A BIRD'S EYE VIEW OF COVID-19 DURING THE FIRST 18 MONTHS OF A PANDEMIC IN A COLLEGE CITY

A Dissertation

by

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ABSTRACT

Introduction, the COVID-19 pandemic entering its third year highlights a need for further information on how SARS-CoV-2 impacts communities. This text establishes the burden of disease on different age groups and minorities, identify predictors for disease severity, as well as the effectiveness of contact tracing. Data from the COVID-19 investigations center is implemented in deterministic mathematical modelling to look at the theoretical effects of different levels of vaccination, earlier vaccination, and reporting levels on an epidemiologic curve. Methods used in this study include univariate, bivariate, and backwards stepwise regression run in Stata 16.1/IC. Mathematical modelling uses both R software package EpiEstim and Matlab to run models. Results highlighted black and Hispanic race/ethnicities are minorities who were adversely affected compared to white, non-Hispanic cases. Comorbidities of diabetes, hypertension, and renal disease were found to increase one's odds of severe disease. Most of the transmission occurred in households, and they often tested for the virus prior to receiving public health guidance from contact tracing. Modeling highlighted that earlier vaccination and or higher vaccination rates would have decreased the number of illnesses and the burden on the local healthcare infrastructure. Discussion, policy makers and healthcare providers can use information regarding who is at higher risk of disease by helping make the public more aware of their increased risk if they fall into a high-risk category. Public health professionals may also encourage those who test positive to not pass on guidance but allow their close contacts to be contacted directly. Lastly, any increase in vaccination can avert cases and decrease the load on the healthcare system.

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NOMENCLATURE

BCHD	Brazos County Health District, Texas
BCS	Cities of Bryan and College Station, Texas
Case	Individual who has tested positive for SARS-CoV-2
CDC	Centers for Disease Control and Prevention
Contact	Individual who was within 6 feet or less, for 15 minutes or more, of someone who tested positive for SARS-CoV-2; also referred as close contact
COVID	Coronavirus Disease
CSTE	Council for State and Territorial Epidemiologists
ELISA	Enzyme-Linked Immunosorbent Assay
NAAT	Nucleic Acid Amplification Test
PCR	Polymerase Chain Reaction
ProMED	Program for Monitoring Emerging Diseases
REDCap	Research Electronic Data Capture
R_0	Reproductive number
SARS-CoV-2	Severe Acute Respiratory Syndrome Coronavirus 2
TX DSHS	Texas Department of State Health Services
WHO	World Health Organization

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1. INTRODUCTION

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a respiratory virus which has led to a reported 513,955,910 confirmed cases of SARS-CoV-2 infection and 6,249,700 deaths globally from December 12, 2019-May 6, 2022 (WHO COVID-19 Dashboard; CDC Museum COVID-19 Timeline, 2022). Within the United States, there have been 80,854,843 confirmed cases reported and 989,435 deaths (WHO COVID-19 Dashboard). Each area is affected by this virus differently, owing to factors such as different population densities, age distributions, and proportion of minorities. The goal of this paper is to begin to understand the burden of infection and disease on Brazos County, Texas. To best comprehend the burden in this geographic region, this introduction discusses the origins of this virus followed by a description of the disease it causes, aims, and policy implications.

Severe acute respiratory syndrome (SARS), a disease caused by a virus in the coronavirus family now known as SARS-CoV-1, became well-known in 2003 after an outbreak emerged in 2002 in the Guangdong Province, China. Throughout the course of the outbreak, from 2002-2003, there were a total of 8,098 cases among 29 countries (CDC MMWR, 2003). The illness caused by this new virus presented as atypical pneumonia but did include milder cases with fever and moderate respiratory symptoms (Zhong et al., 2003). When the disease first emerged, epidemiologists collected contact history, geographic location, select demographic information, and lab results from patients who had this disease (Zhong et al., 2003). Lab tests were conducted with a blood draw and nasopharyngeal (NP) swab. The blood draw was used to test the blood for antibodies against the coronavirus and to look for the blood cell count. The NP swab was used to confirm presence of the virus through culture and isolate a full genomic sequence of this coronavirus (Zhong et al., 2003).

In December 2019, cases of a pneumonia-like illness of unknown origin in the Wuhan Province of China were alerted to the scientific community through ProMED mail, raising concerns about another potential new virus (Bogoch et al., 2020). On January 8, 2020, the pathogen causing these outbreaks was identified as a coronavirus through genetic sequencing (Bogoch et al., 2020). International travel allowed this novel coronavirus to quickly spread throughout the globe leading to a pandemic declaration by the WHO on March 11, 2020 (WHO Director General remarks). The disease caused by this virus was quickly coined 'coronavirus disease 2019' (COVID-19) and the virus designated SARS-CoV-2 by the International Committee on Taxonomy of Viruses (ICTV) (WHO, 2021).

COVID-19 can present as asymptomatic or symptomatic in individuals who test positive for the virus. There are three types of tests most frequently used for COVID-19 as of this writing:

1. Nucleic acid amplification test (NAAT)
2. Rapid antigen test; and
3. Antibody test.

The polymerase chain reaction (PCR) test is a form of a NAAT, and the gold-standard to confirm an acute infection, since it detects genetic material, RNA, of SARS-CoV-2 in the sample; as the most sensitive and specific test for the presence of the virus, it is the most recommended COVID-19 test in the U.S. The rapid antigen test looks for proteins housed on the virus particles themselves. These two tests allow public health surveillance to detect immediate, acute infections, which is essential for enacting public health measures including contact tracing, quarantine, isolation, and outbreak detection.

The antibody test does not necessarily identify an acute infection. This test looks for a humoral immune response in reaction to the virus to detect specific antibodies the person's immune system has produced in response to being exposed to the virus. As antibodies develop over time and may be sustained for months, years, or a lifetime, the presence of antibodies does not indicate if the infection is current.

As a respiratory illness, the virus is spread through respiratory droplets from infected persons. Transmission can occur if an infected person expels respiratory droplets carrying virus particles into the air (where it can be breathed in) or onto another person, and those viral particles are inhaled or otherwise find their way to the respiratory tract of a new individual. Similarly, transmission can occur if a surface is not disinfected between touches of an infected person and another individual, and if an infected person shares food or drink with a previously non infected person. In each instance the viral particles must successfully travel from the infected person, contaminated surface, or contaminated food/drink to the respiratory system of the next person before infection can occur.

An incubation period is the time it takes for an individual to develop symptoms after being exposed to a pathogen. The average incubation period of SARS-CoV-2 is approximately 4 to 5 days. However, this varies person to person and can be up to 14 days (CDC, *Management of Patients with Confirmed 2019-nCoV*). Individuals who are symptomatic for COVID-19 typically recover within 10 days. Symptoms for this disease are variable in general, across age groups and racial/ethnic groups. In addition, symptoms are highly variable from person to person and range from very mild, allergy-like symptoms to more severe disease. Mild symptoms for COVID-19 include a wide range: fever, headache, sore throat, cough, diarrhea, nausea, and loss of taste or smell. Warning signs of COVID-19, or when to seek emergency medical care, include blue lips (indicating there is not enough oxygen getting to the area), trouble breathing, new confusion or disorientation the patient had not previously experienced, and pain or pressure in their chest. If any of these warning signs occur, a patient is encouraged to seek emergency medical care, since they may have or develop complications or severe disease. Severe COVID is defined by the Centers for Disease Control and Prevention (CDC) as an individual who is hospitalized, needs intensive care, requires a ventilator, and/or dies from COVID-19 (CDC: People with Certain Medical Conditions, 2022).

For reasons not yet completely understood, COVID-19 appears to present differently across age groups and disproportionately affects certain ages, races, and ethnicities. For example, young adults (18-29 years), have been seen to have higher prevalence of COVID-19 compared to elderly, indicating a need to understand factors contributing to infection and transmission in young adults, as well as their COVID-19 and healthcare experiences (Malmgren, Guo, & Kaplan, 2021) . Young adults will include those aged 18-29 years as this is the young adult age range CDC reports COVID-19 cases.

1.1 Overall Aims

This research aims to identify the prevalence and behavioral risk factors of SARS-CoV-2 by age group and by severe outcomes of disease. Testing behaviors of individuals reported as a close contact of someone testing positive for SARS-CoV-2 will be described based on the contact tracing data. Using these same data and analyses, mathematical models will be generated for SARS-CoV-2 presenting real-world and alternative scenarios.

1.2 Policy Implications

Policy implications of the research in the following chapters vary. The descriptive focus of COVID-19 symptoms and may bring attention to age groups and or racial or ethnic minorities adversely affected by the disease. Identifying co-morbidities which can lead to greater likelihood of severe COVID-19 can be achieved by analyzing case data. Through these events, policy makers in Texas and or BCS, and similar populations, can use this information to improve public health messaging by targeting groups at higher risk. This can also inform clinical awareness and education for COVID-19 in specific populations.

The contact tracing database can yield fruitful information on what led close contacts to test for SARS-CoV-2 which may be used by policy makers in testing strategies. Limitations from the contact tracing program, such as lack of manpower during outbreaks, can lead to increased funding for these programs to strengthen their efficacy. Depicting vaccination rates in a susceptible population and the timeframe of vaccination campaigns can encourage policy makers to prepare community vaccination plans prior to receiving vaccines.

2. SPECIFIC AIMS

This research, *A Bird's Eye View of COVID-19's Impact on a College City*, aims at understanding the burden of the COVID-19 pandemic on College Station, the largest city in Brazos County, Texas, and home to one of the largest universities in the United States.

Under normal circumstances, the Brazos County Health Department (BCHD) has one full-time epidemiologist that may conduct outbreak investigations. A unique feature of Brazos County is that approximately 25% of the population are comprised of university students, mostly undergraduate, many of whom relocate to the area only during the academic semesters. Due to the large nature of the COVID-19 pandemic and the transitory nature of Brazos County residents, a joint operation was created between Texas A&M University, BCHD, and the Texas Workforce Commission to conduct case investigations and contact tracing during the COVID-19 pandemic.

SARS-CoV-2, the virus causing COVID-19, was confirmed in Brazos County and reported to the public on March 18, 2020. Between March 18, 2020, and November 28, 2021, there have been 33,326 total cases reported in Brazos County. BCHD and local news outlet KBTX regularly publish aggregate numbers of COVID-19 in Brazos County. However, due to the ongoing response, there have been no details made public on the specific characteristics of affected individuals nor the impact that the virus has had on the community. Although there have been demographic and behavioral studies of COVID-19 for other geographic areas, these are not necessarily transportable to Brazos

County because of the unique age demographics and transitory population in Brazos County (Holden et al., 2021; Jacobson, Chang, Shah, Pramanik, & Shah, 2021).

There remains need to detail the COVID-19 experience in terms of case investigations, contact tracing, survey development, data collection, and their challenges. Filling this need may help inform local public health policy decisions regarding SARS-CoV-2 variants of concern or future outbreaks of a similar nature or in similar settings. To best fulfill this objective, I propose the following specific aims:

Aim 1. Define clinical features and outcomes of SARS-CoV-2 infection and identify risk factors for severe outcomes of COVID-19.

Aim 2. Describe testing behaviors in close contacts through the contact tracing in Brazos County.

Aim 3. Gauge the effectiveness of vaccination on the spread of SARS-CoV-2 through factual and counterfactual mathematical scenarios in Brazos County, Texas.

A vast library of data has been collected about COVID-19 in Brazos County, and gleaning valuable information is a direct return on the investment that BCHD and Texas A&M University has poured into the COVID-19 pandemic response in Texas. Through this information, policy makers in Brazos County will be able to see which ethnicities and age groups were most affected by the virus and how. Furthermore, the influence that the local COVID-19 mandates and SARS-CoV-2 screening policies had will be displayed through this research. The expectation of this project is that it will provide justification for designing future outbreak response in a college-centered town.

3. BEHAVIORS, SEVERITY, AND SYMPTOMS OF CASES, OH MY!

3.1. Introduction

Public health surveillance is the ongoing collection, analysis, and interpretation of health-related data (CDC, Introduction to Public Health, 2014). Through the interpretation of public health data, recommendations can be made to policy makers to produce interventions and prevent negative health outcomes. Infectious disease (ID) surveillance is a subset of public health surveillance with the purpose of collecting ongoing, systematic information in relation to an infectious disease or diseases. ID surveillance can be employed to identify the prevalence and/or incidence of a disease in an area, and if any age groups or minorities are adversely affected by the disease and is the primary tool in detecting patterns and changes in patterns that occur. Surveillance of COVID-19 is an important component of ID surveillance to arise in the past few years because the burden it poses to age groups, and racial or ethnic minorities is still being explored. This surveillance will allow public health professionals to act and intervene on behalf of those adversely affected by disease to work to mitigate their risk.

The working case definition for COVID-19 is divided by the World Health Organization (WHO) into three components: confirmed, probable, or suspected case of SARS-CoV-2 infection (WHO, 2020).

A *confirmed case* is defined as:

A. Anyone identified as having a positive SARS-CoV-2 nucleic acid amplification test (NAAT) (WHO, 2020).

B. Tested positive on a SARS-CoV-2 antigen test, and meeting probable or suspected case definition (WHO, 2020).

C. Or an asymptomatic individual is a contact of a probable or confirmed case and tested positive on a SARS-CoV-2 rapid antigen test (WHO, 2020).

A *probable case* can be those who do not have a positive PCR test but:

A. Meet clinical criteria and are epidemiologically linked to probable or confirmed COVID-19 case(s) or associated with a cluster of COVID-19 illness (WHO, 2020); or

B. Had loss of taste or smell without any other clinical or epidemiologic criteria (WHO, 2020); or

C. Had chest imaging consistent with COVID-19 (WHO, 2020); or

D. Or have died due to acute respiratory distress and are connected to a COVID-19 case(s) (WHO, 2020).

A *suspected case* has not tested positive for SARS-CoV-2 by PCR but meets one of three conditions:

A. They meet clinical and epidemiologic criteria for the disease. Where clinical criteria are acute onset of fever and cough; or acute onset of three or more of the following: fever, cough, weakness/fatigue, headache, myalgia, sore throat, coryza, dyspnea, anorexia/nausea/vomiting, diarrhea, or confusion. Epidemiologic criteria are working within a healthcare setting 14 days prior to symptom onset or traveling to an area with community transmission 14 days prior to symptom onset or residing/working in an area with high risk of transmission of SARS-CoV-2 (such as closed residential settings) (WHO, 2020); or

B. They have severe acute respiratory illness defined as having a fever over 100.4°F, cough within the past ten days, and needing hospitalization (WHO, 2020); or

C. They have a positive SARS-CoV-2 rapid antigen test, but do not meet the epidemiologic criteria or are experiencing symptoms (WHO, 2020).

Although U.S. public health surveillance methods are not subject to case definitions issued by the World Health Organization (WHO), it is important to understand the criteria other countries are using in defining COVID-19 cases. Transmission of disease spreads country to country but not all countries use the same case definitions which may lead to different levels of reporting and surveillance.

The CDC conducts passive surveillance on probable and confirmed cases (CDC, 2021), through reporting in public health surveillance. Public health surveillance can be conducted in different ways, in the case of COVID-19, it relies on an interview. A data collection form (DCF) is created for each nationally reportable infectious disease. When someone tests positive for the disease, the DCF is filled out by interviewing the individual. A DCF contains information on demographics and symptoms but is only used when someone is considered a case. Collecting COVID-19 surveillance data on demographic information can provide public health professionals with evidence on if any demographic group(s) are being disproportionately affected and providing insight to where targeted mitigation efforts might be most needed.

Confirmed cases are only those who have a positive PCR test (CDC, 2021 Case Definition). TX DSHS follows the CDC and CSTE case definitions for COVID-19. The probable case definition CDC uses is defined by the Council of State and Territorial Epidemiologists (CSTE) as "meeting presumptive laboratory evidence or meeting vital records criteria while lacking a confirmatory test or having clinical criteria and epidemiologic ties without a confirmatory or presumptive lab evidence for SARS-CoV-2" (CDC, 2021 Case definition).

Case definitions are a foundation for the surveillance process. COVID-19 public health surveillance involves a multi-step process:

1) An individual tests positive for SARS-CoV-2, thus meeting a CDC case definition for COVID-19.
2) If tested at a clinic, hospital, or SARS-CoV-2 testing site, the individual's SARS-CoV-2 laboratory report is transferred to the nearest Health District or Public Health Department, and later reported onto the state and CDC. If the individual is not tested at one of these locations, their positive case may not reach the local public health authority and be counted in the case counts.
3) An epidemiologist or trained staff member collects data through a COVID-19 case investigation.

4) An epidemiologist enters the individual's information into a state and/or national surveillance database; these databases are used for all nationally reportable infectious diseases.

Close contact is an event defined by the CDC where a person is within ≤6 feet for a duration of ≥15 minutes, with or without a face covering, of another person who has tested positive for SARS-CoV-2, and the contact occurs from 2 days prior to symptom onset or testing positive or while symptoms are present (CDC, How to Determine a Close Contact for COVID-19). For the purpose of this paper, we will refer to an individual in close contact with someone testing positive as a 'contact' and someone who has tested positive for SARS-CoV-2 as a 'case.'

In Brazos County, like others in Texas and the US, public health professionals strive to conduct a case investigation of anyone who meets a CDC case definition for COVID-19 surveillance. Staff who fill this role are called case investigators. A case investigation is where the professional calls the person who has tested positive (confirmed or probable) for SARS-CoV-2 on the phone, explains who they are and how they have the person's phone number, then proceeds to collect essential public health data to fill out the DCF, thus into the surveillance system.

The COVID-19 Operations Center (CoOp) is a joint operation created by the local Texas A&M University (TAMU) and Brazos County Health Department (BCHD). The CoOp was located at the TAMU Health Science Center in Bryan and housed both case investigators and contact tracers. At the CoOp, case investigators strived to collect more than essential public health data. These investigators asked how the individual was feeling, what their symptoms were, and who their close contacts were. In Fall 2020, the CoOp was fully mobilized, and questions were added to the questionnaire including risk factor questions such as attending indoor/outdoor gatherings. Transmission in indoor settings is more common than outdoors, as there can be a higher chance of infectious respiratory droplets spreading person-to-person (Farthing & Lanzas, 2021). Household settings as a venue have been commonly linked to viral transmission (Farthing & Lanzas, 2021). For this reason, small indoor gatherings (<5 people and 5-10 people) will be of study interest. When indoor/outdoor gatherings were added, in addition, a series of TAMU specific questions was also added to ask if they were an undergraduate student, graduate/professional student, member of Greek life, Corps of Cadets, or member or another student organization.

Since March 1, 2020, CDC has been reporting COVID-19 weekly cases per 100,000 population by age, race, ethnicity, and sex (CDC COVID Data Tracker, 2021). CDC reports COVID-19 weekly cases by ten different age groups: 0-4, 5-11, 12-15, 16-17, 18-29, 30-39, 40-49, 50-64, 65-74, and 75+ years (CDC COVID Data Tracker, 2021). The age groups presented in CDC's report are used as a template in this study for data analysis.

This study analyzes COVID-19 public health surveillance data in Brazos County by age category to understand the clinical presentation of COVID-19 and risk factors among different ages in this geographic area. The research goals of this chapter are to present the picture of COVID-19 across age groups to 1) describe the clinical presentation of COVID-19 cases, 2) outline social and behavioral features common to COVID-19 cases; and 3) identify groups at risk of progressing to severe COVID-19.

3.2. Literature Review of SARS-CoV-2 Descriptive Studies

To achieve a better understanding of what has already been described about SARS-CoV-2 infection resulting in COVID-19 and disease outcomes, a literature review was conducted. The literature review was completed using the PubMed database with the timeframe of 2019- present. PubMed primarily houses peer-reviewed journal articles. However, given the rapid nature of the pandemic, there are relevant pre-prints not yet peer reviewed, included in this review.

The literature search was done using the search parameters ("COVID" or "SARS-CoV-2") AND ("symptom" or "clinical") AND ("severity" or "outcome" or "mild") NOT ("vaccine trial" or "clinical trial") yielding 20,302 full text articles as of June 7, 2022.

The mean incubation period of COVID-19 for all ages based on a meta-analysis was 5.1-12.2 days (Quesada et al., 2021; Wong, 2020; Laeurer et al., 2020). Among adults (≥18), the median symptom duration from onset of illness was 4 to 8 days from the test date with longer durations for loss of taste or smell (Tenforde et al., 2020). Median symptom duration for children across two cohorts was 5 days and long illness durations were rarely reported (Molteni et al., 2022). Recovery time for COVID-19 varies depending on disease severity. Individuals who are hospitalized from COVID-19 can spend at least two weeks after discharge recovering from the illness (McArthur et al., 2020).

The most common symptoms for COVID-19 cases over all age groups are fever, cough, loss of taste or smell, fever, and difficulty breathing (Ochani et al., 2021; Kim et al., 2020; Lamberghini & Testai, 2021). Among pediatric COVID-19 cases, Fever and cough have been the most reported symptoms (Chang et al., 2020; Liguoro et al., 2020; de Souza et al., 2020; Alsohime et al., 2020). There is lack of consensus on the most frequent symptoms for young adult and adolescent age groups. Risk of infection for children is higher with household member exposure, travel, or living in an area with high transmission (Chang et al., 2020; Alsohime et al., 2020). Severe disease is more likely in children younger than one year of age or with comorbid conditions (hydronephrosis, leukemia, itussusception) (Gallo et al., 2020; Alsohime et al., 2020). Pediatric mortality rate attributed to COVID-19 has been low, 0.08% (Liguoro et al., 2020). Though further research is needed to identify specific risk factors of severe disease and death among children.

Severe COVID-19 as a syndrome is characterized as having been intubated, hospitalized, or died from the disease. Other forms of severe COVID-19 can lead to acute respiratory distress syndrome (ARDS), and extracorporeal membrane oxygenation (ECMO). Predictors of severe COVID-19 among adults have been identified as individuals over the age of 55 years, multiple co-morbidities, shortness of breath, and low oxygen levels (Gallo et al., 2021; Jain & Yuan, 2020). Obesity, diabetes, cardiovascular disease, chronic lung disease, chronic obstructive pulmonary disease and immunosuppression are among the co-morbidities which may lead to increased risk of death (Gallo et al., 2021). Fatality was highest among cardiovascular disease, diabetes, liver disease, kidney disease, chronic obstructive pulmonary disease, hypertension, and cancer (Gallo et al., 2021; Bansal, 2020; Erener, 2020; Cabibbo et al., 2021; Bohn et al., 2020; Abdi et al., 2020; Hu et al., 2020). In few instances, males have been seen at higher risk of severe disease when compared to females, hypothesized to be due to differences in regulation of the ACE2 enzyme (human angiotensin converting enzyme 2) or higher prevalence of comorbidities in males (Bohn et al., 2020).

The most common symptoms across adult patients not hospitalized were fever, cough, fatigue, congestion, sore throat, diarrhea, abdominal pain (Lee et al., 2020; Gallo et al., 2020; Hu et al., 2020; Bergquist et al., 2020). Hospitalized patients presented with headache, sore throat, congestion, difficulty breathing, gastroenteritis, and coughing up blood (Jin et al., 2020; Wang et al., 2020; Gallo et al., 2021). Among hospitalized COVID-19 patients, hypertension, liver disease, diabetes, and cardiovascular disease stood out as the most frequent pre-existing conditions (Jin et al., 2020; Wang et al., 2020). In terms of race/ethnicity, hospitalized patients represented the following percentages in a retrospective study: 49.5% were non-Hispanic black, 25.5% were other race, and 22.6% were non-Hispanic white (Bergquist et. al, 2020).

Numerous studies looking at the clinical presentation of COVID-19 in their community have been published (Chen et al., 2020; Gou et al., 2020). Yet, the focus of these studies has not included both clinical presentation and epidemiologic characteristics. Nor have young adults, specifically, been the focus of many COVID-19 or SARS-CoV-2 studies. Young adults are a necessary group to study because they have been implicated in COVID-19 transmission as a result of outbreaks on college campuses, and behaviors such as traveling and partying.

3.3 Methods

3.3.1 Study Setting

The BCS area is in the central plains of Texas and home to the "twin cities" of Bryan and College Station within Brazos County. Based on Brazos County 2021 census data, there were 237,032 individuals living in the county with a relatively even distribution of male and female individuals (U.S. Census Bureau, 2022). Ages groups in the Census data were broken down into ages 0-5 (6.1%), 6-18 (20.6%), 19-64 (63.8%), and >65 years (9.5%) (U.S. Census Bureau, 2022). Race and ethnicity in the Census data were divided into race and then Hispanic or Latino. Majority of individuals identified as white (79.6%), followed by black (11.2%) and Asian (6.3%) (U.S. Census Bureau, 2022). Approximately a quarter of individuals identified as Hispanic or Latino (26.2%) and half identified as not Hispanic or Latino (55.2%) (U.S. Census Bureau, 2022).

In 2019, Bryan, Texas had a median household income of $45,771 with a poverty rate of 22.8% (Data USA Bryan, 2021). As of 2019, the median age of the Bryan population was 30.5 years of age, the main racial and ethnic groups were white, non-Hispanic (39.5%), Hispanic (32.5%), and black (16.4%) (Data USA, 2021). In 2019, College Station, TX had a median household income of $45,820 with a poverty rate of 29.6% (Data USA College Station, 2021). As of 2019, the median age in College Station was 23 years of ages, the main racial and ethnic groups were white, non-Hispanic

(64.5%), Hispanic (13.3%), black (12.2%), and Asian (10%) (Data USA College Station, 2021).

BCS is unique in the sense it has a large young adult student population as it is home to Texas A&M University in College Station and Blinn College in Bryan. As of fall 2021, there were 67,133 students enrolled at the Texas A&M University College Station Campus and 6,000 students at Blinn College (Texas A&M University, 2021; Blinn College, 2022). The most recent demographic breakdown as of this writing was for the fall 2020 TAMU student population, including 53.8% male and 46.2% female (Texas A&M University Accountability, 2021). Within the TAMU student population, 55% identified their race as white, 23% were Hispanic or Latino, 9% were Asian, 7% were international students, and 3% were Black or African American (Texas A&M University Accountability, 2021).

As a result of this large student population, BCS is a transient area making travel history an important consideration in facilitating disease transmission. Another unique consideration in this population is the possibility that young adults or college students may behave differently than older adults. These aspects are important to consider because travel and certain behaviors could increase risk of exposure to SARS-CoV-2. Consequently, there may be public health recommendations specific to the BCS area or other geographic locations with large student populations.

3.3.2 Data Collection

COVID-19 data used here were collected on laboratory-confirmed or probable cases reported to BCHD with a case investigation start date between March 16, 2020-July 31, 2021. As there were ongoing COVID-19 case investigations at the time in Brazos County when the study began, cases reported after that date were not included in this study. Data was collected and managed in REDCap through the electronic data capture tools hosted at Texas A&M University (Harris et al., 2009; Harris et al., 2019). Variables included in this dataset are sociodemographic (age [years], date of birth, residence, race, ethnicity, student/daycare status, employment status, health insurance), clinical (symptoms, duration [days]), medical history, behavioral, social characteristics, vaccine preferences, and university specific questions (see Appendix section 1).

Symptoms were collected by reading a list of symptoms and allowing the respondent to reply yes, no, or do not know. After responding to the presence or absence of specific symptoms, respondents were asked if their infection was symptomatic or not and an open-ended question about any other signs or symptoms not listed. Following symptom status questions, respondents were asked about their medical history, vaccination interest, close contacts, and lastly asked about their sociodemographic information. Data was exported from REDCap into Stata 16.1/IC (StataCorp, 2019).

These analyses were conducted in partnership with BCHD, and this analysis was reviewed and approved by the Texas A&M University Institutional Review Board, IRB title: COVID-19 in the Brazos Valley, Principal investigator: Rebecca Fischer, IRB ID: IRB2020-0579D.

3.3.3 Data Analysis

Since we sought to include only confirmed and probable cases, individuals who did not have a confirmed or probable laboratory report on a positive test for SARS-CoV-2 were excluded from this analysis. Residential addresses were tabulated and imported into ArcGIS Pro by zip code for the continental United States; these were geocoded in ArcGIS Pro through the ArcGIS World Geocoding Service. The ArcGIS Pro spatial join geoprocessing tool was used to convert the individual zip code points to the mapped zip code, by using public zip code tabulation areas (ZCTAs) for 2020 (United States Census Bureau, 2021). SARS-CoV-2 PCR test dates and SARS-CoV-2 rapid antigen test dates were combined into a single test date variable. Age at infection was calculated by subtracting the test date from the date of birth. Ten age categories were created for analysis which align with CDC reporting: ages 0-4, 5-11, 12-15, 16-17, 18-29, 30-39, 40-49, 50-64, 65-74, and ≥75 (CDC, 2022). After initial descriptive statistics were presented by these age groups, some groups were collapsed for subsequent analyses, owed to small frequencies in some age groups: ages 0-11, 12-17, 18-29, 30-39, 40-49, 50-64, and ≥65 years. Histograms were made to assess age distribution with kernel and normal densities.

The incubation period (days) was calculated by subtracting the test date from the symptom onset date due to lack of exposure date. Incubation period values over 14 days were removed as representing outliers in the literature. Duration of symptoms (days) was calculated by subtracting the symptom resolution date from the symptom onset date. Any negative values were removed as erroneous. Any individual who had missing information from one of the above dates was given a missing value for incubation period and/or symptom duration. Attack rates were estimated for census age categories and race/ethnicities. Residence types were collapsed into house, apartment, dormitory, supported living, and other. Race categories were collapsed into white, black, Asian, and other. Other race encompasses individual as responding as native Hawaiian or other Pacific Islander, American Indian, Alaskan native, and individuals who self-identified as "other race." Combined race-ethnicity categories were defined as either white, non-Hispanic, Hispanic/Latino, black, Asian, or other.

There was a section in the questionnaire for symptom questions and medical history. In each of these questions, possible responses were yes, no, 'I don't know,' or unknown. Unknown responses were recoded as missing. Questions with these possible responses were collapsed into yes/no responses with unknown classified as missing. There was a free-text field for additional symptoms reported, and the most common was allergy-like symptoms; thus an 'allergy symptoms' variable was created based on individuals who self-reported allergies during the open-ended question. A variable for symptomatic individuals was created, categorized as symptomatic if a respondent answered yes to any symptom questions and asymptomatic if respondent answered no to all symptom questions.

Three syndromes were defined according to standard clinical definitions and were classified using reported symptoms. These included influenza like illness (ILI), gastroenteritis, and severe COVID-19. ILI was defined as someone having fever greater than 100^{o}F, cough, and/or a sore throat (CDC, 2017). Gastroenteritis was defined as having diarrhea and/or vomiting (CDC, 2019). Severe COVID-19 was defined as having been hospitalized, admitted into an intensive care unit (ICU), or intubated (CDC: People with Certain Medical Conditions, 2022).

Descriptive statistics were tabulated for variables of interest and presented as a frequency with proportion (n [%]) for categorical variables or as median and interquartile range (median [range]) for continuous variables. To examine differences in demographics between subjects of different ages we compared with symptoms and severe COVID-19 categories. Chi square analysis including Fisher's exact test, where applicable (when any cell frequency is less than five), is presented for each variable by the collapsed age categories to include the Pearson's chi-square value, Pearson's chi-square p-value. Further chi-square analyses were done to assess the impact of demographics and symptoms on the individual before infection and on outcomes of infection (hospitalization, intensive care unit (ICU), emergency room (ER), and death). In addition, the means of number of contacts per age group was compared by use of a one-way analysis of variance (ANOVA) followed by pairwise comparison of means. A chi-square analysis was then conducted to include the average number of contacts per person who tested positive by each age group.

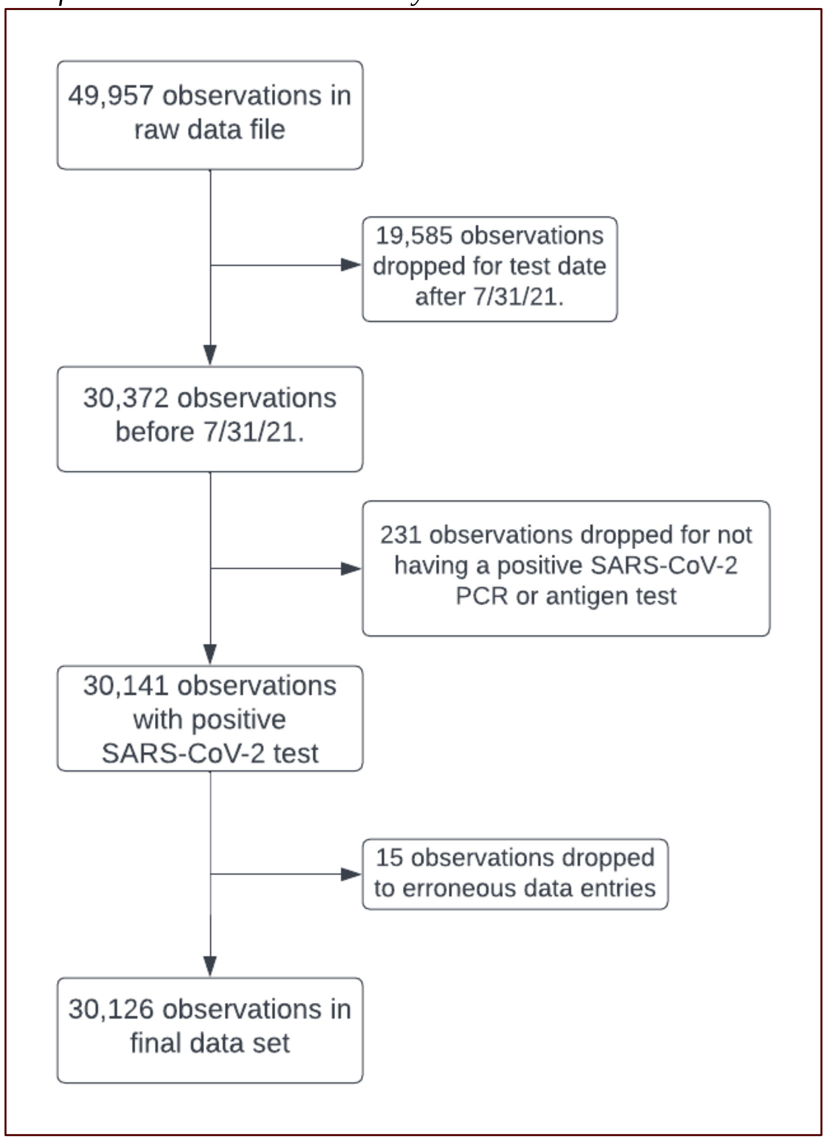
Backwards stepwise logistic regression was done to identify factors which may be associated with higher likelihood of risk factors for illness, and severe disease. Odds ratios were reported with 95% confidence intervals and associated p-values (OR [95% CI]; p-value), anything with a p-value <0.05 was considered statistically significant. Behaviors assessed were attended an indoor gathering in a group of <5 people, attended an indoor gathering of 5-10 people, and traveled in the past 14 days. Variables for these behaviors were identified by running bivariate analysis on demographics, exposure questions, and university affiliation. Significant variables identified through bivariate analysis were used as predictors in regression. Medical outcomes were hospitalization, ICU, ER, severe COVID-19, and death. Variables assessed here were demographics, medical history, receipt of flu shot in prior year, and smoking status. Specific variables within these categories were identified through bivariate analysis. To conduct meaningful regression analysis, ages were further collapsed into decades, from 0-9 years to 90-99 years. For regression, the age group 40-49 was set as the referent group within the decade variable.

A manual backwards stepwise logistic regression method was employed, where a model was first run separately for each outcome of interest that included all the predictors, and individual predictors were removed based on significance level (p-value >0.05) and 95% confidence interval crossing the null value of 1.0. Following the manual backwards stepwise regression, an automated stepwise regression was run to compare the manual backwards stepwise results with the automated backwards stepwise results. Data was analyzed using Stata 16.1/IC (College Station, Texas). Logit and stepwise commands were used in Stata for regression analysis.

3.4. Results

Data was extracted on January 28, 2022, and there were 49,957 observations in the raw data file of the Case database. Of these, there were 19,585 observations excluded for having a SARS-CoV-2 test date after July 31, 2021, and 231 observations dropped for not having a confirmed positive PCR or positive rapid antigen test. An additional fifteen observations were dropped due to multiple missing data points for a total population of 30,126 individuals.

Figure 1: Flowchart of case observations in the study. Flow chart was created in Lucidchart.



3.4.1 Characteristics of study population

Demographics

From March 16, 2020, to July 31, 2022, there were 30,126 individuals reported as having a positive SARS-CoV-2 test in Brazos County, Texas. Among the CDC age categories, there were 528 (1.8%) ages 0-4; 1,192 (4.0%) ages 5-11; 1,022 (3.4%) ages 12-15; 669 (2.2%) ages 16-17; 14,433 (47.9%) ages 18-29; 3,799 (12.6%) ages 30-39; 3.050 (10.1%) ages 40-49; 3,438 (11.4%) ages 50-64; 1,137 (3.8%) ages 65-74; and 785 (2.6%) over age 75. When age categories were re-categorized, there were 1,720 (5.7%) ages 0-11; 1,702 (5.7%) ages 12-17; 14,433 (47.9%) ages 18-29; 3,799 (12.6%) ages 30-39; 3,050 (10.1%) ages 40-49; 3,438 (11.4%) ages 50-64; 1,922 (6.4%) over ages 65, and 0.2% for whom an age was unable to be calculated. Distributions of age frequency are presented below. The median age was 24 years of age with a range of 0 – 101. The majority, 20,987 (69.7%), of the patients were English speaking. Sex was evenly distributed throughout the patients with 15,728 (52%) female and 14,252 (47%) males.

Figure 2: (Left) Ages from U.S. Census data for Brazos County. (Right)Age categories based on Census data for the study population

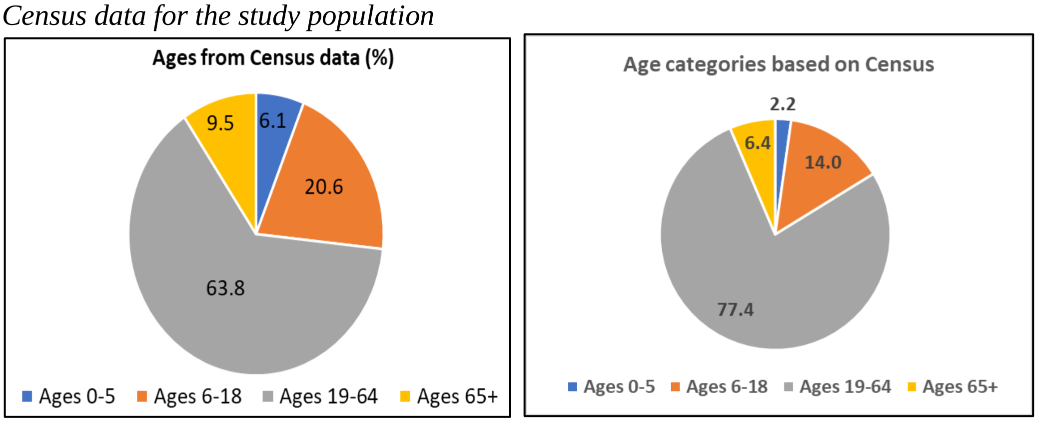


Figure 3: Ages in the study population

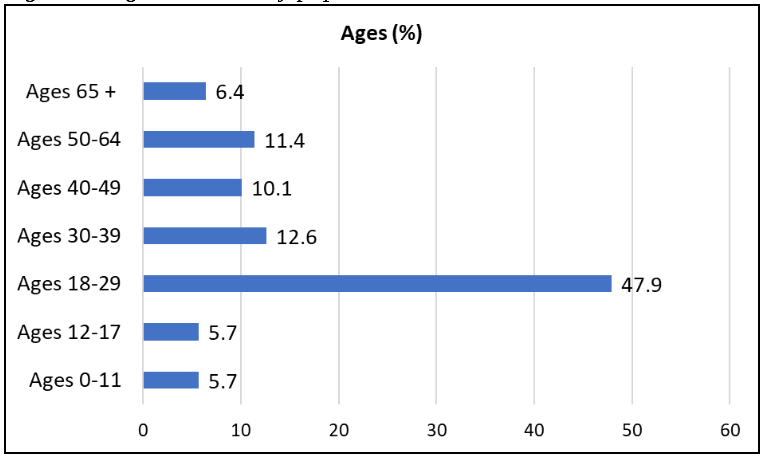


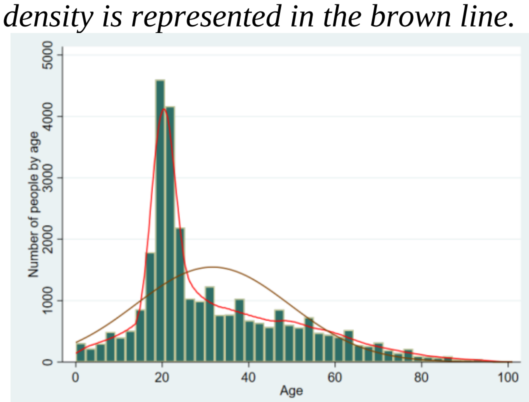
Table 1: Frequency table of age categories, sex, and language in the case database.

	Frequency (n)	Percent (%)
Age (years) according to CDC categories		
Ages 0-4	528	1.8
Ages 5-11	1,192	4.0
Ages 12-15	1,033	3.4
Ages 16-17	669	2.2
Ages 18-29	14,433	47.9
Ages 30-39	3,799	12.6
Ages 40-49	3,050	10.1
Ages 50-64	3,438	11.4
Ages 65-74	1,137	3.8
Ages over 75	785	2.6
Missing or unknown	62	0.2
Age (years)		
Ages 0-11	1,720	5.7
Ages 12-17	1,702	5.7
Ages 18-29	14,433	47.9
Ages 30-39	3,799	12.6
Ages 40-49	3,050	10.1
Ages 50-64	3,438	11.4
Ages 65 +	1,922	6.4
Missing or unknown	62	0.2

Table 1 continued: Frequency table of age categories, sex, and language in the case database.

	Frequency (n)	Percent (%)
Age (years)		
Ages 40 - 49	3,050	10.1
Ages 0 - 9	1,320	4.4
Ages 10 - 19	5,772	19.2
Ages 20 - 29	10,763	35.7
Ages 30 - 39	3,799	12.6
Ages 50 - 59	2,506	8.3
Ages 60 - 69	1,580	5.2
Ages 70 - 70	812	2.7
Ages 80 - 89	345	1.2
Ages 90 - 99	115	0.4
Missing or unknown	64	0.2
Sex		
Female	15,758	52.3
Male	14,252	47.3
Missing or unknown	116	0.4
Language		
English	20,987	69.7
Spanish	871	2.9
Other	25	0.1
Missing or unknown	8,243	27.4
Total	30,126	100.0

Figure 4: Age by frequency below. Kernel density is represented in the red line, normal density is represented in the brown line.



Most (19,254 [66.1%]) individuals identified as white, followed by black (2,431 [8.1%]) and Asian 806 (2.7%). An other category included races such as Native American or other Pacific Islander and American Indian or Alaska Native; 329 (1.1%) identified as other race. Approximately 4,412 (14.7%) did not self-identify a race. Interviewers asked patients if they identified as Hispanic or Latino; 15,500 (51.5%) reported no, not Hispanic or Latino, 9,266 (30.8%) reported yes, and 5,360 (17.8%) with unknown responses. Race and ethnicity variables combined led to 12,268 (40.7%) identifying as white non-Hispanic, 9,135 (30.3%) identified as Hispanic, 2,431 (8.1%) identified as black, 806 (2.7%) identified as Asian, and 67 (0.2%) identified as other race.

The most frequent race/ethnicity with hospitalizations were blacks (10.1%) and Hispanic or Latinos (4.7%). This trend also held across going to an ICU for COVID as well where a proportion of blacks (1.8%) and Hispanic or Latinos (0.7%). Blacks (3.4%) and individuals who self-reported as other race (5.1%) were the most common race/ethnicities reporting going to an ER. Blacks stood out as the only race/ethnicity with a notable proportion of cases with severe COVID (1.3%) and dying of COVID (3.1%).

Figure 5: Percent of race/ethnicity in the study population

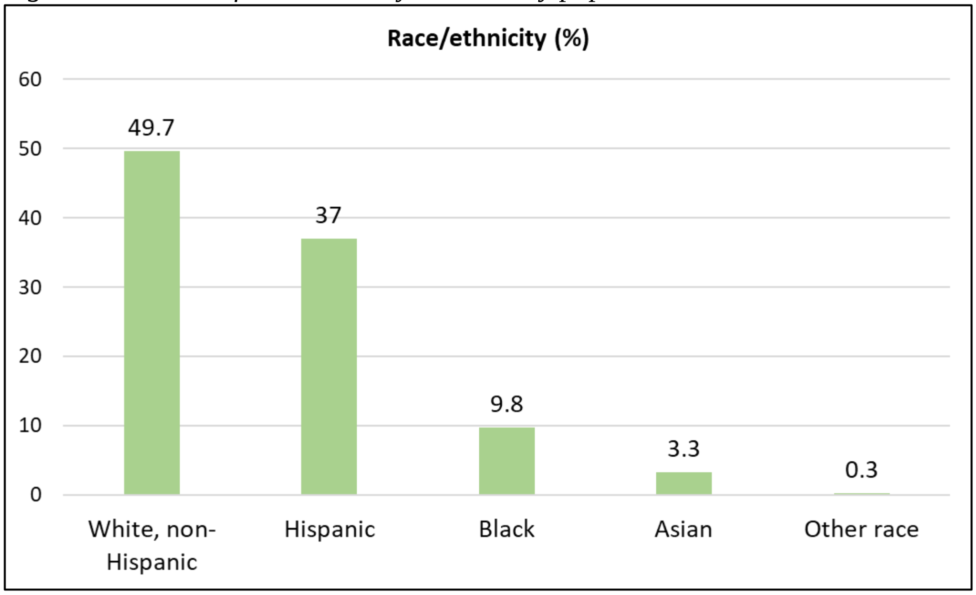


Table 2: Frequency of race, ethnicity, and combined race-ethnicity.

	Frequency (n)	Percent (%)
Race		
White	19,924	66.1
Black	2,431	8.1
Asian	806	2.7
Other	130	0.4
Missing or unknown	6,835	22.7
Hispanic		
No, NOT Hispanic or Latino	15,500	51.5
Yes, Hispanic or Latino	9,266	30.8
Missing or unknown	5,360	17.8
Race/ethnicity		
White, non-Hispanic	12,268	40.7
Hispanic	9,135	30.3
Black	2,431	8.1
Asian	806	2.7
Other race	67	0.2
Missing or unknown	5,419	17.99
Total	30,126	100.0

Table 3: Distribution of race/ethnicity by severe COVID outcomes.

	Race/ethnicity						
	White, non-Hispanic n (column %)	Hispanic n (column %)	Black n (column %)	Asian n (column %)	Other race n (column %)	Total	X2 p-value Pearson X2
Hospitalization							
Yes	336 (3.2)	357 (4.7)	208 (10.1)	19 (2.7)	0 (0.0)	920 (4.4)	210
No	10325 (96.9)	7236 (95.3%)	1,849 (89.9)	698 (97.4)	54 (100.0)	20162 (95.6)	<0.001
Total	10,661	7,593	2,057	717	54	21,082	
ICU							
Yes	41 (0.4)	47 (0.7)	34 (1.8)	0 (0.0)	0 (0.0)	122 (0.6)	53.7
No	9,766 (99.6)	6,574 (99.3)	1,827 (98.2)	664 (100.0)	48 (100.0)	18,879 (99.4)	<0.001
Total	9,807	6,621	1,861	664	48	19,001	
ER							
Yes	196 (2.6)	102 (2.2)	42 (3.4)	11 (1.9)	2 (5.1)	353 (2.5)	8.6
No	7,470 (97.4)	4,642 (97.9)	1,191 (96.6)	561 (98.1)	37 (95.9)	13,901 (97.5)	0.073
Total	7,666	4,744	1,233	572	39		
Severe COVID							
Yes	37 (0.3)	36 (0.5)	27 (1.3)	2 (0.3)	0 (0.0)	102 (0.5)	33.7
No	10,830 (99.7)	7,707 (99.5)	2,092 (98.7)	723 (99.7)	56 (100.0)	21,408 (99.5)	<0.001
Total	10,867	7,743	2,119	725	56	21,510	
Death							
Yes	124 (1.3)	72 (1.1)	61 (3.1)	1 (0.2)	0 (0.0)	258 (1.3)	59.2
No	9,720 (98.7)	6,740 (98.9)	1,894 (96.9)	647 (99.9)	49 (100.0)	19,050 (98.7)	<0.001
Total	9,844	6,812	1,955	648	49	19,308	

A third, 10,124 (33.6%), of the patients were employed while another third had unknown information. The majority of those who provided their residence type, 20,065 (66.6%), reported living in a household. The second most common residence type was apartment with 4,017 (13.3%) individuals.

Table 4: Frequency of employment status and residence type.

	Frequency (n)	Percent (%)
Employed		
No	8,658	28.7
Yes	10,124	33.6
Missing or unknown	11,344	37.7
Residence type		
House	20,065	66.6
Apartment	4,017	13.3
Dormitory	1,192	4.0
Supported living	111	0.4
Other	329	1.1
Missing or unknown	4,412	14.7
Total	30,126	100.0

The map below shows the geographic location of residence for everyone who tested positive through PCR or antigen. As reported by Cases, which were primarily in Texas but were also identified in the following states: Washington, California, Arizona, Colorado, New Mexico, Oklahoma, Iowa, Missouri, Louisiana, Arkansas, Illinois, Alabama, Georgia, South Carolina, and Pennsylvania. Cases in Brazos County are also mapped with zip codes of higher raw case frequency represented by a darker color. Six zip codes in BCS were not successfully mapped in the second figure due to the ZCTA shapefile not including all zip codes represented in BCS. Zip codes not mapped here were 77805 (76 [0.25%]), 77806 (35 [0.12%]), 77841 (30 [0.1%]), 77842 (45 [0.15%]), 77843 (216 [0.72%]), and 77844 (4 [0.01%]) for a total of 406 cases not represented in the second map. The zip codes with the highest frequency of cases were found in College Station (77840 and 77845) out of those mapped here. Individuals appeared outside of BCS when mapping due to individuals being out of town when testing or traveling home following a positive PCR test.

Figure 6: COVID-19 cases by zip code mapped from the BCHD case database.

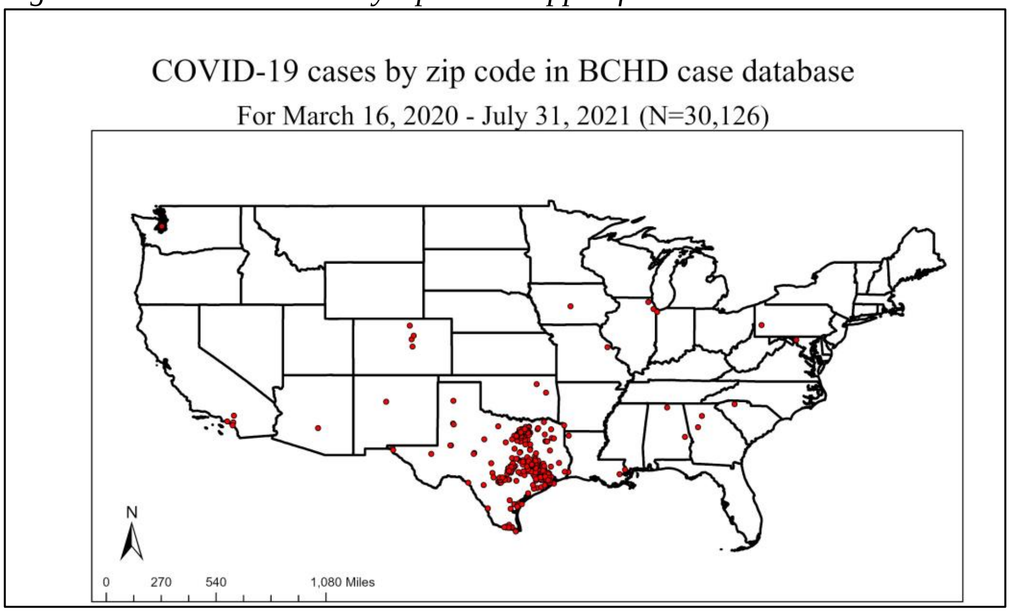
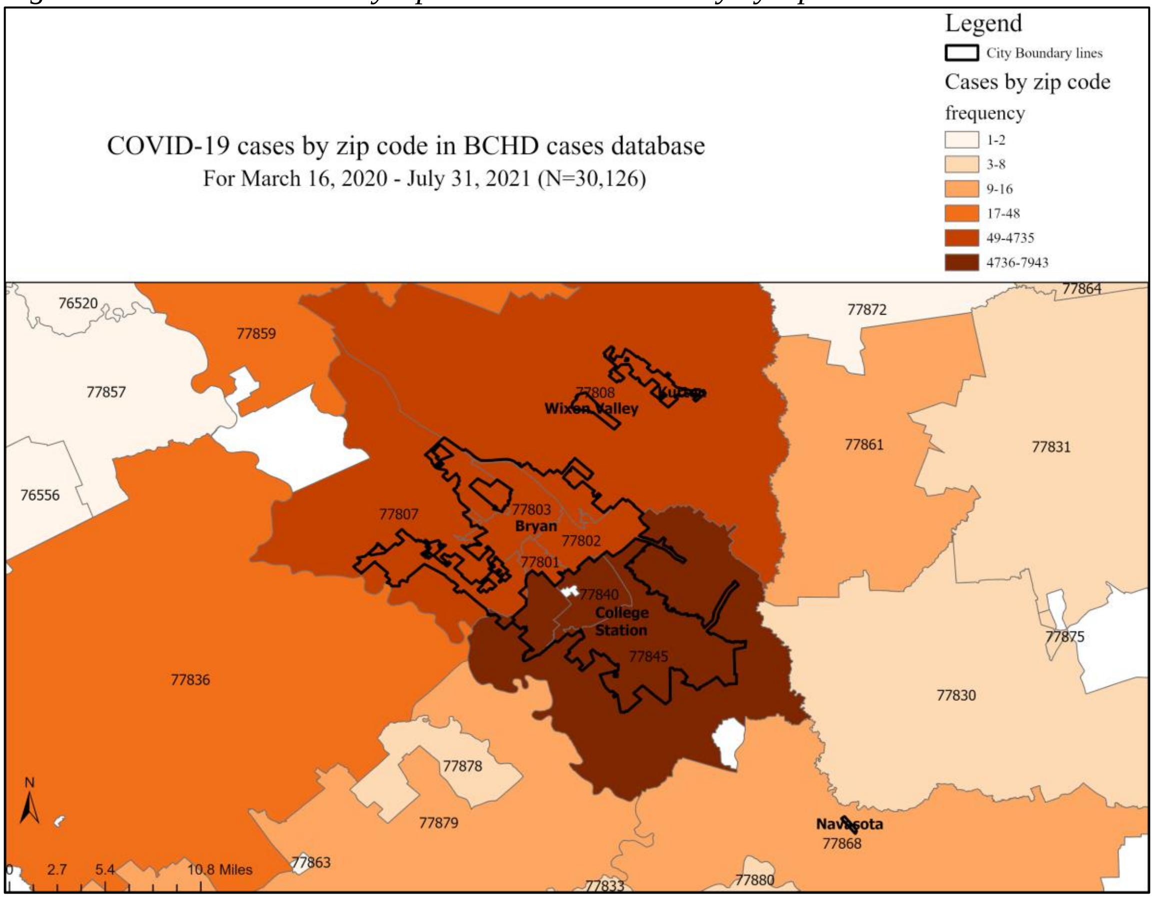
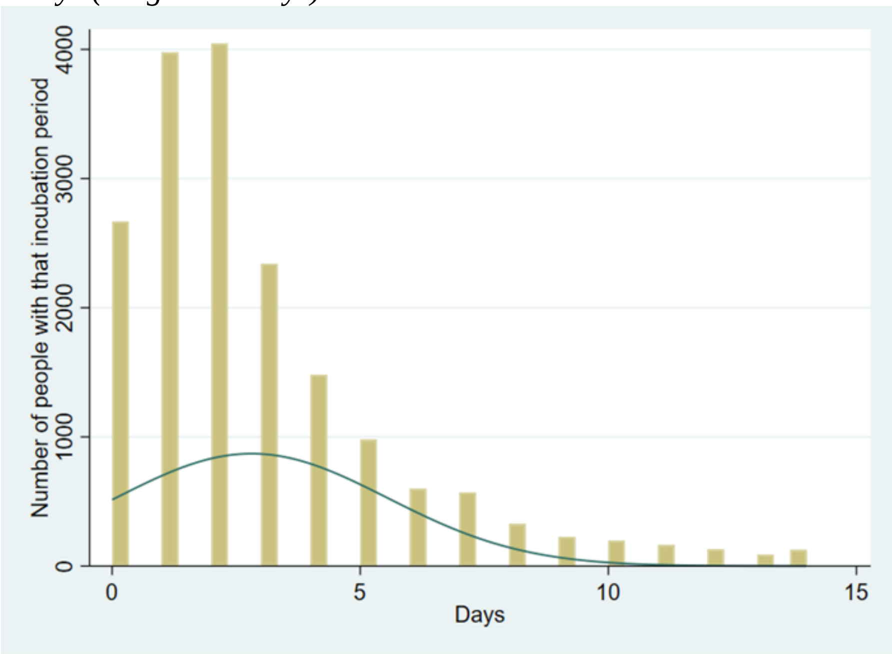


Figure 7: COVID-19 cases by zip code in Brazos County by zip code.



The estimated incubation period had a median of 2 days (range: 0-14 days). The median symptom duration was 6 days (range: 0-97 days). Attack rates by age categories (based on U.S. Census age categories), the highest attack rate was among ages 19-64 (15.4%). Attack rates by race/ethnicity are shown below where the highest attack rate was among Hispanic or Latinos (14.7%).

Figure 8: (top to bottom): (Top) Incubation period estimate graphed with a median of 2 days (range 0-14 days). (Bottom) Symptom duration estimate graphed with a median of 6 days (range 0-97 days).



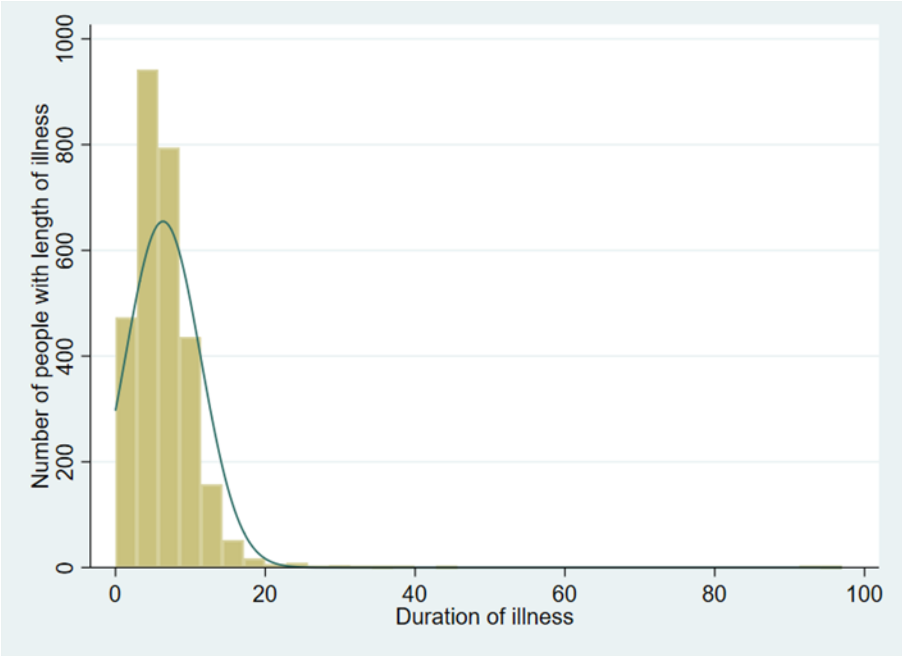


Table 5: Attack rates for ages and race/ethnicities

	Cases in BCHD	Population based on 2021 Census	Reported in Census (%)	Attack rate (%)
Age categories				
Ages 0-5	670	14,459	6.1	4.6
Ages 6-18	4,203	48,829	20.6	8.6
Ages 19-64	23,269	151226	63.8	15.4
Ages 65+	1,922	22518	9.5	8.5
Race/ethnicity				
White, non-Hispanic	12268	130842	55.2	9.4
Black or African American	2431	26548	11.2	9.2
Asian	806	14933	6.3	5.4
Hispanic or Latino	9135	62102	26.2	14.7

Clinical Presentation and medical history

The estimated incubation period was a median of 2 days (range 0-14). Symptom duration was found to have a median of 6 days (range 0-97). Approximately one-quarter of cases (n=7,323) had missing or unknown information on questions about symptoms. The most common symptoms were cough (12,787 [42.5%]), headache (11,961 [39.7%]), and fatigue (10,348 [34.4%]). The least common symptoms were loss of appetite (4,448 [14.8%]), weakness (2,988 [9.9%]), abdominal pain (1,768 [5.9%]), and vomiting (2,706 [9.0%]). Fever was reported by approximately one-third (29.9%).

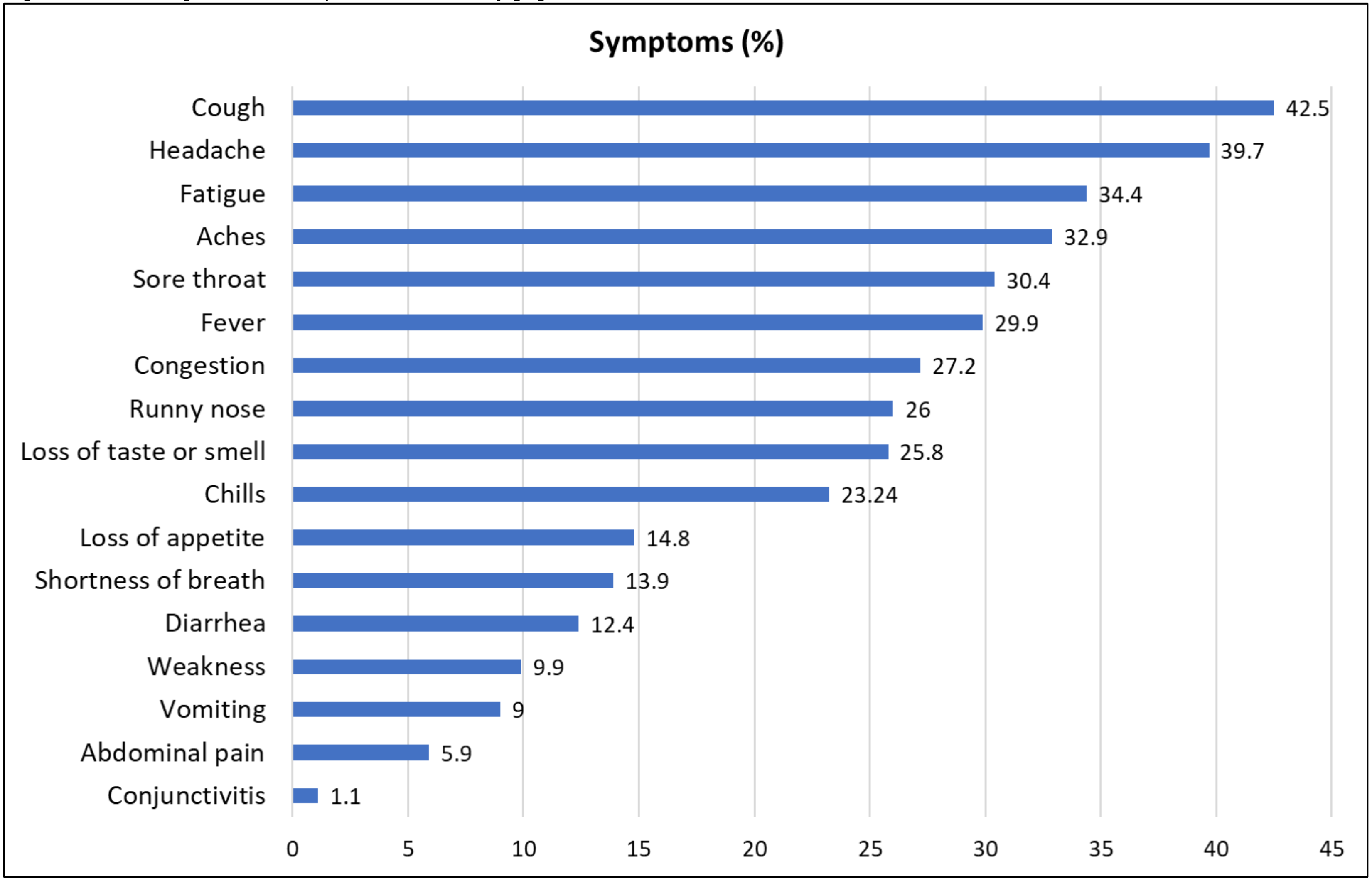
Table 6: Frequency of symptoms in the case database.

	Frequency (n)	Percent (%)
Fever		
No	11,449	38.0
Yes	9,020	29.9
Missing or unknown	9,657	32.1
Cough		
No	8,503	28.2
Yes	12,787	42.5
Missing or unknown	8,836	29.3
Pharyngitis		
No	11,228	37.3
Yes	9,160	30.4
Missing or unknown	9,738	32.3
Shortness of breath		
No	15,189	50.4
Yes	4,192	13.9
Missing or unknown	10,745	35.7
Chills		
No	12,909	42.9
Yes	7,002	23.24
Missing or unknown	10,215	33.9
Headache		
No	8,923	29.6
Yes	11,961	39.7
Missing or unknown	9,242	30.7
Aches		
No	10,587	35.1
Yes	9,914	32.9
Missing or unknown	9,625	32.0
Vomit		
No	16,475	54.7
Yes	2,706	9.0
Missing or unknown	10,945	36.3
Abdominal pain		
No	17,209	57.1
Yes	1,768	5.9
Missing or unknown	11,149	37.0

Table 6 continued: Frequency of symptoms in the case database.

	Frequency	Percent
Diarrhea		
No	15,544	51.6
Yes	3,745	12.4
Missing or unknown	10,837	36.0
Rhinitis		
No	12,231	40.6
Yes	7,829	26.0
Missing or unknown	10,066	33.4
Congestion		
No	12,025	39.9
Yes	8,203	27.2
Missing or unknown	9,898	32.9
Conjunctivitis		
No	18,052	59.9
Yes	321	1.1
Missing or unknown	11,753	39.0
Loss of taste or smell		
No	12,112	40.2
Yes	7,771	25.8
Missing or unknown	10,243	34.0
Fatigue		
No	10,103	33.5
Yes	10,348	34.4
Missing or unknown	9,675	32.1
Weakness		
No	15,763	52.3
Yes	2,988	9.9
Missing or unknown	11,375	37.8
Loss of appetite		
No	14,739	48.9
Yes	4,448	14.8
Missing or unknown	10,939	36.3

Figure 9: Clinical presentation of cases in the study population.



When asked if they felt symptoms, most patients said yes (20,404 [67.7%]). Coding for symptomatic status led to a slightly higher proportion of symptoms (20,537 [68.2%]). Half of the patients met the syndrome criteria for ILI (14,947 [49.6%]). Gastroenteritis syndrome criteria was met by less than a quarter of patients (5,237 [17.7%]). Few patients met the CDC criteria for severe COVID-19 (112 [0.4%]).

Table 7: Frequency of symptomatic status and syndromes

	Frequency (n)	Percent (%)
Patient was asked if they had symptoms		
Yes, had symptoms	20,404	67.7
No, no symptoms	2,896	9.6
Missing or unknown	6,826	22.7
Symptomatic status based on coding		
Symptomatic	20,537	68.2
Asymptomatic	2,266	7.5
Missing or unknown	7,323	24.3
ILI		
No	6,764	22.5
Yes	14,947	49.6
Missing or unknown	8,415	27.9
Gastroenteritis		
No	14,295	47.5
Yes	5,327	17.7
Missing or unknown	10,504	34.9
Severe COVID-19		
No	24,969	82.9
Yes	112	0.4
Missing or unknown	5,045	16.8
Total	30,126	100

Approximately half of the patients did not respond to questions regarding their medical history. A small proportion of patients (less than 10%) answered yes to questions about a history of childhood asthma, immunosuppressed condition, liver disease, renal disease, hypertension, diabetes, cardiovascular disease, or pregnancy. There were 1,000 (3.3%) patients hospitalized for COVID-19 with a small proportion intubated (86 [0.3%]). There were 281 (0.9%) individuals with deaths attributed to COVID-19.

Table 8: Distribution of medical history questions.

	Frequency (n)	Percent (%)
Pregnant		
No	13,429	44.6
Yes	241	0.8
Missing or unknown	16,456	54.6
Diabetes		
No	15,532	51.6
Yes	1,427	4.7
Missing or unknown	13,167	43.7
Cardiovascular disease		
No	16,161	53.6
Yes	673	2.2
Missing or unknown	13,292	44.1
Hypertension		
No	14,705	48.8
Yes	2,489	8.3
Missing or unknown	12,932	42.9
Renal disease		
No	16,443	54.6
Yes	331	1.1
Missing or unknown	13,352	44.3
Liver disease		
No	16,629	55.2
Yes	72	0.2
Missing or unknown	13,425	44.6
Immunosuppressed condition		
No	16,414	54.5
Yes	316	1.1
Missing or unknown	13,396	44.5

Table 8 continued: Distribution of medical history questions.

	Frequency	Percent
Childhood asthma		
No	15,636	51.9
Yes	944	3.1
Missing or unknown	13,546	45.0
Pneumonia		
No	21,251	70.5
Yes	708	2.4
Missing or unknown	8,167	27.1
ARDS		
No	21,618	71.8
Yes	279	0.9
Missing or unknown	8,229	27.3
Abnormal chest x-ray		
No	20,346	67.5
Yes	674	2.2
Missing or unknown	9,106	30.2
Hospitalized		
No	23,326	77.4
Yes	1,000	3.3
Missing or unknown	5,800	19.3
ICU		
No	21,730	72.1
Yes	131	0.4
Missing or unknown	8,265	27.4
ER		
No	16,054	53.3
Yes	410	1.4
Missing or unknown	13,662	45.4
ECMO		
No	21,729	72.1
Yes	62	0.2
Missing or unknown	8,335	27.7
Intubated		
No	21,738	72.2
Yes	86	0.3
Missing or unknown	8,302	27.6

Table 8 continued: Distribution of medical history questions.

	Frequency	Percent
Died		
No	22,340	74.2
Yes	281	0.9
Missing or unknown	7,505	24.9
Total	30,126	100.0

Figure 10: Pre-existing medical conditions for members of the study population.

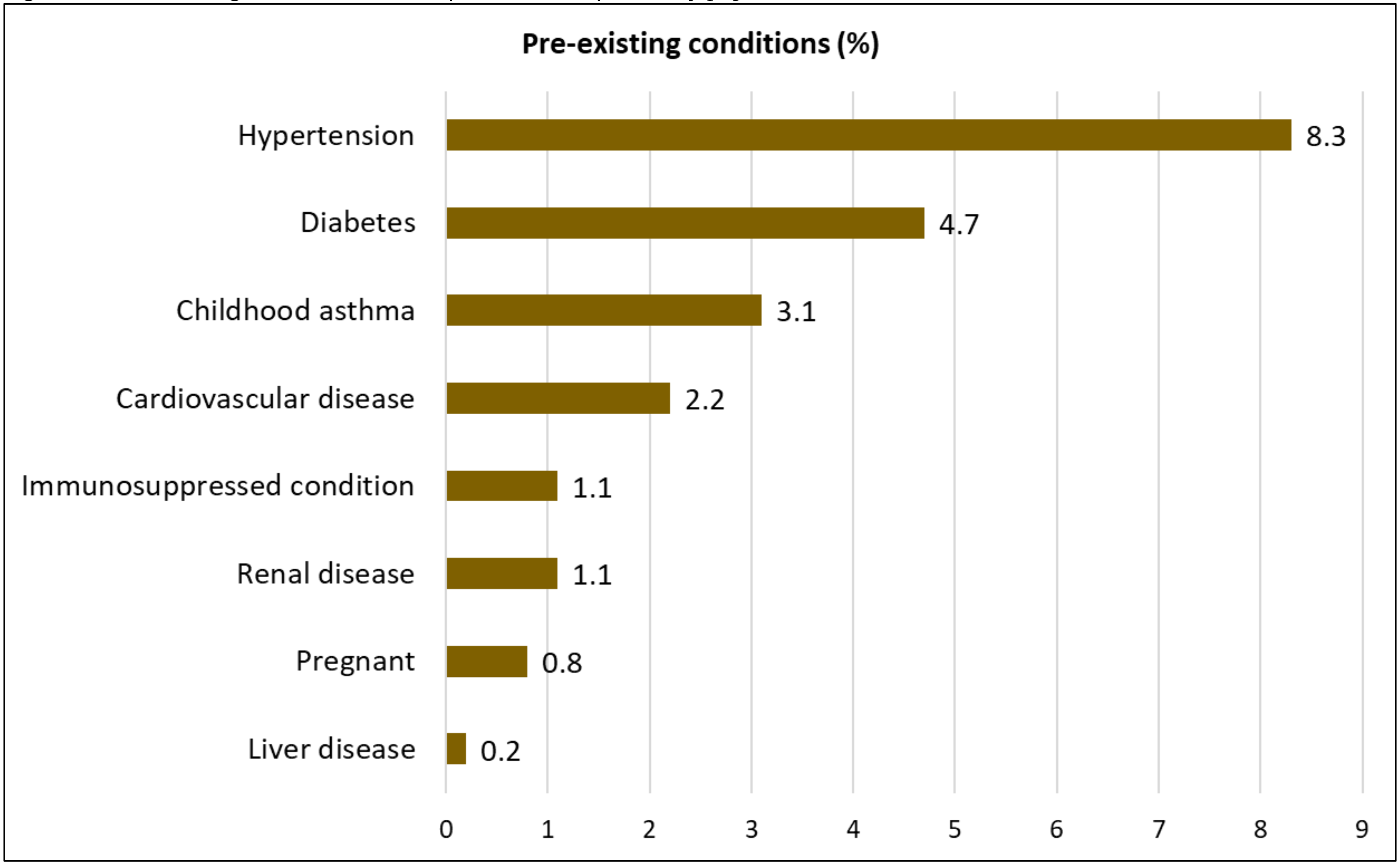
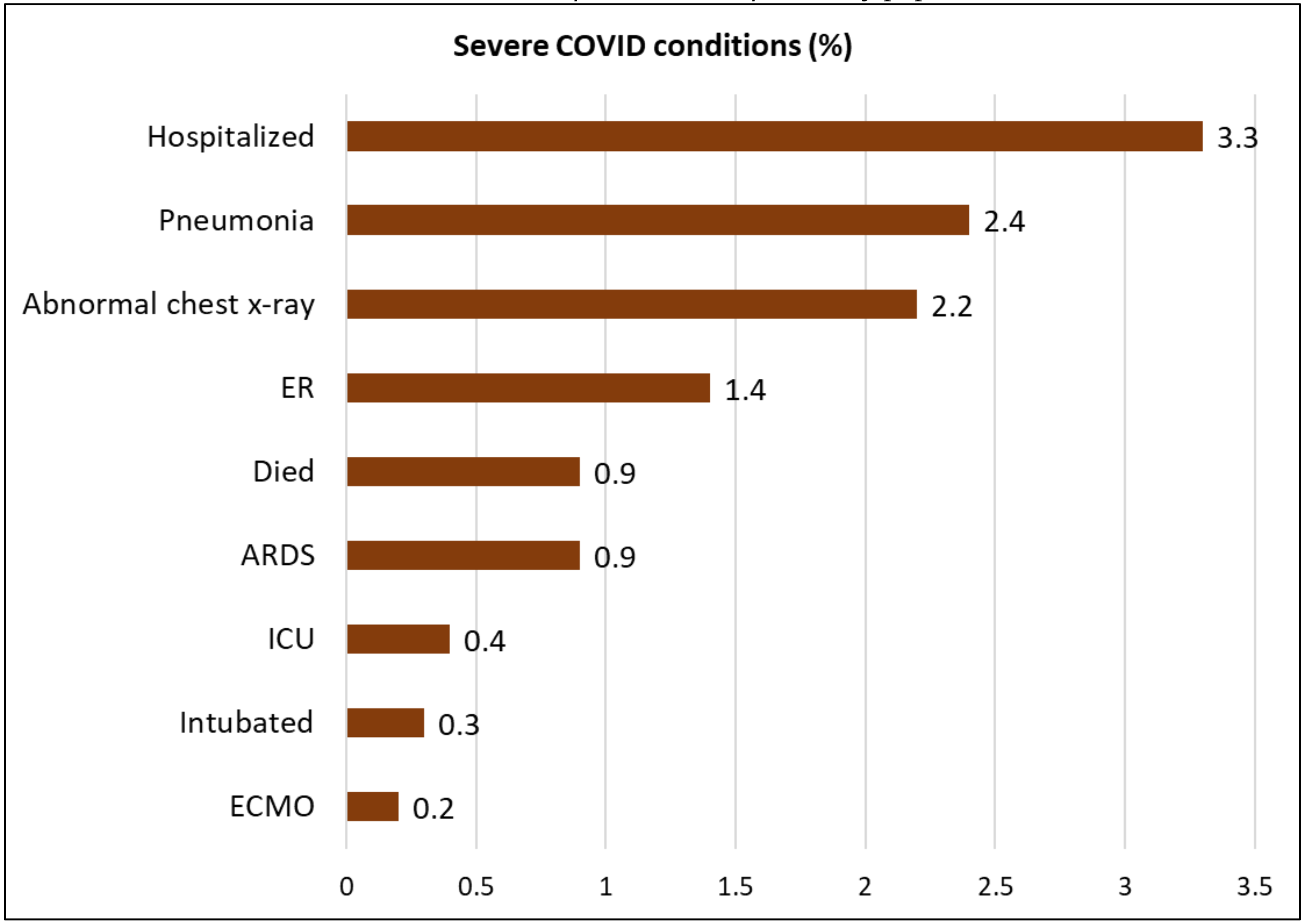
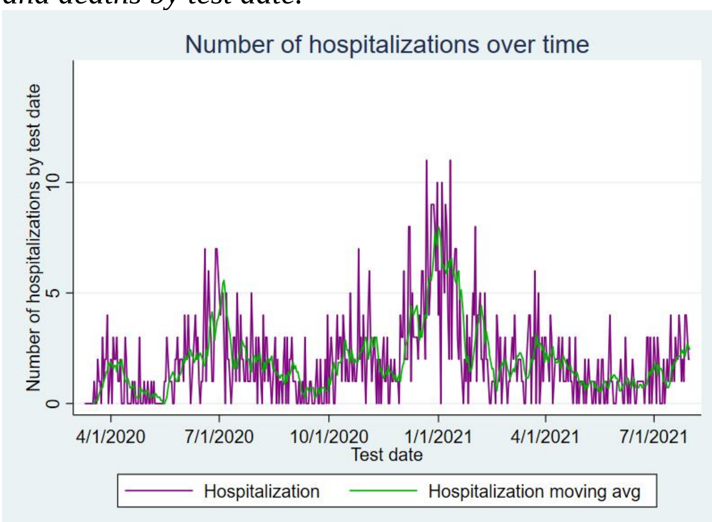


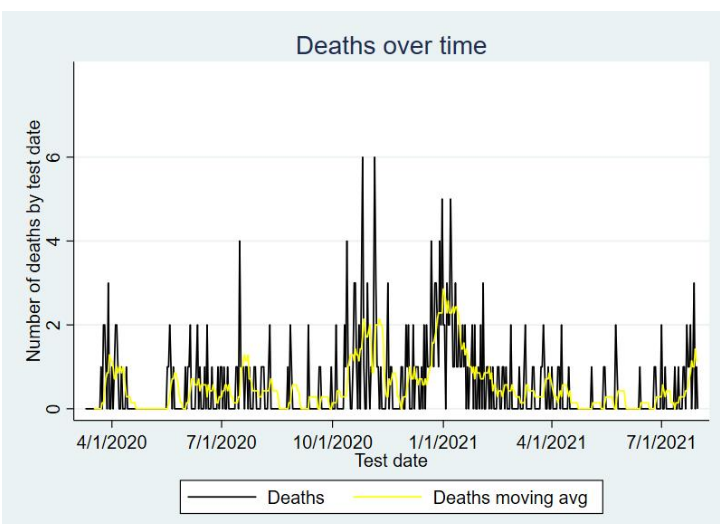
Figure 11: Severe conditions associated with COVID-19 for members of the study populations.

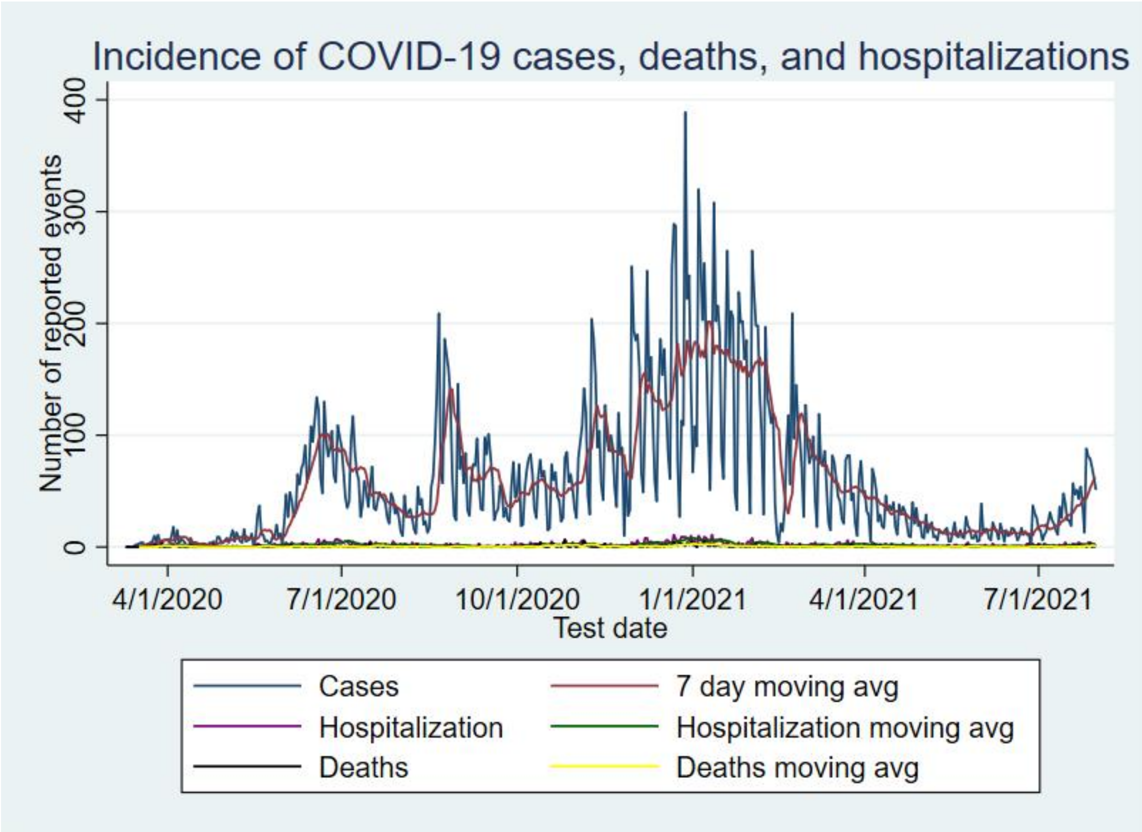


Epidemiologic curves are presented below for the number of cases, the 7-day moving average of cases, hospitalizations, the 7-day moving average of hospitalizations, deaths, and the 7-day moving average of deaths attributed to COVID-19 tied to their respective positive SARS-CoV-2 test date.

Figure 12: Epidemiologic curves from top to bottom: epidemiologic curve for hospitalizations of COVID-19 by test date, epidemiologic curve for deaths of COVID-19 by test date, and epidemiologic curve for combined COVID-19 cases, hospitalizations, and deaths by test date.







Exposure questions

To determine the likelihood of community transmission, patients were asked if knew of their contact with a laboratory confirmed case of COVID-19: 11,631 (38.6%) of patients said yes, 10,027 (33.3%) reported no, and the remaining 8,468 (28.1%) did not respond. Out of those who identified being a close contact, majority (3,400 [81.6%]) attributed their exposure to a household member. The median number of contacts was one, with a range of 0-300. The most common number of household contacts reported was between one and three (3,394 [11.3%]). The median number of household contacts was one, with a range of 0-18. Age distribution is shown below for the number of contacts and subset of household contacts with normal and kernel densities.

Figure 13: Locations the case reported known exposure.

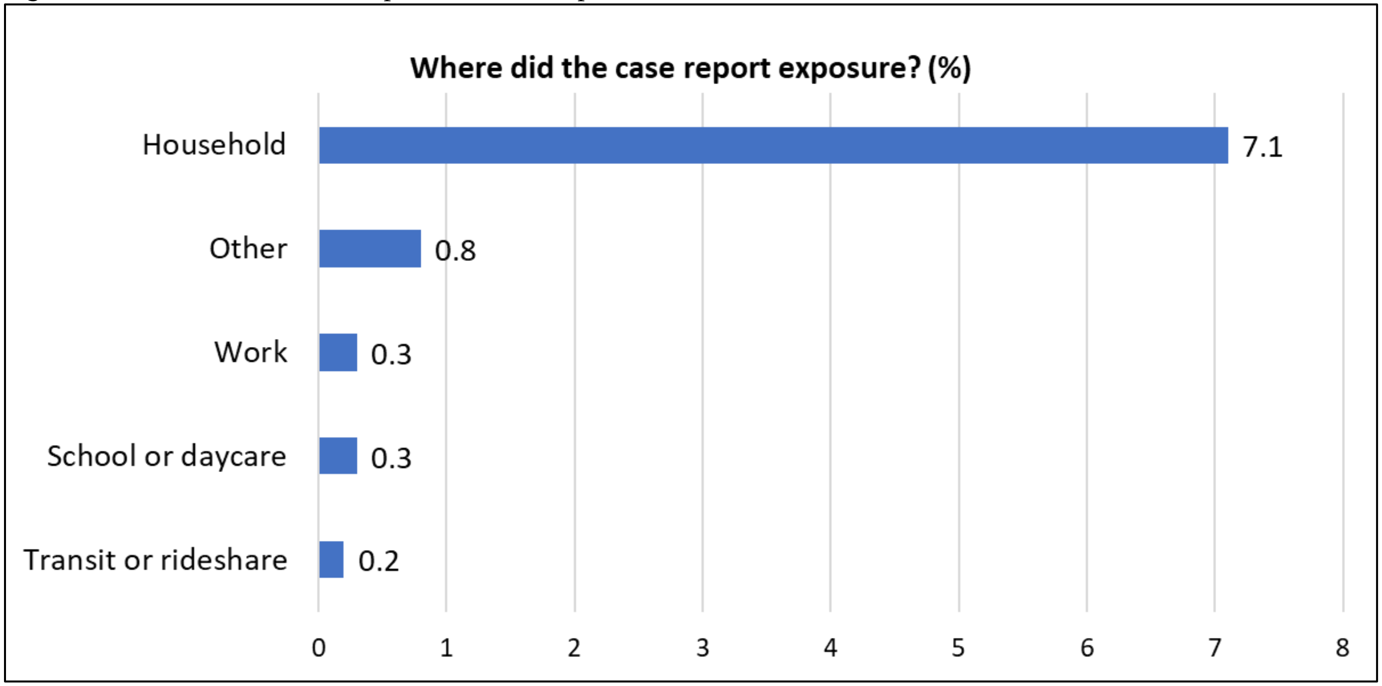


Table 9: Frequency of close contact information

	Frequency (n)	Percent (%)
Did the patient know they had close contact with a laboratory confirmed case?		
Yes	11,631	38.6
No	10,027	33.3
Missing or unknown	8,468	28.1
Was the close contact a household member?		
No	2,140	7.1
Yes	3,400	11.3
Missing or unknown	24,586	81.6
Where did the case report exposure?		
Household	2,151	7.1
School or daycare	92	0.3
Work	86	0.3
Transit or rideshare	60	0.2
Other	247	0.8
Missing or unknown	27,490	91.3
How many contacts did the case report?		
0 contacts	3,548	11.8
1-2 contacts	6,123	20.3
3-4 contacts	3,043	10.1
5-10 contacts	1,439	4.8
11-20 contacts	169	0.6
21-49 contacts	27	0.1
over 50 contacts	16	0.1
Missing or unknown	15,761	52.3
How many household contacts did the case report?		
0 household contacts	3,093	10.3
1-3 household contacts	3,394	11.3
4-6 household contacts	1,274	4.2
over 7 household contacts	101	0.3
Missing or unknown	22,264	73.9
Total	30,126	100.0

Figure 14: Number of number of contacts reported per case with a range of 0-25 contacts: distribution of contacts per case, distribution of contacts per case with kernel and normal densities (kernel density is orange, normal density is brown).

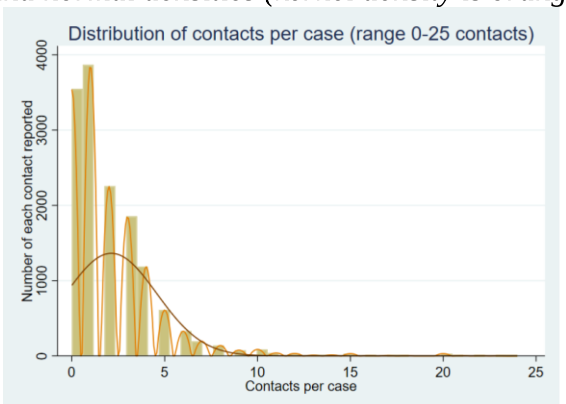


Figure 15: Number of close contacts reported by the case.

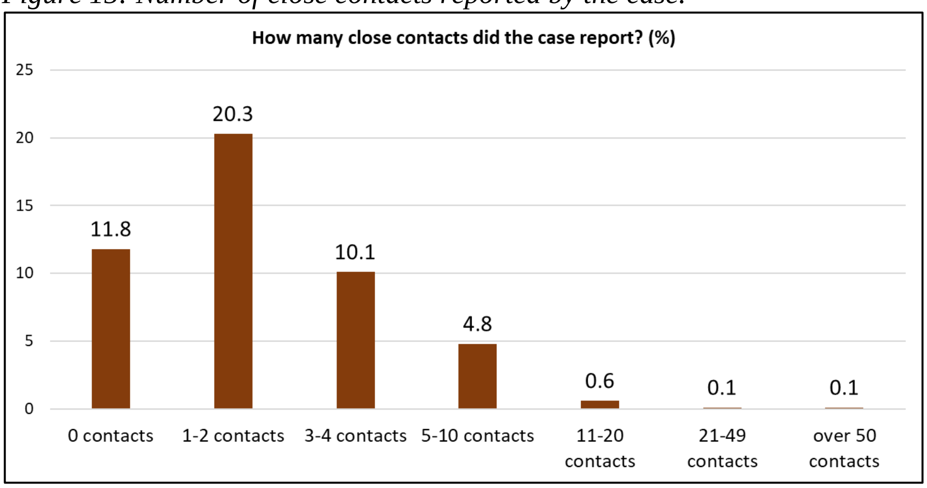
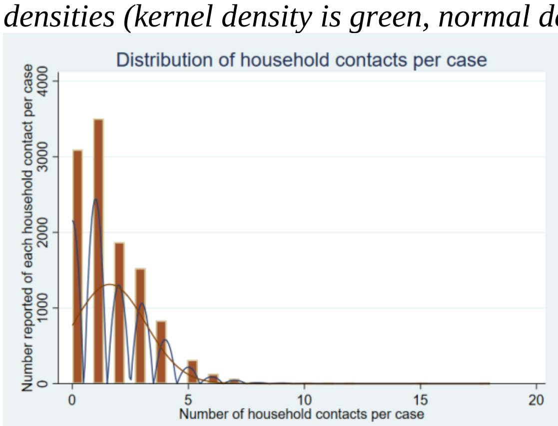


Figure 16: Number of household contacts reported per case: distribution of household contacts per case, distribution of household contacts per case with kernel and normal densities (kernel density is green, normal density is brown).



Behaviors, risk factors, and other exposures

Half of the patients reported not traveling (16,547 [54.9%]) outside of their city of residence in the past 14 days with a small proportion confirming that they had traveled (4,075 [13.5%]). Patients were asked how often they reported wearing a face mask or facial covering. The highest proportion of patients said always (3,224 [10.7%]), followed by sometimes (337 [1.1%]) and never (86 [0.3%]). Within the series of risk factor questions, the most common risk factors were going to a grocery store in person (2,279 [7.6%]), visiting a restaurant in person (1,285 [4.3%]), and working in person (1,284 [4.0%]). In terms of social gatherings, indoor gatherings of less than 5 and indoor gatherings of 5-10 were the social settings reported most often. Frequency of cases attending indoor gatherings >10 people are included in the appendix.

Figure 17: Most common in-person activities reported.

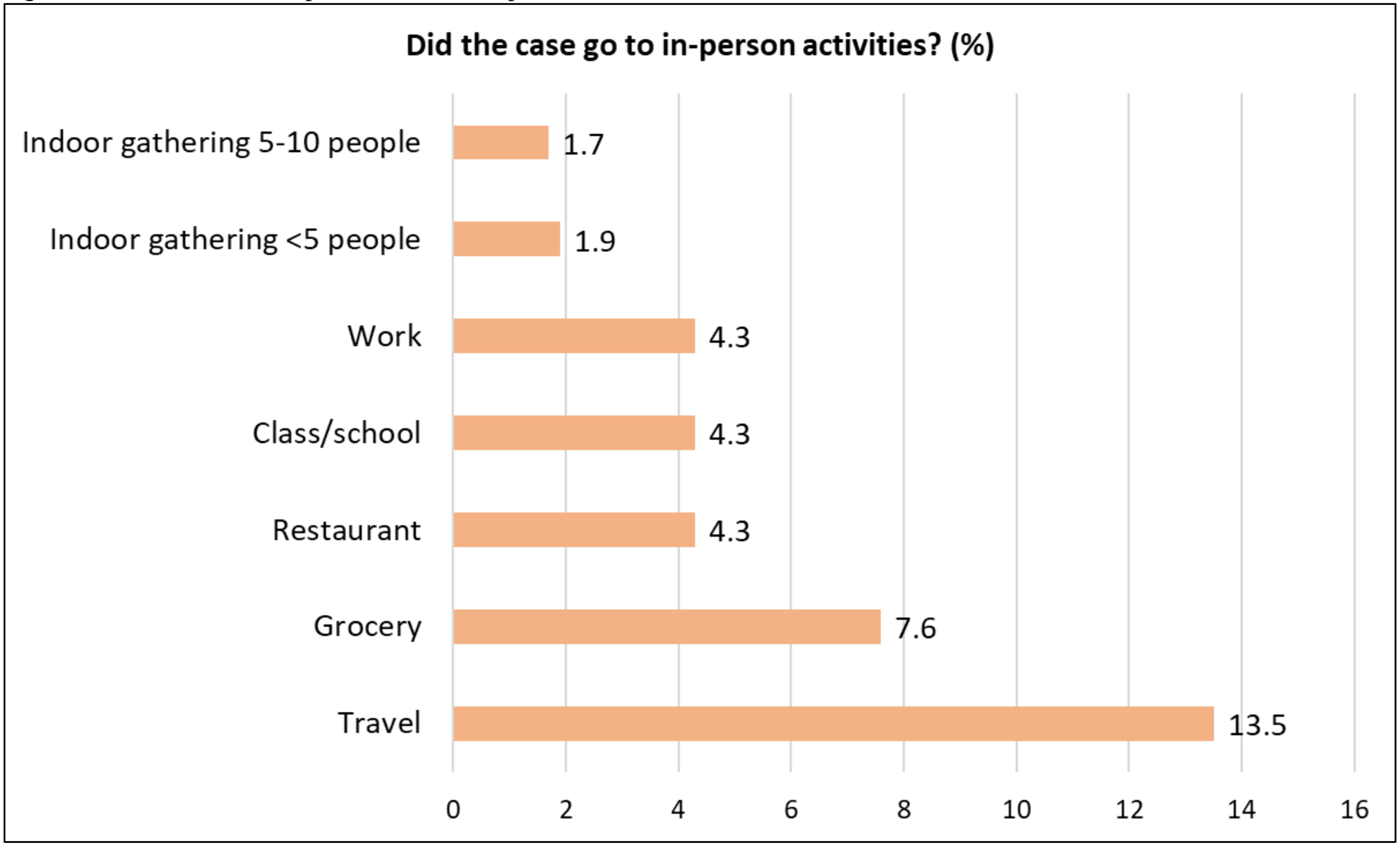


Table 10: Frequency of risk factors in the data set.

	Frequency (n)	Percent (%)
Did the case travel in the past 14 days?		
Yes	4,075	13.5
No	16,547	54.9
Missing or unknown	9,504	31.6
How often did the case report wearing a face mask or face covering?		
Always	3,224	10.7
Sometimes	337	1.1
Never	86	0.3
Missing or unknown	26,479	87.9
Did the case go to the grocery in person?		
Unchecked	27,847	92.4
Checked	2,279	7.6
Did the case go to a restaurant in person?		
Unchecked	28,841	95.7
Checked	1,285	4.3
Did the case work in person?		
Unchecked	28,842	95.7
Checked	1,284	4.3
Did the case go to an indoor gathering with less than 5?		
Unchecked	29,558	98.1
Checked	568	1.9
Did the case go to an indoor gathering with 5 to 10 people?		
Unchecked	29,601	98.3
Checked	525	1.7

Vaccines

By July 31, 2021, questions about COVID vaccination were added to the interview and 4,286 (14%) individuals had provided their vaccination status. When asked if they would get an FDA approved COVID-19 vaccine when it becomes available to them, 1,208 (4%) said yes, and 1,056 (3.5%) were undecided. The most common COVID-19 vaccine distributed based on this data was Moderna (175 [0.6%]) followed by Pfizer (101 [0.3%]); 99% of observations were unknown.

Table 11: Frequency of vaccination questions

	Frequency (n)	Percent (%)
Have you received any dose of an FDA approved COVID-19 vaccine?		
No	3,836	12.7
Yes, 1 dose	219	0.7
Yes, 2 doses	231	0.8
Missing or unknown	25,840	85.8
If vaccinated, did you receive Moderna?		
Unchecked	29,951	99.4
Checked	175	0.6
If vaccinated, did you receive Pfizer?		
Unchecked	30,025	99.7
Checked	101	0.3
Did you receive Johnson & Johnson?		
Unchecked	30,081	99.9
Checked	45	0.2
If fully vaccinated, is this considered a breakthrough infection?		
No	45	10.0
Yes	198	44.0
Cannot be determined	14	3.1
Missing or unknown if vaccinated	193	42.9
Total	450	100.0
If not vaccinated, when an FDA approved COVID-19 vaccine becomes available to you, do you plan to get it?		
No, definitely not	131	0.4
Probably no	133	0.4
Probably yes	393	1.3
Yes, definitely	1,208	4.0
Not sure	1,056	3.5
Missing or unknown	27,205	90.3
Total	30,126	100.0

University questions

The patients within the dataset were divided into affiliated with the university or not. Those affiliated with the university identified based on coding comprised a little over a quarter of patients (8,437 [28%]) within this time frame. A large proportion of university affiliated patients identified as undergraduate students (4,832 [28%]), while only a small amount were graduate or professional students (560 [1.9%]). Extracurricular activities identified were Greek life (554 [1.8%]), student athlete (259 [0.9%]), Corps of Cadets (379 [1.3%]), and member of a student organization (903 [3.0%]).

Table 12: Frequency of university question responses

	Frequency (n)	Percent (%)
Affiliated with the university		
No	21,689	72.0
Yes	8,437	28.0
Indicate student classification: Undergrad		
Unchecked	25,294	84.0
Checked	4,832	16.0
Indicate student classification: Graduate or Professional		
Unchecked	29,566	98.1
Checked	560	1.9
Is the student a member of a Fraternity or Sorority		
Unchecked	29,572	98.2
Checked	554	1.8
Is the student a Clinical Learner		
Unchecked	30,094	99.9
Checked	32	0.1
Is the student a student athlete		
Unchecked	29,867	99.1
Checked	259	0.9
Is the student a student employee		
Unchecked	29,664	98.5
Checked	462	1.5
Is the student a member of the Corps of Cadets		
Unchecked	29,747	98.7
Checked	379	1.3
Is the student a member of student org.		
Unchecked	29,223	97.0
Checked	903	3.0
Total	30,126	100.0

3.4.2 Characteristics by Age Group

Across each adult age category, there were slightly more females than males ($p<0.001$). Though in children under 18 years of age, there were slightly more males than females. There were more English speakers in ages 18-29 years (98.9%) than in any other age group ($p<0.001$). Young adults were found to have significantly more English speakers than non-English speakers when compared to adults over 30 years ($p<0.001$). When comparing white, non-Hispanic to Hispanic or Latino individuals, adults over 18 were less often reported or self-identified as Hispanic or Latino ($p<0.001$). The most common residence type for every age category was private residence or house. Though adults were significantly more often to be reported as living in apartments than in houses when compared to children under 18 (<0.001).

Table 13: Demographics of study population by age

		Age Group, years n (%)							Total*	X^2 p-value Pearson X^2
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 14,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		
Sex										
	Female	827 (48.3)	847 (49.9)	7,550 (52.5)	2,022 (53.5)	1,619 (53.3)	1,836 (53.6)	1,031 (53.7)	15,732 (52.5)	0.001
	Male	886 (51.7)	851 (50.1)	6,831 (47.5)	1,761 (46.6)	1,420 (46.7)	1,591 (46.4)	888 (46.3)	14,228 (47.5)	21.8
	Total*	1,713	1,698	14,381	3,783	3,039	3,427	1,919	29,960	
Primary Language										
	English	922 (91.7)	999 (92.2)	11,122 (98.9)	2,399 (94.0)	1,927 (90.7)	2,237 (92.7)	1,340 (94.8)	20,946 (95.9)	<0.001
	Spanish	82 (8.2)	84 (7.8)	112 (1.0)	152 (6.0)	195 (9.2)	174 (7.2)	70 (5.0)	869 (4.0)	599.3
	Other	2 (0.2)	1 (0.1)	10 (0.1)	2 (0.1)	3 (0.1)	3 (0.1)	4 (0.2)	25 (0.1)	
	Total*	1,006	1,084	11,244	2,553	2,125	2,414	1,414	21,840	
Residence type										
	House	1,340 (93.1)	1,252 (93.4)	8,070 (63.5)	2,824 (89.3)	2,348 (92.7)	2,768 (94.8)	1,430 (91.2)	20,032 (78.0)	4700.0
	Apartment	76 (5.3)	57 (4.3)	3,290 (25.9)	299 (9.5)	142 (5.6)	106 (3.6)	40 (2.6)	4,010 (15.6)	<0.001
	Dormitory	0 (0.0)	9 (0.7)	1,178 (9.3)	0 (0.0)	1 (0.0)	1 (0.0)	0 (0.0)	1,189 (4.6)	
	Supported living	1 (0.1)	0 (0.0)	2 (0.0)	2 (0.1)	2 (0.1)	14 (0.5)	90 (5.7)	111 (0.4)	
	Other	22 (1.5)	23 (1.7)	166 (1.3)	37 (1.2)	41 (1.6)	31 (1.1)	8 (0.5)	328 (1.3)	
	Total*	1,439	1,341	12,706	3,162	2,534	2,920	1,568	25,670	
Race/ethnicity										
	White, non-Hispanic	419 (29.5)	427 (31.5)	7,029 (57.9)	1,185 (38.5)	958 (40.1)	1,334 (47.7)	901 (60.4)	12,253 (49.7)	1500.0
	Hispanic	764 (53.8)	730 (53.8)	3,715 (30.6)	1,414 (46.0)	1,094 (45.8)	1,031 (36.9)	371 (24.9)	9,119 (37.0)	<0.001
	Black	212 (14.9)	175 (12.9)	786 (6.5)	380 (12.4)	292 (12.2)	379 (13.6)	203 (13.6	2,427 (9.8)	
	Asian	25 (1.8)	19 (1.4)	574 (4.7)	86 (2.8)	41 (1.7)	42 (1.5)	18 (1.2)	805 (3.3)	
	Other race	1 (0.1)	5 (0.4)	38 (0.3)	11 (0.4)	3 (0.1)	9 (0.3)	0 (0.0)	67 (0.3)	
	Total*	1,421	1,356	12,142	3,076	2,388	2,795	1,493	24,671	

*Total may not equal number of observations in the data set for all variables because of missing values

Table 14: Sex of children aged 0-17 compared to adults over 18.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-17 3,422 (column %)	18+ 26,642 (column %)		**Pearson X^2**
Sex				
Female	1,674 (49.1)	14,058 (53.0)	15,732 (52.5)	18.2
Male	1,737 (50.9)	12,491 (47.1)	14,228 (47.5)	<0.001
Total	3,411	26,549	29,960	

Table 15: Language of young adults to adults over 30.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433(column %)	30+ 12,209(column %)		**Pearson X^2**
Language				
English speakers	11,122 (98.9)	7,903 (92.9)	19,025 (96.3)	493.7
Other language	122 (1.1)	603 (7.1)	725 (3.7)	<0.001
Total	11,244	8,506		

Table 16: Hispanic/Latino of minors compared to over 18 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-17 3,422 (column %)	18+ 26,642 (column %)		**Pearson X^2**
Hispanic or Latino				
White, non-Hispanic	846 (35.4)	11,407 (59.7)	12,253 (57.0)	509.3
Hispanic	1,542 (64.6)	7,707 (40.3)	8,249 (43.0)	<0.001
Total	2,388	19,114	21,502	

Table 17: House of apartment living in ages under 18 compared to over 18 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-17 3,422 (column %)	18+ 26,642 (column %)		**Pearson X^2**
House or apt				
House	2,592 (95.1)	17,440 (81.8)	20,032 (83.3)	307.8
Apartment	133 (4.9)	3,877 (18.2)	4,010 (16.7)	<0.001
Total	2,725	21,317	24,042	

The most common symptoms in children ages 0-11 were fever (45.0%) and cough (37.7%). Cough (44.0%) and sore throat (41.9%) were the most common symptoms in children 12-17 years. The most often reported symptoms in young adults were headache (69%) and cough (59%), other adult age categories shared these as the most frequent clinical symptom apart from ages 65 and older which infrequently reported headache (30.7%). The youngest and oldest age groups (0-11 and 65+) had the lowest proportions of individuals reporting headache or aches associated with this illness.

Children ages 0-11 years reported sore throat less often than any other age group (18.8%). Sore throat was reported most often by young adults (54.7%) but was reported less often at 5-10% intervals with each older age group.

Very few children aged 0-11 years reported loss of taste or smell (7.4%) or loss of appetite. These were more frequent in adolescents, as over a quarter of children aged 12-17 years reported loss of taste or smell (31.7%) but very few identified a loss of appetite (12.8%). A 2x2 analysis revealed that loss of taste or smell was significantly more common in adolescents than in children (31.7%, $p<0.001$). Further analysis into loss of taste or smell demonstrated that this symptom was more common in adults over 18 (40.9%, $p<0.001$) than in those under 18 years of age. Half of young adults 18-29 years of age reported loss of taste or smell. Ages 30-39 years and 40-49 years had similar reports of loss of taste or smell at 47.8% and 42.3%, respectively. Adults aged 60-64 years had 34.2% reporting loss of taste or smell. Across age groups, loss of appetite was not a common symptom. Loss of appetite was not significantly different between children and adolescents (12.8%, $p=0.051$). However, loss of appetite was significantly more common (24.3% $p<0.001$) in adults over 18 than those under 18.

Table 18: Clinical presentation by age group

		Age Group, years n (%)							Total*	X^2 p-value Pearson X^2
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 4,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		
Symptomatic										
	Yes	753 (69.9)	941 (81.1)	10,183 (88.8)	2,563 (90.4)	2,126 (91.6)	2,440 (89.5)	1,362 (81.5)	20,368 (87.6)	488.8
	No	324 (30.1)	219 (18.9)	1,283 (11.2)	273 (9.6)	196 (8.4)	287 (10.5)	309 (18.5)	2,891 (12.4)	<0.001
	Total	1,077	1,160	11,466	2,836	2,322	2,727	1,671	23,259	
Fever										
	Yes	416 (45.0)	375 (39.0)	4,109 (40.4)	1,190 (48.5)	1,035 (50.8)	1,261 (52.2)	618 (42.0)	9,004 (44.1)	191.2
	No	409 (55.0)	587 (61.0)	6,068 (59.6)	1,264 (51.5)	1,001 (49.2)	1,155 (47.8)	852 (58.0)	11,436 (56.0)	<0.001
	Total	925	962	10,177	2,454	2,036	2,416	1,470	20,440	
Cough										
	Yes	347 (37.7)	427 (44.0)	6,247 (59.0)	1,667 (65.0)	1,431 (67.1)	1,721 (68.4)	922 (59.4)	12,762 (60.0)	444.0
	No	573 (62.3)	544 (56.0)	4,350 (41.1)	899 (35.0)	701 (32.9)	797 (31.7)	631 (40.6)	8,495 (40.0)	<0.001
	Total	920	971	10,597	2,566	2,132	2,518	1,553	21,257	
Sore throat										
	Yes	163 (18.8)	411 (41.9)	5,709 (54.7)	1,030 (43.4)	763 (39.1)	767 (33.0)	301 (21.2)	9,144 (44.9)	1100.0
	No	703 (81.2)	570 (58.1)	4,734 (45.3)	1,346 (56.7)	1,189 (60.9)	1,559 (67.0)	1,116 (78.8)	11,217 (55.1)	<0.001
	Total	866	981	10,443	2,376	1,952	2,326	1,417	20,361	
Headache										
	Yes	206 (23.8)	492 (49.9)	6,783 (63.9)	1,512 (60.6)	1,226 (59.8)	1,287 (53.5)	439 (30.7)	11,945 (57.3)	1100.0
	No	659 (76.2)	494 (50.1)	3,837 (36.1)	984 (39.4)	824 (40.2)	1,121 (46.6	992 (69.3)	8,911 (42.7)	<0.001
	Total	865	986	10,620	2,496	2,050	2,408	1,431	20,586	
Aches										
	Yes	105 (12.4)	282 (30.2)	5,070 (49.1)	1,401 (56.9)	1,206 (59.2)	1,328 (54.8)	503 (34.9)	9,895 (48.3)	877.3
	No	742 (87.6	652 (69.8)	5,255 (50.9)	1,061 (43.1)	833 (40.9)	1,094 (45.2)	940 (65.1)	10,577 (51.7)	<0.001
	Total	847	934	10,325	2,462	2,039	2,422	1,443	20,472	
Loss of taste/smell										
	Yes	62 (7.4)	293 (31.7)	4,426 (43.7)	1,126 (47.8)	822 (42.3)	781 (34.2)	249 (18.0)	7,759 (39.1)	828.4
	No	777 (92.6)	631 (68.3)	5,707 (56.3)	1,229 (52.2)	1,123 (57.7)	1,501 (65.8)	1,132 (82.0)	12,100 (60.9)	<0.001
	Total	839	924	10,133	2,355	1,945	2,282	1,381	19,859	
Loss of appetite										
	Yes	83 (9.9)	113 (12.8)	2,419 (24.8)	536 (24.3)	444 (23.9)	565 (25.4)	278 (20.1)	4,438 (23.2)	166.0
	No	759 (90.1)	767 (87.2)	7,350 (75.2)	1,673 (75.7)	1,412 (76.1)	1,660 (74.6)	1,104 (79.9)	14,725 (76.8)	<0.001
	Total	842	880	9,769	2,209	1,856	2,225	1,382	19,163	

Table 19: Comparing loss of taste or smell among minors.

	Age groups (years) n (%)		**Total**	**X^2 p-value**
	0-11 839 (column %)	12-17 924 (column %)		**Pearson X^2**
Loss of taste/smell				
Yes	62 (7.4)	293 (31.7)	355 (20.1)	161.7
No	777 (92.6)	631 (68.3)	1,408 (79.9)	<0.001
Total	839	924	1,763	

Table 20: Comparing loss of appetite among minors.

	Age groups (years) n (%)		**Total**	**X^2 p-value**
	0-11 842 (column %)	12-17 880 (column %)		**Pearson X^2**
Loss of appetite				
Yes	83 (9.9)	113 (12.8)	196 (11.4)	3.8
No	759 (90.1)	767 (87.2)	1,526 (88.6)	0.051
Total	842	880	1,722	

Table 21: Comparing loss of taste/smell between minors and adults.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-17 1,763 (column %)	18+ 18,096 (column %)		**Pearson X^2**
Loss of taste/smell				
Yes	355 (20.1)	7,404 (40.9)	7,759 (39.1)	291.4
No	1,408 (79.9)	10,692 (59.1)	12,100 (60.9)	<0.001
Total	1,763	18,096	19,859	

Table 22: Comparing loss of appetite between minors and adults.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-17 1,722 (column %)	18+ 17,441 (column %)		**Pearson X^2**
Loss of appetite				
Yes	196 (11.4)	4,242 (24.3)	4,438 (23.2)	147.5
No	1,526 (88.6)	13,199 (75.7)	14,725 (76.8)	<0.001
Total	1,722	17,441	19,163	

Slightly under half (43.9%) of children aged 0-11 years of age had ILI, which is a decrease in ILI prevalence compared to adolescents (59.2%). Each adult age category had ILI prevalence at approximately 70% except for adults aged 65 and older whose ILI prevalence was like adolescents (59.5%). Gastroenteritis was not common (<40% in all age groups) but was most prevalent in those adults aside from those over 65 years of age. Severe COVID-19 was not present in children. All adult age categories had low proportions of severe COVID-19 but the highest prevalence (3.8%) was in those aged 65 years and older.

Table 23: Syndromes across age groups.

		Age Group, years n (%)							Total*	X^2 p-value
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 4,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		Pearson X^2
ILI										
	Yes	410 (43.9)	607 (59.2)	7,749 (71.4)	1,875 (71.7)	1,566 (72.7)	1,788 (70.3)	925 (59.5)	14,920 (68.8)	438.2
	No	523 (56.1)	418 (40.8)	3,100 (28.6)	741 (28.3)	588 (27.3)	756 (29.7)	630 (40.5)	6,756 (31.2)	<0.001
	Total	933	1,025	10,849	2,616	2,154	2,544	1,555	21,676	
Gastroenteritis										
	Yes	153 (17.8)	139 (15.6)	2,618 (26.4)	738 (32.2)	593 (30.8)	729 (32.0)	350 (24.8)	5,320 (27.2)	176.2
	No	708 (82.2)	755 (84.5)	7,318 (73.7)	1,551 (67.8)	1,331 (69.2)	1,552 (68.0)	1,062 (75.2)	14,277 (72.9)	<0.001
	Total	861	894	9,936	2,289	1,924	2,281	1,412	19,597	
Severe COVID										
	Yes	0 (0.0)	0 (0.0)	4 (0.0)	7 (0.2)	10 (0.4)	26 (0.9)	65 (3.8)	112 (0.5)	498.5
	No	1,237 (100.0)	1,384 (100.0)	12,026 (100.0)	3,149 (99.8)	2,473 (99.6)	2,997 (99.1)	1,667 (96.3)	24,933 (99.6)	<0.001
	Total	1,237	1,384	12,030	3,156	2,483	3,023	1,732	25,045	

In children aged 0-11 years, diabetes, immunocompromised condition, and childhood asthma were less common than in children 12-17 years though these relationships were not statistically significant. Cardiovascular disease and hypertension were more prevalent in children aged 0-11 years than in children aged 12-17 years, though these were also not statistically significant relationships.

The prevalence of chronic health conditions in this study population increased with adult age (young adults to ages 30+) except for childhood asthma ($p<0.001$). Diabetes was reported in 1.3% of individuals aged 18-29 years less than all other adults aged 30-39 years (7.3%), adults aged 40-49 years (16%), adults aged 50-64 years (23.2%), and adults over 65 years old (32%). CVD was reported in 1% or less of individuals aged 12-39 years, 3.1% of adults aged 40-49 years, 8.6% of adults aged 50-64 years and 28% of those 65 years and older. Hypertension was reported in less than 1% of children aged 12-17, 1.6% of young adults aged 18-29 years, 10.8% of adults aged 30-39 years, 25.7% of adults aged 40-49 years, 42% of adults aged 50-64 years, and 56.2% of adults aged 65 years and older. Renal disease was reported in less than 2% of individuals under 49 years of age but was higher in ages 50-64 years (5%), and of those aged 65 years and older (12.15%).

Liver disease was reported in less than 1% of individuals aged 49 years and younger, 1.3% in those aged 50-64 years, and 1.7% in ages 65 years and older. Immune compromising conditions was reported in less than 1% of children, 1.3% of ages 18-29 years, 1.5% of 30-39 years, 2.5% of ages 40-49, 3.7% of ages 50-64 years, and 4.5% of ages over 65 years. Childhood asthma was reported in 5.2% of children ages 0-11 years, 5.7% of children aged 12-17 years, 8.7% of ages 18-29 years, 2.6% of ages 30-39, and less than 2% of those over 40 years of age.

Table 24: Pre-existing conditions across age

		Age Group, years n (%)							Total*	X^2 p-value
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 4,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		Pearson X^2
Diabetes										
	Yes	4 (0.6)	10 (1.3)	112 (1.3)	139 (7.3)	258 (16.0)	473 (23.2)	431 (32.0)	1,427 (8.4)	2300.0
	No	706 (99.4)	736 (98.7)	8,452 (98.7)	1,777 (92.8)	1,358 (84.0)	1,570 (76.9)	917 (68.0)	15,516 (91.6)	<0.001
	Total	710	746	8,564	1,916	1,616	2,043	1,348	16,943	
Cardiovascular disease										
	Yes	6 (0.8)	1 (0.1)	50 (0.6)	19 (1.0)	49 (3.1)	171 (8.6)	376 (28.0)	672 (4.0)	2500.0
	No	707 (99.2)	743 (99.9)	8,494 (99.4)	1,867 (99.0)	1,539 (96.9)	1,830 (91.5)	966 (72.0)	16,146 (96.0)	<0.001
	Total	713	744	8,544	1,886	1,588	2,001	1,342	16,818	
Hypertension										
	Yes	6 (0.8)	3 (0.4)	138 (1.6)	208 (10.8)	428 (25.7)	899 (42.0)	802 (56.2)	2,484 (14.5)	4900.0
	No	707 (99.2)	742 (99.6)	8,418 (98.4)	1,721 (89.2)	1,238 (74.3)	1,241 (58.0)	625 (43.8)	14,692 (85.5)	<0.001
	Total	713	745	8,556	1,929	1,666	2,140	1,427	17,176	
Renal disease										
	Yes	3 (0.4)	4 (0.5)	16 (0.2)	22 (1.2)	29 (1.8)	100 (5.0)	157 (12.1)	331 (2.0)	947.5
	No	707 (99.6)	742 (99.5)	8,527 (99.8)	1,867 (98.8)	1,555 (98.2)	1,889 (95.0)	1,140 (87.9)	16,427 (98.0)	<0.001
	Total	710	746	8,543	1,889	1,584	1,989	1,297	16,758	
Liver disease										
	Yes	1 (0.1)	0 (0.0)	5 (0.1)	8 (0.4)	12 (0.8)	25 (1.3)	21 (1.7)	72 (0.4)	112.7
	No	707 (99.9)	744 (100.0)	8,528 (99.9)	1,874 (99.6)	1,570 (99.2)	1,943 (98.7)	1,247 (98.3)	16,613 (99.6)	<0.001
	Total	708	744	8,533	1,882	1,582	1,968	1,268	16,685	
Immunocompromised conditions										
	Yes	3 (0.4)	6 (0.8)	108 (1.3)	29 (1.5)	39 (2.5)	73 (3.7)	57 (4.5)	315 (1.9)	115.2
	No	706 (99.6)	738 (99.2)	8,421 (98.7)	1,854 (98.5)	1,554 (97.6)	1,907 (96.3)	1,219 (95.5)	16,399 (98.1)	<0.001
	Total	709	744	8,529	1,883	1,593	1,980	1,276	16,714	
Childhood asthma										
	Yes	37 (5.2)	42 (5.7)	740 (8.7)	48 (2.6)	27 (1.7)	32 (1.7)	15 (1.2)	941 (5.7)	326.8
	No	672 (94.8)	699 (94.3)	7,785 (91.3)	1,799 (97.4)	1,530 (98.3)	1,905 (98.4)	1,232 (98.8)	15,622 (94.3)	<0.001
	Total	709	741	8,525	1,847	1,557	1,937	1,247	16,563	

Table 25: Comparing prevalence of diabetes in children aged 0-11 years to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-11 1,720 (column %)	12-17 1,702 (column %)		**Pearson X^2**
Diabetes				
Yes	4 (0.6)	10 (1.3)	14 (1.0)	2.3
No	706 (99.4)	736 (98.7)	1,442 (99.0)	0.129
Total	710	746	1,456	

Table 26: Comparing prevalence of diabetes in young adults versus adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433 (column %)	30+ 12,209 (column %)		**Pearson X^2**
Diabetes				
Yes	112 (1.3)	1,301 (18.8)	1,413 (9.1)	1400
No	8,452 (98.7)	5,622 (81.2)	14,074 (90.9)	<0.001
Total	8,564	6,923	15,487	

Table 27: Comparing prevalence of cardiovascular disease in children aged 0-11 years to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-11 1,720 (column %)	12-17 1,702 (column %)		**Pearson X^2**
Cardiovascular disease				
Yes	6 (0.8)	1 (0.1)	7 (0.5)	3.8
No	707 (99.2)	743 (99.9)	1,450 (99.5)	0.051
Total	713	744	1,457	

Table 28: Comparing prevalence of cardiovascular disease in young adults versus adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433 (column %)	30+ 12,209 (column %)		**Pearson X^2**
Cardiovascular disease				
Yes	50 (0.6)	615 (9.0)	665 (4.3)	651.6
No	8,494 (99.4)	6,202 (90.9)	14,696 (95.7)	<0.001
Total	8,544	6,817	15,361	

Table 29: Comparing prevalence of hypertension in children aged 0-11 years to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value Pearson X^2**
	0-11 1,720 (column %)	12-17 1,702 (column %)		
Hypertension				
Yes	6 (0.8)	3 (0.4)	9 (0.6)	1.1
No	707 (99.2)	742 (99.6)	1,449 (99.4)	0.285
Total	713	745	1,458	

Table 30: Comparing prevalence of hypertension in young adults versus adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value Pearson X^2**
	18-29 14,433 (column %)	30+ 12,209 (column %)		
Hypertension				
Yes	138 (1.6)	2,337 (32.6)	2,475 (15.8)	2800
No	8,418 (98.4)	4,825 (67.4)	13,243 (84.3)	<0.001
Total	8,556	7,162	15,718	

Table 31: Comparing prevalence of renal disease in children aged 0-11 years to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value Pearson X^2**
	0-11 1,720 (column %)	12-17 1,702 (column %)		
Renal disease				
Yes	3 (0.4)	4 (0.5)	7 (0.5)	0.1
No	707 (99.5)	742 (99.5)	1,449 (99.5)	0.754
Total	710	746	1,456	

Table 32: Comparing prevalence of renal disease in young adults versus adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value Pearson X^2**
	18-29 14,433 (column %)	30+ 12,209 (column %)		
Renal disease				
Yes	16 (0.2)	308 (4.6)	324 (2.1)	347.6
No	8,527 (99.8)	6,451 (95.4)	14,978 (97.9)	<0.001
Total	8,543	6,759	15,302	

Table 33: Comparing liver disease in children aged 0-11 to those aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-11 1,720 (column %)	12-17 1,702 (column %)		**Pearson X^2**
Liver disease				
Yes	1 (0.1)	0 (0.0)	1 (0.1)	1.1
No	707 (99.9)	744 (100.0)	1,451 (99.9)	0.305
Total	708	744	1,452	

Table 34: Comparing prevalence of liver disease in young adults to adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433 (column %)	30+ 12,209 (column %)		**Pearson X^2**
Liver disease				
Yes	5 (0.1)	66 (0.9)	71 (0.5)	69.4
No	8,528 (99.9)	6,634 (99.0)	15,162 (99.5)	<0.001
Total	8,533	6,700	15,233	

Table 35: Comparing prevalence of immunocompromised children aged 0-11 to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-11 1,720 (column %)	12-17 1,702 (column %)		**Pearson X^2**
Immunosuppressed				
Yes	3 (0.4)	6 (0.8)	9 (0.6)	0.87
No	706 (99.6)	738 (99.2)	1,444 (99.4)	0.352
Total	709	744	1,453	

Table 36: Comparing prevalence of immunosuppressed conditions in young adults to adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433 (column %)	30+ 12,209 (column %)		**Pearson X^2**
Immunosuppressed				
Yes	108 (1.3)	198 (2.9)	306 (2.0)	53.7
No	8,421 (98.7)	6,534 (97.1)	14,955 (97.9)	<0.001
Total	8,529	6,732	15,261	

Table 37: Comparing prevalence of childhood asthma in children aged 0-11 to aged 12-17 years.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	0-11 1,720 (column %)	12-17 1,702 (column %)		**Pearson X^2**
Childhood asthma				
Yes	37 (5.2)	42 (5.7)	79 (5.5)	0.14
No	672 (94.8)	699 (94.3)	1,371 (94.6)	0.706
Total	709	741	1,450	

Table 38: Comparing prevalence of childhood asthma in young adults to adults over 30 years of age.

	Age groups (years) N (%)		**Total**	**X^2 p-value**
	18-29 14,433 (column %)	30+ 12,209 (column %)		**Pearson X^2**
Childhood asthma				
Yes	740 (8.7)	122 (1.9)	862 (5.7)	322.2
No	7,785 (91.3)	6,466 (98.2)	14,251 (94.3)	<0.001
Total	8,525	6,588	15,113	

When asked if they had close contact with a prior confirmed laboratory case of COVID-19, 75.5% of children ages 0-11 years yes, which was a higher percentage than children ages 12-17 years (75.5%). Each adult age group had relatively even distributions of knowing the individual who exposed them and not knowing who exposed them. Both children ages 0-11 years and 12-17 years had majority (88.6% and 80%) reporting close contact with a household member. Ages 18-29 had half report close contact with a household member while ages 30-65+ years reported between 60%-72% household contacts. Majority of each age group reported a household exposure while a minority (4.6%) of ages 18-29 years reported exposure at school.

Table 39: Comparing known exposures across different age groups.

		Age Group, years n (%)							Total*	X^2 p-value Pearson X^2
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 4,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		
Close contact with confirmed case										
	Yes	829 (75.5)	735 (63.9)	5,470 (52.0)	1,383 (52.2)	1,151 (52.9)	1,296 (51.1)	750 (50.0)	11,614 (53.7)	287.9
	No	269 (24.5)	416 (36.1)	5,046 (48.0)	1,267 (47.8)	1,023 (47.1)	1,242 (48.9)	750 (50.0)	10,013 (46.3)	<0.001
	Total	1,098	1,151	10,516	2,650	2,174	2,538	1,500	21,627	
Was the close contact a household member?										
	Yes	398 (88.6)	300 (80.0)	1,360 (50.3)	356 (61.1)	356 (68.1)	405 (68.0)	221 (72.2)	3,396 (61.4)	370.6
	No	51 (11.4)	75 (20.0)	1,342 (49.7)	227 (38.9)	167 (31.9)	191 (32.1)	85 (27.8)	2,138 (38.6)	<0.001
	Total	449	375	2,702	583	523	596	306	5,534	
Where did the case report exposure?										
	Household	118 (98.3)	93 (93.0)	1,430 (73.7)	147 (78.6)	140 (84.9)	154 (85.1)	59 (86.8)	2,141 (77.5)	115.9
	Community	0 (0.0)	2 (2.0)	120 (6.2)	6 (3.2)	5 (3.0)	3 (1.7)	1 (1.5)	137 (5.0)	<0.001
	School or daycare	0 (0.0)	2 (2.0)	84 (4.3)	4 (2.1)	2 (1.2)	0 (0.0)	0 (0.0)	92 (3.3)	
	Work	0 (0.0)	0 (0.0)	53 (2.7)	14 (7.5)	9 (5.5)	9 (5.0)	1 (1.5)	86 (3.1)	
	Transit or rideshare	1 (0.8)	0 (0.0)	50 (2.6)	4 (2.1)	0 (0.0)	3 (1.7)	1 (1.5)	59 (2.1)	
	Other	1 (0.8)	3 (3.0)	203 (10.5)	12 (6.4)	9 (5.5)	12 (6.6)	6 (8.8)	246 (8.9)	
	Total	120	100	1,940	187	165	181	68	2,761	

Very few individuals under the age of 30 years experienced a severe medical outcome. Ages 30-39 years reported hospitalization less frequently (3%) than adults 40-49 (5.4%), ages 50-64 years (9.1%) and in ages over 65 years (24.3%). Going to an ICU was reported most often in ages over 65 (4.1%) and less often in ages 50-64 (1.4%). Similarly, the highest percentage of intubation was reported in adults over 65 years (2.5%), adults aged 50-64 reported intubation less than half as often (1.1%). Furthermore, death was reported infrequently across age groups but most often in adults over 65 years (11.5%).

Table 40: Comparing known severe outcomes across different age groups

		Age Group, years n (%)							**Total***	**X^2 p-value Pearson X^2**
		0-11 1,720 (row%)	12-17 1,702 (%)	18-29 4,433 (%)	30-39 3,799 (%)	40-49 3,050 (%)	50-64 3,438 (%)	65 + 1,922 (%)		
Hospitalized										
	Yes	8 (0.7)	6 (0.4)	90 (0.8)	92 (3.0)	131 (5.4)	268 (9.1)	402 (24.3)	997 (4.1)	2300.0
	No	1,193 (99.3)	1,344 (99.6)	11,564 (99.2)	2,981 (97.0)	2,281 (94.6)	2,676 (90.9)	1,256 (75.8)	23,295 (95.9)	<0.001
	Total	1,201	1,350	11,654	3,073	2,412	2,944	1,658	24,292	
ICU										
	Yes	2 (0.2)	0 (0.0)	6 (0.1)	10 (0.4)	15 (0.7)	35 (1.4)	63 (4.1)	131 (0.6)	404.7
	No	1,096 (99.8)	1,152 (100.0)	10,559 (99.9)	2,689 (99.6)	2,181 (99.3)	2,551 (98.7)	1,476 (95.9)	21,704 (99.4)	<0.001
	Total	1,098	1,152	10,565	2,699	2,196	2,586	1,539	21,835	
Intubated										
	Yes	0 (0.0)	0 (0.0)	4 (0.0)	2 (0.1)	13 (0.6)	29 (1.1)	38 (2.5)	86 (0.4)	256.7
	No	1,099 (100.0)	1,150 (100.0)	10,546 (100.0)	2,691 (99.9)	2,174 (99.4)	2,558 (98.9)	1,494 (97.5)	21,712 (99.6)	<0.001
	Total	1,099	1,150	10,550	2,693	2,187	2,587	1,532	21,798	
Death										
	Yes	1 (0.1)	0 (0.0)	2 (0.0)	9 (0.3)	14 (0.6)	62 (2.3)	191 (11.5)	279 (1.2)	1600.0
	No	1,134 (99.9)	1,190 (100.0)	10,792 (100.0)	2,808 (99.7)	2,282 (99.4)	2,642 (97.7)	1,469 (88.5)	22,317 (98.8)	<0.001
	Total	1,135	1,190	10,794	2,817	2,296	2,704	1,660	22,596	

3.4.3 Characteristics of those attending an indoor gathering <5 people

Demographics, University affiliation, and select risk factors were evaluated for association with having attended any small indoor gathering (≤5 people) in the 14 days prior to testing positive. Cases who reported attending an indoor gathering of <5 people were most often English speakers (2.7%), and white, non-Hispanic (3.2%) followed by Hispanics (1.2%). In terms of College Station versus Bryan, College Station residents most often reported attending these gatherings (2.8%). The only age groups who reported attending small indoor gatherings were ages 10-19 years (3.1%) and ages 20-29 years (3.1%).

Dormitory (9.9%) and apartment (5.5%) residence types were the most often reported by people attending these small gatherings. Employed individuals (2.3%) reported attending these gatherings slightly more often unemployed (3.6%). Cases who reported being a student or daycare attendee (4.8%) reported attending small gatherings more than those who were not (1.0%).

Few healthcare workers (1.2%) reported going to an indoor gathering of less than five people. Cases who knew their confirmed prior contact did not often report going to small gatherings (1.6%), though those who did not know their index case more often reported this (3.3%); respectively, these proportions were like those who knew they had close contact with a household member. The most known location of exposure was school or daycare (10.9%) and transit or rideshare (10.0%). A higher proportion (6.6%)

of those affiliated with the university reported going to an indoor gathering than those who were not (0.04%).

Table 41: Demographics of attending an indoor gathering of <5.

	Indoor gathering <5 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	20,423 (97.3)	564 (2.7)	20,987	22.7
Spanish	870 (99.9)	1 (0.1)	871	<0.001
Other	25 (100)	0 (0.0)	25	
Total	21,318	565	21,883	
Race/ethnicity				
White, non-Hispanic	11,878 (96.8)	390 (3.2)	12,268	177.4
Hispanic	9,024 (98.8)	111 (1.2)	9,135	<0.001
Black	2,423 (99.7)	8 (0.3)	2,431	
Asian	760 (94.3)	46 (5.7)	806	
other race	66 (98.5)	1 (1.5)	67	
Total	28,171 (97.8)	566 (2.3)	28,737	
BCS				
College Station	15,593 (97.2)	453 (2.8)	16,046	206.0
Bryan	13,050 (99.4)	75 (0.6)	13,125	<0.001
Total	28,643 (98.2)	528 (1.8)		
Age (years)				
0-9	1,319 (99.9)	1 (0.1)	1,320	291.9
10-19	5,594 (96.9)	178 (3.1)	5,772	<0.001
20-29	10,430 (96.9)	333 (3.1)	10,763	
30-39	3,784 (99.6)	15 (0.4)	3,799	
40-49	3,038 (99.6)	12 (0.4)	3,050	
50-59	2,492 (99.4)	14 (0.6)	2,506	
60-69	1,572 (99.5)	8 (0.5)	1,580	
70-79	807 (99.4)	5 (0.6)	812	
80-89	345 (100.0)	0 (0.0)	345	
90-99	115 (100.0)	0 (0.0	115	
Total	29,496 (98.1)	566 (1.9)	30,062	

Table 42: Exposure characteristics of attending an indoor gathering of <5.

	Indoor gathering <5 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Residence type				
House	19,848 (98.9)	217 (1.1)	20,065	659.4
Apartment	3,794 (94.5)	223 (5.5)	4,017	<0.001
Dormitory	1,074 (90.1)	118 (9.9)	1,192	
Supported living	111 (100.0)	0 (0.0)	111	
other	323 (98.2)	6 (1.8)	329	
Total	25,150 (97.8)	564 (2.2)	25,714	
Employed				
Yes	9,891 (97.7)	233 (2.3)	10,124	28.1
No	8,346 (96.4)	312 (3.6)	8,658	<0.001
Total	18,237 (97.1)	545 (2.9)	18,782	
Student or daycare attendee				
Yes	9,729 (95.2)	493 (4.8)	10,222	158.0
No	5,426 (99.0)	53 (1.0)	5,479	<0.001
Total	15,155 (96.5)	546 (3.5)	15,701	
Healthcare worker				
Yes	1,021 (98.8)	12 (1.2)	1, 033	8.3
No	20,018 (97.4)	535 (2.6)	20,553	0.004
Total	21,039 (97.5)	547 (2.5)	21,586	
Close contact with a case				
Yes	11,420 (98.2)	211 (1.8)	10,027	46.0
No	9,701 (96.8)	326 (3.3)	11,631	<0.001
Total	21,121 (97.5)	537 (2.5)	21,658	
Close contact with household				
Yes	3,347 (98.4)	53 (1.6)	3,400	44.1
No	2,043 (95.5)	97 (4.5)	2,140	<0.001
Total	5,390	150	5,540	
Location of exposure				
Household	2,029 (94.6)	116 (5.4)	2,145	12.2
Community	128 (92.8)	10 (7.3)	138	0.033
School or daycare	82 (89.1)	10 (10.9)	92	
Work	79 (91.9)	7 (8.1)	86	
Transit or rideshare	54 (90.0)	6 (10.0)	60	
Other	224 (90.7)	23 (9.3)		
Total	2,596 (93.8)	172 (6.2)		
Affiliated with the university				
Yes	7,878 (93.4)	559 (6.6)	21,689	1400
No	21,680 (99.9)	9 (0.04)	8,437	<0.001
Total	29,558 (98.1)	568 (1.9)	30,126	

3.4.4 Characteristics of those attending an indoor gathering of 5-10 people

The variable of if the case attended an indoor gathering of 5-10 was tested with demographics, select other exposure questions, and university affiliation. Individuals attending indoor gatherings of 5-10 mainly identified as English speakers (2.2%), other race (4.5%), Asian (4.1%), and White, non-Hispanic. College Station residents (2.5%) more often reported attending these gatherings than residents of Bryan (0.7%). The main age groups attending were ages 10-19 years (2.7%) and ages 20-29 years (2.8%).

Dormitory (7.9%) and apartment (4.8%) were the most common residence types reporting attending an indoor gathering of 5-10 people. There was a relatively even distribution of employed (2.0%) to unemployed (3.4%) attending these gatherings. Student or daycare attendees (4.3%) more often reported attending an indoor gathering of 5-10 people than those who were not a student or daycare attendee (1.3%).

A small percentage of healthcare workers (1.0%) reported going to these events. Those who knew their index case (1.9%) and it was a household member (1.6%) less often reported going to small indoor gatherings than those who did not report these exposures. Exposure locations where individuals also reported going to these gatherings were school or daycare (14.1%) and community (8.7%). Approximately 6% of those affiliated with the university reported going to an indoor gathering of 5-10 people

Table 43: Characteristics of those attending an indoor gathering of 5-10 people.

	Indoor gathering 5-10 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	20,470 (97.5)	517 (2.2)	20,987	11.5
Spanish	865 (99.3)	6 (0.7)	871	0.003
Other	24 (96.0)	1 (4.0)	25	
Total	21,539 (97.6)	524 (2.4)	21,883	
Race/ethnicity				
White, non-Hispanic	11,902 (97.0)	366 (3.0)	12,268	142.2
Hispanic	9,030 (98.9)	105 (1.2)	9,135	<0.001
Black	2,423 (99.7)	8 (0.3)	2,431	
Asian	773 (95.9)	33 (4.1)	806	
other race	64 (95.5)	3 (4.5)	67	
Total	24,192 (97.9)	515 (2.1)	24,707	
BCS				
College Station	15,638 (97.5)	408 (2.5)	16,046	148.4
Bryan	13,035 (99.3)	90 (0.69)	13,125	<0.001
Total	28,673 (98.3)	498 (1.7)	29,171	
Age (years)				
0-9	1,319 (99.9)	1 (0.1)	1,320	235.2
10-19	5,616 (97.3)	156 (2.7)	5,772	<0.001
20-29	10,460 (97.2)	303 (2.8)	10,763	
30-39	3,781 (99.5)	18 (0.5)	3,799	
40-49	3,032 (99.4)	18 (0.6)	3,050	
50-59	2,490 (99.4)	16 (0.6)	2,506	
60-69	1,574 (99.6)	6 (0.4)	1,580	
70-79	809 (99.6)	3 (0.4)	812	
80-89	344 (99.7)	1 (0.3)	345	
90-99	115 (100.0)	0 (0.0)	115	
Total	29,540	522	30,062	

Table 44: Risk characteristics of those who reported an indoor gathering of 5-10 people.

	Indoor gathering 5-10 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Residence type				
House	19,834 (98.9)	231 (1.2)	20,065	437.7
Apartment	3,825 (95.2)	192 (4.8)	4,017	<0.001
Dormitory	1,098 (92.1)	94 (7.9)	1,192	
Supported living	111 (100.0)	0 (0.0)	111	
other	323 (98.2)	6 (1.8)	329	
Total	25,191	523	25,714	
Employed				
Yes	9,920 (98.0)	204 (2.0)	8,658	35.0
No	8,363 (96.6)	295 (3.4)	10,124	<0.001
Total	18,283 (97.3)	499 (2.7)	18,782	
Student or daycare attendee				
Yes	9,779 (95.7)	443 (4.3)	5,479	106.9
No	5,410 (98.7)	69 (1.3)	10,222	<0.001
Total	15,189 (96.7)	512 (3.3)		
Healthcare worker				
Yes	1,023 (99.0)	10 (1.0)	1,033	9.1
No	20,053 (97.6)	500 (2.4)	20,553	0.002
Total	21,076 (97.6)	510 (2.4)	21,586	
Close contact with a case				
Yes	11,415 (98.1)	216 (1.9)	11,631	19.8
No	9,750 (97.2)	277 (2.8)	10,027	<0.001
Total	21,165 (97.7)	493 (2.3)	21,658	
Close contact with household				
Yes	3,345 (98.4)	55 (1.6)	3,400	67.1
No	2,021 (94.4)	119 (5.6)	2,140	<0.001
Total	5,366 (96.9)	174 (3.1)	5,540	
Location of exposure				
Household	2,035 (94.9)	110 (5.1)	2,145	17.9
Community	126 (91.3)	12 (8.7)	138	0.003
School or daycare	79 (85.9)	13 (14.1)	92	
Work	84 (97.7)	2 (2.3)	86	
Transit or rideshare	56 (93.3)	4 (6.7)	60	
Other	232 (93.9)	15 (6.1)	247	
Total	2,612 (94.4)	156 (5.6)	2,768	
Affiliated with the university				
Yes	7,931 (94.0)	506 (6.0)	8,437	1200
No	21,670 (99.9)	19 (0.1)	21,689	<0.001
Total	29,601 (98.3)	525 (1.7)		

3.4.5 Characteristics of people who reported travel in past 14 days

The variable of if the case traveled in the past 14 days was tested with demographics, other select exposure questions, and university affiliation. Travelers were most often English speakers (21%), white, non-Hispanic (25.4%) and Asian (25.4%). In terms of College Station to Bryan residents, College Station residents (23.9%) reported traveling more often than those in Bryan (13.9%). Ages 20-29 years (25.2%) were the main age group reporting travel closely followed by ages 10-19 years (20.1%).

Residence type reported by cases traveling were apartment (27.6%), dormitory (24.3%), other (18.3%), and house (18.2%). Employed cases (22.8%) reported travel more commonly than unemployed (18.9%). Approximately a quarter of cases who identified as being a student or daycare attendee reported travel (24.8%). Cases who knew their index case (17.9%) and they had close contact with a household member (16.1%) less often reported traveling than those who did not. Transit or rideshare was the most frequently cited location of exposure (36.4%). Work (25.9%), household (22.6%), and community (22.4%) were other specific locations of exposure mentioned among those who reported travel. When comparing travel to university affiliation, about a quarter of those reporting travel in the 14 days prior to test date also reported university affiliation (27.6%).

Table 45: Characteristics of cases reporting travel in the 14 days prior to test date or symptom onset.

	Travel n (%)		Total	X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	13,086 (79.0)	3,482 (21.0)	16,568	63.9
Spanish	716 (90.4)	76 (9.6)	792	<0.001
Other	13 (100.0)	0 (0.0)	13	
Total	13,815 (79.5)	3,558 (20.5)	17,373	
Race/ethnicity				
White, non-Hispanic	7,027 (74.6)	2,396 (25.4)	9,423	263.6
Hispanic	5,253 (84.2)	985 (15.8)	6,238	<0.001
Black	1,422 (85.6)	240 (14.4)	1,662	
Asian	490 (74.6)	167 (25.4)	657	
other race	36 (80.0)	9 (20.0)	45	
Total	14,228 (78.9)	3,797 (21.1)	18,025	
BCS				
College Station	8,674 (76.1)	2,723 (23.9)	11,397	312.8
Bryan	7,414 (86.1)	1,194 (13.9)	8,608	<0.001
Total	16,088 (80.4)	3,917 (19.6)	20,005	
Age (years)				
0-9	716 (92.6)	57 (7.4)	773	337.5
10-19	3,196 (79.9)	804 (20.1)	4,000	<0.001
20-29	5,624 (74.8)	1,896 (25.2)	7,520	
30-39	2,053 (83.6)	402 (16.4)	2,455	
40-49	1,722 (84.9)	307 (15.1)	2,029	
50-59	1,425 (83.0)	293 (17.1)	1,718	
60-69	920 (81.4)	210 (18.6)	1,130	
70-79	520 (85.8)	86 (14.2)	606	
80-89	255 (95.5)	12 (4.5)	267	
90-99	91 (96.8)	3 (3.2)	94	
Total	16,522 (80.2)	4,070 (19.8)	20,592	

Table 46: Risk characteristics compared to traveling in the 14 days prior to test date or symptom onset.

	Travel n (%)		Total	X^2 p-value
	No (row %)	Yes (row %)		Pearson X^2
Residence type				
House	12,331 (81.8)	2,738 (18.2)	15,069	184.4
Apartment	2,501 (72.4)	953 (27.6)	3,454	<0.001
Dormitory	806 (75.7)	259 (24.3)	1,065	
Supported living	81 (97.6)	2 (2.4)	83	
other	224 (81.8)	50 (18.3)	274	
Total	15,943 (79.9)	4,002 (20.1)	19,945	
Employed				
Yes	7,261 (77.2)	2,139 (22.8)	9,400	37.9
No	6,319 (81.1)	1,474 (18.9)	7,793	<0.001
Total	13,580 (79.0)	3,613 (21.0)	17,193	
Student or daycare attendee				
Yes	6,528 (75.2)	2,150 (24.8)	8,678	46.2
No	4,110 (80.3)	1,011 (19.7)	5,121	<0.001
Total	10,638 (77.1)	3,161 (22.9)	13,799	
Healthcare worker				
Yes	788 (83.0)	162 (17.1)	950	5.4
No	15,153 (79.9)	3,819 (20.1)	18,972	0.021
Total	15,941 (80.0)	3,981 (20.0)	19,922	
Close contact with a case				
Yes	8,422 (82.1)	1,840 (17.9)	10,262	26.1
No	7,301 (79.2)	1,920 (20.8)	9,221	<0.001
Total	15,723 (80.7)	3,760 (19.3)	19,483	
Close contact with household				
Yes	2,644 (83.9)	506 (16.1)	3,150	88.8
No	1,517 (73.2)	555 (26.8)	2,072	<0.001
Total	4,161 (79.7)	1,061 (20.3)	5,222	
Location of exposure				
Household	1,523 (77.4)	444 (22.6)	1,967	18.8
Community	97 (77.6)	28 (22.4)	125	0.002
School or daycare	79 (86.8)	12 (13.2)	91	
Work	60 (74.1)	21 (25.9)	81	
Transit or rideshare	35 (63.6)	20 (36.4)	55	
Other	164 (69.2)	73 (30.8)	237	
Total	1,958 (76.6)	598 (23.4)	2,556	
Affiliated with the university				
Yes	5,337 (72.4)	2,039 (27.6)	7,376	450.1
No	11,210 (84.6)	2,036 (15.4)	13,246	<0.001
Total	16,547 (80.2)	4,075 (19.8)	20,622	

3.4.6 Characteristics of hospitalized cases.

Hospitalization and bivariate analysis were done for demographics, medical history, and a few risk factor questions (flu shot status and smoking status). Those with significant relationships are presented below.

Other language speakers (11.8%) and Spanish speakers (6.6%) were hospitalized more than English speakers (3.8%). Black or African American cases (10.1%) were hospitalized more than any other race or ethnicity. When comparing Bryan cases to those in College Station, the percentage of Bryan cases hospitalized (6.4%) was nearly three times higher than those of College Station (2.4%). Children represented a small proportion of hospitalizations at less than 1% per child/adolescent age group. The most common ages hospitalized were elderly, namely, ages 80-89 years (35.1%) and 90-99 years (43.4%). The most common residence type for hospitalized cases was supported living (39.8%). There were more unemployed cases (6.2%) reporting hospitalization than employed (3.0%). Student or daycare attendees were also infrequently reported among hospitalizations (0.3%).

A small proportion of pregnant women reported hospitalization because of COVID-19 (10.0%). The least common comorbid condition among hospitalizations was childhood asthma (1.5%). Other comorbidities reported among hospitalizations were renal disease (40.8%), cardiovascular disease (34.0%), liver disease (22.9%), diabetes (22.6%), hypertension (20.4%), and immunocompromised (13.1%). A small proportion of current/former smokers (8.1%) and people with a flu shot in the past year (2.9%) were also hospitalized.

Table 47: Characteristics of hospitalized cases.

	Hospitalized n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	17,639 (96.2)	694 (3.8)	18,333	19.7
Spanish	776 (93.4)	55 (6.6)	831	<0.001
Other	15 (88.2)	2 (11.8)	17	
Total	18,430 (96.1)	751 (3.9)	19,181	
Race/ethnicity				
White, non-Hispanic	10,325 (96.9)	336 (3.2)	10,661	210.0
Hispanic	7,236 (95.3)	357 (4.7)	7,593	<0.001
Black	1,849 (89.9)	208 (10.1)	2,057	
Asian	698 (97.4)	19 (2.7)	717	
other race	54 (100.0)	0 (0.0)	54	
Total	20,162 (95.6)	920 (4.4)	21,082	
BCS				
College Station	12,816 (97.6)	316 (2.4)	13,132	231.0
Bryan	9,871 (93.6)	673 (6.4)	10,544	<0.001
Total	22,687 (95.8)	989 (4.2)	23,676	
Age (years)				
0-9	927 (99.3)	7 (0.8)	934	2600
10-19	4,652 (99.6)	19 (0.4)	4,671	<0.001
20-29	8,522 (99.1)	78 (0.9)	8,600	
30-39	2,981 (97.0)	92 (3.0)	3,073	
40-49	2,281 (94.6)	131 (5.4)	2,412	
50-59	1,956 (91.6)	179 (8.4)	2,135	
60-69	1,177 (86.7)	180 (13.3)	1,357	
70-79	544 (77.3)	160 (22.7)	704	
80-89	198 (64.9)	107 (35.1)	305	
90-99	56 (56.6)	43 (43.4)	99	
Total	23,294 (95.9)	996 (4.1)	24,290	
Residence type				
House	16,595 (95.5)	780 (4.5)	17,375	445.0
Apartment	3,535 (98.0)	74 (2.1)	3,609	<0.001
Dormitory	1,067 (99.9)	1 (0.1)	1,068	
Supported living	65 (60.2)	43 (39.8)	108	
Other	277 (93.6)	19 (6.4)	296	
Total	21,539 (95.9)	917 (4.1)	22,456	

Table 47 continued: Characteristics of hospitalized cases.

	Hospitalized n(%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Employment				
Yes	9,403 (97.0)	290 (3.0)	9,693	106.1
No	7,594 (93.8)	501 (6.2)	8,095	<0.001
Total	16,997 (95.6)	791 (4.5)	17,788	
Student or Daycare				
Yes	9,054 (99.7)	31 (0.3)	9,085	657.7
No	4,827 (91.8)	430 (8.2)	5,257	<0.001
Total	13,881 (96.8)	461 (3.2)	14,342	

Table 48: Risk characteristics of hospitalized cases

	Hospitalized n (%)			X^2
	No (row %)	Yes (row %)	Total	p-value Pearson X^2
Pregnant				
Yes	206 (90.0)	23 (10.0)	229	16.1
No	12,400 (95.5)	579 (4.5)	12,979	<0.001
Total	12,606 (95.4)	602 (4.6)	13,208	
Diabetes				
Yes	1,067 (77.4)	311 (22.6)	1,378	1000
No	14,637 (96.9)	475 (3.1)	15,112	<0.001
Total	15,704 (95.2)	786 (4.8)	16,490	
Cardiovascular disease				
Yes	431 (66.0)	222 (34.0)	653	1300
No	15,177 (96.5)	548 (3.5)	15,725	<0.001
Total	15,608 (95.3)	770 (4.7)	16,378	
Hypertension				
Yes	1,885 (79.6)	484 (20.4)	2,369	1400
No	13,993 (97.6)	344 (2.4)	14,337	<0.001
Total	15,878 (95.0)	828 (5.0)	16,706	
Renal disease				
Yes	189 (59.3)	130 (40.8)	319	965.7
No	15,381 (96.1)	623 (3.9)	16,004	<0.001
Total	(95.4)15,570	753 (4.6)	16,323	
Liver disease				
Yes	54 (77.1)	16 (22.9)	70	56.4
No	15,476 (95.7)	704 (4.4)	16,180	<0.001
Total	15,530 (95.6)	720 (4.4)	16,250	
Immunocompromised				
Yes	266 (86.9)	40 (13.1)	306	54.1
No	15,284 (95.7)	687 (4.3)	15,971	<0.001
Total	15,550 (95.5)	727 (4.5)	16,277	
Childhood asthma				
Yes	913 (98.5)	14 (1.5)	927	19.7
No	14,503 (95.4)	698 (4.6)	15,201	<0.001
Total	15,416 (95.6)	712 (4.4)	16,128	
Smoking status				
Current/former smoker	1,847 (91.9)	162 (8.1)	2,009	119.1
Never smoked	14,760 (96.8)	481 (3.2)	15,241	<0.001
Total	16,607 (96.3)	643 (3.7)	17,250	
Flu shot status				
Yes	6,134 (97.1)	185 (2.9)	6,319	17.3
No	7,643 (98.1)	145 (1.9)	7,788	<0.001
Total	13,777 (97.7)	330 (2.3)	14,107	

3.4.7 Characteristics of cases going to an ICU

Demographics, medical history, and select risk factor questions (flu shot status and smoking status) were characteristics of cases going to an ICU presented. Black or African American cases (1.8%) was the most common race/ethnicity going to an ICU. When comparing cases residing in Bryan versus College Station, there were more ICU cases in Bryan (0.9%). The most common ages who reported going to an ICU were ages 70-79 years (3.3%), 80-89 years (6.1%), and 90-99 years (8.7%). Supported living (9.3%) was the most frequently reported residence type for cases going to an ICU. Very few of cases going to an ICU were employed (0.3%) or a student/daycare attendee (0.1%).

Renal disease (6.8%) and cardiovascular disease (6.2%) were the most common pre-existing condition in cases who went to an ICU. Other comorbidities reported in cases who went to an ICU were diabetes (4.4%), hypertension (3.0%), and immunocompromised conditions (2.1%). A small proportion of current/former smokers (0.8%) also reported going to an ICU.

Table 49: Characteristics of cases going to an ICU.

	ICU n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	17,467 (99.5)	89 (0.5)	17,556	10.8
Spanish	803 (99.6)	3 (0.4)	806	0.005
Other	15 (93.8)	1 (6.3)	16	
Total	18,285 (99.5)	93 (0.5)	18,378	
Race/ethnicity				
White, non-Hispanic	9,766 (99.6)	41 (0.4)	9,807	53.7
Hispanic	6,574 (99.3)	47 (0.7)	6,621	<0.001
Black	1,827 (98.2)	34 (1.8)	1,861	
Asian	664 (100.0)	0 (0.0)	664	
other race	48 (100.0)	0 (0.0)	48	
Total	18,879 (99.4)	122 (0.6)	19,001	
BCS				
College Station	12,002 (99.7)	42 (0.4)	12,044	30.4
Bryan	9,166 (99.1)	87 (0.9)	9,253	<0.001
Total	21,168 (99.4)	129 (0.6)	21,297	
Age (years)				
0-9	847 (99.9)	1 (0.1)	848	479.2
10-19	4,135 (99.9)	2 (0.1)	4,137	<0.001
20-29	7,825 (99.9)	5 (0.1)	7,830	
30-39	2,689 (99.6)	10 (0.4)	2,699	
40-49	2,181 (99.3)	15 (0.7)	2,196	
50-59	1,852 (99.0)	19 (1.0)	1,871	
60-69	1,189 (97.4)	32 (2.6)	1,221	
70-79	639 (96.7)	22 (3.3)	661	
80-89	261 (93.9)	17 (6.1)	278	
90-99	84 (91.3)	8 (8.7)	92	
Total	21,702 (99.4)	131 (0.6)	21,833	
Residence type				
House	16,309 (99.4)	96 (0.6)	16,405	142.9
Apartment	3,370 (99.7)	10 (0.3)	3,380	<0.001
Dormitory	1,023 (99.9)	1 (0.1)	1,024	
Supported living	88 (90.7)	9 (9.3)	97	
Other	282 (99.7)	1 (0.4)	283	
Total	21,072 (99.5)	117 (0.6)	21,189	

Table 49 continued: Characteristics of cases going to an ICU

	ICU n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Employment				
Yes	9,334 (99.7)	28 (0.3)	9,362	38.8
No	7,601 (98.9)	82 (1.1)	7,683	<0.001
Total	16,935 (99.4)	110 (0.7)	17,045	
Student or Daycare				
Yes	8,634 (99.9)	4 (0.1)	8,638	101.3
No	4,981 (98.7)	67 (1.3)	5,048	<0.001
Total	13,615 (99.5)	71 (0.5)	13,686	

Table 50: Risk characteristics of cases going to an ICU.

	ICU n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Diabetes				
Yes	1,257 (95.6)	58 (4.4)	1,315	294.7
No	14,485 (99.7)	50 (0.3)	14,535	<0.001
Total	15,742 (99.3)	108 (0.7)	15,850	
Cardiovascular disease				
Yes	571 (93.8)	38 (6.2)	609	304.0
No	15,068 (99.6)	65 (0.4)	15,133	<0.001
Total	15,639 (99.4)	103 (0.7)	15,742	
Hypertension				
Yes	2,190 (97.0)	67 (3.0)	2,257	207.2
No	13,761 (99.7)	41 (0.3)	13,802	<0.001
Total	15,951 (99.3)	108 (0.7)	16,059	
Renal disease				
Yes	275 (93.2)	20 (6.8)	295	176.9
No	15,311 (99.5)	81 (0.5)	15,392	<0.001
Total	15,586 (99.4)	101 (0.6)	15,687	
Immunocompromised				
Yes	284 (97.9)	6 (2.1)	290	9.3
No	15,268 (99.4)	95 (0.6)	15,363	0.002
Total	15,552 (99.4)	101 (0.7)	15,653	
Childhood asthma				
Yes	865 (100.0)	0 (0.0)	865	5.9
No	14,536 (99.3)	99 (0.7)	14,635	0.015
Total	15,401 (99.4)	99 (0.6)	15,500	
Smoking status				
Current/former smoker	1,910 (99.2)	16 (0.8)	1,926	10.3
Never smoked	14,609 (99.7)	50 (0.3)	14,659	0.001
Total	16,519 (99.6)	66 (0.4)	16,585	

3.4.8 Characteristics of cases going to an ER

Demographics, medical history, and select risk factor question (flu shot status and smoking status) characteristics of cases going to an ER were analyzed through bivariate analysis. Those with significant relationships are presented here. Demographics and going to an ER held no statistically significant relationship.

Comorbidities of cardiovascular disease (4.9%), renal disease (5.9%), and hypertension (3.6%) were reported by cases going to an ER. Additionally, cases who reported a flu shot in the prior year (2.4%) more often reported going to an ER than those who had not had a flu shot (2.1%).

Table 51: Risk characteristics for cases who went to an ER.

	ER n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Cardiovascular disease				
Yes	307 (95.1)	16 (4.9)	323	8.7
No	11,376 (97.6)	277 (2.4)	11,653	0.003
Total	11,683 (97.6)	293 (2.4)	11,976	
Hypertension				
Yes	1,397 (96.4)	52 (3.6)	1,449	9.8
No	10,494 (97.8)	241 (2.2)	10,735	0.002
Total	11,891 (97.6)	293 (2.4)	12,184	
Renal disease				
Yes	128 (94.1)	8 (5.9)	136	6.9
No	11,526 (97.6)	283 (2.4)	11,809	0.009
Total	11,654 (97.6)	291 (2.4)	11,945	
Flu shot status				
Yes	4,627 (96.6)	164 (3.4)	4,791	17.5
No	5,688 (97.9)	122 (2.1)	5,810	<0.001
Total	10,315 (97.3)	286 (2.7)	10,601	

3.4.9 Characteristics for cases with severe COVID-19

Characteristics for cases with severe COVID-19 (combined hospitalization or ICU or intubation or death) were looked at through bivariate analysis. The most common race/ethnicity reported for cases with severe COVID was Black or African American (1.3%). When comparing those living in Bryan versus College Station, Bryan residents more often reported severe COVID (0.8%). Cases 19 years and under did not report severe COVID. It was rarely reported in middle-aged adults such as ages 30-39 (0.2%) and most reported in ages 80-89 years5.0%) and 90-99 years (8.2%). The residence type cases with severe COVID most often reported was in a supported living facility (7.3%). Only 1 case with severe COVID reported being a student/daycare attendee but those who did not identify as a student/daycare attendee (1.0%) reported severe COVID more often. Employment (0.1%) and unemployment (0.7%) were not regularly reported among severe COVID cases.

The most common comorbidities reported among severe COVID cases were renal disease (4.6%) and cardiovascular disease (4.2%). Less frequently reported were diabetes (3.1%), liver disease (2.9%), and hypertension (2.5%). Current or former smokers (0.4%) were identified in severe COVID cases slightly more often than cases who never smoked (0.2%).

Table 52: Characteristics of severe COVID-19 cases.

	Severe COVID-19 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Language				
English	18,782 (99.6)	72 (0.4)	18,854	11.8
Spanish	834 (99.5)	4 (0.5)	838	0.003
Other	18 (94.7)	1 (5.3)	19	
Total	19,634 (99.6)	77 (0.4)	19,711	
Race/ethnicity				
White, non-Hispanic	10,830 (99.7)	37 (0.3)	10,867	33.7
Hispanic	7,707 (99.5)	36 (0.5)	7,743	<0.001
Black	2,092 (98.7)	27 (1.3)	2,119	
Asian	723 (99.7)	2 (0.3)	725	
other race	56 (100.0)	0 (0.0)	56	
Total	21,408 (99.5)	102 (0.5)	21,510	
BCS				
College Station	13,503 (99.8)	25 (0.2)	13,528	49.0
Bryan	10,770 (99.2)	86 (0.8)	10,856	<0.001
Total	24,273 (99.5)	111 (0.5)	24,384	
Age (years)				
0-9	960 (100.0)	0 (0.0)	960	539.1
10-19	4,828 (100.0)	0 (0.0)	4,828	<0.001
20-29	8,859 (99.9)	4 (0.1)	8,863	
30-39	3,149 (99.8)	7 (0.2)	3,156	
40-49	2,473 (99.6)	10 (0.4)	2,483	
50-59	2,179 (99.3)	16 (0.7)	2,195	
60-69	1,370 (97.9)	30 (2.1)	1,400	
70-79	707 (97.3)	20 (2.8)	727	
80-89	305 (95.0)	16 (5.0)	321	
90-99	101 (91.8)	9 (8.2)	110	
Total	24,931 (99.6)	112 (0.5)	25,043	
Residence type				
House	17,757 (99.6)	81 (0.5)	17,838	147.0
Apartment	3,659 (99.9)	3 (0.1)	3,662	<0.001
Dormitory	1,125 (100.0)	0 (0.0)	1,125	
Supported living	102 (92.7)	8 (7.3)	110	
Other	300 (100.0)	0 (0.0)	300	
Total	22,943 (99.6)	92 (0.4)	23,035	

Table 52 continued: Characteristics of severe COVID-19 cases

	Severe COVID-19 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Employment				
Yes	9,785 (99.9)	15 (0.1)	9,800	35.8
No	8,169 (99.3)	60 (0.7)	8,229	<0.001
Total	17,954 (99.6)	75 (0.4)	18,029	
Student or Daycare				
Yes	9,280 (99.9)	1 (0.0)	9,281	87.0
No	5,290 (99.0)	52 (1.0)	5,342	<0.001
Total	14,570 (99.6)	53 (0.4)	14,623	

Table 53: Risk characteristics of severe COVID-19 cases

	Severe COVID-19 n (%)			X^2
	No (row %)	Yes (row %)	Total	p-value Pearson X^2
Diabetes				
Yes	1,355 (96.9)	43 (3.1)	1,398	218.7
No	15,218 (99.8)	36 (0.2)	15,254	<0.001
Total	16,573 (99.5)	79 (0.5)	16,652	
Cardiovascular disease				
Yes	636 (95.8)	28 (4.2)	664	220.7
No	15,829 (99.7)	46 (0.3)	15,875	<0.001
Total	16,465 (99.6)	74 (0.5)	16,539	
Hypertension				
Yes	2,347 (97.5)	60 (2.5)	2,407	229.5
No	14,439 (99.8)	23 (0.2)	14,462	<0.001
Total	16,786 (99.5)	83 (0.5)	16,869	
Renal disease				
Yes	313 (95.4)	15 (4.6)	328	127.4
No	16,096 (99.6)	59 (0.4)	16,155	<0.001
Total	16,409 (99.6)	74 (0.5)	16,483	
Liver disease				
Yes	68 (97.1)	2 (2.9)	70	9.8
No	16,273 (99.6)	68 (0.4)	16,341	0.002
Total	16,341 (99.6)	70 (0.4)	16,411	
Smoking status				
Current/former smoker	2,019 (99.6)	9 (0.4)	2,028	6.7
Never smoked	15,315 (99.8)	26 (0.2)	15,341	0.01
Total	17,334 (99.8)	35 (0.2)	17,369	

3.4.10 Characteristics of cases who died from COVID-19

Demographics, medical history, and select risk factor questions were analyzed as characteristics of cases who died from COVID-19. There was a similar proportion of female (1.1%) to male (1.4%) cases who died from COVID-19. Black or African Americans cases (3.1%) were the primary race/ethnicity who were reported of dying of COVID-19. When comparing cases residing in Bryan to those residing in College Station, cases in Bryan were more often reported as dying (2.1%). Adults 70-79 years (9.8%) and 90-99 years (29.0%) were the most common ages reported dying of COVID-19. Cases who were reported to reside in supported living were the most common residence type to report dying of COVID-19. Unemployed cases (2.5%) and cases who did not identify as student/daycare attendees (2.9%) were more often reported as dying from COVID than those who did report employment and student/daycare attendance.

Renal disease (16.6%) and cardiovascular disease (14.2%) were the comorbidities reported most often in cases who died of COVID-19. Other comorbidities identified were liver disease (10.0%), diabetes (8.7%), immunocompromised (3.8%), and childhood asthma (0.1%). Current and former smokers (1.8%) were often reported of dying to COVID-19 than those who had never smoked (0.7%). A small percentage of cases who had a flu shot in the past year reported dying of COVID-19 (0.5%).

Table 54: Characteristics for cases who died of COVID-19.

	Dying of COVID-19 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Sex				
Female	11,875 (98.9)	131 (1.1)	12,006	4.8
Male	10,447 (98.6)	150 (1.4)	10,597	0.028
Total	22,322 (98.8)	281 (1.2)	22,603	
Race/ethnicity				
White, non-Hispanic	9,720 (98.7)	124 (1.3)	9,844	59.2
Hispanic	6,740 (98.9)	72 (1.1)	6,812	<0.001
Black	1,894 (96.9)	61 (3.1)	1,955	
Asian	647 (99.9)	1 (0.1)	648	
other race	49 (100.0)	0 (0.0)	49	
Total	19,050 (98.7)	258 (1.3)	19,308	
BCS				
College Station	12,196 (99.4)	77 (0.6)	12,273	92.5
Bryan	9,552 (97.9)	204 (2.1)	9,756	<0.001
Total	21,748 (98.7)	281 (1.3)	22,029	
Age (years)				
0-9	875 (99.9)	1 (0.1)	876	2100
10-19	4,214 (100.0)	0 (0.0)	4,214	<0.001
20-29	8,027 (99.9)	2 (0.02)	8,029	
30-39	2,808 (99.7)	9 (0.3)	2,817	
40-49	2,282 (99.4)	14 (0.6)	2,296	
50-59	1,916 (98.1)	38 (1.9)	1,954	
60-69	1,231 (95.4)	59 (4.6)	1,290	
70-79	628 (90.2)	68 (9.8)	696	
80-89	259 (82.2)	56 (17.8)	315	
90-99	76 (71.0)	31 (29.0)	107	
Total	22,316 (98.8)	278 (1.2)	22,594	
Residence type				
House	16,747 (98.9)	187 (1.1)	16,934	737.8
Apartment	3,338 (99.8)	8 (0.2)	3,346	<0.001
Dormitory	1,019 (100.0)	0 (0.0)	1,019	
Supported living	78 (72.9)	29 (27.1)	107	
Other	292 (99.3)	2 (0.7)	294	
Total	21,474 (99.0)	226 (1.0)	21,700	

Table 54 continued: Characteristics for cases who died of COVID-19.

	Dying of COVID-19 n (%)			
	No (row %)	Yes (row %)	Total	X^2 p-value Pearson X^2
Employment				
Yes	9,391 (99.7)	29 (0.3)	9,420	158.0
No	7,537 (97.5)	192 (2.5)	7,729	<0.001
Total	16,928 (98.7)	221 (1.3)	17,149	
Student or Daycare				
Yes	8,542 (100.0)	0 (0.0)	8,542	250.3
No	5,060 (97.1)	151 (2.9)	5,211	<0.001
Total	13,602 (98.9)	151 (1.1)	13,753	

Table 55: Risk characteristics of cases who died of COVID-19.

	Dying of COVID-19 n (%)			X^2 p-value
	No (row %)	Yes (row %)	Total	Pearson X^2
Diabetes				
Yes	1,245 (91.3)	118 (8.7)	1,363	564.4
No	14,365 (99.3)	105 (0.7)	14,470	<0.001
Total	15,610 (98.6)	223 (1.4)	15,833	
Cardiovascular disease				
Yes	554 (85.8)	92 (14.2)	646	837.5
No	14,961 (99.2)	121 (0.8)	15,082	<0.001
Total	15,515 (98.7)	213 (1.4)	15,728	
Hypertension				
Yes	2,172 (93.3)	156 (6.7)	2,328	556.6
No	13,646 (99.5)	68 (0.5)	13,714	<0.001
Total	15,818 (98.6)	224 (1.4)	16,042	
Renal disease				
Yes	262 (83.4)	52 (16.6)	314	583.7
No	15,200 (99.0)	151 (1.0)	15,351	<0.001
Total	15,462 (98.7)	203 (1.3)	15,665	
Liver disease				
Yes	63 (90.0)	7 (10.0)	70	43.9
No	15,344 (98.8)	187 (1.2)	15,531	<0.001
Total	15,407 (98.8)	194 (1.2)	15,601	
Immunocompromised				
Yes	281 (96.2)	11 (3.8)	292	15.5
No	15,155 (98.8)	183 (1.2)	15,338	<0.001
Total	15,436 (98.8)	194 (1.2)	15,630	
Childhood asthma				
Yes	830 (99.9)	1 (0.1)	831	8.8
No	14,456 (98.7)	188 (1.3)	14,644	0.003
Total	15,286 (98.8)	189 (1.2)	15,475	
Smoking status				
Current/former smoker	1,917 (98.2)	36 (1.8)	1,953	29.1
Never smoked	14,406 (99.3)	98 (0.7)	14,504	<0.001
Total	16,323 (99.2)	134 (0.8)	16,457	
Flu shot status				
Yes	5,944 (99.5)	33 (0.5)	5,977	5.1
No	7,334 (99.7)	22 (0.3)	7,356	0.023
Total	13,278 (99.6)	55 (0.4)	13,333	

3.4.11 Factors with odds of attending an indoor gathering (<5 people)

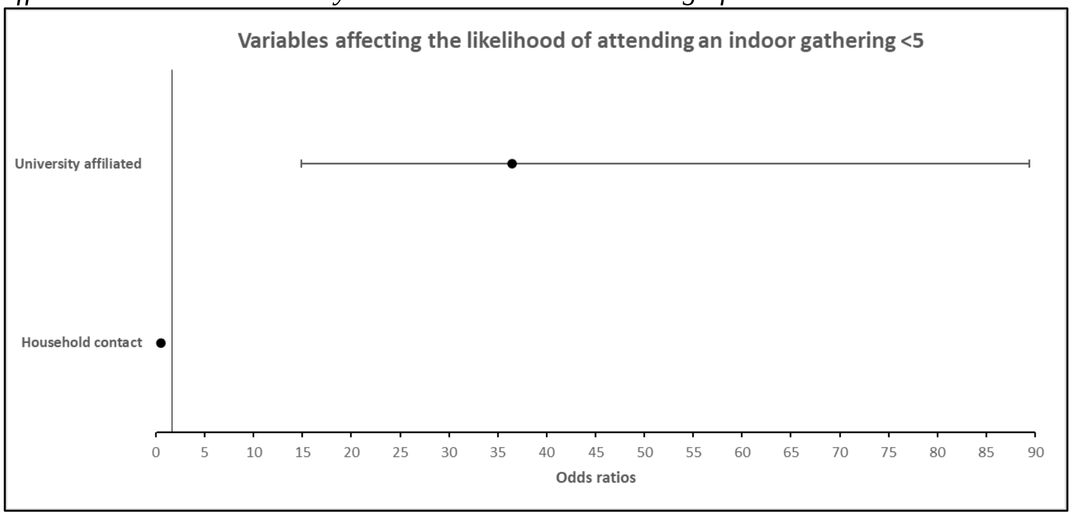
To evaluate the effect of specific factors on if an individual attended an indoor gathering of less than 5 people in 14 days prior to infection, multivariate regression was done. Variables with a p-value of <0.05 in bivariate analysis were language, race/ethnicity, age, College Station versus Bryan, employment status, residence type, student or daycare attendee, healthcare worker, known close contact, household close contact, location of exposure, and if affiliated with the university. Variables kept in the final model were having a household close contact and affiliation with the University.

Regression revealed household close contacts made individuals less likely to attend an indoor gathering of <5 people (OR: 0.5, p=0.001, 95% CI: [0.4-0.8]). Cases who reported affiliation with the university had significantly higher odds of attending these small gatherings (<5 people) than those who were not affiliated with the university (OR: 36.5, p<0.001, 95% CI: [14.9-89.4]).

Table 56: Manual logistic regression for attending an indoor gathering of less than 5 people. Variables included in the model were language, race/ethnicity, age, living in College Station versus Bryan, employment status, residence type, student or daycare status, healthcare worker, known contact with a confirmed case, household close contact, location of exposure, and affiliation with the University. There were 5,540 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Household contact	0.5	0.001	[0.4-0.8]
University affiliated	36.5	p<0.001	[14.9-89.4]

Figure 18: Variables affecting the likelihood of attending an indoor gathering <5 people. Variables included in the model were language, race/ethnicity, age, living in College Station versus Bryan, employment status, residence type, student or daycare status, healthcare worker, known contact with a confirmed case, household close contact, location of exposure, and affiliation with the University. Variables with statistical significance are noted with an asterisk.



3.4.12 Factors with odds of attending an indoor gathering (5-10 people)

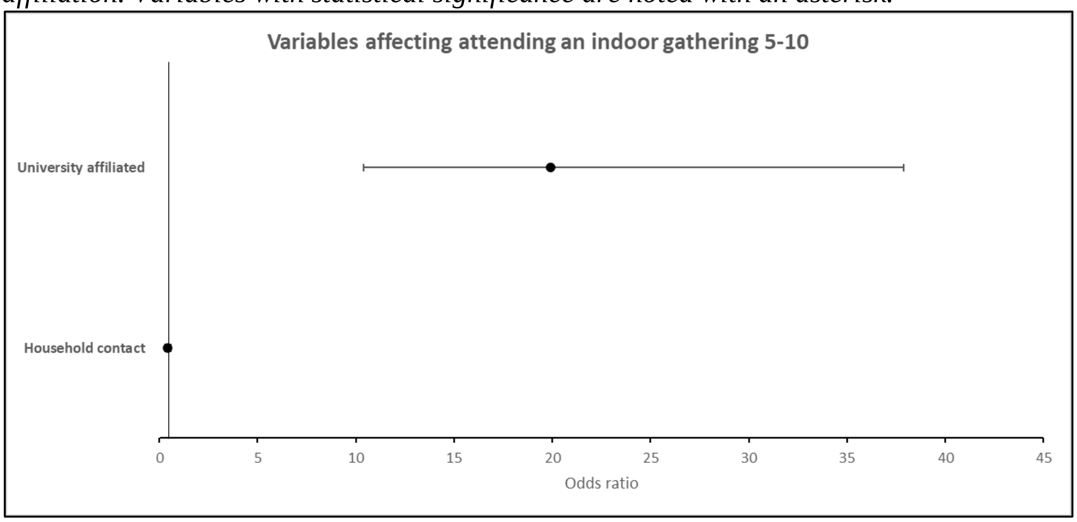
To assess the effect factors on whether a case attended an indoor gathering of 5-10 people in the 14 days prior to illness, multivariate regression was run. Variables identified through bivariate analysis ($p<0.05$) were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment status, student or daycare attendee, healthcare worker status, close contact with a laboratory confirmed case, close contact with a household member, location of exposure, and university affiliation.

Backwards stepwise regression identified cases with a household close contact as having odds less likely to attend an indoor gathering of 5-10 people (OR: 0.4, $p<0.001$, 95% CI: [0.3-0.6]). Cases with university affiliation had higher odds of attending a small gathering of 5-10 people (OR: 19.9, p<0.001, 95% CI: [10.4-37.9]).

Table 57: Manual logistic regression with the outcome of attending an indoor gathering of 5-10 people. Variables included in the model were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment status, student or daycare status, healthcare worker status, known close contact with a case, close contact with a household member, location of exposure, and University affiliation. There were 5,540 people included in the model.

Variable	OR	p-value	95% CI
Household contact	0.4	p<0.001	[0.3-0.6]
University affiliated	19.9	p<0.001	[10.4-37.9]

Figure 19: Likelihood of attending an indoor gathering of 5-10 people. Variables included in the model were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment status, student or daycare status, healthcare worker status, known close contact with a case, close contact with a household member, location of exposure, and University affiliation. Variables with statistical significance are noted with an asterisk.



3.4.13 Factors with odds of traveling in 14 days before test date or symptom onset

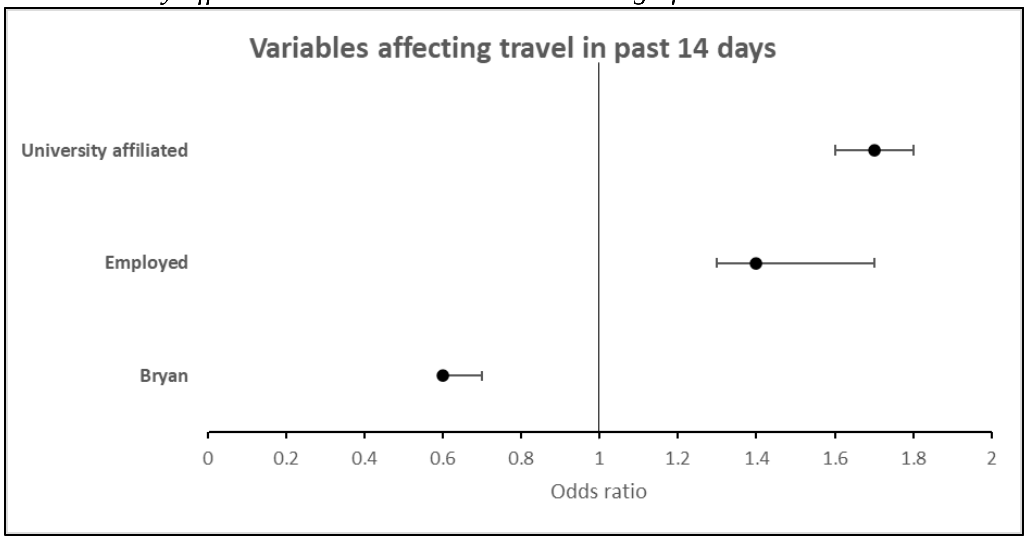
To determine the effect individual factors had on traveling in the 14 days prior to test date or symptom onset, multivariate regression was conducted. Variables pinpointed from bivariate analysis ($p<0.05$) were language, race/ethnicity, living in College Station compared to Bryan, age, residence type, employment, student/daycare attendee, healthcare worker, close contact with a case, close contact with household, location of exposure, and university affiliation. The only variables kept in the model were employment status, living in Bryan compared to College Station, and affiliation with the University.

Backwards stepwise regression identified as those living in Bryan less likely to travel than those who lived in College Station (OR: 0.6, $p<0.001$, 95% CI: [0.6-0.7]). Cases who reported employment were more likely to travel in the past 14 days prior to test date than those who did not report employment (OR: 1.4, $p<0.001$, 95% CI: [1.3-1.7]). In addition, cases reporting affiliation with the university were more likely to travel in 14 days prior to test date than those who did not report university affiliation (OR: 1.7, $p<0.001$, 95% CI: [1.6-1.8]).

Table 58: Manual logistic regression with the outcome of traveling in the past 14 days. Variables included in the model were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment, student/daycare status, healthcare worker status, known close contact with a confirmed case, close contact with a household member, location of exposure, and University affiliation. There were 16,643 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Bryan	0.6	p<0.001	[0.6-0.7]
Employed	1.4	p<0.001	[1.3-1.7]
University affiliated	1.7	p<0.001	[1.6-1.8]

Figure 20: Likelihood of travel in the past 14 days prior to symptom onset or test date. Variables included in the model were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment, student/daycare status, healthcare worker status, known close contact with a confirmed case, close contact with a household member, location of exposure, and University affiliation. Variables with statistical significance are noted with an asterisk.



3.4.14 Factors assessing odds of hospitalization

To assess the effect of unique factors on hospitalization with COVID-19, multivariate regression was run. Variables identified through bivariate analysis (p<0.05) were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment, student or daycare status, pregnancy, diabetes, cardiovascular disease, hypertension, renal disease, liver disease, immunocompromised, childhood asthma, smoking, and flu shot status. Variables kept in the model were sex, race/ethnicity, age, employment status, student/daycare status, diabetes, cardiovascular disease, hypertension, renal disease, and immunocompromised conditions.

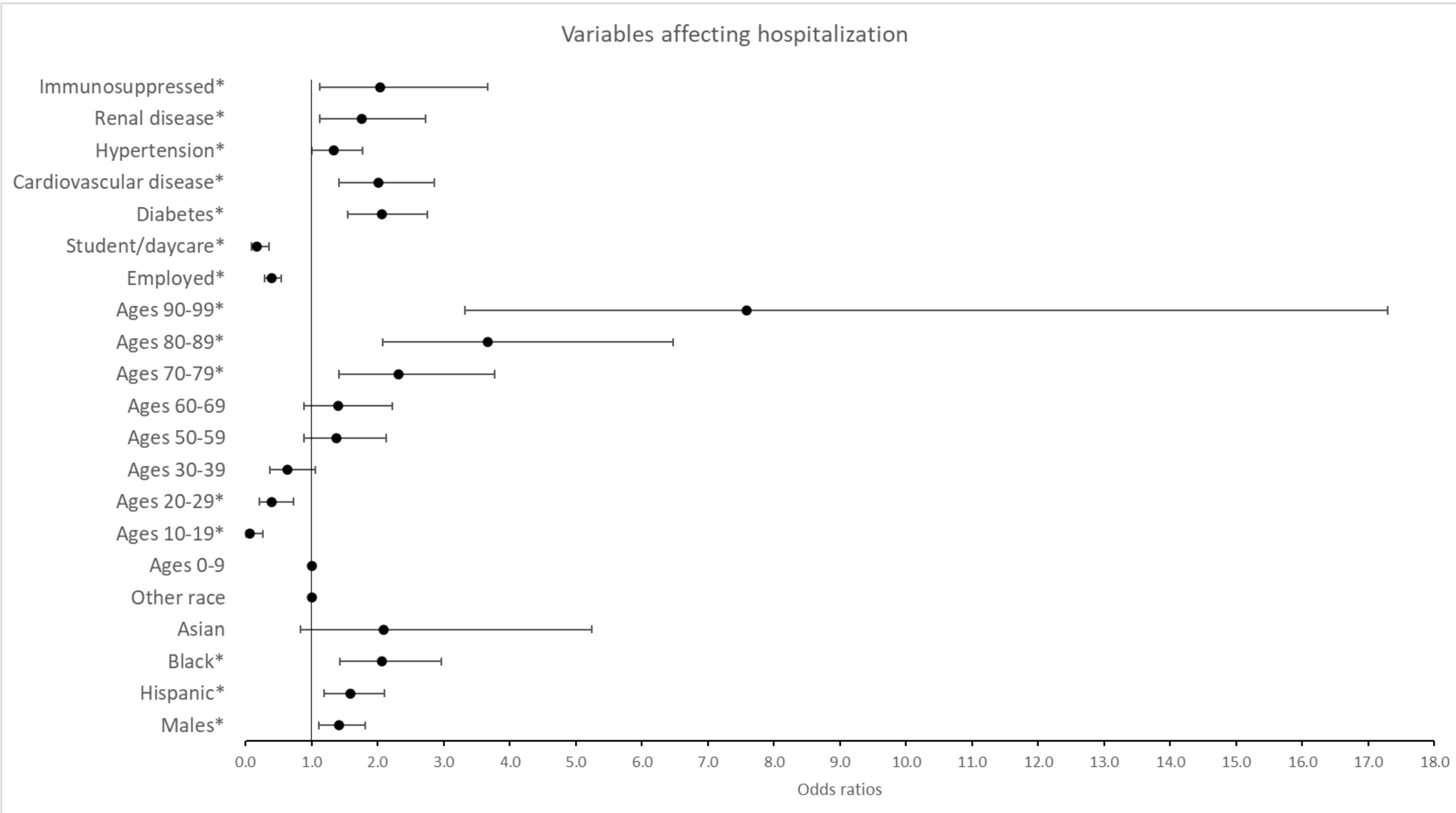
Hispanic or Latino (OR: 1.6, p=0.002, 95% CI: [1.2-2.1]), and black or African American (OR: 2.1, p<0.001, 95% CI: [1.4-3.0] had higher odds of hospitalization than white, non-Hispanic cases. Ages under 39 all had lower odds of hospitalization when compared to ages 40-49 except for ages 0-9. Age groups with the highest odds of hospitalization were 90-99 (OR: 7.6, $p<0.001$, 95% CI: 3.3-17.3]). Cases who reported employment had lower odds of hospitalization than unemployed (OR: 0.4, $p<0.001$, 95% CI: [0.3-0.5]). Additionally, student or daycare attendees had a lower odds of hospitalization when compared to those who were not student or daycare attendees (OR: 0.2, $p<0.001$, 95% CI: [0.1-0.3]).

Five comorbidities were identified as giving cases a higher odds of hospitalization: cardiovascular disease (OR: 2.0, $p<0.001$, 95% CI: [1.4-2.9]), hypertension (OR: 1.3, $p=0.048$, 95% CI: [1.0-1.8]), diabetes (OR: 2.1, $p<0.001$, 95% CI: [1.5-2.8]), renal disease (OR: 1.8, $p=0.013$, 95% CI: [1.1-2.7]), and immunocompromised status (OR: 2.0, $p=0.019$, 95% CI: [1.1-3.7]).

Table 59: Odds of factors affecting hospitalization. Variables included in the model were sex, language, race/ethnicity, living in College Station vs Bryan, age, residence type, employment, student or daycare status, pregnancy status, diabetes, cardiovascular disease, hypertension, renal disease, liver disease, immunocompromised, childhood asthma, smoking, and flu shot status. There were 9,466 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Sex (referent group: female)			
Males	1.4	0.006	[1.1-1.8]
Race/ethnicity (referent group: white, non-Hispanic)			
Hispanic	1.6	0.002	[1.2-2.1]
Black	2.1	<0.001	[1.4-3.0]
Asian	2.1	0.115	[0.8-5.2]
Other	1.0	NA	NA
Age (referent group: ages 40-49)			
Ages 0-9	1.0	NA	NA
Ages 10-19	0.1	<0.001	[0.0-0.3]
Ages 20-29	0.4	0.003	[0.2-0.7]
Ages 30-39	0.6	0.078	[0.4-1.1]
Ages 50-59	1.4	0.152	[0.9-2.1]
Ages 60-69	1.4	0.152	[0.9-2.2]
Ages 70-79	2.3	0.001	[1.4-3.8]
Ages 80-89	3.7	<0.001	[2.1-6.5]
Ages 90-99	7.6	<0.001	[3.3-17.3]
Employed	0.4	<0.001	[0.3-0.5]
Student/daycare	0.2	<0.001	[0.1-0.3]
Diabetes	2.1	<0.001	[1.5-2.8]
Cardiovascular disease	2.0	<0.001	[1.4-2.9]
Hypertension	1.3	0.048	[1.0-1.8]
Renal disease	1.8	0.013	[1.1-2.7]
Immunosuppressed	2.0	0.019	[1.1-3.7]

Figure 21: Likelihood of being hospitalized. Variables included in the model were sex, language, race/ethnicity, living in College Station vs Bryan, age, residence type, employment, student or daycare status, pregnancy status, diabetes, cardiovascular disease, hypertension, renal disease, liver disease, immunocompromised, childhood asthma, smoking, and flu shot status. Variables with statistical significance are noted with an asterisk.



3.4.15 Factors assessing odds of going to an ICU

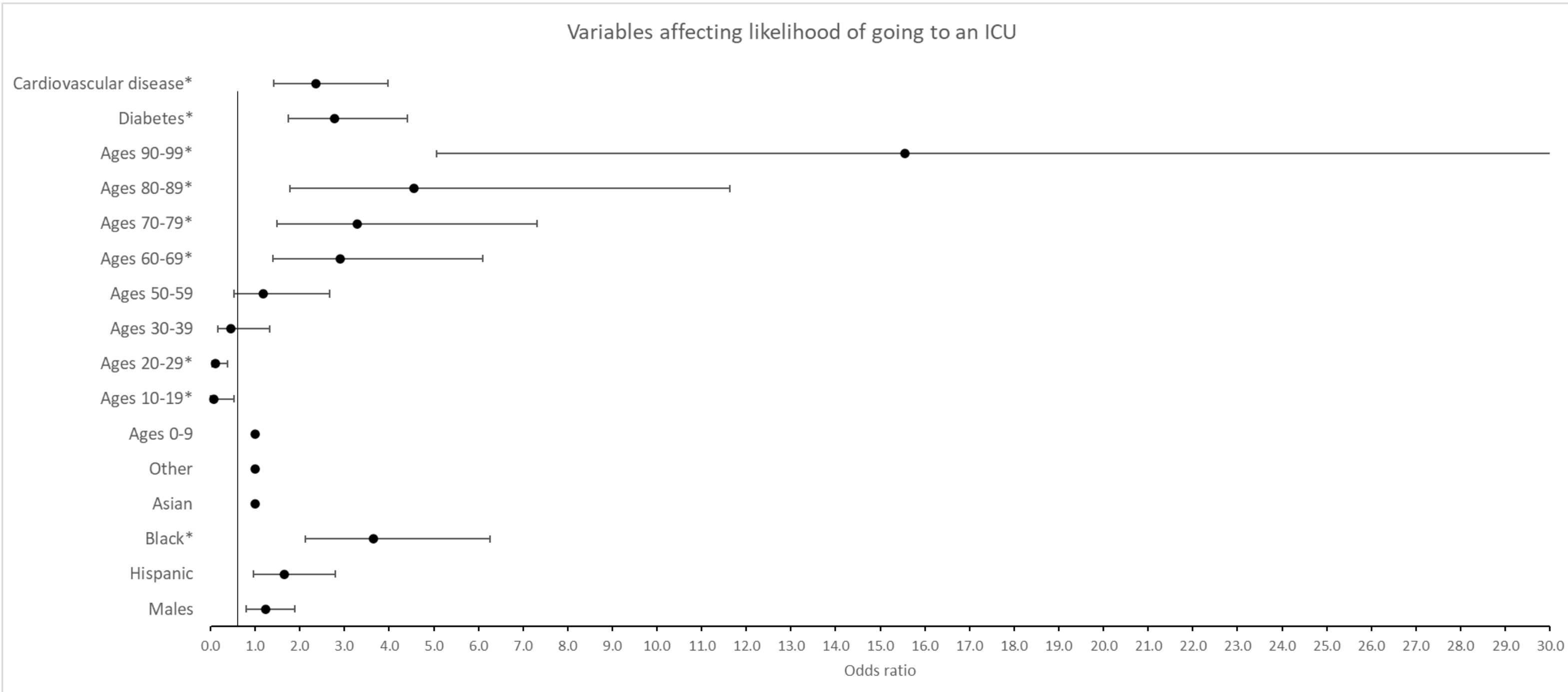
To identify the effect specific factors had on going to an ICU, multivariate regression was conducted. The variables determined to analyze from bivariate analysis ($p<0.05$) were language, race/ethnicity, living in College Station versus Bryan, age, residence type, employment, student/daycare attendee, diabetes, cardiovascular disease, hypertension, renal disease, immunocompromised, childhood asthma, and smoking status. Variables kept in the model were sex, race/ethnicity, age, diabetes, and cardiovascular disease.

One race/ethnicity was identified as significantly affecting going to an ICU when compared to white, non-Hispanics, black or African American (OR: 3.6, $p<0.001$, 95% CI: [2.1-6.3]). Adults aged 60-69 years had higher odds of going to an ICU when compared to those 40-49 years (OR: 2.9, $p=0.005$, 95% CI: [1.4-6.1]). Additionally, adults aged 70-79 years also a higher odd of going to an ICU than those 40-49 years (OR: 3.3, $p=0.003$, 95% CI: [1.5-7.3]). Diabetes (OR: 2.8, $p<0.001$, 95% CI: [1.7-4.4]) and cardiovascular disease (OR: 2.4, $p=0.001$, 95% CI: [1.4-4.0]) were the only comorbidities that affected a case going to the ICU.

Table 60: Factors affecting the odds of going to an ICU. Variables included in the model were sex, language, age, race/ethnicity, living in College Station versus Bryan, residence type, employment status, student or daycare status, diabetes, cardiovascular disease, hypertension, renal disease, immunocompromised status, childhood asthma, and smoking status. There were 13,073 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Sex			
Males	1.2	0.348	[0.8-1.9]
Race/ethnicity			
Hispanic	1.6	0.065	[1.0-2.8]
Black	3.6	<0.001	[2.1-6.3]
Asian	1.0	NA	NA
Other	1.0	NA	NA
Age			
Ages 0-9	1.0	NA	NA
Ages 10-19	0.1	0.01	[0.0-0.5]
Ages 20-29	0.1	0.001	[0.0-0.4]
Ages 30-39	0.5	0.148	[0.2-1.3]
Ages 50-59	1.2	0.683	[0.5-2.7]
Ages 60-69	2.9	0.005	[1.4-6.1]
Ages 70-79	3.3	0.003	[1.5-7.3]
Ages 80-89	4.6	0.002	[1.8-11.6]
Ages 90-99	15.6	<0.001	[5.1-47.8]
Diabetes	2.8	<0.001	[1.7-4.4]
Cardiovascular disease	2.4	0.001	[1.4-4.0]

Figure 22: Likelihood of going to an ICU. Variables included in the model were sex, language, age, race/ethnicity, living in College Station versus Bryan, residence type, employment status, student or daycare status, diabetes, cardiovascular disease, hypertension, renal disease, immunocompromised status, childhood asthma, and smoking status. Variables with statistical significance are noted with an asterisk.



3.4.16 Factors assessing odds of going to an ER

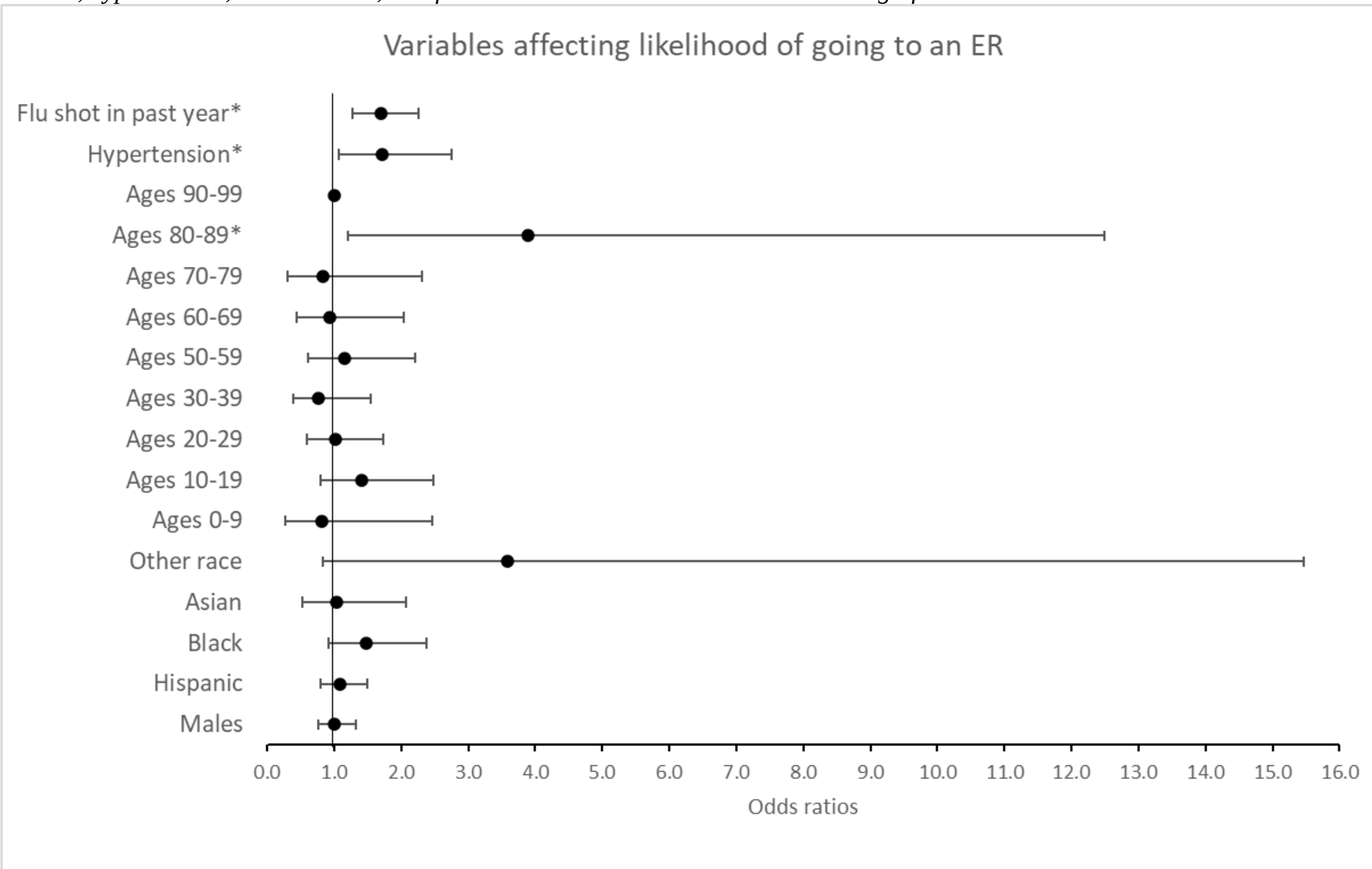
To identify factors which had a specific effect on going to an ER multivariate regression was run. Variables identified based on bivariate analysis ($p<0.05$) were cardiovascular disease, hypertension, renal disease, and flu shot status. Variables kept in the model were sex, race/ethnicity, age, hypertension, and flu shot status.

No race/ethnicities significantly predicted going to an ER. Ages 80-89 was the only age group significantly affecting the odds of going to an ER when compared to ages 40-49 (OR: 3.9, $p=0.023$, 95% CI: [1.2-12.5]). Cases who reported a history of hypertension had a higher odd of going to an ER than those who did not (OR: 1.7, $p=0.025$, 95% CI: [1.1-2.7]). Individuals who had a flu shot in the past year before infection were also more likely to go to an ER than those who had not had a flu shot in the past year (OR: 1.7, $p<0.001$, 95% CI: [1.3-2.3]).

Table 61: Factors with an effect on going to an ER. Variables included in the model were sex, race/ethnicity, age, residence type, cardiovascular disease, hypertension, renal disease, and flu shot status. There were 8,217 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Sex			
Males	1.0	0.967	[0.8-1.3]
Race/ethnicity			
Hispanic	1.1	0.578	[0.8-1.5]
Black	1.5	0.114	[0.9-2.4]
Asian	1.0	0.92	[0.5-2.1]
Other	3.6	0.087	[0.8-15.5]
Age			
Ages 0-9	0.8	0.712	[0.3-2.5]
Ages 10-19	1.4	0.24	[0.8-2.5]
Ages 20-29	1.0	0.969	[0.6-1.7]
Ages 30-39	0.8	0.464	[0.4-1.5]
Ages 50-59	1.2	0.66	[0.6-2.2]
Ages 60-69	0.9	0.872	[0.4-2.0]
Ages 70-79	0.8	0.719	[0.3-2.3]
Ages 80-89	3.9	0.023	[1.2-12.5]
Ages 90-99	1.0	NA	NA
Hypertension	1.7	0.025	[1.1-2.7]
Flu shot in past year	1.7	<0.001	[1.3-2.3]

Figure 23: Likelihood of going to an ER. Variables included in the model were sex, race/ethnicity, age, residence type, cardiovascular disease, hypertension, renal disease, and flu shot status. Variables with statistical significance are noted with an asterisk.



3.4.17 Factors related to severe COVID-19

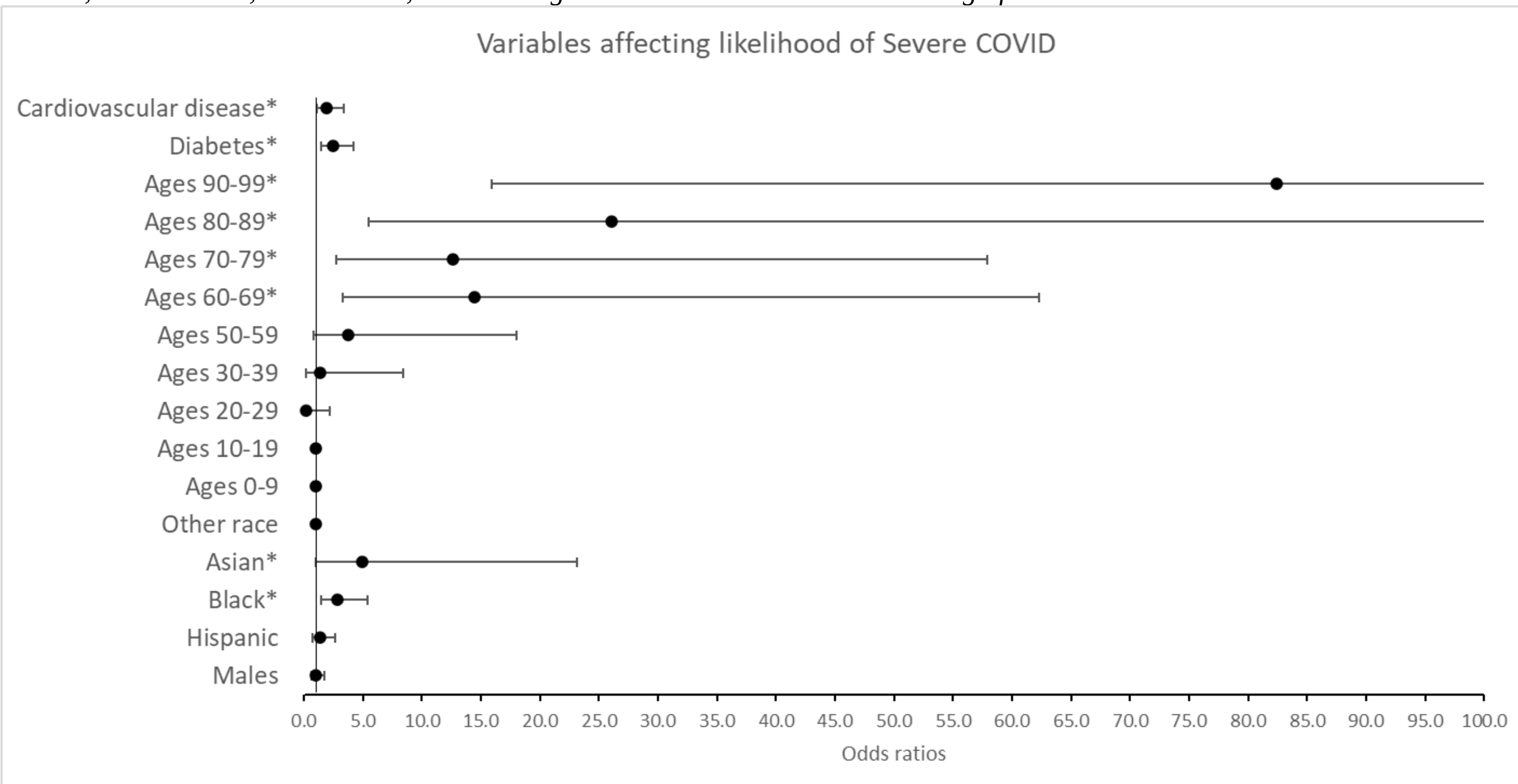
To determine factors with a specific effect on severe COVID-19, multivariate regression was conducted. Variables identified through bivariate analysis ($p<0.05$) were language, race/ethnicity, living in BCS, age, residence type, employment, student or daycare attendee, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, and smoking status. Variables kept in the model were sex, race/ethnicity, age, diabetes, and cardiovascular disease.

Black or African Americans (OR: 2.8, p=0.001, 95% CI: [1.5-5.4]) and Asian cases (OR: 4.9, p=0.043, 95% CI: [1.1-23.1]) had a higher odd of developing severe COVID when compared to white, non-Hispanics. Ages over 60 were more likely to have severe COVID when compared to ages 40-49. Those who had a history of cardiovascular disease had a high odd of severe COVID-19 (OR: 1.9, p=0.029, 95% CI: [1.1-3.4]). The comorbidity with the highest odds of influencing severe COVID-19 was diabetes (OR: 2.5, p=0.001, 95% CI: [1.5-4.3]).

Table 62: Factors which influenced odds of severe COVID-19. Variables included in the model were sex, language, race/ethnicity, living in College Station compared to Bryan, age, residence type, employment status, student or daycare attendee, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, and smoking status. There were 11,348 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Sex			
Males	1.1	0.846	[0.6-1.7]
Race/ethnicity			
Hispanic	1.4	0.321	[0.7-2.6]
Black	2.8	0.001	[1.5-5.4]
Asian	4.9	0.043	[1.1-23.1]
Other	1.0	NA	NA
Age			
Ages 0-9	1.0	NA	NA
Ages 10-19	1.0	NA	NA
Ages 20-29	0.2	0.182	[0.0-2.2]
Ages 30-39	1.4	0.717	[0.2-8.4]
Ages 50-59	3.8	0.092	[0.8-18.0]
Ages 60-69	14.4	<0.001	[3.3-62.3]
Ages 70-79	12.6	0.001	[2.8-57.9]
Ages 80-89	26.1	<0.001	[5.5-123.4]
Ages 90-99	82.4	<0.001	[15.9-426.7]
Diabetes	2.5	0.001	[1.5-4.3]
Cardiovascular disease	1.9	0.029	[1.1-3.4]

Figure 24: Likelihood of developing severe COVID. Variables included in the model were sex, language, race/ethnicity, living in College Station compared to Bryan, age, residence type, employment status, student or daycare attendee, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, and smoking status. Variables with statistical significance are noted with an asterisk.



3.4.18 Factors influencing COVID-19-related Deaths

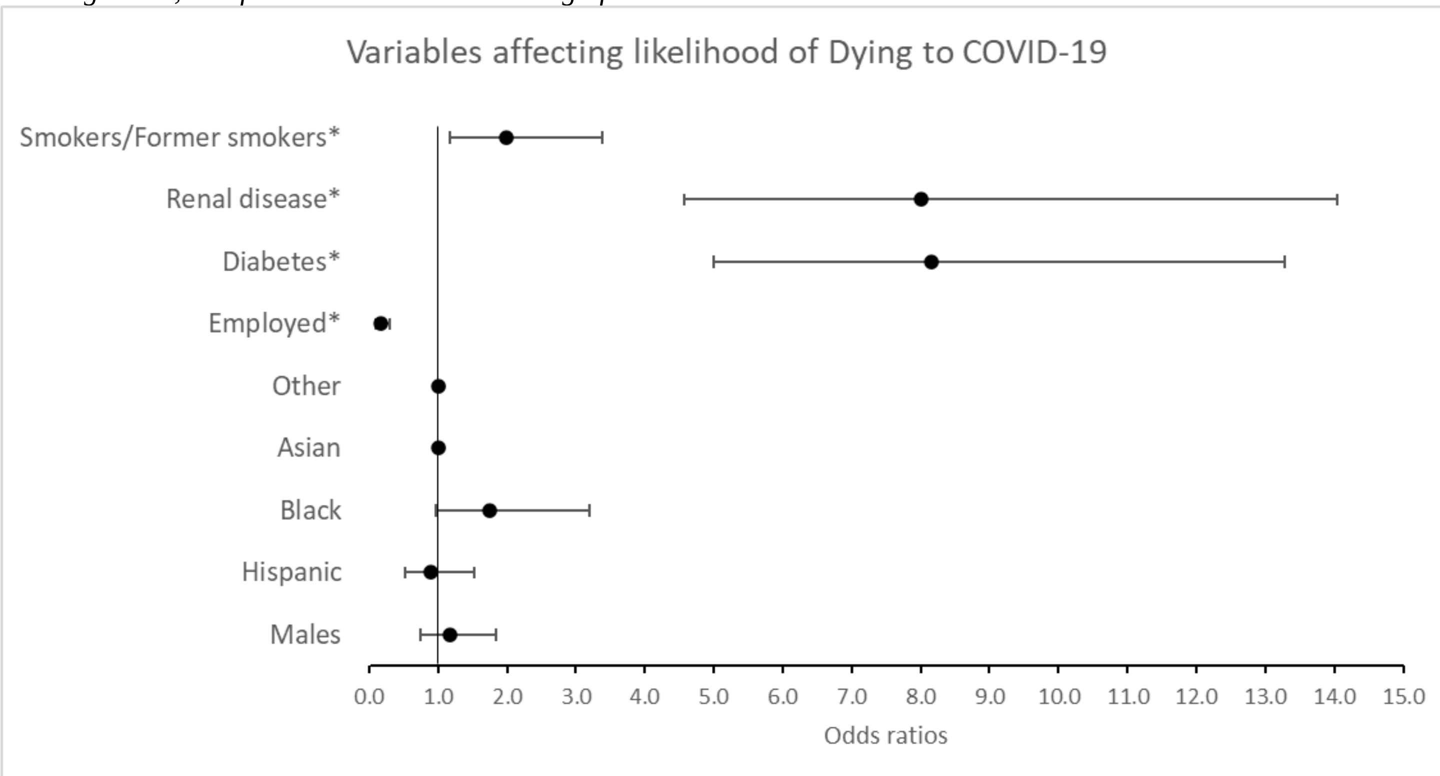
To determine what individual factors had a specific effect on dying of COVID-19, multivariate regression was run. Variables identified through bivariate analysis ($p<0.05$) were sex, race/ethnicity, living in College Station versus Bryan, age, residence type, employment, student or daycare status, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, immunocompromised, childhood asthma, smoking status, and flu shot status. Variables kept in the model were sex, race/ethnicity, employment status, diabetes, renal disease, and smoking status.

The only variable with a protective effect on dying of COVID-19 was employment status (OR: 0.2, $p<0.001$, 95% CI: 0.1-0.3]). Two comorbidities gave cases a higher odd of dying of COVID-19. First, were cases with a history of diabetes were more likely to die of COVID than those who did not (OR: 8.2, $p<0.001$, 95% CI: [5.0-13.3]). Second, cases who reported renal disease had a higher odds of dying of COVID than those who did not (OR: 8.0, $p<0.001$, 95% CI: [4.6-14.0]). Current or former smokers gave cases a higher odds of dying of COVID than cases who reported never smoking (OR: 2.0, $p=0.012$, 95% CI: [1.2-3.4]).

Table 63: Factors affecting COVID-19 deaths. Variables included in the model were sex, race/ethnicity, employment, student or daycare status, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, immunocompromised status, childhood asthma, smoking status, and flu shot status. There were 10,060 people included in the model.

Variable	**OR**	**p-value**	**95% CI**
Sex			
Males	1.2	0.478	[0.8-1.8]
Race/ethnicity			
Hispanic	0.9	0.693	[0.5-1.5]
Black	1.8	0.065	[1.0-3.2]
Asian	1.0	NA	NA
Other	1.0	NA	NA
Employed	0.2	<0.001	[0.1-0.3]
Diabetes	8.2	<0.001	[5.0-13.3]
Renal disease	8.0	<0.001	[4.6-14.0]
Smokers/Former smokers	2.0	0.012	[1.2-3.4]

Figure 25: Likelihood of dying to COVID-19. Variables included in the model were sex, race/ethnicity, employment, student or daycare status, diabetes, hypertension, cardiovascular disease, renal disease, liver disease, immunocompromised status, childhood asthma, smoking status, and flu shot status. Statistical significance is denoted in variables with an asterisk.



3.5 Discussion

COVID in this population reflects what has been reported in the United States. Young adults made up a large proportion of the community and implicated in transmission. Despite a university presence in the community, not all young adults were affiliated with the university. There was evidence of racial and ethnic disparities in this data as well as specific comorbidities affected COVID-19 outcomes.

3.5.1 Risk factors

When assessing race/ethnicity, Hispanic, Asian, and black, individuals had progressively higher odds of hospitalization when compared to white, non-Hispanic people. These odds align with the incidence of hospitalization in these ethnicities as Black cases (10.1%) had the highest percentage of hospitalization among race/ethnicities, followed by Hispanic (4.7%) and Asian (2.7%). Black or African American cases also had a higher odd of going to an ICU, comparable to the high reported incidence of going to an ICU. These people groups are identified as minorities in Brazos County census data as the proportion of these groups is much lower than white, non-Hispanic individuals.

The most often comorbidities significantly affecting severe COVID-19 outcomes were diabetes, cardiovascular disease, hypertension, and renal disease. Diabetes significantly affected one's increased odds of hospitalization, going to an ICU, severe COVID-19, and death. This aligned with several peer-reviewed articles on the COVID-19 risk associated with diabetes (Bansal, 2020; Erener, 2020; Abdi et al., 2020).

Cardiovascular disease gave someone a higher odds of going to an ICU and severe COVID-19. Multiple previously published studies have noted cardiovascular disease increasing one's chance of developing severe COVID (de Carvalho et al., 2020; Bansal, 2020; He et al., 2020). However, a large proportion of individuals with cardiovascular disease are also older than those who do not present with cardiovascular disease with may be a factor in their increased odds of illness (He et al., 2020).

Cases with a history of hypertension gave cases a higher chance of hospitalization and going to an ER. In published studies, hypertension alone did not increase odds of hospitalization or other severe outcome of COVID, only when it was compared with another comorbidity (Killerby et al., 2020; Fresán et al., 2021; Garg et al, 2020). In this sense, the results here are different from published studies because hypertension was the only comorbidity affecting odds of going to an ER.

A case who reported renal disease had a higher chance of hospitalization and dying of COVID-19. Renal disease has been noted as one of the leading risk factors for hospitalization, and other severe COVID outcomes (Oetjens et al., 2020). Specifically, end-stage renal disease, marked as someone on dialysis has been published as a high-risk factor for hospitalization with COVID-19 (Gottlieb et al., 2020; Oetjens et al, 2020). While the questionnaire in this data did not specifically ask about end-stage renal disease, it is still representative of cases who had a form of renal disease.

Cases who reported being a current or former smoker increased their likelihood of dying of COVID-19 when compared to cases who reported never smoking. The relationship between smokers and COVID has also been published in the literature (de

Carvalho et al., 2020). As COVID-19 is caused by a respiratory virus, smoking can detrimentally affect their breathing and lung capacity.

Flu shot status predicting admittance to an ER is important to note for public health implications because it was noted as protecting specifically against admittance to an emergency room because of COVID-19 (Taghioff et. al, 2021). Although there were other predictors in the model, this study contradicting a peer-reviewed article is important to provide evidence against flu shots protecting against COVID-19 and reinforces the CDC's assertion that a flu shot does not help against COVID-19 (CDC 2020 – 2021 flu season, 2021; Taghioff et. al, 2021).

Cases who reported employment were less likely to present with hospitalization, going to an ICU, severe COVID, or dying of COVID. This may be a factor of age, as young ages are more likely to work than elderly and thus less likely to have severe outcomes. This is justified through the odds of hospitalization, as cases below 40 years were less likely to present hospitalization than adults over 40 years.

Other risk factors explored here were attending an indoor gathering of <5 people, of 5-10 people, and traveling in the 14 days prior to test date or symptom onset. Small gatherings were explored as a risk factor because gatherings were strongly discouraged, if not banned throughout the early stages of the pandemic yet these small gatherings were the most reported in the data. The same two variables of having a household contact and university affiliation influenced one's odds of attending a small gathering. Having a household close contact yielded a protective effect, making one less likely to attend a small gathering. Affiliation with the university significantly increased one's likelihood of attending a small indoor gathering.

University affiliation also heightened the likelihood of traveling in the past 14 days. A lot of students and faculty travel to and from the university if their family lives outside of the city or if their place of residence is outside the city. Additionally, employed increased odds of traveling, likely because it provided the monetary means to do so. Cases who lived in Bryan had a lower, or protective, odds of traveling in the past 14 days when compared to cases living in College Station. When comparing the two cities, Bryan has a higher percentage of minorities and a lower median income than College Station.

3.5.2 Epidemiologic characteristics

The estimated incubation period had a median of 2 days (range: 0-14) is shorter than what is found in the literature (5-7 days) (Quesada et al., 2021; Johansson et al., 2021; Elias et al, 2021; Salzberger et al., 2021). There a few main reasons this incubation period may be shorter than that in literature, first, the actual incubation period was unable to be calculated due to lack of exposure date in the data. Second, as the calculation uses date of symptom onset date, recall bias may be a factor if cases do not remember when they first felt symptoms. The highest attack rate present in ages 19-64 was expected as it includes young adults, who comprise a large percentage of the dataset. In terms of race/ethnicity attack rates, Hispanic or Latinos had the highest attack rate demonstrating this community was disproportionately affected by the disease.

The median duration of illness was estimated to be 6 days (range: 0-97 days). This length of symptom duration was like what others have reported in the literature, and the same as a cohort of young cases (Tenforde et al., 2020; Molteni et al., 2021). A duration of illness less than a week is likely attributed to the large young adult population in the data.

In Brazos County, similar to other locales in the US, the first peak of cases was observed in June, 2020, which coincided with the end of state-wide mobility restrictions in Texas (Husch Blackwell, 2020). The next peak was in August/September 2020, which is also when many students were returning to classroom instruction. The highest peak of COVID-19 cases occurred in early January 2021. We observed that the trends in hospitalizations and deaths closely followed that of cases, except for the highest number of deaths occurring in early October 2020. It is possible these individuals were a part of the August/September 2020 peak of cases and were victims of longer COVID than average prior to death. These trends are like those in Texas COVID-19 case reports with the notable exception of a peak following the return to classroom instruction in August 2020 (TX DSHS COVID-19 Dashboard, 2020).

3.5.3 Description of demographics, clinical presentation, and medical history

Out of the individuals for whom age was able to be calculated, the majority were ages 18-29. The majority in this age bracket was expected because of the large young adult population present in the BCS area. Additionally, Texas A&M University required student testing in Spring 2021 which may have raised the number of cases identified among the college student population.

Out of those reporting their employment status, approximately half reported employment while the other half did not. Since most individuals in the dataset were over the age of 18 years, and the largest age category was young adults, this could be attributed to the large student population within Blinn College and TAMU. The most frequent residence types were as expected, including private residence or house, apartment, and dormitories. These were the expected most frequent residence types as it speaks to community members and young adults frequently living in shared housing, apartments, and dormitories.

Regarding clinical presentation, there were differences between the most common symptoms in this study compared to those in the literature. The most common symptoms in this study were cough, headache, and fatigue with the least common symptoms were identified as loss of appetite, weakness, abdominal pain, and vomiting. The literature presents the most common symptoms among non-hospitalized patients as cough, congestion, sore throat, diarrhea, abdominal pain, and vomiting (Lee et al., 2020). The largest difference was among the gastrointestinal symptoms. Gastrointestinal symptoms, namely diarrhea, abdominal pain, and vomiting, were listed as frequent in the literature yet not in this study. Overall, comorbidities were not as high in this data (27.4%) compared to that in another study, those many studies did not have this specific information published (53%) (Djaharuddin et al., 2021). This discrepancy could be due to decreased comorbidities and severe cases in this data as those with liver damage, ARDS, and severe cases have historically had higher incidence of gastrointestinal symptoms (Ye et al., 2020).

Analysis of medical history for individuals testing positive for SARS-CoV-2 was not extensive due to the data available. Most respondents answering no to various comorbidities suggests either few people in the dataset had comorbidities, or they did not want to share the information with the interviewer.

Death and other severe outcomes were rare in this study. Other mortality rates have been listed as 1.2% for the U.S. overall and 7.4% in a specific study (John Hopkins Coronavirus Resource Center, 2020; Nakamichi et al., 2021). Hospitalized cases at 18.4% of their population group (Nakamicihi et al., 2021). Death and severe outcomes of COVID-19 could be underrepresented in this data as answers to the questions relied on the patient's ability to answer or an available proxy for the patient willing to answer.

3.5.4 Differences in clinical presentation for ages.

Across clinical presentation, all symptoms, including symptom status, were significantly associated with age categories. The most common symptoms for young adults, with over 50% responding yes to the symptom, were headache (63.9%), cough (59.0%), pharyngitis (54.7%), and fatigue (52.5%). Despite the conception presented in the media that young adults were likely to be asymptomatic, most young adults (91.3%) in this population were symptomatic. Published academic literature has long since refuted the misconception that young adults will regularly be asymptomatic. However, unless they themselves are in academia, young adults and other members of the public are likely to not be reading peer-reviewed articles. This has significant bearing on public health messaging because the public needs to understand no age group is invulnerable to COVID-19.

Children and elderly age groups had a lower frequency of symptoms compared to other age groups. However, this is likely a direct result of children not understanding signs and symptoms, and therefore being unable to tell someone exactly what hurts. Similarly, elderly individuals often suffer from dementia and can exhibit similar behavior. Unfortunately, dementia was not a question asked in the dataset preventing this theory from being proved.

While less common in children and elderly, ILI was common in each age group. The similarity of COVID-19's clinical presentation to that of influenza reinforces the need for the public to understand their differences. When there are influenza outbreaks, the public is not asked to submit to rigorous public health precautions, testing, isolation, and quarantining. Describing the differences and public health importance of COVID in comparison to influenza may help the public understand why their cooperation with public health measures are appropriate and needed.

Medical history questions were associated with age in each question. When assessing severe outcomes and age, the only severe outcome not significantly associated with age was if a patient was admitted to an emergency room for this illness. The proportion of individuals who responded yes, admitted to an emergency room was similar across all age categories. When comparing age to exposure questions, such as if they had close contact with a laboratory confirmed case and where the case reported exposure, all variables were significantly associated with age.

3.5.5 Describing possible exposures

There were 38.6% of individuals who reported close contact with a laboratory confirmed case of COVID-19, 33.3% who reported no known close contact, and the remaining had no information on this question. The proportion of known close contact to no known close contact provides evidence of community transmission of COVID-19. Individuals who had no known close contact may have contracted the virus anywhere within the Brazos community or perhaps contracted it while traveling. This evidence can support the public health response by demonstrating the prevalence of the virus in the community, and the whole community should work towards ending the outbreak.

Frequent locations of exposure were in the household, school/daycare, or work. Each of these locations put individuals in close quarters with another and limited the ability to physically distance providing ample opportunities for the virus to spread person to person. In terms of number of close contacts, half of the individuals in the dataset did not provide information on the number of people they were in close contact. The median number of contacts identified was one with a mean of 2 (standard deviation 4.5). Based on the histogram of number of contacts, the most frequent number of contacts reported was between zero and two. This was lower than expected given the social behavior of young adults. The mean number of household contacts of two was as expected given family sizes.

The proportion of individuals who reported traveling outside of the city in the past 14 days (13.5%) was lower than expected given the transitory nature of the area. It is possible respondent bias could have played a role in this if the patient believed the case investigator would look down on them. Risk factor questions were added as the pandemic evolved to include items like wearing a face mask. Consequently, the number of people who had the ability to answer these questions was inherently limited. Despite this, there is still value in the reviewing the responses. There was little variation in respondents discussing the frequency of which they wore a face mask or face covering; 88.4% who responded said they always wore a face mask. This statistic may seem slightly surprising at first. However, the public health guidance on face masks changed throughout the course of the pandemic. Additionally, the most widely available face mask has been cloth which are not as effective as surgical or N-95 masks, and this question did not specify what type of face mask they wore most often. In future questionnaires regarding face masks, it would be helpful to include a follow-up on asking the type of face mask worn to help determine the efficacy of the face mask when worn in the public.

Visiting a grocery store in person, a restaurant in person, attending small indoor social gatherings, and working in person were the most common behavioral risk factors. Spread of the virus at indoor gatherings is dependent on those attending the gatherings and risk varies by the precautions attendees take. Grocery stores, restaurants, and workplaces were anticipated as common risk factors as these locations are high touch, surface areas are commonly touched by multiple individuals before it can be cleaned. Many establishments have implemented public health measures since the start of the pandemic in the effort to limit spread of the disease such as cleaning grocery carts when they are returned. However, there is still a level of risk awareness and risk acceptance that must be considered by everyone. Employees at grocery stores and restaurants cannot wipe down every item despite their best efforts. During an infectious disease outbreak, it needs to be ensured the public is aware there is a high level of risk by visiting establishments or attending gatherings, and then they can make an informed decision based on their personal health.

Working in person is similar in the sense that they must understand the risk they are taking by working in person. However, some do not have the choice to not work in person if it is their only job, and they need their livelihood. Consequently, in the current climate, if an employee becomes diagnosed with COVID-19 while working and were able to build a case, employees could sue the business for damages. Moving forward, businesses may want to continue the recommended COVID-19 safety recommendations and add a COVID-19 clause for liability to protect themselves and help make their employees aware of the inherent workplace risk.

3.5.6 Vaccination questions

Vaccine efficacy for COVID-19 vaccines has decreased drastically with the Delta and Omicron variants of concern. Consequently, minimal breakthrough infections were expected in this population prior to the known emergence of the variants. There were 231 (5%) individuals who tested positive for SARS-CoV-2 in this data also identifying as having received two doses of an FDA-approved COVID-19 vaccine. This is in line with expectations since the COVID-19 vaccine is expected to prevent severe disease not infection. Vaccine hesitancy was common when asked if they would get the vaccine when it became available to them. This suggests early efforts to combat vaccine hesitancy need to be heightened when releasing a new vaccine amidst a publicized outbreak. The most frequent COVID-19 FDA approved vaccine to be distributed in this dataset was the Moderna vaccine. The largest source of vaccine distribution in Brazos County was the Brazos County vaccine hub opened in spring 2021. The vaccine hub distributed the Moderna vaccine, which explains the prevalence of the Moderna vaccine.

3.5.8 University questions

The number of people affiliated with the university in this dataset (N=8,347, 28%) was smaller than expected given the influx of people the university brings for faculty, staff, and students. The smaller than expected number of university affiliated cases could be due to students not being required to be in person for classes until the spring 2021 semester, or the number of non-pharmaceutical interventions employed by the university. Approximately half of the university affiliated individuals identified as undergraduate students. There was a mixture of students identifying as part of an organization such as the Corps of Cadets or being a member of Greek life. There were publicized outbreaks within the Corps of Cadets and certain chapters of Greek life from events held and or housing those organizations provided.

3.5.9 Other interesting points of discussion

The cut-off date in the dataset for this analysis was July 31, 2021, despite 19,457 observations in the data having a test date for SARS-CoV-2 after the cut-off date. This cut-off allowed Delta and Omicron variants to be excluded as they did not have known emergence locally before Brazos County. The Delta and Omicron variants of concern have different clinical presentations and behaviors compared to earlier variants of SARS-CoV-2 making this distinction important.

Maps and travel history demonstrate a highly mobile nature of the Brazos County population. In addition to Texas, cases reporting to BCHD represent at least 15 other states. This geographic diversity may be due to students at the University in BCS who also identify a permanent address in another state. Cases were asked separately if they were currently residing at that address, but a different address was not considered when mapping. A magnified map of cases by zip code in the BCS area presents the highest frequency of cases were in College Station. Higher frequency of cases in College Station can be attributed to the spread within social gatherings and publicized outbreaks at Texas A&M University.

3.5.10 Limitations

This dataset is limited by the method in which it was collected. While all case investigators were given the same training and requirements, case investigations were not always administered by the same individual. Following the trainings, employees did not always follow directions, such as not asking all the questions in the questionnaire or pushing the case for their close contacts. The questionnaire also evolved with the pandemic. Questions were added throughout the process depending on changing guidelines (like face masks) or requests from policy makers.

A large limitation of the secondary dataset was differences in employees correctly inputting data into REDCap. When test dates were inputted incorrectly, the CoOp may not have been able to provide accurate isolation guidelines to the case or to any relevant close contacts. Similarly, when test dates or birthdates were inputted incorrectly, the person's age was unable to be calculated with any degree of accuracy. Additionally, some individuals who tested positive for SARS-CoV-2 may not know the answer to a question, and employees were tasked with marking the response as "do not know" instead of leaving it blank or unknown – yet this occurred infrequently.

Efficacy and availability of SARS-CoV-2 tests affects this data as well. Anyone who tested at home after rapid antigen tests were made available or had a false negative on their SARS-CoV-2 test would not have their results passed onto the CoOp or Health Department. Communication between providers with the Health Department was crucial. If a provider did not fax a medical report or did not give complete contact information, the CoOp would not be able to process the report and conduct a case investigation.

Recall bias was a significant issue, especially given the length of the questionnaire in the case investigation. Depending on one's activities, they may not have remembered all their close contacts or activities, thereby hampering the investigation process. Medical history questions such as childhood asthma may or may not be difficult to remember for those in later stages of life.

Limiting the spread of SARS-CoV-2 relied on individuals cooperating with the contact tracing effort and isolation guidelines. Individuals who tested positive for SARS-CoV-2 may not have picked up the phone, preventing the CoOp from checking on them and collecting information. Other cases, after picking up the phone, believed the investigator to be a spam call or solicitor, further contributing to decreased data collection. Some cases regularly did not want to give information on their close contacts, which prevented the CoOp from being able to provide evidence-based public health guidance. Some cases refused to isolate or isolate completely, increasing the chance of them spreading the virus to others.

3.5.11 Concluding thoughts

This study sought to analyze data collected on individuals testing positive for SARS-CoV-2 in Brazos County, Texas to best understand who is at risk and possible behaviors that can affect risk. Out of age groups, young adults were the most represented but were not immune and had similar levels of symptomatic status to other age categories. The most common behavioral risk factors included attending indoor gatherings and traveling outside of their city of residence – often predicted by affiliation with the university.

Hispanic or Latino cases had the highest burden of disease as evidenced by attack rates. However, black individuals, and in some cases, Hispanics were minorities had higher likelihoods of severe disease than other race and ethnicities in the Brazos County community. Clinical presentation and medical history components predicting severe outcomes were shortness of breath, hypertension, diabetes, and cardiovascular disease.

Policy makers can take these highlights and incorporate them into an after-action report to understand how they can mitigate or prevent these minorities in the community from being adversely affected by COVID-19. BCHD can inform the county that Hispanic, or Latinos have been evidence to have higher incidence of disease. Additionally, they, along with blacks or African Americans have been proven to have a higher likelihood of severe disease. Individuals who self-identify as members of these groups could use the information to be mindful of their risk. The comorbidities can also be included as factors for the public to be aware of and better understand their risk. Healthcare providers can inform their patients of medical conditions demonstrated to have an increased likelihood of severe disease. Although notable limitations were present in the data, there is still evidence for improved public health messaging to help ensure risk awareness.

4. CONTACT TRACING AND TESTING OF COVID-19, WHICH CAME FIRST?

4.1. Introduction

4.1.1 Introduction to contact tracing

Contact tracing is the process of identifying individuals who have been in contact with someone with an infectious disease, who may be at risk themselves of having been infected. The process usually involves communicating with the identified individuals to assess their specific risk levels, guiding them on what to watch for in terms of symptoms of disease, and advising them on quarantine, testing, prophylaxis, and other interventions. Through successful contact tracing, the spread of disease can be reduced and ultimately prevented. The definition of contact and the specific guidelines those individuals are given varies by disease, according to the characteristics of the infecting pathogen, disease severity, and potential routes of transmission, and overall public health safety and concerns. For example, contact tracing was used during the 2014 Ebola Virus Disease (EVD) outbreak, where contact was defined as exposure to a case (regardless of confirmed, probable, or suspected status) through sleeping in the same house, contacting the case during illness or burial processes, encountering body fluids, or a baby breastfeeding by a case (Saurabh & Prateek, 2017). In the H1N1 pandemic in 2015, close contacts were considered anyone around a positive case, including healthcare workers; they were requested to stay home for seven days while monitoring symptoms (Rewar, Mirdha, & Rewar, 2016).

4.1.2 Contact tracing and COVID-19

During the COVID-19 pandemic, contact tracing has been used worldwide. However, in this pandemic, the definition of a contact has not been static. Close contact is an event, defined here as, in the COVID-19 pandemic, per CDC, is any individual who has been within six feet or less for 15 minutes or more of one who has tested positive for SARS-CoV-2 (CDC, Contact Tracing for COVID-19). For the ease of discussion, a contact will be referred to as a person here. The process of contact tracing in BCS was the case identified close contacts to the case investigator on the telephone, then the case investigator passed the information along to a contact tracer. Following the receipt of the close contact's information, they call the contact tracer to inform them of their exposure, give guidance on testing and quarantining. The contact tracer will follow-up with the close contact to see how they are doing and if they have tested for the virus.

Here, we look at whether close contacts in BCS during the COVID-19 pandemic complied with recommended SARS-CoV-2 testing windows following notification of potential exposure by the contact tracing program. First, close contacts identified through the BCS contact tracing program are described. Next, a summary of testing behavior is presented as whether SARS-CoV-2 testing occurred after the contact tracing event occurred, with effective contact tracing considered completion of testing following a call from a contact tracer. This small window into the effectiveness of public health messaging about the importance of testing during the appropriate window for the SARS-CoV-2 virus and infection process is assessed by looking at individuals who tested for

SARS-CoV-2 within the recommended window of testing within 3-7 days following exposure.

4.2 Literature Review of Behaviors and Risk Factors of COVID-19

A literature review was done using PubMed to identify existing peer-reviewed articles associated with contact tracing. The search terms used were ("COVID-19" or "SARS-COV-2") AND ("contact" or "close contact" or "contact tracing") yielding 9,291 articles.

At least 54 studies have assessed household transmission and household specific attack rates (Madewell et al., 2020). In these studies, they estimated the secondary attack rate by estimating cases in household contacts and found household contacts greatly contributing to the reproduction number (Arnedo-Pena et al., 2020; Madewell et al, 2020). Symptomatic index cases were found to contribute more to household transmission than if the index case were symptomatic or asymptomatic (Madewell et al, 2020). In these studies, age was most often studied with children being less likely than adults to test positive for SARS-CoV-2 after being exposed than adults (Hua et al., 2020; Arnedo-Pena et al., 2020; Madewell et al, 2020). Close contacts over age 60 were found to be most susceptible to SARS-CoV-2 when compared to other age groups (Madewell et al., 2020; Arnedo-Pena et al., 2020; Hu et al., 2021; Jing et al., 2020). Few studies have found sex significantly associated as a factor in close contacts – those that did found females at higher risk (Madewell et al., 2020; Islam & Noman, 2020; Liu et al., 2020; Yu et al., 2020)

There are two takeaways from these search results: 1) household exposure to SARS-CoV-2 is a proven risk factor through contact tracing, and 2) there are limited studies published on the results of SARS-CoV-2 contact tracing in a university-centered community.

4.3. Methods

4.3.1. Data Collection

The data source is BCHD records, IRB title: COVID-19 in the Brazos Valley, Principal investigator: Rebecca Fischer, IRB ID: IRB2020-0579D.

Data for cases and contacts was collected in the same manner as in Section 1.3.1. The REDCap project databases were made available by the shared data management system by Obeid et al (Obeid et al., 2012). Data was exported from REDCap into Stata/IC on February 1, 2022, with 22,239 observations (StataCorp, 2019).

4.3.2. Data Analysis

The contact database was cleaned in the same manner as in Chapter 1.3.2 apart from coding variables present in the contact database not included in the case database. Residential addresses which were reported for close contacts were tabulated and imported into ArcGIS Pro and geocoded through the ArcGIS World Geocoding Service. The ArcGIS Pro spatial join geoprocessing tool was used to convert the individual zip code points to the mapped zip code, by using public zip code tabulation areas (ZCTAs) for 2020 (United States Census Bureau, 2021). Any close contact whose address was in the continental United States and reported is mapped here.

Age was calculated by subtracting the index case report date from the contact's date of birth and rounding down to the nearest whole number. Age categories were then done in the same manner as in chapter 1, outlined in section 1.3.2. Residence type was coded as private residence, apartment, dormitory, supported living, and other. Race/ethnicity was coded as white, non-Hispanic, Hispanic, black, Asian, other race, and missing race. All variables with a binary no/yes strata were coded as no or yes and other or unknown categories were marked as missing. The contact's relationship to the confirmed case was coded as household/family, roommate, friend, co-worker, and other. The location where a contact was exposed by the case was categorized as household, work, community, contact or case visited home, school/university, and other. Testing in the recommended window for the close contact was calculated by subtracting the test date of the close contact from their exposure date. Testing in the recommended window was then categorized as testing in three to seven days after exposure or testing too early/too late (outside three to seven days); continuous exposures were excluded from this variable.

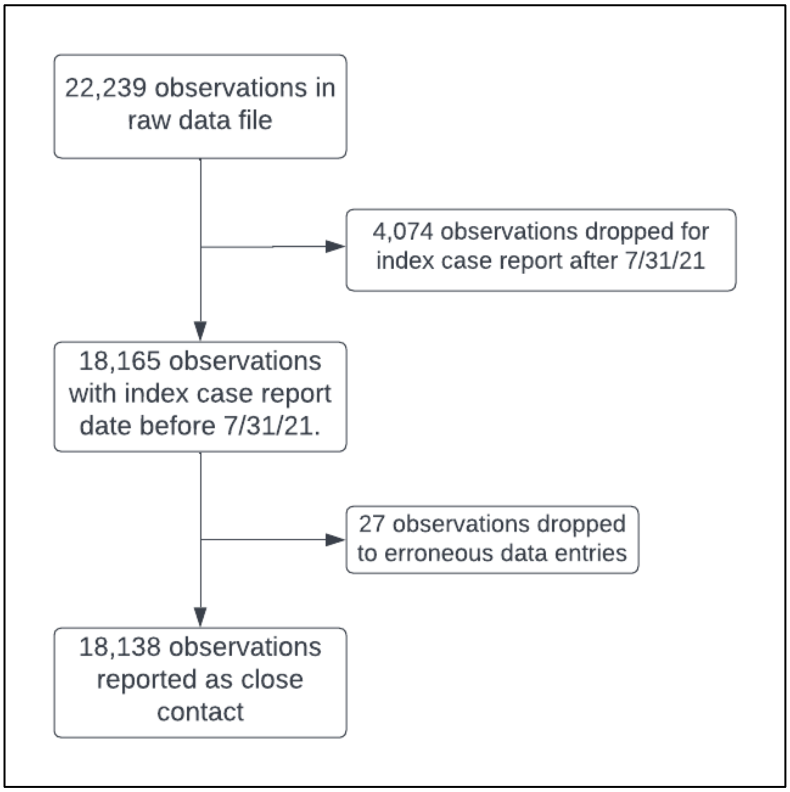
Syndromes were defined as in chapter 1.3.2. Descriptive characteristics of each variable in the contact database were tabulated for bivariate analysis. Bivariate analysis was done for each variable against whether someone tested before or after a call from a contact tracer and for variables against if they tested for SARS-CoV-2 within the recommended window.

Logistic regression was completed for two outcomes with a series of predictors all entered the model and then removed based on p-values (<0.05) and 95% confidence intervals (which do not cross 1.0) of each predictor. The two outcomes assessed here were whether someone tested before or after a call from a contact tracer and if they tested within the recommended window (three to seven days after exposure). Predictors were identified based on significance in chi-square testing. Following logistic regression, stepwise regression was completed with the same predictors.

4.4. Results

Data was extracted on January 28, 2022, and there were 22,239 observations in the raw data file of the Contact database. Of these, 4,074 observations were dropped for having an index case report date after July 31, 2021. An additional 27 observations were dropped to erroneous index case test results for a total sample size of 18,138 observations.

Figure 26: Flowchart of close contacts in the study. Flowchart was created in Lucidchart.



Majority of the close contacts whose addresses were reported were in Texas, isolated close contacts were reported in New Mexico, Colorado, South Carolina, and Georgia. The highest frequency of close contacts reported were in College Station zip codes. Zip codes not mapped here were 77608 (1 [0.01%]), 77805 (14 [0.17%]), 77806 (7 [0.09%]), 77841 (2 [0.02%]), 77842 (7 [0.09]), 77843 (10 [0.12%]), 77847 (1 [0.01%]), and 77849 (2 [0.02%]). This yielded a total of 44 close contacts not mapped.

Figure 27: Close contacts mapped from the BCHD contact database by zip code

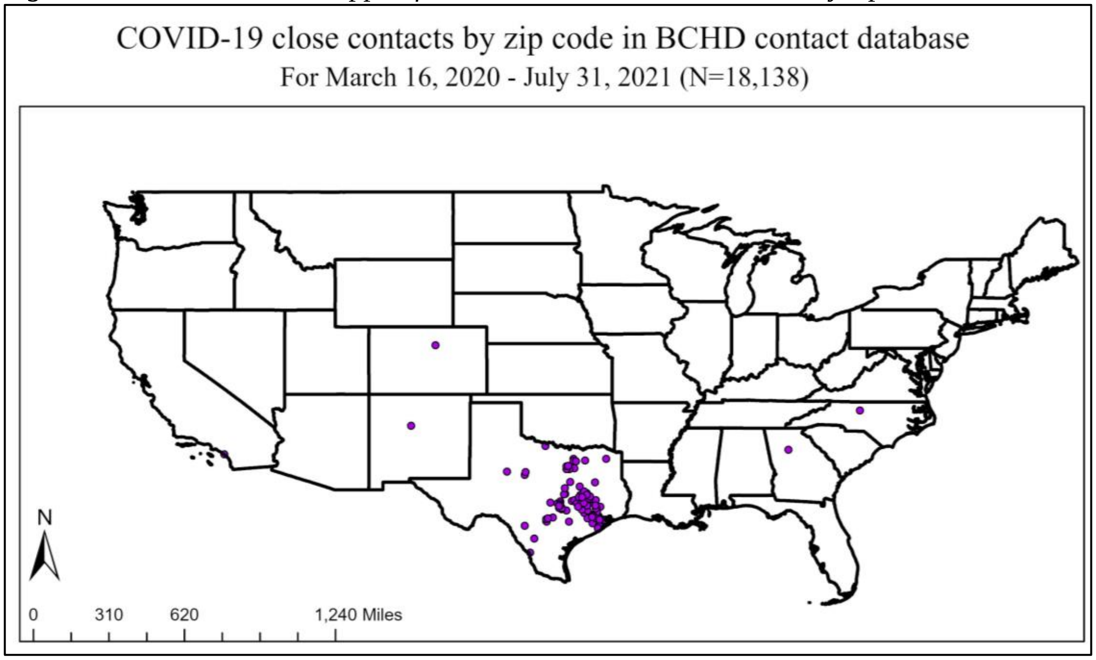
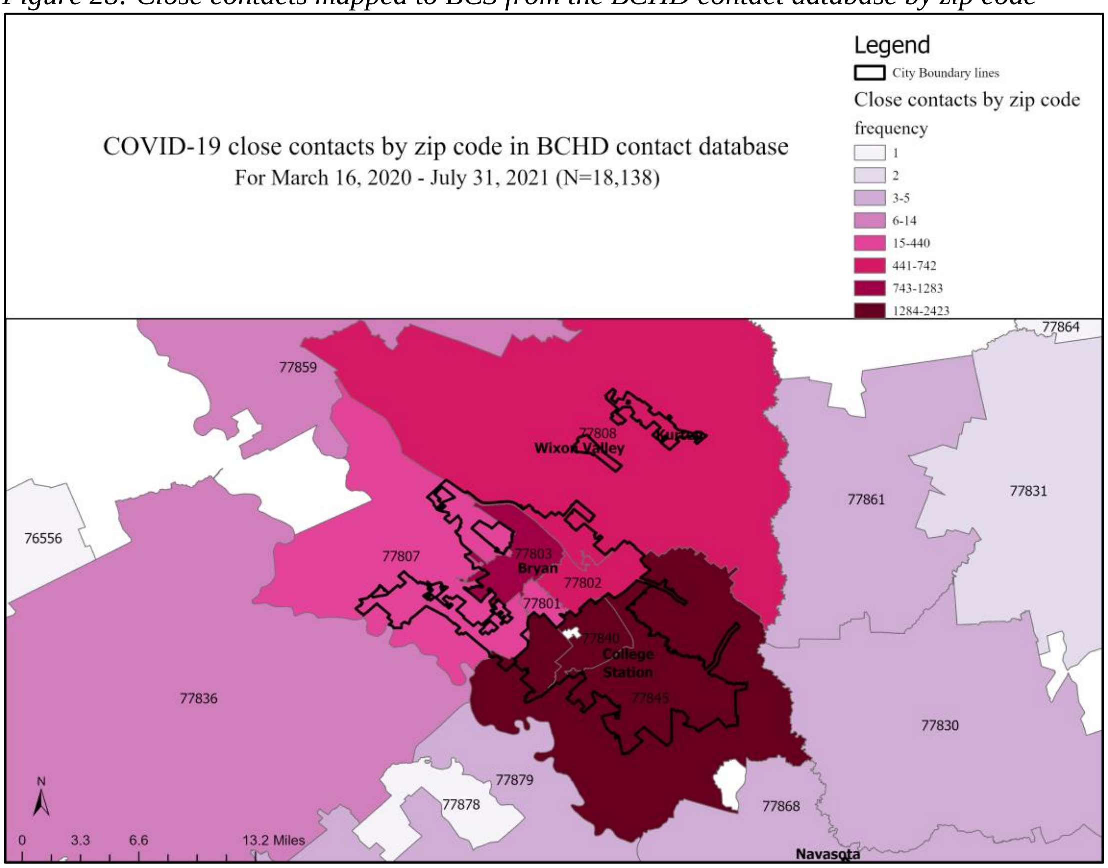


Figure 28: Close contacts mapped to BCS from the BCHD contact database by zip code



4.4.1 Descriptive characteristics

Demographics

From March 16, 2020 to July 31, 2022, there were 18,138 individuals reported as close contacts for COVID-19 in Brazos County, Texas. Most contacts had missing data points throughout the dataset (51.4% missing age, 64.9% missing race). Out of 8,819 respondents, there were 1,330 (7.3%) ages 0-11 years, 845 (4.7%) ages 12-17 years, 3,693 (20.4%) ages 18-29 years, 921 (5.1%) ages 30-39 years, 752 (4.2%) ages 40-49 years, 888 (4.9%) ages 50-64 years, and 390 (2.2%) over ages 65. The primary language spoken out of those who responded was English (91.4%). The median age was 21 with a range of 0-96. Approximately a quarter of individuals did not provide information on their sex, while 7,344 (40.5%) are female and 6,797 (37.5%) male.

Figure 29: Frequency of close contact's ages with kernel and normal density. In the distribution of ages blue line is kernel density and brown line is normal density

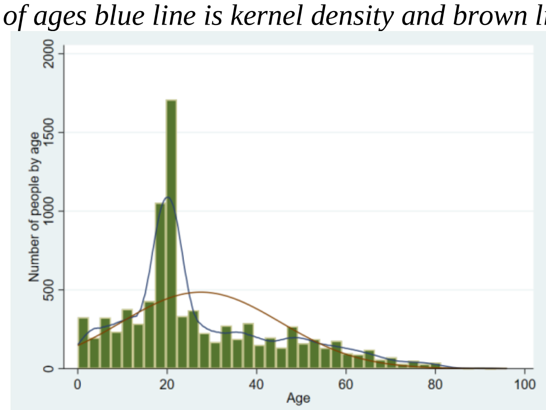


Figure 30: Language reported among close contacts.

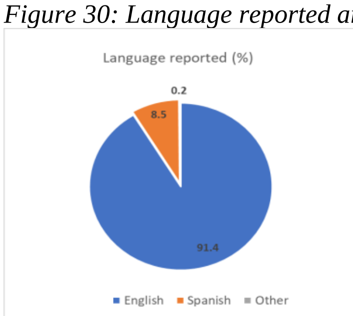


Table 64: Close contact characteristics for age by decade, language, and sex.

	Frequency (n)	Percent (%)
Age (years)		
Ages 0-11	1,330	7.3
Ages 12-17	845	4.7
Ages 18-29	3,693	20.4
Ages 30-39	921	5.1
Ages 40-49	752	4.2
Ages 50-64	888	4.9
Ages 65+	390	2.2
Missing or unknown	9,319	51.4
Age (years)		
Ages 0-9	1,083	6.0
Ages 10-19	2,145	11.8
Ages 20-29	2,640	14.6
Ages 30-39	921	5.1
Ages 40-49	752	4.2
Ages 50-59	658	3.6
Ages 60-69	392	2.2
Ages 70-79	181	1.0
Ages 80-89	36	0.2
Ages 90-99	11	0.1
Missing or unknown	9,319	51.4
Language		
English	7,341	40.47
Spanish	683	3.77
Other	12	0.07
Missing or unknown	10,102	55.7
Sex		
Female	7,344	40.49
Male	6,797	37.47
Missing or unknown	3,997	22.04
Total	18,138	100

Only 6,376 individuals responded to race, leaving most (11,762 [64.8%]) missing. 5,521 (30.4%) self-reported as white, 493 (2.7%) as black, 338 (1.9%) as Asian, and 24 (0.13%) identified as other race. Questionnaire options for ethnicity were

Hispanic or Latino (2,471 [13.6%]), Not Hispanic or Latino (4,233 [23.3%]), and Unknown (11,762 [64.8%]). Race/ethnicity combined reported 3,386 (18.9%) white, non-Hispanic, 2,441 (13.5%) Hispanic, 493 (2.7%) black, 338 (1.9%) Asian, and 11,078 (61.1%) missing race.

Figure 31: Race/ethnicity reported among close contacts

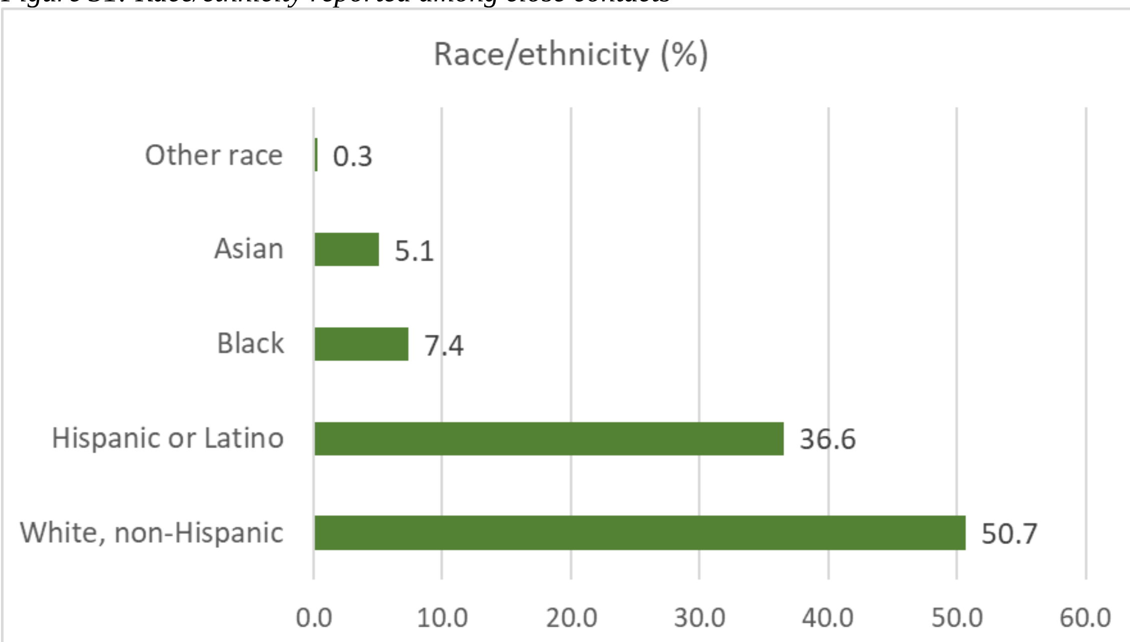


Table 65: Characteristics of close contacts for race, ethnicity, and race/ethnicity

	Frequency (n)	Percent (%)
Race		
White	5,521	30.44
Black	493	2.72
Asian	338	1.86
Other	24	0.13
Missing or unknown	11,762	64.85
Hispanic		
No, NOT Hispanic or Latino	4,233	23.34
Yes, Hispanic or Latino	2,471	13.62
Missing or unknown	11,434	63.04
Race/ethnicity		
White, non-Hispanic	3,386	18.67
Hispanic	2,441	13.46
Black	493	2.72
Asian	338	1.86
Other race	19	0.1
Missing or unknown	11,461	63.19
Total	18,138	100

Most of the close contacts who provided their residence type (5,794 [31.9%]) live in a house. The second most common housing type was apartment (1,256 [6.9%]) followed by dormitory (438 [24%]). Most information in the housing category was unknown (10,592 [58.4%]). Only 1,990 (11%) patients reported as being employed, and 3,900 (21.5%) identified as being a student or daycare attendee.

Figure 32: Residence type reported among close contacts.

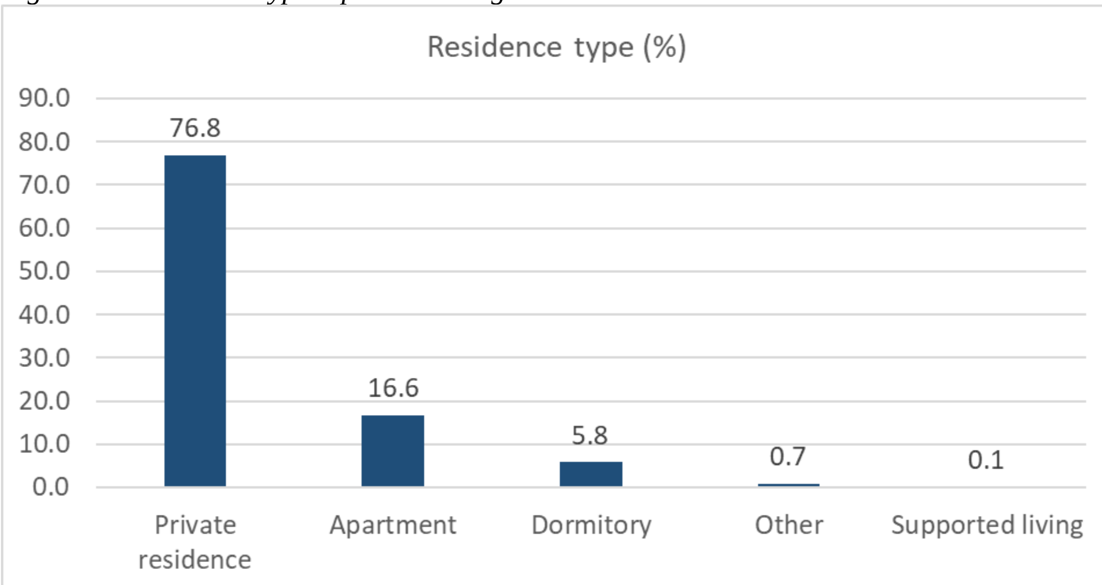


Figure 33: Student/daycare attendees reported among close contacts.

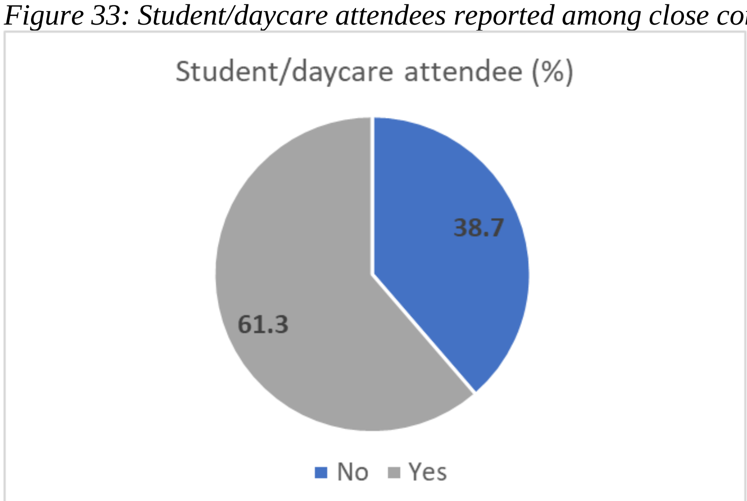


Table 66: Characteristics of close contacts for residence type, employment status, and student or daycare status

	Frequency (n)	Percent (%)
Residence type		
House	5,794	31.94
Apartment	1,256	6.92
Dormitory	438	2.41
Supported living	4	0.02
Other	54	0.3
Missing or unknown	10,592	58.4
Employment status		
Yes	1,990	10.97
No	2,304	12.7
Missing or unknown	13,844	76.33
Student or daycare attendee		
Yes	3,900	21.5
No	2,459	13.56
Missing or unknown	11,779	64.94
Total	18,138	100

Symptoms and medical history

Most close contacts did not report feeling symptoms either through prompting of individual symptoms (fever, cough, etc.) or by asking if they had felt any symptoms (5,972 [32.9%] felt no symptoms; 7,965 [43.9%] missing or unknown). There was a low prevalence of answers to the medical history, risk factors, and behaviors questions.

Figure 34: Clinical presentation among close contacts

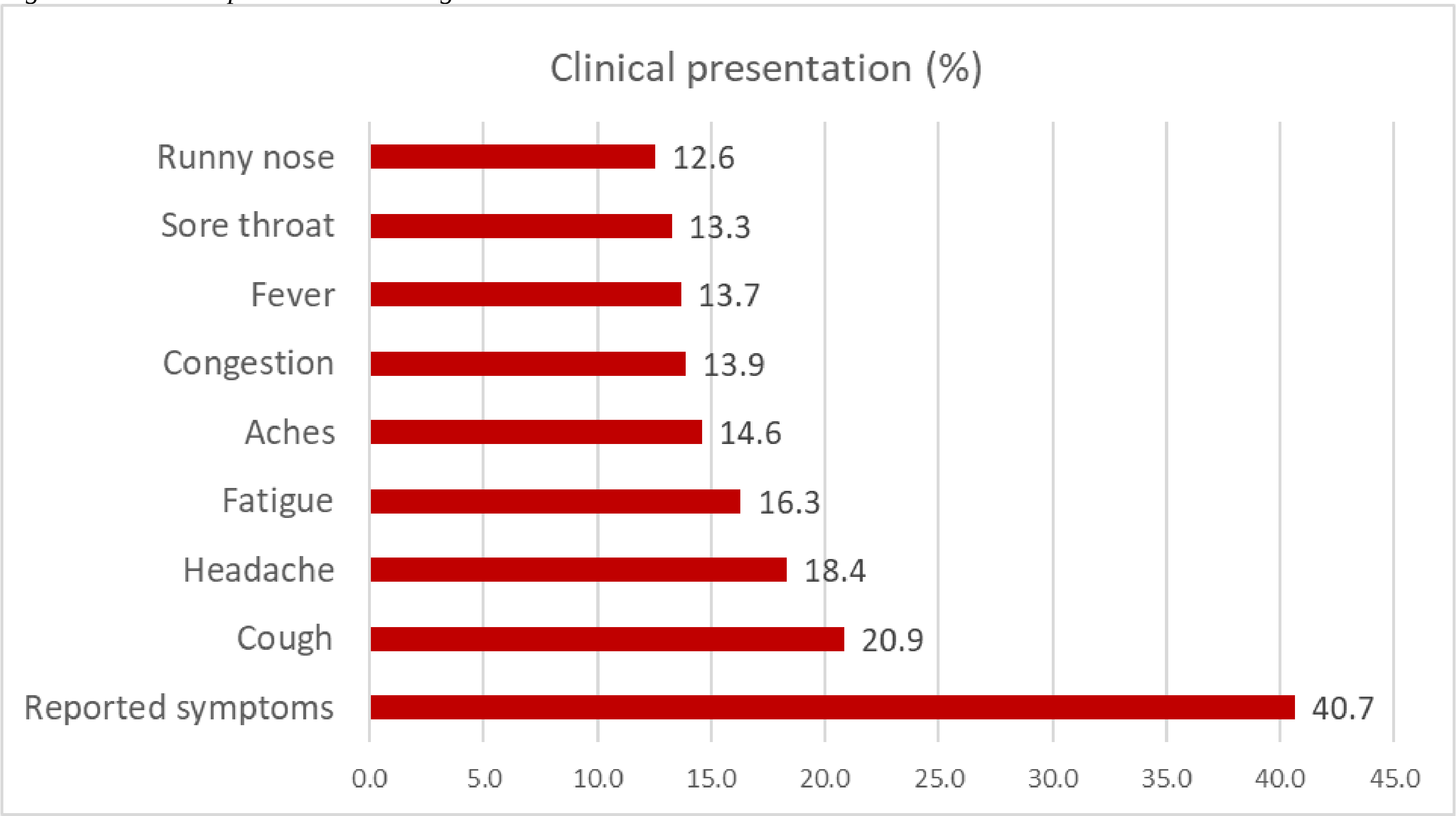


Table 67: Characteristics of close contacts' clinical presentation

Fever	Frequency (n)	Percent (%)
Yes	655	3.61
No	4,140	22.83
Missing or unknown	13,343	73.56
Cough		
Yes	1,027	5.66
No	3,894	21.47
Missing or unknown	13,217	72.87
Sore throat		
Yes	632	3.48
No	4,133	22.79
Missing or unknown	13,373	73.73
Headache		
Yes	888	4.9
No	3,950	21.78
Missing or unknown	13,300	73.33
Aches		
Yes	702	3.87
No	4,101	22.61
Missing or unknown	13,335	73.52
Runny nose		
Yes	592	3.26
No	4,126	22.75
Missing or unknown	13,420	73.99
Congestion		
Yes	654	3.61
No	4,054	22.35
Missing or unknown	13,430	74.04
Fatigue		
Yes	782	4.31
No	4,017	22.15
Missing or unknown	13,339	73.54
Symptoms		
Yes	4,201	23.16
No	5,972	32.93
Missing or unknown	7,965	43.91
Total	18,138	100

Exposure questions

During the initial case investigation with the index case and prior to initiating a call to the close contact, the index case was asked their relationship to the contact in question. 10,191 (56.2%) reported a household or family relationship, 3,255 (18.0%) differentiated the relationship as a roommate, 2,194 (12.1%) said they were friends, 890 (4.9%) reported a co-worker, and 619 (3.4%) listed other relationship. A small percentage of contacts had missing information on their relationship to the index case (989 [5.5%]). When the index case was asked where the exposure most likely occurred, 12,560 (69.3%) reported a household exposure, 802 (4.4%) a workplace exposure, 803 (4.4%) a community exposure, 780 (4.3%) a contact or case visited the home, 228 (1.3%) a school/university exposure, 734 (4.1%) listed other exposure location, and 2,231 (12.3%) had unknown information. Approximately a third of individuals reported on ongoing exposure to their index case, rather than a discrete exposure event, such as living with the index case where physical separation was not possible.

Figure 35: Contact's relationship to their index case

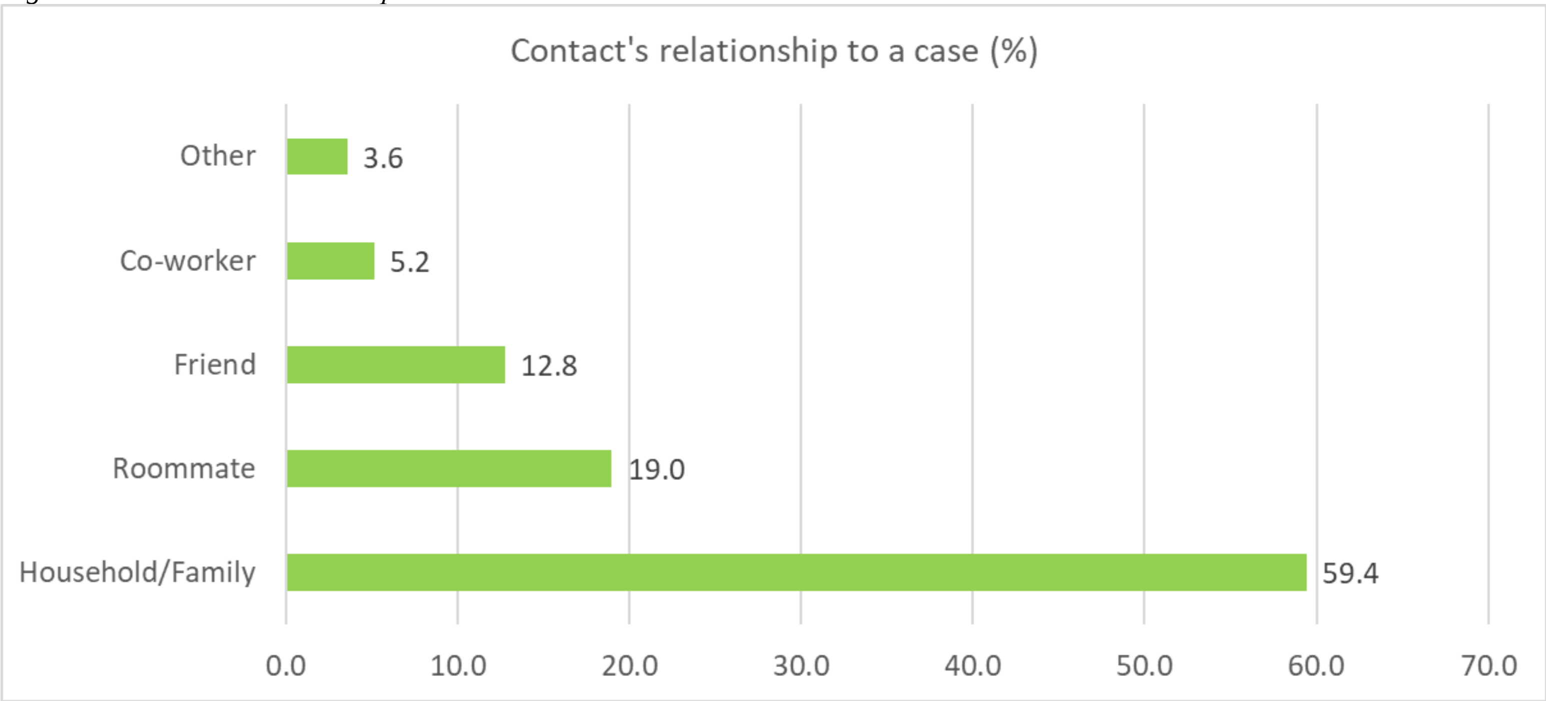


Figure 36: Known location the close contact was exposed.

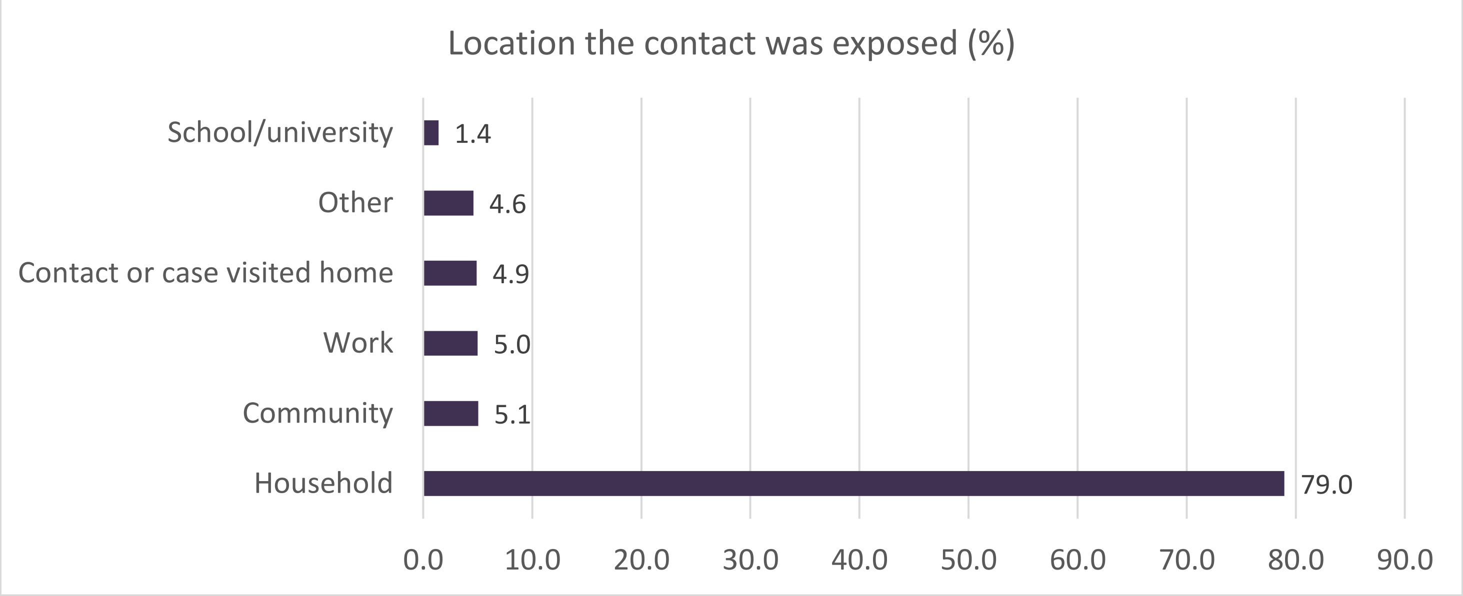


Figure 37: Reported continuous exposure among close contacts

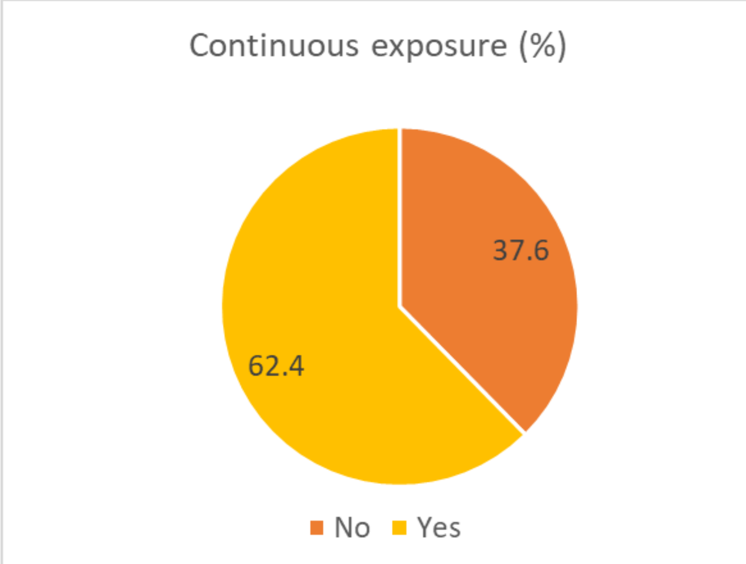


Table 68: Characteristics of exposure questions among close contacts

	Frequency (n)	Percent (%)
Contact's relationship to case		
Household/Family	10,191	56.2
Roommate	3,255	18.0
Friend	2,194	12.1
Co-worker	890	4.9
Other	619	3.4
Missing or unknown	989	5.5
Where did exposure most likely occur?		
Household	12,560	69.3
Work	802	4.4
Community	803	4.4
Contact or case visited home	780	4.3
School/university	228	1.3
Other	734	4.1
Missing or unknown	2,231	12.3
Was there continuous exposure?		
Not continuous exposure	5,449	30.0
Continuous exposure	9,030	49.8
Missing or unknown	3,659	20.2
Total	18,138	100.0

Out of contacts with a specific exposure date, 433 (28.7%) tested less than 3 days after exposure, 511 (33.9%) tested three to five days post exposure, and 564 (37.4%) tested five to ten days after exposure. When categories were collapsed to testing in the recommended window or too early/too late, there was a comparable proportion of individuals in each category. Out of those who provided SARS-CoV-2 testing information to the contact tracer, 3,448 (19.0%) reported testing prior to being called, 441 (2.4%) reported testing after being called, and 14,470 (78.6%) were missing or unknown.

Figure 38: How soon after exposure the close contact was exposed (excluding continuous exposure).

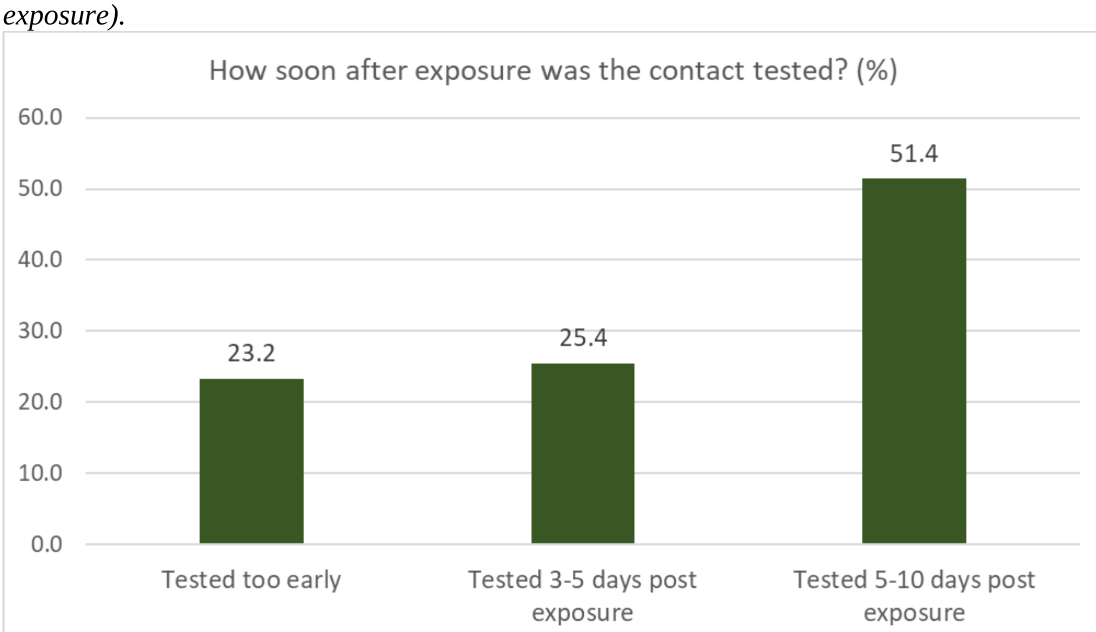


Figure 39: Close contacts who did or did not test in the recommended window (excluding continuous exposure).

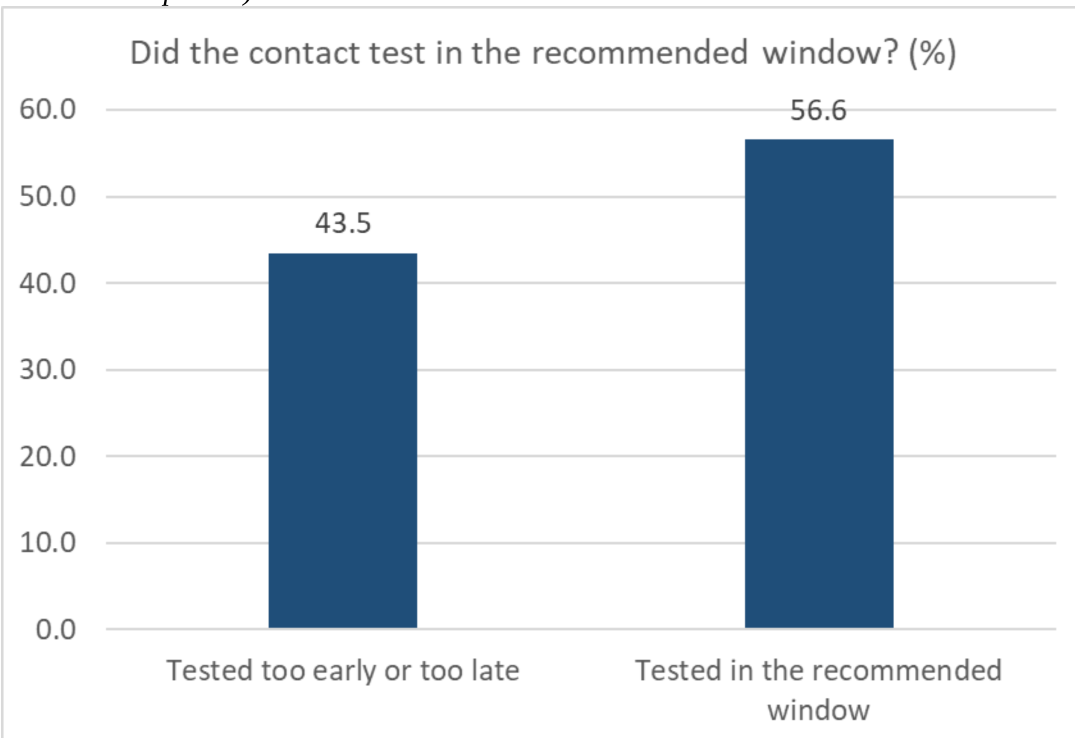


Figure 40: Whether the close contact tested before or after being called by a contact tracer.

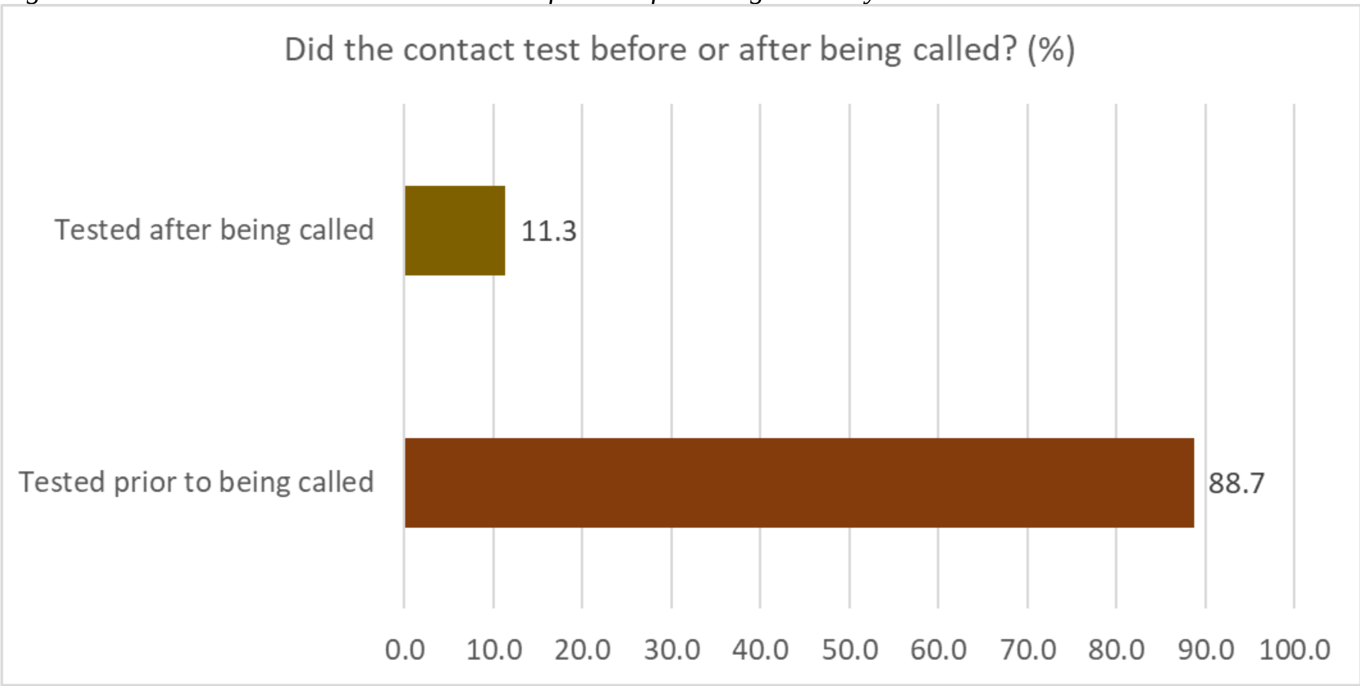


Table 69: Characteristics of close contact testing questions

	Frequency (n)	Percent (%)
How soon after exposure did the contact get tested for COVID-19?		
Tested 1-2 days after exposure	433	2.4
Tested 3-5 days post exposure	511	2.8
Tested 5-10 days after exposure	564	3.1
Missing or unknown	16,630	91.7
Did the contact test in the recommended window?		
Tested too early or too late	810	4.5
Tested in the recommended window	1,054	5.8
Missing or unknown	16,274	89.7
Did the contact get tested before or after being called?		
Tested prior to being called	3,448	19.0
Tested after being called	441	2.4
Missing or unknown	14,249	78.6
Total	18,138	100.0

Contact Tracer Documentation

The contact tracer was required to mark each stage of the contact tracing process with incomplete, unverified, or complete. At the end of the first contact tracing interview, 9,199 (50.7%) were incomplete, 723 (4.0%) were unverified, and 8,216 (45.3%) were complete. At the end of the second contact tracing interview, 16,716 (92.2%) were incomplete, 51 (0.3%) were unverified, and 1,371 (7.6%) were complete. The last step for contact tracers was to fill out the investigator log indicating if they had finished or were closing out the report with the same options of incomplete (5,188 [28.6%]), unverified (156 [0.9%]), and complete (12,794 [70.5%]).

Table 70: Distribution of completed contact interviews

	Frequency (n)	Percent (%)
Did the investigator complete the first contact interview?		
Incomplete	9,199	50.7
Unverified	723	4.0
Complete	8,216	45.3
Total	18,138	100.0
Did the investigator complete the second contact interview?		
Incomplete	16,716	92.2
Unverified	51	0.3
Complete	1,371	7.6
Total	18,138	100.0
Did the investigator complete the investigator log?		
Incomplete	5,188	28.6
Unverified	156	0.9
Complete	12,794	70.5
Total	18,138	100.0

4.4.2 Comparing variables among close contacts

Bivariate analysis was done for two variables: if the close contact tested for SARS-CoV-2 before/after a call from a contact tracer and if the close contact tested in the recommended window. These variables were each compared to demographics, exposure questions, feeling symptoms, medical history, and university affiliation. Chi-square test of association and Fisher's exact test were both used in these comparisons.

Household residence type was related to a close contact testing before being contacted by a contact tracer (X^2 13.5, p=0.009). If a contact felt symptoms, they were more likely to be tested before a contact tracer call (X^2 p<0.001). None of the close contacts' medical history had a significant relationship with their timeframe of being tested based on chi-square p-value above 0.05.

There were multiple behaviors significantly related with the testing timeframe of SARS-CoV-2 before/after a call from a contact tracer. Indoor gatherings of less than five people and attending an indoor gathering of 20 to 50 people had significant associations with testing for SARS-CoV-2 before/after a contact tracing call. Specific locations a close contact visited with a significant a chi square test and testing for SARS-CoV-2 before/after a contact tracing call were visiting a grocery store, gym/fitness center, going to work in person, a library, or doctor's office. Individuals affiliated with the university more frequently tested before being contacted by a contact tracer (X^2 21.3, $p<0.001$).

Table 71: Distribution of variables compared to testing before/after a call from a contact tracer.

	Tested before or after call from contact tracer			X2
	Before n (row %)	After n (row %)	Total	Pearson p-value
Residence type				
House	1,463 (89.0)	180 (11.0)	1,643	13.5
Apartment	537 (85.9)	88 (14.1)	625	0.009
Dormitory	233 (82.9)	48 (17.1)	281	
Supported living	1 (100.0)	0 (0.0)	1	
Other	20 (100.0)	0 (0.0)	20	
Total	2,254 (87.7)	316 (12.3)		
Reported symptoms				
Yes	961 (90.2)	104 (9.8)	1,065	4.2
No	1,700 (87.8)	237 (12.2)	1,937	0.041
Total	2,661 (88.6)	341 (11.4)	3,002	
Indoor gathering <5				
Checked	11 (64.7)	6 (35.3)	17	9.7
Unchecked	3,437 (88.8)	435 (11.2)	3,872	0.002
Total	3,448 (88.7)	441 (11.3)	3,889	
Indoor gathering 20-50				
Checked	1 (33.3)	2 (66.7)	3	9.1
Unchecked	3,447 (88.7)	439 (11.3)	3,886	0.002
Total	3,448 (88.7)	441 (11.3)	3,889	
Grocery				
Checked	236 (83.4)	47 (16.6)	283	8.4
Unchecked	3,212 (89.1)	394 (89.3)	3,606	0.004
Total	3,448 (88.7)	441 (11.3)	283	
Gym or fitness center				
Checked	32 (74.4)	11 (25.6)	43	8.8
Unchecked	3,416 (88.8)	430 (11.2)	3,846	0.003
Total	3,448 (88.7)	441 (11.3)	3,889	
Work in person				
Checked	76 (79.2)	20 (20.8)	96	8.8
Unchecked	3,372 (88.9)	421 (11.1)	3,793	0.003
Total	3,448 (88.7)	441 (11.3)	3,889	
Library				
Checked	8 (61.5)	5 (38.5)	13	9.5
Unchecked	3,440 (88.8)	436 (11.3)	3,876	0.002
Total	3,448 (88.7)	441 (11.3)	3,889	
Doctor’s office				
Checked	48 (78.7)	13 (21.3)	61	6.1
Unchecked	3,400 (88.2)	428 (11.2)	3,828	0.013
Total	3,448 (88.7)	441 (11.3)	3,889	
University affiliation				
Yes	655 (84.0)	125 (16.0)	780	21.3
No	2,793 (89.8)	316 (10.2)	3,109	<0.001
Total	3,448 (88.7)	441 (11.3)		

A contact's relationship to their index case, continuous exposure, location exposure, and known contact with a prior case - each made the contact more likely to be tested for SARS-CoV-2 prior to a contact tracing interview.

Table 72: Comparing exposure between index case and contact

	Tested before or after being called		Total	X2 Pearson p-value
	Before n (row %)	After n (row %)		
Contact's relationship to case				
Household	1,493 (89.4)	178 (10.7)	1,671	21.3
Roommate	931 (89.5)	109 (10.5)	1,040	<0.001
Friend	577 (89.0)	71 (11.0)	648	
Co-worker	197 (79.8)	50 (20.2)	247	
Other	126 (87.5)	18 (12.5)	144	
Total	3,324 (88.6)	426 (11.4)	3,750	
Known prior contact				
Yes	74 (92.5)	6 (7.5)	80	9.5
No	51 (73.9)	18 (26.1)	69	0.002
Total	125 (83.9)	24 (16.1)	149	
Continuous exposure				
Yes	1,483 (91.3)	142 (8.7)	1,625	22.8
No	1,562 (86.1)	253 (13.9)	1,815	<0.001
Total				
Location of known exposure				
Household	2,367 (89.3)	284 (10.7)	2,651	27.7
Work	183 (78.5)	50 (21.5)	233	<0.001
Community	230 (87.8)	32 (12.2)	262	
Contact or Case visited home	136 (91.9)	12 (8.1)	148	
School/university	57 (87.7)	8 (12.3)	65	
Other	165 (91.2)	16 (8.8)	181	
Total	3,138 (88.6)	402 (11.4)	3,540	

Bivariate analysis for individuals testing within the recommended window versus testing too early or too late presented a significant relationship between age, language, and residence type. Each of these relationships were tested through chi-square and Fisher's exact test and had a p-value of <0.05.

Table 73: Descriptive characteristics for the timeframe of testing

	Timeframe tested			X2
	Too early/too late n (row %)	Rec. window n (row %)	Total	Pearson p-value
Age (years)				
0-9	15 (51.7)	14 (48.3)	29	16.5
10-19	203 (48.1)	219 (51.9)	422	0.036
20-29	387 (43.5)	503 (56.5)	890	
30-39	41 (42.7)	55 (57.3)	96	
40-49	20 (30.8)	45 (69.2)	65	
50-59	21 (30.9)	47 (69.1)	68	
60-69	16 (37.2)	27 (62.8)	43	
70-79	4 (44.4)	5 (55.6)	9	
80-89	4 (80.0)	1 (20.0)	5	
Total	711	916	1,627	
Language				
English	678 (43.3)	888 (56.7)	1,566	6.1
Spanish	5 (19.2)	21 (80.8)	26	0.047
Other	2 (50.0)	2 (50.0)	4	
Total	685 (42.9)	911 (57.1)	1,596	
Residence type				
House	263 (46.9)	341 (49.2)	604	8.0
Apartment	180 (43.4)	245 (57.7)	425	0.045
Dormitory	111 (51.6)	104 (48.4)	215	
Other	7 (70.0)	3 (30.0)	10	
Total	561 (44.7)	693 (55.3)	1,254	

4.4.3 Factors related to testing before or after call from a contact tracer

To identify what factors had a specific effect on someone testing before or after a call from a contact tracer, multivariate regression was run. Variables used in the model were identified from bivariate analysis ($p<0.05$) and included residence type, symptomatic status, attending an indoor gathering of less than five people, attending an indoor gathering of 20-50 people, visiting a grocery store, gym or fitness center, working in person, going to a library, going to a doctor's office, affiliated with the university, contact's relationship to the index case, continuous exposure, known prior contact with a case, and location of exposure.

The only variable kept in the model was prior contact with a laboratory confirmed case. Individuals who had close contact with a prior case were more likely to test for SARS-CoV-2 before being called by a contact tracer (OR: 0.2, p=0.004, 95% CI: [0.1-0.6]).

Table 74: Manual logistic regression for the outcome of testing before or after a call from a contact tracer. There were 149 people in the model.

Variable	**OR**	**p-value**	**95% CI**
Prior contact with a case	0.2	0.004	[0.1-0.6]

4.4.4 Factors assessing testing in the recommended window

The specific effect individual factors had on testing in the recommended window was assessed through multivariate regression. Variables identified through bivariate analysis ($p<0.05$) were age, language, residence type and symptomatic status.

The only variable predicting whether a close contact was tested in the recommended window was age. Ages 18-24 (OR: 0.79, p=0.047, 95% CI: [0.62-1.0]) were significantly more likely to test outside of the recommended window when compared to ages 25-64 years.

Table 75: Stepwise logistic regression with the outcome of testing in the recommended window of too early/too late. There were 1,540 people in the model.

Variable	**OR**	**p-value**	**95% CI**
Referent group (ages 25-64)			
Ages 18-24	0.79	0.047	[0.62-1.0]
Ages 65+	0.55	0.120	[0.26-1.2]

4.5. Discussion

4.5.1 Close contacts: demographics, clinical presentation, and medical history

Out of the close contacts who reported their age, the majority fell into the age categories of 0-9 years, 10-19 years, and 20-29 years. The highest proportion of close contacts were young adults in their twenties. These ages were expected to comprise most of the close contacts given the students housed at TAMU and Blinn College. Additionally, children may become close contacts through schools and daycare settings. Regarding language, 40% were English speakers, 4% were Spanish speakers, and about half did not have responses. When asked about ethnicity, 14% identified as Hispanic or Latino, 23% said not Hispanic or Latino but 63% did not have a response to the question. According to U.S. Census data, Brazos County is estimated to have approximately 26% Hispanic or Latino individuals (U.S. Census Bureau, 2020). It is possible the proportion of Hispanic or Latino are underrepresented in this dataset due to a low number of Spanish speaking contact tracers at the CoOp. Trust can also be a concern for this population, Hispanic individuals have been afraid to cooperate with contact tracing efforts due to immigration concerns (Galletly et al., 2021).

Only 4,201 (23.2%) individuals out of the 18,138 who were reported as close contacts reported feeling symptoms of an illness while 43.9% had missing information on symptomatic status. The most common symptoms out of those reported were cough, headache, fatigue, aches, congestion, fever, and sore throat. These symptoms align with most COVID-19 symptoms in the literature apart from gastrointestinal illnesses (Lee et al., 2020). This could be a result of a younger population in the close contact dataset leading to fewer comorbidities which were common with gastrointestinal COVID-19 symptoms.

The most frequent residence types were private residence or house, apartment, and dormitory. These residence types were as expected given the large young adult population in the dataset. In terms of employment status, 13,844 (76.3%) of the observations were missing – out of the respondents (4,294), a slight majority reported unemployed (2,304), while the remaining (1,990) reported employment. Most of the unemployment may be due to majority of close contacts in the young adult or child age groups. Furthermore, when asked if the close contact was a student or daycare attendee, out of respondents (6,359), most (3,900) reported yes, they were a student or daycare attendee. This supports the assertion that employment status was affected by student or daycare attendee status.

Medical history questions were asked of the close contacts. The most frequent comorbidities found among these close contacts were hypertension and a form of asthma (childhood or as an adult). Hypertension and asthma are both comorbidities found often in minorities such as black and Hispanic individuals (Zhang et al., 2019; Kramer et al., 2004). However, in this dataset contrary to literature, the comorbidities in this dataset were primarily in white, non-Hispanic individuals.

4.5.2 Close contacts characteristics of exposure and testing questions

Here, the relationship between the index case and their respective close contacts are discussed. Household and family relationships were the most frequently reported, followed by roommates, friend, and co-worker. Households, families, and roommates were common close contacts living in close quarters with each other. Households were by far the largest location of exposure occurrence. The index case was also asked what date they last exposed the close contact or if there is continuous exposure; most index cases reported continuous exposure. The exposure section tells a story in contact tracing where an individual tests positive for SARS-CoV-2, brings the virus into a home, and exposes people they are living with. In such situations, the case is not able to self-isolate and continuously exposes those they are living with.

Testing questions were divided into how soon after exposure was the close contact tested for SARS-CoV-2 and if they were tested before or after being called by the contact tracer. In the categorized test date of if the close contacts tested too early (433 [2.4%]), three to five days post exposure (511 [2.8%]), and five to ten days after exposure (564 [3.1%]), the proportions of respondents in each category were within one percentage point or less. Similarly, when the categories were collapsed to testing in the recommended window (810 [4.5%]) or too early/too late (1,054 [5.8%]), the categories were within one percentage point or less. This illustrates testing behavior following exposure was inconsistent.

Individuals could have tested too early for several reasons. Some individuals were likely worried and tested immediately, or they wanted a negative test to allow them to participate in events. Individuals could have been tested too late because they did not feel sick and did not want to get tested when they felt healthy. Additionally, some individuals may not have understood the messaging on the best timing to get tested for SARS-CoV-2. Public health messaging could be improved to a lower comprehension level to help ensure messaging reaches people equitably. If more individuals understand the best time to get tested, this can also aid testing infrastructure. In terms of testing infrastructure, the lack of predictability demonstrates testing centers could be quickly overwhelmed leading to delayed testing results and lack of people isolating and or quarantining.

For the question of if the close contact was tested for SARS-CoV-2 before or after being called by a contact tracer, 78.6% of close contacts had missing information, 2.4% tested after being called, and 19.0% had been tested before being called. The reasons for this change can be attributed to several factors. Some individuals did not want to comply with a contact tracer’s request to test again if the close contact tested too early. There was also significant difficulty in reaching people on the phone, which also speaks to the low number of completed contact tracing interviews.

The CoOp partnered with the media and requested the local media spread news about the contact tracing efforts to have more people pick up the phone when called, though this may have left out low-income households. Caller ID did not state the contact tracers were calling from BCHD or the CoOp, so the public was likely skeptical to pick up from an unknown caller. Those who did pick up did not always know the difference between questions a contact tracer would ask and questions a scammer would ask. Then they may have jumped to the conclusions the contact tracer was a scammer and refused to complete the interview.

Each of these factors are valuable lessons to be considered in future contact tracing efforts. The media can be partnered with immediately for streamlined communication with the public at the onset of the outbreak. Through this, public health professionals can communicate what phone number the public should expect to see on caller ID, what questions they will ask, and what questions they will never ask to differentiate from scammers.

4.5.3 Close contacts regression discussion: testing before or after a contact tracer call

Testing for SARS-CoV-2 before or after a call by a contact tracer was predicted by close contacts having prior contact with a confirmed laboratory case. Close contacts who knew they were exposed by someone who tested positive for SARS-CoV-2 were less likely to test after they were called by a contact tracer than those who did not know their index case.

Index cases often reported to the case investigator that they informed their close contacts of the exposure. It is possible the index case could pass on public health guidance from a case investigator, though there is no guarantee the index case would pass on information correctly. For this reason, contact tracing protocols should include guidance to index cases on not relaying testing information but instead encourage their close contacts to wait for a call from a contact tracer. This recommendation only applies for cases who inform their close contacts, which is not always accurate.

4.5.4 Close contacts regression discussion: testing in the recommended window

Testing in the recommended window (three to seven days post exposure) yielded ages 18-24 as the only significant predictor when compared to ages 25-64 years.

This age group could be testing outside of the recommended window for several reasons previously mentioned in this chapter. Most in this age group are in the most common age range for attending a university or college. These individuals may be testing quickly because they need a negative test to attend an event or travel. University student health centers could try to emphasize to students that testing too early would not give them accurate results, possibly putting their friends and family at risk.

4.5.6 Limitations

The contact tracing process and the close contact database have numerous limitations. The contact tracing was completed by a team of contact tracers trained by different individuals. Efficacy of the contact tracers was reliant upon their training; different training circumstances may have contributed to different levels of completion in each contact's file.

Contact tracing relies on information collected from the index case of the close contact. The index case must provide reliable information including, at minimum, the close contact's name, and phone number; if no phone number was available, an email address was accepted. In the case of only having an email address, some individuals were able to be looked up in the TAMU database for their phone number for a contact tracer to call the close contact. If no phone number was found, the close contact was reached out to via email from the CoOp's email address. Yet, in these instances, the email had to be received by the close contact and may have gone into a spam folder.

Many index cases did not want to provide personal information on their friends, viewing it as a violation of their privacy. Those who did provide information, may not have provided accurate information, preventing us from being able to reach those individuals. Regardless of accurate information, a file in the contact database was created for each close contact. A contact tracer attempted to reach every close contact at least three times with at least 24 hours between each attempt. Successful communication relied upon the individual picking up the phone, but caller ID did not always register BCHD. If the individual's caller id did not register BCHD or TAMU, the call may show up as spam, and the close contact would not respond.

There may have also been factors preventing close contacts from getting tested. College Station had more testing sites given the testing program at the University than the City of Bryan. Households in Bryan had lower median income levels and a higher percentage of minorities. One way to prevent this in the future is to set up testing sites by population density so each community has a higher chance of reaching a testing site if needed.

Exposure questions such as continuous exposure, relationship to the close contact, and location of the exposure relied on the memory and cooperation of the index case. Furthermore, some index cases insisted on delivering guidance to the close contact themselves and refused to allow trained contact tracers to communicate with their close contact.

Lastly, the primary effort made by the CoOp and public health professionals was to respond to the active outbreaks in the community. Consequently, when an outbreak of COVID-19 occurred, contact tracers were re-assigned to investigate cases as needed so people currently fighting the disease could get the help and information they need. Each time contact tracers were re-assigned to assist an outbreak, the number of close contacts able to be called decreased. The CoOp was also limited by working space, as only a set number of individuals could work at a given time to maintain physical distancing.

4.5.7 Concluding thoughts

The question of, which came first: contact tracing or testing, was clearly answered in this chapter as most close contacts who reported their testing date were not tested before a call from a contact tracer. This speaks to the limitations of the contact tracing effort as well as the difficulty in reaching contacts on the telephone. However, there are still lessons learned and recommendations made on how future contact tracing efforts could be improved.

5. MATHEMATICAL MODELLING OF COVID-19 ON A UNIVERSITY CAMPUS

5.1 Introduction

Mathematical modelling in infectious disease research is a process to predict and or demonstrate how a pathogen will react and transmit in a community. It has been an evolving practice since its inception with Daniel Bernoulli using mathematical modeling with vaccination and smallpox (Hethcote, 2000). The most widely used and simple model is the linear S-I-R, where each letter represents a compartment in the population: Susceptible, Infected, and Recovered. The S-I-R model can be expanded to represent a group of people exposed to the pathogen to S-E-I-R, where the exposed compartment is set prior to the Infected and Recovered compartments.

In the context of a novel or emerging pathogen such as SARS-CoV-2, the entire population is considered susceptible prior to the start of its spread. SARS-CoV-2 has reached every major continent, infecting people in almost, if not all, countries across the world. Initial research showed everyone who has been infected and recovered from the disease may be considered to have a natural immune response for up to eight months following initial infection (Dan et al., 2020). However, more recent studies have shown natural immunity against SARS-CoV-2 can decay in 90 days (UNMC, 2021).

5.1.1 Introduction to the S-E-I-R model

A mathematical S-E-I-R based model involves setting several parameters. Basic parameters include the population size (N), number of contacts per unit time (C), pathogen infectivity (p), duration of infection (D), incubation period, and basic reproduction number (R_0). Equations for these parameters are shown below.

Equation 1: population size: $N = S + E + I + R$

Equation 2: transmission rate: $\beta = c * p$

Equation 3: force of infection: $\lambda = \frac{\beta * I}{N}$

Equation 4: Recovery rate: $\gamma = \frac{1}{D}$

Equation 5: basic reproductive number: $R_0 = \frac{\beta}{\gamma}$

These parameters can be set based on published literature, based on estimates, or calculated based on a dataset. The Equations of the S-E-I-R model are shown below.

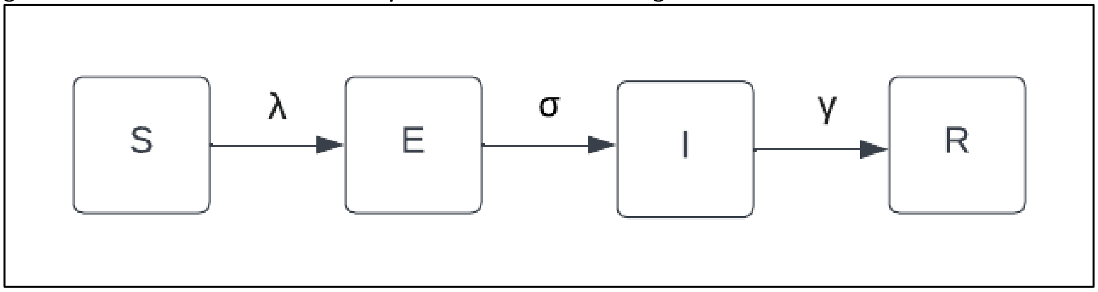
Equation 6: $\frac{dS}{dt} = -\lambda S$

Equation 7: $\frac{dE}{dt} = \lambda S - \sigma E$

Equation 8: $\frac{dI}{dt} = \sigma E - \gamma I$

Equation 9: $\frac{dR}{dt} = \gamma I$

Figure 41: A basic S-E-I-R model, flowchart created using Lucidchart.



However, this basic S-E-I-R model assumes the epidemic takes place in a fully susceptible population, no vaccine is present, and no death. To adjust for death, the mortality rate (μ) needs to be taken into consideration and subtracted from each compartment. After adjusting for the mortality rate, the S-E-I-R equations are as follows (Keeling & Rohani, 2008):

Equation 10: $\frac{dS}{dt} = \mu - (\beta I + \mu)S$

Equation 11: $\frac{dE}{dt} = \beta SI - (\mu + \sigma)E$

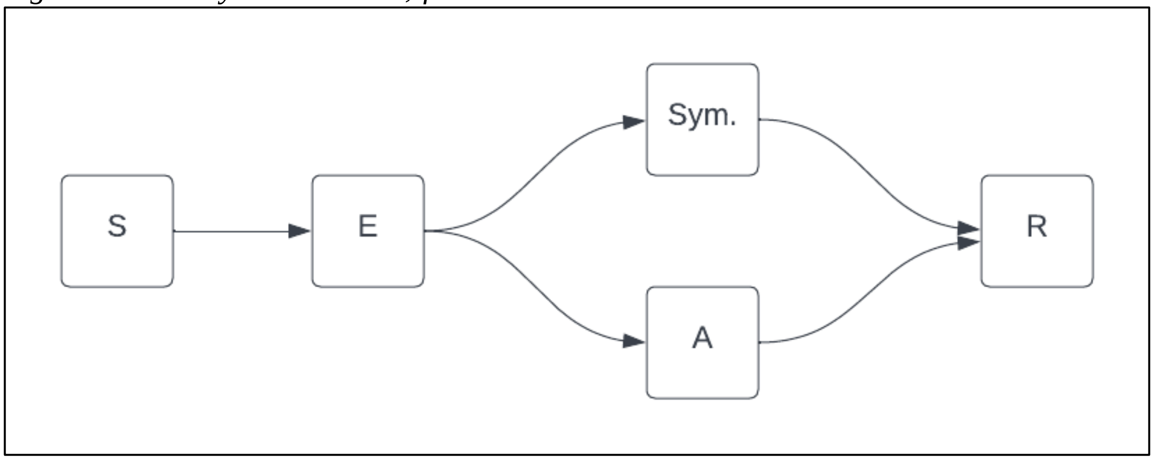
Equation 12: $\frac{dI}{dt} = \sigma E - (\mu + \gamma)I$

Equation 13: $\frac{dR}{dt} = \gamma I - \mu R$

5.1.2 S-E-Sym-A-R model

In an S-E-Sym-A-R model, susceptible individuals move into the exposed compartment before being divided into symptomatic and asymptomatic compartments.

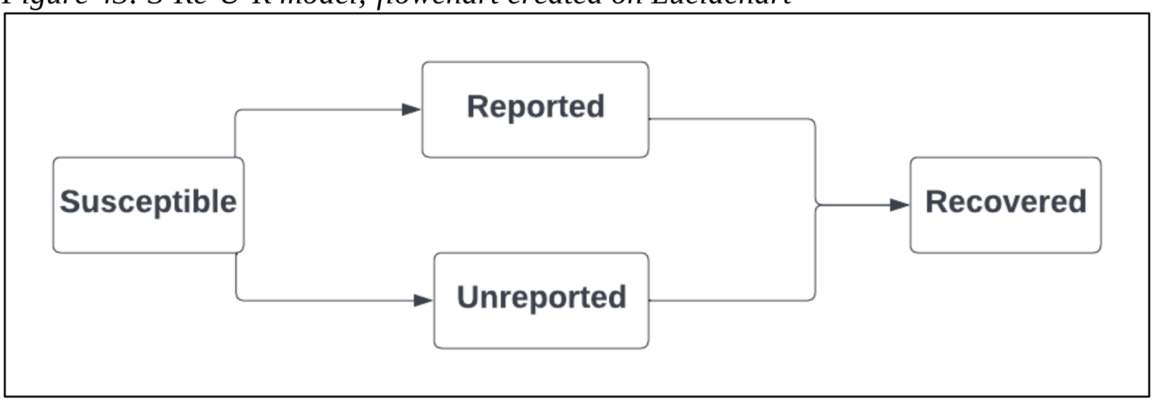
Figure 42: S-E-Sym-A-R model; flowchart created on Lucidchart



5.1.3 S-Re-U-R model

The S-Re-U-R model looks at susceptible, infected/reported, infected/not-reported, and recovered.

Figure 43: S-Re-U-R model; flowchart created on Lucidchart



Equation 14: Susceptible: $\frac{dS}{dt} = \frac{(-\beta * S * (Re + \varepsilon * U))}{N} + \lambda * R$

Equation 15: Reported: $\frac{dRe}{dt} = \frac{pr * (\beta * S * (Re + \varepsilon * U))}{N} - \gamma S * Re$

Equation 16: Unreported: $\frac{dU}{dt} = \frac{(1 - pr) * (\beta * S * (Re + \varepsilon * U))}{N} - \gamma U * U$

Equation 17: Recovered: $\frac{dR}{dt} = \gamma U * U + \gamma S * Re - \lambda * R$

Here, we aim to look at COVID-19 through deterministic models in the Brazos Valley community including factual and counterfactual scenarios. The goal of these models is to look at the impact of different vaccination rates, earlier vaccination, and the effect of cases reporting on the dynamics of COVID-19 in Brazos County.

5.2 Literature Review of COVID-19 mathematical modelling

Although modeling done in this chapter does not model universities or colleges, it does model COVID-19 in a university community. Consequently, reviewing literature on COVID-19 modeling in universities and colleges is useful to understand what COVID-19 modeling in Brazos County, TX may add to the literature.

A literature search in PubMed conducted using the parameters ("SARS-CoV-2" or "COVID-19") AND ("college students" or "university students" or "college student" or "university student") AND ("modelling" or "modeling" or "mathematical modeling" or "mathematical modelling") NOT ("machine learning") generated 64 articles as of November 25, 2021. Several articles looked at a form of modeling SARS-CoV-2 with a university population. One used logistic regression to predict the impact of students spreading the virus to household members and the impact of testing and self-isolation on viral spread (Enright et al., 2021). Regarding the community cases versus young adults, there was modeling looking at the spillover of SARS-CoV-2 from universities into their local community (Pollock et al., 2021).

A separate search using ("SARS-CoV-2" or "COVID-19") AND ("college students" or "university students") AND ("modeling" or "modelling" or "mathematical modeling" or "mathematical modelling") NOT ("mental health" or "depression" or "mental well-being”) NOT (“machine learning”) NOT (“travel ban”) NOT (“e-learning” or “online learning” or “distance education”) NOT (“sleep”) NOT (“social media” or “social network”) NOT (“psychological need”) NOT (“self-determined theory”) NOT (“religiosity”) generated 14 articles. These articles are the focus of the review since they include the target population and exclude topics not prevalent in the later modeling. One article used standard S-E-I-R models on university populations for SARS-CoV-2 (Lopman et al., 2021). Simulated modeling with Bluetooth devices was done in Denmark to simulate transmission in a college setting (Hambridge, Kahn, & Onnela, 2021). A published review presented a comparison of different university modeling papers including their model, population source, and interventions (Christensen et al., 2020).

Although these models cover the target population of a university campus, the data source does not present a factual and counterfactual model of interventions and their estimated effect on a university community.

The literature has, however, presented important information to be considered for modelers and for those studying university transmission. Dormitories were cited as a large source of transmission (Enright et. al, 2021). An intrinsic piece of university outbreaks found through modeling was the importance of students adhering to testing and self-isolation when testing positive for SARS-CoV-2 (Enright et. al, 2021). University outbreaks contributed to outbreaks in their respective communities (Pollock et. al, 2021). However, in the case of University of California (UC) campuses, the proportion of students testing positive was lower than the young adult age group in the surrounding population (Pollock et. al, 2021). S-E-I-R models by Emory University support this assertion as they conducted modeling for their population and found compliance with testing, quarantine, and isolation reduced cumulative incidence of cases (Lopman et. al, 2021). This suggests University mitigation policies or recommendations can reinforce models looking to provide evidence for universities remaining open during an outbreak.

5.3 Methods

5.3.1 Data collection

Data was extracted from the case and contact databases from the CoOp referenced in chapters 1 and 2 from September 1, 2020 – March 31, 2021. The parameter definitions are presented in the table in section 3.3.2 S-Re-U-R model. Parameter calculations are explained in section 3.3.2 S-Re-U-R model.

5.3.2 Data analysis for calculating R_t

Case data was imported into Stata 16.1/IC and close contacts were matched to their associated case through the BCHD ID of the index case. Serial interval was calculated by subtracting the symptom onset date of the close contact from that of the index case. Negative serial intervals and those over 30 were identified as erroneous and marked as missing. Serial intervals between 0 and 29 were used to calculate the mean and standard deviation of the serial interval. The R package: EpiEstim was installed into RStudio version 4.0.4 (Cori et. al, 2021). R code was written based on a vignette using EpiEstim (Cori, 2021). This was used to calculate R_0 using the incidence of COVID-19 cases from September 1, 2020 – March 31, 2020, population size from this timeframe, and the generation time, which was estimated from the mean and standard deviation of the serial interval. R code produced reproduction numbers using the parametric serial interval method. The parametric serial interval method yields the time start, time end, mean R_t, median R_t, standard deviation, and quantiles (0.025, 0.05, 0.25, 0.75, 0.95, 0.975).

5.3.3 S-Re-U-R model

A Susceptible –Reported – Unreported – Recovered (S-I-A-R) model (figure below) was created to match the data to the model and was set to have R_t derived from the model. R_t was derived from the model using equation 18 below.

Equation 18: $R_t = \frac{pr * \beta(t)}{\gamma_{Re}} + \frac{(1-pr) * \varepsilon * \beta(t)}{\gamma_U}$

Where $\beta(t) = q * c(t)$ with q being the probability of infection per contact and $c(t)$ is the contact rate, which is assumed to vary over time, and is estimated through model matching to the data. Model matching was done by matching the daily incidence $pr * q * c(t) * (Re + \varepsilon * U)$ of reported cases to the daily reported cases data.

Figure 43: S-Re-U-R model, flowchart created using Lucidchart

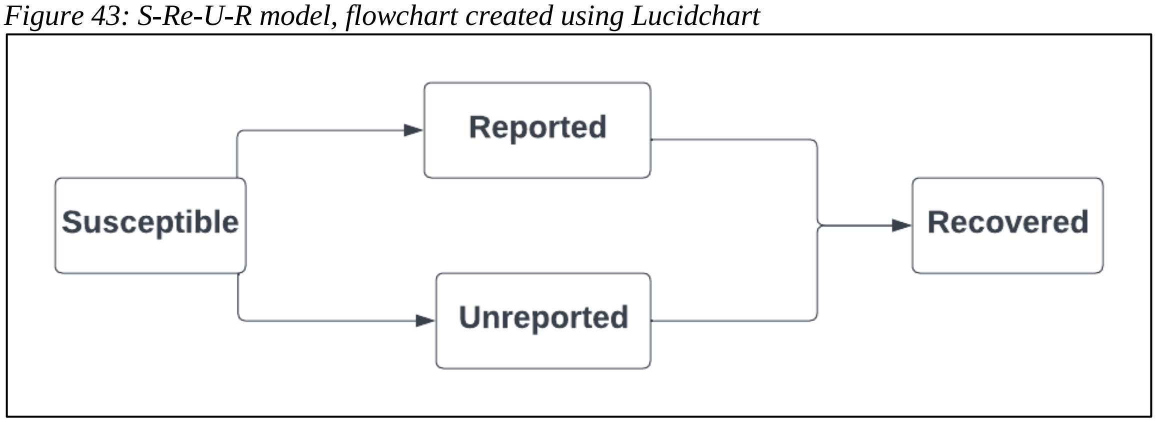


Table 76: Definition of Parameters used in equations for the S-Re-U-R model

Parameter definition	Parameter symbol	Parameter values
Population	N	233849
Number of contacts per unit time	c	Derived from model
Transmission risk per contact	q	0.75
Relative infectivity of symptomatic to pre-symptomatic	ε	0.55
Recovery rate	γ	1/8
Proportion of symptomatic cases reported	pr	0.25

The population size of 233,849 was taken from the population of Brazos County in April 2020 based of Census data (U.S. Census Bureau, 2020). The recovery rate was calculated by subtracting the date of symptom resolution from the date of symptom onset to be six days with a standard deviation of three and a half days. Based off average recovery time in the data, the recovery rate was set at 1/6 with an added two days for the pre-symptomatic period yielding 1/8. Epsilon, the estimated relative infectivity of symptomatic to pre-symptomatic/asymptomatic, was estimated to be 0.55 based off an estimate in the literature (Li et al., 2020). The 0.25 proportion of symptomatic cases reported was from a CDC estimate using February 2020 – September 2021 data (CDC Estimated COVID-19 Burden, 2021).

The S-Re-U-R model was generated with a baseline matching the data. A second model, shown parallel to the baseline is the effect of additional vaccination based on the rate of vaccination in Brazos County, TX of 240 individuals vaccinated/day, and taking Moderna's vaccine efficacy of 91% with two doses into account (prior to Delta and Omicron variants) (IHME, 2022). The vaccination rates modeled were no added vaccination, vaccination rate of 240 people/day, vaccination doubled for 480 people/day, vaccination tripled for 720 people/day, and vaccination rate halved for 120 people/day. The number and percentage of averted cases with varying vaccination rates was calculated and tabulated. A counterfactual model presenting earlier vaccination start dates in Brazos County, TX was done to compare the change in cases with the baseline data. Vaccination start dates included January 8, 2021, December 13, 2020 (DSHS phase 1A start date), December 1, 2020, and October 30, 2020 (DSHS, 2022).

An additional S-Re-U-R model presenting the effect altering reported cases (pr) has on the model was conducted to show a decrease and increase in pr. Reporting changes of the baseline 25% pr to 50% and to 12% were modeled below.

5.3.4 Vaccination in the S-Re-U-R model

Vaccination is accounted for in the S-Re-U-R model by the baseline data divided into two sections by date. The first section is September 1, 2020 (day 0) through January 8, 2021 (day 130) representing the time modeled prior to vaccination in Brazos County, Texas. In the first section of the baseline model, vaccination rate is set to zero to signify no vaccination in the historical data. In the baseline model, the second section of the model is January 9, 2020 (day 131) through the end of time modeled, March 31, 2021 (day 212) with no added vaccination. The baseline model is matched to the historical data considering vaccination within the data.

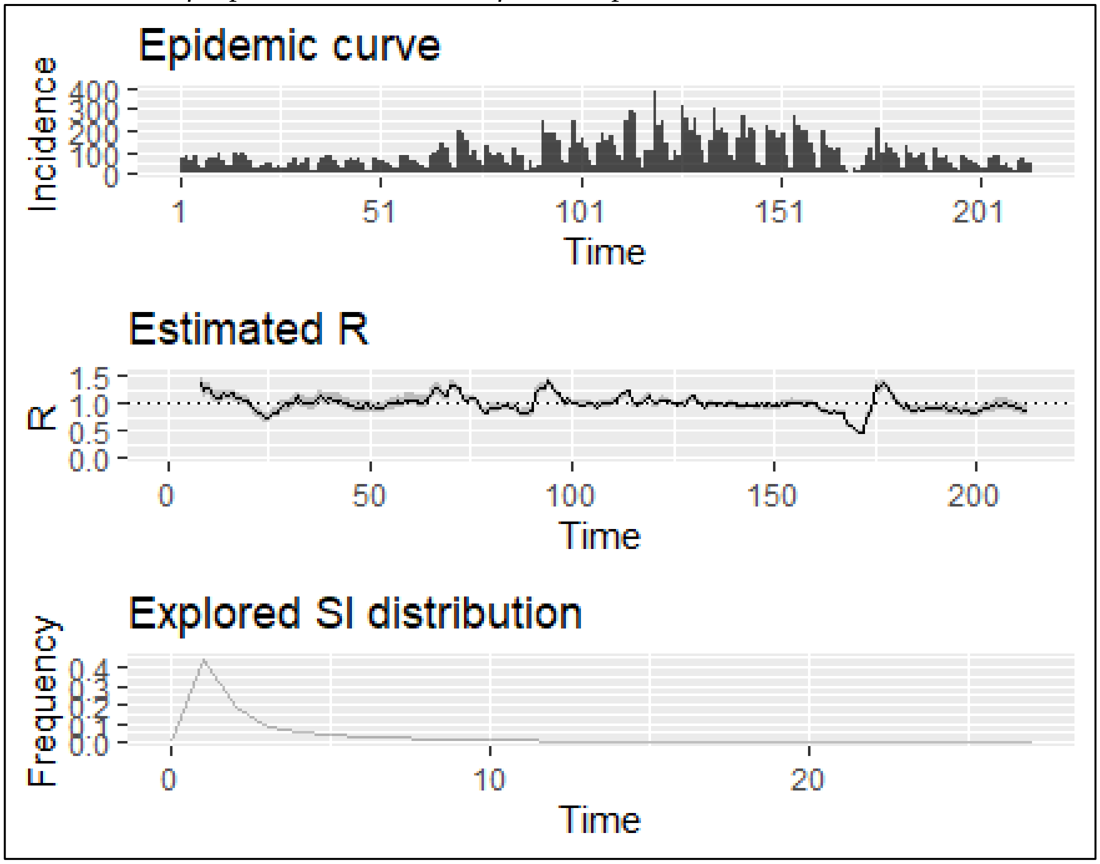
When additional vaccination was modeled, the second section of the model is still January 9, 2020 (day 131) through the end of the time modeled, March 31, 2021 (day 212). However, here, additional vaccination rate was set to 240 individuals vaccinated per day (0.00108 x 0.91 vaccine efficacy for 0.009828). This vaccination rate is designed to account for an approximate 240 individuals vaccinated in Brazos County per day. However, this vaccination rate is in addition to vaccination in the historical data.

5.4 Results

5.4.1 Calculating R_t

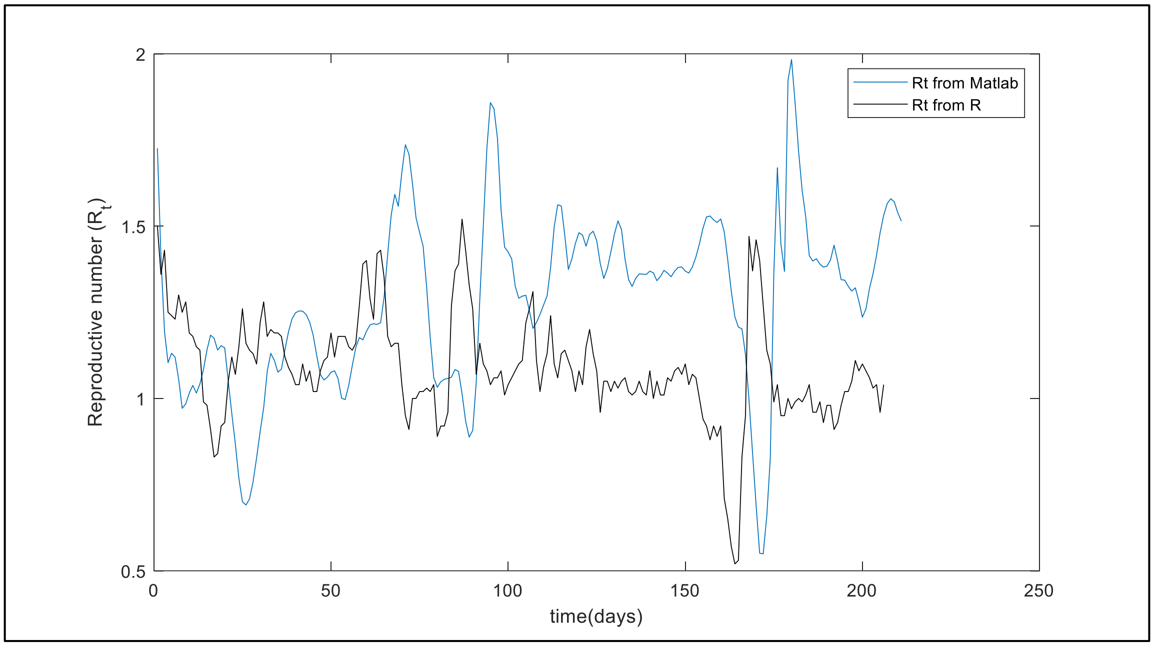
The mean serial interval from September 1, 2020 – April 1, 2020, was calculated to be 3.8 with a standard deviation of 5.2. The first six reproduction numbers estimated were 1.5, 1.36, 1.43, 1.25, 1.24, and 1.23 leading to an average R_0 of 1.33. The EpiEstim estimated R_t over time for the duration of the outbreak by using the serial interval standard deviation and mean given to it. The EpiEstim package in R has been widely used by modelers and public health professionals to calculate R_0 from reported cases data.

Figure 44: Estimate of reproduction numbers from R EpiEstim based on the data.



The graph of R_t below presents R_t changing over time for both R_t calculated in the EpiEstim software and in the Matlab model. When compared to the Matlab model, the parametric serial interval method of calculating R_t in the EpiEstim model appears to have calculated R_t as a seven-day moving average. Peaks in the outbreaks are modeled approximately seven days earlier in the EpiEstim model than shown in the Matlab model. Additionally, the peaks are not as pronounced in the EpiEstim model showing an overall lower R_t over time.

Figure 45: Rt as calculated from the EpiEstim package in R compared to R_t calculated in Matlab.



5.4.2 S-Re-U-R model results – no additional intervention

In the S-Re-U-R models below, data from the case database was matched in the model. The figure of daily identified cases presents the baseline data in the model closely mirroring the data in addition to vaccination if there was constant vaccination of 240 people vaccinated/day.

Figure 46: S-Re-U-R baseline model with additional vaccination for reported, and unreported.

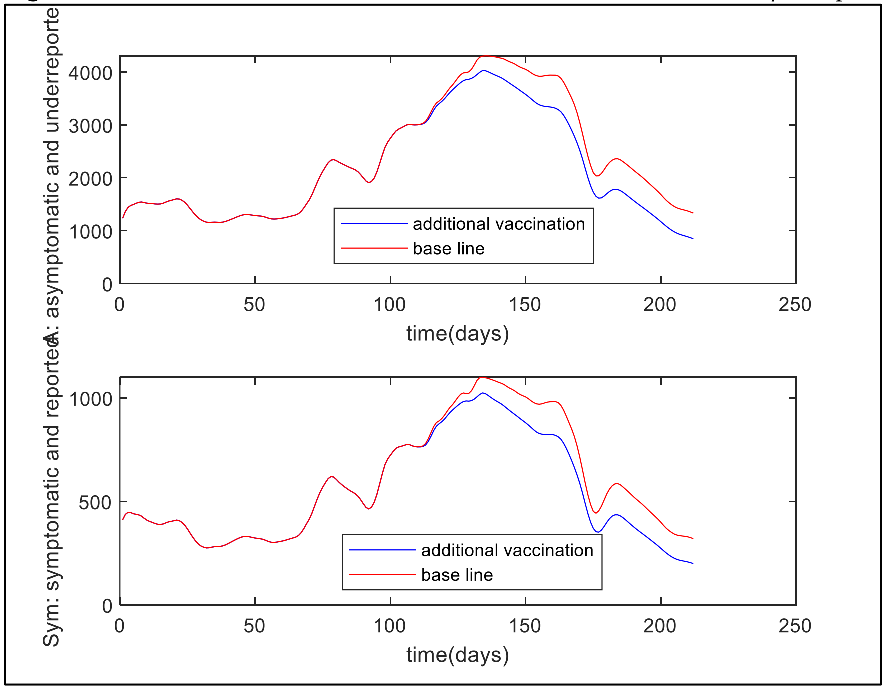


Figure 47: S-Re-U-R baseline model with additional vaccination for total cases

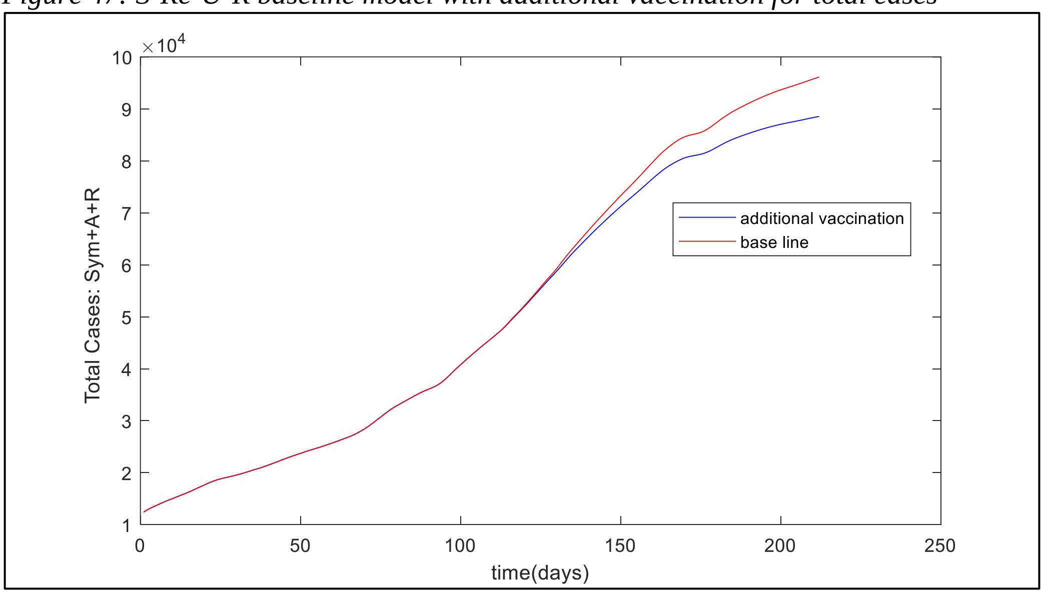


Figure 48: S-Re-U-R baseline model for total active cases

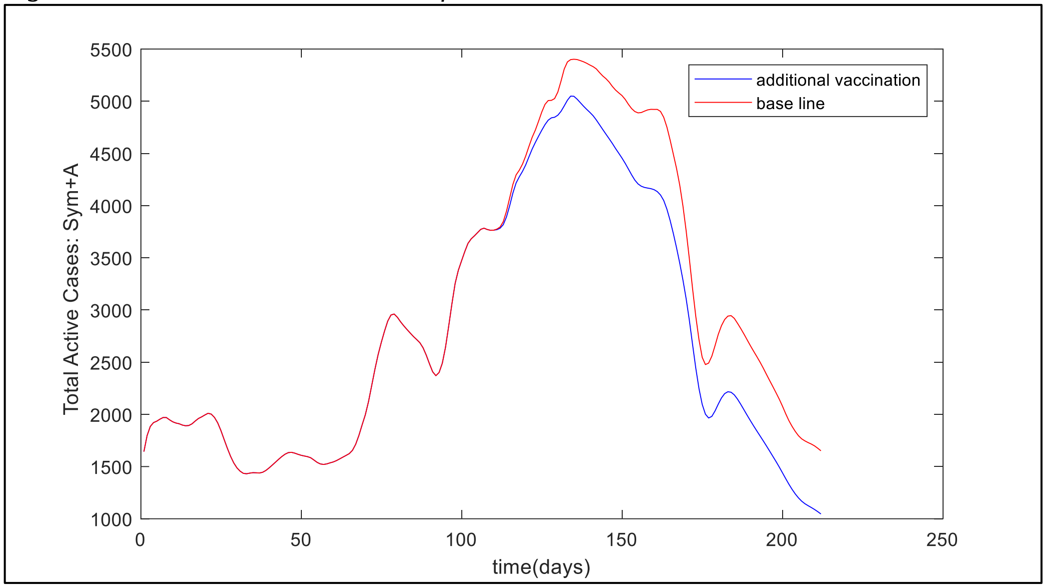
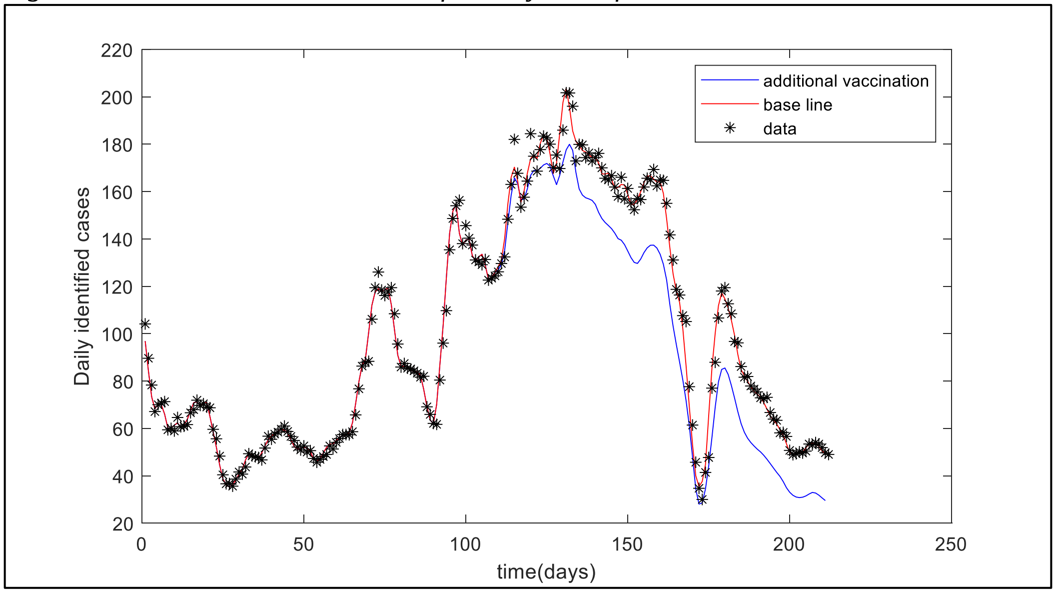


Figure 49: S-Re-U-R baseline model for daily identified cases



5.4.3 Scenarios of different vaccination rates

S-Re-U-R model with different vaccination rates is shown below where the baseline of no added vaccination is closely aligned with the data points. Any increase in vaccination, regardless of half the vaccine rate or triple the vaccine rate demonstrates an overall decrease in cases of COVID-19. When the vaccination rate is halved, 3% of total cases are prevented, with vaccination rate tripled, up to 16% of total cases are prevented.

Figure 50: S-Re-U-R model with different vaccination rates over total cases

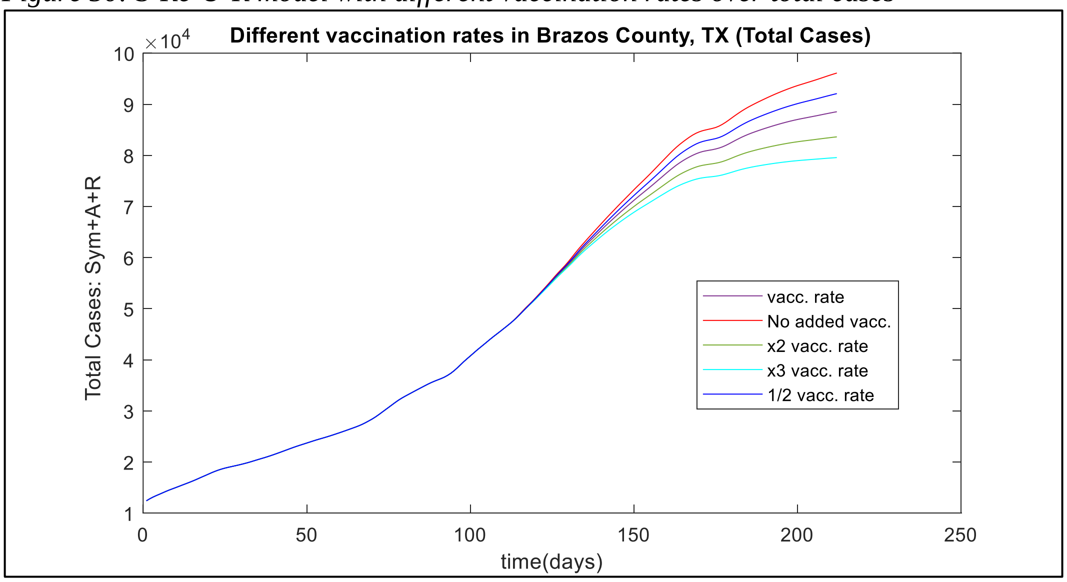


Figure 51: S-Re-U-R model with different vaccination rates over total active cases

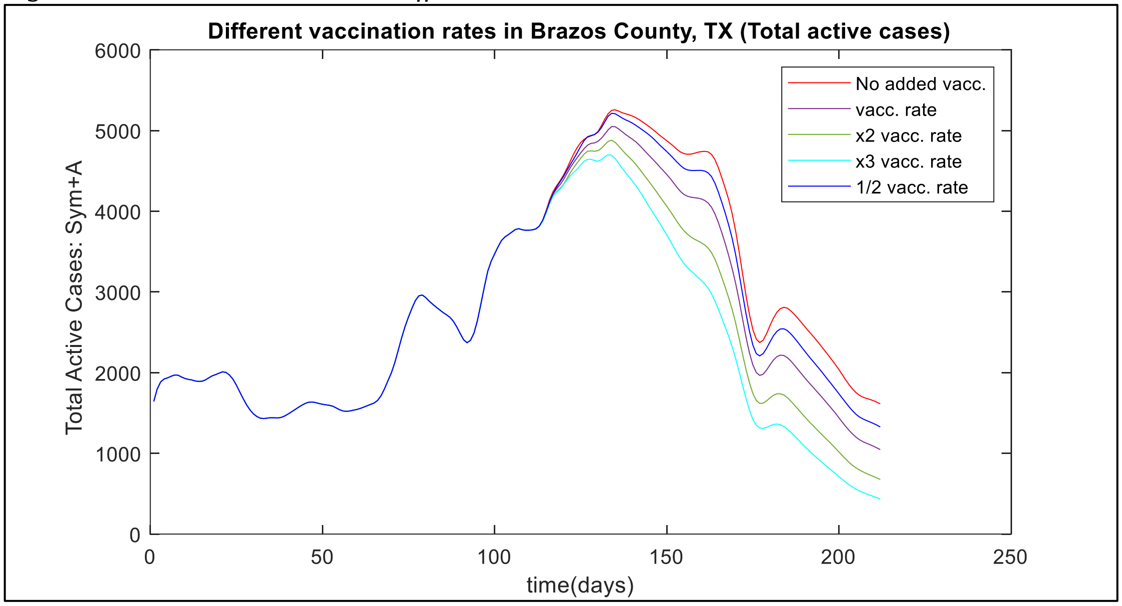


Figure 52: S-Re-U-R model with different vaccination rates over daily identified cases

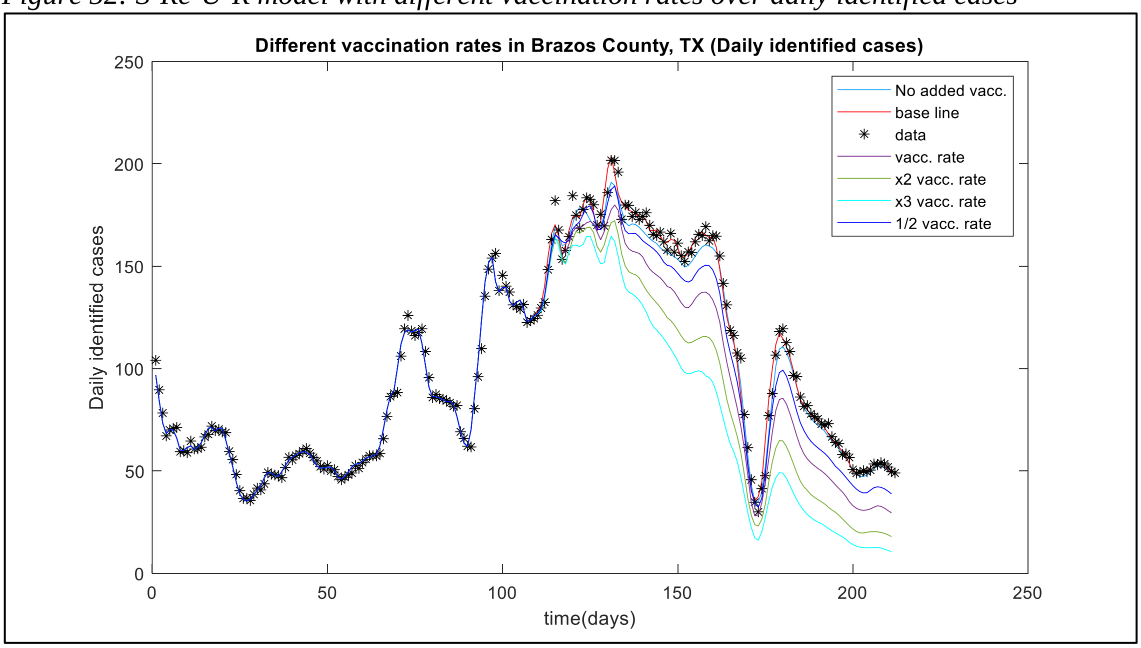


Table 77: S-Re-U-R model with different vaccination rates and the associated averted cases

No added Vacc.		½ Vacc. Rate		Vacc. Rate		x2 Vacc. Rate		x3 Vacc. Rate	
Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases
12426	1643	12426	1643	12426	1643	12426	1643	12426	1643
94753	1613	92088	1327	88544	1046	83627	676	79571	434
Averted cases		2665	285	6209	567	11126	936	15181	1178
% Averted		3	18	7	35	12	58	16	73

5.4.4 Scenarios of earlier vaccination dates

A counterfactual S-Re-U-R of earlier vaccination start dates highlights the cases of COVID-19 which would have been prevented if a constant vaccination rate of 240 people/day were started earlier in the pandemic in Brazos County. This model presents vaccination start dates of January 8, 2021 (Brazos County vaccination start), December 13, 2020 (DSHS phase 1A start), December 1, 2020, and October 30, 2020 (DSHS, 2022). Vaccination starting on December 13, 2020, would have prevented approximately

5% of total cases. Vaccination on December 1, 2020, and October 30, 2020, would have prevented approximately 8% and 17% of cases in Brazos County, respectively.

Figure 53: S-Re-U-R counterfactual model of earlier vaccination start dates over total cases

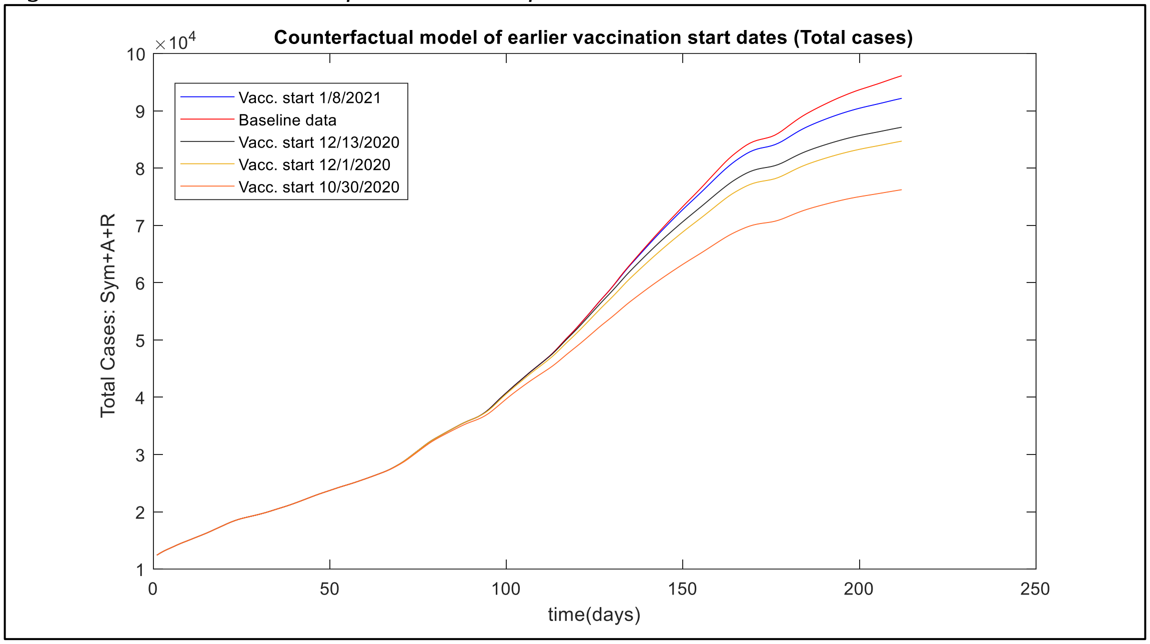


Figure 54: S-Re-U-R counterfactual model of earlier vaccination start dates over total active cases

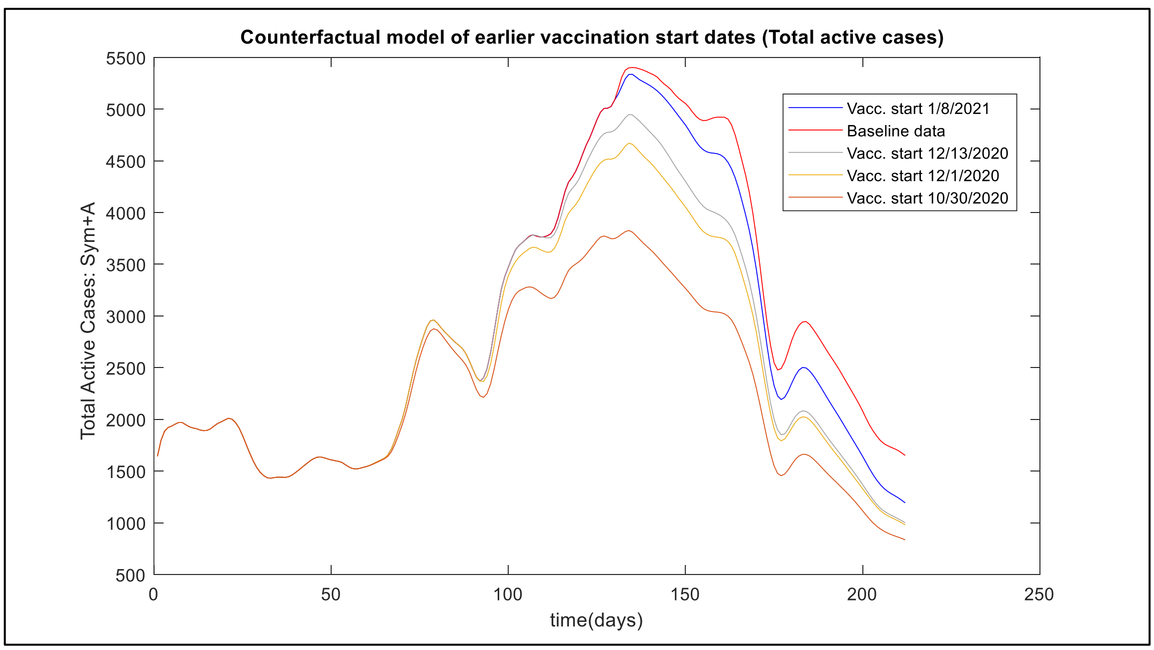


Figure 55: S-Re-U-R counterfactual model of earlier vaccination start dates over daily identified cases

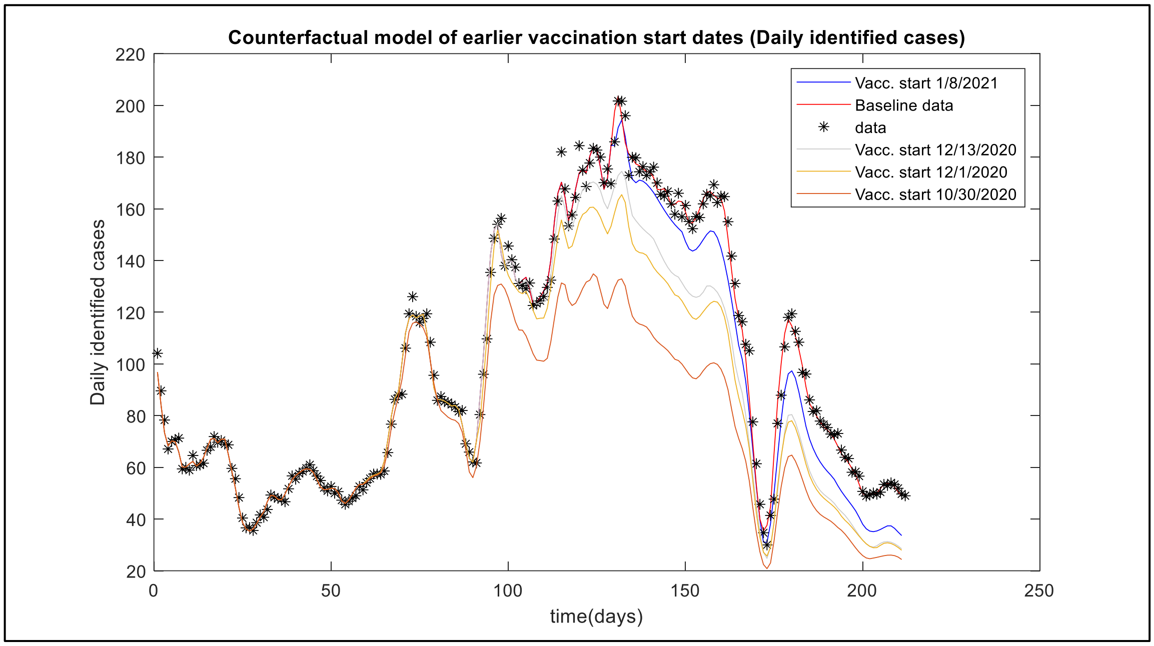


Table 78: S-Re-U-R counterfactual model of earlier vaccination start dates and the associated averted cases.

Day 130		Day 104		Day 92		Day 60	
1/8/2021 Vacc. Start		12/13/2020 Vacc. Start		12/1/2020 Vacc. Start		10/30/2020 Vacc. Start	
Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases
12426	1643	12426	1643	12426	1643	12426	1643
92169	1192	87125	1000	84697	980	76220	835
Averted cases		5044	193	7472	212	15949	358
% Averted cases		5	16	8	18	17	30

5.4.5 Scenarios of reporting changes

S-Re-U-R model with reporting changes over time is presented below. In the baseline data, reporting (pr) is representative of the 1 in 4 or 25% of COVID-19 infections reported based on CDC information (CDC Estimated COVID-19 Burden, 2021). In the model below, three scenarios are presented with the baseline data: 25% reporting with vaccination of 240 people/day, 50% reporting and vaccination of 240 people/day, and 12% reporting and 240 people/day. There is an inverse relationship between reporting and the number of cases in this model. When reporting was increased, the epidemic curve decreased, and when reporting was decreased, the epidemic curve increased. A similar inverse relationship is shown in R_t over time.

Figure 56: S-Re-U-R model reporting changes over total cases

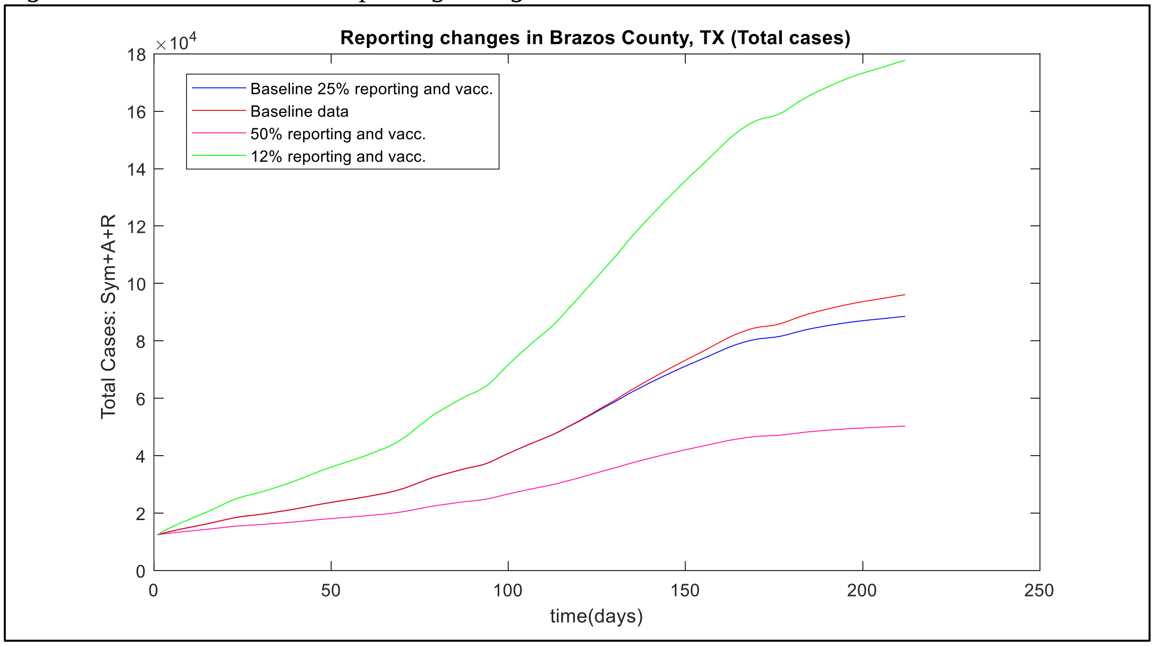


Figure 57: S-Re-U-R model reporting changes over total active cases

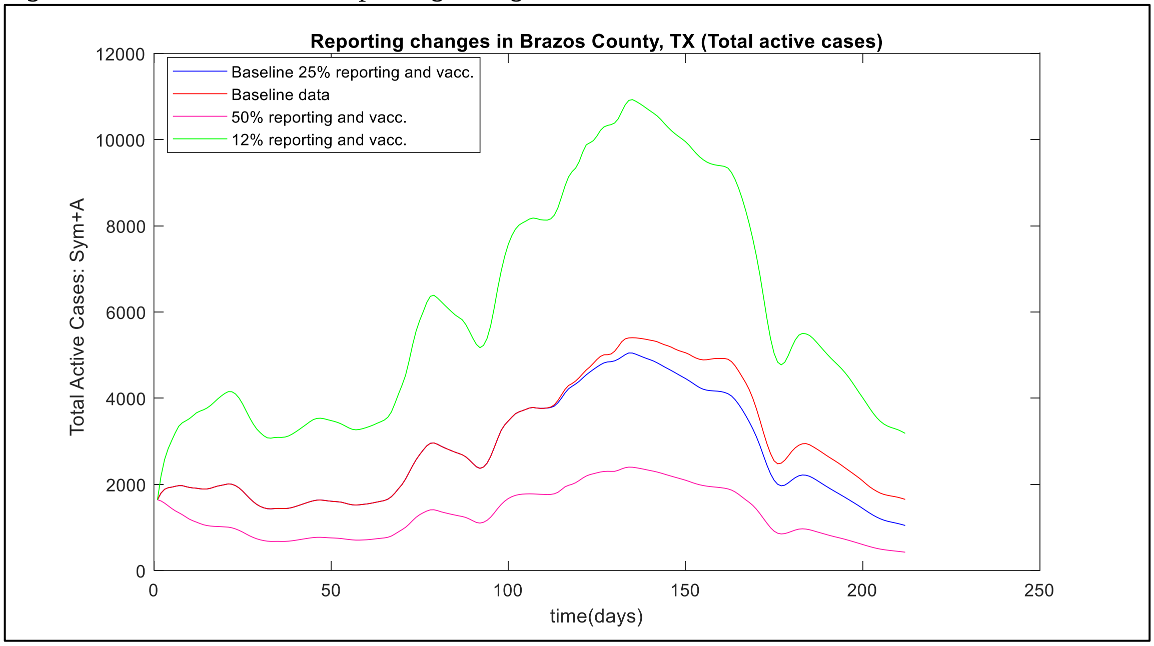


Figure 58: S-Re-U-R model reporting changes over daily identified cases

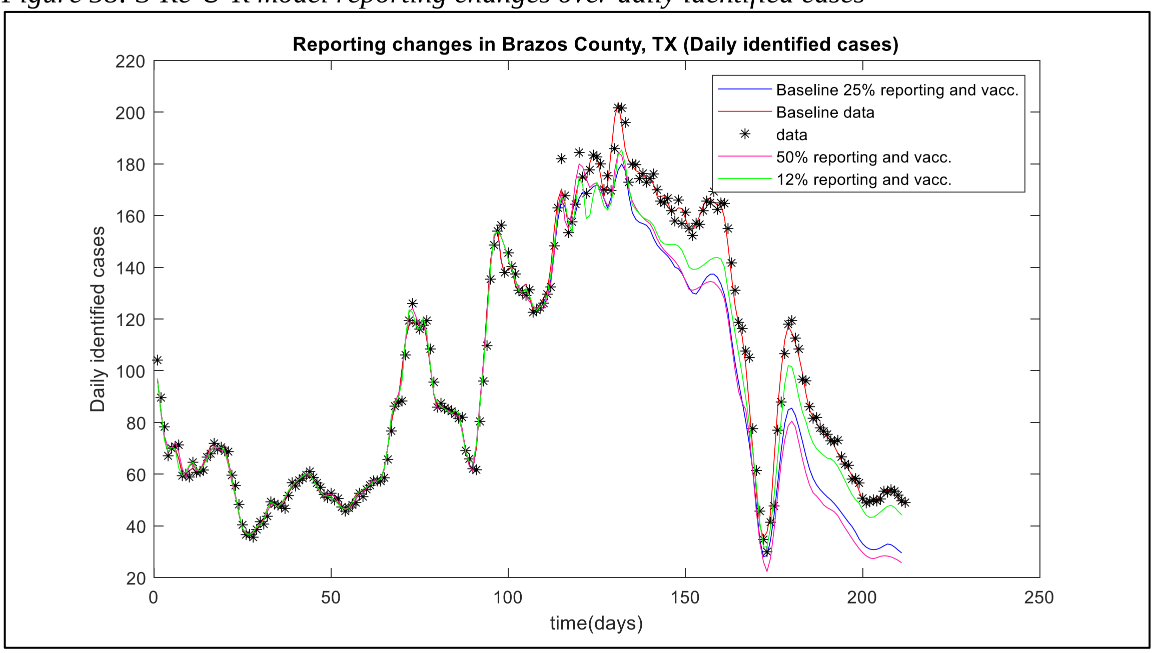


Figure 59: S-Re-U-R model reporting changes over R_t

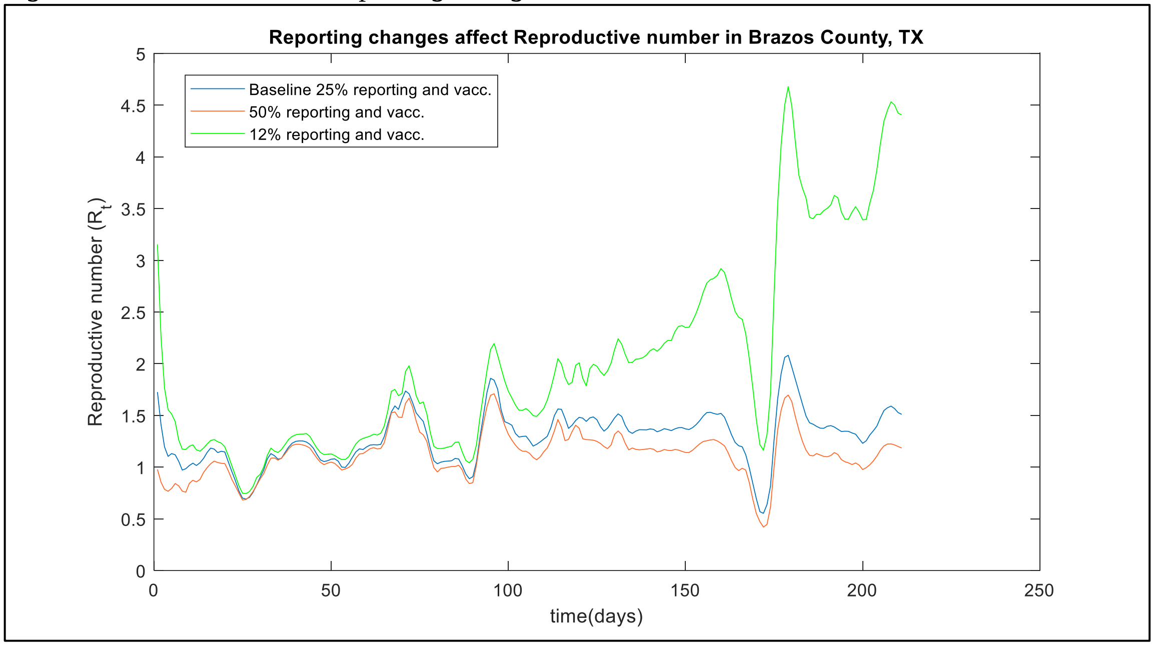


Table 79: S-Re-U-R model reporting changes and the associated difference in cases

Baseline reporting 25%		50% reporting and vacc.		12% reporting and vacc.	
Total cases	Active cases	Total cases	Active cases	Total cases	Active cases
12426	1643	12426	1643	12426	1643
88544	1046	50329	426	177796	3183
Change in cases		38215	620	89252	2137
% Change in cases		43	59	101	204

5.5 Discussion

Given the evolving history of infectious disease modeling, it stands to reason that with each emerging disease, there is something new to be gleaned from the disease, and a way the new information can add to the body of knowledge on infectious disease modeling. Models of SARS-CoV-2 have been used to present alternative scenarios for events, communities, and interventions. Here, models of SARS-CoV-2 are discussed with the reproductive number derived from different methods, and interventions. The interventions modeled are different vaccination rates, earlier vaccination rates, and change in reporting.

5.5.1 Discussing R_t methods

The two methods presented for calculating R_t were the EpiEstim parametric serial interval, and a formula built within Matlab are graphed together in Figure 13. The parametric serial interval relies upon an accurate serial interval standard deviation and mean fed into the program. This is inherently limited by data used to calculate the two values. An advantage to the parametric serial interval method is it does not rely on discrete data being fed into the program, unlike other methods in EpiEstim such as the non-parametric method (Cori, 2021). A disadvantage to this method is it does not consider changes within the data by relying on the serial interval standard deviation and mean.

The formula within Matlab used to calculate R_t included the reporting estimate from CDC, average recovery from the data, and relative infectivity from the literature (CDC Estimated COVID-19 Burden, 2021; Li et al., 2020). These parameters are the same as those used in the S-Re-U-R model, which mirrors incidence of cases in Brazos County as seen in Figure 20.

The two trends of R_t over time are parallel at times, such as days 120 to 150 (January 2021). However, given the stark differences between the methods, the parametric serial interval technique in EpiEstim is not a reliable indicator for transmission in Brazos County during this SARS-CoV-2 outbreak. It is suggested that without reliable, discrete data, using parameters to calculate Rt over time is a more effective tool for tracking disease over time.

5.5.2 Discussing S-Re-U-R model – no additional intervention

All the scenarios here use historical data from Brazos County to derive the parameters, and or to compare with the scenarios. During the timeframe of September 1, 2020 – April 1, 2021, a small proportion of Brazos County was vaccinated inferring some vaccination in the baseline historical data. Main peaks in the data are in early December 2020, late December 2020 – early January 2021, and mid-January 2021. The vaccination rate in Brazos County began at 240 people vaccinated per day leading to that as the baseline vaccination rate for the area.

The S-Re-U-R model graphs the matched historical data over time alongside additional vaccination introduced on January 8, 2021. The additional vaccination line shows a decrease in incidence when 240 people were vaccinated per day in Brazos County. Despite this vaccination rate being derived from Brazos County data, it does not depict the actual vaccination in the area. This evidence demonstrates historical vaccination numbers cannot be modeled through a vaccination rate. Consequently, whenever vaccination is introduced to a population, it should be modeled through data. This is helpful for modelers and epidemiologists to best understand the effect a vaccine is having on a population after its introduction.

5.5.3 Discussing different vaccination rates

Despite historical vaccination in the data, any amount of vaccination in the model led to a decrease in total cases. The scenarios presented depict the change in cases with no added vaccination, 120 people vaccinated per day, 240 people vaccinated per day, 480 people vaccinated per day, and 720 people vaccinated per day. Changing the number of people vaccinated did not alter the baseline scenario but instead depicted side by side how the epidemic curve would decrease if the given vaccination rate occurred.

Initial changes in vaccination prevented 3% of people from infection based on Table 156. When vaccination rate was tripled, as many as 16% of total cases were prevented. A decrease in COVID-19 cases translates to less people needing care and a lower burden on the local healthcare infrastructure. Any increase in vaccination rate may have assuaged the burden the pandemic has placed on the healthcare. In future vaccination campaigns, public health can strive to be clearer on when groups of individuals are qualified to receive a vaccine. Throughout Texas, there was inconsistent messaging on vaccination availability which may have hindered the number of people getting vaccinated.

5.5.4 Discussing earlier vaccination dates

Counterfactual scenarios of earlier vaccination start dates were presented in section 3.4.4. Vaccinating phase 1A individuals against SARS-CoV-2 reportedly began in Texas on December 13, 2020, though vaccinations were not reported in Brazos County until January 8, 2021 (DSHS, 2022). For this reason, the counterfactual scenarios of earlier vaccination dates were shown to highlight the total number of active cases over time.

Earlier start dates of December 13, 2020, December 1, 2020, and October 30, 2020 were selected and graphed in parallel. The expected rise in cases (early December 2020, late December 2020-early January 2021, mid-January 2021) was still seen in each of the scenarios. Though the spike in cases in mid-January 2021 was less pronounced with earlier vaccination based.

Despite a constant vaccination rate, the percentage of avoided cases with earlier vaccination start dates is like when the vaccination rate was increased. Table 156 shows 16% of total cases averted when vaccination was tripled, and in table 157, 17% of total cases were averted when vaccination began in late October 2020. Through these scenarios, an importance is placed on more vaccination in general. Increasing the vaccination rate has the potential to drastically decrease total cases, but so does a constant vaccination rate at an earlier date.

5.5.5 Discussing reporting changes

In section 5.4.5, scenarios are presented where all variables stay constant except for reporting SARS-CoV-2 infections. These scenarios depict the baseline of 25% reporting, 50% reporting, and 12% reporting of cases.

Intuitively, one might think an increase in case reporting would lead to an increase in the number of cases. However, the scenarios here on reporting changes show an inverse relationship between the level of case reporting and the total number of cases. This inverse relationship is due to the set-up of equations in the model. In the equations, the number of cases is divided by the proportion of cases reported in the process of deriving c, the contact rate. This suggests using historical data to portray the effects of underreporting or other reporting changes of an infectious disease may not be ideal and instead a model for reporting changes should be designed for that express purpose.

5.5.6 Policy implications

Given the start date of phase 1A in Texas was December 13, 2020 but vaccination reported in Brazos County, Texas until January 8, 2020, vaccination start-up locally could be improved. Beginning vaccination at the rate of 240 people vaccinated per day on December 13th as opposed to January 8th would have prevented 5,044 or 5% of total cases. The scenarios presented here provide evidence that earlier vaccination would have mitigated COVID-19 spread in Brazos County.

Public announcements were made about the progress and anticipated arrival of a COVID-19 vaccine. Robert Redfield, former CDC director, announced a COVID-19 vaccine could be available to healthcare workers as early as November 2020 (Lovelace Jr., B. & Higgins-Dunn, N., 2020). Former President Trump optimistically stated a COVID-19 could begin distribution as early as October 2020 (Lovelace Jr., B. & Higgins-Dunn, N., 2020). Based on this information, it is recommended that in the future, as soon as politicians begin announcing anticipated release of a vaccine, policy makers develop a plan to distribute to the vaccine. Following such a plan, as soon as they are given approval, distribution of the vaccine could begin in earnest.

While politicians may have known a vaccine was coming, they may not have had all the information to formulate an appropriate plan. They did not know how much of the vaccine would be made available to them. Additionally, previous vaccines did not require cold storage, but the COVID-19 vaccine did so previous vaccine storage facilities would not have been able to store the COVID vaccine. The lessons learned from this chapter have implications for future epidemics. Policy makers and local public health can work on developing a flexible, scalable vaccine distribution campaign to work for their locale in any situation. If the vaccine distribution plan is flexible, they can design it to be applicable to a vaccine which requires cold or room temperature storage. If the vaccine distribution is scalable, then they will prepare multiple locations for storage and or distribution as needed. Such a distribution plan would not be easy. However, flexible and scalable systems have been designed for other applications such as the Incident Command System (ICS) suggesting public health, policy makers, and engineers could work together to develop such a plan.

5.5.7 Limitations

There are several limitations with the models presented here. First, they rely on secondary data collected from the CoOp. This data is then inherently limited by the collection process. For example, there was different training of employees, and a small proportion of individuals testing positive for SARS-CoV-2 refused to adhere with a case investigation.

When R_t was calculated using EpiEstim, the serial interval had to first be calculated by matching close contacts to their index case before preforming the calculation. This relied on both the case and contact responding to an interviewer and recalling when each of their symptom onset dates were. There was likely a severe underestimation of serial interval due to the lack of respondents. Using the serial interval, R_t was then estimated. To graph R_t, the highest quantile of R_t, 97.5%, was used for the modeling to control for underreporting within the data. However, this highest quantile of R_t was likely still to be an underestimation in the data. Across U.S. counties, the median R_t was found to be 1.66 yet the highest R_t calculated in this study was 1.33 (Sy, White, & Nichols, 2021). When R_t was produced from the model it was, on average, lower than 1.66.

When assessing vaccination as an intervention, historical vaccine data was not able to be employed in the model. Daily vaccination data for Brazos County is available to the public in graphical form but not tabulated where it can be transferred into a model. This limits the true vaccine intervention able to be modelled.

5.5.8 Concluding thoughts

Infectious disease modeling has been demonstrated to provide support for methods to mitigate outbreaks. The effect increased rates of vaccination can have here as well as counterfactual scenarios of earlier vaccination are both presented as able to avert the number of COVID-19 cases. It is suggested policy makers have a vaccine distribution plan scalable and flexible to meet the needs of an emerging response.

6. THEMATIC CONCLUSION

Challenges, takeaways, and lessons learned of the COVID-19 response in Brazos County, Texas have been presented here. Evolving public health guidance led to rapid changes in the response, throughout the pandemic. The COVID-19 Operations Center was mobilized in summer of 2020 and was demobilized in spring 2022. While this study excluded data collected after July 31, 2021, the takeaways and lessons learned are widely applicable.

Individuals who tested positive for SARS-CoV-2 were largely cooperative with case investigations but were hesitant to provide personal information of themselves or their close contacts. Although community transmission was present, majority of transmission occurred between family members and friends who knew each other. They then quickly tested for the virus, often without waiting for official public health guidance. Some transmission and testing burden may have been avoided if vaccination had begun earlier than it did.

Regardless of vaccination, public health professionals worked tirelessly throughout the course of the pandemic to help by providing guidance. They spoke to cases and close contacts. Data they collected brought to light the burden on Hispanic and Latinos. Recommendations have been made on ways public health can improve their response, should such a situation occur in the future.

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APPENDIX A

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A.1 Questionnaire and REDCap codebook for people who tested positive for SARS-CoV-2

#	Variable / Field Name	Field Label *Field Note*	Field Attributes (Field Type, Validation, Choices, Calculations, etc.)
Instrument: **Demographics** (demographics)			Collapse
1	bchd_id	BCHD Case ID	text
2	date_investigate	Start Date of Case Investigation	text (date_mdy, Min: 0017-03-20), Required
3	name_first	First Name	text, Required, Identifier
4	name_mi	M.I.	text
5	name_late	Last Name	text, Required, Identifier
6	dob	Date of birth	text (date_mdy), Required, Identifier
7	age	Age (years)	calc Calculation: rounddown(datediff([dob], [date_investigate],"y","mdy"))
8	language	Language:	dropdown (autocomplete) 0 English 1 Spanish 8 Other 9 Unknown
9	clinic	Reporting Clinic / Physician Name	text
10	parent_name Show the field ONLY if: [age] < 18	Section Header: *Contact Information* Name of child's Parent	text
11	address_county	Just to confirm, what is the County of Residence? Where the individual usually lives, such as where the COVID-19 CASE would be reported to the local health authority.	text
12	address	Street Address	text, Identifier
13	address_city	City	text, Identifier
14	address_zip	Zip Code	text (zipcode), Identifier

15	residencetype	Residence Type	dropdown 0 Private residence 15 Apartment 16 Nursing Home 17 Dormitory 1 Homeless 2 Homeless shelter 3 Assisted living facility 4 Longterm acute care 5 Longterm care facility 6 Rehabilitation facility 7 Hospice 8 State supported Living facility 9 Military base 10 Quarantine facility military or other 11 Hotel 12 Jail 13 Prison 14 Detention facility 20 Other 21 Unknown
16	address_temp Show the field ONLY if: [address_temp_yn]="1"	Please give the address where you are currently located Street Address with Apartment or Unit number City, State, Zip, County This information can be used to provide resources and other information during your isolation/quarantine and can be used in case of emergency, such as if you tell us you need emergency aid or for informing 911 or Emergency personnel to wear Protection if they need to render aid at your address.	notes
17	residencetype_other Show the field ONLY if: [residencetype] = '20'	Other type of Residence	text
18	residencetype_facilityname Show the field ONLY if: [residencetype] = '20' or [residencetype] = '16' or [residencetype] = '2' or [residencetype] = '3' or [residencetype] = '4' or [residencetype] = '5' or [residencetype] = '6' or [residencetype] = '7' or [residencetype] = '8' or [residencetype] = '9' or [residencetype] = '10' or [residencetype] = '11' or [residencetype] = '12' or [residencetype] = '13' or [residencetype] = '14'	Name of Facility	text
19	address_temp_yn	Are you currently residing or living/sleeping at this address? Answer No if you are temporarily relocated away from your usual residence.	radio 0 Yes, this is my current residence 1 No, I am currently staying somewhere else
20	phone	Preferred Phone number *Include Area Code*	text (phone), Identifier
21	phone_alt	Alt Phone Number	text (phone)
22	phone_othr	Other contact	text
23	email	E-mail	text (email), Identifier

		Sex	dropdown 0 Female 1 Male 9 Unknown
25	race	Race	dropdown 0 White 1 Black 2 Asian 3 Hawaiian or Other Pacific Islander 4 Native American Alaskan 9 Unknown / Not Reported 7 Other
26	hispanic	Hispanic	dropdown 1 Yes, Hispanic or Latino 0 No, NOT Hispanic or Latino 9 Unknown / Not Reported Custom alignment: RH
27	resident_us	US Resident?	dropdown 0 Yes, US Resident 1 No, NOT US Resident 9 Unknown / Not Reported Custom alignment: RH
28	occupation_yn	Employed?	dropdown 1 Yes 0 No 9 Unknown
29	occup_type Show the field ONLY if: [occupation_yn] = '1'	Occupation	text
30	occup_name Show the field ONLY if: [occupation_yn] = '1'	Employer *If Texas A&M Employee, enter "TAMU"*	text
31	date_work Show the field ONLY if: [occupation_yn] = '1'	Last date at Work	text (date_mdy)
32	hc_work_yn	Is the patient a health care worker?	dropdown 0 No 1 Yes 9 Unknown
33	hc_ptcare Show the field ONLY if: [exp_case] = '1' or [exp_case] = '9'	In the prior 14 days, Did the case provide care for a COVID-19 patient?	dropdown 0 No 1 Yes 9 Unknown
34	student_yn	Student (or Daycare attendee)?	dropdown 1 Yes 0 No 9 Unknown

35	school_name Show the field ONLY if: [student_yn] = '1'		
36	affiliation_tamu_student Show the field ONLY if: [student_yn] = '1'	Please indicate Student classification(s) / Affiliation(s) *Mark all that apply*	checkbox 60 | affiliation_tamu_student___60 | Undergraduate Student 61 | affiliation_tamu_student___61 | Graduate or Professional Student 52 | affiliation_tamu_student___52 | Fraternity / Sorority Member 56 | affiliation_tamu_student___56 | Clinical Learner 57 | affiliation_tamu_student___57 | Student Athlete 58 | affiliation_tamu_student___58 | Student Employee 59 | affiliation_tamu_student___59 | Corps of Cadets 80 | affiliation_tamu_student___80 | Member of Student Organization 98 | affiliation_tamu_student___98 | Other 99 | affiliation_tamu_student___99 | Unknown Custom alignment: LV
37	affiliation_tamu_hclab	Please indicate if work (paid or unpaid) in Laboratory or Healthcare setting:	checkbox 54 | affiliation_tamu_hclab___54 | Healthcare Setting - Human 56 | affiliation_tamu_hclab___56 | Healthcare Setting - Animal 55 | affiliation_tamu_hclab___55 | Laboratory Setting 98 | affiliation_tamu_hclab___98 | Other 99 | affiliation_tamu_hclab___99 | Unknown 0 | affiliation_tamu_hclab___0 | None
38	sx_fever	Section Header: *I want to know if you have experienced any signs of illness. I'm going to read a list of symptoms, and I will ask you to tell me if you have have experienced any of these.* Fever	radio (Matrix) 1 | Yes 0 | No 9 | Unknown
39	sx_cough	Cough	radio (Matrix) 1 | Yes 0 | No 9 | Unknown
40	sx_pharyngitis	Sore throat	radio (Matrix) 1 | Yes 0 | No 9 | Unknown
41	sx_sob	Shortness of Breath	radio (Matrix) 1 | Yes 0 | No 9 | Unknown

		Chills	radio (Matrix) 1 Yes 0 No 9 Unknown
43	sx_headache	Headache	radio (Matrix) 1 Yes 0 No 9 Unknown
44	sx_aches	Muscle aches / Body aches	radio (Matrix) 1 Yes 0 No 9 Unknown
45	sx_vomit	Vomiting / Nausea	radio (Matrix) 1 Yes 0 No 9 Unknown
46	sx_abdpain	Abdominal pain	radio (Matrix) 1 Yes 0 No 9 Unknown
47	sx_diarrhea	Diarrhea	radio (Matrix) 1 Yes 0 No 9 Unknown
48	sx_rhinitis	Runny nose	radio (Matrix) 1 Yes 0 No 9 Unknown
49	sx_congestion	Congestion	radio (Matrix) 1 Yes 0 No 9 Unknown
50	sx_conjunct	Conjunctivitis	radio (Matrix) 1 Yes 0 No 9 Unknown
51	sx_taste	Loss of Smell / Taste	radio (Matrix) 1 Yes 0 No 9 Unknown
52	sx_fatigue	Fatigue	radio (Matrix) 1 Yes 0 No 9 Unknown
53	sx_weakness	Weakness	radio (Matrix) 1 Yes 0 No 9 Unknown

		Loss of Appetite	radio (Matrix) 1 Yes 0 No 9 Unknown
55	sx_fevertemp Show the field ONLY if: [sx_fever] = '1'	Fever Temp (*F)	text (number, Min: 90, Max: 110)
56	sx_other	Specify other symptoms:	text
57	sx_yn	Experienced any Symptoms?	dropdown 1 Yes 0 No 9 Unknown
58	sx_date Show the field ONLY if: [sx_yn] = '1' or [sx_yn] = '9'	Date of Symptom Onset	text (date_mdy, Min: 0001-03-20)
59	sx_daystiltoday Show the field ONLY if: [sx_yn] = '1' or [sx_yn] = '9'	Number of days since Symptom Onset	calc Calculation: datediff([sx_date], [date_report],"d","mdy")
60	onset_unk Show the field ONLY if: ([sx_yn] = '1' or [sx_yn] = '9') a nd [sx_date]=""	Unknown (onset date)	radio 1 Unknown
61	symp_res_yn Show the field ONLY if: [sx_yn] = '1' or [sx_yn] = '9'	Current symptom state	radio 1 Still symptomatic 0 Symptoms resolved 9 Unknown
62	symp_res_dt Show the field ONLY if: [symp_res_yn] = '0'	Date of symptom resolution	text (date_mdy) Field Annotation: @HIDEBUTTON
63	comments	General Comments	notes
64	demographics_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **History** (history)			Collapse
65	exp_case	Section Header: *[name_irst] [name_late] In the 14 days Prior to Illness or if asymptomatic, 14 days prior to Positive Test* In the prior 14 days, Did patient have close contact with a laboratory-confirmed COVID-19 case?	dropdown 0 No 1 Yes 9 Unknown
66	exp_case_hh Show the field ONLY if: [exp_case] = '1'	Was the Close Contact Case a Household Member?	dropdown 0 No 1 Yes 9 Unknown
67	medhx_none	Section Header: *Medical Conditions & Past History: Does the Patient have any Health Conditions?* None	radio (Matrix) 1 Yes 0 No 9 Unknown

		Unknown	radio (Matrix) 1 Yes 0 No 9 Unknown
69	pregnant_yn	If female, currently pregnant	radio (Matrix) 1 Yes 0 No 9 Unknown
70	medhx_diabetes_yn	Diabetes Mellitus	radio (Matrix) 1 Yes 0 No 9 Unknown
71	medhx_cvd_yn	Cardiovascular disease	radio (Matrix) 1 Yes 0 No 9 Unknown
72	medhx_htn	Hypertension	radio (Matrix) 1 Yes 0 No 9 Unknown
73	medhx_cld_yn	Chronic Lung Disease (asthma/emphysema/COPD)	radio (Matrix) 1 Yes 0 No 9 Unknown
74	medhx_renaldis_yn	Renal disease	radio (Matrix) 1 Yes 0 No 9 Unknown
75	medhx_liverdis_yn	Liver disease	radio (Matrix) 1 Yes 0 No 9 Unknown
76	medhx_immsupp_yn	Immunocompromised condition	radio (Matrix) 1 Yes 0 No 9 Unknown
77	medhx_childasthma	Childhood asthma	radio (Matrix) 1 Yes 0 No 9 Unknown
78	medhx_other	Specify any other chronic diseases or comorbid conditions:	text

			0 No - I have not had a positive PCR or Antigen test 1 Yes - I had a positive PCR test result 2 Yes - I had a positive Antigen test but did not have a positive PCR test result 3 I think so - I tested positive for antibodies, but I didn't have a positive PCR or Antigen test 4 I think so - I had symptoms after exposure to a known case, but I didn't have a positive PCR or Antigen test 5 I think so - A doctor told me that I had COVID-19 or probably had it, but I didn't have a positive PCR or Antigen test Custom alignment: LV
80	reinfection_date Show the field ONLY if: [reinfection]>'0'	When did you have COVID-19 or SARS-CoV-2 infection? Please give the start date of infection (i.e. the first positive test result or the date of symptom start, whichever is earlier). If they had more than one infection (i.e. greater than 90 days apart), list the most recent episode.	text (date_mdy) Custom alignment: LV
81	smoke	Smoking Status	radio 0 Never smoker 1 Former smoker 2 Current smoker 9 Unknown
82	flushot	Has had Flu shot within the prior 1 year?	dropdown 0 No 1 Yes 9 Unknown
83	insured	Does the Case have Health Insurance?	dropdown 0 No 1 Yes 9 Unknown
84	isolation	Is the Case Isolating at Home?	dropdown 0 No 1 Yes 2 Yes - Partial 9 Unknown
85	isolation_start Show the field ONLY if: [isolation] = '1'	What was the first date of Isolation?	text (date_mdy)
86	report_source	Source of Reported Case	radio 0 Clinical referral 1 Contact tracing 2 Facility Screening 3 Occupational Screening 8 Other 9 Unknown
87	studyid_contact Show the field ONLY if: [report_source] = '1'	If contact tracing, What was BCHD Contact ID assigned to this Person?Enter patient's contact ID if he/she was previously a contact that has been under investigation through contact-tracing.	text

88	report_source_other Show the field ONLY if: [report_source] = '8'	Other reporting source	text
89	pets_yn	Do you have pets in your household?	dropdown 1 Yes 0 No 9 Unknown
90	vaccinated_yn	Have you received any dose of an FDA-approved COVID-19 vaccine?	radio 1 Yes, 1 dose 2 Yes, 2 doses 0 No
91	vaccine_label Show the field ONLY if: [vaccinated_yn]='1' or [vaccin ated_yn]='2'	Which Vaccine did you receive?	checkbox 0 vaccine_label___0 Moderna 1 vaccine_label___1 Pfizer 2 vaccine_label___2 Johnson & Johnson 3 vaccine_label___3 AstraZeneca 7 vaccine_label___7 Vaccine not listed above, from a foreign country 8 vaccine_label___8 Vaccine other than above 9 vaccine_label___9 I don't know which
92	vaccine_county Show the field ONLY if: [vaccinated_yn]='1' or [vaccin ated_yn]='2'	Where did you get vaccinated?	checkbox 0 vaccine_county___0 Brazos County 1 vaccine_county___1 Another county in Texas 2 vaccine_county___2 Another state, not Texas 3 vaccine_county___3 Outside the US 9 vaccine_county___9 I don't know
93	vaccine_dosedate Show the field ONLY if: [vaccinated_yn]='1' or [vaccin ated_yn]='2'	When was your latest dose received? If you don't know the exact date of your latest shot, please give your best estimate.	text (date_mdy)
94	vaccine_break Show the field ONLY if: [vaccinated_yn]='1' or [vaccin ated_yn]='2'	Is this considered a 'breakthrough infection'? In other words, Did this episode occur AT LEAST 2 WEEKS AFTER the individual was FULLY VACCINATED (2 doses of Pfizer, Moderna, or AstraZeneca OR 1 dose of J&J). Cannot be determined if: Vaccinated but cannot estimate last dose date Vaccinated but unknown label/manufacturer Vaccinated other than Pfizer, Moderna, AstraZeneca or J&J Other reasons - check with epi lead	radio 1 Yes 0 No 9 Cannot be Determined
95	vaccine_yn Show the field ONLY if: [vaccinated_yn]='0'	When an FDA-approved COVID-19 vaccine becomes available to you, do you plan to get vaccinated?	radio 1 YES, definitely 2 Probably yes 9 I'm not sure 8 Probably not 0 NO, definitely not
96	tamuresearch_yn	Would you be willing to receive an email communication about opportunities to participate in COVID related research at Texas A&M?	dropdown 1 Yes 0 No 9 Unknown

97	history_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Contact with Prior Case** (contacts)			Collapse
98	exp_travel	Section Header: *[name_irst] [name_late] In the 14 days Prior to Illness or if asymptomatic, 14 days prior to Positive Test* In the prior 14 days, Did the case travel outside of their city of residence?	dropdown 0 No 1 Yes 9 Unk
99	exp_travel_state Show the field ONLY if: [exp_travel] = '1'	If travel to other City or State, specify:	text
100	exp_travel_othcountry Show the field ONLY if: [exp_travel] = '1'	If travel to non-US country, specify	text
101	exp_returntravel_date Show the field ONLY if: [exp_travel] = '1'	Date of departure from last travel	text (date_mdy)
102	exp_travel_date Show the field ONLY if: [exp_travel] = '1'	Date of return from last travel	text (date_mdy)

103	social_venue	In the 7 days prior to your symptom onset (or 7 days before the positive test), which of the following have you been to?	checkbox

0	social_venue___0	Grocery store
1	social_venue___1	Restaurant for Dine-in
2	social_venue___2	Bar
3	social_venue___3	Gym or Fitness center
5	social_venue___5	Wedding
6	social_venue___6	Salon or Barber shop
7	social_venue___7	Class/School, in-person
29	social_venue___29	Work, in-person
8	social_venue___8	Library
23	social_venue___23	Doctor's Office or Health Clinic
24	social_venue___24	Any theme park or water park
9	social_venue___9	Texas A&M Memorial Student Center
30	social_venue___30	Texas A&M Student Orientation
14	social_venue___14	Any Indoor gathering, < 5 attendees
15	social_venue___15	Any Indoor gathering, 5 to < 10 attendees
16	social_venue___16	Any Indoor gathering, 10 to < 20 attendees
17	social_venue___17	Any Indoor gathering, 20 to < 50 attendees
11	social_venue___11	Any Indoor gathering, 50+ attendees
18	social_venue___18	Any Outdoor gathering, < 5 attendees
19	social_venue___19	Any Outdoor gathering, 5 to < 10 attendees
20	social_venue___20	Any Outdoor gathering, 10 to < 20 attendees
21	social_venue___21	Any Outdoor gathering, 20 to < 50 attendees
13	social_venue___13	Any Outdoor gathering, 50+ attendees
12	social_venue___12	Any Outdoor gathering, < 50 attendees
10	social_venue___10	Any Indoor gathering, < 50 attendees
99	social_venue___99	None of these
22	social_venue___22	Texas Renaissance Festival
25	social_venue___25	Texas A&M Midnight Yell Practice
26	social_venue___26	Texas A&M Breakaway
27	social_venue___27	Santa's Wonderland
28	social_venue___28	Texas A&M Graduation Ceremony

Field Annotation: @HIDECHOICE='10','12','22','25', '26', '27', '28'

104	act_facemask	In the 7 days prior to your symptom onset (or 7 days before the positive test), How often did you wear a face mask or barrier that covers your nose and mouth when leaving your home?	radio 1 Always 2 Sometimes 0 Never
105	close_contacts	Section Header: *Close Contacts of [name_irst] [name_late]* Contacts identified in the TAMU Reporting Portal: *List one person per line: Full Name, Relationship, Area Code+Cell Number, Email Address, Exposure Date*	notes Custom alignment: LH
106	close_contacts_community	Additional Close Contacts identified through Case Investigation: *List one person per line: Full Name, Relationship, Area Code+Cell Number, Email Address, Exposure Date, Notes*	notes Custom alignment: LV
107	close_contacts_class	Any other Event Exposures from TAMU Portal: What in-person classes or events did the individual attend starting from 48 hours before symptoms started? or 48 hours before diganosis, suspicion, or notification?	notes
108	cluster	List any suspected OUTBREAK this patient is associated with.	text
109	contacts_number	Total Number of Contacts	text
110	contacts_number_hh	Number of Household Contacts *Subset of the Above # who are Household Members*	text
111	casecontact_id_1	Section Header: *If this Case is Linked to Previous Cases or Contacts List all Existing Cases and Contacts with Whom the Patient has had Contact* Name or ID of Prior Case Contact:	text
112	casecontact_relationship_1 Show the field ONLY if: [casecontact_id_1] > '"0"'	Relationship to Existing Case/Contact	dropdown 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other
113	casecontact_exposure_1 Show the field ONLY if: [casecontact_id_1] > '"0"'	Where did Exposure occur?	dropdown 1 Household 2 Healthcare setting 3 Workplace 4 Daycare 5 At School 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
114	casecontact_date_1 Show the field ONLY if: [casecontact_id_1] > '"0"'	What is the last date of the exposure? In other words, what is the last time this person was exposed to the prior case? For an exposed contact, this is the start date of the quarantine period. If the exposure is still happening, such as they cannot physically separate in the home, the last exposure will be in the future, on the last date of the case isolation period.	text (date_mdy)

115	casecontact_id_2 Show the field ONLY if: [casecontact_id_1] > '"0"'	Name or ID of Prior Case Contact	text
116	casecontact_relationship_2 Show the field ONLY if: [casecontact_id_2] > '"0"'	Relationship to Existing Case/Contact	dropdown 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other
117	casecontact_exposure_2 Show the field ONLY if: [casecontact_id_2] > '"0"'	Where did Exposure occur?	dropdown 1 Household 2 Healthcare setting 3 Work 4 Daycare 5 School/University 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
118	casecontact_date_2 Show the field ONLY if: [casecontact_id_2] > '"0"'	What is the last date of the exposure? In other words, what is the last time this person was exposed to the prior case? For an exposed contact, this is the start date of the quarantine period. If the exposure is still happening, such as they cannot physically separate in the home, the last exposure will be in the future, on the last date of the case isolation period.	text (date_mdy)
119	casecontact_id_3 Show the field ONLY if: [casecontact_id_2] > '"0"'	Name or ID of Prior Case Contact	text
120	casecontact_relationship_3 Show the field ONLY if: [casecontact_id_3] > '"0"'	Relationship to Existing Case/Contact	dropdown 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other

121	casecontact_exposure_3 Show the field ONLY if: [casecontact_id_3] > "0"	Where did Exposure occur?	dropdown 1 Household 2 Healthcare setting 3 Work 4 Daycare 5 School/University 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
122	casecontact_date_3 Show the field ONLY if: [casecontact_id_3] > "0"	What is the last date of the exposure? In other words, what is the last time this person was exposed to the prior case? For an exposed contact, this is the start date of the quarantine period. If the exposure is still happening, such as they cannot physically separate in the home, the last exposure will be in the future, on the last date of the case isolation period.	text (date_mdy)
123	casecontact_id_4 Show the field ONLY if: [casecontact_id_3] > "0"	Name or ID of Prior Case Contact	text
124	casecontact_relationship_4 Show the field ONLY if: [casecontact_id_4] > "0"	Relationship to Existing Case/Contact	dropdown 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other
125	casecontact_exposure_4 Show the field ONLY if: [casecontact_id_4] > "0"	Where did Exposure occur?	dropdown 1 Household 2 Healthcare setting 3 Work 4 Daycare 5 School/University 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
126	casecontact_date_4 Show the field ONLY if: [casecontact_id_4] > "0"	What is the last date of the exposure? In other words, what is the last time this person was exposed to the prior case? For an exposed contact, this is the start date of the quarantine period. If the exposure is still happening, such as they cannot physically separate in the home, the last exposure will be in the future, on the last date of the case isolation period.	text (date_mdy)
127	casecontact_id_5 Show the field ONLY if: [casecontact_id_4] > "0"	Name or ID of Prior Case Contact	text

128	casecontact_relationship_5 Show the field ONLY if: [casecontact_id_5] > '"0"'		1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other
129	casecontact_exposure_5 Show the field ONLY if: [casecontact_id_5] > '"0"'	Where did Exposure occur?	dropdown 1 Household 2 Healthcare setting 3 Work 4 Daycare 5 School/University 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
130	casecontact_date_5 Show the field ONLY if: [casecontact_id_5] > '"0"'	What is the last date of the exposure? In other words, what is the last time this person was exposed to the prior case? For an exposed contact, this is the start date of the quarantine period. If the exposure is still happening, such as they cannot physically separate in the home, the last exposure will be in the future, on the last date of the case isolation period.	text (date_mdy)
131	study_comments	Comments and Notes about Contacts	notes
132	notes_general	Any other notes from the TAMU Portal	notes
133	contacts_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Hospitalization** (hospitalization_death)			Collapse
134	hosp_yn	Section Header: *Hospitalization & Fatality Record for [name_irst] [name_late]* Was the patient hospitalized?	dropdown 0 No 1 Yes 9 Unknown
135	hosp_dateadmit Show the field ONLY if: [hosp_yn] = '1'	If yes, admission date	text (date_mdy) Field Annotation: @HIDEBUTTON
136	hosp_datedc Show the field ONLY if: [hosp_yn] = '1'	If yes, discharge date	text (date_mdy) Field Annotation: @HIDEBUTTON
137	icu_yn	Was the patient admitted to an intensive care unit (ICU)?	dropdown 0 No 1 Yes 9 Unknown

138	er_yn Show the field ONLY if: [hosp_yn]='0' or [hosp_yn]='9'		0 No 1 Yes 9 Unknown
139	icu_dateadmit Show the field ONLY if: [icu_yn] = '1'	If yes, admission date	text (date_mdy) Field Annotation: @HIDEBUTTON
140	icu_datedc Show the field ONLY if: [icu_yn] = '1'	If yes, discharge date	text (date_mdy) Field Annotation: @HIDEBUTTON
141	ecmo_yn	Did the patient receive extracorporeal membrane oxygenation (ECMO)?	dropdown 1 Yes 0 No 9 Unknown
142	mechvent_yn	Did the patient receive mechanical ventilation (MV)/intubation?	dropdown 1 Yes 0 No 9 Unknown
143	dx_ekg	Did the patient have an Abnormal EKG?	dropdown 1 Yes 0 No 9 Unknown
144	mechvent_dur Show the field ONLY if: [mechvent_yn] = '1'	If yes, total days with MV (days)	text (number)
145	dx_pneumonia	Was the Patient diagnosed with pneumonia?	dropdown 0 No 1 Yes 9 Unknown
146	dx_ards	Was the Patient diagnosed with acute respiratory distress syndrome?	dropdown 0 No 1 Yes 9 Unknown
147	dx_xray	Did the patient have an Abnormal Chest X-ray?	dropdown 1 Yes 0 No 9 Unknown
148	death_yn	Did the patient die as a result of this illness?	radio 1 Yes 0 No 9 Unknown
149	death_dt Show the field ONLY if: [death_yn] = '1'	Date of Death	text (date_mdy) Field Annotation: @HIDEBUTTON
150	death_unk Show the field ONLY if: [death_yn] = '1'	Date of Death Unknown	radio 1 Unknown
151	notes_hosp_hx	Comments and Additional Notes on Hospitalization or Death	notes

	te	Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Laboratory Testing & Results** (laboratory_testing_results)			Collapse
153	spec_npswab1_dt	PCR: Collection date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
154	spec_npswab1_type	PCR: Specimen Type - 1	dropdown 0 Nasopharyngeal (NP) swab 1 Oral (mouth) swab 2 Nasal (nostril) swab 3 Saliva or Drool 4 Blood 5 Other
155	spec_npswab1_id	PCR: Specimen ID - 1	text
156	spec_npswab1_dtresult	PCR: Result date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
157	spec_npswab1_result	PCR: Result - 1	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
158	spec_npswab1site	PCR: Lab Name - 1	text
159	spec_npswab1_variant	PCR: Viral variant/type - 1	text
160	spec_npswab2_dt	PCR: Collection date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
161	spec_npswab2_type	PCR: Specimen Type - 2	dropdown 0 Nasopharyngeal (NP) swab 1 Oral (mouth) swab 2 Nasal (nostril) swab 3 Saliva or Drool 4 Blood 5 Other
162	spec_npswab2_id	PCR: Specimen ID - 2	text
163	spec_npswab2_dtresult Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Result date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
164	spec_npswab2result Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Result - 2	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
165	spec_npswab2site Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Lab Name - 2	text

166	spec_npswab2_variant Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Viral variant/type - 2	text
167	spec_ag1_dt	Antigen: Collection date - 1 (i.e. Rapid Test)	text (date_mdy) Field Annotation: @HIDEBUTTON
168	spec_ag1_type Show the field ONLY if: [spec_ag1_dt] > "0"	Antigen: Specimen Type - 1	dropdown 0 Nasopharyngeal (NP) swab 1 Oral (mouth) swab 2 Nasal (nostril) swab 3 Saliva or Drool 4 Blood 5 Other
169	spec_ag1_id Show the field ONLY if: [spec_ag1_dt] > "0"	Antigen: Specimen ID - 1	text
170	spec_ag1_dtresult Show the field ONLY if: [spec_ag1_dt] > "0"	Antigen: Result date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
171	spec_ag1_result Show the field ONLY if: [spec_ag1_dt] > "0"	Antigen: Result - 1	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
172	spec_ag1_site Show the field ONLY if: [spec_ag1_dt] > "0"	Antigen: Lab Name - 1	text
173	spec_ab1_dt	Antibody: Collection date - 1 (i.e. Blood Test)	text (date_mdy) Field Annotation: @HIDEBUTTON
174	spec_ab1_type Show the field ONLY if: [spec_ab1_dt] > "0"	Antibody: Specimen Type - 1	dropdown 4 Blood
175	spec_ab1_id Show the field ONLY if: [spec_ab1_dt] > "0"	Antibody: Specimen ID - 1	text
176	spec_ab1_dtresult Show the field ONLY if: [spec_ab1_dt] > "0"	Antibody: Result date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
177	spec_ab1_result Show the field ONLY if: [spec_ab1_dt] > "0"	Antibody: Result - 1	dropdown 1 Positive, Not otherwise specified 6 Positive-IgM 7 Positive-IgG 8 Positive-IgM and IgG 2 Negative 3 Pending 4 Not Done 5 Indeterminate
178	spec_ab1_site Show the field ONLY if: [spec_ab1_dt] > "0"	Antibody: Lab Name - 1	text
179	spec_otherspecimen1_spec	Other specimen type - 1	text

180	spec_otherspecimen1_dt Show the field ONLY if: [spec_otherspecimen1_spec] > ''	Other: Collection date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
181	spec_otherspecimen1result Show the field ONLY if: [spec_otherspecimen1_spec] > ''	Other: Result - 1	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
182	spec_otherspecimen1_dtresult Show the field ONLY if: [spec_otherspecimen1_spec] > ''	Other: Result date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
183	spec_otherspecimen1site Show the field ONLY if: [spec_otherspecimen1_spec] > ''	Other: Lab Name - 1	text
184	spec_otherspecimen2_spec	Other specimen type - 2	text
185	spec_otherspecimen2_dt Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Collection date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
186	spec_otherspecimen2_dtresult Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Result date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
187	spec_otherspecimen2site Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Lab Name - 2	text
188	spec_otherspecimen2result Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Result - 2	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
189	resp_flua_ag	Section Header: *Respiratory Diagnostic Testing* Influenza A Rapid Ag	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
190	resp_flub_ag	Influenza B Rapid Ag	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done

		Influenza A PCR	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
192	resp_flub_pcr	Influenza B PCR	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
193	resp_rsv	RSV	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
194	resp_hm	H. metapneumovirus	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
195	resp_pi	Parainfluenza (1-4)	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
196	resp_adv	Adenovirus	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
197	resp_rhino	Rhinovirus/enterovirus	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
198	resp_cov	Coronavirus (OC43, 229E, HKU1, NL63)	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
199	resp_mp	M. pneumoniae	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done

		C. pneumoniae	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
201	resp_gas	Group A Strep	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
202	resp_other	Other positive pathogens	radio (Matrix) 1 Positive 2 Negative 3 Pending 4 Not Done
203	lab_notes	Notes about Testing	notes
204	laboratory_testing_results_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Investigator Log** (investigator_log)			Collapse
205	interview_name	Section Header: *Investigation Completed: [name_irst] [name_late]* Investigator Name	text
206	interview_phone	Investigator Phone Number	text (phone)
207	casestatus	Case Status	radio, Required 1 Laboratory Confirmed Case 0 Probable Case 2 Suspect Case 5 Pending 9 Indeterminate or Status Unknown
208	interview_final	Investigation Closed Reason	checkbox 0 interview_final___0 Interview Completed 1 interview_final___1 Partial Interview Completed 2 interview_final___2 Non-Response 3 interview_final___3 No Contact Information Available 4 interview_final___4 Refusal 7 interview_final___7 Test determined to be Negative or Inconclusive (Not a Case) 6 interview_final___6 Reported through TAMU Portal 5 interview_final___5 Out of County

209	collect_source	Report Data Collected from (check all that apply):	checkbox 0 collect_source___0 Patient Interview 1 collect_source___1 Medical Record 2 collect_source___2 Parent 3 collect_source___3 Family Member 8 collect_source___8 Other Source 9 collect_source___9 Unknown Field Annotation: @HIDDEN
210	date_dshsreport	Date BCHD Reported/counted as a Case *Assigned by BCHD (From Patient Tracker)*	text (date_mdy)
211	dshsreport_ready	Case ready for Submission to DSHS Data Managers Only	dropdown 1 Yes 0 No
212	dshsreport_submitdate	Date Case transferred to DSHS Database for Submission	text (date_mdy)
213	dshsreport_submitted	Case transferred to DSHS Database for Submission	dropdown 1 Yes 0 No
214	instruct_isolate_case_sx Show the field ONLY if: [sx_yn] = '1' or [sx_date] > ''	Section Header: *Isolation Guidelines* This individual should remain in isolation, physically separated from others, for 10 days, beginning on [sx_date]. Also, must be symptom free for 24-hours before released from Isolation. Use the calendar below to calculate the date the individual can be released from Self-Isolation.	descriptive
215	instruct_isolate_case_asx Show the field ONLY if: [sx_yn] = '0' or [sx_yn] = '9' or [sx_yn] = ''	This individual should remain in isolation, physically separated from others, for 10 days, beginning on [spec_npswab1_dt]. Also, must be symptom free for 24-hours before released from Isolation. Use the calendar below to calculate the date the individual can be released from Self-Isolation.	descriptive
216	instruct_isolate_case	You are requested to remain in isolation and avoid any contact with others as much as possible. You are not allowed to go to work or school. You should remain in your home but separate from others, include family members and other people living in your house. This will help keep you from spreading the virus to others. You are required to isolate, even if you don't feel sick, since you can still spread the virus to people you come into contact with. Self-monitor your health, and seek medical attention if you feel worse, especially if you have any difficulty breathing. Please follow these instructions until the end of the day on your last day of isolation, which is: *Select Isolation End Date using the above formula.*	text (date_mdy) Custom alignment: LV Field Annotation: @HIDEBUTTON
217	call_date_1	Section Header: *Investigator Call Log* Date & Time	text (datetime_mdy)
218	call_notes_1	Notes & Investigator *Include Investigator Name*	notes
219	call_date_2 Show the field ONLY if: [call_date_1] > '"0"'	Date & Time	text (datetime_mdy)
220	call_notes_2 Show the field ONLY if: [call_date_1] > '"0"'	Notes & Investigator *Include Investigator Name*	notes
221	call_date_3 Show the field ONLY if: [call_date_2] > '"0"'	Date & Time	text (datetime_mdy)
222	call_notes_3 Show the field ONLY if: [call_date_2] > '"0"'	Notes & Investigator *Include Investigator Name*	notes

			9 Don't Use - Italo - Epi Lead 11 Don't Use - Matt - Epi Lead 29 Don't Use - Tykeara - Epi Lead 204 Don't Use - Amber - Epi Lead 203 Don't Use - Suyash - Data Manager 34 Don't Use - Tifany - Data Manager 98 Clendenin - Faculty 99 Fischer - Faculty
228	interview_date	Investigation Completed or Closed Date	text (date_mdy)
229	interview_medrec	Medical Records	file
230	spec_npswab1_report	Laboratory Report provided by Respondent	file
231	interview_medrecportal	TAMU Report Form	file
232	investigator_log_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Isolation Clearance** (isolation_clearance) Enabled as survey			Collapse
233	release2	Section Header: *Formal Letter of Release from COVID-19 Isolation* Name: [demographics][name_first] [demographics][name_late]Date of Birth: [demographics][dob]	descriptive
234	the_individual_referenced2	To Whom it May Concern: The individual referenced above has participated in a COVID-19 investigation and has been given instructions to isolate by a member of the Texas A&M University COVID Investigation & Operations Team. The COVID Ops center is an official entity of the Brazos County Health District and Texas A&M University System, and the formal instructions provided in this letter apply to the individual named above. This individual is to remain in isolation through the end of the day on [instruct_isolate_case], as long as the individual has been without symptoms for at least 24 hours.This release from isolation is specific to the individual named in this letter only and cannot be extended to another individual. This letter serves as official notice of isolation. This isolation period may only be reduced by a Brazos County health official. The isolation period may be extended by a physician if certain conditions are met, such as if the individual experiences a worsening of condition or is hospitalized, or if symptoms persist.Any specific question or concern regarding this document may be directed to covid@tamu.edu. COVID Investigations & Operations Center, An Interagency solution to stop the spread of COVID-19	descriptive
235	isolation_clearance_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Covid19 Document Submission** (covid19_test_submission) Enabled as survey			Collapse
236	instruct_uploadfile	Howdy! Use this form to upload documentation to your Texas A&M COVID Operations Center investigator. This upload portal is secure and private, and your information is always protected.	descriptive
237	date_fileupload1	What is today's Date	text (date_mdy)
238	file_upload1	File Upload:	file
239	file_notes1	Please provide any additional information or comments here that your investigator will need to review your documentation or help with your case management.	notes

		File Upload:	file
		What is today's Date	text (date_mdy)
		Please provide any additional information or comments here that your investigator will need to review your documentation or help with your case management.	notes
243	covid19_test_submission_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **TAMU Portal Responses** (tamu_portal_responses) Collapse			
244	text_portal	The below responses are imported from the TAMU COVID-19 Reporting Portal and may be useful when conducting the investigation. However, you do not need to fill in answers here.	descriptive
245	reporter_tamu	Origin of TAMU Reprort	radio 0 Self - I am reporting my own confirmed or suspected COVID-19 illness 1 Supervisor 2 HR Representative 3 Administrative staff 4 Faculty Member/Advisor 8 COVID Ops Team Member 9 Other
246	designat_tamu Show the field ONLY if: [occup_name] = 'TAMU' or [school_name] = 'TAMU'	Primary Role at Texas A&M	radio 0 Student (including student worker) 1 Staff 2 Faculty 3 Postdoc, Resident, or Fellow 4 Contract Worker 5 Other 9 Unknown
247	report_casestatus	This report is about a (select one):	radio 0 Laboratory confirmed case, with positive test result 1 Symptomatic person without laboratory test results 2 Close contact of or potentially exposed to COVID-19 Case 9 Unknown
248	interview_closed	File Closed due to	checkbox 0 interview_closed___0 Out of County (Brazos and Hunt Counties are active) 1 interview_closed___1 Individual's Lab Test returned Negative Result 2 interview_closed___2 Added to Case database 3 interview_closed___3 Added to Contact database 4 interview_closed___4 Non-response 5 interview_closed___5 Insufficient Contact information Provided
249	notes_coop		notes Custom alignment: LV

250	notes_coop_document	Relevant Document Upload	file
251	comments_cf66c6	Please provide any details or additional information you think would be helpful to know.	notes
252	affiliation_tamu	Please indicate any Texas A&M affiliations: *Mark all that apply*	checkbox 0 | affiliation_tamu___0 | Health Science Center (HSC) 1 | affiliation_tamu___1 | Texas A&M System (TAMUS) 10 | affiliation_tamu___10 | Texas A&M University (TAMU) 2 | affiliation_tamu___2 | AgriLife 3 | affiliation_tamu___3 | Center for Applied Technology (TCAT) 4 | affiliation_tamu___4 | Engineering Experiment Station (TEES) 5 | affiliation_tamu___5 | Engineering Extension Service (TEEX) 6 | affiliation_tamu___6 | Forest Service (TFS) 7 | affiliation_tamu___7 | Transportation Institute (TTI) 11 | affiliation_tamu___11 | College of Veterinary Medicine 8 | affiliation_tamu___8 | Veterinary Medicine & Diagnostic Laboratory (TVMDL) 9 | affiliation_tamu___9 | Veterinary Medicine Teaching Hospital (VMTH) 12 | affiliation_tamu___12 | College of Medicine 31 | affiliation_tamu___31 | Higher Education Center at McAllen 32 | affiliation_tamu___32 | School of Law 33 | affiliation_tamu___33 | Texas A&M University at Galveston 34 | affiliation_tamu___34 | Texas A&M University - Commerce 35 | affiliation_tamu___35 | Texas A&M University at Qatar 50 | affiliation_tamu___50 | Corps of Cadets 51 | affiliation_tamu___51 | Texas A&M Athletics 54 | affiliation_tamu___54 | Involved in Healthcare (Human or Animal) 55 | affiliation_tamu___55 | Laboratory Personnel 60 | affiliation_tamu___60 | Custodial Staff 98 | affiliation_tamu___98 | Other 99 | affiliation_tamu___99 | Unknown Custom alignment: LV
253	housingbldg_tamu_report	Residence Building Name/Number *e.g. SPHA*	text
254	date_tamu_campus	When was the individual last on campus? *MM-DD-YYYY*	text (date_mdy) Field Annotation: @HIDEBUTTON
255	hcare_tamu	Has medical care been sought?	radio 1 | Yes 0 | No 9 | Unknown

256	date_report_tamu	Date Reported to TAMU *MM-DD-YYYY*	text (date_mdy, Min: 2020-03-01)
257	uin_tamu	Section Header: *Information on Individual with Conirmed or Suspected COVID-19* UIN, if known	text (number), Identifier Field Annotation: @HIDDEN-PDF
258	phone_work	Office Phone Number *Include Area Code*	text (phone), Identifier Field Annotation: @HIDDEN-PDF
259	contact_tamu_qty	What is the estimated number of other individuals impacted?	text
260	labpos_tamu	Was there a laboratory test with a Positive result for COVID-19?	radio 1 Yes 0 No 9 Unknown
261	locate_tamu	Is the individual physically located on campus at this time?	radio 1 Yes 0 No 9 Unknown
262	contact_date_tamu	If known, what date was the prior contact with the Positive or Suspected COVID-19 case? *MM-DD-YYYY*	text (date_mdy)
263	affilitation_other_tamu	Specify Other Affiliation(s)	text
264	date_tamu_result	Date test results were Received, if known *MM-DD-YYYY*	text (date_mdy) Field Annotation: @HIDEBUTTON
265	name_tamu_reporter	Name of person making this Report *First Name Last Name*	text
266	role_tamu_reporter	Title of person making this Report *e.g. Department Chair*	text
267	school_tamu	School/College *e.g. School of Public Health*	text
268	school_tamu_3	Department/Unit/Laboratory Name *e.g. Department of Environmental & Occupational Health*	text
269	bldg_tamu_report	Building Name/Number *e.g. SPHA*	text
270	close_contacts_2	What areas of campus did the individual visit while symptomatic and 48 hours before symptoms started? If no symptoms, what areas did the individual visit starting 48 hours before diganosis, suspicion, or report? Please list locations visited/worked. Please be specific (buildings, halls, rooms).	notes
271	city_tamu_report	City/Location *e.g. College Station*	text
272	email_reporter_tamu	E-mail Address of person making report	text (email)
273	phone_tamu_reporter	Phone Number of person making this report *Include Area Code*	text (phone), Identifier
274	date_tamu_notif	What date were you notified of the Positive or Suspected COVID-19 Case? *MM-DD-YYYY*	text (date_mdy)
275	report_yn	Have you reported the confirmed or suspected event to your supervisor, HR liaison, Principal Investigator, or TAMU designee?	radio 1 Yes 0 No 9 Unknown

276	instruct_private	The information provided in this report will be protected and kept private to the full extent possible. Information will be used by Texas A&M designated officers for Risk Management and to ensure the health and safety of the Texas A&M family. Please ensure you have provided accurate information that can be used to help protect others. Information will also be used by the Texas A&M COVID Investigation & Operations Center to help conduct the Case Investigation and Contact Tracing by the local Health Authority.	descriptive
277	covid19_questionnaire_complete	covid19_questionnaire_complete	text
278	covid19_questionnaire_timestamp	covid19_questionnaire_timestamp	text (datetime_mdy)
279	covid_report_form_complete	covid_report_form_complete	text
280	covid_report_form_timestamp	covid_report_form_timestamp	text (datetime_mdy)
281	covid_ops_action_complete	covid_ops_action_complete	text
282	reportid_report_tamu	TAMU Portal Report Tracking number	text
283	tamu_portal_responses_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Retired Questions - Do Not Use** (retired_questions_do_not_use)			Collapse
284	retired	These are old questions no longer in use.	descriptive
285	social_renaissance	During the prior 14 days, Did you attend the Texas Renaissance Festival?	dropdown 0 No 1 Yes 2 Unknown
286	football_nov28	For the Texas A&M Football game on NOV 28 vs LSU, please indicate all of your game related activities:	checkbox 1 football_nov28___1 Pre-game social activity or event 2 football_nov28___2 Watch party, indoor 3 football_nov28___3 Watch party, outdoor 4 football_nov28___4 Attended game at the Stadium 5 football_nov28___5 Post-game social activity or event 6 football_nov28___6 Watch at home, alone or with household/roommates 7 football_nov28___7 Worked at the Stadium during the game 0 football_nov28___0 None

			1 | football_nov7___1 | Pre-game social activity or event 2 | football_nov7___2 | Watch party, indoor 3 | football_nov7___3 | Watch party, outdoor 4 | football_nov7___4 | Attended game at the Stadium 5 | football_nov7___5 | Post-game social activity or event 6 | football_nov7___6 | Watch at home, alone or with household/roommates 0 | football_nov7___0 | None
288	football_oct31	For the Texas A&M Football game on OCT 31 vs Arkansas, please indicate all of your game related activities:	checkbox 1 | football_oct31___1 | Pre-game social activity or event 2 | football_oct31___2 | Watch party, indoor 3 | football_oct31___3 | Watch party, outdoor 4 | football_oct31___4 | Attended game at the Stadium 5 | football_oct31___5 | Post-game social activity or event 6 | football_oct31___6 | Watch at home, alone or with household/roommates 7 | football_oct31___7 | Worked at the Stadium during the game 0 | football_oct31___0 | None
289	football_oct17	For the Texas A&M Football game on OCT 17 @ Mississippi State, please indicate all of your game related activities:	checkbox 1 | football_oct17___1 | Pre-game social activity or event 2 | football_oct17___2 | Watch party, indoor 3 | football_oct17___3 | Watch party, outdoor 4 | football_oct17___4 | Attended game at the Stadium 5 | football_oct17___5 | Post-game social activity or event 6 | football_oct17___6 | Watch at home, alone or with household/roommates 0 | football_oct17___0 | None
290	football_oct10	For the Texas A&M Football game on OCT 10 vs Florida, please indicate all of your game related activities:	checkbox 1 | football_oct10___1 | Pre-game social activity or event 2 | football_oct10___2 | Watch party, indoor 3 | football_oct10___3 | Watch party, outdoor 4 | football_oct10___4 | Attended game at the Stadium 5 | football_oct10___5 | Post-game social activity or event 6 | football_oct10___6 | Watch at home, alone or with household/roommates 7 | football_oct10___7 | Worked at the Stadium during the game 0 | football_oct10___0 | None

			1 football_oct3___1 Pre-game social activity or event 2 football_oct3___2 Watch party, indoor 3 football_oct3___3 Watch party, outdoor 4 football_oct3___4 Attended game at the Stadium 5 football_oct3___5 Post-game social activity or event 6 football_oct3___6 Watch at home, alone or with household/roommates 0 football_oct3___0 None
292	football_sept26	For the Texas A&M Football game on SEPT 26th vs Vanderbilt, please indicate all of your game related activities:	checkbox 1 football_sept26___1 Pre-game social activity or event 2 football_sept26___2 Watch party, indoor 3 football_sept26___3 Watch party, outdoor 4 football_sept26___4 Attended game at the Stadium 5 football_sept26___5 Post-game social activity or event 6 football_sept26___6 Watch at home, alone or with household/roommates 7 football_sept26___7 Worked at the Stadium during the game 0 football_sept26___0 None
293	exp_pui	Did patient have close contact with a PUI (person under investigation, who is not a laboratory-confirmed case)?	dropdown 0 No 1 Yes 9 Unknown
294	date_report	Date Case reported to BCHD	text (date_mdy, Min: 0017-03-20)
295	hc_visit_yn	In the prior 14 days, Was the patient in a healthcare facility (as a patient, worker or visitor) ?	dropdown 0 No 1 Yes, as Patient 2 Yes, as Worker 3 Yes, as Visitor 4 Yes (Other/Unknown) 9 Unknown
296	hc_visit_spec Show the field ONLY if: [hc_visit_yn] = '1'	Describe healthcare visit or Facility	text
297	test_file	TEST FILE	file
298	tracer_pending	Pending Contact Tracing	radio 0 Pending - Assigned to Tracer 1 Tracer Review Complete
299	tracer_assigned	Assigned Contact Tracer *Do not Edit*	dropdown 105 - - BCHD - - - 200 BCHD - Investigator 13 Nabihah - Investigator 16 Rachel - Investigator 206 Adrianne - Investigator

			20 Don't Use - Caroline - Epi Lead 9 Don't Use - Italo - Epi Lead 11 Don't Use - Matt - Epi Lead 29 Don't Use - Tykeara - Epi Lead 204 Don't Use - Amber - Epi Lead 203 Don't Use - Suyash - Data Manager 34 Don't Use - Tifany - Data Manager 98 Clendenin - Faculty 99 Fischer - Faculty
300	case_casecontacts Show the field ONLY if: [exp_case] = '1'	List Names and/or ID numbers of any other COVID cases that are linked to this Case	text
301	retired_questions_do_not_use_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete

A.2 Code for case database

```
*Coding for case database started on 1.31.22*

*Coding for ASTMH abstract*
*Calculate incubation period: test date to symptom start date
gen incubationperiod=test_date2 - sx_date_raw
tab incubationperiod, missing
replace incubationperiod=. if incubationperiod<0
replace incubationperiod=. if incubationperiod>101
tab incubationperiod, missing

gen incubationperiodnew=test_date2 - sx_date_raw
tab incubationperiodnew, missing
replace incubationperiodnew=. if incubationperiodnew<0
replace incubationperiodnew=. if incubationperiodnew>14
tab incubationperiodnew, missing

*Symptom duration calculation: symptom start date to symptom end date
gen symptomduration=  symp_res_dt_raw-   sx_date_raw
tab symptomduration, missing
replace symptomduration=. if symptomduration<0
replace symptomduration=. if symptomduration>101
tab symptomduration, missing

gen symptomduration=  symp_res_dt_raw-   sx_date_raw
tab symptomduration, missing
replace symptomduration=. if symptomduration<0
tab symptomduration, missing
replace symptomduration=. if symptomduration>101
tab symptomduration, missing


*COVID resolution is infection date to symptom end date
gen resolution= test_date2-symp_res_dt_raw
tab resolution, missing
replace resolution=. if resolution<0
replace resolution=. if resolution>100
tab resolution, missing

*Coding for modeling parameters*
*calculate recovery rate*
gen recoveryrate=symp_res_dt_raw-test_date2
```

```
tab recoveryrate, missing
replace recoveryrate=. if recoveryrate>100
replace recoveryrate=. if recoveryrate<0
tab recoveryrate, missing

*Calculating difference between symptom onset and test date*
gen symponset=test_date2 - sx_date_raw
tab symponset, missing
replace symponset=. if symponset<-30
replace symponset=. if symponset>30

*If negative, tested before symptom onset - likely due to contact tracing or
*required to test
*If positive, tested after symptom onset


*Coding for age categories*

gen test_date= max(spec_npswab1_dt_raw, spec_npswab2_dt_raw, spec_ag1_dt_raw)

tab test_date

format test_date %tdCCYY.NN.DD
tab test_date

*Went through and manually fixed test dates*
*Dropping test dates after July 31, 2021*
drop if test_date>22492

gen age_calc=((test_date -dob_raw)/365.25)
replace age_calc = round(age_calc,0.1)
list age_calc in 1/10

gen age_calc2=floor(age_calc/10)
drop age_calc2
gen age_calc_r=round(age_calc)
gen age_calc_f=floor(age_calc)
drop age_calc_r
*age_calc_f rounds down*


**re-coding after adjusting dates that were off*

gen test_date2= max(spec_npswab1_dt_raw, spec_npswab2_dt_raw, spec_ag1_dt_raw)
```

```
tab test_date2

format test_date2 %tdCCYY.NN.DD
tab test_date2
drop if test_date2>22492

gen age_calc2=((test_date2 -dob_raw)/365.25)
replace age_calc2 = round(age_calc2,0.1)
list age_calc2 in 1/10


gen age_calc_r2=round(age_calc2)
gen age_calc_f2=floor(age_calc2)


*age_calc_f rounds down*
*age categories based off CDC COVID-19 reporting*
gen age_coded2=.
*age 0 - 4*
replace age_coded2=0 if (age_calc_f2 >= 0) & (age_calc_f2 <= 4)
*age 5 - 11*
replace age_coded2=1 if (age_calc_f2 >=5) & (age_calc_f2 <=11)
*age 12 - 15*
replace age_coded2=2 if (age_calc_f2 >= 12) & (age_calc_f2<= 15)
*age 16 - 17*
replace age_coded2=3 if (age_calc_f2 >= 16) & (age_calc_f2 <= 17)
*age 18 - 29*
replace age_coded2=4 if (age_calc_f2 >= 18) & (age_calc_f2 <= 29)
*age 30 - 39*
replace age_coded2=5 if (age_calc_f2 >= 30) & (age_calc_f2 <= 39)
*age 40 - 49*
replace age_coded2=6 if (age_calc_f2 >= 40) & (age_calc_f2 <= 49)
*age 50 - 64*
replace age_coded2=7 if (age_calc_f2 >= 50) & (age_calc_f2 <= 64)
*age 65 - 74*
replace age_coded2=8 if (age_calc_f2 >= 65) & (age_calc_f2 <= 74)
*age 75+*
replace age_coded2=9 if (age_calc_f2>=75) & (age_calc_f2 <=110)
tab age_coded2

label define agelabel 0 "Ages 0 - 4" 1 "Ages 5 - 11" 2 "Ages 12 - 15" 3 "Ages 16 - 17" 4
"Ages 18 - 29" 5 "Ages 30 - 39" 6 "Ages 40 - 49" 7 "Ages 50 - 64" 8 "Ages 65 - 74" 9
"Ages over 75"
```

```
label values age_coded2 agelabel

*over and under 18*
gen eighteenage_coded=.
replace eighteenage_coded=0 if (age_calc_f2 >=0) & (age_calc_f2 <=17)
*aggregate all ages over 18*
replace eighteenage_coded=1 if (age_calc_f2 >=18) & (age_calc_f2 <=110)

label define aggregate_age 0 "All ages under 18" 1 "All ages over 18"
label values eighteenage_coded aggregate_age
tab eighteenage_coded, missing

*18 and then each decade of life*
gen decade=.
replace decade=0 if (age_calc_f2 >=0) & (age_calc_f2 <=17)
replace decade=1 if (age_calc_f2 >= 18) & (age_calc_f2 <= 29)
replace decade=2 if (age_calc_f2 >= 30) & (age_calc_f2 <= 39)
replace decade=3 if (age_calc_f2 >= 40) & (age_calc_f2 <= 49)
replace decade=4 if (age_calc_f2 >= 50) & (age_calc_f2 <= 59)
replace decade=5 if (age_calc_f2 >= 60) & (age_calc_f2 <= 69)
replace decade=6 if (age_calc_f2 >= 70) & (age_calc_f2 <= 79)
replace decade=7 if (age_calc_f2 >= 80) & (age_calc_f2 <= 89)
replace decade=8 if (age_calc_f2 >= 90) & (age_calc_f2 <= 99)
label define decadelabel 0 "ages under 18" 1 "18 - 29" 2 "30 - 39" 3 "40 - 49" 4 "50 - 59"
5 "60 - 69" 6 "70 - 79" 7 "80 - 89" 8 "90 - 99"
label values decade decadelabel
tab decade, missing


gen decadenew=.
replace decadenew=0 if (age_calc_f2 >=0) & (age_calc_f2 <=9)
replace decadenew=1 if (age_calc_f2 >=10) & (age_calc_f2<=19)
replace decadenew=2 if (age_calc_f2>=20) & (age_calc_f2<=29)
replace decadenew=3 if (age_calc_f2>=30) & (age_calc_f2<=39)
replace decadenew=4 if (age_calc_f2 >= 40) & (age_calc_f2 <= 49)
replace decadenew=5 if (age_calc_f2 >= 50) & (age_calc_f2 <= 59)
replace decadenew=6 if (age_calc_f2 >= 60) & (age_calc_f2 <= 69)
replace decadenew=7 if (age_calc_f2 >= 70) & (age_calc_f2 <= 79)
replace decadenew=8 if (age_calc_f2 >= 80) & (age_calc_f2 <= 89)
replace decadenew=9 if (age_calc_f2 >= 90) & (age_calc_f2 <= 99)
label define decadelabel2 0 "ages 0 - 9" 1 "ages 10 - 19" 2 "ages 20 - 29" 3 "ages 30 -
39" 4 "ages 40 - 49" 5 "ages 50 - 59" 6 "ages 60 - 69" 7 "ages 70 - 79" 8 "ages 80 - 89" 9
"ages 90 - 99"
label values decadenew decadelabel2
```

```
tab decadenew


gen decade2=.
*referent group is now 40 - 49*
replace decade2=0 if (age_calc_f2 >= 40) & (age_calc_f2 <= 49)
replace decade2=1 if (age_calc_f2 >=0) & (age_calc_f2 <=9)
replace decade2=2 if (age_calc_f2 >=10) & (age_calc_f2<=19)
replace decade2=3 if (age_calc_f2>=20) & (age_calc_f2<=29)
replace decade2=4 if (age_calc_f2>=30) & (age_calc_f2<=39)
replace decade2=5 if (age_calc_f2 >= 50) & (age_calc_f2 <= 59)
replace decade2=6 if (age_calc_f2 >= 60) & (age_calc_f2 <= 69)
replace decade2=7 if (age_calc_f2 >= 70) & (age_calc_f2 <= 79)
replace decade2=8 if (age_calc_f2 >= 80) & (age_calc_f2 <= 89)
replace decade2=9 if (age_calc_f2 >= 90) & (age_calc_f2 <= 99)

label define decade2label 0 "ages 40 - 49" 1 "ages 0 - 9" 2 "ages 10 - 19" 3 "ages 20 -
29" 4 "ages 30 - 39" 5 "ages 50 - 59" 6 "ages 60 - 69" 7 "ages 70 - 79" 8 "ages 80 - 89" 9
"ages 90 - 99"
label values decade2 decade2label
tab decade2

gen minors=.
replace minors=0 if (age_calc_f2 >=0) & (age_calc_f2 <=11)
replace minors=1 if (age_calc_f2 >=12) & (age_calc_f2 <=17)
tab minors
label define minorslabel 0 "ages 0-11" 1 "ages 12-7"
label values minors minorslabel
tab minors, missing

gen youngadults=.
replace youngadults=0 if (age_calc_f2 >= 18) & (age_calc_f2 <= 29)
replace youngadults=1 if (age_calc_f2 >=30) & (age_calc_f2 <=110)
label define young 0 "ages 18-29" 1 "ages 30+"
label values youngadults young
tab youngadults, missing

*Code language*
*Omitting Unknown language*
gen language_coded=.
replace language_coded=0 if language_raw==0
replace language_coded=1 if language_raw==1
replace language_coded=8 if language_raw==8
label define languagelabel 0 "English" 1 "Spanish" 8 "Other"
```

```
label values language_coded languagelabel
tab language_coded

gen language_new=.
replace language_new=0 if language_raw==0
replace language_new=1 if language_raw==1 | language_raw==8
label define langlabel 0 "English" 1 "Other language"
label values language_new langlabel
tab language_new, missing

*Code sex*
*Omitting sex unknown*
gen sex_coded=.
replace sex_coded=0 if sex_raw==0
replace sex_coded=1 if sex_raw==1
label define sexlabel 0 "Female" 1 "Male"
label values sex_coded sexlabel
tab sex_coded

*Code and collapse residence type*
gen residencetype_coded=.
replace residencetype_coded=0 if residencetype_raw==0
replace residencetype_coded=1 if residencetype_raw==15
replace residencetype_coded=2 if residencetype_raw==17
*residence type=3 if supported living*
replace residencetype_coded=3 if residencetype_raw==3 | residencetype_raw== 4 |
residencetype_raw== 7 |residencetype_raw==6 | residencetype_raw== 8 |
residencetype_raw==16
*residencetype_coded=8 if other
replace residencetype_coded=8 if residencetype_raw==20 | residencetype_raw==1 |
residencetype_raw==2 | residencetype_raw== 9 | residencetype_raw==10
|residencetype_raw==11 | residencetype_raw==14

label define residencetypelabel2 0 "House" 1 "Apartment" 2 "Dormitory" 3 "Supported
living" 8 "Other"
label values residencetype_coded residencetypelabel2
tab residencetype_coded

gen apthouse=.
replace apthouse=0 if residencetype_raw==0
replace apthouse=1 if residencetype_raw==15
label define apt 0 "House" 1 "Apartment"
label values apthouse apt
tab apthouse, missing
```

```
*Code and collapse race*
gen race_coded=.
replace race_coded=0 if race_raw==0
replace race_coded=1 if race_raw==1
replace race_coded=2 if race_raw==2
replace race_coded=8 if race_raw==8 | race_raw==4 | race_raw==3

label define racelabel2 0 "White" 1 "Black" 2 "Asian"  8 "Other"
label values race_coded racelabel2
tab race_coded

*code for hispanic*
gen hispanic_coded=.
replace hispanic_coded=0 if hispanic_raw==0
replace hispanic_coded=1 if hispanic_raw==1

label define hispaniclabel 0 "No, NOT Hispanic or Latino" 1 "Yes, Hispanic or Latino"
label values hispanic_coded hispaniclabel
tab hispanic_coded

*race and ethnicity*
gen race_ethnicity=.
replace race_ethnicity=0 if hispanic_raw==1 & race_raw==0
replace race_ethnicity=1 if hispanic_raw==1 & race_raw==1
replace race_ethnicity=2 if hispanic_raw==1 & race_raw==2
replace race_ethnicity=3 if hispanic_raw==0 & race_raw==0
replace race_ethnicity=4 if hispanic_raw==0 & race_raw==1
replace race_ethnicity=5 if hispanic_raw==0 & race_raw==2
replace race_ethnicity=6 if hispanic_raw==0 & race_raw==4
replace race_ethnicity=7 if hispanic_raw==0 & race_raw==3

label define race_ethnicitylabel  0 "Hispanic, White" 1 "Hispanic, Black" 2 "Hispanic,
Asian" 3 "White, non-Hispanic" 4 "Black, non-Hispanic" 5 "Asian, non-Hispanic" 6
"American Indian or Alaska Native, non-Hispanic" 7 "Native Hawaiian or Other Pacific
Islander, non-Hispanic"
label values race_ethnicity race_ethnicitylabel
tab race_ethnicity

*https://doh.wa.gov/sites/default/files/legacy/Documents/1500//RaceEthnGuidelines.pdf
*
gen race_ethnicity_recode=.
*White, non-Hispanic*
replace race_ethnicity_recode=0 if hispanic_raw==0 & race_raw==0
```

```
*Hispanic, White*
replace race_ethnicity_recode=1 if hispanic_raw==1 & race_raw==0
*Black, non-Hispanic*
replace race_ethnicity_recode=2 if hispanic_raw==0 & race_raw==1
*Asian, non-Hispanic*
replace race_ethnicity_recode=3 if hispanic_raw==0 & race_raw==2
*Hispanic, Black*
replace race_ethnicity_recode=4 if hispanic_raw==1 & race_raw==1


label define race_ethnicityrecolabel2 0 "White, non-Hispanic" 1 "Hispanic, White" 2
"Black, non-Hispanic" 3 "Asian, non-Hispanic" 4 "Hispanic, Black"
label values race_ethnicity_recode race_ethnicityrecolabel2
tab race_ethnicity_recode, missing

*Recoding race_ethnicity* **Don't use this one.
gen race_ethnicity_new=.
*White, non-Hispanic*
replace race_ethnicity_new=0 if hispanic_raw==0 & race_raw==0
*Hispanic, White*
replace race_ethnicity_new=1 if hispanic_raw==1 & race_raw==0
*Black, non-Hispanic*
replace race_ethnicity_new=2 if hispanic_raw==0 & race_raw==1
*Asian, non-Hispanic*
replace race_ethnicity_new=3 if hispanic_raw==0 & race_raw==2
*Hispanic, Other*
replace race_ethnicity_new=4 if hispanic_raw==1 & race_coded==8
*Non-Hispanic, Other*
replace race_ethnicity_new=8 if hispanic_raw==0 & race_coded==8 | race_coded==.

label define raceethnicitylabel2 0 "White, non-Hispanic" 1 "Hispanic, White" 2 "Black,
non-Hispanic" 3 "Asian, non-Hispanic" 4 "Hispanic, Other" 8 "Non-Hispanic, Other"
label values race_ethnicity_new raceethnicitylabel2
tab race_ethnicity_new, missing

*Recoding race_ethnicity after talking to Dr. Fischer*
gen race_ethnicity_again=.
*White,non-Hispanic*
replace race_ethnicity_again=0 if hispanic_raw==0 & race_raw==0
*Hispanic*
replace race_ethnicity_again=1 if hispanic_raw==1
*Black*
replace race_ethnicity_again=2 if race_raw==1
*Asian*
```

```
replace race_ethnicity_again=3 if race_raw==2
*Other race*
replace race_ethnicity_again=6 if race_raw==8
*Missing race*
replace race_ethnicity_again=7 if race_raw==.
label define raceagainlabel 0 "White, non-Hispanic" 1 "Hispanic" 2 "Black" 3 "Asian" 6
"Other race" 7 "Missing race"
label values race_ethnicity_again raceagainlabel
tab race_ethnicity_again, missing


gen race_ethnicity_v5=.
*Other race*
replace race_ethnicity_v5=4 if race_coded==8
*Missing race*
replace race_ethnicity_v5=8 if race_coded==.
*White,non-Hispanic*
replace race_ethnicity_v5=0 if hispanic_raw==0 & race_raw==0
*Hispanic*
replace race_ethnicity_v5=1 if hispanic_raw==1
*Black*
replace race_ethnicity_v5=2 if race_raw==1
*Asian*
replace race_ethnicity_v5=3 if race_raw==2
label define raceeth 4 "Other race" 8 "Missing race" 0 "White, non-Hispanic" 1
"Hispanic" 2 "Black" 3 "Asian"
label values race_ethnicity_v5 raceeth
tab race_ethnicity_v5, missing

gen race_eth=.
*Other race*
replace race_eth=4 if race_coded==8
*White, non-Hispanic*
replace race_eth=0 if hispanic_raw==0 & race_raw==0
*Hispanic*
replace race_eth=1 if hispanic_raw==1
*Black*
replace race_eth=2 if race_raw==1
*Asian*
replace race_eth=3 if race_raw==2
label define neww 0 "White, non-Hispanic" 1 "Hispanic" 2 "Black" 3 "Asian" 4 "Other
race"
label values race_eth neww
tab race_eth, missing
```

```
gen hispanicwhite=.
*White, non-Hispanic*
replace hispanicwhite=0 if race_raw==0 & hispanic_raw==0
*Hispanic*
replace hispanicwhite=1 if hispanic_raw==1
label define hispan 0 "White, non-Hispanic" 1 "Hispanic"
label values hispanicwhite hispan
tab hispanicwhite

*Code for employed*
gen employed_coded=.
replace employed_coded=0 if occupation_yn_raw==0
replace employed_coded=1 if occupation_yn_raw==1

label define employedlabel 0 "No" 1 "Yes"
label values employed_coded employedlabel
tab employed_coded

*code for symptoms*
gen fever_coded=.
replace fever_coded=0 if sx_fever_raw==0
replace fever_coded=1 if sx_fever_raw==1

label define symptoms 0 "No" 1 "Yes"
label values fever_coded symptoms

gen cough_coded=.
replace cough_coded=0 if sx_cough_raw==0
replace cough_coded=1 if sx_cough_raw==1

label values cough_coded symptoms
tab cough_coded

gen pharyngitis_coded=.
replace pharyngitis_coded=0 if sx_pharyngitis_raw==0
replace pharyngitis_coded=1 if sx_pharyngitis_raw==1

label values pharyngitis_coded symptoms
tab pharyngitis_coded

gen sob_coded=.
replace sob_coded=0 if sx_sob_raw==0
replace sob_coded=1 if sx_sob_raw==1
```

```
label values sob_coded symptoms
tab sob_coded

gen chills_coded=.
replace chills_coded=0 if sx_chills_raw==0
replace chills_coded=1 if sx_chills_raw==1

label values chills_coded symptoms
tab chills_coded

gen headache_coded=.
replace headache_coded=0 if sx_headache_raw==0
replace headache_coded=1 if sx_headache_raw==1

label values headache_coded symptoms
tab headache_coded

gen aches_coded=.
replace aches_coded=0 if sx_aches_raw==0
replace aches_coded=1 if sx_aches_raw==1

label values aches_coded symptoms
tab aches_coded

gen vomit_coded=.
replace vomit_coded=0 if sx_vomit_raw==0
replace vomit_coded=1 if sx_vomit_raw==1

label values vomit_coded symptoms
tab vomit_coded

gen abdpain_coded=.
replace abdpain_coded=0 if sx_abdpain_raw==0
replace abdpain_coded=1 if sx_abdpain_raw==1

label values abdpain_coded symptoms
tab abdpain_coded

gen diarrhea_coded=.
replace diarrhea_coded=0 if sx_diarrhea_raw==0
replace diarrhea_coded=1 if sx_diarrhea_raw==1

label values diarrhea_coded symptoms
```

```
tab diarrhea_coded

gen rhinitis_coded=.
replace rhinitis_coded=0 if sx_rhinitis_raw==0
replace rhinitis_coded=1 if sx_rhinitis_raw==1

label values rhinitis_coded symptoms
tab rhinitis_coded

gen congestion_coded=.
replace congestion_coded=0 if sx_congestion_raw==0
replace congestion_coded=1 if sx_congestion_raw==1

label values congestion_coded symptoms
tab congestion_coded

gen conjunct_coded=.
replace conjunct_coded=0 if sx_conjunct_raw==0
replace conjunct_coded=1 if sx_conjunct_raw==1

label values conjunct_coded symptoms
tab conjunct_coded

gen taste_coded=.
replace taste_coded=0 if sx_taste_raw==0
replace taste_coded=1 if sx_taste_raw==1

label values taste_coded symptoms
tab taste_coded

gen fatigue_coded=.
replace fatigue_coded=0 if sx_fatigue_raw==0
replace fatigue_coded=1 if sx_fatigue_raw==1

label values fatigue_coded symptoms
tab fatigue_coded

gen weakness_coded=.
replace weakness_coded=0 if sx_weakness_raw==0
replace weakness_coded=1 if sx_weakness_raw==1

label values weakness_coded symptoms
tab weakness_coded
```

```
gen hyporexia_coded=.
replace hyporexia_coded=0 if sx_hyporexia_raw==0
replace hyporexia_coded=1 if sx_hyporexia_raw==1

label values hyporexia_coded symptoms
tab hyporexia_coded


*Need to drop everyone who is not a positive case - include PCR positive and *
*antigen positive*
gen pos_cases=.
replace pos_cases=0 if spec_npswab1_result_raw==1 | spec_npswab2result_raw==1 |
spec_ag1_result_raw==1
drop if pos_cases==.

*Asymptomatic - asked*
gen asymptomatic_asked=.
replace asymptomatic_asked=0 if sx_yn_raw==0
replace asymptomatic_asked=1 if sx_yn_raw==1
label values asymptomatic_asked symptoms
tab asymptomatic_asked

*Asymptomatic coding, if person responded no (0) to all symptoms then yes, they're
asymptomatic*
gen asymptomatic_coded=.
replace asymptomatic_coded=0 if fever_coded==1 | cough_coded==1 |
pharyngitis_coded==1 | sob_coded==1 | chills_coded==1 | headache_coded==1 |
aches_coded==1 | vomit_coded==1 | abdpain_coded==1 |diarrhea_coded==1 |
rhinitis_coded==1 | congestion_coded==1 | conjunct_coded==1 | taste_coded==1 |
fatigue_coded==1 | weakness_coded==1 | hyporexia_coded==1

replace asymptomatic_coded=1 if fever_coded==0 & cough_coded==0 &
pharyngitis_coded==0 & sob_coded==0 & chills_coded==0 & headache_coded==0 &
aches_coded==0 & vomit_coded==0 & abdpain_coded==0 & diarrhea_coded==0 &
rhinitis_coded==0 & congestion_coded==0 & conjunct_coded==0 & taste_coded==0 &
fatigue_coded==0 & weakness_coded==0 & hyporexia_coded==0

label define asymptomaticlabel 0 "No, NOT asymptomatic" 1 "Yes, asymptomatic"
label values asymptomatic_coded asymptomaticlabel

*Medical history*
gen medicalhistory_none=.
replace medicalhistory_none=0 if medhx_none_raw==0
replace medicalhistory_none=1 if medhx_none_raw==1
```

```
label values medicalhistory_none symptoms
tab medicalhistory_none

gen medicalhistory_unknown=.
replace medicalhistory_unknown=0 if medhx_unknown_raw==0
replace medicalhistory_unknown=1 if medhx_unknown_raw==1
label values medicalhistory_unknown symptoms
tab medicalhistory_unknown

gen pregnant_coded=.
replace pregnant_coded=0 if pregnant_yn_raw==0
replace pregnant_coded=1 if pregnant_yn_raw==1

label values pregnant_coded symptoms
tab pregnant_coded

gen diabetes_coded=.
replace diabetes_coded=0 if medhx_diabetes_yn_raw==0
replace diabetes_coded=1 if medhx_diabetes_yn_raw==1
label values diabetes_coded symptoms
tab diabetes_coded

gen cvd_coded=.
replace cvd_coded=0 if medhx_cvd_yn_raw==0
replace cvd_coded=1 if medhx_cvd_yn_raw==1
label values cvd_coded symptoms
tab cvd_coded

gen cvd_codedmiss=.
replace cvd_codedmiss=0 if medhx_cvd_yn_raw==0 | medhx_cvd_yn_raw==.
replace cvd_codedmiss=1 if medhx_cvd_yn_raw==1
labe values cvd_codedmiss symptoms
tab cvd_codedmiss

gen htn_coded=.
replace htn_coded=0 if medhx_htn_raw==0
replace htn_coded=1 if medhx_htn_raw==1
label values htn_coded symptoms
tab htn_coded

gen htn_codedmiss=.
replace htn_codedmiss=0 if medhx_htn_raw==0 | medhx_htn_raw==.
replace htn_codedmiss=1 if medhx_htn_raw==1
label values htn_codedmiss symptoms
```

```
tab htn_codedmiss

gen cld_coded=.
replace cld_coded=0 if medhx_cld_yn_raw==0
replace cld_coded=1 if medhx_cld_yn_raw==1
label values cld_coded symptoms
tab cld_coded

gen cld_codedmiss=.
replace cld_codedmiss=0 if medhx_cld_yn_raw==0 | medhx_cld_yn_raw==.
replace cld_codedmiss=1 if medhx_cld_yn_raw==1
label values cldmiss symptoms
tab cld_codedmiss, missing

gen renaldis_coded=.
replace renaldis_coded=0 if medhx_renaldis_yn_raw==0
replace renaldis_coded=1 if medhx_renaldis_yn_raw==1
label values renaldis_coded symptoms
tab renaldis_coded

gen liverdis_coded=.
replace liverdis_coded=0 if medhx_liverdis_yn==0
replace liverdis_coded=1 if medhx_liverdis_yn==1
label values liverdis_coded symptoms
tab liverdis_coded

gen immsupp_coded=.
replace immsupp_coded=0 if medhx_immsupp_yn_raw==0
replace immsupp_coded=1 if medhx_immsupp_yn_raw==1
label values immsupp_coded symptoms
tab immsupp_coded

gen immsupp_codedmiss=.
replace immsupp_codedmiss=0 if medhx_immsupp_yn_raw==0 |
medhx_immsupp_yn_raw==.
replace immsupp_codedmiss=1 if medhx_immsupp_yn_raw==1
label values immsupp_codedmiss symptoms
tab immsupp_codedmiss, missing

gen childasthma_coded=.
replace childasthma_coded=0 if medhx_childasthma_raw==0
replace childasthma_coded=1 if medhx_childasthma_raw==1
label values childasthma_coded symptoms
tab childasthma_coded
```

```
gen childasthma_codedmiss=.
replace childasthma_codedmiss=0 if medhx_childasthma_raw==0 |
medhx_childasthma_raw==.
replace childasthma_codedmiss=1 if medhx_childasthma_raw==1
label values childasthma_codedmiss symptoms
tab childasthma_codedmiss

gen comorbidities=.
replace comorbidities=0 if medhx_immsupp_yn_raw==0 & medhx_liverdis_yn==0 &
medhx_renaldis_yn_raw==0 & medhx_cld_yn_raw==0 & medhx_htn_raw==0 &
medhx_cvd_yn_raw==0 & medhx_diabetes_yn_raw==0

replace comorbidities=1 if medhx_immsupp_yn_raw==1 | medhx_liverdis_yn==1 |
medhx_renaldis_yn_raw==1 | medhx_cld_yn_raw==1 | medhx_htn_raw==1 |
medhx_cvd_yn_raw==1 | medhx_diabetes_yn_raw==1

label values comorbidities symptoms
tab comorbidities

*coding for us resident*
gen resident_coded=.
replace resident_coded=0 if resident_us_raw==1
replace resident_coded=1 if resident_us_raw==0

label define residentlabel 0 "No, NOT US resident" 1 "Yes, US resident"
label values resident_coded residentlabel
tab resident_coded

*coding for Is the patient a healthcare worker?*
gen healthcareworker_coded=.
replace healthcareworker_coded=0 if hc_work_yn_raw==0
replace healthcareworker_coded=1 if hc_work_yn_raw==1

label define healthcareworkerlabel 0 "No" 1 "Yes"
label values healthcareworker_coded healthcareworkerlabel
tab healthcareworker_coded

*In the past 14 days did the patient have close contact with a laboratory-confirmed
COVID-19?*
gen exp_case_coded=.
replace exp_case_coded=0 if exp_case_raw==0
replace exp_case_coded=1 if exp_case_raw==1
label define exp_case_label 0 "No" 1 "Yes"
```

```
label values exp_case_coded exp_case_label
tab exp_case_coded

*Was the close contact a household member? *
gen exp_case_hh_coded=.
replace exp_case_hh_coded=0 if exp_case_hh_raw==0
replace exp_case_hh_coded=1 if exp_case_hh_raw==1
label define exp_case_hh_label 0 "No" 1 "Yes"
label values exp_case_hh_coded exp_case_hh_label
tab exp_case_hh_coded

*Did the patient provide care for a COVID-19 patient?*
gen ptcare_coded=.
replace ptcare_coded=0 if hc_ptcare==0
replace ptcare_coded=1 if hc_ptcare==1
label define ptcare_label 0 "No" 1 "Yes"
label values ptcare_coded ptcare_label
tab ptcare_coded

*Is the patient a student or daycare attendee?*
gen student_or_daycare=.
replace student_or_daycare=0 if student_yn_raw==0
replace student_or_daycare=1 if student_yn_raw==1
label define student_yn_label 0 "No" 1 "Yes"
label values student_or_daycare student_yn_label
tab student_or_daycare

*smoking_coded*
gen smoking_coded=.
replace smoking_coded=0 if smoke_raw==0
replace smoking_coded=1 if smoke_raw==1 | smoke_raw==2
label define smokerlabel 0 "Not a smoker" 1 "Current or former smoker"
label values smoking_coded smokerlabel
tab smoking_coded

*flushot_coded to yes or no*
gen flushot_coded=.
replace flushot_coded=0 if flushot_raw==0
replace flushot_coded=1 if flushot_raw==1
label define flushotlabel 0 "No flu shot in past year" 1 "Had flu shot in past year"
label values flushot_coded flushotlabel
tab flushot_coded

*Has health insurance recoded to yes or no*
```

```
gen insured_coded=.
replace insured_coded=0 if insured_raw==0
replace insured_coded=1 if insured_raw==1
label define insurelabel 0 "No insurance" 1 "Yes, insurance"
label values insured_coded insurelabel
tab insured_coded

*Is the case isolating at home?*
gen isolating_coded=.
replace isolating_coded=0 if isolation_raw==0
replace isolating_coded=1 if isolation_raw==1
replace isolating_coded=2 if isolation_raw==2
*where 0 is No, not isolating *
*where 1 is yes, isolating *
*where 2 is yes, partial isolating*
label define isolationlabel 0 "Not isolating" 1 "Yes, isolating" 2 "Partial isolation"
label values isolating_coded isolationlabel
tab isolating_coded

*Does the patient have pets in their household? *
gen pets_coded=.
replace pets_coded=0 if pets_yn_raw==0
replace pets_coded=1 if pets_yn_raw==1
* where 0 is no and 1 is yes*
label define petslabel 0 "No" 1 "Yes"
label values pets_coded petslabel
tab pets_coded

*source of reported case*
gen reported_case_coded=.
replace reported_case_coded=0 if report_source_raw==0
replace reported_case_coded=1 if report_source_raw==1
replace reported_case_coded=2 if report_source_raw==2
replace reported_case_coded=3 if report_source_raw==3
replace reported_case_coded=8 if report_source_raw==8
*where 0 is Clinical referral*
*where 1 is contact tracing, 2 is facility screening *
*3 is occupational screening and 8 is other*
label define reportedcaselabel 0 "Clinical referral" 1 "Contact tracing" 2 "Facility
screening" 3 "Occupational screening" 8 "Other"
label values reported_case_coded reportedcaselabel
tab reported_case_coded

*In the past 14 days did the case travel outside their city of residence?*
```

```
gen travel_coded=.
replace travel_coded=0 if exp_travel_raw==0
replace travel_coded=1 if exp_travel_raw==1
label define travellabel 0 "No" 1 "Yes"
label values travel_coded travellabel
tab travel_coded

*undergrad*
gen undergrad= affiliation_tamu_student60_raw
*grad or professional*
gen grad= affiliation_tamu_student61_raw
*Fraternity/sorority*
gen greeklife= affiliation_tamu_student52_raw
*student athlete*
gen studentathlete= affiliation_tamu_student57_raw
*Corps of Cadets*
gen corpsofcadets= affiliation_tamu_student59_raw
*Member of student org*
gen memberstudentorg= affiliation_tamu_student80_raw

*zipcode*
gen zip_new=address_zip_raw

gen zipcode=.
*zipcodes in Bryan, TX*
replace zipcode=77801 if address_zip_raw=="77801"
replace zipcode=77802 if address_zip_raw=="77802"
replace zipcode=77803 if address_zip_raw=="77803"
replace zipcode=77805 if address_zip_raw=="77805"
replace zipcode=77806 if address_zip_raw=="77806"
replace zipcode=77807 if address_zip_raw=="77807"
replace zipcode=77808 if address_zip_raw=="77808"
*zipcodes in College Station, TX*
replace zipcode=77802 if address_zip_raw=="77802"
replace zipcode=77840 if address_zip_raw=="77840"
replace zipcode=77841 if address_zip_raw=="77841"
replace zipcode=77842 if address_zip_raw=="77842"
replace zipcode=77843 if address_zip_raw=="77843"
replace zipcode=77844 if address_zip_raw=="77844"
replace zipcode=77845 if address_zip_raw=="77845"
tab zipcode

gen BCS=.
*College Station = 0*
```

```
replace BCS=0 if zipcode==77802 | zipcode==77840 | zipcode==77841 |
zipcode==77842 | zipcode==77843 | zipcode==77844 | zipcode==77845
*Bryan = 1*
replace BCS=1 if zipcode==77801 | zipcode==77802 | zipcode==77803 |
zipcode==77805 | zipcode==77806 | zipcode==77807 | zipcode==77808
label define BCSlabel 0 "College Station" 1 "Bryan"
label values BCS BCSlabel
tab BCS


*In past 7 days before symptom onset or before positive test, did the patient go to the
grocery store?*
label define socialbehaviorlabel 0 "Unchecked" 1 "Checked"
gen grocery_coded=.
replace grocery_coded=0 if social_venue0_raw==0
replace grocery_coded=1 if social_venue0_raw==1
*where 0 is unchecked, 1 is checked
label values grocery_coded socialbehaviorlabel
tab grocery_coded

gen restaurant_coded=.
replace restaurant_coded=0 if social_venue1_raw==0
replace restaurant_coded=1 if social_venue1_raw==1
label values restaurant_coded socialbehaviorlabel
tab restaurant_coded

gen bar_coded=.
replace bar_coded=0 if social_venue2_raw==0
replace bar_coded=1 if social_venue2_raw==1
label values bar_coded socialbehaviorlabel
tab bar_coded

gen gym_fitness_coded=.
replace gym_fitness_coded=0 if social_venue3_raw==0
replace gym_fitness_coded=1 if social_venue3_raw==1
label values gym_fitness_coded socialbehaviorlabel
tab gym_fitness_coded

gen wedding_coded=.
replace wedding_coded=0 if social_venue5_raw==0
replace wedding_coded=1 if social_venue5_raw==1
label values wedding_coded socialbehaviorlabel
tab wedding_coded
```

```
gen salon_barber_coded=.
replace salon_barber_coded=0 if social_venue6_raw==0
replace salon_barber_coded=1 if social_venue6_raw==1
label values salon_barber_coded socialbehaviorlabel
tab salon_barber_coded

gen class_school_coded=.
replace class_school_coded=0 if social_venue7_raw==0
replace class_school_coded=1 if social_venue7_raw==1
label values class_school_coded socialbehaviorlabel
tab class_school_coded

gen work_inperson_coded=.
replace work_inperson_coded=0 if social_venue29_raw==0
replace work_inperson_coded=1 if social_venue29_raw==1
label values work_inperson_coded socialbehaviorlabel
tab work_inperson_coded

gen library_coded=.
replace library_coded=0 if social_venue8_raw==0
replace library_coded=1 if social_venue8_raw==1
label values library_coded socialbehaviorlabel
tab library_coded

gen doctorsoffice_coded=.
replace doctorsoffice_coded=0 if social_venue23_raw==0
replace doctorsoffice_coded=1 if social_venue23_raw==1
label values doctorsoffice_coded socialbehaviorlabel
tab doctorsoffice_coded

gen themepark_coded=.
replace themepark_coded=0 if social_venue24_raw==0
replace themepark_coded=1 if social_venue24_raw==1
label values themepark_coded socialbehaviorlabel
tab themepark_coded

gen tamu_msc_coded=.
replace tamu_msc_coded=0 if social_venue9_raw==0
replace tamu_msc_coded=1 if social_venue9_raw==1
label values tamu_msc_coded socialbehaviorlabel
tab tamu_msc_coded

gen tamu_studentorientation_coded=.
replace tamu_studentorientation_coded=0 if social_venue30_raw==0
```

```
replace tamu_studentorientation_coded=1 if social_venue30_raw==1
label values tamu_studentorientation_coded socialbehaviorlabel
tab tamu_studentorientation_coded

gen indoor_lessthan5=.
replace indoor_lessthan5=0 if social_venue14_raw==0
replace indoor_lessthan5=1 if social_venue14_raw==1
label values indoor_lessthan5 socialbehaviorlabel
tab indoor_lessthan5

gen indoor_5to10=.
replace indoor_5to10=0 if social_venue15_raw==0
replace indoor_5to10=1 if social_venue15_raw==1
label values indoor_5to10 socialbehaviorlabel
tab indoor_5to10

gen indoor_10to20=.
replace indoor_10to20=0 if social_venue16_raw==0
replace indoor_10to20=1 if social_venue16_raw==1
label values indoor_10to20 socialbehaviorlabel
tab indoor_10to20

gen indoor_20to50=.
replace indoor_20to50=0 if social_venue17_raw==0
replace indoor_20to50=1 if social_venue17_raw==1
label values indoor_20to50 socialbehaviorlabel
tab indoor_20to50

gen indoor_over50=.
replace indoor_over50=0 if social_venue11_raw==0
replace indoor_over50=1 if social_venue11_raw==1
label values indoor_over50 socialbehaviorlabel
tab indoor_over50

gen outdoor_lessthan5=.
replace outdoor_lessthan5=0 if social_venue18_raw==0
replace outdoor_lessthan5=1 if social_venue18_raw==1
label values outdoor_lessthan5 socialbehaviorlabel
tab outdoor_lessthan5

gen outdoor_5to10=.
replace outdoor_5to10=0 if social_venue19_raw==0
replace outdoor_5to10=1 if social_venue19_raw==1
label values outdoor_5to10 socialbehaviorlabel
```

```
tab outdoor_5to10

gen outdoor_10to20=.
replace outdoor_10to20=0 if social_venue20_raw==0
replace outdoor_10to20=1 if social_venue20_raw==1
label values outdoor_10to20 socialbehaviorlabel
tab outdoor_10to20

gen outdoor_20to50=.
replace outdoor_20to50=0 if social_venue21_raw==0
replace outdoor_20to50=1 if social_venue21_raw==1
label values outdoor_20to50 socialbehaviorlabel
tab outdoor_20to50

gen outdoor_over50=.
replace outdoor_over50=0 if social_venue13_raw==0
replace outdoor_over50=1 if social_venue13_raw==1
label values outdoor_over50 socialbehaviorlabel
tab outdoor_over50

gen anyindoor_lessthan50=.
replace anyindoor_lessthan50=0 if social_venue10_raw==0
replace anyindoor_lessthan50=1 if social_venue10_raw==1
label values anyindoor_lessthan50 socialbehaviorlabel
tab anyindoor_lessthan50

gen anyoutdoor_lessthan50=.
replace anyoutdoor_lessthan50=0 if social_venue12_raw==0
replace anyoutdoor_lessthan50=1 if social_venue12_raw==1
label values anyoutdoor_lessthan50 socialbehaviorlabel
tab anyoutdoor_lessthan50

gen nosocial=.
replace nosocial=0 if social_venue99_raw==0
replace nosocial=1 if social_venue99_raw==1
label values nosocial socialbehaviorlabel
tab nosocial

gen ren_fest=.
replace ren_fest=0 if social_venue22_raw==0
replace ren_fest=1 if social_venue22_raw==1
label values ren_fest socialbehaviorlabel
tab ren_fest
```

```
gen midnightyell=.
replace midnightyell=0 if social_venue25_raw==0
replace midnightyell=1 if social_venue25_raw==1
label values midnightyell socialbehaviorlabel
tab midnightyell

gen breakaway=.
replace breakaway=0 if social_venue26_raw==0
replace breakaway=1 if social_venue26_raw==1
label values breakaway socialbehaviorlabel
tab breakaway

gen santa_wonderland=.
replace santa_wonderland=0 if social_venue27_raw==0
replace santa_wonderland=1 if social_venue27_raw==1
label values santa_wonderland socialbehaviorlabel
tab santa_wonderland

gen tamu_graduation=.
replace tamu_graduation=0 if social_venue28_raw==0
replace tamu_graduation=1 if social_venue28_raw==1
label values tamu_graduation socialbehaviorlabel
tab tamu_graduation

gen facemask_coded=.
replace facemask_coded=0 if act_facemask_raw==1
replace facemask_coded=1 if act_facemask_raw==2
replace facemask_coded=2 if act_facemask_raw==0
label define facemasklabel3 0 "Always" 1 "Sometimes" 2 "Never"
label values facemask_coded facemasklabel3
tab facemask_coded

gen pneumonia_coded=.
replace pneumonia_coded=0 if dx_pneumonia_raw==0
replace pneumonia_coded=1 if dx_pneumonia_raw==1
label values pneumonia_coded symptoms
tab pneumonia_coded

gen abnormal_ekg=.
replace abnormal_ekg=0 if dx_ekg_raw==0
replace abnormal_ekg=1 if dx_ekg_raw==1
label values abnormal_ekg symptoms
tab abnormal_ekg
```

```
gen ards=.
replace ards=0 if dx_ardx_raw==0
replace ards=1 if dx_ardx_raw==1
label values ards symptoms
tab ards

gen xray_coded=.
replace xray_coded=0 if dx_xray_raw==0
replace xray_coded=1 if dx_xray_raw==1
label values xray_coded symptoms
tab xray_coded

*Was the patient hospitalized?
gen hosp_coded=.
replace hosp_coded=0 if hosp_yn_raw==0
replace hosp_coded=1 if hosp_yn_raw==1
label values hosp_coded symptoms
tab hosp_coded

*Was the patient admitted to an ICU?*
gen icu_coded=.
replace icu_coded=0 if icu_yn_raw==0
replace icu_coded=1 if icu_yn_raw==1
label values icu_coded symptoms
tab icu_coded

*Was the patient treated in a hospital ER?*
gen er_coded=.
replace er_coded=0 if er_yn_raw==0
replace er_coded=1 if er_yn_raw==1
label values er_coded symptoms
tab er_coded

gen ecmo_coded=.
replace ecmo_coded=0 if ecmo_yn_raw==0
replace ecmo_coded=1 if ecmo_yn_raw==1
label values ecmo_coded symptoms
tab ecmo_coded

gen intubation_coded=.
replace intubation_coded=0 if mechvent_yn_raw==0
replace intubation_coded=1 if mechvent_yn_raw==1
label values intubation_coded symptoms
tab intubation_coded
```

```
*Did the patient die as a result of this illness? *
gen death_coded=.
replace death_coded=0 if death_yn_raw==0
replace death_coded=1 if death_yn_raw==1
label values death_coded symptoms
tab death_coded

*Positive PCR results*
gen pos_cases=.
replace pos_cases=0 if spec_npswab1_result_raw==1 | spec_npswab2result_raw==1
label define pos_caselabel 0 "Positive case"
label values pos_cases pos_caselabel
tab pos_cases

*hospitalization*
gen hospitalization=.
replace hospitalization=1 if  hosp_yn_raw==1
label define hospitallabel 1 "Hospitalized"
label values hospitalization hospitallabel
tab hospitalization

gen test_date_timeseries=test_date2
format test_date_timeseries %tdCCYY.NN.DD

egen test_timeseries=group (test_date_timeseries)
tsset test_timeseries

*TAMU affiliated*
gen tamu_affiliated=.
*affiliation 0 is no*
replace tamu_affiliated=0 if affiliation_tamu_student60_raw==0 |
affiliation_tamu_student61_raw==0 | affiliation_tamu_student52_raw==0 |
affiliation_tamu_student56_raw==0 | affiliation_tamu_student57_raw==0 |
affiliation_tamu_student58_raw==0 | affiliation_tamu_student59_raw==0 |
affiliation_tamu_student80_raw==0 | affiliation_tamu4_raw==0 | affiliation_tamu0_raw
==0 | affiliation_tamu1_raw==0 | affiliation_tamu10_raw==0 |
affiliation_tamu2_raw==0 | affiliation_tamu3_raw==0 | affiliation_tamu5_raw==0 |
affiliation_tamu6_raw==0 | affiliation_tamu7_raw==0 | affiliation_tamu11_raw==0|
affiliation_tamu8_raw==0 | affiliation_tamu9_raw==0| affiliation_tamu12_raw==0 |
affiliation_tamu31_raw==0 | affiliation_tamu32_raw==0 | affiliation_tamu33_raw==0 |
affiliation_tamu50_raw==0 | affiliation_tamu51_raw==0 | affiliation_tamu54_raw==0 |
affiliation_tamu55_raw==0 | affiliation_tamu60_raw==0 | affiliation_tamu98_raw==0 |
```

```
affiliation_tamu_hclab54_raw==0 | affiliation_tamu_hclab56_raw==0 |
affiliation_tamu_hclab55_raw==0 | affiliation_tamu_hclab98_raw==0

*Affiliation 1 is yes*
replace tamu_affiliated=1 if affiliation_tamu_student60_raw==1 |
affiliation_tamu_student61_raw==1 | affiliation_tamu_student52_raw==1 |
affiliation_tamu_student56_raw==1 | affiliation_tamu_student57_raw==1 |
affiliation_tamu_student58_raw==1 | affiliation_tamu_student59_raw==1 |
affiliation_tamu_student80_raw==1 | affiliation_tamu4_raw==1 | affiliation_tamu0_raw
==1 | affiliation_tamu1_raw==1 | affiliation_tamu10_raw==1 |
affiliation_tamu2_raw==1 | affiliation_tamu3_raw==1 | affiliation_tamu4_raw==1 |
affiliation_tamu5_raw==1 | affiliation_tamu6_raw==1 | affiliation_tamu7_raw==1 |
affiliation_tamu11_raw==1| affiliation_tamu8_raw==1 | affiliation_tamu9_raw==1 |
affiliation_tamu12_raw==1 | affiliation_tamu31_raw==1 | affiliation_tamu32_raw==1 |
affiliation_tamu33_raw==1 | affiliation_tamu50_raw==1 | affiliation_tamu51_raw==1 |
affiliation_tamu54_raw==1 | affiliation_tamu55_raw==1 | affiliation_tamu60_raw==1 |
affiliation_tamu98_raw==1 | affiliation_tamu_hclab54_raw==1 |
affiliation_tamu_hclab56_raw==1 | affiliation_tamu_hclab98_raw==1 |
reporter_tamu_raw==0
label define affiliationlabel 0 "Not affiliated with TAMU" 1 "Affiliated with TAMU"
label values tamu_affiliated affiliationlabel
tab tamu_affiliated

*DSHS ready to report to the state*
*Also using as a marker to decide which individuals are Brazos valley only
gen dshs_ready=.
replace dshs_ready=0 if dshsreport_ready_raw==0 | dshsreport_ready_raw==.
replace dshs_ready=1 if dshsreport_ready_raw==1
label define DSHSlabel 0 "Not ready to submit to DSHS" 1 "DSHS ready"
label values dshs_ready DSHSlabel
tab dshs_ready

*Coding for flu-like illness syndrome*
*Per CDC, influenza like illness (ILI) is defined as fever 100 or greater, a cough, and or
sore throat*
*https://www.cdc.gov/vaccines/pubs/surv-manual/chpt06-
influenza.html#:~:text=For%20this%20system%2C%20ILI%20is,known%20cause%20
other%20than%20influenza.*

gen fever_over100=.
replace fever_over100=0 if cc_sx_fevertemp_raw<100
replace fever_over100=1 if cc_sx_fevertemp_raw>=100
label define feverlabel 0 "Fever less than 100" 1 "Fever 100 or greater"
label values fever_over100 feverlabel
```

```
tab fever_over100

*Coding for influenza like illness*
gen ili_coded=.
replace ili_coded=0 if fever_over100==0 & cough_coded==0 | pharyngitis_coded==0
replace ili_coded=1 if fever_over100==1 & cough_coded==1 | pharyngitis_coded==1
label define ili_label 0 "Does not meet ILI syndrome" 1 "Meets ILI syndrome"
label values ili_coded ili_label
tab ili_coded

*gastroenteritis - characterized by diarrea and or vomiting*
*https://www.cdc.gov/disasters/disease/infectevac.html*
gen gastroenteritis_coded=.
replace gastroenteritis_coded=0 if diarrhea_coded==0 | vomit_coded==0
replace gastroenteritis_coded=1 if diarrhea_coded==1 | vomit_coded==1
label define gastroenteritislabel 0 "No gastroenteritis" 1 "gastroenteritis"
label values gastroenteritis_coded gastroenteritislabel
tab gastroenteritis_coded


*Coding for allergy syndrome*
*create duplicate of other symptoms*
gen other_symptoms=sx_other_raw
compare other_symptoms sx_other_raw
describe other_symptoms

gen allergy_symptoms= "allergy" if other_symptoms=="ALLERGY, LEGPAIN" |
other_symptoms=="Allergic rhinitis, COVID19, Influenza, Sinusitis, URI" |
other_symptoms=="Allergies" | other_symptoms=="Allergies with nasal congestion" |
other_symptoms=="Allergy Symptoms" | other_symptoms=="Allergy like symptoms" |
other_symptoms=="Allergy like symptoms; sneezing" | other_symptoms=="Congestion,
allergies"| other_symptoms=="Ear Infection, Allergies" | other_symptoms=="Had flu
shot 2 weeks ago, regular seasonal allergies, I do not know weather to list wet cough as a
cough since I was informed that it covid coughs are dry." | other_symptoms=="None (I
have had a minor cough since the 6th but it seemed consistent with allergies. Serious
symptoms didnt start showing up until recently which is why i got tested)" |
other_symptoms=="SINUS PRESSURE, ALLERGIES, EAR PAIN" |
other_symptoms=="Seasonal Allergies" | other_symptoms=="allergies" |
other_symptoms=="allergy" | other_symptoms=="sneezing, allergy symptoms"
tab allergy_symptoms

gen allergy_num ="1" if allergy_symptoms=="allergy"
tab allergy_num
```

```
gen allergy_num_new2=.
replace allergy_num_new2=1 if allergy_num_new==1
replace allergy_num_new2=0 if allergy_num_new==.
label define allergylabel 0 "Did not specify allergies or unknown" 1 "Allergies"
label values allergy_num_new2 allergylabel
rename allergy_num_new2 allergy_coded
tab allergy_coded

label define allergylabel2 0 "Did not specify allergies or unknown" 1 "Reported
allergies"
label values allergy_coded allergylabel2
tab allergy_coded

*Severe illness for COVID-19*
*https://www.cdc.gov/coronavirus/2019-ncov/need-extra-precautions/people-with-
medical-conditions.html*
gen severe_coded=.
replace severe_coded=1 if hosp_coded==1 | icu_coded==1 | intubation_coded==1 |
death_coded==1
replace severe_coded=0 if hosp_coded==0 | icu_coded==0 | intubation_coded==0 |
death_coded==0
label define severelabel 0 "Not severe COVID-19" 1 "Severe COVID-19"
label values severe_coded severelabel
tab severe_coded

*Re-coding age*

*age_calc_f rounds down*
*age categories based off CDC COVID-19 reporting*
gen age_recode=.
*age 0 - 11*
replace age_recode=0 if (age_calc_f2 >= 0) & (age_calc_f2 <= 11)
*age 12 - 17*
replace age_recode=1 if (age_calc_f2 >= 12) & (age_calc_f2<= 17)
*age 18 - 29*
replace age_recode=2 if (age_calc_f2 >= 18) & (age_calc_f2 <= 29)
*age 30 - 39*
replace age_recode=3 if (age_calc_f2 >= 30) & (age_calc_f2 <= 39)
*age 40 - 49*
replace age_recode=4 if (age_calc_f2 >= 40) & (age_calc_f2 <= 49)
*age 50 - 64*
replace age_recode=5 if (age_calc_f2 >= 50) & (age_calc_f2 <= 64)
*age 65 +*
replace age_recode=6 if (age_calc_f2 >= 65) & (age_calc_f2 <= 110)
```

```
tab age_recode

label define agerecodelabel 0 "Ages 0 - 11" 1 "Ages 12 - 17" 2 "Ages 18 - 29" 3 "Ages
30 - 39" 4 "Ages 40 - 49" 5 "Ages 50 - 64" 6 "Ages 65 +"
label values age_recode agerecodelabel

gen reported_exposure=.
replace reported_exposure=0 if casecontact_exposure_1_raw==1 |
casecontact_exposure_2_raw==1 | casecontact_exposure_3_raw==1 |
casecontact_exposure_4_raw==1 | casecontact_exposure_5_raw==1

replace reported_exposure=1 if casecontact_exposure_1_raw==9 |
casecontact_exposure_2_raw==9 | casecontact_exposure_4_raw==9

replace reported_exposure=2 if casecontact_exposure_1_raw==5 |
casecontact_exposure_1_raw==4 | casecontact_exposure_2_raw==5 |
casecontact_exposure_2_raw==4

replace reported_exposure=3 if casecontact_exposure_1_raw==3 |
casecontact_exposure_2_raw==3 | casecontact_exposure_3_raw==3 |
casecontact_exposure_4_raw==3 | casecontact_exposure_5_raw==3

replace reported_exposure=4 if casecontact_exposure_1_raw==6 |
casecontact_exposure_1_raw==7 | casecontact_exposure_3_raw==7 |
casecontact_exposure_4_raw==7

replace reported_exposure=5 if casecontact_exposure_1_raw==2 |
casecontact_exposure_1_raw==8 | casecontact_exposure_1_raw==10 |
casecontact_exposure_2_raw==10 | casecontact_exposure_4_raw==10 |
casecontact_exposure_5_raw==10


label define reportedexposurelabel2 0 "Household" 1 "Community" 2 "School or
Daycare" 3 "Work" 4 "Transit or Rideshare" 5 "Other"
label values reported_exposure reportedexposurelabel2
tab reported_exposure, missing

*Coding for contacts*
gen num_contacts="unknown" if contacts_number_raw=="unknown"
replace num_contacts="unknown" if
contacts_number_raw=="unkown"|contacts_number_raw=="unknwon" |
contacts_number_raw=="unknown - works as a nurse"
replace num_contacts="unknown" if contacts_number_raw=="unknown  "
```

```
replace num_contacts="unknown" if contacts_number_raw=="unknonw"|
contacts_number_raw=="unknoiwn"| contacts_number_raw=="unkn"
replace num_contacts="unknown" if contacts_number_raw=="unk "|
contacts_number_raw=="un k"| contacts_number_raw=="un" |
contacts_number_raw=="uknown"
replace num_contacts="unknown" if contacts_number_raw=="unk"
replace contacts_number_raw="unknown" if contacts_number_raw=="o" |
contacts_number_raw=="n/a" | contacts_number_raw== "contacts" |
contacts_number_raw=="Case is not sure" | contacts_number_raw==" - "
|contacts_number_raw=="unknown"
replace num_contacts="unknown" if contacts_number_raw== "06-May"|
contacts_number_raw=="07-May" | contacts_number_raw=="10-Jun" |
contacts_number_raw=="Declined" | contacts_number_raw=="UNK"|
contacts_number_raw=="UNKNOWN"
replace num_contacts="unknown" if contacts_number_raw=="UNKNOWN  " |
contacts_number_raw=="Uknown "| contacts_number_raw=="Uknown"
replace num_contacts="unknown" if contacts_number_raw=="Unk" |
contacts_number_raw=="Unknown "
replace num_contacts="unknown" if contacts_number_raw=="Unknown" |
contacts_number_raw=="Unknown  "
replace num_contacts="unknown" if contacts_number_raw=="Unknwon " |
contacts_number_raw=="Unkown" | contacts_number_raw=="Unkown" |
contacts_number_raw=="Unknwon"
replace num_contacts="unknown" if contacts_number_raw==" "
replace num_contacts="unknown" if contacts_number_raw==""
replace num_contacts="unknown" if contacts_number_raw=="'more than she can
count'"
replace num_contacts="0" if contacts_number_raw=="none" |
contacts_number_raw=="0" | contacts_number_raw=="0 "
|contacts_number_raw=="NONE REPORTED"
replace num_contacts="unknown" if contacts_number_raw=="None reported"
|contacts_number_raw=="none"

replace num_contacts="1" if contacts_number_raw=="1"
replace num_contacts="2" if contacts_number_raw=="2" | contacts_number_raw=="2+"
| contacts_number_raw==">1" | contacts_number_raw=="a few"
replace num_contacts="3" if contacts_number_raw=="3" | contacts_number_raw=="at
least 3"| contacts_number_raw=="2 or 3" | contacts_number_raw=="1-3"

replace num_contacts="4" if contacts_number_raw=="4" |
contacts_number_raw=="maybe 4" | contacts_number_raw=="<5" |
contacts_number_raw=="3-4" | contacts_number_raw=="at least 4" |
contacts_number_raw=="3+" | contacts_number_raw=="3 to 4"
```

```
replace num_contacts="5" if contacts_number_raw=="5" |
contacts_number_raw=="about 5"| contacts_number_raw=="3-5" |
contacts_number_raw=="3 to 5"| contacts_number_raw=="4-5" |
contacts_number_raw=="approx 5"| contacts_number_raw=="4+"|
contacts_number_raw=="4 to 5"| contacts_number_raw=="4 or 5" |
contacts_number_raw=="4 to 6"

replace num_contacts="6" if contacts_number_raw=="6" |
contacts_number_raw=="about 6"| contacts_number_raw=="5-6" |
contacts_number_raw=="approx. 6" | contacts_number_raw==">5"|
contacts_number_raw=="> 5"

replace num_contacts="7" if contacts_number_raw=="7"| contacts_number_raw=="6 or
7"| contacts_number_raw=="6-7" | contacts_number_raw=="6 to 7" |
contacts_number_raw=="6-7" | contacts_number_raw=="5-7" |
contacts_number_raw=="2-11"


replace num_contacts="11" if contacts_number_raw=="11" |
contacts_number_raw=="10 to 12"| contacts_number_raw=="10 - 12"

replace num_contacts="8" if contacts_number_raw=="8"|
contacts_number_raw=="about 8" | contacts_number_raw=="7 - 8" |
contacts_number_raw=="5-10" | contacts_number_raw=="5 - 10"


replace num_contacts="9" if contacts_number_raw=="9" |
contacts_number_raw=="<10" | contacts_number_raw=="9 (6-7 family members)"|
contacts_number_raw=="8-9" | contacts_number_raw=="8 - 9"|
contacts_number_raw=="8 to 10"| contacts_number_raw=="7-10"

replace num_contacts="10" if contacts_number_raw=="10" |
contacts_number_raw==">10" | contacts_number_raw=="10 at most"|
contacts_number_raw=="approx. 10" | contacts_number_raw=="about 10" |
contacts_number_raw=="10+" | contacts_number_raw=="approx 10" |
contacts_number_raw=="approx 10?"

replace num_contacts="20" if contacts_number_raw=="20" |
contacts_number_raw=="10 to 20"
replace num_contacts="14" if contacts_number_raw=="14" |
contacts_number_raw=="about 14"| contacts_number_raw=="<15"|
contacts_number_raw=="10 to 18"
replace num_contacts="12" if contacts_number_raw=="12"
```

```
replace num_contacts="15" if contacts_number_raw=="15" |
contacts_number_raw=="15+"| contacts_number_raw=="approx. 15"|
contacts_number_raw=="between 10 to 20"

replace num_contacts="20" if contacts_number_raw==">20" |
contacts_number_raw==">20" | contacts_number_raw=="about 20" |
contacts_number_raw=="15 to 20" | contacts_number_raw=="15-20" |
contacts_number_raw=="approx. 20"

replace num_contacts="13" if contacts_number_raw=="13" |
contacts_number_raw=="12-15"| contacts_number_raw=="10-15"
|contacts_number_raw=="10 to 15"| contacts_number_raw=="10 - 15"

replace num_contacts="16" if contacts_number_raw=="16" |
contacts_number_raw=="12-20"
replace num_contacts="17" if contacts_number_raw=="17"|
contacts_number_raw=="15 - 20"
replace num_contacts="18" if contacts_number_raw=="18"
replace num_contacts="21" if contacts_number_raw=="21"
|contacts_number_raw=="over 20"
replace num_contacts="22" if contacts_number_raw=="22"
replace num_contacts="100" if contacts_number_raw=="100" |
contacts_number_raw==">100"
replace num_contacts="30" if contacts_number_raw=="30" |
contacts_number_raw=="30+"
replace num_contacts="28" if contacts_number_raw=="28"
replace num_contacts="24" if contacts_number_raw=="24"
replace num_contacts="25" if contacts_number_raw=="25"|
contacts_number_raw=="20 to 30"
replace num_contacts="50" if contacts_number_raw=="50" |
contacts_number_raw=="at least 50" | contacts_number_raw==">50?"|
contacts_number_raw=="50 +"
replace num_contacts="52" if contacts_number_raw=="52"
replace num_contacts="29" if contacts_number_raw=="29"
replace num_contacts="62" if contacts_number_raw=="62"
replace num_contacts="42" if contacts_number_raw=="42"
replace num_contacts="41" if contacts_number_raw=="41"
replace num_contacts="300" if contacts_number_raw=="300"
replace num_contacts="100" if contacts_number_raw=="> 100"
replace num_contacts="40" if contacts_number_raw=="40+"
replace num_contacts="61" if contacts_number_raw=="61"
replace num_contacts="175" if contacts_number_raw=="175"
replace num_contacts="55" if contacts_number_raw=="50 to 60"
```

```
replace num_contacts="88" if contacts_number_raw=="between 75 to 100 - through work"
replace num_contacts="65" if contacts_number_raw=="approx 60 to 70"
replace num_contacts="23" if contacts_number_raw=="20 to 25"| contacts_number_raw== "20-25"
replace num_contacts="27" if contacts_number_raw=="25 to 30"

gen num_contacts_num=num_contacts
destring num_contacts_num, generate(number_contacts) force


gen number_contacts_categorized=.
replace number_contacts_categorized=0 if number_contacts==0
replace number_contacts_categorized=1 if (number_contacts >=1) & (number_contacts<=4)
replace number_contacts_categorized=2 if (number_contacts>=5) & (number_contacts<=10)
replace number_contacts_categorized=3 if (number_contacts>=11) & (number_contacts<=20)
replace number_contacts_categorized=4 if (number_contacts>=21) & (number_contacts<=49)
replace number_contacts_categorized=5 if (number_contacts>=50) & (number_contacts<=176)
label define contactslabel 0 "0" 1 "1 - 4" 2 "5 - 10" 3 "11 - 20" 4 "21 - 49" 5 "over 50"
label values number_contacts_categorized contactslabel
tab number_contacts_categorized, missing

gen contacts_recode=.
replace contacts_recode=0 if number_contacts==0
replace contacts_recode=1 if (number_contacts >=1) & (number_contacts<=2)
replace contacts_recode=2 if (number_contacts >=3) & (number_contacts<=4)
replace contacts_recode=3 if (number_contacts>=5) & (number_contacts<=10)
replace contacts_recode=4 if (number_contacts>=11) & (number_contacts<=20)
replace contacts_recode=5 if (number_contacts>=21) & (number_contacts<=49)
replace contacts_recode=6 if (number_contacts>=50) & (number_contacts<=180)
label define contactsrecodelabel 0 "0" 1 "1 - 2" 2 "3 - 4" 3 "5 - 10" 4 "11 - 20" 5 " 21 - 49" 6 "over 50 contacts"
label values contacts_recode contactsrecodelabel
tab contacts_recode, missing

*Coding for household*
gen household_contacts="unknown" if contacts_number_hh_raw=="unknown"
```

```
replace household_contacts="unknown" if contacts_number_hh_raw=="" |
contacts_number_hh_raw==" " | contacts_number_hh_raw=="unknwon" |
contacts_number_hh_raw=="she is staying upstairs away from her.."

replace household_contacts="unknown" if contacts_number_hh_raw=="u/k" |
contacts_number_hh_raw=="unk" | contacts_number_hh_raw=="unkn" |
contacts_number_hh_raw=="unknoiwn"| contacts_number_hh_raw=="unknow" |
contacts_number_hh_raw=="-" | contacts_number_hh_raw=="NONE REPORTED"|
contacts_number_hh_raw=="UNK"

replace household_contacts="unknown" if contacts_number_hh_raw=="UNKNOWN" |
contacts_number_hh_raw=="Unk" |contacts_number_hh_raw=="Unknown" |
contacts_number_hh_raw=="o" | contacts_number_hh_raw=="she is staying upstairs
away from her parents" | contacts_number_hh_raw=="Unknown " |
contacts_number_hh_raw=="Unkown" | contacts_number_hh_raw=="41"

replace household_contacts="0" if contacts_number_hh_raw=="0" |
contacts_number_hh_raw=="N/A" | contacts_number_hh_raw=="none" |
contacts_number_hh_raw=="na"

replace household_contacts="1" if contacts_number_hh_raw=="1" |
contacts_number_hh_raw=="1 - K. Patterson - sibling"| contacts_number_hh_raw=="At
least 1" | contacts_number_hh_raw=="at least 1"

replace household_contacts="2" if contacts_number_hh_raw=="2" |
contacts_number_hh_raw=="2 children" | contacts_number_hh_raw=="2+" |
contacts_number_hh_raw==">1"

replace household_contacts="3" if contacts_number_hh_raw=="3" |
contacts_number_hh_raw=="2-3" | contacts_number_hh_raw=="3w"

replace household_contacts="4" if contacts_number_hh_raw=="4" |
contacts_number_hh_raw=="3-4"

replace household_contacts="5" if contacts_number_hh_raw=="5"
replace household_contacts="6" if contacts_number_hh_raw=="6"
replace household_contacts="7" if contacts_number_hh_raw=="7"
replace household_contacts="8" if contacts_number_hh_raw=="8"
replace household_contacts="9" if contacts_number_hh_raw=="9"
replace household_contacts="10" if contacts_number_hh_raw=="10"
replace household_contacts="11" if contacts_number_hh_raw=="11"
replace household_contacts="12" if contacts_number_hh_raw=="12"
replace household_contacts="15" if contacts_number_hh_raw=="15"
replace household_contacts="18" if contacts_number_hh_raw=="18  freshmen"
```

```
gen household_contacts_num=household_contacts
destring household_contacts_num, generate(number_household) force

gen householdcontacts_categorized=.
replace householdcontacts_categorized=0 if number_household==0
replace householdcontacts_categorized=1 if (number_household>=2) &
(number_household<=3)
replace householdcontacts_categorized=2 if (number_household>=4) &
(number_household<=6)
replace householdcontacts_categorized=3 if (number_household>=7) &
(number_household<=19)

label define householdlabel2 0 "0" 1 "1 - 3" 2 "4 - 6" 3 "7 - 18"
label values householdcontacts_categorized householdlabel2
tab householdcontacts_categorized, missing


**estimating serial interval*
gen serialinterval=sx_date_raw - cc_sx_date_raw
gen serialinterval2=serialinterval
replace serialinterval2=. if (serialinterval>=49) & (serialinterval<=380)
replace serialinterval2=. if serialinterval<0
```

A.3 Complete distribution of variables in case database

Table 1: Frequency of age, language, and sex in case database.

Variable	Frequency	Percent
Age		
Ages 0 - 11	1,720	5.7
Ages 12 - 17	1,702	5.7
Ages 18 - 29	14,433	47.9
Ages 30 - 39	3,799	12.6
Ages 40 - 49	3,050	10.1
Ages 50 - 64	3,438	11.4
Ages 65 +	1,922	6.4
.	62	0.2
Total	30,126	100.0
Age by decade		
Ages 40 - 49	3,050	10.1
Ages 0 - 9	1,320	4.4
Ages 10 - 19	5,772	19.2
Ages 20 - 29	10,763	35.7
Ages 30 - 39	3,799	12.6
Ages 50 - 59	2,506	8.3
Ages 60 - 69	1,580	5.2
Ages 70 - 70	812	2.7
Ages 80 - 89	345	1.2
Ages 90 - 99	115	0.4
.	64	0.2
Total	30,126	100.0
Language		
English	20,987	69.7
Spanish	871	2.9
Other	25	0.1
.	8,243	27.4
Sex		
Female	15,758	52.3
Male	14,252	47.3
.	116	0.4

Table 2: Frequency of race, ethnicity, and race/ethnicity in case database.

Variable		Frequency	Percent
Race			
	White	19,924	66.1
	Black	2,431	8.1
	Asian	806	2.7
	Other	130	0.4
	.	6,835	22.7
Hispanic			
	No, NOT Hispanic or Latino	15,500	51.5
	Yes, Hispanic or Latino	9,266	30.8
	.	5,360	17.8
Race/ethnicity			
	White, non-Hispanic	12,268	40.7
	Hispanic	9,135	30.3
	Black	2,431	8.1
	Asian	806	2.7
	Other race	67	0.2
	Missing race	4,030	13.4
	.	1,389	4.6

Table 3: Frequency of employment status and residence type in case database

Variable		Frequency	Percent
Employed			
	No	8,658	28.7
	Yes	10,124	33.6
	.	11,344	37.7
Residence type			
	House	20,065	66.6
	Apartment	4,017	13.3
	Dormitory	1,192	4.0
	Supported living	111	0.4
	Other	329	1.1
	.	4,412	14.7

Table 4: Frequency of symptoms in case database

Variable	Frequency	Percent
Fever		
No	11,449	38.0
Yes	9,020	29.9
.	9,657	32.1
Cough		
No	8,503	28.2
Yes	12,787	42.5
.	8,836	29.3
Pharyngitis		
No	11,228	37.3
Yes	9,160	30.4
.	9,738	32.3
Shortness of breath		
No	15,189	50.4
Yes	4,192	13.9
.	10,745	35.7
Chills		
No	12,909	42.9
Yes	7,002	23.24
.	10,215	33.9
Headache		
No	8,923	29.6
Yes	11,961	39.7
.	9,242	30.7
Aches		
No	10,587	35.1
Yes	9,914	32.9
.	9,625	32.0
Vomit		
No	16,475	54.7
Yes	2,706	9.0
.	10,945	36.3
Abdominal pain		
No	17,209	57.1

Yes	1,768	5.9
.	11,149	37.0
Diarrhea		
No	15,544	51.6
Yes	3,745	12.4
.	10,837	36.0
Rhinitis		
No	12,231	40.6
Yes	7,829	26.0
.	10,066	33.4
Congestion		
No	12,025	39.9
Yes	8,203	27.2
.	9,898	32.9
Conjunctivitis		
No	18,052	59.9
Yes	321	1.1
.	11,753	39.0
Loss of taste or smell		
No	12,112	40.2
Yes	7,771	25.8
.	10,243	34.0
Fatigue		
No	10,103	33.5
Yes	10,348	34.4
.	9,675	32.1
Weakness		
No	15,763	52.3
Yes	2,988	9.9
.	11,375	37.8
Loss of appetite		
No	14,739	48.9
Yes	4,448	14.8
.	10,939	36.3

Table 5: Symptom and syndrome status in case database.

	Frequency	Percent
Patient was asked if they had symptoms		
No, no symptoms	2,896	9.6
Yes, had symptoms	20,404	67.7
.	6,826	22.7
Aymptomatic based on coding		
No, not asymptomatic	20,537	68.2
Yes, asymptomatic	2,266	7.5
.	7,323	24.3
Patient meets ILI criteria		
No	6,764	22.5
Yes	14,947	49.6
.	8,415	27.9
Patient meets gastroenteritis criteria		
No	14,295	47.5
Yes	5,327	17.7
.	10,504	34.9
Patient meets severe COVID		
No	24,969	82.9
Yes	112	0.4
.	5,045	16.8
Total	30,126	100

Table 6: Medical history questions

Variable	Frequency	Percent
Pregnant?		
No	13,429	44.6
Yes	241	0.8
.	16,456	54.6
Diabetes		
No	15,532	51.6
Yes	1,427	4.7
.	13,167	43.7
Cardiovascular disease		
No	16,161	53.6
Yes	673	2.2
.	13,292	44.1
Hypertension		
No	14,705	48.8
Yes	2,489	8.3
.	12,932	42.9
Renal disease		
No	16,443	54.6
Yes	331	1.1
.	13,352	44.3
Liver disease		
No	16,629	55.2
Yes	72	0.2
.	13,425	44.6
Immunosuppressed condition		
No	16,414	54.5
Yes	316	1.1
.	13,396	44.5
Childhood asthma		
No	15,636	51.9
Yes	944	3.1
.	13,546	45.0

Table 7: Frequency of severe conditions associated with COVID-19 in case database.

Variable	Frequency	Percent
Was the patient diagnosed with pneumonia?		
No	21,251	70.5
Yes	708	2.4
.	8,167	27.1
Was the patient diagnosed with acute respiratory distress syndrome (ARDS)?		
No	21,618	71.8
Yes	279	0.9
.	8,229	27.3
Was the patient diagnosed with an abnormal chest x-ray?		
No	20,346	67.5
Yes	674	2.2
.	9,106	30.2
Was the patient hospitalized due to this illness?		
No	23,326	77.4
Yes	1,000	3.3
.	5,800	19.3
Was the patient admitted to an Intensive Care Unit (ICU) for this illness?		
No	21,730	72.1
Yes	131	0.4
.	8,265	27.4
Was the patient admitted to an Emergency Room for this illness?		
No	16,054	53.3
Yes	410	1.4
.	13,662	45.4
Was the patient given extracorporeal membrane oxygenation (ECMO)?		
No	21,729	72.1
Yes	62	0.2
.	8,335	27.7
Was the patient intubated?		
No	21,738	72.2
Yes	86	0.3
.	8,302	27.6
Did the patient die of this illness?		
No	22,340	74.2
Yes	281	0.9
.	7,505	24.9

Table 8: Frequency of exposure questions in case database.

Variable	Frequency	Percent
Is the patient a healthcare worker?		
No	20,553	68.2
Yes	1,033	3.4
.	8,540	28.4
Did the patient have close contact with a laboratory confirmed case?		
No	10,027	33.3
Yes	11,631	38.6
.	8,468	28.1
Was the close contact a household member?		
No	2,140	7.1
Yes	3,400	11.3
.	24,586	81.6
Where did the case report exposure?		
Household	2,151	7.1
School or daycare	92	0.3
Work	86	0.3
Transit or Rideshare	60	0.2
Other	247	0.8
.	27,490	91.3
How many contacts did the case report?		
0 contacts	3,548	11.8
1 -2 contacts	6,123	20.3
3- 4 contacts	3,043	10.1
5 - 10 contacts	1,439	4.8
11 - 20 contacts	169	0.6
21 - 49 contacts	27	0.1
over 50 contacts	16	0.1
.	15,761	52.3
How many household contacts did the case report?		
0 household contacts	3,093	10.3
1 - 3 household contacts	3,394	11.3
4 - 6 household contacts	1,274	4.2
7 household contacts +	101	0.3
.	22,264	73.9
Did patient provide care for a COVID-19 patient?		
No	11,069	36.7

Yes	571	1.9
.	18,486	61.4
Is the patient a student or daycare attendee?		
No	5,479	18.2
Yes	10,222	33.9
.	14,425	47.9

Table 9: Other exposure questions in the case database.

Variable	Frequency	Percent
Is the patient a current or former smoker?		
Never smoked	15,635	51.9
Current or former smoker	2,073	6.9
.	12,418	41.2
Did the patient have a flu shot in the past year?		
No	7,880	26.2
Yes	6,417	21.3
.	15,829	52.5
Did the patient have health insurance at time of interview?		
No health insurance	1,138	3.8
Yes, health insurance	8,474	28.1
.	20,514	68.1
Has the patient been isolating?		
No	953	3.2
Yes	18,142	60.2
Partial isolation	216	0.7
.	10,815	35.9
Did the patient have pets in their household?		
No	4,877	16.2
Yes	3,663	12.2
.	21,586	71.7
How was the case reported?		
Clinical referral	23,069	76.6
Contact tracing	1,960	6.5
Facility screening	357	1.2
Occupational screening	452	1.5
Other	941	3.1
.	3,347	11.1

Table 10: Frequency of vaccine questions in case database.

Variable	Frequency	Percent
Have you received any dose of an FDA approved COVID-19 vaccine?		
No	3,836	12.7
Yes, 1 dose	219	0.7
Yes, 2 doses	231	0.8
.	25,840	85.8
Did you receive Moderna?		
Unchecked	29,951	99.4
Checked	175	0.6
Did you receive Pfizer?		
Unchecked	30,025	99.7
Checked	101	0.3
Did you receive Johnson & Johnson?		
Unchecked	30,081	99.9
Checked	45	0.2
Is this considered a breakthrough infection?		
No	45	0.2
Yes	198	0.7
Cannot be determined	14	0.1
.	29,869	99.2
When an FDA approved COVID-19 vaccine becomes available to you, do you plan to get it?		
No, definitely not	131	0.4
Yes, definitely	1,208	4.0
Probably yes	393	1.3
Probably no	133	0.4
Not sure	1,056	3.5
.	27,205	90.3

Table 11: Frequency of exposure and risk factor questions in case database

Variable	Frequency	Percent
Did the patient travel in the past 14 days?		
No	16,547	54.9
Yes	4,075	13.5
.	9,504	31.6
How often did the patient report wearing a face mask or face covering?		
Always	3,224	10.7
Sometimes	337	1.1
Never	86	0.3
.	26,479	87.9
Did the patient go to the grocery in person?		
Unchecked	27,847	92.4
Checked	2,279	7.6
Did the patient go to a restaurant in person?		
Unchecked	28,841	95.7
Checked	1,285	4.3
Did the patient go to a bar in person?		
Unchecked	29,681	98.5
Checked	445	1.5
Did the patient go to a gym or fitness center in person?		
Unchecked	29,405	97.6
Checked	721	2.4
Did the patient go to a wedding in person?		
Unchecked	30,071	99.8
Checked	55	0.2
Did the patient go to a salon or barber shop in person?		
Unchecked	30,004	99.6
Checked	122	0.4
Did the patient go to class or school in person?		
Unchecked	29,212	97.0
Checked	914	3.0
Did the patient work in person?		
Unchecked	28,842	95.7
Checked	1,284	4.3
Did the patient visit a library in person?		
Unchecked	29,994	99.6
Checked	132	0.4
Did the patient visit a doctor's office or clinic in person?		

Unchecked	29,537	98.0
Checked	589	2.0
Did the patient visit a theme park or water park?		
Unchecked	30,110	100.0
Checked	16	0.1
Did the patient visit the TAMU MSC?		
Unchecked	29,625	98.3
Checked	501	1.7

Table 12: Frequency of social behaviors in case database

Variable	Frequency	Percent
Did the patient go to an indoor gathering with less than 5?		
Unchecked	29,558	98.1
Checked	568	1.9
Did the patient go to an indoor gathering with 5 to 10 people?		
Unchecked	29,601	98.3
Checked	525	1.7
Did the patient go to an indoor gathering with 10 to 20 people?		
Unchecked	29,823	99.0
Checked	303	1.0
Did the patient go to an indoor gathering with 20 to 50 people?		
Unchecked	29,944	99.4
Checked	182	0.6
Did the patient go to an indoor gathering with over 50 people?		
Unchecked	29,910	99.3
Checked	216	0.7
Did the patient go to an outdoor gathering with less than 5 people?		
Unchecked	29,996	99.6
Checked	130	0.4
Did the patient go to an outdoor gathering with 5 to 10 people?		
Unchecked	29,944	99.4
Checked	182	0.6
Did the patient go to an outdoor gathering with 10 to 20 people?		
Unchecked	29,981	99.5
Checked	145	0.5
Did the patient go to an outdoor gathering with 20 to 50 people?		
Unchecked	30,013	99.6
Checked	113	0.4

Did the patient go to an outdoor gathering with over 50 people?		
Unchecked	29,973	99.5
Checked	153	0.5
Did the patient report no social gathering?		
Unchecked	29,260	97.1
Checked	866	2.9
Did the patient report going to Texas Renaissance Festival?		
Unchecked	30,109	99.9
Checked	17	0.1
Did the patient report going to Midnight Yell?		
Unchecked	30,121	100.0
Checked	5	0.0
Did the patient report going to Breakaway?		
Unchecked	30,085	99.9
Checked	41	0.1
Did the patient report going to Santa's Wonderland?		
Unchecked	30,110	100.0
Checked	16	0.1
Did the patient report going to TAMU graduation?		
Unchecked	30,111	100.0
Checked	15	0.1

Table 13: Questions for University affiliation in case database.

Variable	Frequency	Percent
Is the patient affiliated with the university?		
No	21,689	72.0
Yes	8,437	28.0
Indicate student classification: Undergrad		
Unchecked	25,294	84.0
Checked	4,832	16.0
Indicate student classification: Graduate or Professional		
Unchecked	29,566	98.1
Checked	560	1.9
Indicate student classification: Fraternity or Sorority		
Unchecked	29,572	98.2
Checked	554	1.8
Indicate student classification: Clinical Learner		
Unchecked	30,094	99.9

Checked	32	0.1
Indicate student classification: Student athlete		
Unchecked	29,867	99.1
Checked	259	0.9
Indicate student classification: Student employee		
Unchecked	29,664	98.5
Checked	462	1.5
Indicate student classification: Corps of Cadets		
Unchecked	29,747	98.7
Checked	379	1.3
Indicate student classification: Member of student org.		
Unchecked	29,223	97.0
Checked	903	3.0
Indicate student classification: other		
Unchecked	29,940	99.4
Checked	186	0.6
Indicate work in healthcare setting: Human		
Unchecked	29,685	98.5
Checked	441	1.5
Indicate work in healthcare setting: Animal		
Unchecked	30,034	99.7
Checked	92	0.3
Indicate work in healthcare setting: laboratory		
Unchecked	29,441	97.7
Checked	685	2.3
Indicate work in healthcare setting: other		
Unchecked	29,793	98.9
Checked	333	1.1

A.4 Questionnaire and REDCap codebook for people who were within proximity to those testing positive for SARS-CoV-2

Collapse all instruments

#	Variable / Field Name	Field Label *Field Note*	Field Attributes (Field Type, Validation, Choices, Calculations, etc.)
Instrument: **Index Case and Exposure Information** (index_case_and_exposure_information)			Collapse
1	record_id	Record	text
2	bchd_id	Temporary BCHD ID	text
3	bchid_index	Section Header: *Information about the Laboratory-Con rmed Referrent Case* BCHD ID of Index Case	text
4	index_name_last	Last name of Case	text, Required, Identifier
5	index_name_first	First name of Case	text, Identifier
6	index_date_report	Date of Case report	text (date_mdy)
7	index_date_sxonset	Date of Case Symptom Onset	text (date_mdy)
8	asymptomatic Show the field ONLY if: [index_date_sxonset] < '"0"'	Index Case is Completely asymptomatic	dropdown 1 Yes 0 No 9 Unknown
9	index_date_result	Date of Case Positive Test Result	text (date_mdy)
10	relationship	What is the Contact's relationship to the confirmed case?	dropdown, Identifier 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family 5 Friend 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate 10 Other
11	otherrelationship_spec Show the field ONLY if: [relationship] = '10'	Relationship- Specify if Other	text, Identifier
12	index_date_exposure_on	Does this Contact having ongoing or continuous Exposure to the Case? For example, household members usually have continued exposure to their case.	dropdown 1 Yes 2 No 9 Unknown
13	index_date_exposure Show the field ONLY if: [index_date_exposure_on] = '2' or [index_date_exposure_on] = '9'	Date of Contact's Last Exposure to Case:	text (date_mdy)

14	exposure	Where was the Contact exposed to Case? In what location did the exposure most likely occur?	dropdown 1 Household 2 Healthcare setting 3 Work 4 Daycare 5 School/University 6 Transit 7 Rideshare 8 Hotel 9 Community 11 Case visited Contact home 12 Contact visited Case home 10 Other
15	exposure_workplace Show the field ONLY if: [exposure] = '3'	Employer and Location:	text
16	exposure_school Show the field ONLY if: [exposure] = '4' or [exposure] = '5'	School and Location:	text
17	exposure_hcare Show the field ONLY if: [exposure] = '2'	Facility and Location:	text
18	exposure_other_spec Show the field ONLY if: [exposure] = '10' and [exposure] = '8' and [exposure] = '7' and [exposure] = '6'	Specify the Exposure location	text
19	sympstatus1	Has Contact had any symptoms of an illness?	dropdown 1 Yes 0 No 9 Unknown
20	test1_yn	Has Contact already been tested for COVID-19?	dropdown 1 Yes 0 No 9 Unknown
21	comments	Comments	notes
22	exp_case	Section Header: *Information from the TAMU Portal* Was there known prior contact with a Positive or Suspected COVID-19 case?	dropdown 1 Yes 0 No 9 Unknown
23	contact_date_tamu	What date was the prior contact with the Positive or Suspected COVID-19 case? *MM-DD-YYYY*	text (date_mdy)
24	casecontact_id_1	Name of the Positive COVID-19 case	text

25	casecontact_relationship_1	Relationship	dropdown 1 Spouse/Partner 2 Child 3 Parent 11 Sibling 4 Other Family Member 5 Friend / Acquaintance 6 Healthcare Worker 7 Co-Worker 8 Classmate 9 Roommate / Housemate 10 Other
26	casecontact_exposure_1	Where did the Exposure most likely occur?	dropdown 1 Household 2 Healthcare setting 3 Workplace 4 Daycare 5 At School 6 Transit 7 Rideshare 8 Hotel 9 Community 10 Other
27	index_case_and_exposure_information_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Contact Interview - Demographics** (contact_interview_demographics)			Collapse
28	date_investigate_contact	Start Date of Contact Tracking	text (date_mdy, Min: 0017-03-20)
29	days_report_interview1	# of Days since Contact Identified	calc Calculation: datediff([date_investigate_contact],[index_date_report],"d","mdy")
30	name_first	Section Header: *Information on the Individual in Close Contact with a Case* First Name	text, Identifier
31	name_mi	Middle Initial	text
32	name_late	Last Name	text, Identifier
33	dob	Date of birth	text (date_mdy), Identifier
34	age	Age (years)	calc Calculation: rounddown(datediff([dob],"today","y","mdy"))
35	age_manual Show the field ONLY if: [age] = ''	Please enter Age (years)	text (number)
36	name_parent Show the field ONLY if: [age] < 18 or ([age_manual] < 18 and [age_manual]>0)	If patient is a Child, Parent or Guardian Name	text

37	language	Preferred Language	dropdown 0 English 1 Spanish 8 Other 9 Unknown
38	phone	Phone number *Include Area Code*	text (phone), Identifier
39	email	E-mail	text (email), Identifier
40	address	Address Be sure to include any UNIT #, such as apartment, dorm room, or unit number.	notes, Identifier
41	address_city	City	text, Identifier
42	address_zip	Zip Code	text (zipcode), Identifier
43	address_temp_yn	Are you currently residing or living/sleeping at this address? Answer No if you are temporarily relocated away from your usual residence.	radio 0 Yes, this is my current residence 1 No, I am currently staying somewhere else
44	address_temp Show the field ONLY if: [address_temp_yn] = '1'	Please give the address where you are currently locatedStreet Address with Apartment or Unit numberCity, State, Zip, CountyThis information can be used to provide resources and other information during your isolation/quarantine and can be used in case of emergency, such as if you tell us you need emergency aid or for informing 911 or Emergency personnel to wear Protection if they need to render aid at your address.	notes
45	address_county	County of Residence	text
46	residencetype	Residence Type	dropdown 0 Private residence 15 Apartment 17 Dormitory 16 Nursing Home 1 Homeless 2 Homeless shelter 3 Assisted living facility 4 Longterm acute care facility 5 Longterm care facility 6 Rehabilitation facility 7 Hospice 8 State supported Living facility 9 Military base 10 Quarantine facility military or other 11 Hotel 12 Jail 13 Prison 14 Detention facility 20 Other 21 Unknown

47	residencetype_facilityname Show the field ONLY if: [residencetype] = '20' or [residencetype] = '16' or [residencetype] = '2' or [residencetype] = '3' or [residencetype] = '4' or [residencetype] = '5' or [residencetype] = '6' or [residencetype] = '7' or [residencetype] = '8' or [residencetype] = '9' or [residencetype] = '10' or [residencetype] = '11' or [residencetype] = '12' or [residencetype] = '13' or [residencetype] = '14'	Name of Facility	text
48	residencetype_other Show the field ONLY if: [residencetype] = '20'	Other type of Residence	text
49	sex	Sex	dropdown 0 Female 1 Male 9 Other / Unknown
50	race	Race	dropdown 0 White 1 Black / African American 2 Asian 3 Native Hawaiian or Other Pacific Islander 4 American Indian/Alaska Native 5 Other 9 Unknown / Not Reported
51	race_spec Show the field ONLY if: [race] = '5'	Other specified race	text
52	hispanic	Hispanic	radio 0 No 1 Yes 2 Unknown Custom alignment: RH
53	student_yn	Is a Student or Daycare attendee?	dropdown 1 Yes 0 No 9 Unknown
54	school_name Show the field ONLY if: [student_yn] = '1'	School or Daycare Name:	text

55	affiliation_tamu_student Show the field ONLY if: [student_yn] = '1' or [designat_tamu]='0'		60 | affiliation_tamu_student___60 | Undergraduate Student 61 | affiliation_tamu_student___61 | Graduate or Professional Student 52 | affiliation_tamu_student___52 | Fraternity / Sorority Member 56 | affiliation_tamu_student___56 | Clinical Learner 57 | affiliation_tamu_student___57 | Student Athlete 58 | affiliation_tamu_student___58 | Student Employee 59 | affiliation_tamu_student___59 | Corps of Cadets 80 | affiliation_tamu_student___80 | Member of Student Organization 98 | affiliation_tamu_student___98 | Other 99 | affiliation_tamu_student___99 | Unknown Custom alignment: LV
56	occupation_yn	Employed?	dropdown 1 | Yes 0 | No 9 | Unknown
57	occup_type Show the field ONLY if: [occupation_yn] = '1'	Occupation	text
58	occup_name Show the field ONLY if: [occupation_yn] = '1'	Employer *If Texas A&M Employee, enter "TAMU"*	text
59	uin_tamu	UIN	text (number), Identifier Field Annotation: @HIDDEN-PDF
60	affiliation_tamu_hclab	Please indicate if work (paid or unpaid) in Laboratory or Healthcare setting:	checkbox 54 | affiliation_tamu_hclab___54 | Healthcare Setting - Human 56 | affiliation_tamu_hclab___56 | Healthcare Setting - Animal 55 | affiliation_tamu_hclab___55 | Laboratory Setting 98 | affiliation_tamu_hclab___98 | Other 99 | affiliation_tamu_hclab___99 | Unknown 0 | affiliation_tamu_hclab___0 | None Custom alignment: LV
61	hc_work_yn	Is patient a healthcare worker?	dropdown 0 | No 1 | Yes 9 | Unknown
62	contact_interview_demographics_complete	Section Header: *Form Status* Complete?	dropdown 0 | Incomplete 1 | Unverified 2 | Complete

Instrument: **Contact Interview - 1** (contact_interview_1) Collapse

63	instruct_1	Please answer all these questions about [name_first]. If you are answering for someone else, such as a child, please remember to answer all questions for that person.	descriptive
64	cc_sx_fever	Section Header: *I want to know if you have experienced any signs of illness. I'm going to read a list of symptoms, and I will ask you to tell me if you have have experienced any of these.* Fever	radio (Matrix) 1 Yes 0 No 9 Unknown
65	cc_sx_cough	Cough	radio (Matrix) 1 Yes 0 No 9 Unknown
66	cc_sx_pharyngitis	Sore throat	radio (Matrix) 1 Yes 0 No 9 Unknown
67	cc_sx_sob	Shortness of Breath	radio (Matrix) 1 Yes 0 No 9 Unknown
68	cc_sx_chills	Chills	radio (Matrix) 1 Yes 0 No 9 Unknown
69	cc_sx_headache	Headache	radio (Matrix) 1 Yes 0 No 9 Unknown
70	cc_sx_aches	Muscle aches / Body aches	radio (Matrix) 1 Yes 0 No 9 Unknown
71	cc_sx_vomit	Vomiting / Nausea	radio (Matrix) 1 Yes 0 No 9 Unknown
72	cc_sx_abdpain	Abdominal pain	radio (Matrix) 1 Yes 0 No 9 Unknown
73	cc_sx_diarrhea	Diarrhea	radio (Matrix) 1 Yes 0 No 9 Unknown
74	cc_sx_rhinitis	Runny nose	radio (Matrix) 1 Yes 0 No 9 Unknown

		Congestion	radio (Matrix) 1 Yes 0 No 9 Unknown
76	cc_sx_conjunct	Conjunctivitis	radio (Matrix) 1 Yes 0 No 9 Unknown
77	cc_sx_taste	Loss of Smell / Taste	radio (Matrix) 1 Yes 0 No 9 Unknown
78	cc_sx_fatigue	Fatigue	radio (Matrix) 1 Yes 0 No 9 Unknown
79	cc_sx_weakness	Weakness	radio (Matrix) 1 Yes 0 No 9 Unknown
80	cc_sx_hyporexia	Loss of Appetite	radio (Matrix) 1 Yes 0 No 9 Unknown
81	cc_sx_rash	Rash	radio (Matrix) 1 Yes 0 No 9 Unknown
82	cc_sx_fevertemp Show the field ONLY if: [cc_sx_fever] = '1'	Fever Temp (*F)	text (number, Min: 90, Max: 110)
83	cc_sx_other	Specify other symptoms:	text
84	cc_sx_yn	Experienced any Symptoms?	dropdown 1 Yes 0 No 9 Unknown
85	cc_sx_date Show the field ONLY if: [cc_sx_yn] = '1' or [cc_sx_yn] = '9'	Date of Symptom Onset	text (date_mdy, Min: 0001-03-20)
86	cc_symp_res_yn Show the field ONLY if: [cc_sx_yn] = '1'	Current symptom state	radio 1 Still symptomatic 0 Symptoms resolved 9 Unknown
87	cc_symp_res_dt Show the field ONLY if: [cc_symp_res_yn] = '0'	Date of symptom resolution	text (date_mdy)

		Section Header: *Past or Present Health Conditions* None	radio (Matrix) 1 Yes 0 No 9 Unknown
89	medhx_unknown	Unknown	radio (Matrix) 1 Yes 0 No 9 Unknown
90	medhx_diabetes_yn	Diabetes Mellitus	radio (Matrix) 1 Yes 0 No 9 Unknown
91	hypertension	Hypertension	radio (Matrix) 1 Yes 0 No 9 Unknown
92	medhx_cvd_yn	Cardiovascular/Heart disease	radio (Matrix) 1 Yes 0 No 9 Unknown
93	medhx_immsupp_yn	Immunocompromised condition	radio (Matrix) 1 Yes 0 No 9 Unknown
94	medhx_eczema	Eczema	radio (Matrix) 1 Yes 0 No 9 Unknown
95	medhx_asthma_adult_yn	Asthma	radio (Matrix) 1 Yes 0 No 9 Unknown
96	medhx_asthma_yn	Childhood Asthma	radio (Matrix) 1 Yes 0 No 9 Unknown
97	medhx_cld_yn	Other Lung Disease (e.g. emphysema/COPD)	radio (Matrix) 1 Yes 0 No 9 Unknown
98	medhx_apnea_yn	Sleep Apnea	radio (Matrix) 1 Yes 0 No 9 Unknown
99	pregnant_yn Show the field ONLY if: [sex] = '0'	If female, currently pregnant	radio (Matrix) 1 Yes 0 No 9 Unknown

		Current smoker	radio (Matrix) 1 Yes 0 No 9 Unknown
101	smoke_former_yn	Former smoker	radio (Matrix) 1 Yes 0 No 9 Unknown
102	otherdis_spec	Specify other health conditions or chronic diseases	text
103	vaccinated_yn	Have you received any dose of an FDA-approved COVID-19 vaccine?	radio 1 Yes, 1 dose 2 Yes, 2 doses 0 No
104	vaccine_opp	You may be interested in Prevent COVID U, a National study about coronavirus infection after being vaccinated. Texas A&M is making the study available to young adults in Texas. You can learn more about how to get paid for getting vaccinated and tested: PreventCovidU.org.	descriptive
105	vaccine_label Show the field ONLY if: [vaccinated_yn]='1' or [vaccinated_yn]='2'	Which Vaccine did you receive?	checkbox 0 vaccine_label___0 Moderna 1 vaccine_label___1 Pfizer 2 vaccine_label___2 Johnson & Johnson 7 vaccine_label___7 Vaccine not listed above, from a foreign country 8 vaccine_label___8 Vaccine other than above 9 vaccine_label___9 I don't know which
106	vaccine_county Show the field ONLY if: [vaccinated_yn]='1' or [vaccinated_yn]='2'	Where did you get vaccinated?	checkbox 0 vaccine_county___0 Brazos County 1 vaccine_county___1 Another county in Texas 2 vaccine_county___2 Another state, not Texas 3 vaccine_county___3 Outside the US 9 vaccine_county___9 I don't know
107	vaccine_date Show the field ONLY if: [vaccinated_yn]='1' or [vaccinated_yn]='2'	When was your last dose received?If you don't know the exact date of your latest shot, please estimate as best you can what date.	text (date_mdy)
108	vaccine_yn Show the field ONLY if: [vaccinated_yn]='0'	When an FDA-approved COVID-19 vaccine becomes available to you, do you plan to get vaccinated?	radio 1 YES, definitely 2 Probably yes 9 I'm not sure 8 Probably not 0 NO, definitely not

<table>
<tr>
<td>109</td>
<td>social_venue</td>
<td>In the past 7 days, which of the following have you been to?</td>
<td>checkbox
<table>
<tr><td>0</td><td>social_venue___0</td><td>Grocery store</td></tr>
<tr><td>1</td><td>social_venue___1</td><td>Restaurant for Dine-in</td></tr>
<tr><td>2</td><td>social_venue___2</td><td>Bar</td></tr>
<tr><td>3</td><td>social_venue___3</td><td>Gym or Fitness center</td></tr>
<tr><td>5</td><td>social_venue___5</td><td>Wedding</td></tr>
<tr><td>6</td><td>social_venue___6</td><td>Salon or Barber shop</td></tr>
<tr><td>7</td><td>social_venue___7</td><td>Class/School, in-person</td></tr>
<tr><td>29</td><td>social_venue___29</td><td>Work, in-person</td></tr>
<tr><td>8</td><td>social_venue___8</td><td>Library</td></tr>
<tr><td>23</td><td>social_venue___23</td><td>Doctor's Office or Health Clinic</td></tr>
<tr><td>24</td><td>social_venue___24</td><td>Any theme park or water park</td></tr>
<tr><td>9</td><td>social_venue___9</td><td>Texas A&M Memorial Student Center</td></tr>
<tr><td>30</td><td>social_venue___30</td><td>Texas A&M Student Orientation/Conference</td></tr>
<tr><td>14</td><td>social_venue___14</td><td>Any Indoor gathering, < 5 attendees</td></tr>
<tr><td>15</td><td>social_venue___15</td><td>Any Indoor gathering, 5 to < 10 attendees</td></tr>
<tr><td>16</td><td>social_venue___16</td><td>Any Indoor gathering, 10 to < 20 attendees</td></tr>
<tr><td>17</td><td>social_venue___17</td><td>Any Indoor gathering, 20 to < 50 attendees</td></tr>
<tr><td>11</td><td>social_venue___11</td><td>Any Indoor gathering, 50+ attendees</td></tr>
<tr><td>18</td><td>social_venue___18</td><td>Any Outdoor gathering, < 5 attendees</td></tr>
<tr><td>19</td><td>social_venue___19</td><td>Any Outdoor gathering, 5 to < 10 attendees</td></tr>
<tr><td>20</td><td>social_venue___20</td><td>Any Outdoor gathering, 10 to < 20 attendees</td></tr>
<tr><td>21</td><td>social_venue___21</td><td>Any Outdoor gathering, 20 to < 50 attendees</td></tr>
<tr><td>13</td><td>social_venue___13</td><td>Any Outdoor gathering, 50+ attendees</td></tr>
<tr><td>12</td><td>social_venue___12</td><td>Any Outdoor gathering, < 50 attendees</td></tr>
<tr><td>10</td><td>social_venue___10</td><td>Any Indoor gathering, < 50 attendees</td></tr>
<tr><td>99</td><td>social_venue___99</td><td>None of these</td></tr>
<tr><td>25</td><td>social_venue___25</td><td>Texas A&M Midnight Yell Practice</td></tr>
<tr><td>26</td><td>social_venue___26</td><td>Texas A&M Breakaway</td></tr>
<tr><td>27</td><td>social_venue___27</td><td>Santa's Wonderland</td></tr>
<tr><td>22</td><td>social_venue___22</td><td>Texas Renaissance Festival</td></tr>
<tr><td>28</td><td>social_venue___28</td><td>Texas A&M Graduation Ceremony</td></tr>
</table>
Field Annotation: @HIDECHOICE='10','12','22','25', '26', '27','28'</td>
</tr>
</table>

		During the prior 7 days, How often did you wear a face mask or barrier that covers your nose and mouth when leaving your home?	checkbox 1 act_facemask___1 Always 2 act_facemask___2 Sometimes 0 act_facemask___0 Never
111	flushot	Received Flu Shot in the Prior 1 year?	dropdown 1 Yes 0 No 9 Unknown
112	healthins	Has health insurance?	dropdown 1 Yes 0 No 9 Unknown
113	date_work Show the field ONLY if: [occupation_yn] = '1'	Last date at Work	text (date_mdy)
114	isolation	Is the Case Isolating at Home?	dropdown 0 No 1 Yes 2 Yes - Partial 9 Unknown
115	isolation_start Show the field ONLY if: [isolation] = '1'	What was the first date of Isolation?	text (date_mdy)
116	tamuresearch_yn	Would you be interested in learning about opportunities to participate in COVID/SARS-CoV-2 research at Texas A&M?	dropdown 1 Yes 0 No 9 Unknown or Undecided
117	days_indexexp_interview1	# of Days since Exposure to Index Case	calc Calculation: datediff([date_start_investig], [index_date_exposure],"d","mdy")
118	days_indexsxexp_interview1	# of Days between Symptom onset of Case and Exposure	calc Calculation: datediff([index_date_exposure], [index_date_sxonset],"d","mdy")
119	instruct_isolate_time1 Show the field ONLY if: [index_date_exposure] > '"0"'	This individual should remain isolated for 14 days, beginning on [index_date_exposure]. Use the calendar below to calculate the date the individual can be released from Self-Quarantine.	descriptive
120	instruct_isolate_date1 Show the field ONLY if: [index_date_exposure] > '"0"'	You are requested to remain in quarantine and avoid any contact with others as much as possible. You should not go to work or school. You should remain in your home but separate from others, include family members and other people living in your house. This will help keep others safe by limiting transmission of the virus to other people. Please follow these instructions until: *Select Isolation End Date using the above formula.*	text (date_mdy) Custom alignment: LV Field Annotation: @HIDEBUTTON
121	days_indexsx_interview1	# of Days since Symptom onset of Index Case	calc Calculation: datediff([date_start_investig], [index_date_sxonset],"d","mdy")
122	instruct_test_time Show the field ONLY if: [index_date_exposure] > '"0"'	This individual should be tested, the ideal timeframe for testing is at day 5 following [index_date_exposure], but at the very least testing should be at least 3 days from this date. Use the calendar below to calculate the date this individual should be tested.	descriptive

123	instruct_test_time1b Show the field ONLY if: ([index_date_exposure] = '' or [index_date_exposure_on] = '1')	This individual should be tested, the ideal timeframe for testing is at day 5 following [index_date_result]. Use the calendar below to calculate the date this individual should be tested.	descriptive
124	instruct_isolate_date2	We are sending you to be tested for COVID-19. You may go to any testing site that you like, such as a doctor's office, urgent care clinic, or hospital testing site, or other place that offers COVID-19 testing. Visit www.brazoshealth.org for some testing sites we know about. Please tell the clinic staff that the Health Department told you that you need to be tested. Even if you do not have symptoms, it is important for you to get the test. If you have any difficulty receiving the test, or if the clinic sends you away, please let us know right away. We can also provide a letter to the clinic for you if they ask for one. The Health Department does not provide testing or pay for testing, and we do not know how much testing costs. But some clinics do offer low-cost or no-cost testing if you do not have health insurance and are unable to pay. Please make arrangements to get your COVID-19 test on: *Select Test Date using the above formula.*	text (date_mdy) Custom alignment: LV Field Annotation: @HIDEBUTTON
125	test_referral	Interviewer referred Contact for Testing	dropdown 1 Yes 0 No 9 Unknown
126	date_followup	Date Investigator will Follow-up with Contact	text (date_mdy)
127	case_casecontacts Show the field ONLY if: [exp_case] = '1'	List Names and/or ID numbers of any other COVID cases that are linked to this Case	text
128	interviewer_name_1	Interviewer Name	text
129	interviewer_date1	Date Interview Completed	text (date_mdy)
130	interviewer_tele	Interviewer telephone number	text (phone)
131	final_notes	Any additional comments/notes?	notes
132	contact_interview_1_complet e	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Contact Interview - 2** (contact_interview_2)			Collapse
133	date_investigate2	Section Header: *Please answer all of these questions about [name_ rst] [name_last]. Age: [age] [name_parent] Language: [language] Phone: [phone]* Date Follow-Up contact is Initiated: *MM-DD-YYYY*	text (date_mdy)
134	days_report_interview2	# of Days since Contact Identified	calc Calculation: datediff([date_investigate2], [index_date_report],"d","mdy")
135	days_indexsx_interview2	# of Days since Symptom onset of Index Case	calc Calculation: datediff([date_investigate2], [index_date_sxonset],"d","mdy")
136	days_indexexp_interview2	# of Days since Exposure to Index Case	calc Calculation: datediff([date_investigate2], [index_date_exposure],"d","mdy")
137	contact_has_continued_expo	Contact has continued exposure to case? [index_date_exposure_on]	descriptive

		Section Header: *Has [name_ rst] experienced any signs of illness, including but not limited to the following symptoms:* Fever	radio (Matrix) 1 Yes 0 No 9 Unknown Field Annotation: Subjective or Objective
139	sx_cough_yn_2	Cough	radio (Matrix) 1 Yes 0 No 9 Unknown
140	sx_chills_yn_2	Chills	radio (Matrix) 1 Yes 0 No 9 Unknown
141	sx_myalgia_yn_2	Muscle aches / Body aches (myalgia)	radio (Matrix) 1 Yes 0 No 9 Unknown
142	sx_runnose_yn_2	Runny nose (rhinorrhea)	radio (Matrix) 1 Yes 0 No 9 Unknown
143	sx_sthroat_yn_2	Sore throat	radio (Matrix) 1 Yes 0 No 9 Unknown
144	sx_sob_yn_2	Shortness of breath (dyspnea)	radio (Matrix) 1 Yes 0 No 9 Unknown
145	sx_nauseavomit_yn_2	Nausea or Vomiting	radio (Matrix) 1 Yes 0 No 9 Unknown
146	sx_headache_yn_2	Headache	radio (Matrix) 1 Yes 0 No 9 Unknown
147	sx_taste_yn_2	Loss of Smell / Taste	radio (Matrix) 1 Yes 0 No 9 Unknown
148	sx_pinkeye_yn_2	Conjunctivitis / "pink eye"	radio (Matrix) 1 Yes 0 No 9 Unknown

		Fatigue	radio (Matrix) 1 Yes 0 No 9 Unknown
150	sx_congest_yn_2	Congestion	radio (Matrix) 1 Yes 0 No 9 Unknown
151	sx_other_2	Specify any other symptoms	text
152	onset_dt_2 Show the field ONLY if: [sx_fever_yn_2] = '1' or [sx_chills_yn_2] = '1' or [sx_myalgia_yn_2] = '1' or [sx_runnose_yn_2] = '1' or [sx_sthroat_yn_2] = '1' or [sx_cough_yn_2] = '1' or [sx_sob_yn_2] = '1' or [sx_nauseavomit_yn_2] = '1' or [sx_headache_yn_2] = '1' or [sx_taste_yn_2] = '1' or [sx_pinkeye_yn_2] = '1' or [sx_congest_yn_2] = '1' or [sx_other_2] <> ''	Symptom onset date When is the first time the above symptoms appeared?	text (date_mdy)
153	sympstatus2 Show the field ONLY if: [symp_res_yn] = '1' or [symp_res_yn] = '9'	Symptoms present	radio 1 Symptomatic 0 Asymptomatic 9 Unknown
154	symp_res_dt_2 Show the field ONLY if: [onset_dt_2] > '"0"'	If had symptoms, date of symptom resolution	text (date_mdy)
155	test1_yn_2	Has been tested for COVID-19	dropdown 1 Yes 0 No 9 Unknown
156	test_referral_2	Interviewer referred Contact for Testing	dropdown 1 Yes 0 No 9 Unknown
157	interviewer_name_2	Interviewer Name	text
158	date_interview2	Date of Interview	text (date_mdy)
159	followup1_comments	Comments	notes
160	contact_interview_2_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Laboratory Testing Results** (laboratory_testing_results)			Collapse
161	priorpositive_report	Prior Test Results Documentation	file
162	spec_npswab1_dt	NP Swab: Collection date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON

163	spec_npswab1_type	PCR: Specimen Type - 1	dropdown 0 Nasopharyngeal (NP) swab 1 Oral (mouth) swab 2 Nasal (nostril) swab 3 Saliva or Drool 4 Blood 5 Other
164	spec_npswab1_dtresult	PCR Swab: Result date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
165	spec_npswab1_result Show the field ONLY if: [spec_npswab1_dt] > "0"	PCR: Result - 1	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
166	spec_npswab1site Show the field ONLY if: [spec_npswab1_dt] > "0"	PCR: Testing Site Name - 1	text
167	spec_npswab1_id	PCR: Specimen ID - 1	text
168	spec_npswab1_report	PCR: Laboratory Report	file
169	spec_npswab2_dt	PCR: Collection date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
170	spec_npswab2_result Show the field ONLY if: [spec_npswab2_dt] >"0"	PCR: Result - 2	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
171	spec_npswab2_dtresult Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Result date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
172	spec_npswab2site Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR: Testing Site Name - 2	text
173	spec_npswab3_dt	PCR: Collection date - 3	text (date_mdy) Field Annotation: @HIDEBUTTON
174	spec_npswab3site Show the field ONLY if: [spec_npswab3_dt] >"0"	PCR: Testing Site - 3	text
175	spec_npswab3stateresult Show the field ONLY if: [spec_npswab3_dt] > "0"	PCR: State Result - 3	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
176	spec_otherspecimen1_dt	Other Specimen: Collection date - 1	text (date_mdy) Field Annotation: @HIDEBUTTON
177	spec_otherspecimen1_type Show the field ONLY if: [spec_otherspecimen1_dt] > "0"	Other Specimen Type - 1	text

	t Show the field ONLY if: [spec_otherspecimen1_spec] > ''		text (date_mdy) Field Annotation: @HIDEBUTTON
179	spec_otherspecimen1site Show the field ONLY if: [spec_otherspecimen1_dt] > "0"	Other Specimen: Testing Site - 1	text
180	spec_otherspecimen1_pcr Show the field ONLY if: [spec_otherspecimen1_dt] > 0	Other Specimen: PCR Result - 1	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
181	spec_otherspecimen1_igm Show the field ONLY if: [spec_otherspecimen1_dt] > "0"	Other Specimen: IgM Result - 1	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
182	spec_otherspecimen1_igg Show the field ONLY if: [spec_otherspecimen1_dt] >"0"	Other Specimen: IgG Result - 1	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
183	spec_otherspecimen2_dt	Other Specimen: Collection date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
184	spec_otherspecimen2_type Show the field ONLY if: [spec_otherspecimen2_dt] > "0"	Other: Local Specimen Type- 2	text
185	spec_otherspecimen2site Show the field ONLY if: [spec_otherspecimen2_dt] > "0"	Other Specimen: Testing site - 2	text
186	spec_otherspecimen2_pcr Show the field ONLY if: [spec_otherspecimen2_dt] > "0"	Other Specimen: PCR Result - 2	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
187	spec_otherspecimen2_igm Show the field ONLY if: [spec_otherspecimen2_dt] > "0"	Other Specimen: IgM Result - 2	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate

188	spec_otherspecimen2_igg Show the field ONLY if: [spec_otherspecimen2_dt] > "0"		1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
189	spec_otherspecimen3_dt	Other Specimen: Collection date - 3	text (date_mdy) Field Annotation: @HIDEBUTTON
190	spec_otherspecimen3_spec Show the field ONLY if: [spec_otherspecimen3_dt] > "0"	Other specimen type - 3	text
191	spec_otherspecimen3site Show the field ONLY if: [spec_otherspecimen3_dt] > "0"	Other Specimen: Testing Site - 3	text
192	spec_otherspecimen3_pcr Show the field ONLY if: [spec_otherspecimen3_dt] > "0"	Other Specimen: PCR Result - 3	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
193	spec_otherspecimen3_igm Show the field ONLY if: [spec_otherspecimen3_dt] >"0"	Other Specimen: IgM Result - 3	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
194	spec_otherspecimen3_igg Show the field ONLY if: [spec_otherspecimen3_dt] > "0"	Other Specimen: IgG Result - 3	radio 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
195	lab_notes	Notes about Testing	notes
196	aboratory_testing_results_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Investigator Log** (investigator_log)			Collapse
197	interview_date_contact	Section Header: *Investigation Completed: [name_ rst] [name_late]* Investigation Completed or Closed Date	text (date_mdy)
198	interview_name	Investigator Name	text
199	investigator_phone	Investigator Phone Number	text (phone)

			0 | interview_final___0 | Interview Completed 1 | interview_final___1 | Partial Interview Completed 2 | interview_final___2 | Non-Response 3 | interview_final___3 | No/Insufficient Contact Information Available 4 | interview_final___4 | Refusal 5 | interview_final___5 | Out of County 10 | interview_final___10 | Out of County - TAMU System 6 | interview_final___6 | Reported through TAMU Portal 20 | interview_final___20 | Status changed to CASE
201	refused_testing	Mark if:	checkbox 1 | refused_testing___1 | Contact declined/refused Testing 0 | refused_testing___0 | Contact was Unable to Obtain Test
202	contact_casestatus	What is the current COVID-19 case status of this person? Confirmed case - Laboratory detection (PCR)Probable case - Close contact with case + Any symptoms presentSuspected case - Close contact with caseNot a case - No symptoms and laboratory confirmed Negative	radio 1 | Laboratory Confirmed Case 2 | Probable Case 3 | Suspected Case 4 | Not a Case 5 | Deemed not an actual exposure 9 | Unknown
203	collect_source	Report Data Collected from (check all that apply):	checkbox 0 | collect_source___0 | Patient Interview 1 | collect_source___1 | Medical Record 2 | collect_source___2 | Parent 3 | collect_source___3 | Family Member 8 | collect_source___8 | Other Source 9 | collect_source___9 | Unknown
204	contact_caseid Show the field ONLY if: [contact_casestatus] = '1'	New BCHD Case ID	text
205	interview_assigned_pending	Referred to Case Investigator	checkbox 1 | interview_assigned_pending___1 | Pending - Referred to Investigator
206	interview_assigned	Assigned Case Investigator *Do not Edit*	dropdown (autocomplete) 105 | - - BCHD - - - 24 | Heidi - Investigator 103 | Javier - Investigator 13 | Nabihah - Investigator 18 | Paula - Investigator 16 | Rachel - Investigator 200 | BCHD - Investigator 70 | - 206 | Adrianne - Tracer 92 | Ahmed - Tracer

			57 Don't Use - Sruthi - Tracer 35 Don't Use - Thomas - Tracer 76 Don't Use - Zacary A - Tracer 12 Don't Use - Alyssa - Epi Lead 20 Don't Use - Caroline - Epi Lead 9 Don't Use - Italo - Epi Lead 98 Clendenin - Faculty 99 Fischer - Faculty
218	interview_medrec	Associated Records	file
219	investigator_log_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Quarantine Release** (quarantine_release) Enabled as survey Collapse			
220	release1	Section Header: *Instructions for Release from COVID-19 Quarantine* Name: [initiate_contact_i_arm_1][name_first] [initiate_contact_i_arm_1][name_late] Date of Birth: [initiate_contact_i_arm_1][dob]	descriptive
221	the_individual_referenced	To Whom it May Concern: The individual referenced above has participated in a COVID-19 investigation and has been given instructions to quarantine by a member of the COVID Investigation & Operations Team. The COVID Ops center is an interagency partnership between Texas A&M University and the Brazos County Health District. This individual is released from quarantine as of [initiate_contact_i_arm_1] [instruct_isolate_date1].This release from quarantine is specific to the individual named in this letter only and cannot be extended to another individual. This letter serves as official notice from the authorized investigator. The quarantine period may not be shortened by any other entity or person. The quarantine period may be extended if certain conditions are met, such as a re-occurrence of exposure to this individual.Any specific question or concern regarding this document may be directed to covid@tamu.edu. COVID Investigations & Operations Center, An Interagency solution to stop the spread of COVID-19	descriptive
222	quarantine_release_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Covid19 Document Submission** (covid19_document_submission) Enabled as survey Collapse			
223	instruct_uploadfile	Howdy! Use this form to upload documentation to your Texas A&M COVID Operations Center investigator. This upload portal is secure and private, and your information is always protected.	descriptive
224	date_fileupload1	What is today's Date	text (date_mdy)
225	file_upload1	File Upload:	file
226	file_notes1	Please provide any additional information or comments here that your investigator will need to review your documentation or help with your case management.	notes
227	file_upload2	File Upload:	file
228	date_fileupload2	What is today's Date	text (date_mdy)
229	file_notes2	Please provide any additional information or comments here that your investigator will need to review your documentation or help with your case management.	notes

230	covid19_document_submission_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete
Instrument: **Tamu Portal Responses** (tamu_portal_responses)			Collapse
231	designat_tamu	Primary Role at Texas A&M	radio 0 Student (including student worker) 1 Staff 2 Faculty 3 Postdoc, Resident, or Fellow 4 Contract Worker 5 Other 9 Unknown
232	reportid_report_tamu	Unique Person ID *TAMU Portal Report ID*	text
233	date_report_tamu	Date Reported to TAMU *MM-DD-YYYY*	text (date_mdy, Min: 2020-03-01)
234	text_portal	The below responses are imported from the TAMU COVID-19 Reporting Portal and may be useful when conducting the investigation. However, you do not need to fill in answers here.	descriptive
235	report_casestatus	This report is about a (select one):	radio 0 Person who received a positive test result for CoVID-19 (a laboratory confirmed case) 1 Person who has symptoms and may have COVID-19 but has not been tested or has test resultss that are pending (suspected case) 2 Person who has been exposed to someone who received a positive test result for COVID-19 9 Unknown
236	reporter_tamu	Origin of Initial TAMU Report	radio 0 Self - I am reporting my own confirmed or suspected COVID-19 illness or exposure 1 Supervisor 2 HR Representative 3 Administrative staff 4 Faculty Member 9 Other
237	affiliation_sublist_tamu Show the field ONLY if: [affiliation_tamus]='4'	You have selected Texas A&M University as your primary institution. Please select the most applicable affiliation. You may select more than one.	checkbox, Required 1 affiliation_sublist_tamu___1 Bush School of Government & Public Service 2 affiliation_sublist_tamu___2 College of Agriculture & Life Sciences 3 affiliation_sublist_tamu___3 College of Architecture 4 affiliation_sublist_tamu___4 College of Education & Human Development 96 affiliation_sublist_tamu___96 College of Engineering 5 affiliation_sublist_tamu___5 College of Geosciences

6	affiliation_sublist_tamu___6	College of Liberal Arts
7	affiliation_sublist_tamu___7	College of Science
8	affiliation_sublist_tamu___8	College of Veterinary Medicine & Biomedical Sciences
9	affiliation_sublist_tamu___9	Corps of Cadets
10	affiliation_sublist_tamu___10	Division of Finance & Operations
11	affiliation_sublist_tamu___11	Division of Human Resources & Org Effectiveness
12	affiliation_sublist_tamu___12	Division of Information Technology
13	affiliation_sublist_tamu___13	Division of Marketing & Communications
14	affiliation_sublist_tamu___14	Division of Research
15	affiliation_sublist_tamu___15	Division of Student Affairs
16	affiliation_sublist_tamu___16	Higher Education Center at McAllen
17	affiliation_sublist_tamu___17	Mays Business School
18	affiliation_sublist_tamu___18	Mays Houston City Centre Campus
19	affiliation_sublist_tamu___19	Office of Government Relations
20	affiliation_sublist_tamu___20	Office of the Provost
21	affiliation_sublist_tamu___21	Office of Risk, Ethics, and Compliance
22	affiliation_sublist_tamu___22	School of Innovation
23	affiliation_sublist_tamu___23	School of Law
25	affiliation_sublist_tamu___25	Texas A&M Athletics
97	affiliation_sublist_tamu___97	Texas A&M Transportation Institute - Affiliated Faculty or Student Employee
26	affiliation_sublist_tamu___26	University Libraries
24	affiliation_sublist_tamu___24	SSC Services
27	affiliation_sublist_tamu___27	Chartwells
98	affiliation_sublist_tamu___98	Other

			99 | affiliation_sublist_tamu___99 | Unknown Custom alignment: LV
238	affiliation_tamus	Please indicate one primary Texas A&M University System institution or agency affiliation:	radio 4 | Texas A&M University 1 | Prairie View A&M University 2 | Tarleton State University 3 | Texas A&M International University 5 | Texas A&M University at Galveston 6 | Texas A&M University at Qatar 7 | Texas A&M University Health Science Center 8 | Texas A&M University-Central Texas 9 | Texas A&M University-Commerce 10 | Texas A&M University-Corpus Christi 11 | Texas A&M University-Kingsville 12 | Texas A&M University-San Antonio 13 | Texas A&M University-Texarkana 14 | West Texas A&M University 15 | The Texas A&M University Systems Offices 16 | Texas A&M AgriLife Extension 17 | Texas A&M AgriLife Research 18 | Texas A&M Engineering Experiment Station 19 | Texas A&M Engineering Extension Service 20 | Texas A&M Forest Service 21 | Texas A&M Transportation Institute 22 | Texas A&M Veterinary Medical Diagnostic Laboratory 23 | Texas Division of Emergency Management 98 | Other 99 | Unknown Custom alignment: LV

239	affiliation_sublist_hsc Show the field ONLY if: [affiliation_tamus] = '7'	You have selected Texas A&M University Health Science Center as your primary institution. Please select the most applicable affiliation. You may select more than one.	checkbox 1 affiliation_sublist_hsc___1 College of Dentistry 2 affiliation_sublist_hsc___2 College of Medicine 3 affiliation_sublist_hsc___3 College of Nursing 4 affiliation_sublist_hsc___4 College of Pharmacy 5 affiliation_sublist_hsc___5 School of Public Health 6 affiliation_sublist_hsc___6 Center for Craniofacial Research 7 affiliation_sublist_hsc___7 Center for Innovation in Advanced Development & Manufacturing 8 affiliation_sublist_hsc___8 Center for Health Organization Transformation 9 affiliation_sublist_hsc___9 Center for Population Health & Aging 10 affiliation_sublist_hsc___10 Coastal Bend Health Education Center 11 affiliation_sublist_hsc___11 Family Care - Bryan 12 affiliation_sublist_hsc___12 Family Care - Navasota 13 affiliation_sublist_hsc___13 Family Care - Victoria 14 affiliation_sublist_hsc___14 Global Institute for Hispanic Health 15 affiliation_sublist_hsc___15 Healthy South Texas 16 affiliation_sublist_hsc___16 HSC Administrative Unit 17 affiliation_sublist_hsc___17 Institute of Biosciences & Technology 18 affiliation_sublist_hsc___18 Psychiatry & Behavioral Health 19 affiliation_sublist_hsc___19 Rural & Community Health Institute 20 affiliation_sublist_hsc___20 Telebehavioral Health 98 affiliation_sublist_hsc___98 Other 99 affiliation_sublist_hsc___99 Unknown Custom alignment: LV

240	affiliation_tamu_housing	Please indicate Housing:	radio 1 Fraternity / Sorority House 2 University Dormitory 3 University Apartment 4 Off-Campus in Private Residence 98 Other 99 Unknown
241	housingbldg_tamu_report Show the field ONLY if: [affiliation_tamu_housing] = '1' or [affiliation_tamu_housing] = '2' or [affiliation_tamu_housing] = '3'	Residence Building Name/Number *e.g. SPHA*	text
242	affiliation_tamu_remote	Please specify how current interactions are carried out at TAMU/TAMUS:	radio 1 Working or Attending classes Remotely/Online only 2 Working or Attending classes In-Person only 3 Working or Attending classes using a combination of In-Person and Remote/Online 99 Unknown
243	pets_yn	Do you have pets (dogs, cats, or other mammals) in your household?	dropdown 1 Yes 0 No 9 Unknown
244	notes_general	Any other notes from the TAMU Portal	notes
245	notes_coop		notes Custom alignment: LV
246	notes_coop_document	Relevant Document Upload	file
247	comments_cf66c6	Please provide any details or additional information you think would be helpful to know.	notes
248	name_tamu_reporter	Name of person making this Report *First Name Last Name*	text
249	role_tamu_reporter	Title of person making this Report *e.g. Department Chair*	text
250	school_tamu	School/College *e.g. School of Public Health*	text
251	school_tamu_3	Department/Unit/Laboratory Name *e.g. Department of Environmental & Occupational Health*	text
252	bldg_tamu_report	Building Name/Number	text
253	city_tamu_report	City/Location *e.g. College Station*	text
254	email_reporter_tamu	E-mail Address of person making report	text (email)
255	phone_tamu_reporter	Phone Number of person making this report *Include Area Code*	text (phone), Identifier
256	date_tamu_notif	What date were you notified of the Positive or Suspected COVID-19 Case? *MM-DD-YYYY*	text (date_mdy)
257	labpos_tamu	Was there a laboratory test with a Positive result for COVID-19?	radio 1 Yes 0 No 9 Unknown
258	date_tamu_result	Date test results were Received, if known *MM-DD-YYYY*	text (date_mdy) Field Annotation: @HIDEBUTTON

259	report_yn	Have you reported the confirmed or suspected event to your supervisor, HR liaison, Principal Investigator, or TAMU designee?	radio 1 Yes 0 No 9 Unknown
260	close_contacts_2	What areas of campus did the individual visit while symptomatic and 48 hours before symptoms started? If no symptoms, what areas did the individual visit starting 48 hours before diganosis, suspicion, or report? Please list locations visited/worked. Please be specific (buildings, halls, rooms).	notes
261	covid19_questionnaire_complete	covid19_questionnaire_complete	text
262	covid19_questionnaire_timestamp	covid19_questionnaire_timestamp	text (datetime_mdy)
263	covid_report_form_complete	covid_report_form_complete	text
264	covid_report_form_timestamp	covid_report_form_timestamp	text (datetime_mdy)

265	affiliation_tamu	Question Retired - - Please indicate any Texas A&M affiliations: *Mark all that apply*	checkbox 0 | affiliation_tamu___0 | Health Science Center (HSC) 1 | affiliation_tamu___1 | Texas A&M System (TAMUS) 10 | affiliation_tamu___10 | Texas A&M University (TAMU) 2 | affiliation_tamu___2 | AgriLife 3 | affiliation_tamu___3 | Center for Applied Technology (TCAT) 4 | affiliation_tamu___4 | Engineering Experiment Station (TEES) 5 | affiliation_tamu___5 | Engineering Extension Service (TEEX) 6 | affiliation_tamu___6 | Forest Service (TFS) 7 | affiliation_tamu___7 | Transportation Institute (TTI) 11 | affiliation_tamu___11 | College of Veterinary Medicine 8 | affiliation_tamu___8 | Veterinary Medicine & Diagnostic Laboratory (TVMDL) 9 | affiliation_tamu___9 | Veterinary Medicine Teaching Hospital (VMTH) 12 | affiliation_tamu___12 | College of Medicine 31 | affiliation_tamu___31 | Higher Education Center at McAllen 32 | affiliation_tamu___32 | School of Law 33 | affiliation_tamu___33 | Texas A&M University at Galveston 34 | affiliation_tamu___34 | Texas A&M University - Commerce 35 | affiliation_tamu___35 | Texas A&M University at Qatar 50 | affiliation_tamu___50 | Corps of Cadets 51 | affiliation_tamu___51 | Texas A&M Athletics 54 | affiliation_tamu___54 | Involved in Healthcare (Human or Animal) 55 | affiliation_tamu___55 | Laboratory Personnel 60 | affiliation_tamu___60 | Custodial Staff 98 | affiliation_tamu___98 | Other 99 | affiliation_tamu___99 | Unknown Custom alignment: LV
266	tamu_portal_responses_complete	Section Header: *Form Status* Complete?	dropdown 0 | Incomplete 1 | Unverified 2 | Complete
Instrument: **Don't Use - Retired Questions** (dont_use_retired_questions)			Collapse
267	old_questions_that_have_be	Old questions that have been retired	descriptive

			1 football_nov28___1 Pre-game social activity or event 2 football_nov28___2 Watch party, indoor 3 football_nov28___3 Watch party, outdoor 4 football_nov28___4 Attended game at the Stadium 5 football_nov28___5 Post-game social activity or event 6 football_nov28___6 Watched at home, alone or with household/roommates 7 football_nov28___7 Worked at the Stadium during the game 0 football_nov28___0 None
269	football_nov7	For the Texas A&M Football game on NOV 7 @ South Carolina, please indicate all of your game related activities:	checkbox 1 football_nov7___1 Pre-game social activity or event 2 football_nov7___2 Watch party, indoor 3 football_nov7___3 Watch party, outdoor 4 football_nov7___4 Attended game at the Stadium 5 football_nov7___5 Post-game social activity or event 6 football_nov7___6 Watched at home, alone or with household/roommates 0 football_nov7___0 None
270	football_oct31	For the Texas A&M Football game on OCT 31 vs Arkansas, please indicate all of your game related activities:	checkbox 1 football_oct31___1 Pre-game social activity or event 2 football_oct31___2 Watch party, indoor 3 football_oct31___3 Watch party, outdoor 4 football_oct31___4 Attended game at the Stadium 5 football_oct31___5 Post-game social activity or event 6 football_oct31___6 Watched at home, alone or with household/roommates 7 football_oct31___7 Worked at the Stadium during the game 0 football_oct31___0 None
271	football_oct17	For the Texas A&M Football game on OCT 17 @ Mississippi State, please indicate all of your game related activities:	checkbox 1 football_oct17___1 Pre-game social activity or event 2 football_oct17___2 Watch party, indoor 3 football_oct17___3 Watch party, outdoor 4 football_oct17___4 Attended game at the Stadium 5 football_oct17___5 Post-game social activity or event 6 football_oct17___6 Watched at home, alone or with household/roommates 0 football_oct17___0 None

272	football_oct10	For the Texas A&M Football game on OCT 10 vs Florida, please indicate all of your game related activities:	checkbox 1 football_oct10___1 Pre-game social activity or event 2 football_oct10___2 Watch party, indoor 3 football_oct10___3 Watch party, outdoor 4 football_oct10___4 Attended game at the Stadium 5 football_oct10___5 Post-game social activity or event 6 football_oct10___6 Watched at home, alone or with household/roommates 7 football_oct10___7 Worked at the Stadium during the game 0 football_oct10___0 None
273	football_oct3	For the Texas A&M Football game on OCT 3 @ Alabama, please indicate all of your game related activities:	checkbox 1 football_oct3___1 Pre-game social activity or event 2 football_oct3___2 Watch party, indoor 3 football_oct3___3 Watch party, outdoor 4 football_oct3___4 Attended game at the Stadium 5 football_oct3___5 Post-game social activity or event 6 football_oct3___6 Watched at home, alone or with household/roommates 0 football_oct3___0 None
274	football_sept26	For the Texas A&M Football game on SEPT 26 vs Vanderbilt, please indicate all of your game related activities:	checkbox 1 football_sept26___1 Pre-game social activity or event 2 football_sept26___2 Watch party, indoor 3 football_sept26___3 Watch party, outdoor 4 football_sept26___4 Attended game at the Stadium 5 football_sept26___5 Post-game social activity or event 6 football_sept26___6 Watched at home, alone or with household/roommates 7 football_sept26___7 Worked at the Stadium during the game 0 football_sept26___0 None
275	student_locatoin Show the field ONLY if: [student_yn] = '1'	School or Daycare and Location:	text
276	interview_date	Investigation Completed Date	text (date_dmy)
277	date_start_investig	Contact Investigation Start Date	text (date_mdy)
278	name_last	Last Name	text, Identifier
279	res_county	County of residence	text Custom alignment: RH

		Section Header: *Symptoms, clinical course, past medical history and social history: Within the past 14 days, has [name_ rst] had any of the following symptoms?* Fever or felt feverish	radio (Matrix) 1 Yes 0 No 9 Unknown Field Annotation: Objective or Subjective
281	sx_chills_yn	Chills	radio (Matrix) 1 Yes 0 No 9 Unknown
282	sx_cough_yn	Cough (new onset or worsening of chronic cough)	radio (Matrix) 1 Yes 0 No 9 Unknown
283	sx_myalgia_yn	Muscle aches (myalgia)	radio (Matrix) 1 Yes 0 No 9 Unknown
284	sx_runnose_yn	Runny nose (rhinorrhea)	radio (Matrix) 1 Yes 0 No 9 Unknown
285	sx_sthroat_yn	Sore throat	radio (Matrix) 1 Yes 0 No 9 Unknown
286	sx_sob_yn	Shortness of breath (dyspnea)	radio (Matrix) 1 Yes 0 No 9 Unknown
287	sx_nauseavomit_yn	Nausea or Vomiting	radio (Matrix) 1 Yes 0 No 9 Unknown
288	sx_headache_yn	Headache	radio (Matrix) 1 Yes 0 No 9 Unknown
289	sx_taste_yn	Loss of Smell/Taste	radio (Matrix) 1 Yes 0 No 9 Unknown
290	sx_pinkeye_yn	Conjunctivitis / "pink eye"	radio (Matrix) 1 Yes 0 No 9 Unknown

		Fatigue	radio (Matrix) 1 Yes 0 No 9 Unknown
292	sx_congest_yn	Sinus or Nasal Congestion	radio (Matrix) 1 Yes 0 No 9 Unknown
293	sx_rash_yn	Rash	radio (Matrix) 1 Yes 0 No 9 Unknown
294	sx_back_pain_yn	Back pain	radio (Matrix) 1 Yes 0 No 9 Unknown
295	sx_other	Please list any other symptoms during the past 14 days:	text
296	onset_dt Show the field ONLY if: [sx_fever_yn] = '1' or [sx_chills_yn] = '1' or [sx_cough_yn] = '1' or [sx_myalgia_yn] = '1' or [sx_runnose_yn] = '1' or [sx_sthroat_yn] = '1' or [sx_sob_yn] = '1' or [sx_nauseavomit_yn] = '1' or [sx_headache_yn] = '1' or [sx_taste_yn] = '1' or [sx_pinkeye_yn] = '1' or [sx_fatigue_yn] = '1' or [sx_congest_yn] = '1' or [sx_rash_yn] = '1' or [sx_back_pain_yn] = '1' or [sx_other] > '"0"'	When is the first day you felt ill with any or these symptoms?	text (date_mdy)
297	symp_res_yn Show the field ONLY if: [sx_fever_yn] = '1' or [sx_chills_yn] = '1' or [sx_cough_yn] = '1' or [sx_myalgia_yn] = '1' or [sx_runnose_yn] = '1' or [sx_sthroat_yn] = '1' or [sx_sob_yn] = '1' or [sx_nauseavomit_yn] = '1' or [sx_headache_yn] = '1' or [sx_taste_yn] = '1' or [sx_pinkeye_yn] = '1' or [sx_fatigue_yn] = '1' or [sx_congest_yn] = '1' or [sx_rash_yn] = '1' or [sx_back_pain_yn] = '1' or [sx_other] > '"0"'	Are any symptoms still present?	radio 1 Yes, Still symptomatic 0 No, Symptoms have resolved 9 Unknown symptom status
298	symp_res_dt Show the field ONLY if: [symp_res_yn] = '0'	Date of symptom resolution	text (date_mdy) Field Annotation: @HIDEBUTTON
299	smoke	Smoking Status	radio 0 Never smoker 1 Former smoker 2 Current smoker 9 Unknown

		E-Cigarette Use or Vaping	radio 0 Never user 1 Former user 2 Current user 9 Unknown
301	insured	Does the Case have Health Insurance?	dropdown 0 No 1 Yes 9 Unknown
302	self_isolation	Already self isolating?	dropdown 1 Yes 2 No 3 Partial 4 Unk
303	self_isolation_date Show the field ONLY if: [self_isolation] = '1' or [self_isolation] = '3'	Isolation Start Date	text
304	prior_testing_documentatio	Prior Testing Documentation	file
305	spec_npswab2result Show the field ONLY if: [spec_npswab2_dt] > "0"	PCR Swab: Result - 2	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
306	spec_otherspecimen1_spec	Other specimen type - 1	text
307	spec_otherspecimen2_spec	Other specimen type - 2	text
308	spec_otherspecimen1result Show the field ONLY if: [spec_otherspecimen1_spec] > ''	Other: Result - 1	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate
309	spec_otherspecimen2_dtresult Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Result date - 2	text (date_mdy) Field Annotation: @HIDEBUTTON
310	spec_otherspecimen2result Show the field ONLY if: [spec_otherspecimen2_spec] > ''	Other: Result - 2	dropdown 1 Positive 2 Negative 3 Pending 4 Not Done 5 Indeterminate

311	report_source	Source of Reported Case	radio 0 Clinical referral 1 Contact tracing 2 Facility Screening 3 Occupational Screening 8 Other 9 Unknown
312	dont_use_retired_questions_complete	Section Header: *Form Status* Complete?	dropdown 0 Incomplete 1 Unverified 2 Complete

A.5 Code for contact database

```
*Coding for contact database 4.2.22*


*if I drop based off exposure date, it drops those with continuous exposure*
*dropped 14,628 observations, undid that

*drop based on case report date*
drop if index_date_report_raw>22492

gen sex_coded=.
replace sex_coded=0 if sex_raw==0
replace sex_coded=1 if sex_raw==1
label define sexlabel 0 "Female" 1 "Male"
label values sex_coded sexlabel
tab sex_coded

gen language_coded=.
replace language_coded=0 if language_raw==0
replace language_coded=1 if language_raw==1
replace language_coded=8 if language_raw==8
label define languagelabel 0 "English" 1 "Spanish" 8 "Other"
label values language_coded languagelabel
tab language_coded

*Calculate age*
gen age_calc=((index_date_report_raw -dob_raw)/365.25)
replace age_calc=round(age_calc,0.1)
gen age_calc_f=floor(age_calc)
tab age_calc_f


*age categories based off CDC COVID-19 reporting*
gen age_coded2=.
*age 0 - 4*
replace age_coded2=0 if (age_calc_f >= 0) & (age_calc_f <= 4)
*age 5 - 11*
replace age_coded2=1 if (age_calc_f >=5) & (age_calc_f <=11)
*age 12 - 15*
replace age_coded2=2 if (age_calc_f >= 12) & (age_calc_f<= 15)
*age 16 - 17*
replace age_coded2=3 if (age_calc_f>= 16) & (age_calc_f <= 17)
*age 18 - 29*
replace age_coded2=4 if (age_calc_f >= 18) & (age_calc_f <= 29)
```

```
*age 30 - 39*
replace age_coded2=5 if (age_calc_f >= 30) & (age_calc_f <= 39)
*age 40 - 49*
replace age_coded2=6 if (age_calc_f >= 40) & (age_calc_f <= 49)
*age 50 - 64*
replace age_coded2=7 if (age_calc_f>= 50) & (age_calc_f <= 64)
*age 65 - 74*
replace age_coded2=8 if (age_calc_f >= 65) & (age_calc_f <= 74)
*age 75+*
replace age_coded2=9 if (age_calc_f >=75) & (age_calc_f <=110)
label define agelabel 0 "Ages 0 - 4" 1 "Ages 5 - 11" 2 "Ages 12 - 15" 3 "Ages 16 - 17" 4 "Ages 18 -
29" 5 "Ages 30 - 39" 6 "Ages 40 - 49" 7 "Ages 50 - 64" 8 "Ages 65 - 74" 9 "Ages over 75"
label values age_coded2 agelabel
tab age_coded2

gen age_recode=.
*age 0 - 11*
replace age_recode=0 if (age_calc_f >= 0) & (age_calc_f <= 11)
*age 12 - 17*
replace age_recode=1 if (age_calc_f >= 12) & (age_calc_f<= 17)
*age 18 - 29*
replace age_recode=2 if (age_calc_f >= 18) & (age_calc_f <= 29)
*age 30 - 39*
replace age_recode=3 if (age_calc_f >= 30) & (age_calc_f <= 39)
*age 40 - 49*
replace age_recode=4 if (age_calc_f >= 40) & (age_calc_f <= 49)
*age 50 - 64*
replace age_recode=5 if (age_calc_f >= 50) & (age_calc_f <= 64)
*age 65 +*
replace age_recode=6 if (age_calc_f >= 65) & (age_calc_f <= 110)
tab age_recode

label define agerecodelabel 0 "Ages 0 - 11" 1 "Ages 12 - 17" 2 "Ages 18 - 29" 3 "Ages 30 - 39" 4
"Ages 40 - 49" 5 "Ages 50 - 64" 6 "Ages 65 +"
label values age_recode agerecodelabel

gen decade2=.
*referent group is now 40 - 49*
replace decade2=0 if (age_calc_f >= 40) & (age_calc_f <= 49)
replace decade2=1 if (age_calc_f >=0) & (age_calc_f <=9)
replace decade2=2 if (age_calc_f >=10) & (age_calc_f<=19)
replace decade2=3 if (age_calc_f>=20) & (age_calc_f<=29)
replace decade2=4 if (age_calc_f>=30) & (age_calc_f<=39)
replace decade2=5 if (age_calc_f >= 50) & (age_calc_f <= 59)
replace decade2=6 if (age_calc_f >= 60) & (age_calc_f <= 69)
```

```
replace decade2=7 if (age_calc_f >= 70) & (age_calc_f <= 79)
replace decade2=8 if (age_calc_f >= 80) & (age_calc_f <= 89)
replace decade2=9 if (age_calc_f >= 90) & (age_calc_f <= 99)

label define decade2label 0 "ages 40 - 49" 1 "ages 0 - 9" 2 "ages 10 - 19" 3 "ages 20 - 29" 4
"ages 30 - 39" 5 "ages 50 - 59" 6 "ages 60 - 69" 7 "ages 70 - 79" 8 "ages 80 - 89" 9 "ages 90 - 99"
label values decade2 decade2label
tab decade2

*Code and collapse residence type*
gen residencetype_coded=.
replace residencetype_coded=0 if residencetype_raw==0
replace residencetype_coded=1 if residencetype_raw==15
replace residencetype_coded=2 if residencetype_raw==17
*residence type=3 if supported living*
replace residencetype_coded=3 if residencetype_raw==3 | residencetype_raw== 4 |
residencetype_raw== 7 |residencetype_raw==6 | residencetype_raw== 8 |
residencetype_raw==16
*residencetype_coded=8 if other
replace residencetype_coded=8 if residencetype_raw==20 | residencetype_raw==1 |
residencetype_raw==2 | residencetype_raw== 9 | residencetype_raw==10
|residencetype_raw==11 | residencetype_raw==14

label define residencetype_label 0 "Private Residence" 1 "Apartment" 2 "Dormitory" 3
"Supported living" 8 "Other"
label values residencetype_coded residencetype_label
tab residencetype_coded

*Code and collapse race*
gen race_coded=.
replace race_coded=0 if race_raw==0
replace race_coded=1 if race_raw==1
replace race_coded=2 if race_raw==2
replace race_coded=8 if race_raw==8 | race_raw==4 | race_raw==3

label define racelabel 0 "White" 1 "Black" 2 "Asian"  8 "Other"
label values race_coded racelabel
tab race_coded


gen race_ethnicity_v5=.
*Other race*
replace race_ethnicity_v5=4 if race_coded==8
*Missing race*
replace race_ethnicity_v5=8 if race_coded==.
```

```
*White,non-Hispanic*
replace race_ethnicity_v5=0 if hispanic_raw==0 & race_raw==0
*Hispanic*
replace race_ethnicity_v5=1 if hispanic_raw==1
*Black*
replace race_ethnicity_v5=2 if race_raw==1
*Asian*
replace race_ethnicity_v5=3 if race_raw==2
label define raceeth 4 "Other race" 8 "Missing race" 0 "White, non-Hispanic" 1 "Hispanic" 2
"Black" 3 "Asian"
label values race_ethnicity_v5 raceeth
tab race_ethnicity_v5, missing


*code for hispanic*
gen hispanic_coded=.
replace hispanic_coded=0 if hispanic_raw==0
replace hispanic_coded=1 if hispanic_raw==1

label define hispanic_label 0 "No, NOT Hispanic or Latino" 1 "Yes, Hispanic or Latino"
label values hispanic_coded hispanic_label
tab hispanic_coded

*https://doh.wa.gov/sites/default/files/legacy/Documents/1500//RaceEthnGuidelines.pdf*
gen race_ethnicity_recode=.
*White, non-Hispanic*
replace race_ethnicity_recode=0 if hispanic_raw==0 & race_raw==0
*Hispanic, White*
replace race_ethnicity_recode=1 if hispanic_raw==1 & race_raw==0
*Black, non-Hispanic*
replace race_ethnicity_recode=2 if hispanic_raw==0 & race_raw==1
*Asian, non-Hispanic*
replace race_ethnicity_recode=3 if hispanic_raw==0 & race_raw==2
*Hispanic, Black*
replace race_ethnicity_recode=4 if hispanic_raw==1 & race_raw==1


label define race_ethnicityrecolabel2 0 "White, non-Hispanic" 1 "Hispanic, White" 2 "Black,
non-Hispanic" 3 "Asian, non-Hispanic" 4 "Hispanic, Black"
label values race_ethnicity_recode race_ethnicityrecolabel2
tab race_ethnicity_recode, missing

gen race_eth=.
*Other race*
replace race_eth=4 if race_coded==8
```

```
*White, non-Hispanic*
replace race_eth=0 if hispanic_raw==0 & race_raw==0
*Hispanic*
replace race_eth=1 if hispanic_raw==1
*Black*
replace race_eth=2 if race_raw==1
*Asian*
replace race_eth=3 if race_raw==2
label define neww 0 "White, non-Hispanic" 1 "Hispanic" 2 "Black" 3 "Asian" 4 "Other race"
label values race_eth neww
tab race_eth, missing

*Code for employed*
gen employed_coded=.
replace employed_coded=0 if occupation_yn_raw==0
replace employed_coded=1 if occupation_yn_raw==1

label define employed_label 0 "No" 1 "Yes"
label values employed_coded employed_label
tab employed_coded

*Contact's relationship to the confirmed case*
gen relationship_coded=.
replace relationship_coded=0 if relationship_raw==1 | relationship_raw==2
|relationship_raw==3 | relationship_raw==11 | relationship_raw==4
replace relationship_coded=1 if relationship_raw==9
replace relationship_coded=2 if relationship_raw==5
replace relationship_coded=3 if relationship_raw==7
replace relationship_coded=8 if relationship_raw==10 | relationship_raw==6 |
relationship_raw==8
label define relationshiplabelfinal 0 "Household/Family" 1 "Roommate" 2 "Friend" 3 "Co-
worker" 8 "Other"
label values relationship_coded relationshiplabelfinal
tab relationship_coded

*Does contact have continuous exposure to the case?*
gen continuous_exposure_coded=.
replace continuous_exposure_coded=0 if index_date_exposure_on_raw==2
replace continuous_exposure_coded=1 if index_date_exposure_on_raw==1
*where 0 is no and 1 is yes*
label define continuousexposurelabel 0 "Not continuous exposure" 1 "Continuous exposure"
label values continuous_exposure_coded continuousexposurelabel
tab continuous_exposure_coded

*Where was the Contact exposed to the Case? In what location did the exposure
```

```
*most likely occur?*
gen exposure_coded=.
*Household 13,7111
replace exposure_coded=0 if exposure_raw==1
*Work 1,021*
replace exposure_coded=1 if exposure_raw==3
*Community 905*
replace exposure_coded=2 if exposure_raw==9
*Case or contact visited home 878*
replace exposure_coded=3 if exposure_raw==11 | exposure_raw==12
*School/university* 368*
replace exposure_coded=4 if exposure_raw==5
*Other where Other is Other + hotel + daycare+ transit + rideshare
replace exposure_coded=8 if exposure_raw==10 | exposure_raw==4 | exposure_raw==8 |
exposure_raw==4 | exposure_raw==6 | exposure_raw==7
label define exposure_label 0 "Household" 1 "Work" 2 "Community" 3 "Contact or Case visited
home" 4 "School/university" 8 "Other"
label values exposure_coded exposure_label
tab exposure_coded

*Has Contact had symptoms of an illness?*
gen symptomstatus_coded=.
replace symptomstatus_coded=0 if sympstatus1_raw==0
replace symptomstatus_coded=1 if sympstatus1_raw==1
label define symptomstatus_label 0 "No" 1 "Yes"
label values symptomstatus_coded symptomstatus_label
tab symptomstatus_coded

*Has Contact already been tested for COVID-19?*
*this is one method, the individual was asked by the caller*
*will follow-up by coding with Dr. Fischer's recommendation of test date- call date*
*the above will see if they got tested prior to being asked or after being asked*
gen alreadytested=.
replace alreadytested=0 if test1_yn_raw==0
replace alreadytested=1 if test1_yn_raw==1
label define alreadytestedlabel 0 "No" 1 "Yes"
label values alreadytested alreadytestedlabel
tab alreadytested


***There are 13050 observations with a call 1 date aka call_date_1**
**7635 with a test date*
**22,239 total observations*

*Dr. Fischer's recommendation of test date - call date*
```

```
gen test_date_coded=max(spec_npswab1_dt_raw, spec_npswab2_dt_raw,
spec_npswab3_dt_raw)
tab test_date_coded

format test_date_coded %tdCCYY.NN.DD
tab test_date_coded
*creating duplicate of call_date_1_raw*
gen calldate1=call_date_1_raw
format calldate1 %tCMonth_dd,_CCYY_HH:MM

*Below formula does not calculate correctly*
gen testdate_minus_calldate=(test_date_coded-calldate1)
*16,781 missing values generated*
*5458 observations with a testdate_minus_calldate

generate newcalldate = dofc(calldate1)
format %td newcalldate test_date_coded
generate test_since_call=.
replace test_since_call=test_date_coded-newcalldate


gen test_since_call_coded= (test_since_call>0) if test_since_call !=.

label define testcall_label 0 "Tested prior to being called" 1 "Tested after being called"
label values test_since_call_coded testcall_label
tab test_since_call_coded


*Did the interviewer refer the Contact for testing? *
gen referred_testing=.
replace referred_testing=0 if test_referral_raw==0 | test_referral_2_raw==0
replace referred_testing=1 if test_referral_raw==1 | test_referral_2_raw==1
label define referrallabel 0 "No" 1 "Yes"
label values referred_testing referrallabel
tab referred_testing

label define symptoms 0 "No" 1 "Yes"

*Coding for symptoms in contact database*
gen fever_coded=.
replace fever_coded=0 if cc_sx_fever_raw==0 | sx_fever_yn_2_raw==0
replace fever_coded=1 if cc_sx_fever_raw==1 | sx_fever_yn_2_raw==1
label values fever_coded symptoms
tab fever_coded
```

```
gen cough_coded=.
replace cough_coded=0 if cc_sx_cough_raw==0 |sx_cough_yn_2_raw==0
replace cough_coded=1 if cc_sx_cough_raw==1 | sx_cough_yn_2_raw==1
label values cough_coded symptoms
tab cough_coded

gen pharyngitis_coded=.
replace pharyngitis_coded=0 if cc_sx_pharyngitis_raw==0 | sx_sthroat_yn_2_raw==0
replace pharyngitis_coded=1 if cc_sx_pharyngitis_raw==1 | sx_sthroat_yn_2_raw==1
label values pharyngitis_coded symptoms
tab pharyngitis_coded

gen sob_coded=.
replace sob_coded=0 if cc_sx_sob_raw==0 | sx_sob_yn_2_raw==0
replace sob_coded=1 if cc_sx_sob_raw==1 | sx_sob_yn_2_raw==1
label values sob_coded symptoms
tab sob_coded

gen chills_coded=.
replace chills_coded=0 if cc_sx_chills_raw==0 | sx_chills_yn_2_raw==0
replace chills_coded=1 if cc_sx_chills_raw==1 | sx_chills_yn_2_raw==1
label values chills_coded symptoms
tab chills_coded

gen headache_coded=.
replace headache_coded=0 if cc_sx_headache_raw==0 | sx_headache_yn_2_raw==0
replace headache_coded=1 if cc_sx_headache_raw==1 | sx_headache_yn_2_raw==1
label values headache_coded symptoms
tab headache_coded

gen aches_coded=.
replace aches_coded=0 if cc_sx_aches_raw==0 | sx_myalgia_yn_2_raw==0
replace aches_coded=1 if cc_sx_aches_raw==1 | sx_myalgia_yn_2_raw==1
label values aches_coded symptoms
tab aches_coded

gen vomit_coded=.
replace vomit_coded=0 if cc_sx_vomit_raw==0 | sx_nauseavomit_yn_2_raw==0
replace vomit_coded=1 if cc_sx_vomit_raw==1 | sx_nauseavomit_yn_2_raw==1
label values vomit_coded symptoms
tab vomit_coded

gen abdpain_coded=.
replace abdpain_coded=0 if cc_sx_abdpain_raw==0
replace abdpain_coded=1 if cc_sx_abdpain_raw==1
```

```
label values abdpain_coded symptoms
tab abdpain_coded

gen diarrhea_coded=.
replace diarrhea_coded=0 if cc_sx_diarrhea_raw==0
replace diarrhea_coded=1 if cc_sx_diarrhea_raw==1
label values diarrhea_coded symptoms
tab diarrhea_coded

gen rhinitis_coded=.
replace rhinitis_coded=0 if cc_sx_rhinitis_raw==0 | sx_runnose_yn_2_raw==0
replace rhinitis_coded=1 if cc_sx_rhinitis_raw==1 | sx_runnose_yn_2_raw==1
label values rhinitis_coded symptoms
tab rhinitis_coded

gen congestion_coded=.
replace congestion_coded=0 if cc_sx_congestion_raw==0 | sx_congest_yn_2_raw==0
replace congestion_coded=1 if cc_sx_congestion_raw==1| sx_congest_yn_2_raw==1
label values congestion_coded symptoms
tab congestion_coded

gen conjunct_coded=.
replace conjunct_coded=0 if cc_sx_conjunct_raw==0 | sx_pinkeye_yn_2_raw==0
replace conjunct_coded=1 if cc_sx_conjunct_raw==1 | sx_pinkeye_yn_2_raw==1
label values conjunct_coded symptoms
tab conjunct_coded

gen taste_coded=.
replace taste_coded=0 if cc_sx_taste_raw==0 | sx_taste_yn_2_raw==0
replace taste_coded=1 if cc_sx_taste_raw==1 | sx_taste_yn_2_raw==1
label values taste_coded symptoms
tab taste_coded

gen fatigue_coded=.
replace fatigue_coded=0 if cc_sx_fatigue_raw==0 | sx_fatigue_yn_2_raw==0
replace fatigue_coded=1 if cc_sx_fatigue_raw==1 | sx_fatigue_yn_2_raw==1
label values fatigue_coded symptoms
tab fatigue_coded

gen weakness_coded=.
replace weakness_coded=0 if cc_sx_weakness_raw==0
replace weakness_coded=1 if cc_sx_weakness_raw==1
label values weakness_coded symptoms
tab weakness_coded
```

```
gen hyporexia_coded=.
replace hyporexia_coded=0 if cc_sx_hyporexia_raw==0
replace hyporexia_coded=1 if cc_sx_hyporexia_raw==1
label values hyporexia_coded symptoms
tab hyporexia_coded

gen rash_coded=.
replace rash_coded=0 if cc_sx_rash_raw==0 | sx_rash_yn_raw==0
replace rash_coded=1 if cc_sx_rash_raw==1 | sx_rash_yn_raw==1
label values rash_coded symptoms
tab rash_coded

*Coding medical history*
gen diabetes_coded=.
replace diabetes_coded=0 if medhx_diabetes_yn_raw==0
replace diabetes_coded=1 if medhx_diabetes_yn_raw==1
label values diabetes_coded symptoms
tab diabetes_coded

gen hypertension_coded=.
replace hypertension_coded=0 if hypertension_raw==0
replace hypertension_coded=1 if hypertension_raw==1
label values hypertension_coded symptoms
tab hypertension_coded

gen cvd_coded=.
replace cvd_coded=0 if medhx_cvd_yn_raw==0
replace cvd_coded=1 if medhx_cvd_yn_raw==1
label values cvd_coded symptoms
tab cvd_coded

gen immuno_coded=.
replace immuno_coded=0 if medhx_immsupp_yn_raw==0
replace immuno_coded=1 if medhx_immsupp_yn_raw==1
label values immuno_coded symptoms
tab immuno_coded

gen eczema_coded=.
replace eczema_coded=0 if medhx_eczema_raw==0
replace eczema_coded=1 if medhx_eczema_raw==1
label values eczema_coded symptoms
tab eczema_coded

gen asthma_adult_coded=.
replace asthma_adult_coded=0 if medhx_asthma_adult_yn_raw==0
```

```
replace asthma_adult_coded=1 if medhx_asthma_adult_yn_raw==1
label values asthma_adult_coded symptoms
tab asthma_adult_coded

gen asthma_child_coded=.
replace asthma_child_coded=0 if medhx_asthma_yn_raw==0
replace asthma_child_coded=1 if medhx_asthma_yn_raw==1
label values asthma_child_coded symptoms
tab asthma_child_coded

gen cld_coded=.
replace cld_coded=0 if medhx_cld_yn_raw==0
replace cld_coded=1 if medhx_cld_yn_raw==1
label values cld_coded symptoms
tab cld_coded

gen apnea_coded=.
replace apnea_coded=0 if medhx_apnea_yn_raw==0
replace apnea_coded=1 if medhx_apnea_yn_raw==1
label values apnea_coded symptoms
tab apnea_coded

gen pregnant_coded=.
replace pregnant_coded=0 if pregnant_raw==0
replace pregnant_coded=1 if pregnant_raw==1
label values pregnant_coded symptoms
tab pregnant_coded

*Asymptomatic based on interviewer*
gen asymptomatic_asked=.
replace asymptomatic_asked=0 if cc_sx_yn_raw==0 | sympstatus1_raw==0
replace asymptomatic_asked=1 if cc_sx_yn_raw==1 | sympstatus1_raw==1
label define asymptomaticlabel 0 "No symptoms" 1 "Reported symptoms"
label values asymptomatic_asked asymptomaticlabel
tab asymptomatic_asked

*Asymptomatic coding, if person responded no (0) to all symptoms then yes, they're
asymptomatic*
gen feelingsymptoms_coded=.
replace feelingsymptoms_coded=1 if fever_coded==1 | cough_coded==1 |
pharyngitis_coded==1 | sob_coded==1 | chills_coded==1 | headache_coded==1 |
aches_coded==1 | vomit_coded==1 | abdpain_coded==1 |diarrhea_coded==1 |
rhinitis_coded==1 | congestion_coded==1 | conjunct_coded==1 | taste_coded==1 |
fatigue_coded==1 | weakness_coded==1 | hyporexia_coded==1
```

```
replace feelingsymptoms_coded=0 if fever_coded==0 & cough_coded==0
&pharyngitis_coded==0 & sob_coded==0 & chills_coded==0 & headache_coded==0 &
aches_coded==0 & vomit_coded==0 & abdpain_coded==0 & diarrhea_coded==0 &
rhinitis_coded==0 & congestion_coded==0 & conjunct_coded==0 & taste_coded==0 &
fatigue_coded==0 & weakness_coded==0 & hyporexia_coded==0

label define feelingsymptomslabel 0 "No symptoms" 1 "Feeling symptoms"
label values feelingsymptoms_coded feelingsymptomslabel
tab feelingsymptoms_coded

*Received flu shot in prior 1 year? *
gen flushot_coded=.
replace flushot_coded=0 if flushot_raw==0
replace flushot_coded=1 if flushot_raw==1
label values flushot_coded symptoms
tab flushot_coded

*Smoking status*
gen smoke_coded=.
replace smoke_coded=0 if smoke_raw==0  |smoke_curr_yn_raw==0 |
smoke_former_yn_raw==0
replace smoke_coded=1 if smoke_raw==1 | smoke_curr_yn_raw==1 |
smoke_former_yn_raw==1
label define smokelabel 0 " Never smoker" 1 "Former or Current smoker"
label values smoke_coded smokelabel
tab smoke_coded

*Possible other exposures*
label define sociallabel 0 "Unchecked" 1 "Checked"
gen grocery_coded=.
replace grocery_coded=0 if social_venue0_raw==0
replace grocery_coded=1 if social_venue0_raw==1
*where 0 is unchecked and 1 is checked*
label values grocery_coded sociallabel
tab grocery_coded

gen restaurant_coded=.
replace restaurant_coded=0 if social_venue1_raw==0
replace restaurant_coded=1 if social_venue1_raw==1
label values restaurant_coded sociallabel
tab restaurant_coded

gen bar_coded=.
replace bar_coded=0 if social_venue2_raw==0
replace bar_coded=1 if social_venue2_raw==1
```

```
label values bar_coded sociallabel
tab bar_coded

gen gym_coded=.
replace gym_coded=0 if social_venue3_raw==0
replace gym_coded=1 if social_venue3_raw==1
label values gym_coded sociallabel
tab gym_coded

gen wedding_coded=.
replace wedding_coded=0 if social_venue5_raw==0
replace wedding_coded=1 if social_venue5_raw==1
label values wedding_coded sociallabel
tab wedding_coded

gen salonbarber_coded=.
replace salonbarber_coded=0 if social_venue6_raw==0
replace salonbarber_coded=1 if social_venue6_raw==1
label values salonbarber_coded sociallabel
tab salonbarber_coded

gen classschool_coded=.
replace classschool_coded=0 if social_venue7_raw==0
replace classschool_coded=1 if social_venue7_raw==1
label values classschool_coded sociallabel
tab classschool_coded

gen work_inperson_coded=.
replace work_inperson_coded=0 if social_venue29_raw==0
replace work_inperson_coded=1 if social_venue29_raw==1
label values work_inperson_coded sociallabel
tab work_inperson_coded

gen library_coded=.
replace library_coded=0 if social_venue8_raw==0
replace library_coded=1 if social_venue8_raw==1
label values library_coded sociallabel
tab library_coded

gen doctoroffice_coded=.
replace doctoroffice_coded=0 if social_venue23_raw==0
replace doctoroffice_coded=1 if social_venue23_raw==1
label values doctoroffice_coded sociallabel
tab doctoroffice_coded
```

```
gen themepark_coded=.
replace themepark_coded=0 if social_venue24_raw==0
replace themepark_coded=1 if social_venue24_raw==1
label values themepark_coded sociallabel
tab themepark_coded

gen tamu_msc_coded=.
replace tamu_msc_coded=0 if social_venue9_raw==0
replace tamu_msc_coded=1 if social_venue9_raw==1
label values tamu_msc_coded sociallabel
tab tamu_msc_coded

gen tamu_student_orientation=.
replace tamu_student_orientation=0 if social_venue30_raw==0
replace tamu_student_orientation=1 if social_venue30_raw==1
label values tamu_student_orientation sociallabel
tab tamu_student_orientation

gen indoor_lessthan5=.
replace indoor_lessthan5=0 if social_venue14_raw==0
replace indoor_lessthan5=1 if social_venue14_raw==1
label values indoor_lessthan5 sociallabel
tab indoor_lessthan5

gen indoor_5to10=.
replace indoor_5to10=0 if social_venue15_raw==0
replace indoor_5to10=1 if social_venue15_raw==1
label values indoor_5to10 sociallabel
tab indoor_5to10

gen indoor_10to20=.
replace indoor_10to20=0 if social_venue16_raw==0
replace indoor_10to20=1 if social_venue16_raw==1
label values indoor_10to20 sociallabel
tab indoor_10to20

gen indoor_20to50=.
replace indoor_20to50=0 if social_venue17_raw==0
replace indoor_20to50=1 if social_venue17_raw==1
label values indoor_20to50 sociallabel
tab indoor_20to50

gen indoor_over50=.
replace indoor_over50=0 if social_venue11_raw==0
replace indoor_over50=1 if social_venue11_raw==1
```

```
label values indoor_over50 sociallabel
tab indoor_over50

gen outdoor_lessthan5=.
replace outdoor_lessthan5=0 if social_venue18_raw==0
replace outdoor_lessthan5=1 if social_venue18_raw==1
label values outdoor_lessthan5 sociallabel
tab outdoor_lessthan5

gen outdoor_5to10=.
replace outdoor_5to10=0 if social_venue19_raw==0
replace outdoor_5to10=1 if social_venue19_raw==1
label values outdoor_5to10 sociallabel
tab outdoor_5to10

gen outdoor_10to20=.
replace outdoor_10to20=0 if social_venue20_raw==0
replace outdoor_10to20=1 if social_venue20_raw==1
label values outdoor_10to20 sociallabel
tab outdoor_10to20

gen outdoor_20to50=.
replace outdoor_20to50=0 if social_venue21_raw==0
replace outdoor_20to50=1 if social_venue21_raw==1
label values outdoor_20to50 sociallabel
tab outdoor_20to50

gen outdoor_over50=.
replace outdoor_over50=0 if social_venue13_raw==0
replace outdoor_over50=1 if social_venue13_raw==1
label values outdoor_over50 sociallabel
tab outdoor_over50

gen outdoor_lessthan50=.
replace outdoor_lessthan50=0 if social_venue12_raw==0
replace outdoor_lessthan50=1 if social_venue12_raw==1
label values outdoor_lessthan50 sociallabel
tab outdoor_lessthan50

gen indoor_lessthan50=.
replace indoor_lessthan50=0 if social_venue10_raw==0
replace indoor_lessthan50=1 if social_venue10_raw==1
label values indoor_lessthan50 sociallabel
tab indoor_lessthan50
```

```
*Does the contact have pets?*
gen pets_coded=.
replace pets_coded=0 if pets_yn_raw==0
replace pets_coded=1 if pets_yn_raw==1
label values pets_coded symptoms
tab pets_coded

*Create tamu affiliated variable*
gen tamu_affiliated=.
replace tamu_affiliated=0 if affiliation_tamu_student61_raw==0 |
affiliation_tamu_student52_raw==0 | affiliation_tamu_student56_raw==0 |
affiliation_tamu_student57_raw==0 | affiliation_tamu_student58_raw==0 |
affiliation_tamu_student59_raw==0 | affiliation_tamu_student80_raw==0 |
affiliation_tamu_student98_raw==0 | affiliation_tamu_hclab54_raw==0 |
affiliation_tamu_hclab56_raw==0 | affiliation_tamu_hclab55_raw==0 |
affiliation_tamu_hclab98_raw==0 | affiliation_sublist_tamu1_raw==0 |
affiliation_sublist_tamu2_raw==0 | affiliation_sublist_tamu3_raw==0 |
affiliation_sublist_tamu4_raw==0 | affiliation_sublist_tamu96_raw==0 |
affiliation_sublist_tamu5_raw==0 | affiliation_sublist_tamu6_raw==0 |
affiliation_sublist_tamu7_raw==0 | affiliation_sublist_tamu8_raw==0 |
affiliation_sublist_tamu9_raw==0 | affiliation_sublist_tamu10_raw==0 |
affiliation_sublist_tamu11_raw==0 | affiliation_sublist_tamu12_raw==0 |
affiliation_sublist_tamu13_raw==0 | affiliation_sublist_tamu14_raw==0 |
affiliation_sublist_tamu15_raw==0 | affiliation_sublist_tamu16_raw==0 |
affiliation_sublist_tamu17_raw==0 | affiliation_sublist_tamu18_raw==0 |
affiliation_sublist_tamu19_raw==0 | affiliation_sublist_tamu20_raw==0 |
affiliation_sublist_tamu21_raw==0 | affiliation_sublist_tamu22_raw==0 |
affiliation_sublist_tamu23_raw==0 | affiliation_sublist_tamu25_raw==0 |
affiliation_sublist_tamu97_raw==0 | affiliation_sublist_tamu26_raw==0 |
affiliation_sublist_tamu24_raw==0 | affiliation_sublist_tamu27_raw==0 |
affiliation_sublist_tamu98_raw==0

replace tamu_affiliated=1 if affiliation_tamu_student61_raw==1 |
affiliation_tamu_student52_raw==1 | affiliation_tamu_student56_raw==1 |
affiliation_tamu_student57_raw==1 | affiliation_tamu_student58_raw==1 |
affiliation_tamu_student59_raw==1 | affiliation_tamu_student80_raw==1 |
affiliation_tamu_student98_raw==1| affiliation_tamu_hclab54_raw==1 |
affiliation_tamu_hclab56_raw==1 | affiliation_tamu_hclab55_raw==1 |
affiliation_tamu_hclab98_raw==1 | affiliation_sublist_tamu1_raw==1 |
affiliation_sublist_tamu2_raw==1 | affiliation_sublist_tamu3_raw==1 |
affiliation_sublist_tamu4_raw==1 | affiliation_sublist_tamu96_raw==1 |
affiliation_sublist_tamu5_raw==1 | affiliation_sublist_tamu6_raw==1 |
affiliation_sublist_tamu7_raw==1 | affiliation_sublist_tamu8_raw==1 |
affiliation_sublist_tamu9_raw==1 | affiliation_sublist_tamu10_raw==1|
affiliation_sublist_tamu11_raw==1 | affiliation_sublist_tamu12_raw==1 |
```

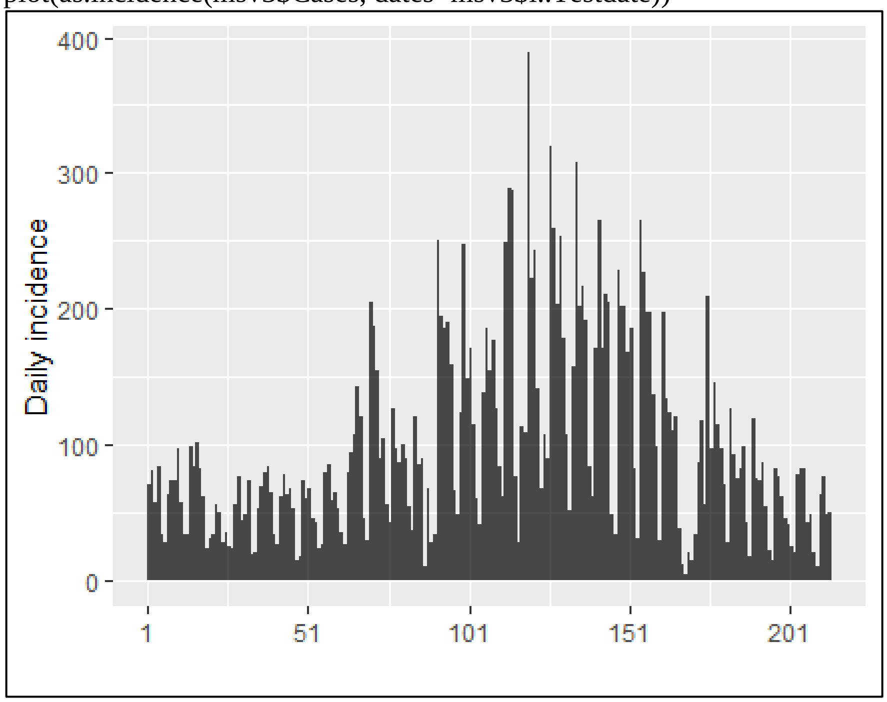
```
affiliation_sublist_tamu13_raw==1 | affiliation_sublist_tamu14_raw==1 |
affiliation_sublist_tamu15_raw==1 | affiliation_sublist_tamu16_raw==1 |
affiliation_sublist_tamu17_raw==1 | affiliation_sublist_tamu18_raw==1 |
affiliation_sublist_tamu19_raw==1 | affiliation_sublist_tamu20_raw==1 |
affiliation_sublist_tamu21_raw==1 | affiliation_sublist_tamu22_raw==1 |
affiliation_sublist_tamu23_raw==1 | affiliation_sublist_tamu25_raw==1 |
affiliation_sublist_tamu97_raw==1 | affiliation_sublist_tamu26_raw==1 |
affiliation_sublist_tamu24_raw==1 | affiliation_sublist_tamu27_raw==1 |
affiliation_sublist_tamu98_raw==1

label define tamu_affiliatedlabel 0 "Not affiliated with TAMU" 1 "Affiliated with TAMU"
label values tamu_affiliated tamu_affiliatedlabel
tab tamu_affiliated

gen student_coded=.
replace student_coded=0 if student_yn_raw==0
replace student_coded=1 if student_yn_raw==1
label define studentlabel 0 "No" 1 "Yes"
label values student_coded studentlabel
tab student_coded

*Was there known prior contact with a positive or confirmed COVID-19 case?*
gen prior_contact_coded=.
replace prior_contact_coded=0 if exp_case_raw==0
replace prior_contact_coded=1 if exp_case_raw==1
label define contactlabel 0 "No" 1 "Yes"
label values prior_contact_coded contactlabel
tab prior_contact_coded

*Did the contact say that they were tested at any point during the contact tracing process? *
gen tested=.
replace tested=0 if test1_yn_raw==0  |  test1_yn_2_raw==0
replace tested=1 if test1_yn_raw==1 |  test1_yn_2_raw==1
label define testlabel 0 "No" 1 "Yes"
label values tested testlabel
tab tested

*Calculating if the contact got tested when they should have*
gen collectiondate=.
replace collectiondate=max(spec_npswab1_dt_raw, spec_npswab2_dt_raw,
spec_npswab3_dt_raw, spec_otherspecimen1_dt_raw, spec_otherspecimen2_dt,
spec_otherspecimen3_dt)

format collectiondate %tdCCYY.NN.DD
tab collectiondate, missing
```

```
*Calculate collection date of close contact - exposure date *
gen correcttestdate=collectiondate-index_date_exposure_raw
tab correcttestdate, missing

replace correcttestdate=. if correcttestdate<=0
tab correcttestdate, missing
replace correcttestdate=. if correcttestdate>=20
tab correcttestdate, missing

*categorize correct test date*
gen categorizecorrecttestdate=.
replace categorizecorrecttestdate=0 if correcttestdate==1 | correcttestdate==2
replace categorizecorrecttestdate=1 if (correcttestdate>3) & (correcttestdate<=5)
replace categorizecorrecttestdate=2 if (correcttestdate>5) & (correcttestdate<=10)
label define cattestdatelabel 0 "tested too early" 1 "tested 3 - 5 days post exposure" 2 "tested 5
- 10 days after exposure"
label values categorizecorrecttestdate cattestdatelabel
tab categorizecorrecttestdate, missing

*Recoding correct test date*
gen cor_testdate=.
replace cor_testdate=0 if correcttestdate==1 | correcttestdate==2 | (correcttestdate>7 &
correcttestdate<=20)
replace cor_testdate=1 if (correcttestdate>=3) & (correcttestdate<=7)
label define cortestdate 0 "tested too early or too late" 1 "tested in the recommended window"
label values cor_testdate cortestdate
tab cor_testdate, missing

*Coding for flu-like illness syndrome*
*Per CDC, influenza like illness (ILI) is defined as fever 100 or greater, a cough, and or sore
throat*
*https://www.cdc.gov/vaccines/pubs/surv-manual/chpt06-
influenza.html#:~:text=For%20this%20system%2C%20ILI%20is,known%20cause%20other%20t
han%20influenza.*

gen fever_over100=.
replace fever_over100=0 if cc_sx_fevertemp_raw<100
replace fever_over100=1 if cc_sx_fevertemp_raw>=100
label define feverlabel 0 "Fever less than 100" 1 "Fever 100 or greater"
label values fever_over100 feverlabel
tab fever_over100

*Coding for influenza like illness*
gen ili_coded=.
```

```
replace ili_coded=0 if fever_over100==0 & cough_coded==0 | pharyngitis_coded==0
replace ili_coded=1 if fever_over100==1 & cough_coded==1 | pharyngitis_coded==1
label define ili_label 0 "Does not meet ILI syndrome" 1 "Meets ILI syndrome"
label values ili_coded ili_label
tab ili_coded

*gastroenteritis - characterized by diarrea and or vomiting*
*https://www.cdc.gov/disasters/disease/infectevac.html*
gen gastroenteritis_coded=.
replace gastroenteritis_coded=0 if diarrhea_coded==0 | vomit_coded==0
replace gastroenteritis_coded=1 if diarrhea_coded==1 | vomit_coded==1
label define gastroenteritislabel 0 "No gastroenteritis" 1 "gastroenteritis"
label values gastroenteritis_coded gastroenteritislabel
tab gastroenteritis_coded
```

A.6 R code for calculating R_0 and output

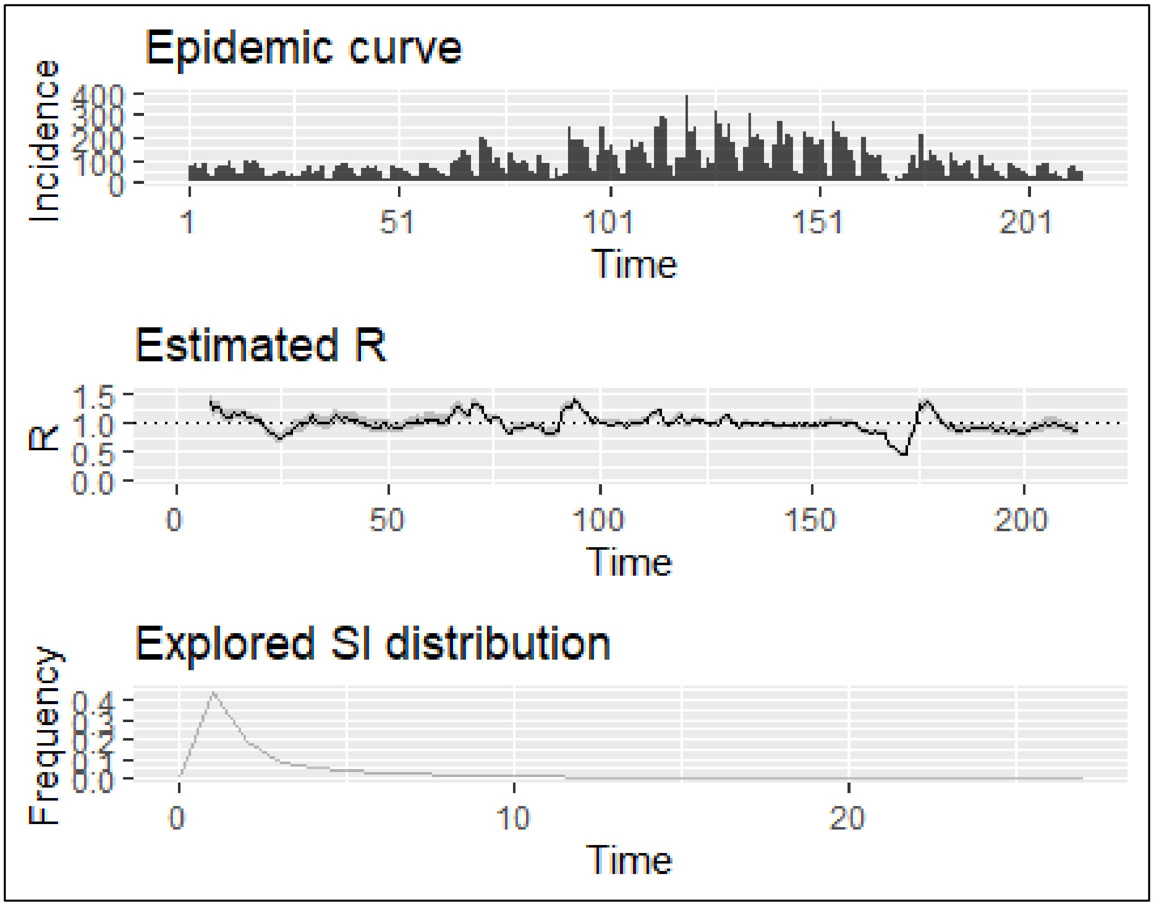
```
install.packages("rlang", dependencies=TRUE)
install.packages("vctrs", dependencies=TRUE)
install.packages("EpiEstim", dependencies=TRUE)
install.packages("incidence", dependencies=TRUE)
install.packages("writexl", dependencies=TRUE)

library(EpiEstim)
library(ggplot2)
library(writexl)
library(EpiEstim)
library(incidence)
library(vctrs)
library(ggplot2)


msv3<-read.csv("C:\\Users\\alyss\\OneDrive - Texas A&M
University\\Dissertation\\Data\\Modelingsubsetv3.csv")

head(msv3$Cases)
library(incidence)
plot(as.incidence(msv3$Cases, dates=msv3$ï..Testdate))
```



```
mydata<-read.table("C:\\Users\\alyss\\OneDrive - Texas A&M
University\\Dissertation\\Data\\Modelingsubsetv3.csv", header=TRUE, sep=",")

library(EpiEstim)
res_parametric_si<-estimate_R(msv3$Cases,
method="parametric_si",config=make_config(list(mean_si=3.8, std_si=5.2)))
head(res_parametric_si$R)
t_start t_end  Mean(R)     Std(R) Quantile.0.025(R) Quantile.0.05(R) Quantile.0.25(R)
Median(R) Quantile.0.75(R) Quantile.0.95(R)
1       2     8 1.366402 0.06659434         1.238980        1.258740        1.320914  1.365320
1.410710        1.477753
2       3     9 1.234719 0.06075653         1.118494        1.136511        1.193214  1.233722
1.275137        1.336325
3       4    10 1.305330 0.06132974         1.187878        1.206116        1.263457  1.304369
1.346156        1.407820
4       5    11 1.136007 0.05503972         1.030679        1.047016        1.098415  1.135118
1.172631        1.228030
5       6    12 1.126923 0.05453563         1.022557        1.038745        1.089676  1.126044
1.163212        1.218101
6       7    13 1.122721 0.05401692         1.019332        1.035373        1.085830  1.121854
1.158667        1.213023
  Quantile.0.975(R)
1          1.499971
2          1.356605
3          1.428239
4          1.246386
5          1.236288
6          1.231031
```

First six values of mean(R): 1.37, 1.23, 1.31, 1.14, 1.13, 1.12
Average first 6 values of R: 1.22

```
plot(res_parametric_si, legend=FALSE)
```




```
res_parametric_si<-estimate_R(msv3$Cases,
method="parametric_si",config=make_config(list(mean_si=3.8, std_si=5.2)))
head(res_parametric_si$R)
res_parametric_si
options(max.print=10000)#change global options
x<-res_parametric_si$R
write_xlsx(x,path= "R.xlsx", col_names=TRUE)
```

A.7 Matlab code for models

%SIARv3

```
function  yprime = SIARv3(t,y, params)

% %parameters for SEEIAR-V dissertation model
%   S = susceptible population
%   Sym = reported cases/infections
%   A = unreported cases/infections
%   R = Recovered (got sick, now recovered and immune, or died :( )
%   N = total population = (S + Sym + A + R)
%

  Data_array = params.Data_array;
           % Table of: time    cases

    min_t = Data_array(1,1);
      n_table = length(Data_array(:,1) );
    max_t = Data_array(n_table,1);
     t_val = max( min_t, min( t, max_t) );
   Reported_cases = interp1( Data_array(:,1), Data_array(:,2), t_val); %
Linear interpolation

%    min_t = Data_array(1,1);
%       n_table = length(Data_array(:,1) );
%     max_t = Data_array(n_table,1);
%      t_val = max( min_t, min( t, max_t) );
%    c = interp1(Data_array(:,1),Data_array(:,3), t_val);

   gammaA = params.gammaA;
   gammaS = params.gammaS;
   lambda = params.lambda;
   q = params.q;
   eps = params.eps;
   pr = params.pr;

   N = params.N;

     S = y(1);
     Sym = y(2);
     A = y(3);
     R = y(4);
     Rr = y(5);
     CI = y(6);

     yprime = zeros(6,1);

     %pr = min(1,Reported_cases/((beta*S*(Sym+eps*A)/N)));% reporting rate
```

```
    c = Reported_cases/(pr*q*S*(Sym+eps*A)/N); %derive what c is ;
reported_cases divided by what incidence is
    beta = (c)*q;%Brazos average household size

    yprime(1) = (-beta*S*(Sym+eps*A)/N)+lambda*R;
    yprime(2) = pr*(beta*S*(Sym+eps*A)/N)-gammaS*Sym;
    yprime(3) = (1-pr)*(beta*S*(Sym+eps*A)/N)-gammaA*A;
    yprime(4) = gammaS*Sym+gammaA*A-lambda*R;
    yprime(5) = c; %dummy variable for contact rate
    yprime(6) = pr*beta*S*(Sym+eps*A)/N; %dummy variable for reported
incidence to compare to the data
```

%SIARv3_only

```
function  yprime = SIAR_Vonlyv3(t,y, params)

% %parameters for SEEIAR-V dissertation model
%   S = susceptible population
%   Sym = reported cases/infections
%   A = unreported cases/infections
%   R = Recovered (got sick, now recovered and immune, or died :( )
%   N = total population = (S + Sym + A + R)
%

  Data_array = params.Data_array;
  Rr = params.c;
          % Table of: time    cases

    min_t = Data_array(1,1);
      n_table = length(Data_array(:,1) );
    max_t = Data_array(n_table,1);
     t_val = max( min_t, min( t, max_t) );
   c = interp1( Data_array(2:end,1), Rr(:,1), t_val); % Linear interpolation

%    min_t = Data_array(1,1);
%       n_table = length(Data_array(:,1) );
%     max_t = Data_array(n_table,1);
%      t_val = max( min_t, min( t, max_t) );
%    c = interp1(Data_array(:,1),Data_array(:,3), t_val);

   gammaA = params.gammaA;
   gammaS = params.gammaS;
   lambda = params.lambda;
   v=params.v;
   q = params.q;
   eps = params.eps;
   pr = params.pr;

   beta = (c)*q;

   N = params.N;

     S = y(1);
     Sym = y(2);
     A = y(3);
     R = y(4);
     V = y(5);%vaccination instead of contact
     CI = y(6);%remains reported incidence

     yprime = zeros(6,1);

     yprime(1) = (-beta*S*(Sym+eps*A)/N)-v*S+lambda*R;
```

```
yprime(2) = pr*(beta*S*(Sym+eps*A)/N)-gammaS*Sym;
yprime(3) = (1-pr)*(beta*S*(Sym+eps*A)/N)-gammaA*A;
yprime(4) = gammaS*Sym+gammaA*A-lambda*R;
yprime(5) = v*S;
yprime(6) = pr*beta*S*(Sym+eps*A)/N;
```

```
clear all
```

%parameters for SIAR-V dissertation model

```
%   S = susceptible population
%   Sym = reported cases/infections
%   A = unreported cases/infactions
%   R = Recovered (got sick, now recovered and immune, or died :( )
%   N = total population = (S + Sym + A + R)
%
%    dS/dt = (-beta*S*(Sym+eps*A)/N)-v*S
%    dSym/dt = pr*(+beta*S*(Sym+eps*A)/N)-gammaS*Sym
%    dA/dt = (1-pr)*(+beta*S*(Sym+eps*A)/N)-gammaA*A
%    dR/dt = gamma*Sym+gamma*A+v*S

%   this file passes "seir.m" function to ode solver
%     ode systen is specified in "seir.m" file
 S_0 =221423;  %233849 is population of Brazos County April 2020
https://www.census.gov/quickfacts/brazoscountytexas
 Sym_0 = 353+0.25*(107+124); %The 0.25 takes into account underreporting
based on CDC data.
 A_0 = 1059+0.75*(107+124);    %Need to do 353*3 and replace 235 with that
value, this will take into account under-reporting
 R_0 = 10783;         % initial recovered (not to be confused with R_zero,
below)
 V_0 = 0;                % initially, no one has recovered

   %  params is a structure used to pass parameters to the
%   ODE solver

   params.N = S_0 + Sym_0 + A_0 + R_0 + V_0;  % N = total population

 params.gammaS= 1./6; %based on average time between symptom onset on test
result (3 days + 1 day to wait for result) + 2 days pre-symptoms infection
 params.gammaA = 1./8; %based on recovery in data (6 days from onset to test
result) + 2 days pre-sympt
 params.q = 0.75;% https://www.pnas.org/doi/full/10.1073/pnas.2019324117;
probablity of transmission - 0.5
 params.eps = 0.55; % from
https://www.science.org/doi/full/10.1126/science.abb3221; study was done from
people in China
 params.lambda = 0;%1/180; %average duration to reinfection (immunity loss or
new variants infection)
 params.pr = 0.25; %https://www.cdc.gov/coronavirus/2019-ncov/cases-
updates/burden.html; reporting rate fixed at 25%
 %array below - 3rd column is contacts; currently not being used. Decreased
 %amount of contacts with peak of cases shows people might not be reporting
 %their contacts
     Data_array =  [1.0   104.1  1.1;
2.0   89.6   1.1;
3.0   78.3   1.2;
4.0   67.1   1.2;
```

```
5.0    70.0   1.3;
6.0    70.7   1.3;
7.0    71.3   1.4;
8.0    59.4   1.5;
9.0    60.0   1.6;
10.0   58.9   1.7;
11.0   64.6   1.7;
12.0   60.7   1.5;
13.0   60.9   1.6;
14.0   61.6   1.5;
15.0   66.6   1.4;
16.0   67.9   1.4;
17.0   71.9   1.4;
18.0   69.7   1.3;
19.0   70.4   1.4;
20.0   69.0   1.4;
21.0   68.7   1.4;
22.0   59.6   1.4;
23.0   55.6   1.4;
24.0   48.3   1.4;
25.0   40.4   1.4;
26.0   36.6   1.5;
27.0   36.7   1.7;
28.0   35.6   1.7;
29.0   38.6   1.9;
30.0   41.6   1.9;
31.0   40.7   1.8;
32.0   43.7   1.8;
33.0   49.3   1.8;
34.0   48.4   1.7;
35.0   48.0   1.8;
36.0   47.7   1.5;
37.0   46.7   1.5;
38.0   51.7   1.5;
39.0   56.7   1.5;
40.0   55.4   1.6;
41.0   57.6   1.6;
42.0   58.4   1.6;
43.0   59.7   1.9;
44.0   61.0   1.8;
45.0   58.7   1.8;
46.0   56.6   1.7;
47.0   54.9   1.6;
48.0   52.1   1.4;
49.0   50.9   1.4;
50.0   52.6   1.4;
51.0   50.0   1.3;
52.0   50.6   1.3;
53.0   47.3   1.3;
54.0   45.7   1.3;
55.0   46.9   1.5;
56.0   48.1   1.4;
```

```
57.0  49.0  1.2;
58.0  52.6  1.2;
59.0  51.3  1.3;
60.0  54.1  1.4;
61.0  55.7  1.5;
62.0  57.4  1.5;
63.0  57.4  1.5;
64.0  57.3  1.6;
65.0  58.6  1.7;
66.0  65.7  1.7;
67.0  76.7  1.7;
68.0  86.3  1.5;
69.0  87.9  1.4;
70.0  88.3  1.3;
71.0  106.1 1.3;
72.0  119.4 1.2;
73.0  126.0 1.2;
74.0  118.4 1.1;
75.0  116.1 1.1;
76.0  117.6 1.2;
77.0  119.4 1.2;
78.0  108.4 1.2;
79.0  95.6  1.1;
80.0  85.9  1.1;
81.0  87.4  1.1;
82.0  85.4  1.2;
83.0  85.1  1.1;
84.0  84.3  1.1;
85.0  83.3  1.1;
86.0  81.6  1.1;
87.0  82.0  1.0;
88.0  69.1  1.0;
89.0  65.9  0.9;
90.0  62.1  0.9;
91.0  61.7  0.9;
92.0  80.4  1.0;
93.0  96.0  1.1;
94.0  109.7 1.1;
95.0  135.4 1.3;
96.0  148.6 1.2;
97.0  154.0 1.2;
98.0  156.3 1.3;
99.0  138.0 1.2;
100.0 145.6 1.2;
101.0 140.3 1.2;
102.0 137.4 1.3;
103.0 131.1 1.2;
104.0 130.3 1.3;
105.0 129.1 1.2;
106.0 131.3 1.3;
107.0 122.6 1.2;
108.0 123.4 1.1;
```

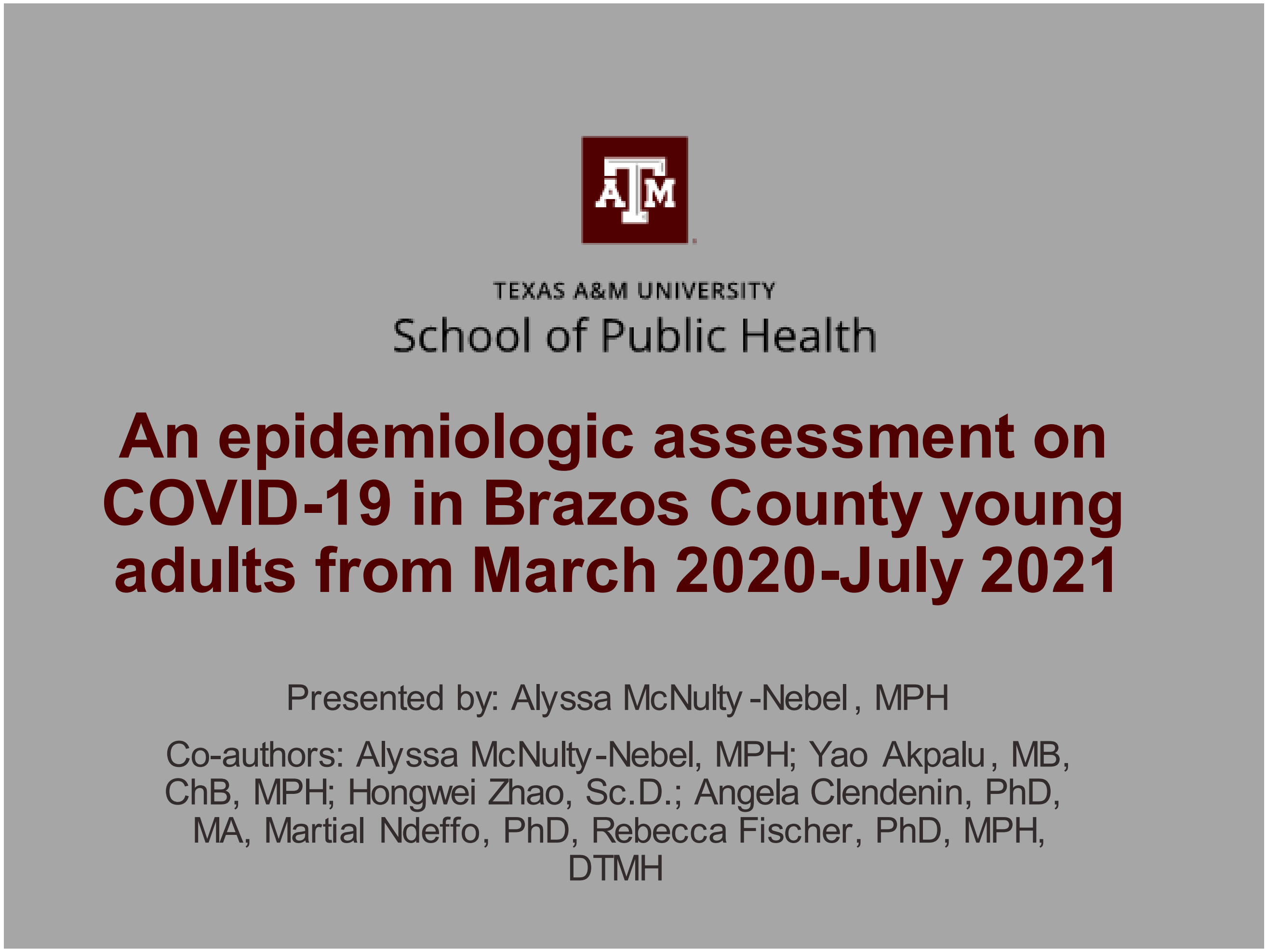
```
109.0  124.4  1.0;
110.0  126.1  0.9;
111.0  129.6  0.8;
112.0  132.4  0.8;
113.0  148.3  0.7;
114.0  163.0  0.7;
115.0  182.0  0.6;
116.0  167.7  0.5;
117.0  153.4  0.6;
118.0  157.6  0.6;
119.0  164.4  0.6;
120.0  184.4  0.7;
121.0  174.9  0.7;
122.0  168.6  0.7;
123.0  177.7  0.7;
124.0  183.4  0.7;
125.0  182.7  0.6;
126.0  180.0  0.7;
127.0  170.1  0.6;
128.0  175.4  0.6;
129.0  169.7  0.6;
130.0  185.9  0.6;
131.0  201.7  0.7;
132.0  201.6  0.7;
133.0  196.0  1.1;
134.0  172.9  1.1;
135.0  179.9  1.1;
136.0  179.7  1.1;
137.0  174.3  1.1;
138.0  176.3  1.1;
139.0  172.9  1.3;
140.0  174.3  0.9;
141.0  176.1  0.8;
142.0  170.0  0.9;
143.0  165.6  1.0;
144.0  164.9  1.0;
145.0  166.7  1.0;
146.0  161.9  0.8;
147.0  157.9  0.6;
148.0  166.0  0.7;
149.0  156.9  0.7;
150.0  161.3  0.6;
151.0  155.1  0.6;
152.0  152.3  0.7;
153.0  157.0  0.6;
154.0  156.6  0.7;
155.0  161.9  0.7;
156.0  165.6  0.7;
157.0  165.0  0.7;
158.0  169.3  0.6;
159.0  162.4  0.6;
160.0  164.9  0.6;
```

```
161.0  164.7  0.7;
162.0  155.0  0.7;
163.0  141.7  0.7;
164.0  131.1  0.7;
165.0  118.7  0.8;
166.0  116.3  0.8;
167.0  107.6  0.7;
168.0  105.1  0.6;
169.0  77.6   0.5;
170.0  61.4   0.5;
171.0  45.7   0.5;
172.0  34.7   0.4;
173.0  30.0   0.5;
174.0  41.4   0.6;
175.0  47.7   0.6;
176.0  77.0   0.7;
177.0  87.9   0.8;
178.0  106.6  0.8;
179.0  118.0  0.9;
180.0  119.4  0.9;
181.0  112.6  0.8;
182.0  108.4  0.9;
183.0  96.7   0.8;
184.0  96.1   0.8;
185.0  86.1   0.9;
186.0  81.6   0.9;
187.0  81.9   0.9;
188.0  77.9   0.9;
189.0  76.6   0.9;
190.0  75.4   0.9;
191.0  72.9   0.9;
192.0  72.6   0.8;
193.0  73.1   0.8;
194.0  66.7   0.8;
195.0  63.9   0.7;
196.0  63.4   0.7;
197.0  58.1   0.6;
198.0  58.3   0.6;
199.0  56.6   0.6;
200.0  50.7   0.5;
201.0  48.9   0.6;
202.0  49.3   0.7;
203.0  50.1   0.8;
204.0  49.6   0.8;
205.0  50.4   0.9;
206.0  53.4   0.9;
207.0  53.0   0.9;
208.0  54.0   0.8;
209.0  53.4   0.7;
210.0  51.9   0.7;
211.0  49.7   0.7;
212.0  49.0   0.7];
```

```
    params.Data_array = Data_array;
%
  tspan = [1:212];  % time in days for the whole data set
  %Assumes the model should be able to replicate the data almost exactly.
  %Daily number of reported cases from the model should be the data. Not
  %fitting, just saying the model should generate the number of daily
  %number of cases.

 yinit = zeros(6,1);
 yinit(1) = S_0;
 yinit(2) = Sym_0;
 yinit(3) = A_0;
 yinit(4) = R_0;

[t1,y1] = ode45(@SIARv3, tspan, yinit, [], params);

tv=130; %time vaccination
yinit = y1(tv,:);
yinit(5)=V_0;
params.c = (y1(2:end,5)-y1(1:end-1,5));% daily contact rate
tspan =[tv:212]; %110 does not have to be 110; its the start date of vacc. If
I change this make sure I change it on yinit too.
params.v = 0.0009828;
[t2,y2] = ode45(@SIAR_Vonlyv3, tspan, yinit, [], params);

t0 = [[1:tv] t2(2:end)'];
y0 = [y1(1:tv,:)' y2(2:end,:)'];

t = t0';
y = y0';

 figure;%blue is enhanced vaccination and red is no added vaccination
  subplot(2,1,2), plot( t, y(:,2),'b-');
  hold on; plot(t,y1(:,2),'r-')
  legend('additional vaccination','base line')
   xlabel('time(days)');
   ylabel('Sym: symptomatic and reported');

   subplot(2,1,1), plot( t, y(:,3),'b-');
   hold on; plot(t, y1(:,3),'r-')
   legend('additional vaccination','base line')
   xlabel('time(days)');
   ylabel('A: asymptomatic and underreported');

%
 total_cases(:,1) = y(:,2) + y(:,3) + y(:,4);
 total_cases_b(:,1) = y1(:,2) + y1(:,3) + y1(:,4);

figure;
```

```
 plot( t, total_cases(:,1),'b-');
 hold on; plot(t, total_cases_b,'r-')
 legend('additional vaccination','base line')
 xlabel('time(days)');
 ylabel('Total Cases: Sym+A+R ');

figure;
  total_cases_active(:,1) = y(:,2) + y(:,3);
  total_cases_active_b(:,1) = y1(:,2) + y1(:,3);
  plot( t, total_cases_active,'b-');
  hold on; plot(t, total_cases_active_b,'r-')
 legend('additional vaccination','base line')
   xlabel('time(days)');
   ylabel('Total Active Cases: Sym+A ');
figure
plot(y(2:end,6)-y(1:end-1,6),'b-')
  hold  on; plot(y1(2:end,6)-y1(1:end-1,6),'r-')
  hold on
  plot(Data_array(:,1),Data_array(:,2),'*k');
  legend('additional vaccination','base line','data')
   xlabel('time(days)');
   ylabel('Daily identified cases');

   figure
  plot(params.q*(y1(2:end,5)-y1(1:end-1,5)).*(params.pr/params.gammaS + (1-
params.pr)*params.eps/params.gammaA))% R0=pr*beta/(gamma*S)+1-
pr*eps*(beta/gamma*A)
   ylabel('Reproductive number (R_t)')
   xlabel('time(days)')
```

A.8 Diseases in Nature Presentation



Outline

- Learning objectives
- Interagency cooperation
- Methods for current analysis
- Statistics in Brazos County
- Young adults in the dataset
- Clinical presentation
- Behaviors & risk factors
- Strengths
- Continuing research
- Limitations
- Conclusions
- References
- Questions

Learning objectives

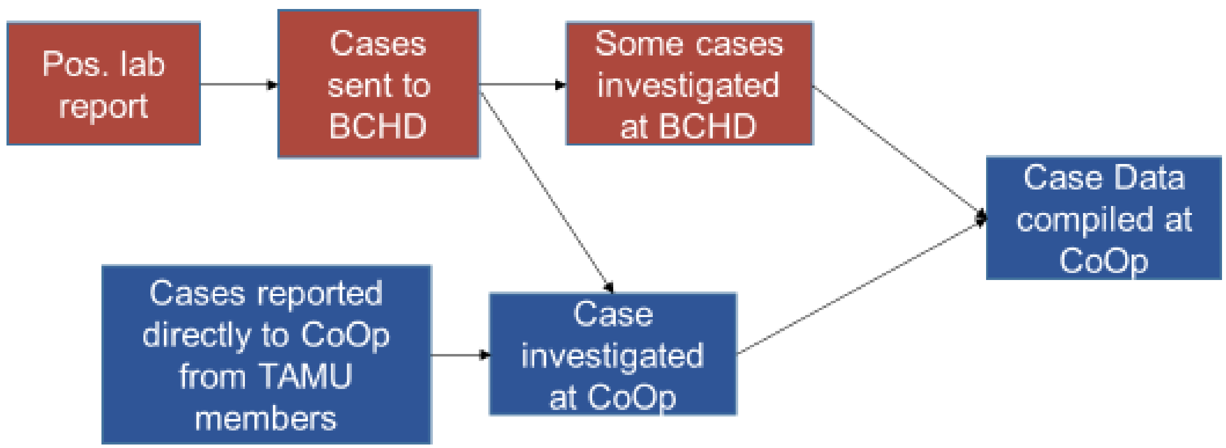
- Unique interagency partnership between public health and academia that augmented COVID-19 response & reporting capacity.
- Describe characteristics of the young adults who tested positive for SARS-CoV-2 in the Brazos County.
- Describe clinical signs, symptoms, and severity of COVID-19 in young adults.

Interagency cooperation

- Brazos County Health Department (BCHD) partnered with Texas A&M University (TAMU)
- COVID-19 Operations (CoOp) established by TAMU Public Health faculty.
  - Faculty had worked side by side with BCHD epidemiology since March 2020

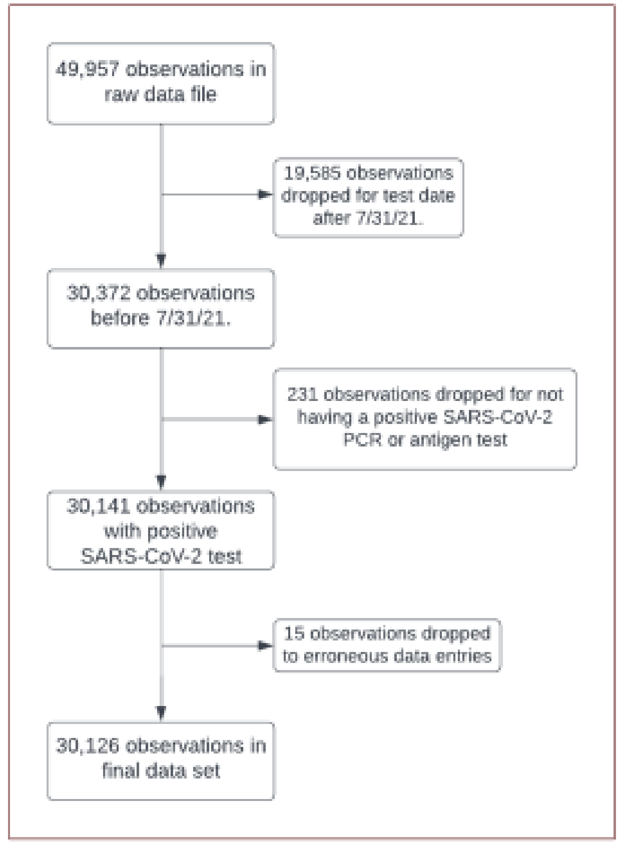
Interagency cooperation cont'd

- COVID-19 case investigators and contact tracers were at BCHD and the CoOp.
- Situational awareness between CoOp, TAMU, and BCHD



Methods

- Cases were entered into the Research Electronic Data Capture (REDCap) software
- For this analysis, included data on cases thru July 31, 2021
- Data cleaned in STATA 16.1/IC

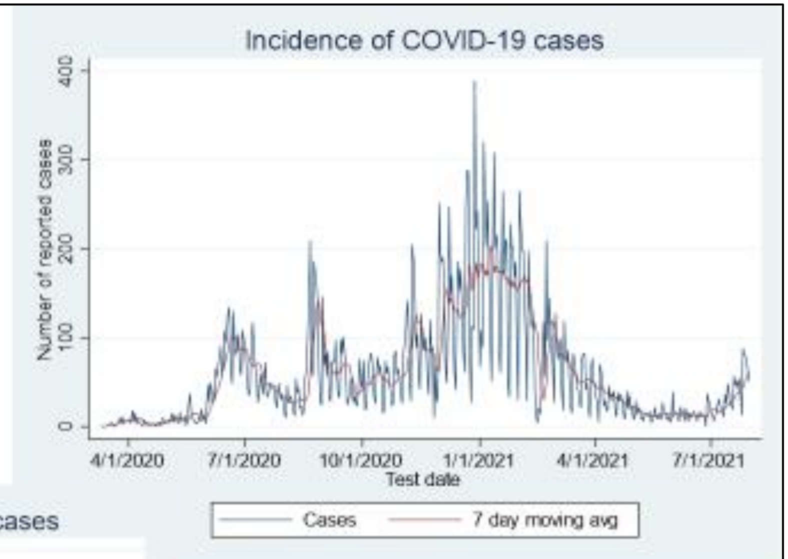


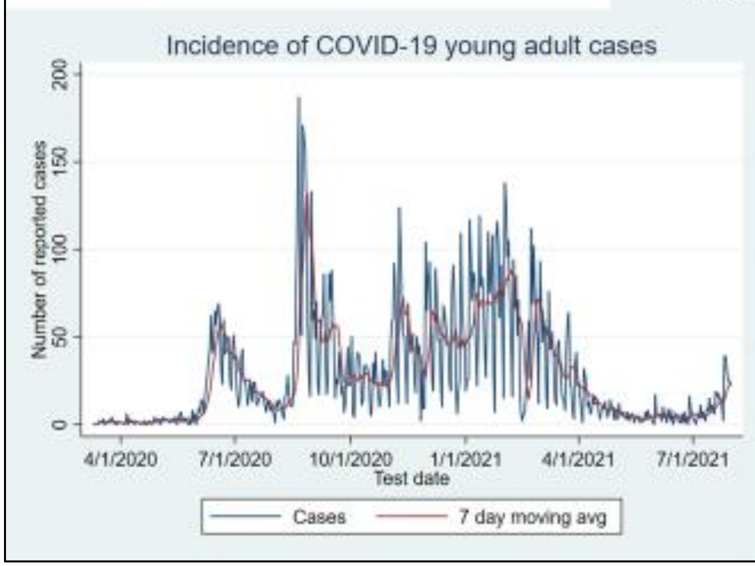
Methods cont'd

- Self-reporting filled gaps where labs may not have otherwise made it to reporting systems
- May include some individuals later not included in BCHD data
  - Residence determined elsewhere
  - Testing occurred elsewhere
- Includes probable & confirmed cases
- Excludes individuals reporting without confirmed or probable laboratory testing
- University testing programs and expanded campus test availability may have increased case numbers over what otherwise may have been observed in the young adult population

COVID-19 in Brazos County

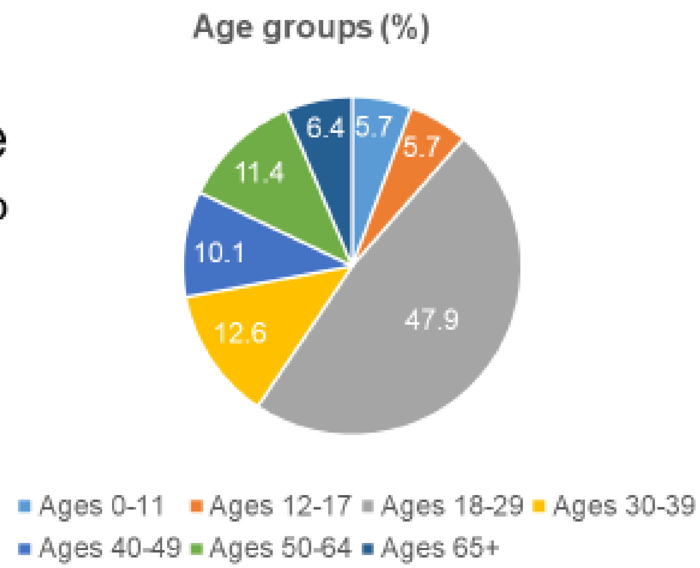
- Home to Texas A&M, one of the largest public universities in the U.S.
  - Opportunity to look at unique young adult population
- As of June 2, 2022 there have been[1]:
  - 55,672 cases of COVID-19 reported
  - 415 deaths reported
- From March 17, 2020-July 31, 2021, in the data:
  - 30,126 cases of COVID-19
  - 281 deaths
  - Data precedes known emergence of Delta (B.1.617.2) and Omicron (B.1.1.529) variants


Incidence of COVID-19 cases
Number of reported cases
0
100
200
300
400
4/1/2020
7/1/2020
10/1/2020
1/1/2021
4/1/2021
7/1/2021
Test date
Cases
7 day moving avg


Incidence of COVID-19 young adult cases
Number of reported cases
0
50
100
150
200
4/1/2020
7/1/2020
10/1/2020
1/1/2021
4/1/2021
7/1/2021
Test date
Cases
7 day moving avg

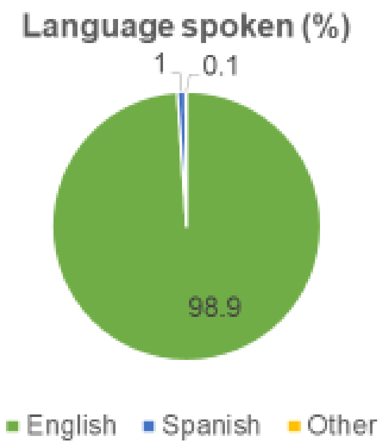
Young adults in the data

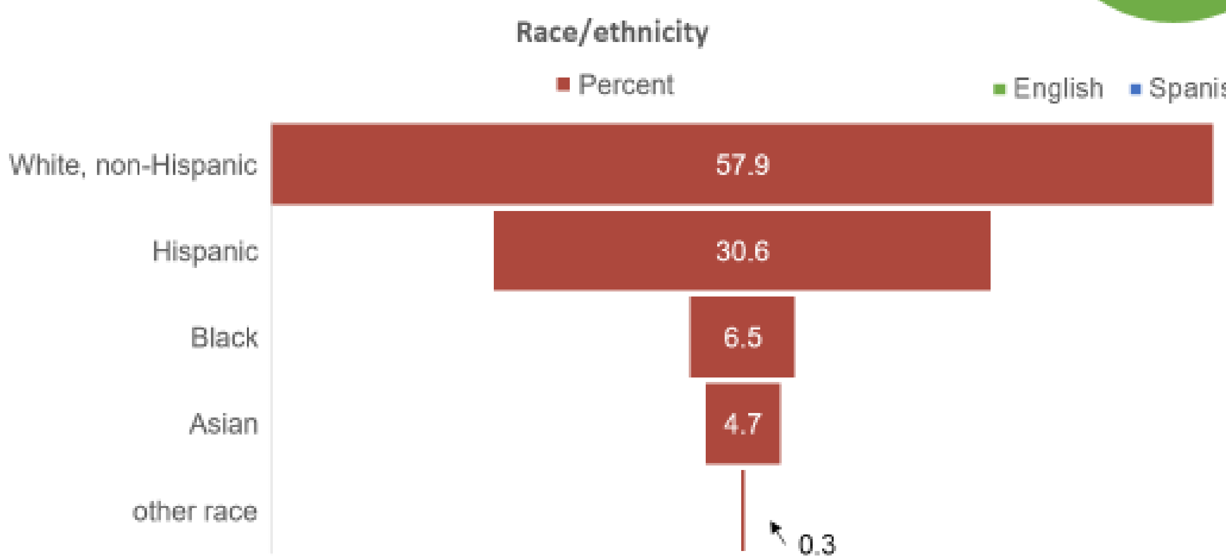
- Young adults defined here as 18-29 years of age
- 14,433 young adults in the dataset, comprising 47.9% of total cases
- 2 young adults died of COVID
- The rest of this presentation will focus specifically on young adults



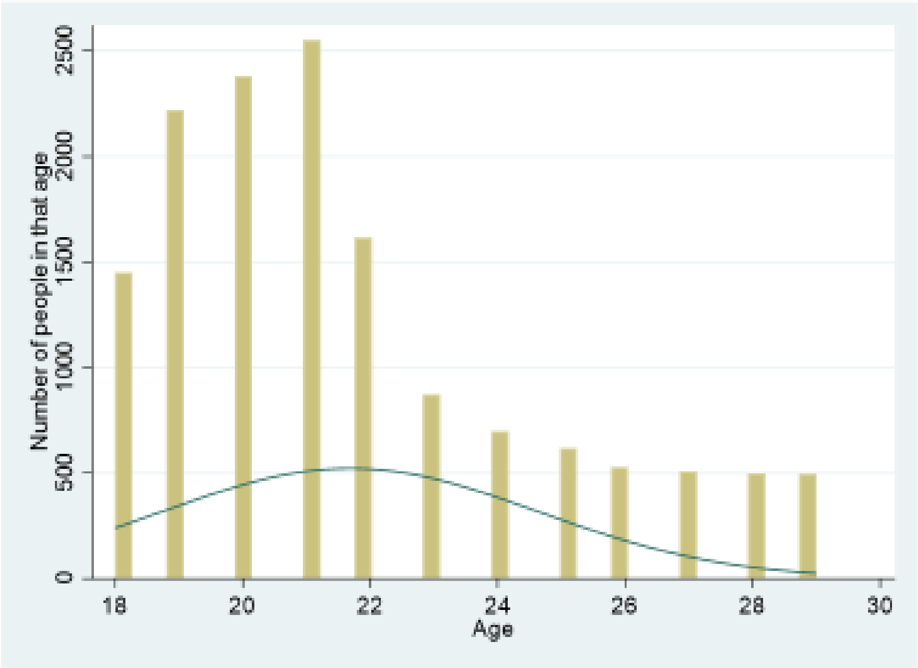

Demographics

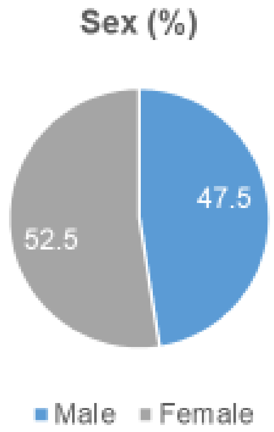
- Majority reported as English speakers (98.9%), about half were White, non-Hispanic (57.9%)



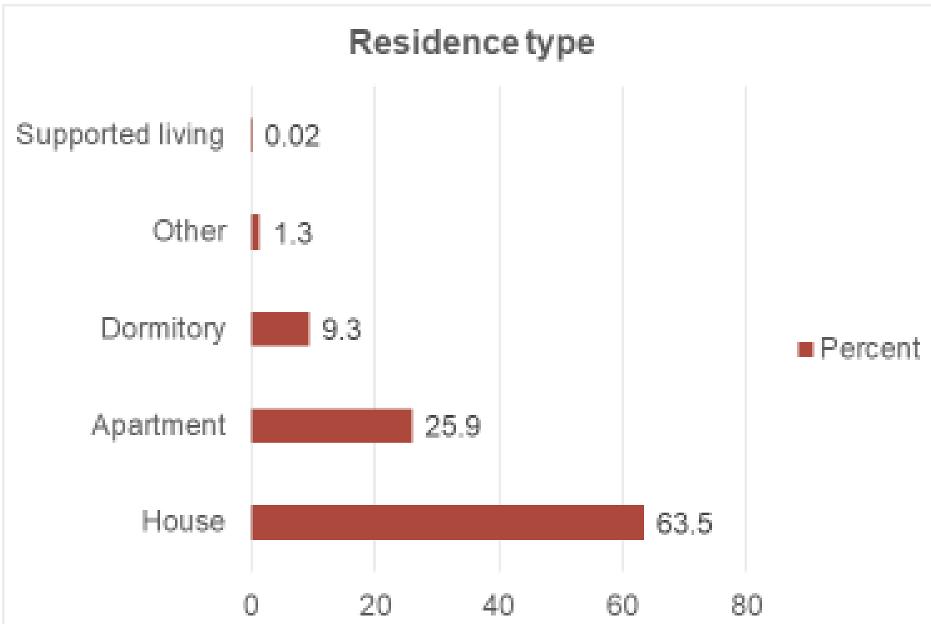


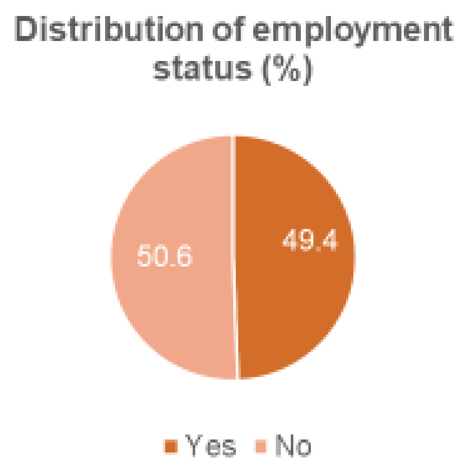
- Relatively even distribution of male (47.5%) and female (52.5%)
- Most common ages in young adults were 19-21





- Most reported living in a house (63.5%) followed by apartment (25.9%)
- Half were employed (50.6%)

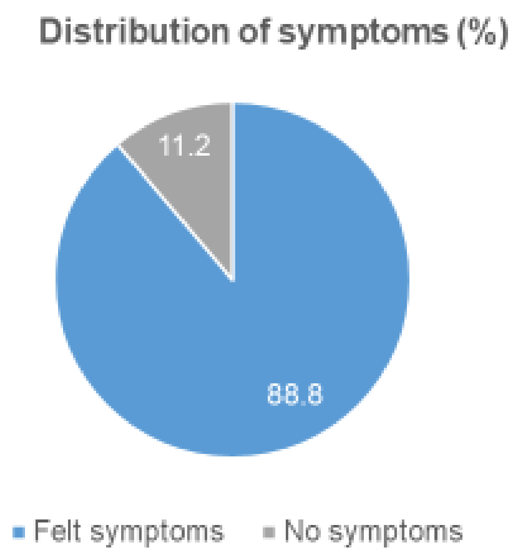


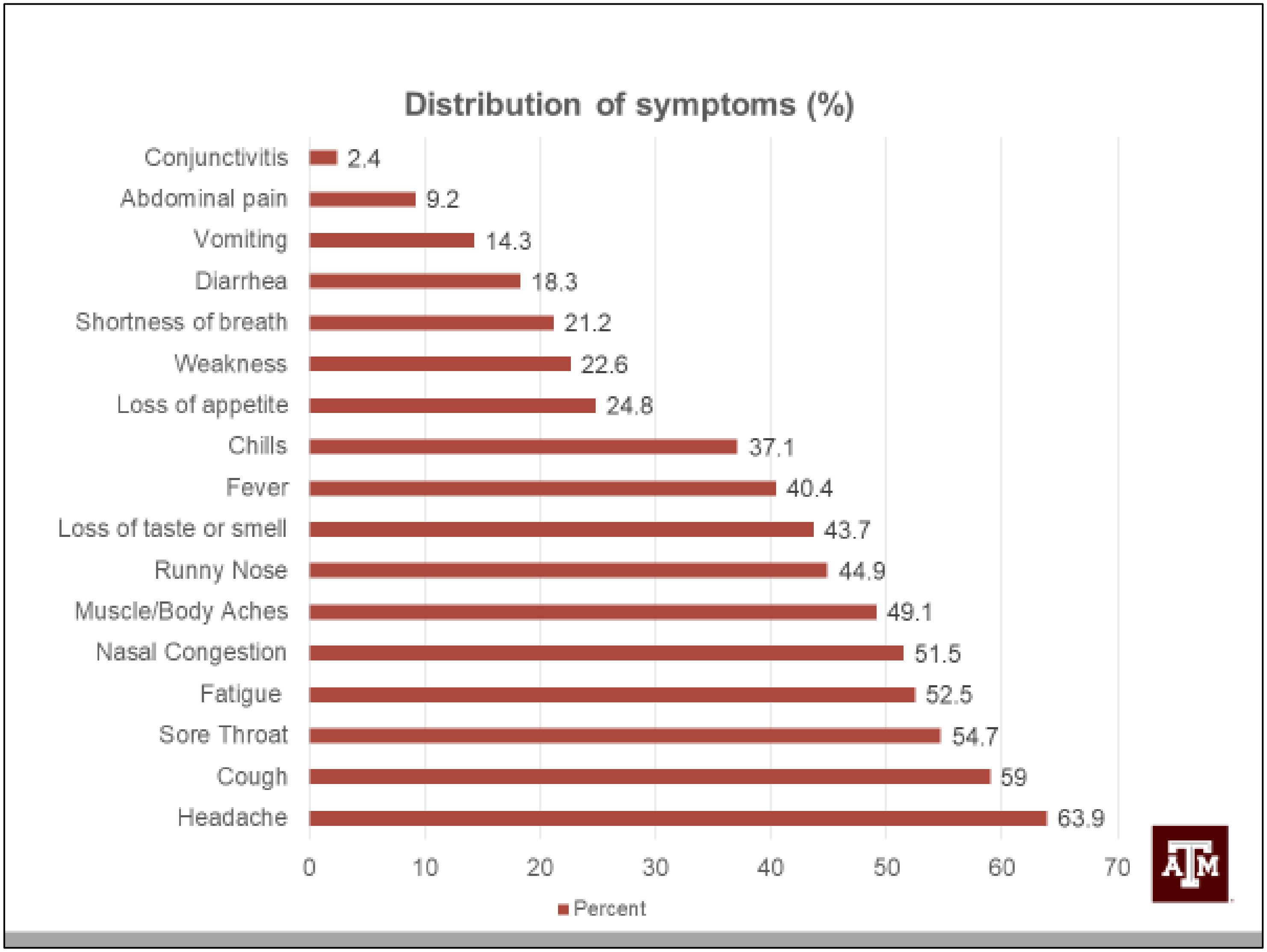


Clinical presentation

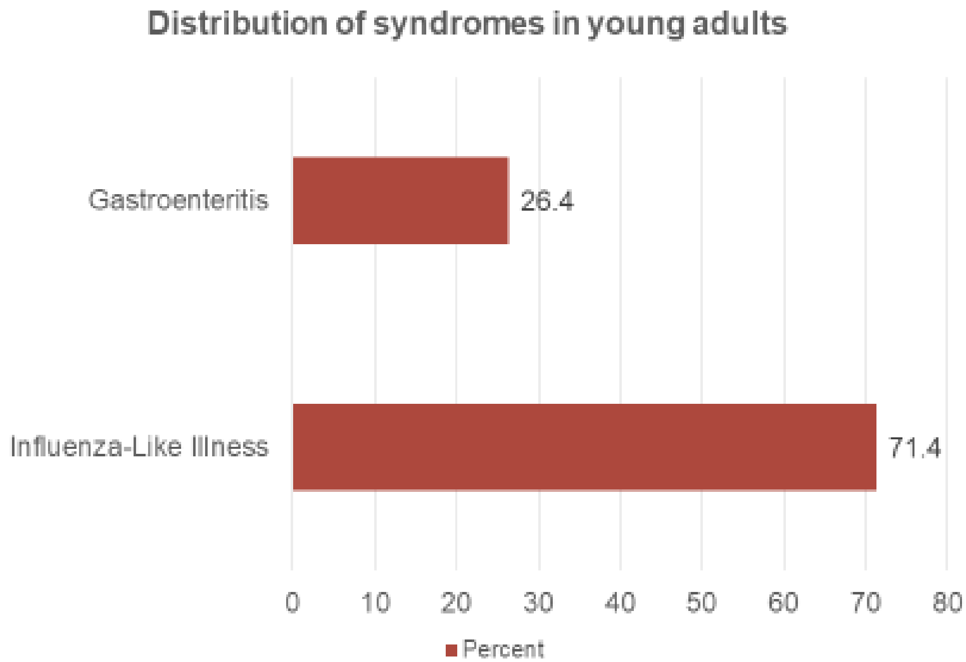
Symptom status

- Most young adults had some symptoms of illness, despite often being characterized as having a sense of invincibility[2,3].



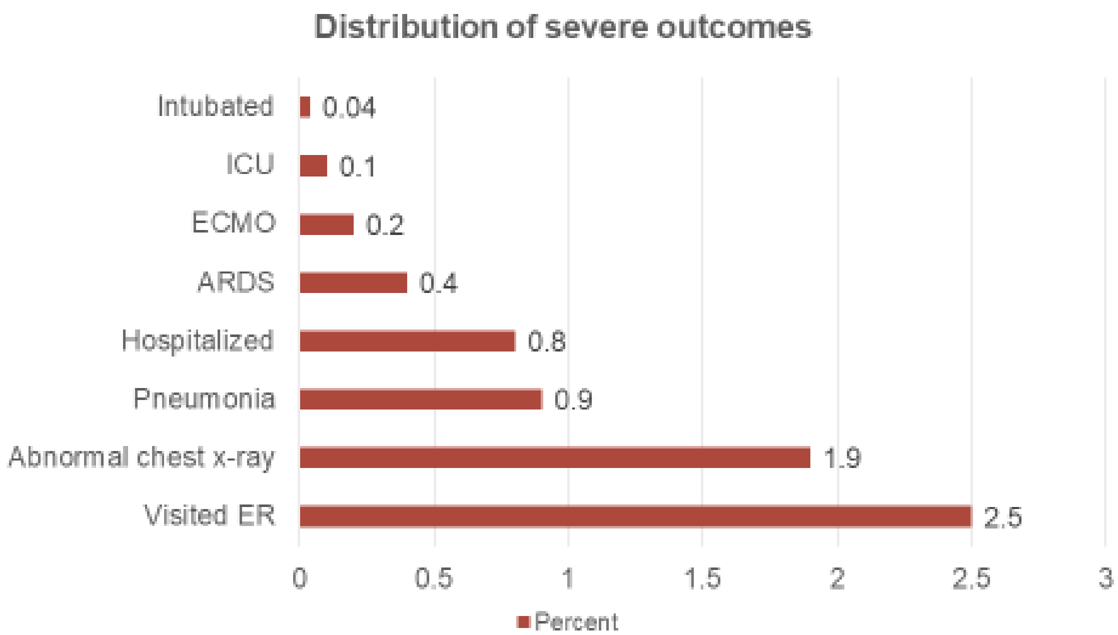

Distribution of symptoms (%)
Conjunctivitis
Abdominal pain
Vomiting
Diarrhea
Shortness of breath
Weakness
Loss of appetite
Chills
Fever
Loss of taste or smell
Runny Nose
Muscle/Body Aches
Nasal Congestion
Fatigue
Sore Throat
Cough
Headache
2.4
9.2
14.3
18.3
21.2
22.6
24.8
37.1
40.4
43.7
44.9
49.1
51.5
52.5
54.7
59
63.9
0
10
20
30
40
50
60
70
Percent

- Influenza-like illness (ILI) defined as having fever greater than 100ºF, cough, and/or sore throat.
- Gastroenteritis defined as having diarrhea and/or vomiting
- Gastrointestinal symptoms were not common in young adults (73.7%)



Severe outcomes

- Young adults were not exempt from severe outcomes of COVID-19



ECMO: Extracorporeal membrane oxygenation
ARDS: Acute respiratory distress syndrome

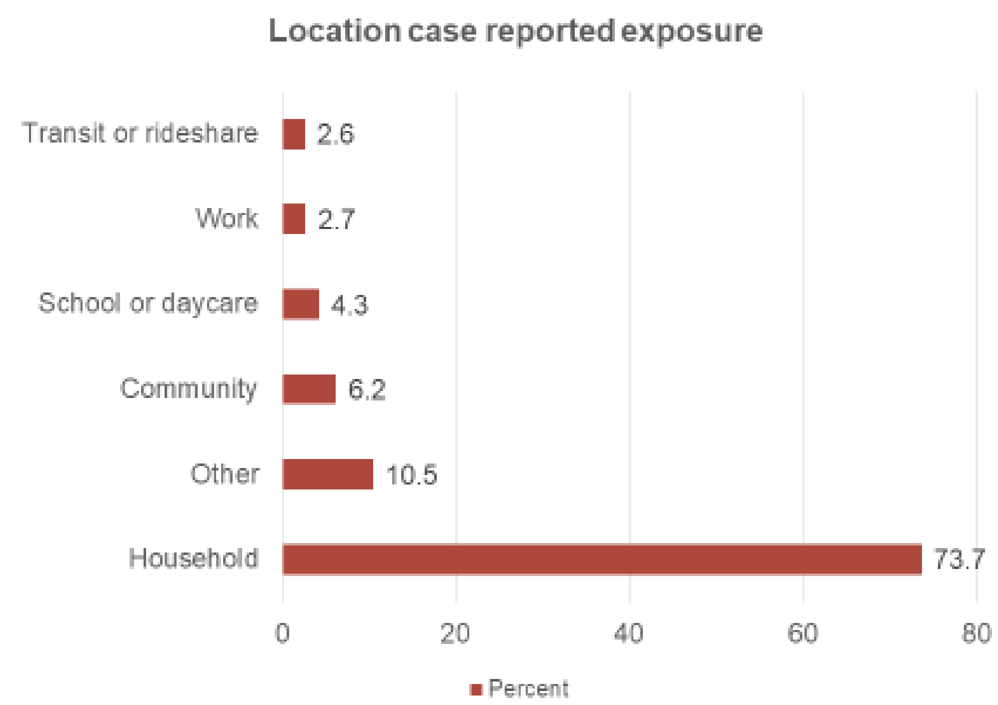
Case fatality in Brazos County

- Overall case fatality for this set of data was 1.26%
- Case fatality rate for young adult subset was 2/10704 = 0.02%

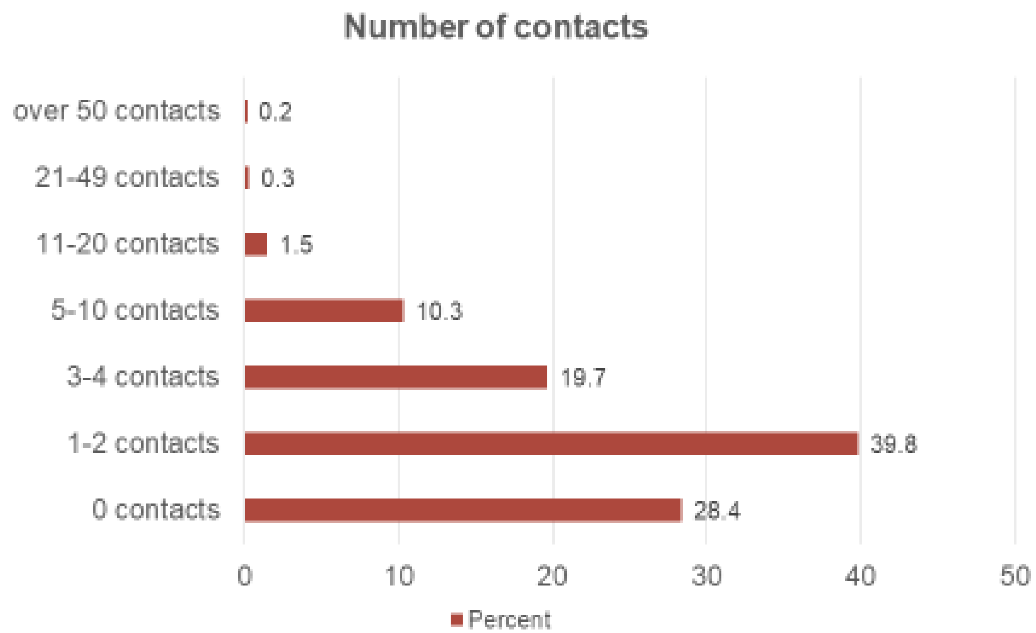
- Observed case fatality rate for the U.S. population is estimated at 1.2%[4]
- Approximate case fatality rate for U.S. young adults is 0.04%[5,6]

Select Behaviors and other Risk Factors

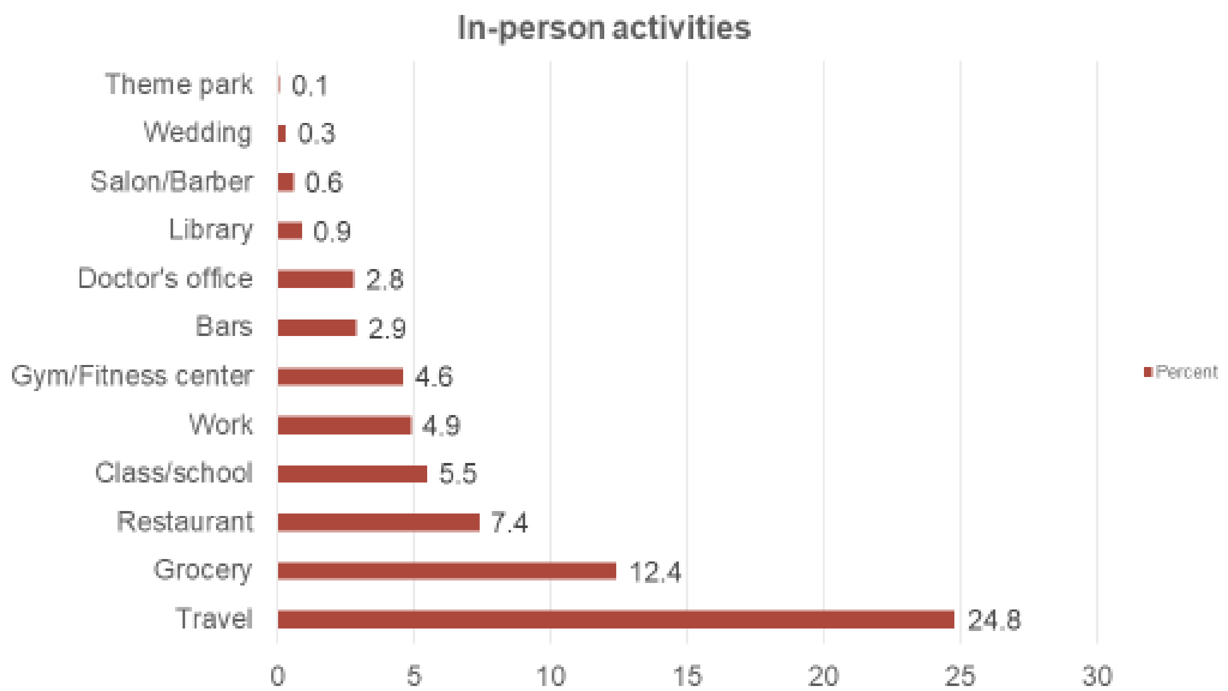
Where did the case report exposure?



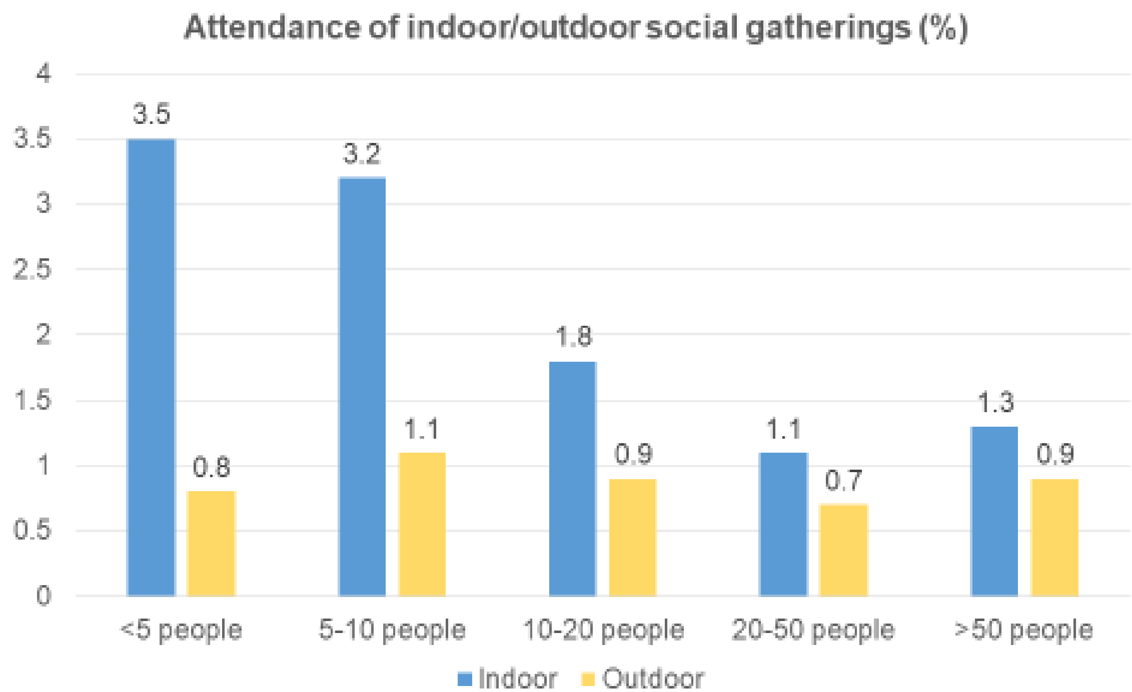
How many close contacts did young adults have?



Did young adults attend in-person activities?

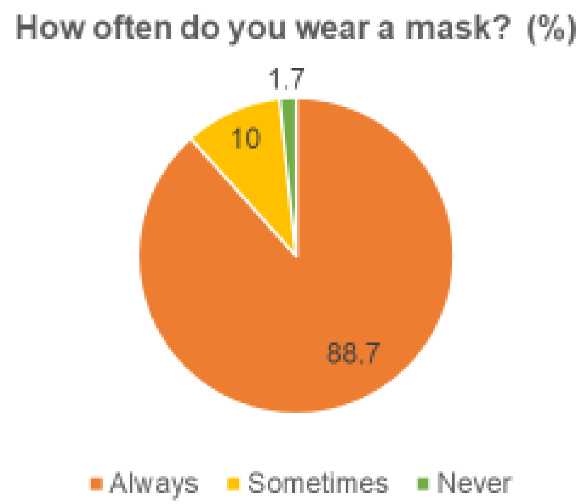


Did young adults attend in-person social gatherings?



How often do young adults wear a face mask (outside of the home) 7 days prior to symptom onset or positive test?

- Total young adult respondents: 2,788
- Only 19.3% of young adults in the data responded
- Majority reported always wearing a mask.



Strengths

- Potentially enriched young adult population
- University testing & reporting strategies means that even asymptomatic individuals could be tested and included in this analysis
- Interagency partnership meant capacity to investigate cases maximize
- Secure data entry, storage, analysis, transfers supported by TAMU SPH, Administration, IT
- Information on individual cases were NOT reported back to TAMU, meaning that BCHD confidentiality was maintained (unidirectional information flow)
- Situational awareness provided by epidemiology experts at TAMU & BCHD

Continuing research

- Analysis of full COVID-19 case database
- Identifying predictors for severe COVID-19 outcomes
- Analysis of close contact database
- Determining predictors for testing for SARS-CoV-2 in the recommended window

Limitations

- Difficulty reaching cases on the phone
- Participant bias
  - Young adults may have answered questions based on what they believed the investigator wanted to hear.
  - Fear of providing information to CoOp linked to school
  - Fear of providing personal details to an unknown entity
  - Don't know their county of 'residence'
- Potential underreporting
  - Fear of being quarantined/isolated
  - Fear of stigma
- Not testing
  - Lack of awareness on symptoms
  - Lack of familiarity with free test availability
  - Misinformation about types of tests and utility of each
  - Fear of testing positive
  - Inability to be contact traced and learn of exposure

Conclusions

- Similar to what is reported for the US in general, most infections were reported in young adults.
- Majority of young adults here did not participate in specific high-risk behaviors for virus transmission
  - Most reported wearing masks and having few close contacts during the time period analyzed
- Rarely identified as having asymptomatic COVID
  - Contrary to generalization that young adults are least affected by COVID, they bear most of the infections and most manifest symptoms, suggesting young adults account for a high proportion of COVID illnesses
  - If most infections result during symptomatic illness, this age group could be contributing to a substantial proportion of transmission
- There is limited evidence in this study for young adult social behaviors contributing to transmission.
- Cases largely referenced that they traced their exposures to their own households/homes, rather than other locations, such as school or work.
- Precautions, such as those implemented at Texas A&M and other schools and universities can help limit spread in that setting

References

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2. Brar, E., Saxena, A., Dukler, C., Xu, F., Saxena, D., Brar, P. C., ... & Li, X. (2021). Vaping, SARS-CoV-2, and multisystem inflammatory syndrome: a perfect storm. Frontiers in Pediatrics, 9.
3. Tam, C. C., Qiao, S., & Li, X. (2022). Factors associated with decision making on COVID-19 vaccine acceptance among college students in South Carolina. Psychology, Health & Medicine, 27(1), 150-161.
4. John Hopkins Coronavirus Resource Center. 2022. Mortality Analyses. https://coronavirus.jhu.edu/data/mortality
5. Centers for Disease Control and Prevention. 2022. Weekly Updates by Select Demographic and Geographic Characteristics. https://www.cdc.gov/nchs/nvss/vsrr/covid_weekly/index.htm#SexAndAge
6. Statista. 2022. Total number of COVID-19 cases by age U.S. 2022. https://www.statista.com/statistics/1254271/us-total-number-of-covid-cases-by-age-group/

Questions?

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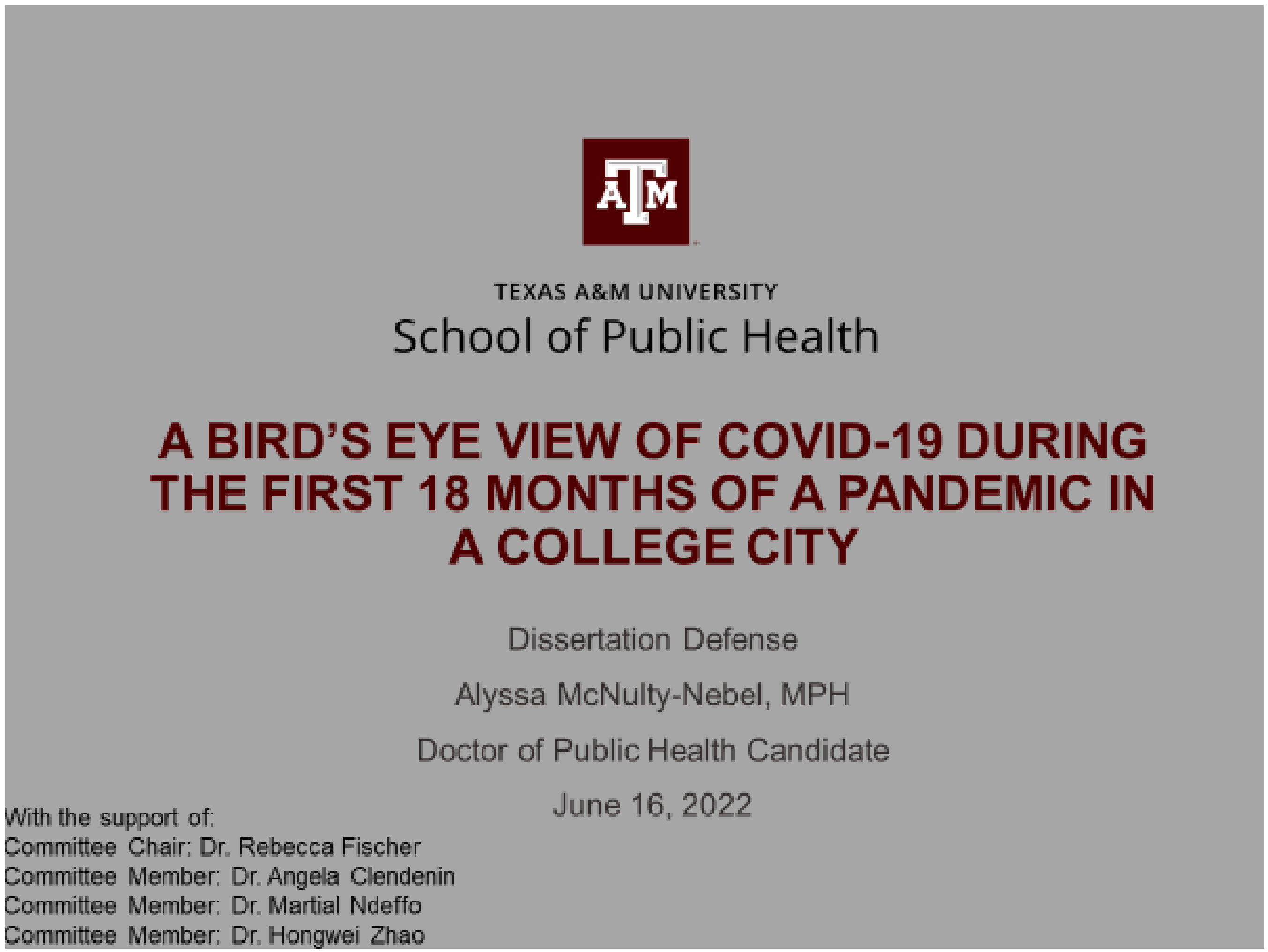
For correspondence, please contact Dr. Rebecca Fischer at rfischer@tamu.edu

A.9 Defense presentation



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Outline

- Introduction
- Chapter 1: Behaviors, Severity, and Symptoms of Cases, oh my!
- Chapter 2: Contact Tracing and Testing of COVID-19, Which Came First?
- Chapter 3: Mathematical Modelling of COVID-19 in a University City
- Future research/next steps
- Conclusions
- Acknowledgements
- Questions

Introduction

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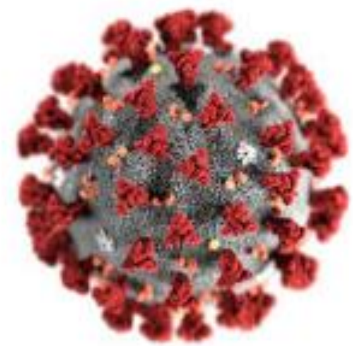
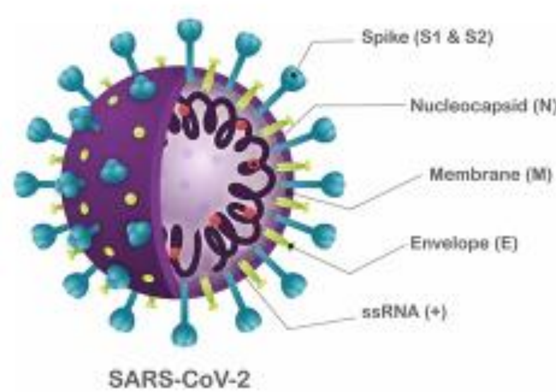
Origins of the virus



- Coronaviruses (CoV) are a family of viruses
  - All have an enveloped single-stranded RNA genome
- Main types of coronaviruses:
  - Severe acute respiratory virus (SARS), well-known for an outbreak in 2002-2003 in China
  - Middle eastern respiratory virus (MERS), first known case was in Jordan, 2012
  - Severe acute respiratory virus 2 (SARS-CoV-2), originated in Wuhan province of China in December 2019



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Disease caused by SARS-CoV-2

- Coronavirus disease 2019 (COVID-19)
- Pandemic caused by COVID-19 was declared on March 11, 2020 by WHO
- Spread through respiratory droplets containing virus
  - Can be transferred if droplets are breathed in, come in close contact with someone who has it, or touch a surface with virus on it

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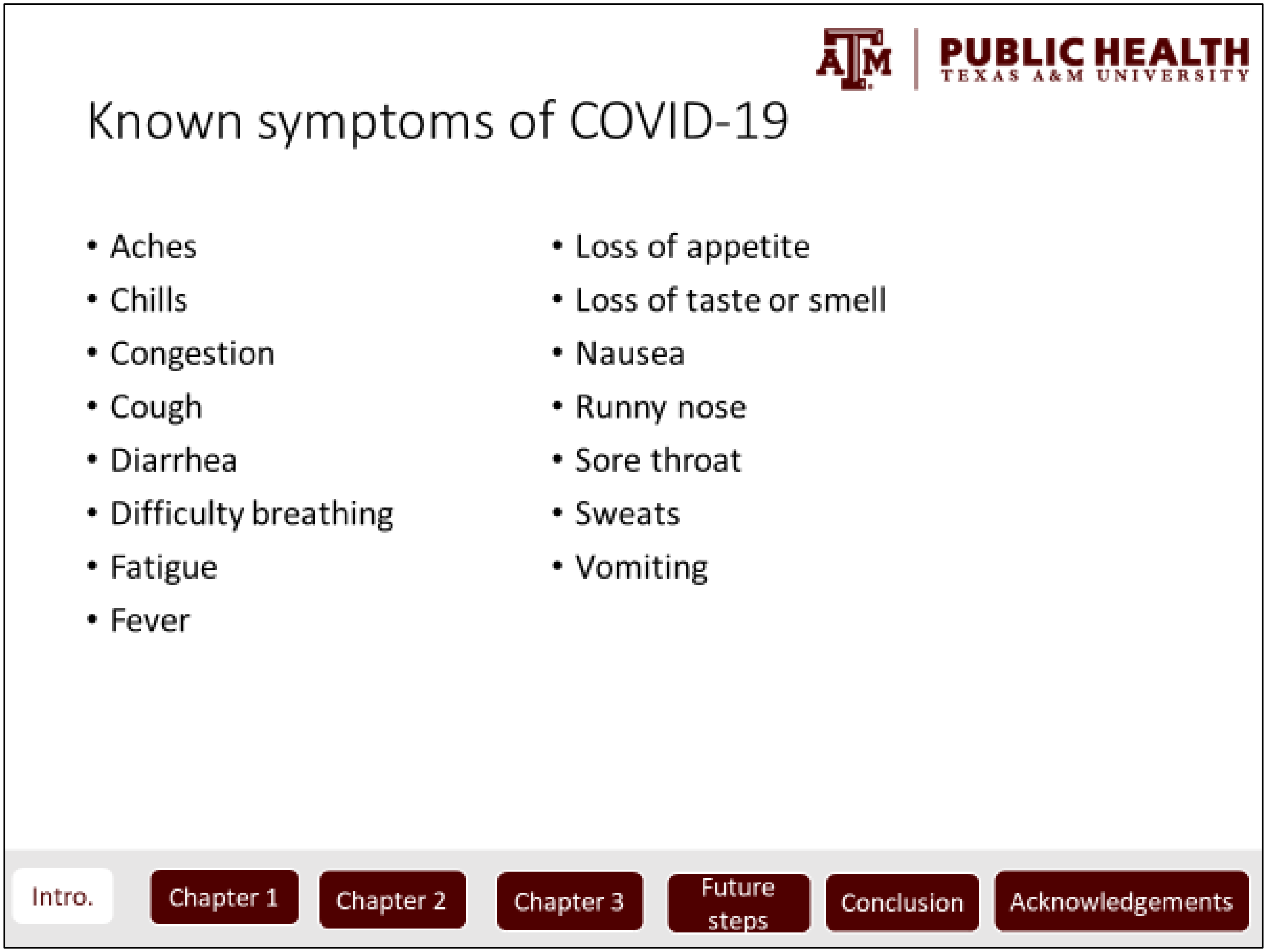
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Known symptoms of COVID-19
• Aches
• Chills
• Congestion
• Cough
• Diarrhea
• Difficulty breathing
• Fatigue
• Fever
• Loss of appetite
• Loss of taste or smell
• Nausea
• Runny nose
• Sore throat
• Sweats
• Vomiting
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Ways to get tested for COVID-19

- Polymerase chain reaction (PCR)
  - Uses a cheek or nasal swab
  - Detects genetic material (RNA) of the virus
  - Gold-standard to identify an acute infection

- Rapid antigen test
  - Uses a cheek or nasal swab
  - Detects proteins on the virus particles

- Antibody test
  - Uses a small blood sample
  - Detects antibodies produced by the individual in response to the virus
  - Does not identify an acute, current infection

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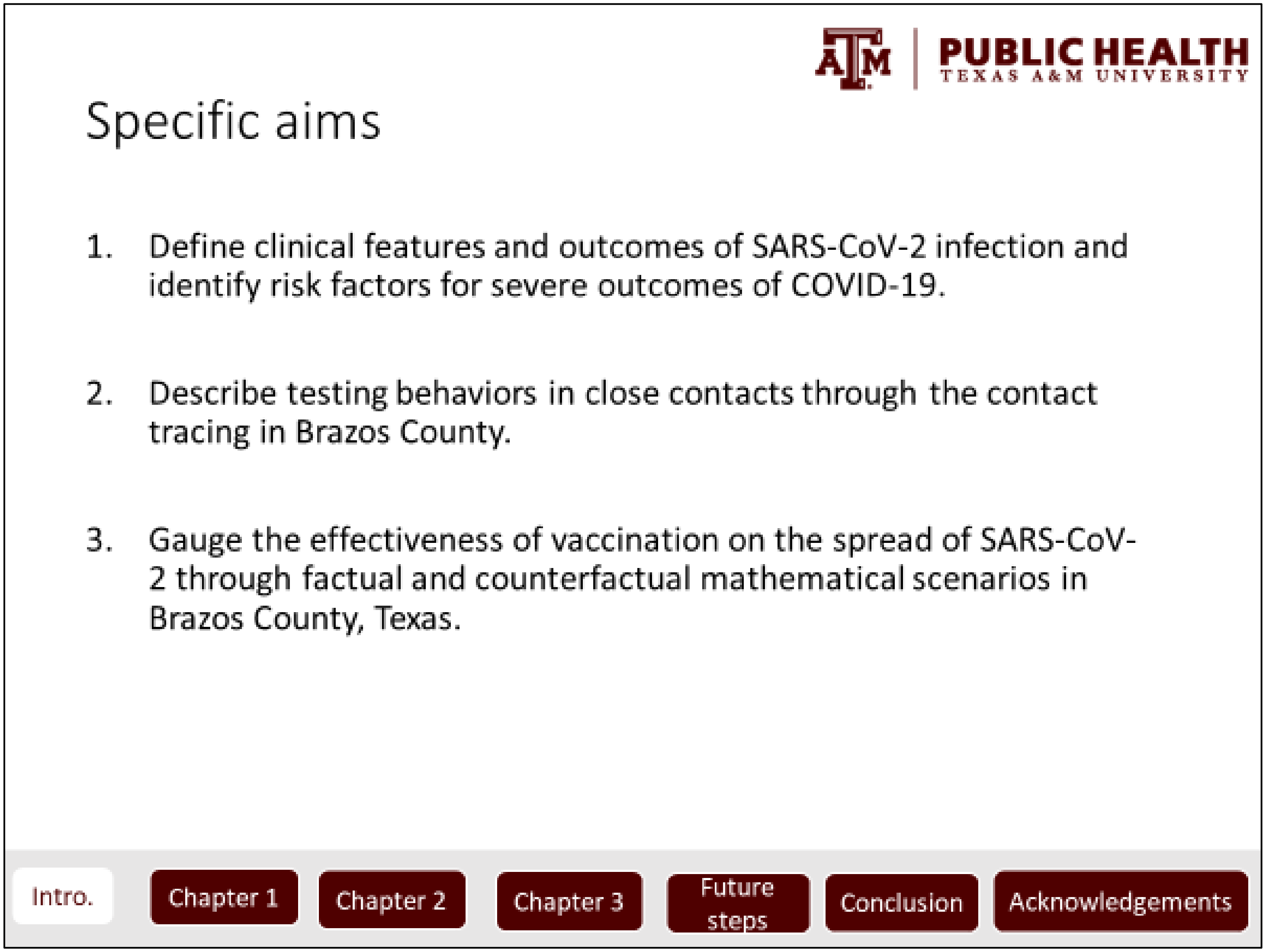
Why get tested for COVID-19?

- PCR and rapid antigen tests allow for identifying current infections
- Identifying current infections can aid in public health measures such as:
  - Outbreak identification
  - Contact tracing
  - Isolation guidelines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Specific aims
1. Define clinical features and outcomes of SARS-CoV-2 infection and identify risk factors for severe outcomes of COVID-19.
2. Describe testing behaviors in close contacts through the contact tracing in Brazos County.
3. Gauge the effectiveness of vaccination on the spread of SARS-CoV-2 through factual and counterfactual mathematical scenarios in Brazos County, Texas.
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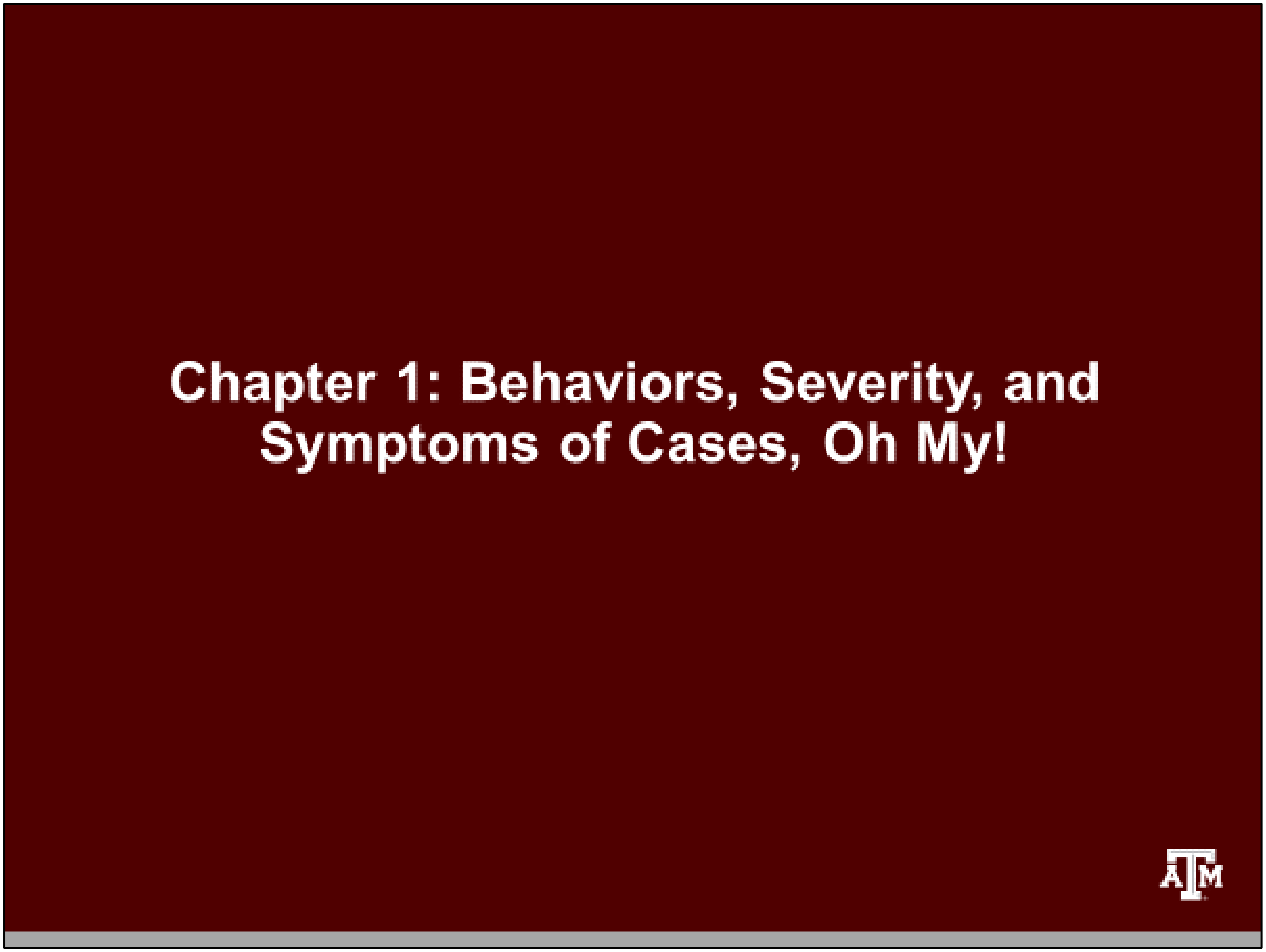
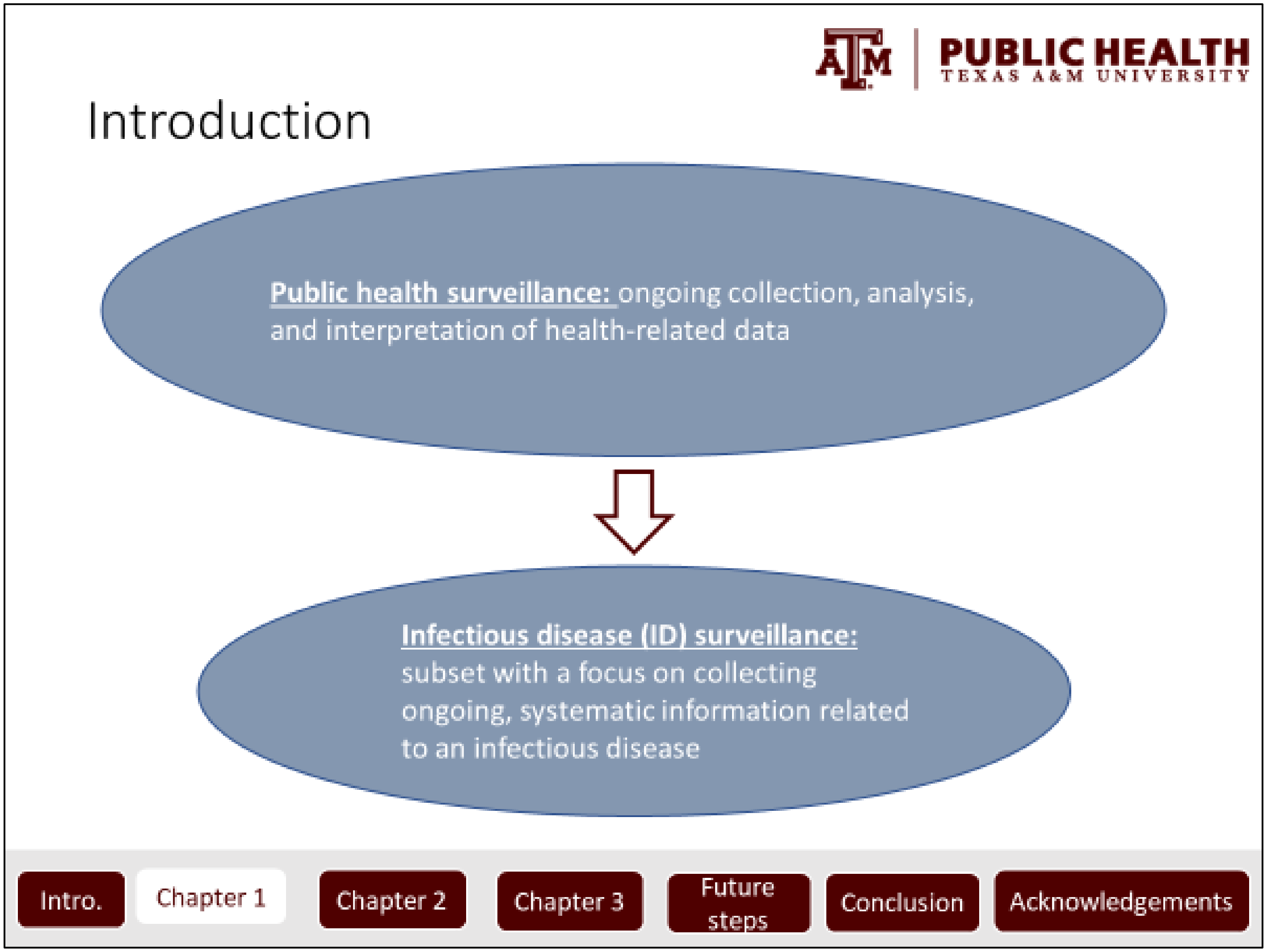

Chapter 1: Behaviors, Severity, and
Symptoms of Cases, Oh My!


PUBLIC HEALTH
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Introduction
Public health surveillance: ongoing collection, analysis, and interpretation of health-related data
Infectious disease (ID) surveillance: subset with a focus on collecting ongoing, systematic information related to an infectious disease
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Case definitions for COVID-19

- Confirmed case – meets confirmatory laboratory evidence
  - PCR test
  - Or SARS-CoV-2 found through genomic sequencing
- Probable case – meets presumptive laboratory evidence (positive antigen test)
  - Or meets vital records criteria with no positive PCR test
  - Or meets clinical AND epidemiologic linkage with no positive PCR or rapid antigen test
- Suspect case – meets supportive laboratory evidence with no history of being confirmed or probable case
  - Positive antibody test
  - Or detecting viral antigen in autopsy

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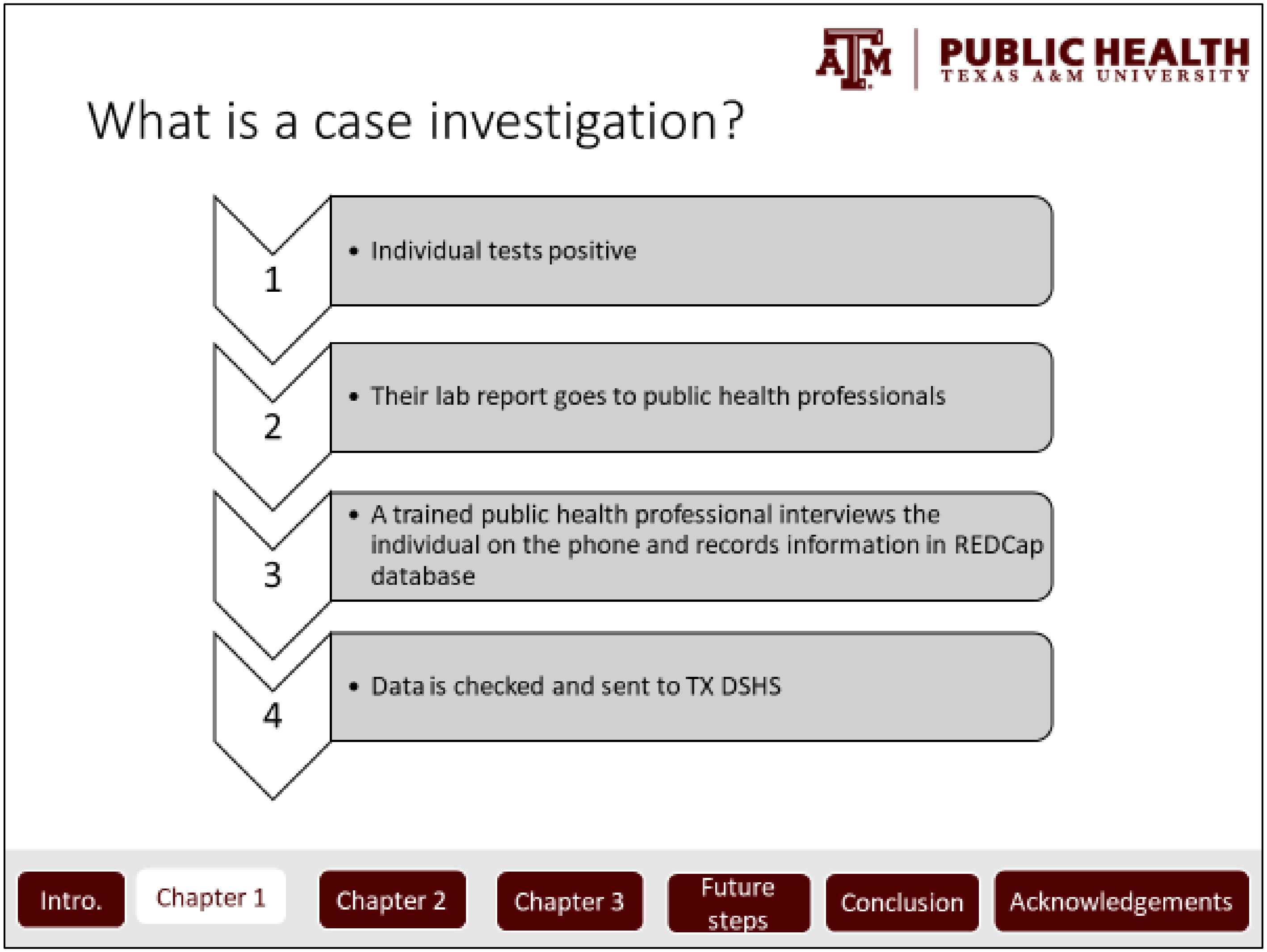
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What is a case investigation?
1
• Individual tests positive
2
• Their lab report goes to public health professionals
3
• A trained public health professional interviews the individual on the phone and records information in REDCap database
4
• Data is checked and sent to TX DSHS
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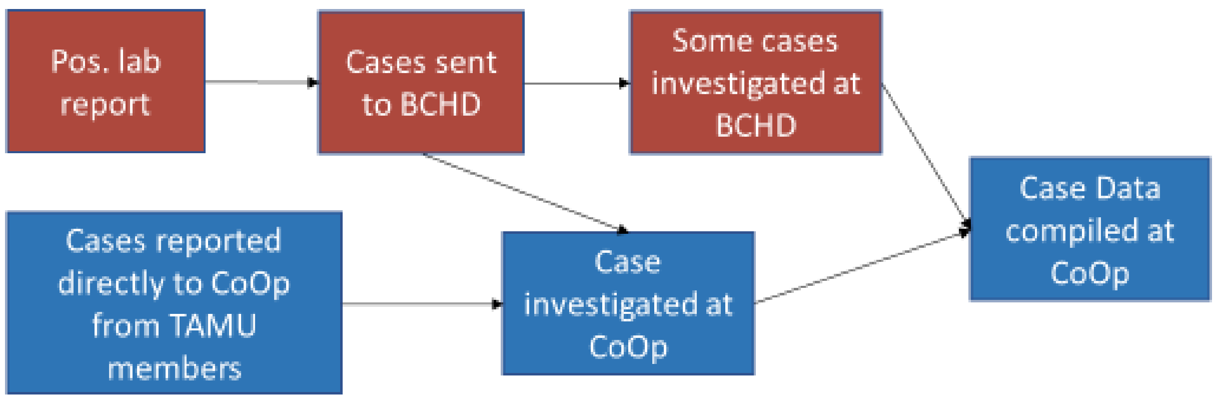
Interagency cooperation

- Brazos County Health Department (BCHD) partnered with Texas A&M University (TAMU) to respond to COVID locally
- COVID-19 Operations (CoOp) was created by TAMU Public Health faculty in cooperation with other university partners, BCHD, TX Workforce Commission
- Case investigators were located at both BCHD and CoOp
- Situational awareness between CoOp, TAMU, and BCHD



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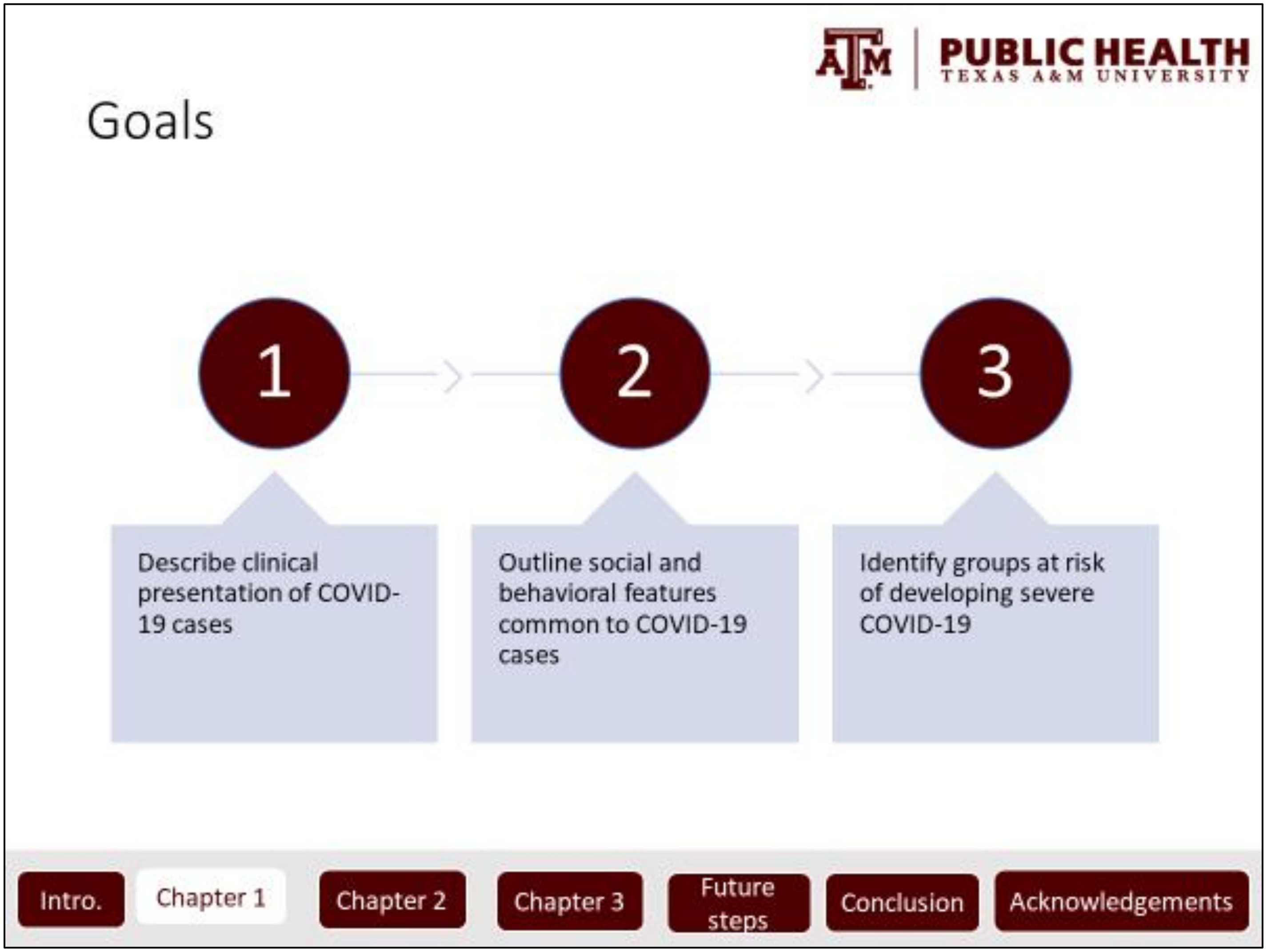
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Goals
1
2
3
Describe clinical presentation of COVID-19 cases
Outline social and behavioral features common to COVID-19 cases
Identify groups at risk of developing severe COVID-19
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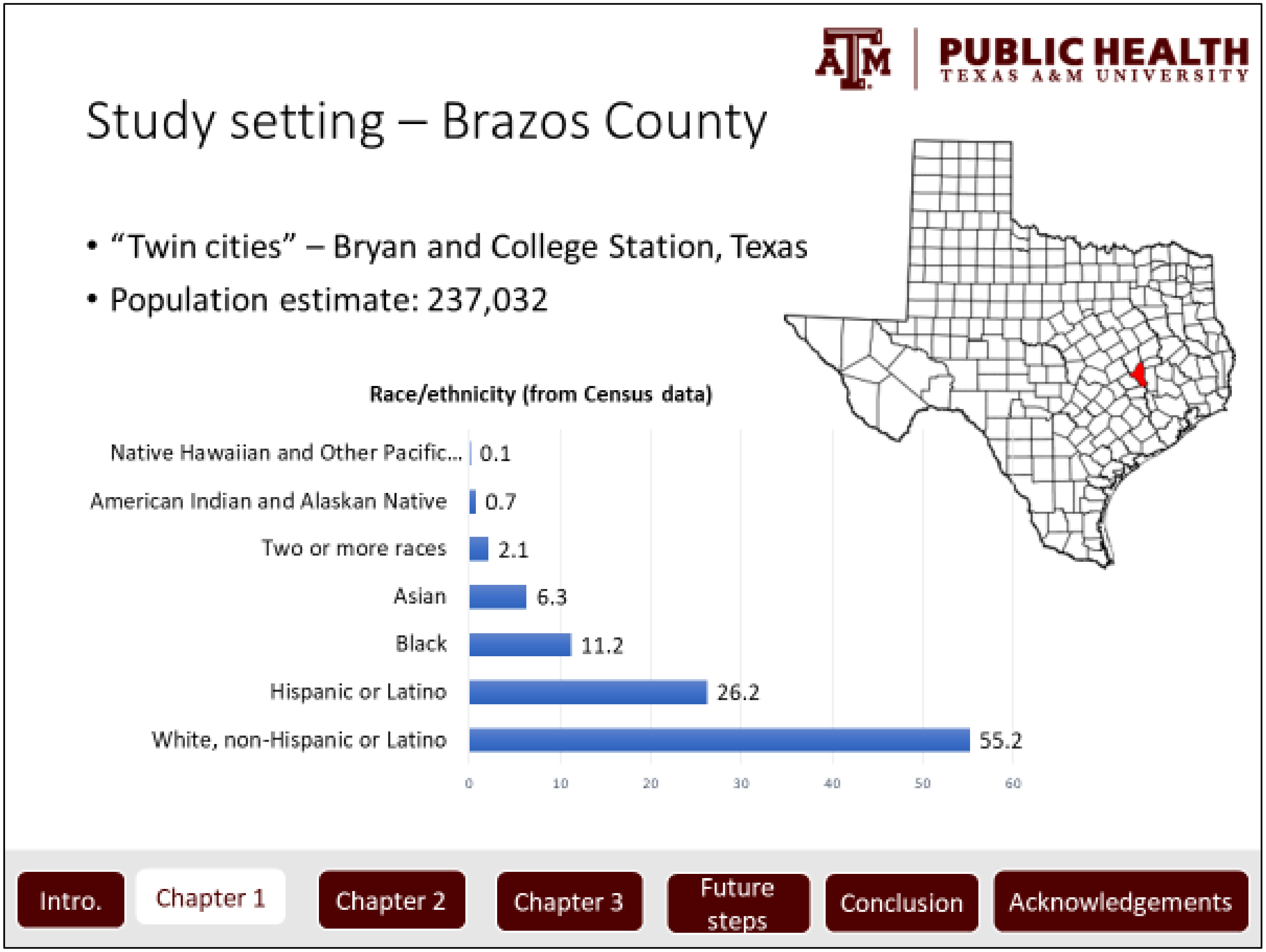
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Study setting – Brazos County
• "Twin cities" – Bryan and College Station, Texas
• Population estimate: 237,032
Race/ethnicity (from Census data)
Native Hawaiian and Other Pacific... 0.1
American Indian and Alaskan Native 0.7
Two or more races 2.1
Asian 6.3
Black 11.2
Hispanic or Latino 26.2
White, non-Hispanic or Latino 55.2
0
10
20
30
40
50
60
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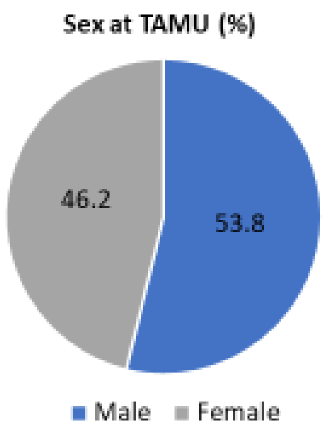
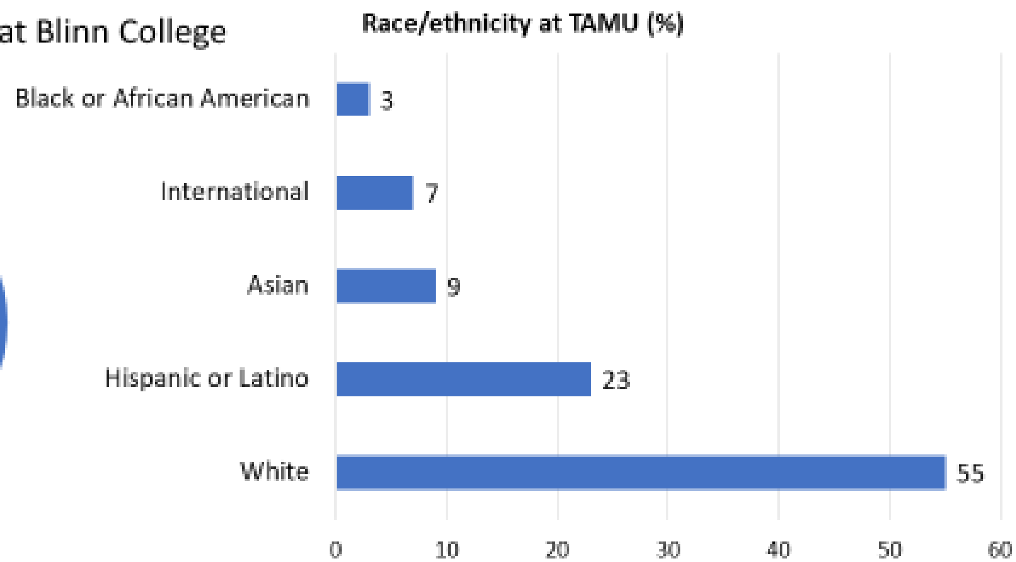
Study setting

- BCS is home to Texas A&M University (College Station) and Blinn College (Bryan)
    - 67,133 students at A&M as of Fall 2021
    - 26,000 faculty and staff
    - 6,000 students at Blinn College





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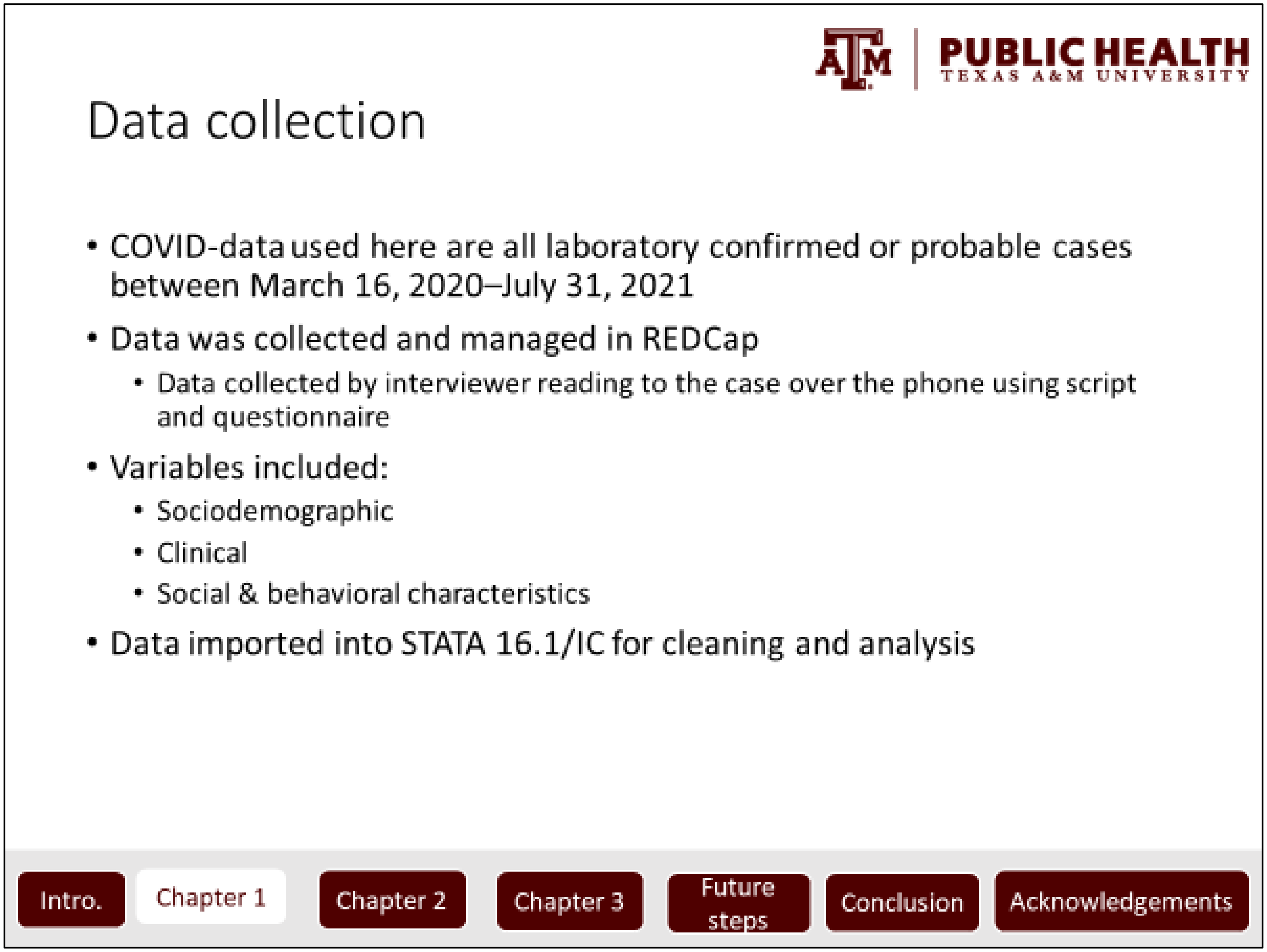
PUBLIC HEALTH
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Data collection
• COVID-data used here are all laboratory confirmed or probable cases between March 16, 2020–July 31, 2021
• Data was collected and managed in REDCap
• Data collected by interviewer reading to the case over the phone using script and questionnaire
• Variables included:
• Sociodemographic
• Clinical
• Social & behavioral characteristics
• Data imported into STATA 16.1/IC for cleaning and analysis
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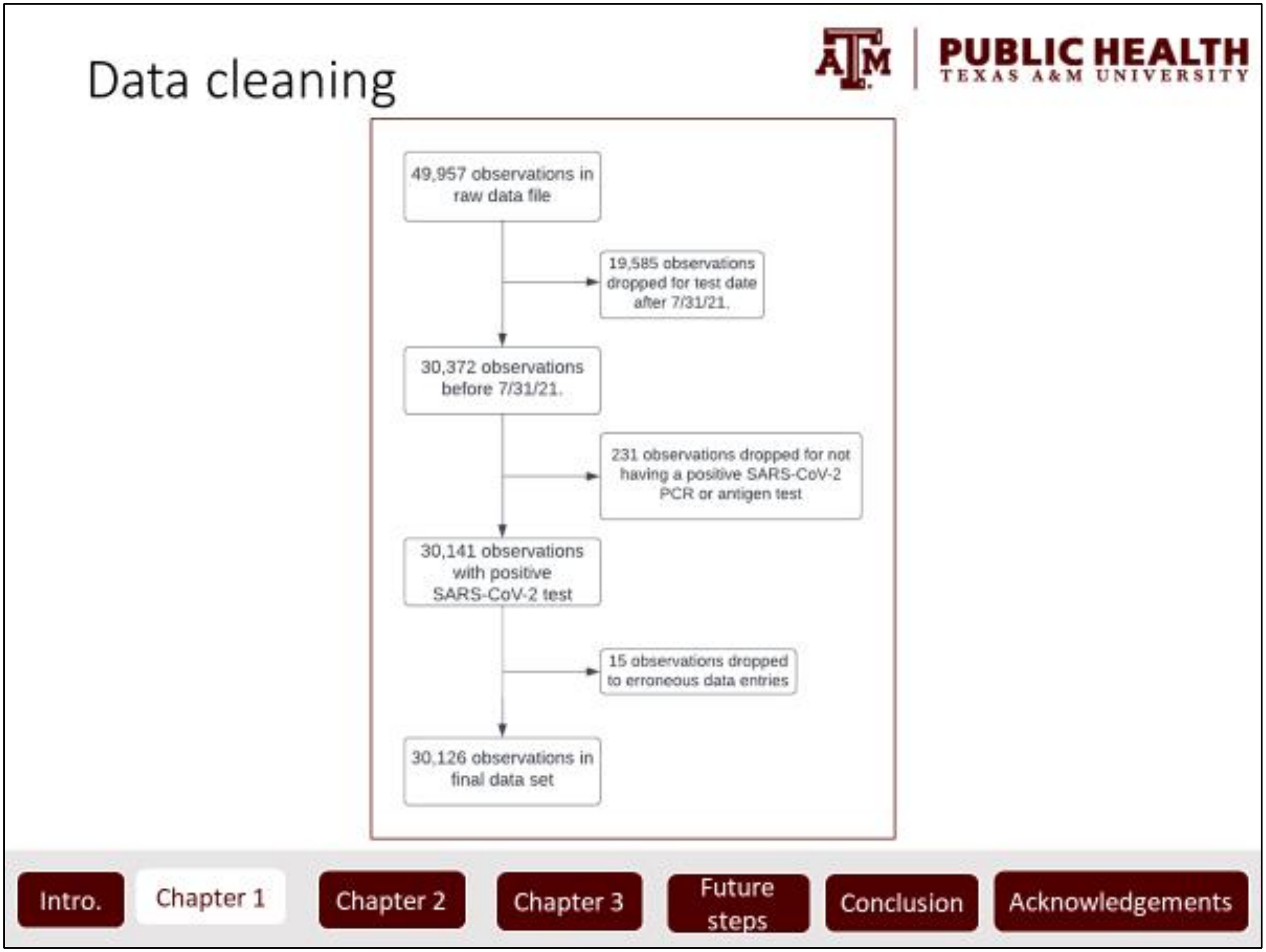
Data cleaning
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49,957 observations in raw data file
19,585 observations dropped for test date after 7/31/21.
30,372 observations before 7/31/21.
231 observations dropped for not having a positive SARS-CoV-2 PCR or antigen test
30,141 observations with positive SARS-CoV-2 test
15 observations dropped to erroneous data entries
30,126 observations in final data set
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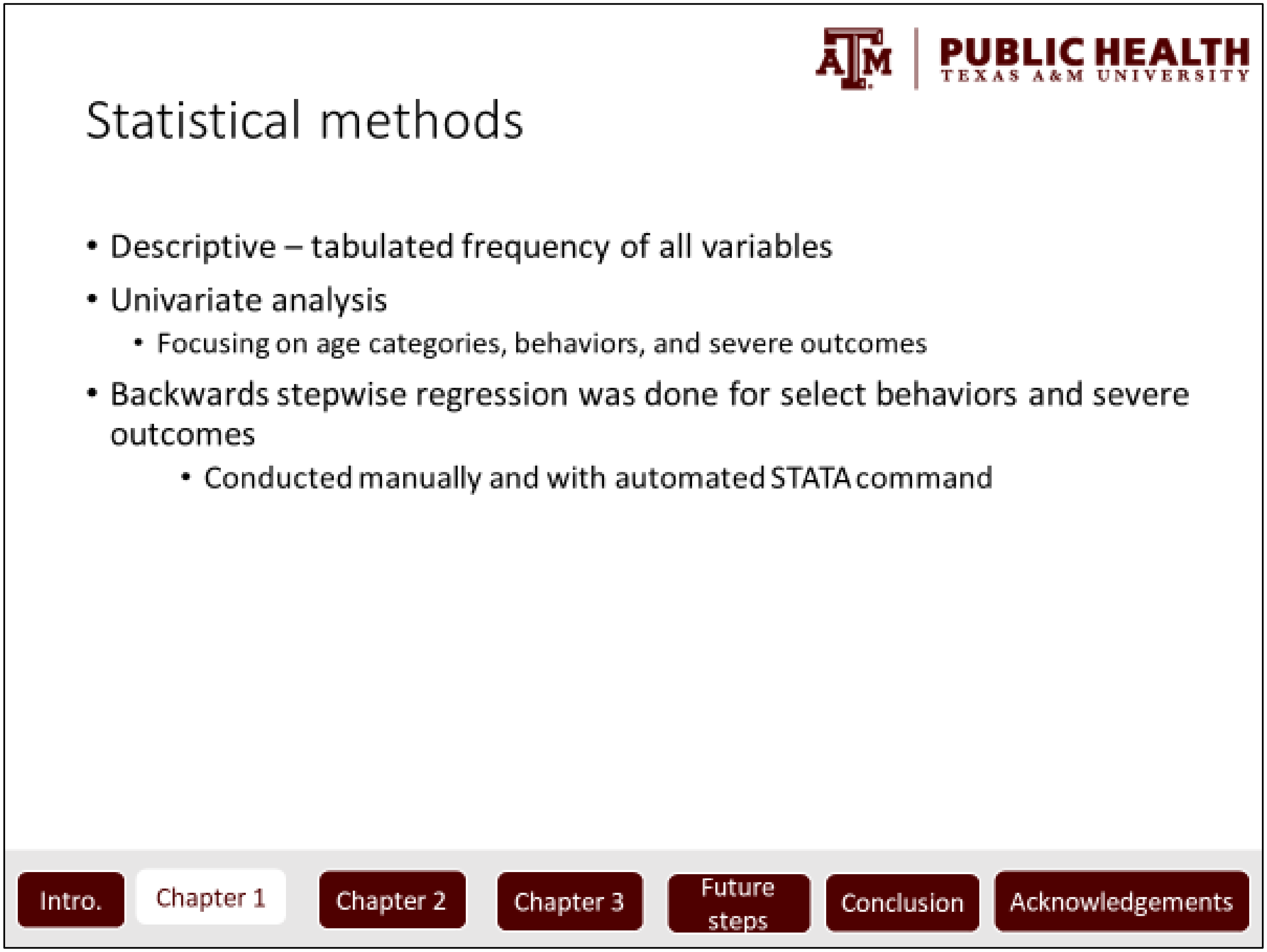
Data analysis

- Age at infection calculated by subtracting test date from date of birth
  - Calculated age used to create age categories
- *Do not know* or *unknown* responses were marked missing
- Syndromes were defined and coded based on clinical definitions
  - Influenza-like illness (ILI): fever greater than 100°F, cough, and/or sore throat
  - Gastroenteritis: diarrhea and/or vomiting
  - Severe COVID: hospitalized, admitted to an intensive care unit (ICU), or intubated
- Incubation period estimated from test date and symptom onset date
  - Not calculated accurately due to no exposure date
- Duration of illness calculated as time between symptom resolution and symptom onset date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Statistical methods
• Descriptive – tabulated frequency of all variables
• Univariate analysis
• Focusing on age categories, behaviors, and severe outcomes
• Backwards stepwise regression was done for select behaviors and severe outcomes
• Conducted manually and with automated STATA command
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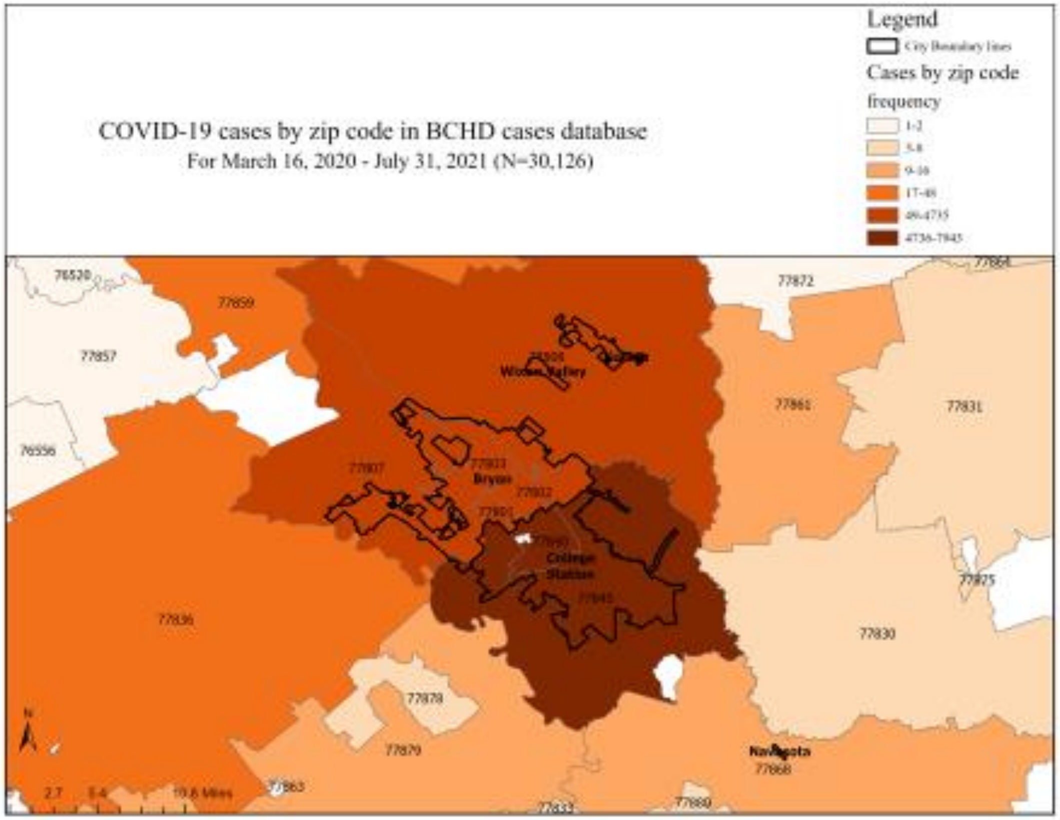
Location of cases



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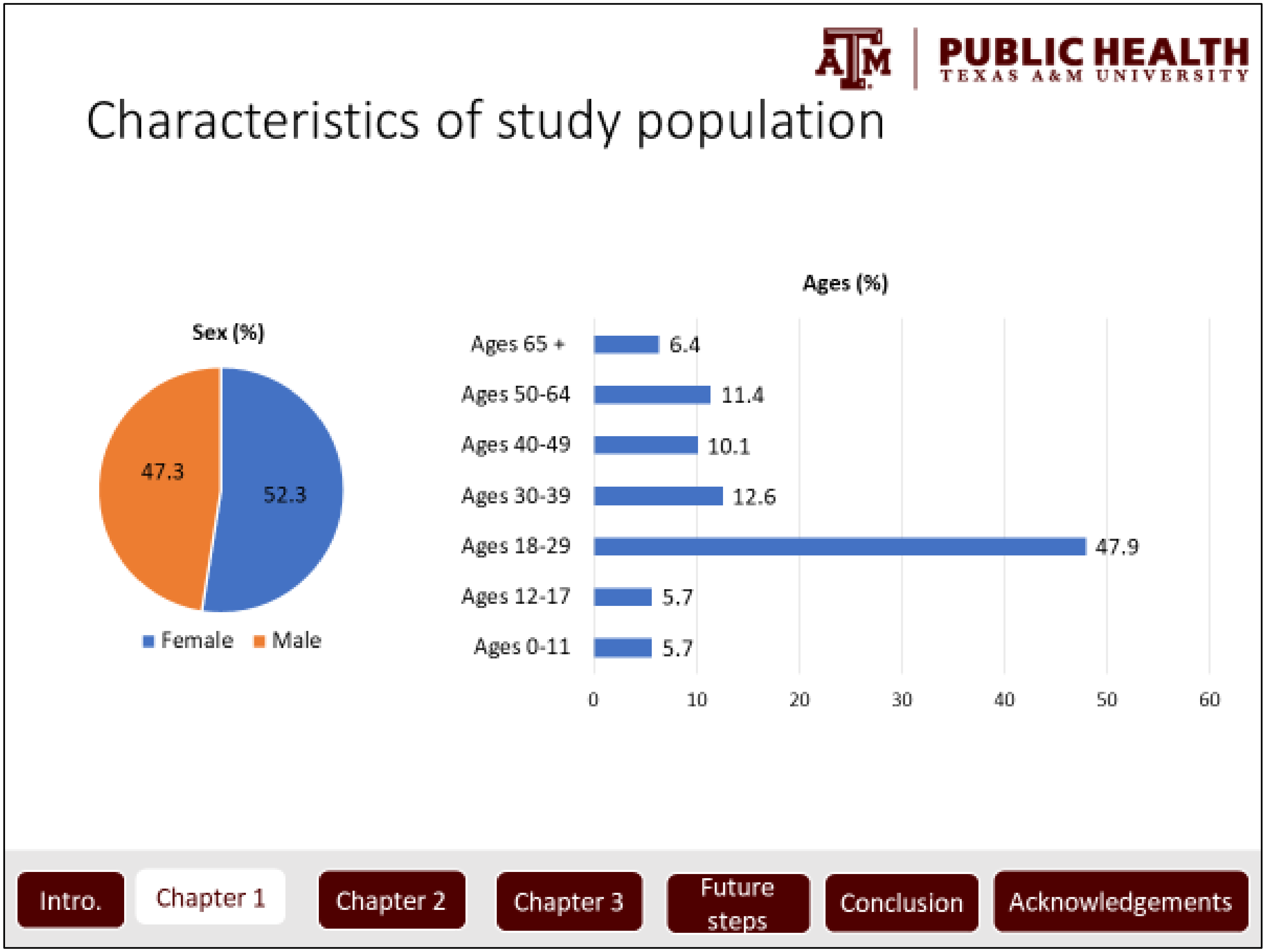
ATM | PUBLIC HEALTH
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Characteristics of study population
Sex (%)
47.3
52.3
Female
Male
Ages (%)
Ages 65 +
6.4
Ages 50-64
11.4
Ages 40-49
10.1
Ages 30-39
12.6
Ages 18-29
47.9
Ages 12-17
5.7
Ages 0-11
5.7
0
10
20
30
40
50
60
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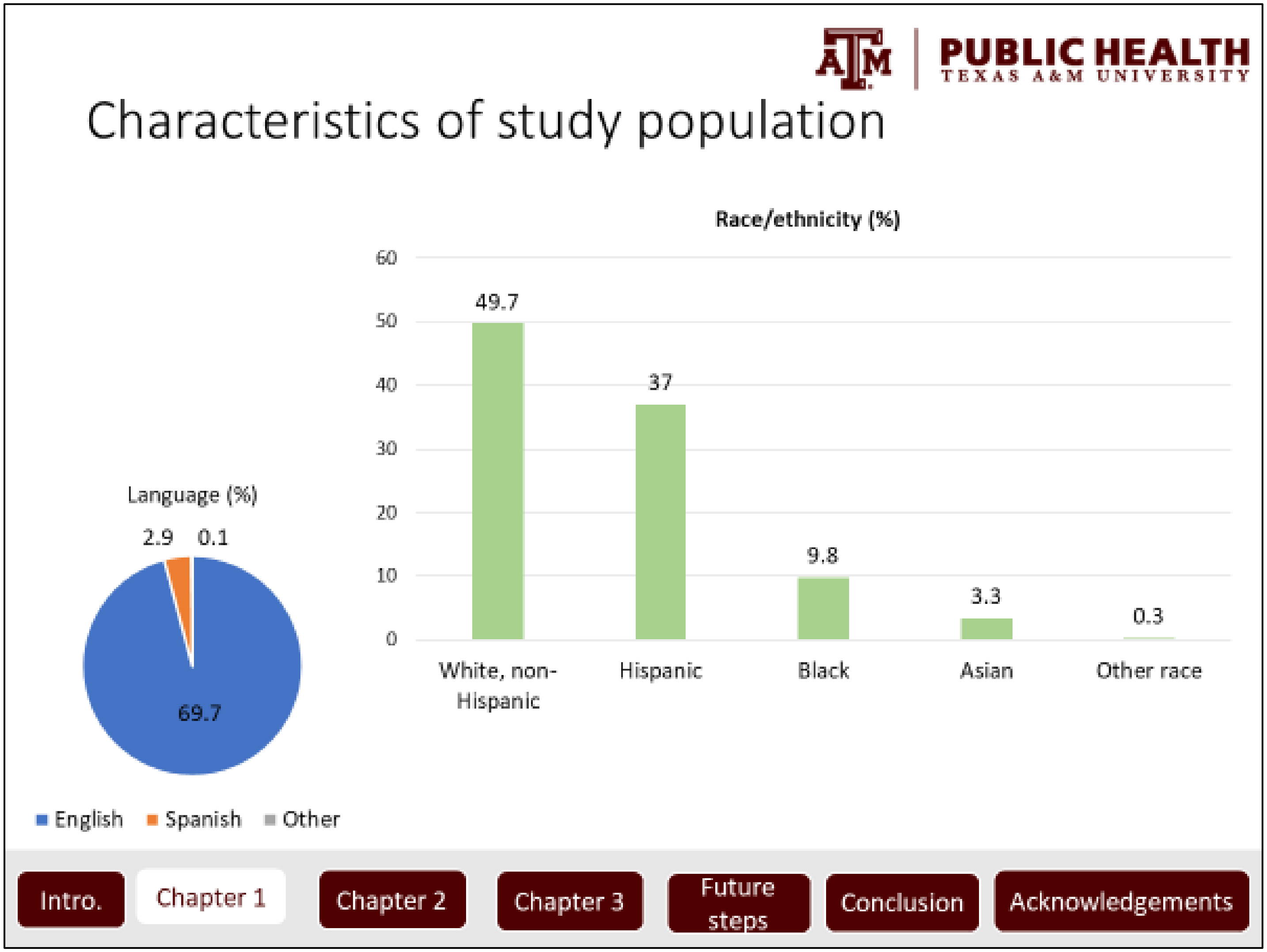
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Characteristics of study population
Race/ethnicity (%)
60
50
40
30
20
10
0
49.7
37
9.8
3.3
0.3
White, non-Hispanic
Hispanic
Black
Asian
Other race
Language (%)
2.9
0.1
69.7
English
Spanish
Other
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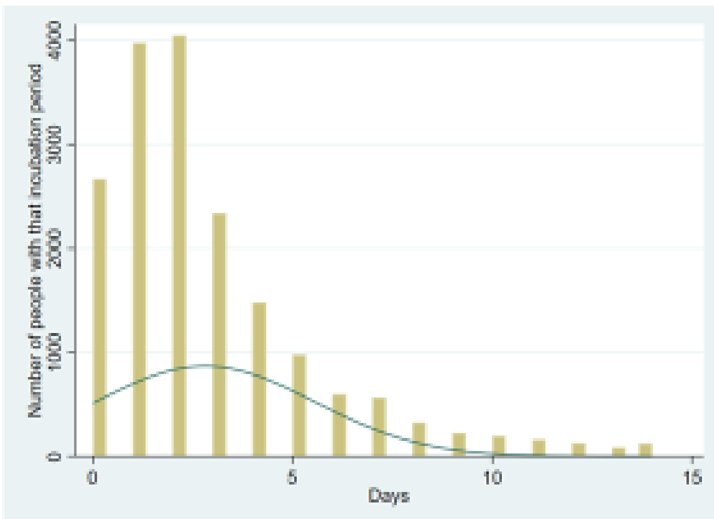
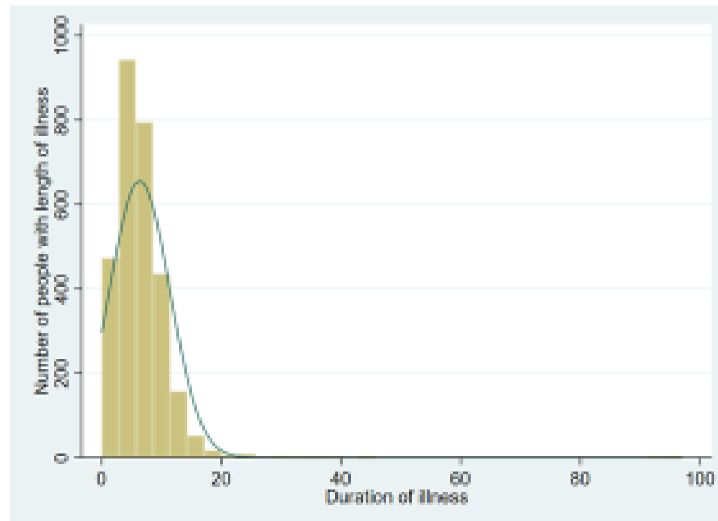
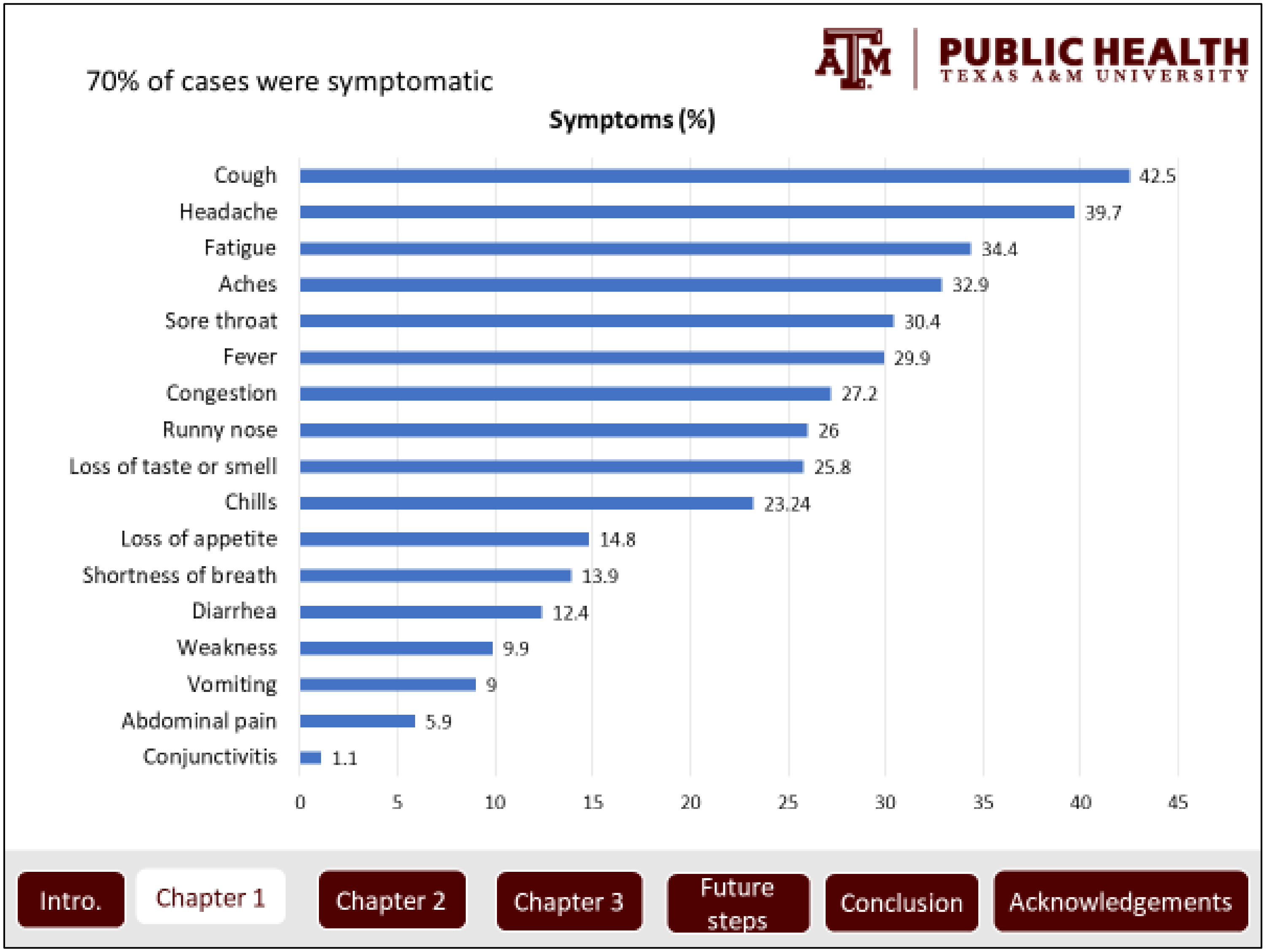
Incubation period estimate
- Median: 2 days (range: 0-14)



Symptom duration estimate
- Median: 6 days (0-97 days)





70% of cases were symptomatic
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Symptoms (%)
Cough 42.5
Headache 39.7
Fatigue 34.4
Aches 32.9
Sore throat 30.4
Fever 29.9
Congestion 27.2
Runny nose 26
Loss of taste or smell 25.8
Chills 23.24
Loss of appetite 14.8
Shortness of breath 13.9
Diarrhea 12.4
Weakness 9.9
Vomiting 9
Abdominal pain 5.9
Conjunctivitis 1.1
0 5 10 15 20 25 30 35 40 45
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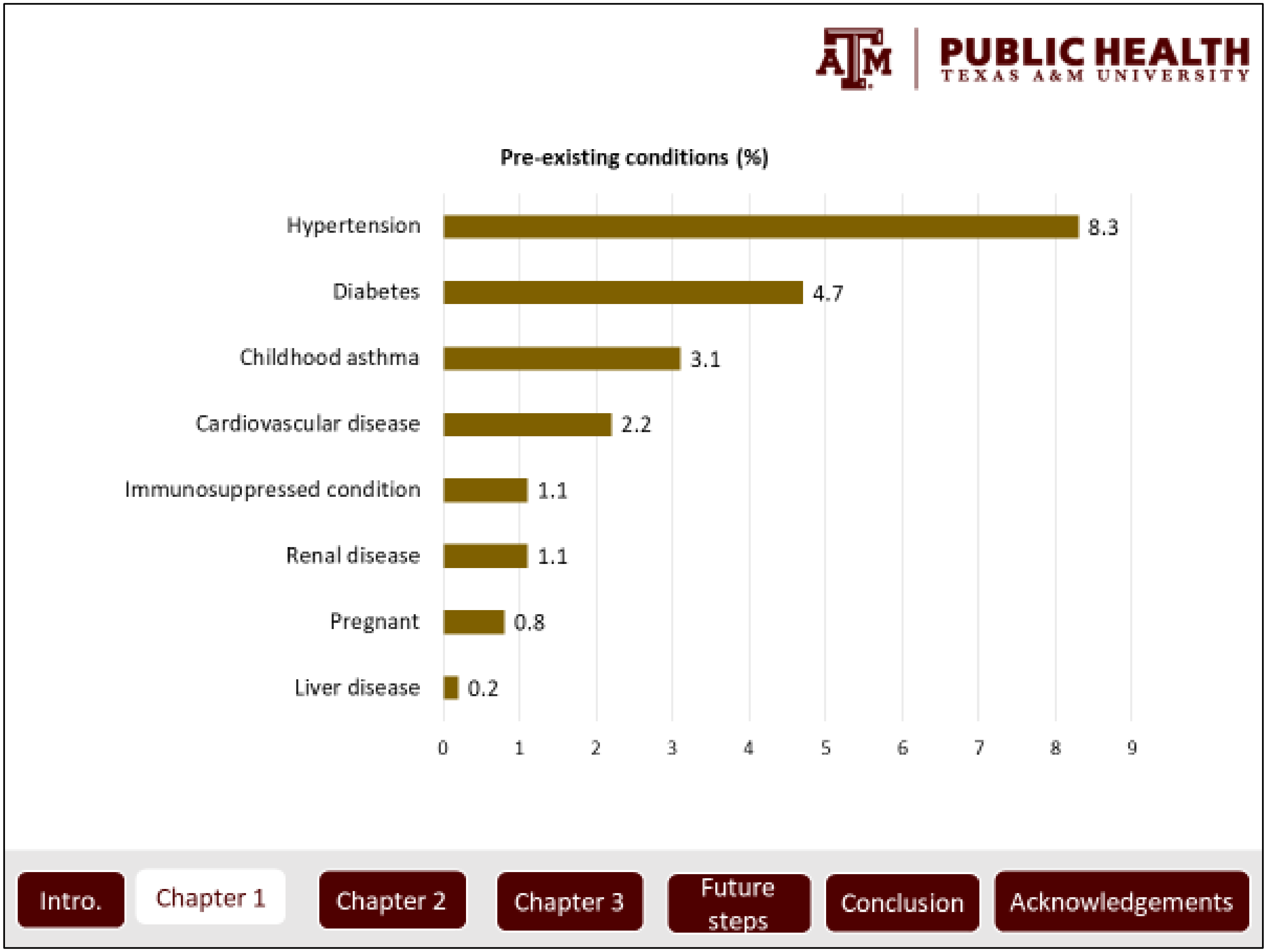
PUBLIC HEALTH
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Pre-existing conditions (%)
Hypertension
Diabetes
Childhood asthma
Cardiovascular disease
Immunosuppressed condition
Renal disease
Pregnant
Liver disease
8.3
4.7
3.1
2.2
1.1
1.1
0.8
0.2
0
1
2
3
4
5
6
7
8
9
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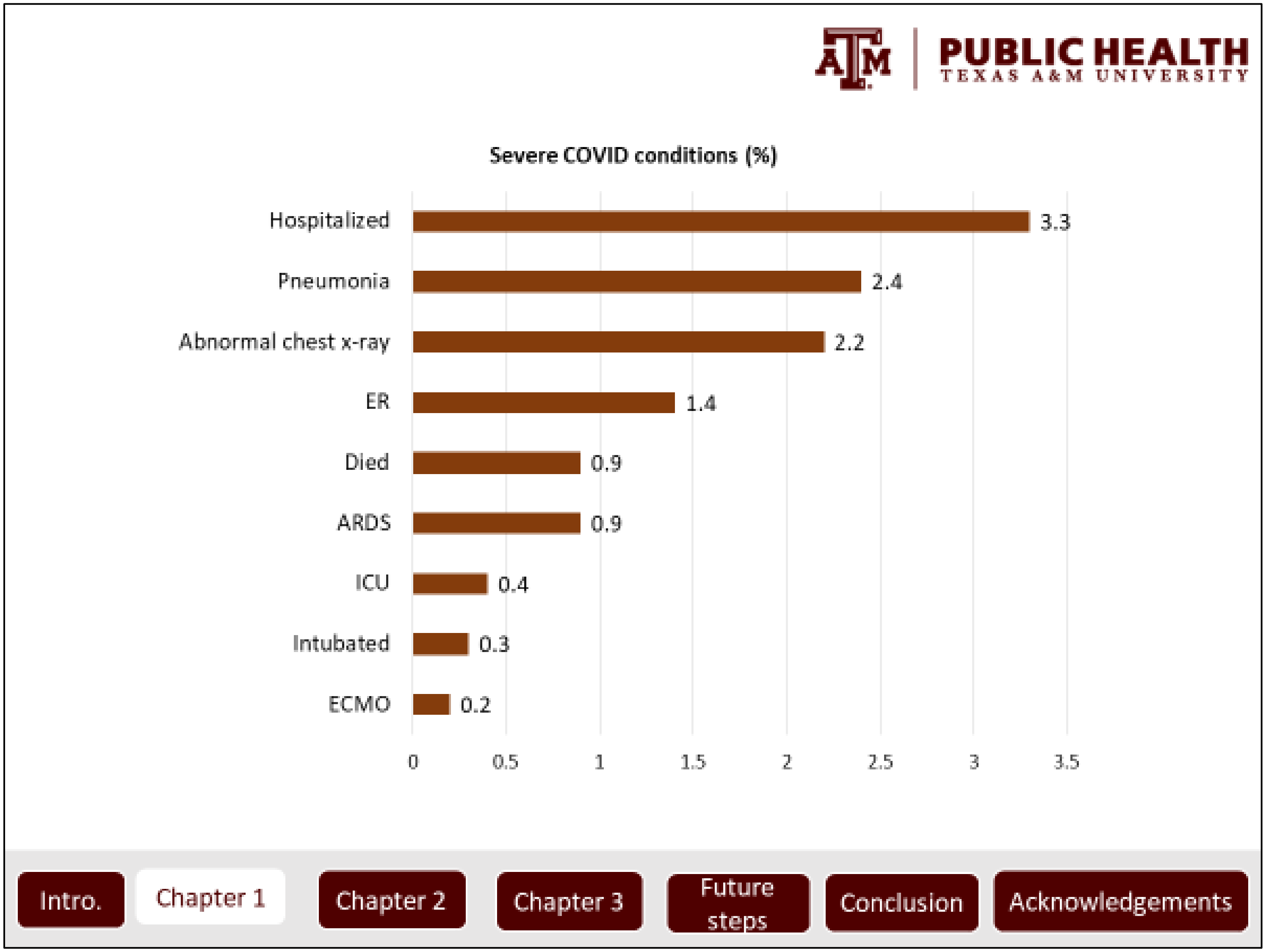
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Severe COVID conditions (%)
Hospitalized 3.3
Pneumonia 2.4
Abnormal chest x-ray 2.2
ER 1.4
Died 0.9
ARDS 0.9
ICU 0.4
Intubated 0.3
ECMO 0.2
0 0.5 1 1.5 2 2.5 3 3.5
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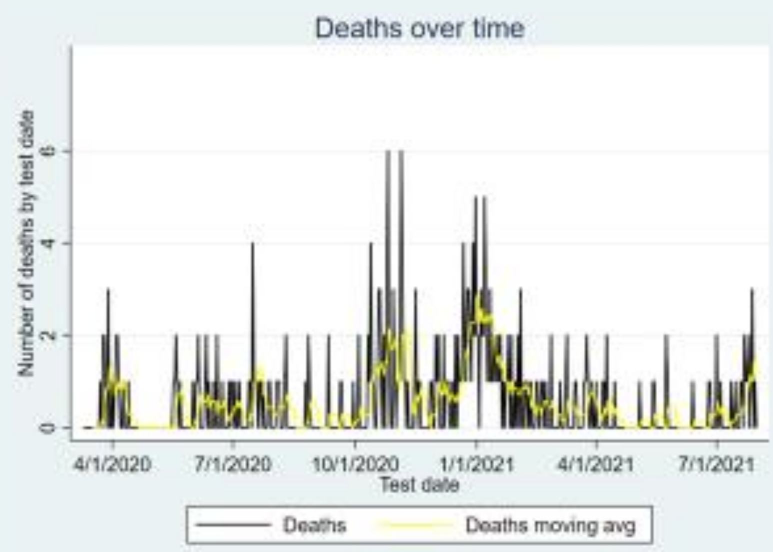

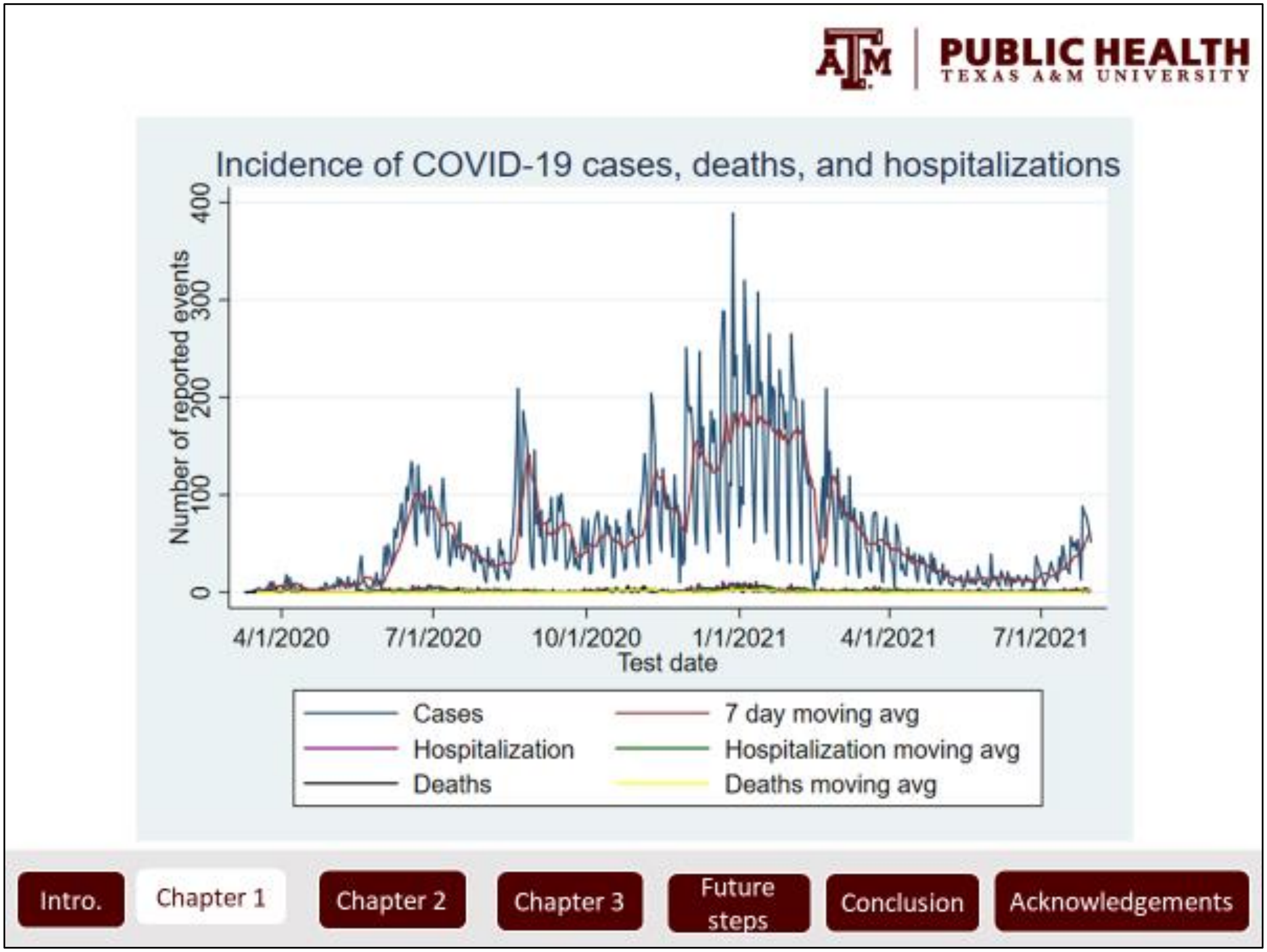
PUBLIC HEALTH
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Incidence of COVID-19 cases, deaths, and hospitalizations
Number of reported events
0
100
200
300
400
4/1/2020
7/1/2020
10/1/2020
1/1/2021
4/1/2021
7/1/2021
Test date
Cases
7 day moving avg
Hospitalization
Hospitalization moving avg
Deaths
Deaths moving avg
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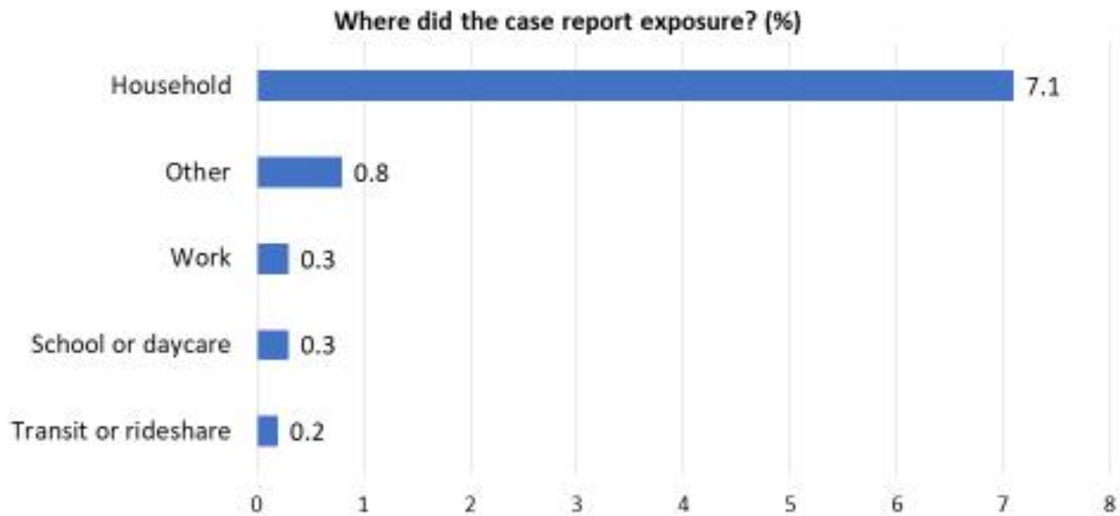
Exposure

- Known prior contact with a confirmed case → 38.6%
- Close contact was a household member → 11.3%



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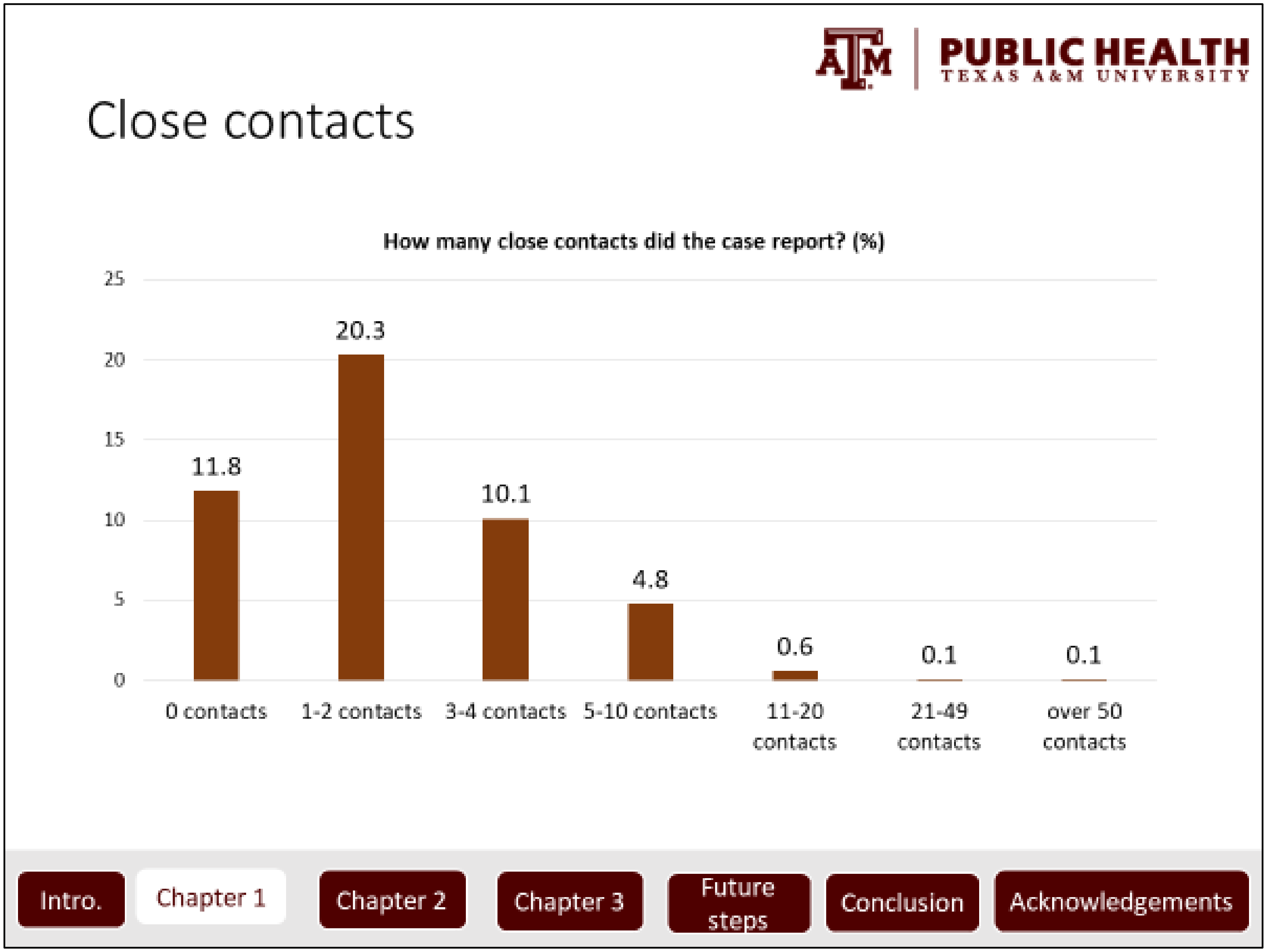
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Close contacts
How many close contacts did the case report? (%)
25
20
15
10
5
0
11.8
20.3
10.1
4.8
0.6
0.1
0.1
0 contacts
1-2 contacts
3-4 contacts
5-10 contacts
11-20 contacts
21-49 contacts
over 50 contacts
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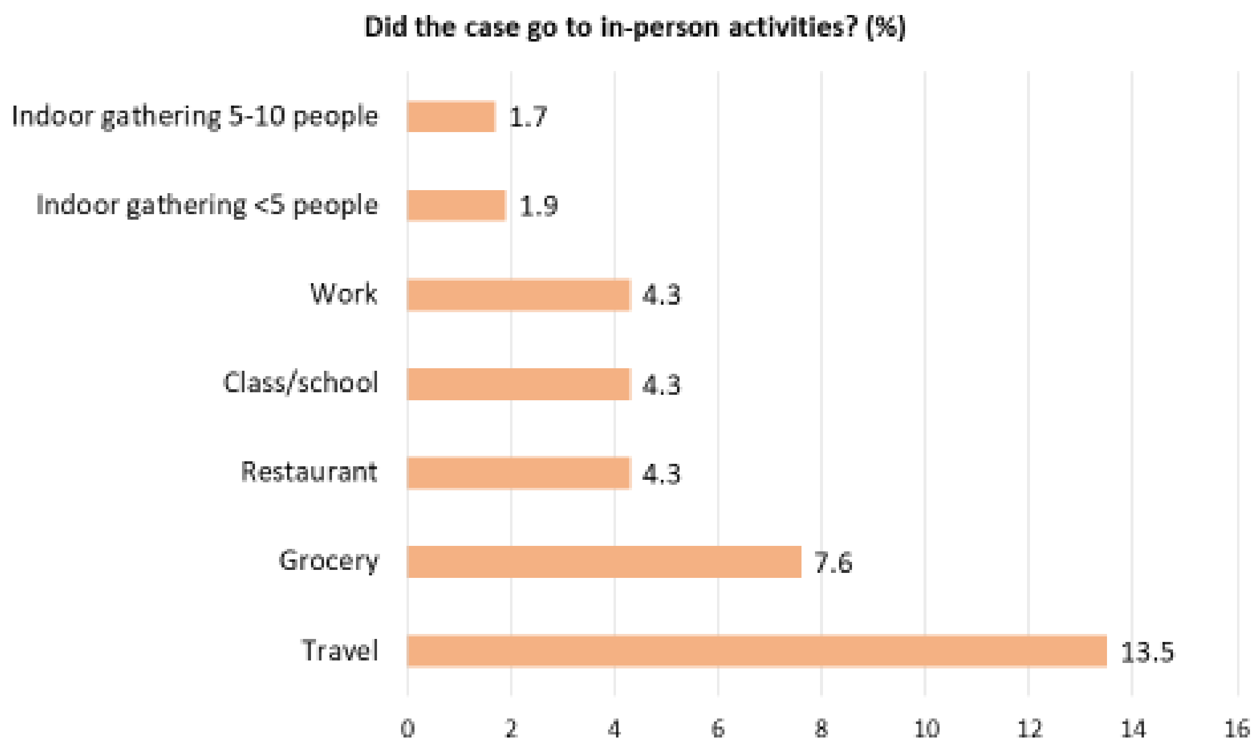
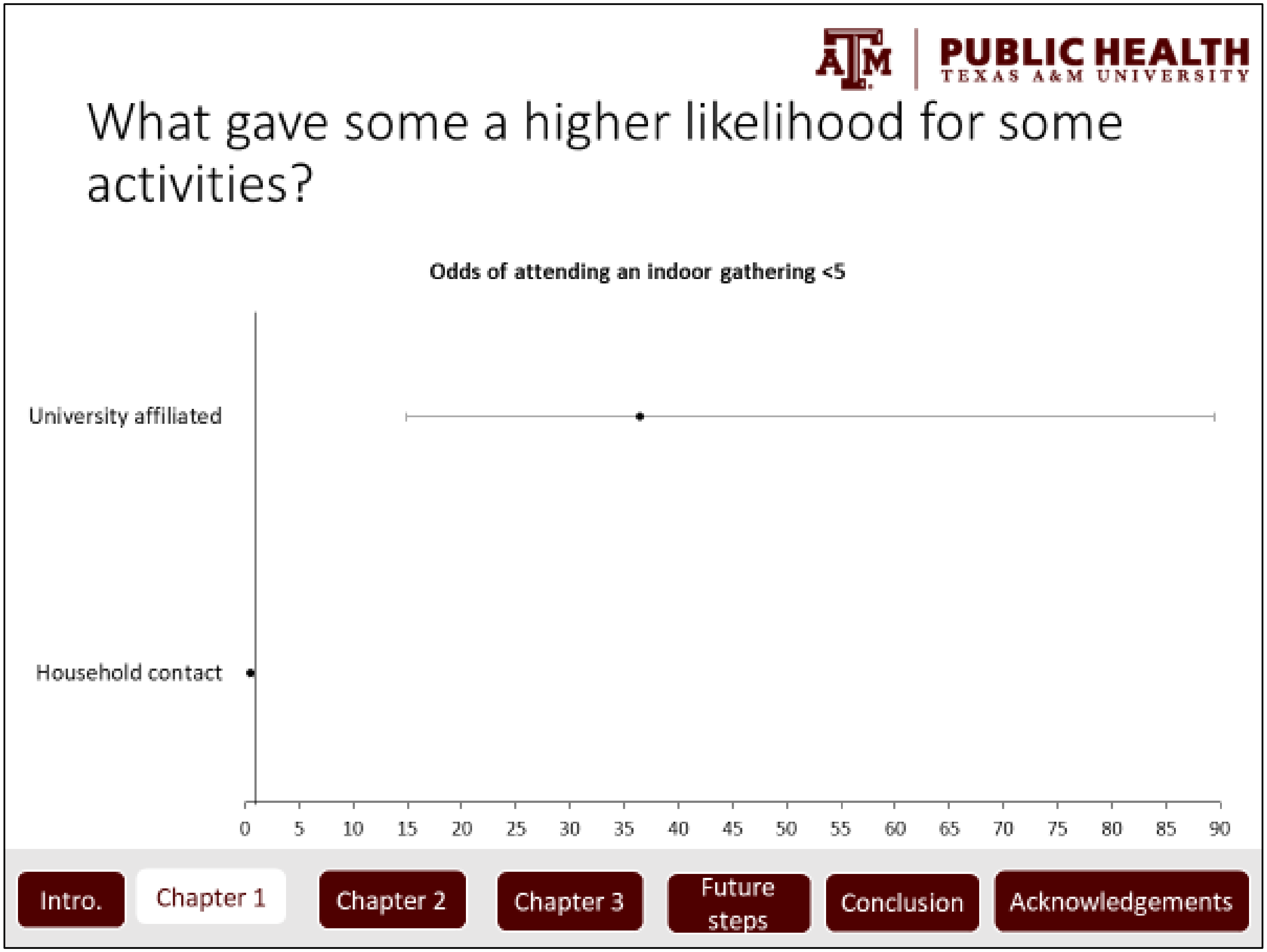
Activities


Did the case go to in-person activities? (%)
Indoor gathering 5-10 people
1.7
Indoor gathering <5 people
1.9
Work
4.3
Class/school
4.3
Restaurant
4.3
Grocery
7.6
Travel
13.5
0
2
4
6
8
10
12
14
16



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What gave some a higher likelihood for some activities?
Odds of attending an indoor gathering <5
University affiliated
Household contact
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
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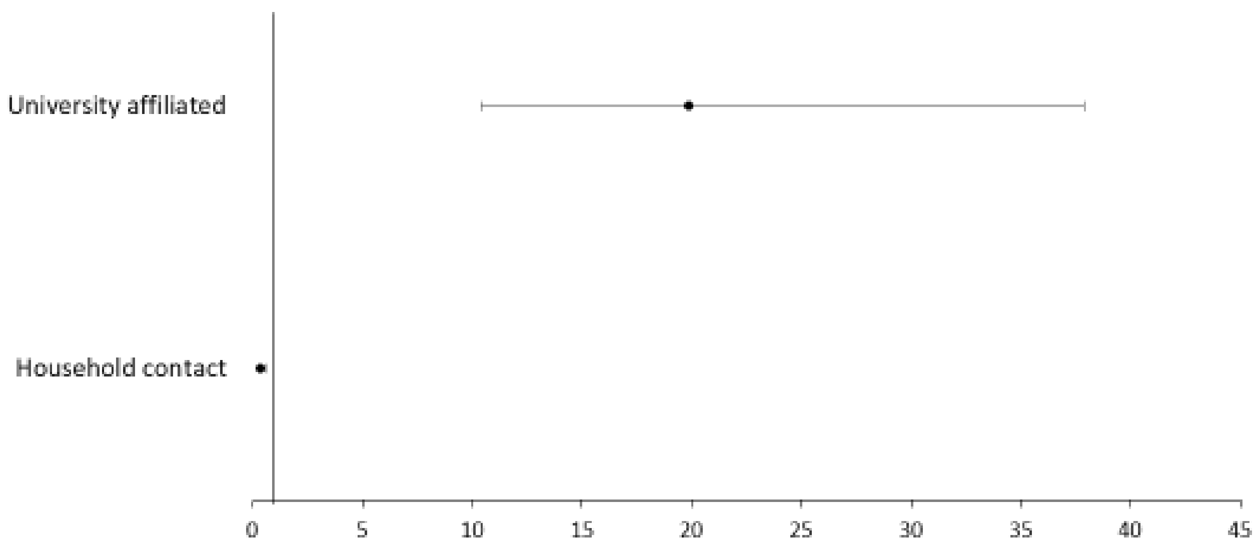
What gave some a higher likelihood for some activities?

Odds of attending an indoor gathering 5-10



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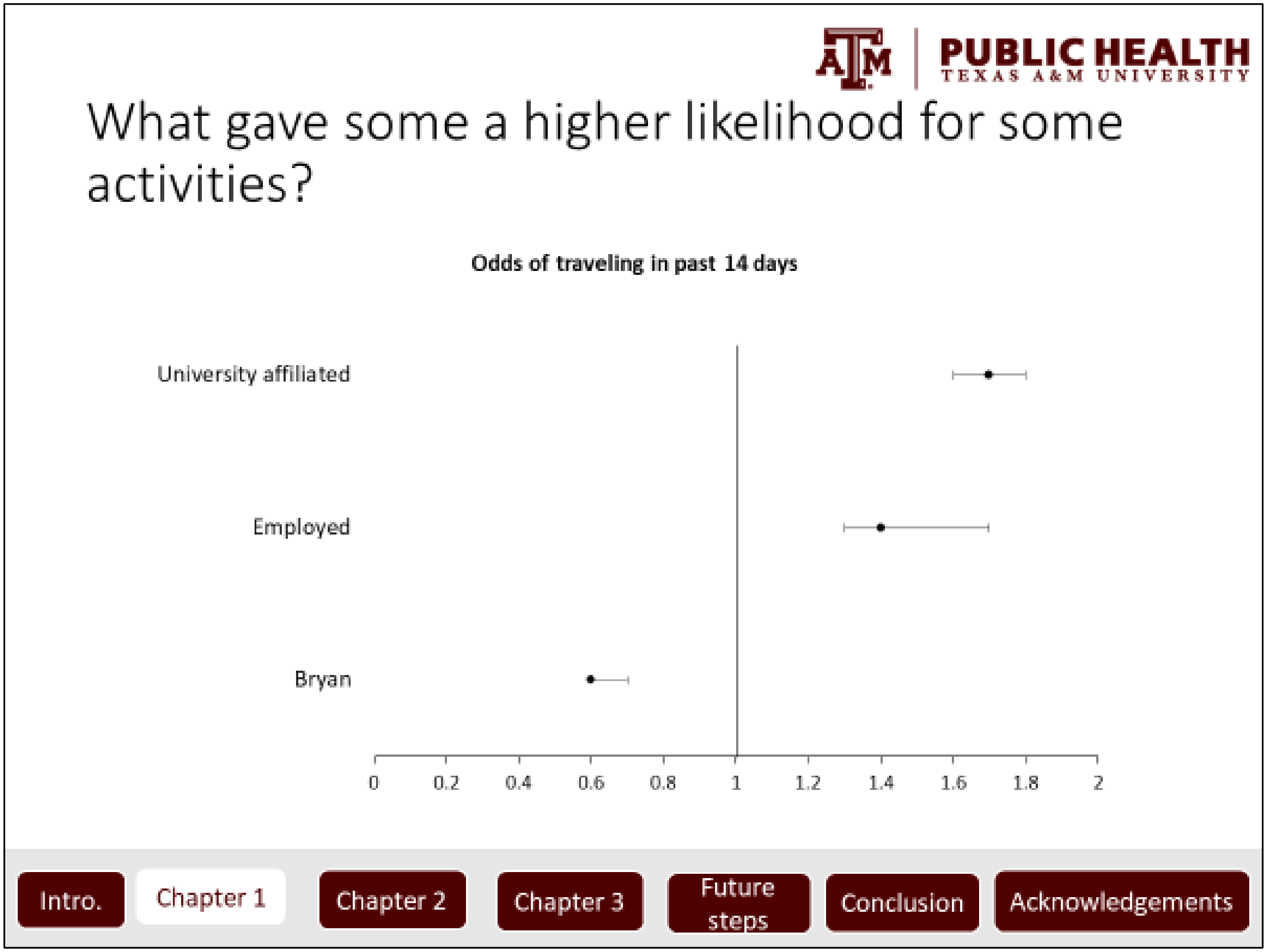
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
What gave some a higher likelihood for some activities?
Odds of traveling in past 14 days
University affiliated
Employed
Bryan
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2
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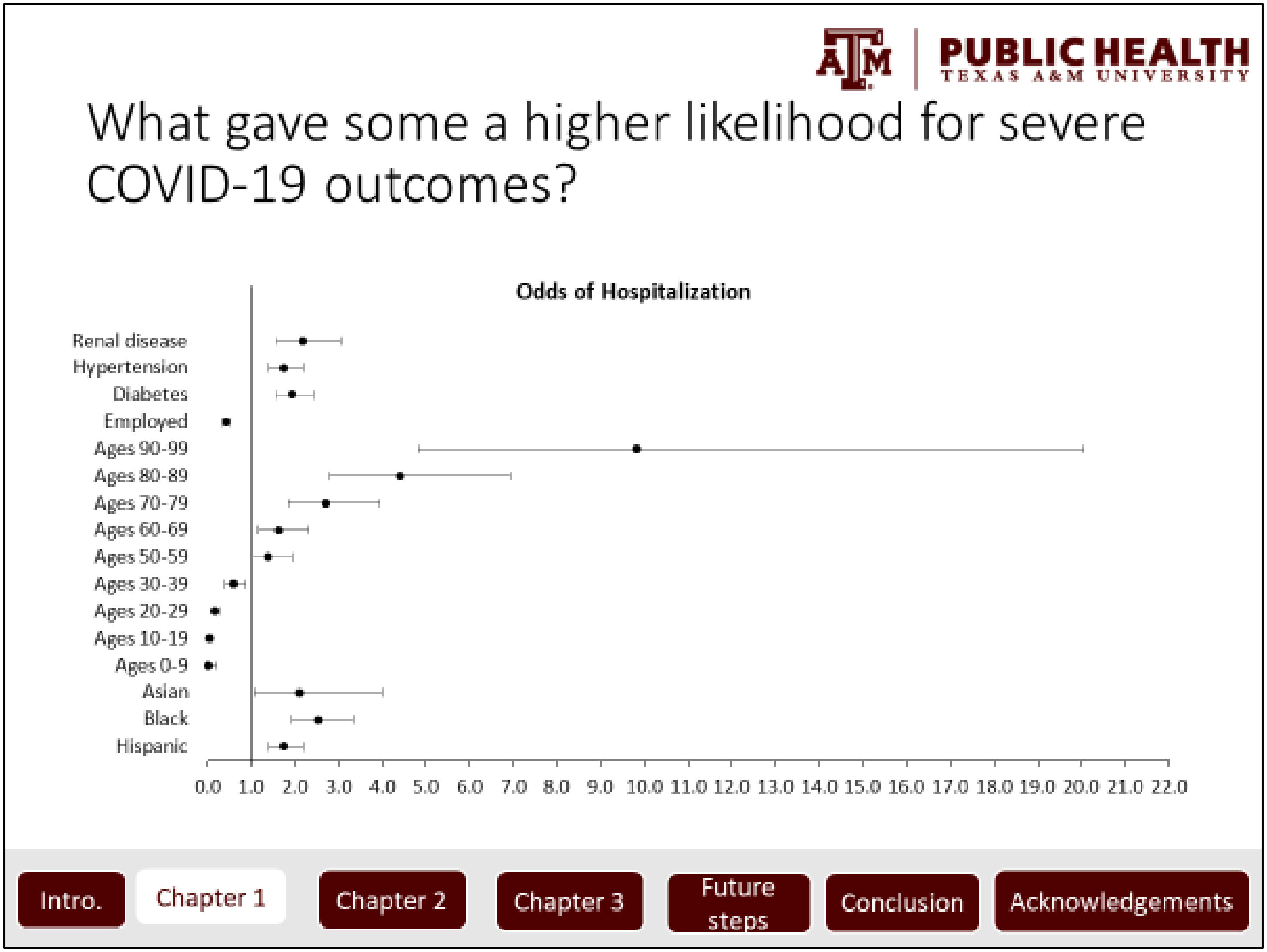
PUBLIC HEALTH
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What gave some a higher likelihood for severe COVID-19 outcomes?
Odds of Hospitalization
Renal disease
Hypertension
Diabetes
Employed
Ages 90-99
Ages 80-89
Ages 70-79
Ages 60-69
Ages 50-59
Ages 30-39
Ages 20-29
Ages 10-19
Ages 0-9
Asian
Black
Hispanic
0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 21.0 22.0
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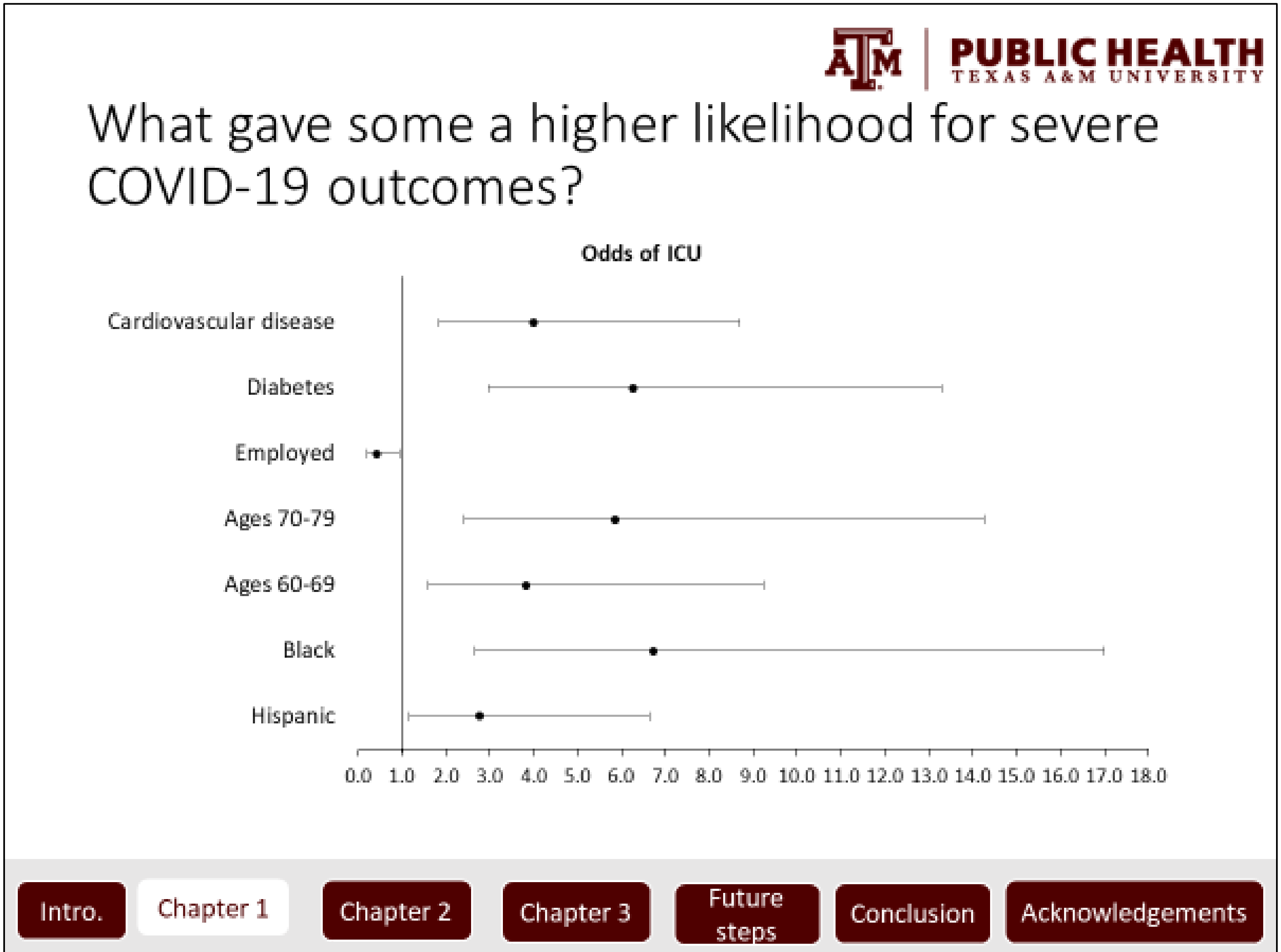
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
What gave some a higher likelihood for severe COVID-19 outcomes?
Odds of ICU
Cardiovascular disease
Diabetes
Employed
Ages 70-79
Ages 60-69
Black
Hispanic
0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0
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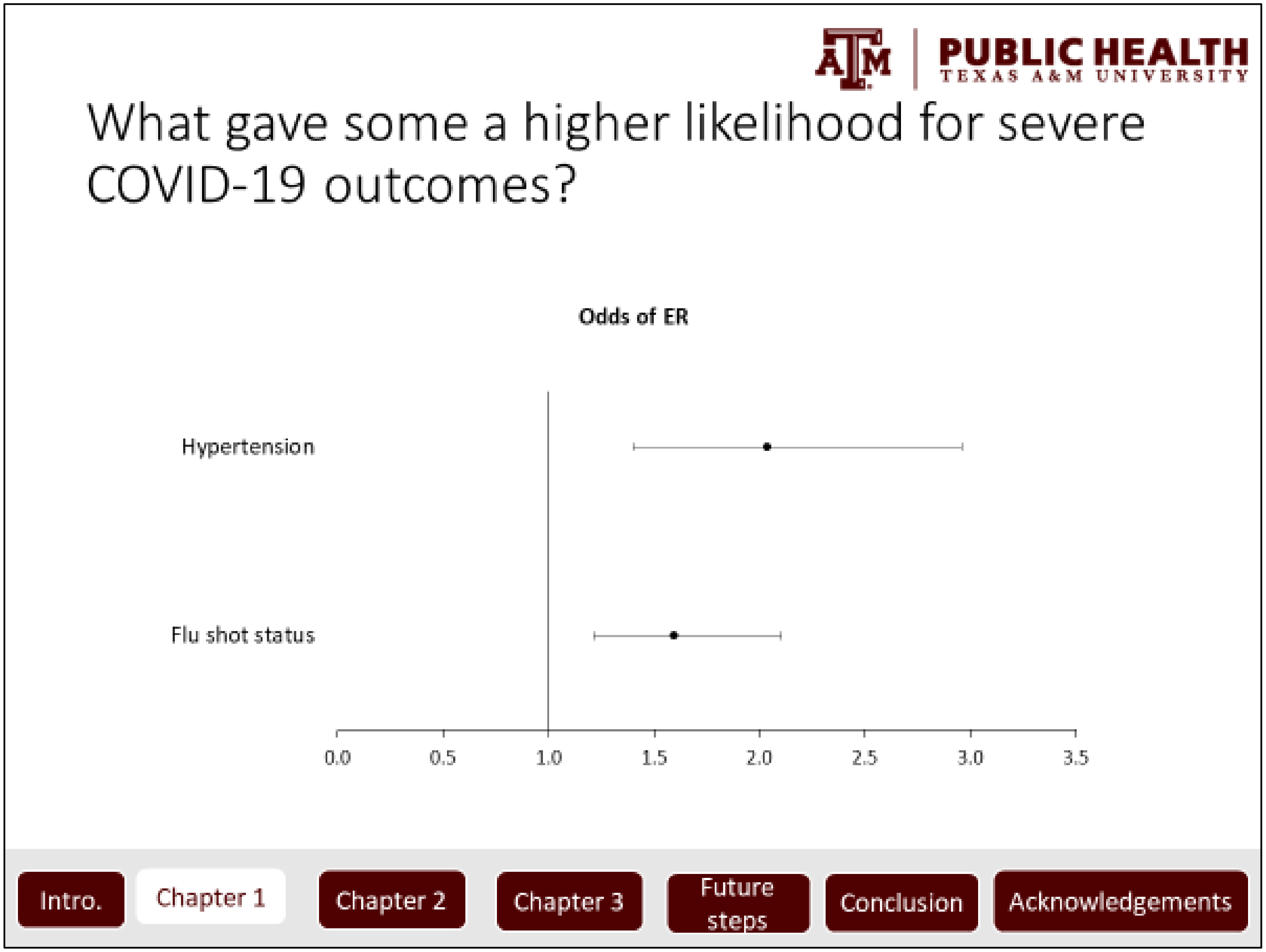
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
What gave some a higher likelihood for severe COVID-19 outcomes?
Odds of ER
Hypertension
Flu shot status
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
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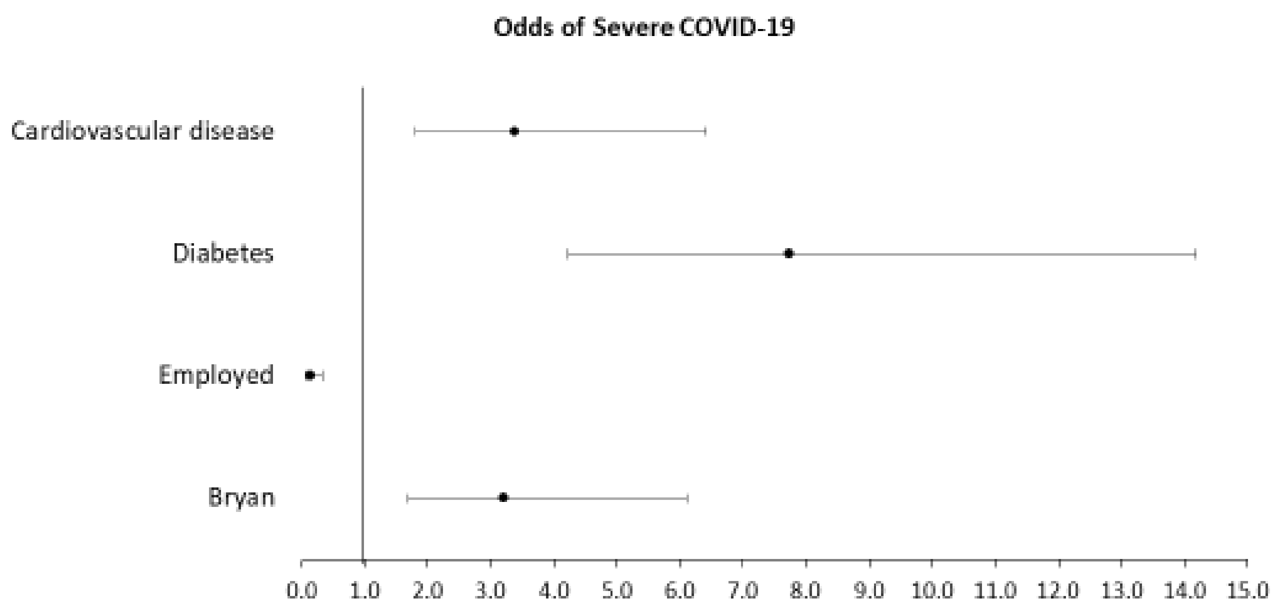
What gave some a higher likelihood for severe COVID-19 outcomes?



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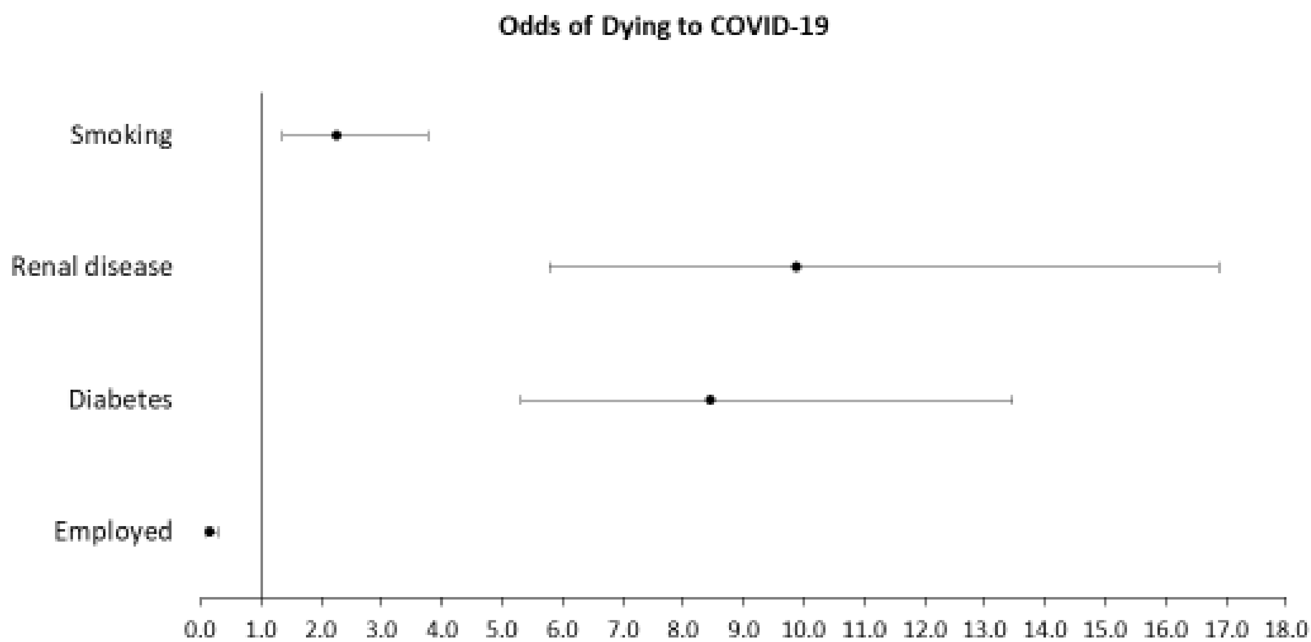
What gave some a higher likelihood for severe COVID-19 outcomes?



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Limitations

- Questionnaire evolved with the pandemic
- Differences in inputting data
- Provider not giving accurate/complete contact information of the case
- Difficulty reaching people on the phone
- Recall bias
- Backlog of cases

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Conclusions

- Young adults most represented age group and not immune to the virus
- Most common behavioral risk factors were attending indoor gatherings and traveling outside city of residence
- Minorities were at higher risk of severe disease
  - Black
  - Hispanic
- Co-morbidities put individuals at higher risk of severe disease
  - Cardiovascular disease
  - Diabetes
  - Hypertension
  - Renal disease
- Policy makers can make these groups aware of their higher risk

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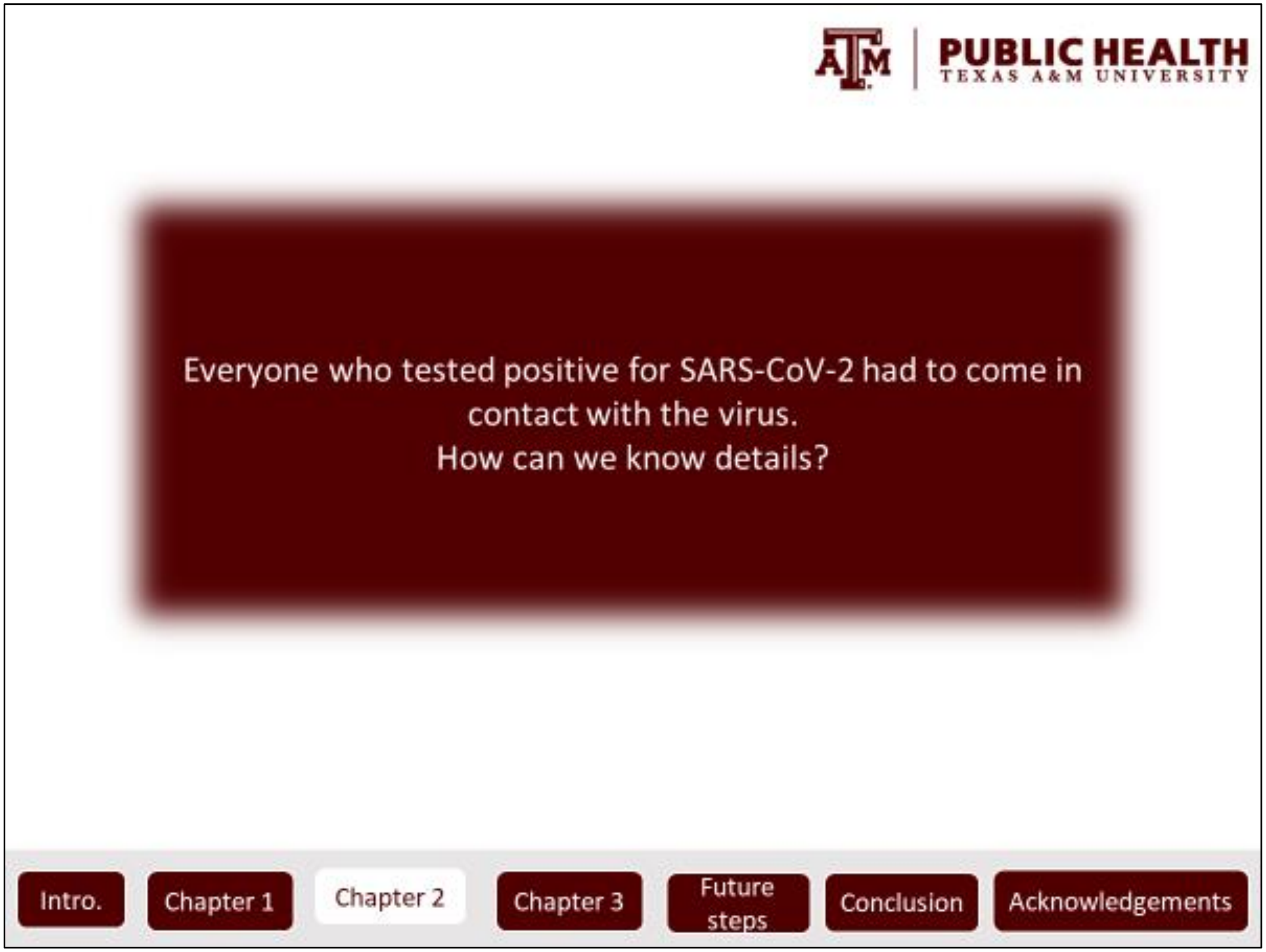
Chapter 2: Contact Tracing and Testing of COVID-19, Which Came First?


PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Everyone who tested positive for SARS-CoV-2 had to come in contact with the virus.
How can we know details?
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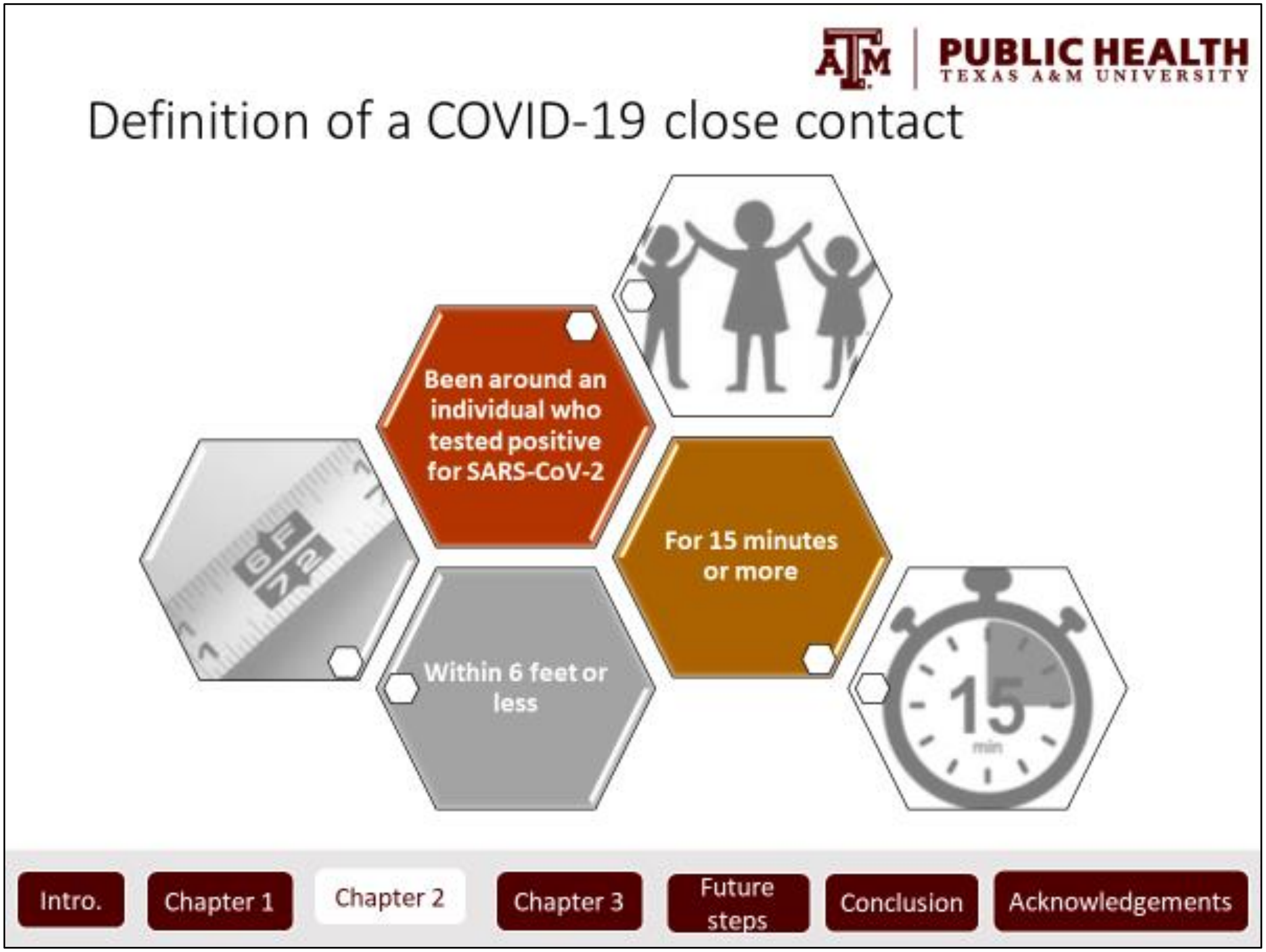
Contact tracing

- Process of speaking with someone who has been near those with an infectious disease and warning them to watch for disease symptoms and requesting quarantine.

- The contact tracing concept is not new
  - John Snow and cholera (1854)
  - Mary Mallon and typhoid (1906)
  - HIV (1988)
  - Ebola outbreak (2014)
  - H1N1 (2015).....
  - COVID-19


PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Definition of a COVID-19 close contact
Been around an individual who tested positive for SARS-CoV-2
For 15 minutes or more
Within 6 feet or less
15
min
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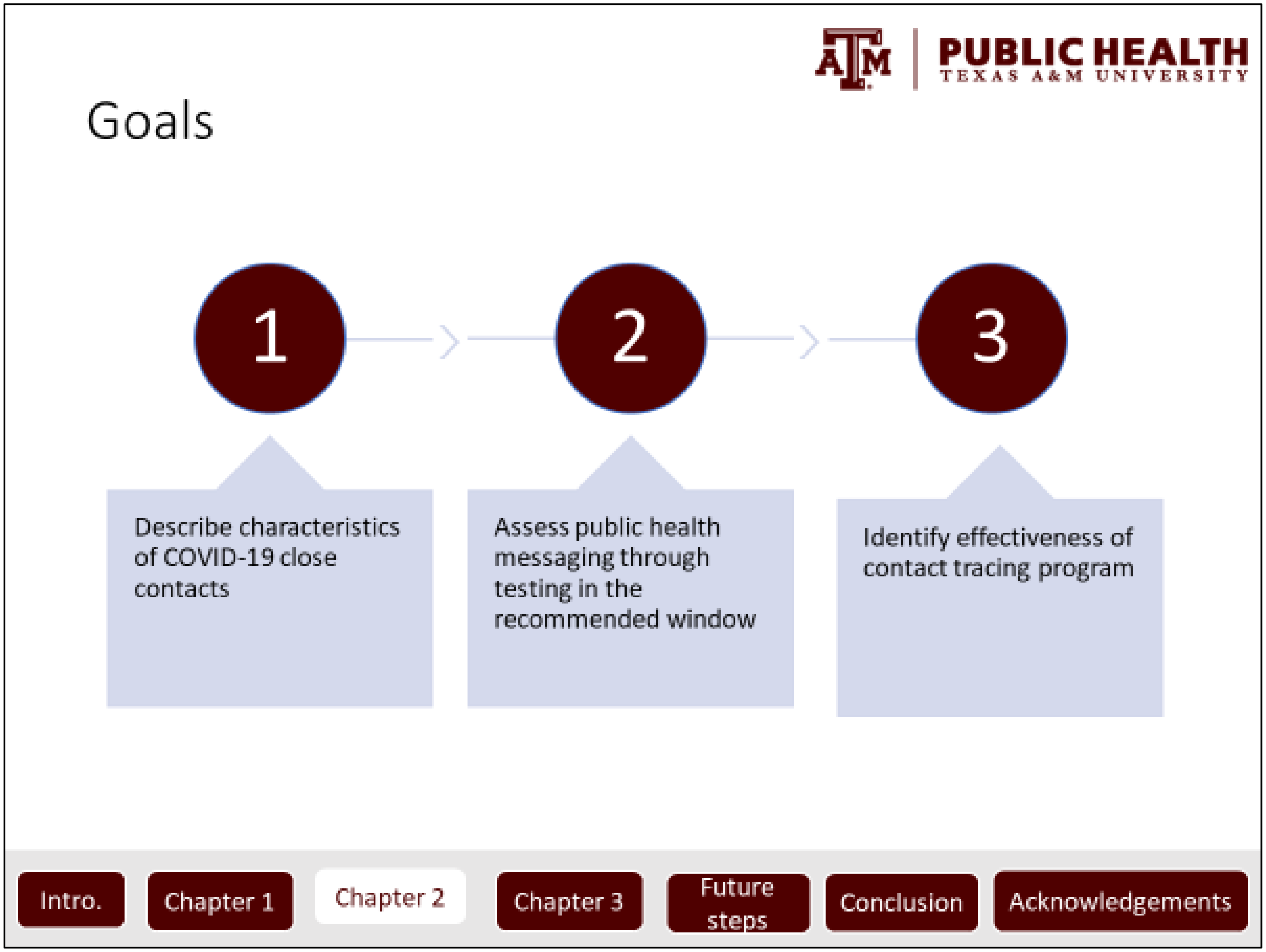
COVID-19 contact tracing process

Person tests positive for SARS-CoV-2

Case investigator calls case.

Information on close contacts is passed on to contact tracer

Contact tracer calls close contact to give guidance


PUBLIC HEALTH
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Goals
1
2
3
Describe characteristics of COVID-19 close contacts
Assess public health messaging through testing in the recommended window
Identify effectiveness of contact tracing program
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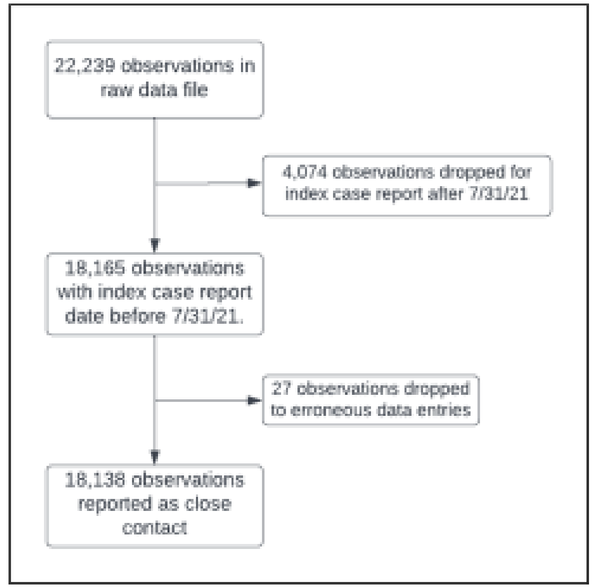
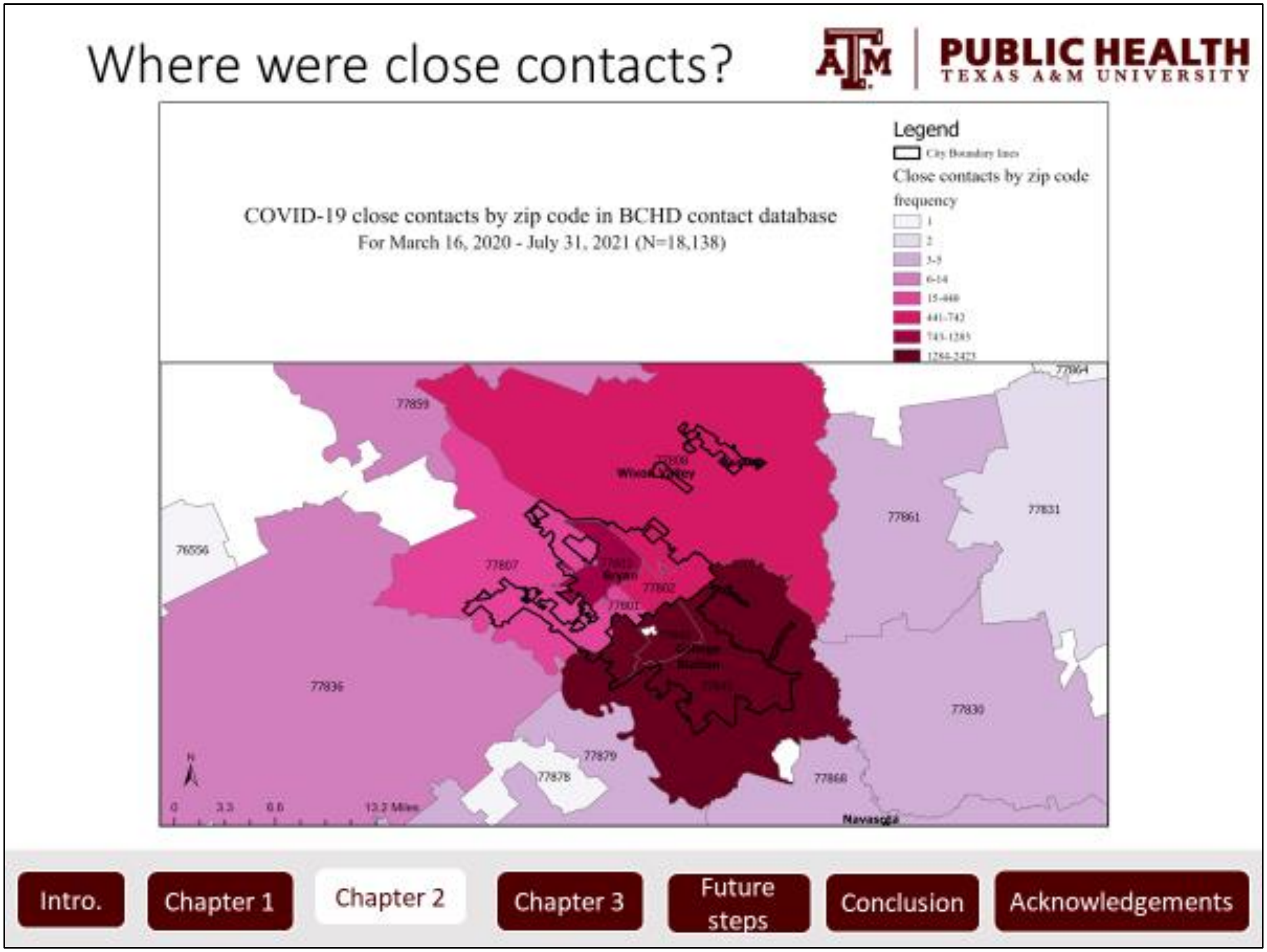
Methods

- All data collected was provided by the case and/or contact
- Data entered into the REDCap software
- Included data on contacts thru July 31, 2021
- Data cleaned in the same manner as chapter 1
    - STATA 16.1/IC
- Variables unique to this data included questions such as:
    - Relationship between confirmed case and close contact





Where were close contacts?
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
COVID-19 close contacts by zip code in BCHD contact database
For March 16, 2020 - July 31, 2021 (N=18,138)
Legend
City Boundary lines
Close contacts by zip code frequency
1
2
3-5
6-14
441-742
77859
77861
77831
76556
77807
77836
77830
77879
77878
77868
Navasota
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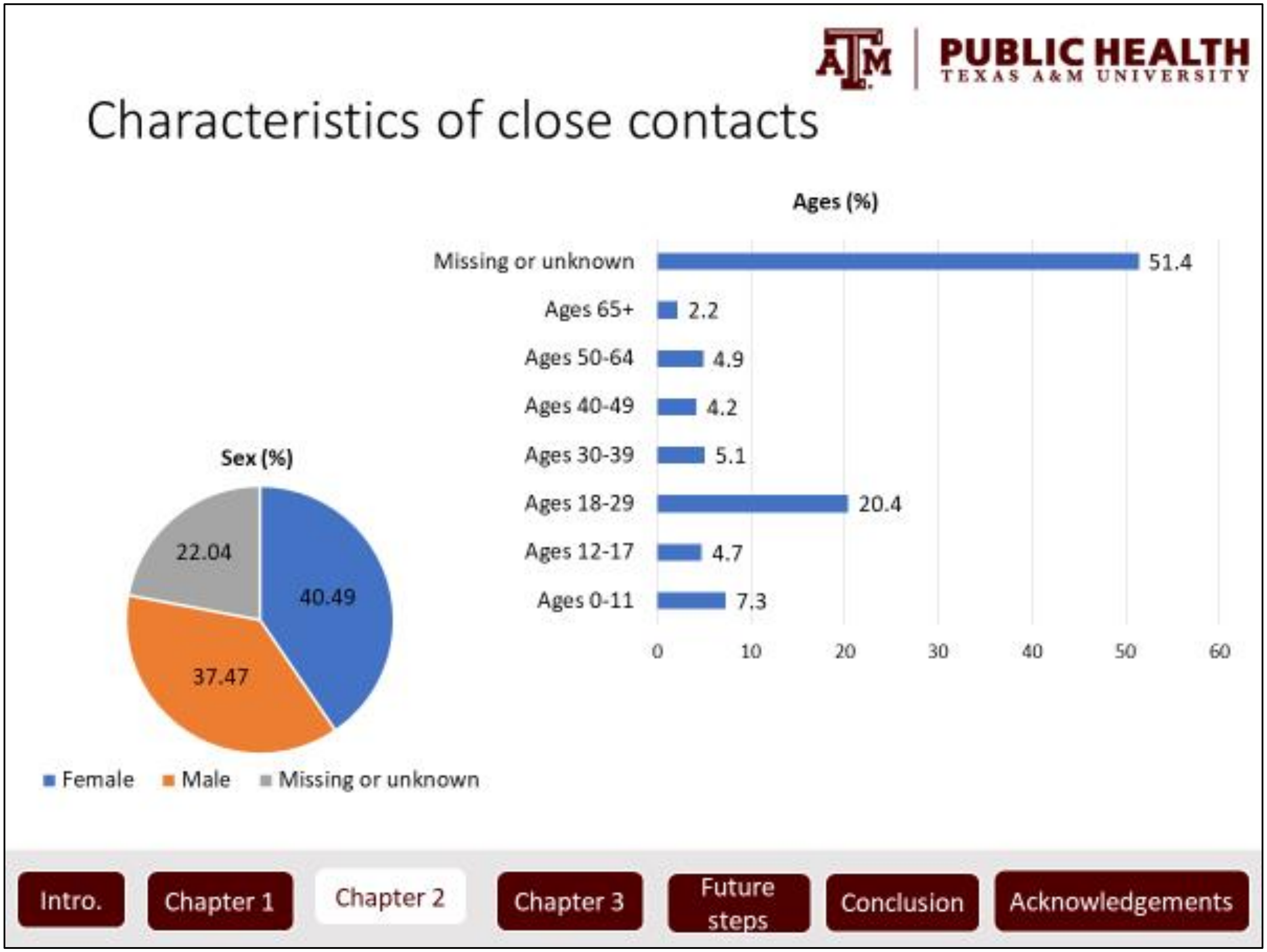
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Characteristics of close contacts
Sex (%)
22.04
40.49
37.47
Female
Male
Missing or unknown
Ages (%)
Missing or unknown 51.4
Ages 65+ 2.2
Ages 50-64 4.9
Ages 40-49 4.2
Ages 30-39 5.1
Ages 18-29 20.4
Ages 12-17 4.7
Ages 0-11 7.3
0 10 20 30 40 50 60
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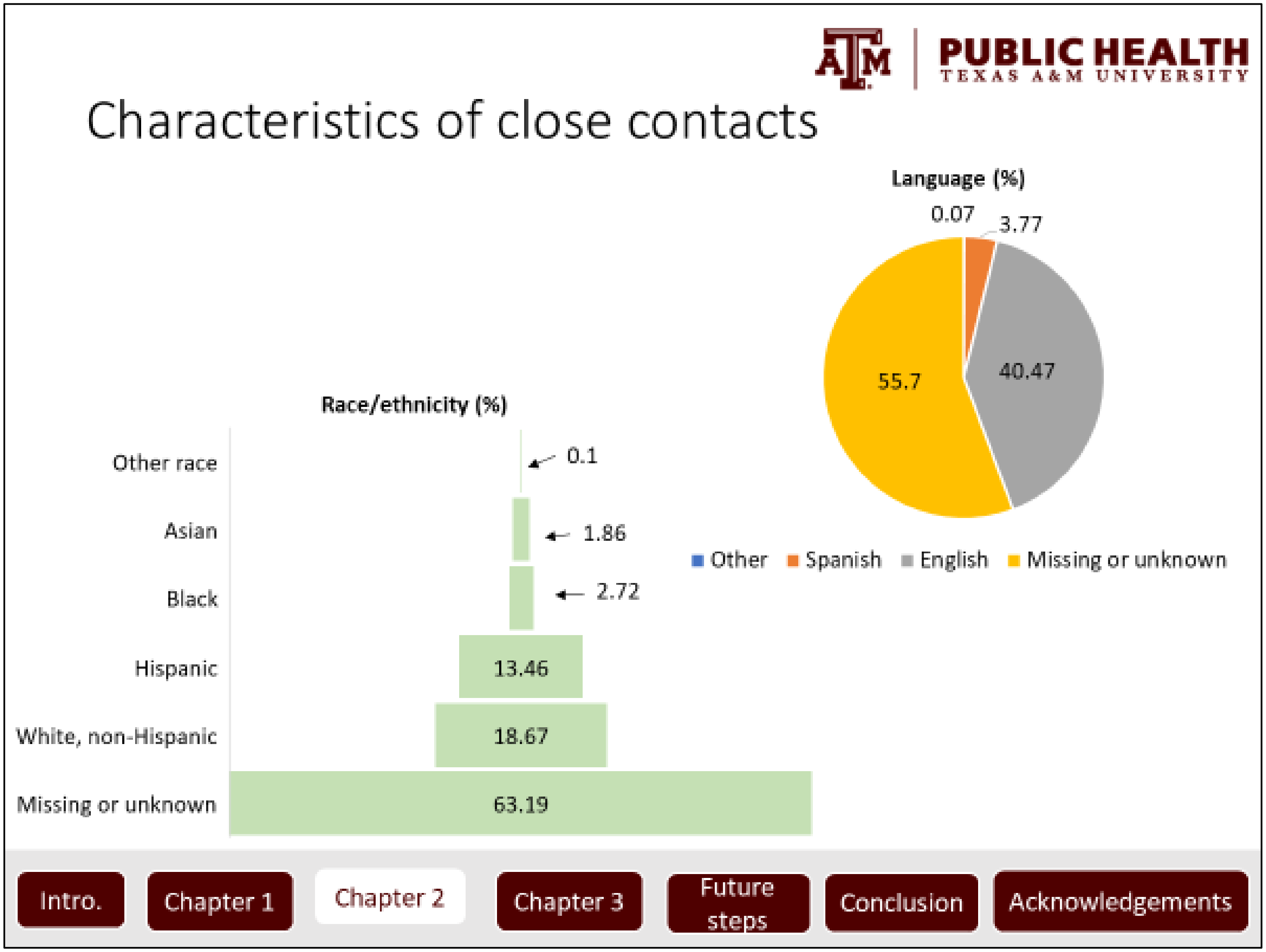

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Characteristics of close contacts
Language (%)
0.07
3.77
55.7
40.47
Other
Spanish
English
Missing or unknown
Race/ethnicity (%)
Other race
Asian
Black
Hispanic
White, non-Hispanic
Missing or unknown
0.1
1.86
2.72
13.46
18.67
63.19
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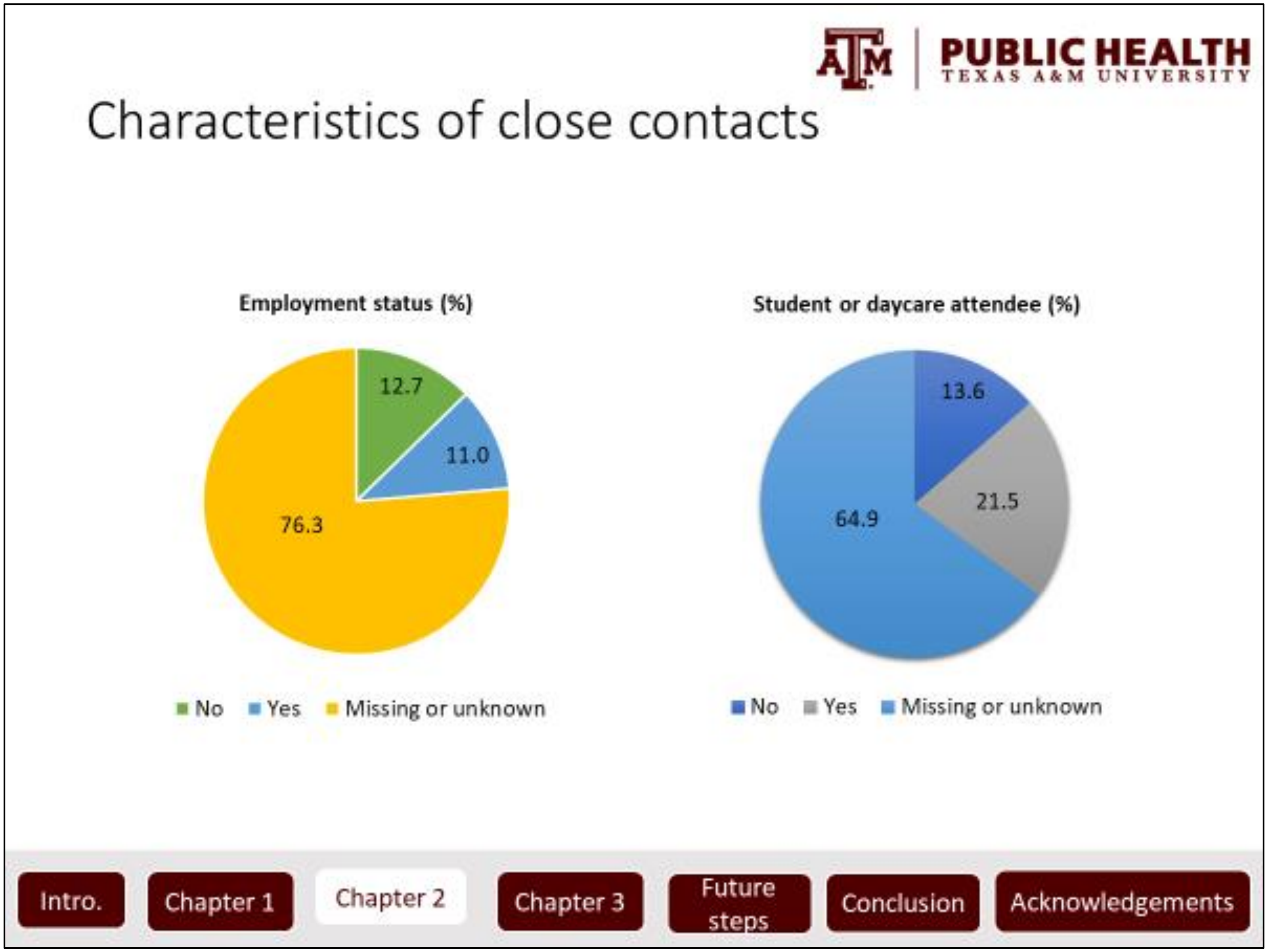
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Characteristics of close contacts
Employment status (%)
12.7
11.0
76.3
No
Yes
Missing or unknown
Student or daycare attendee (%)
13.6
21.5
64.9
No
Yes
Missing or unknown
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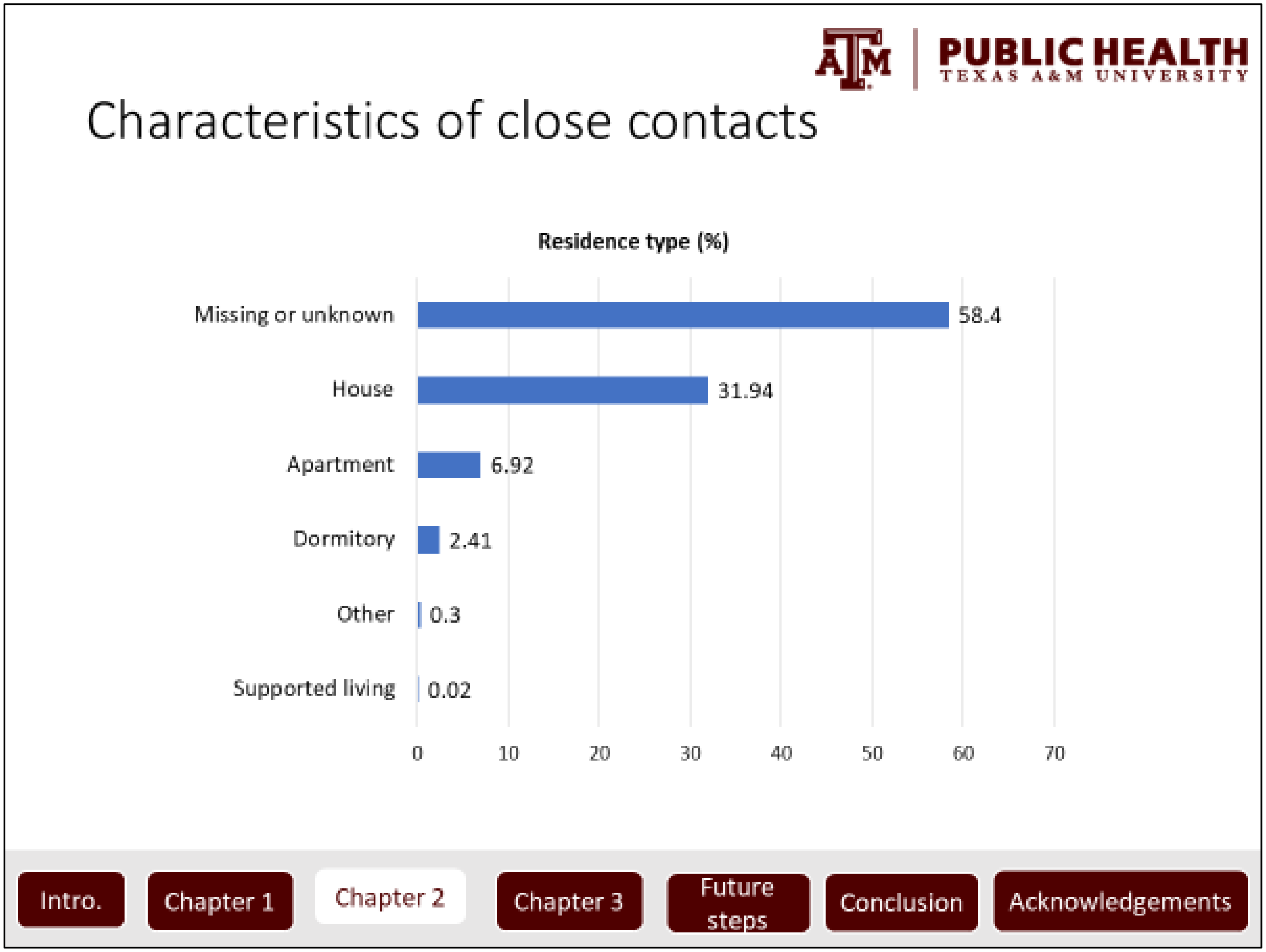
PUBLIC HEALTH
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Characteristics of close contacts
Residence type (%)
Missing or unknown
58.4
House
31.94
Apartment
6.92
Dormitory
2.41
Other
0.3
Supported living
0.02
0
10
20
30
40
50
60
70
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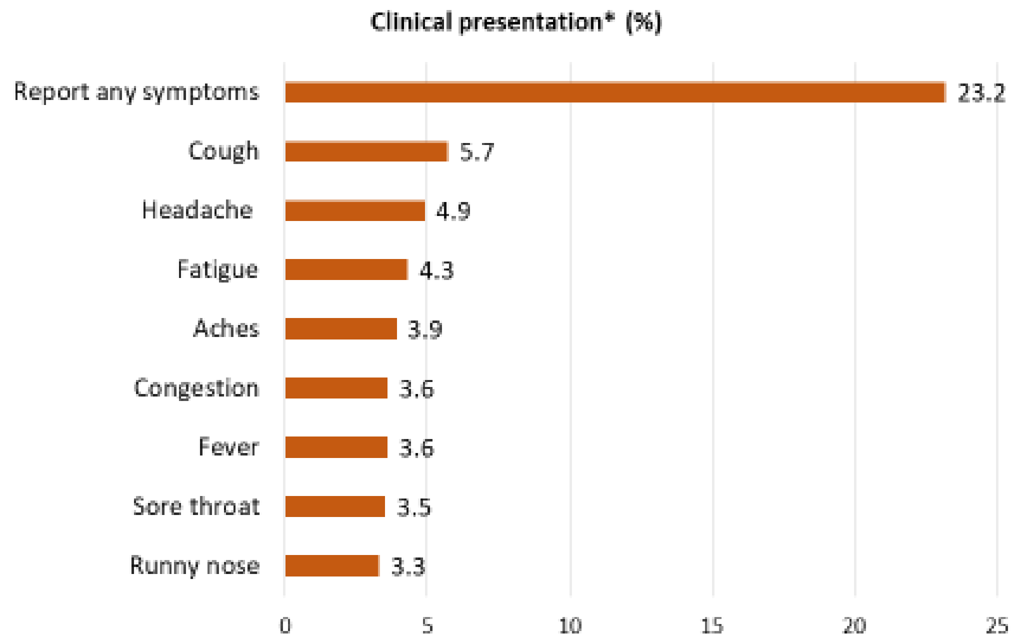
Clinical presentation of close contacts



*Each individual symptom question had >70% missing, symptomatic status had >40% missing

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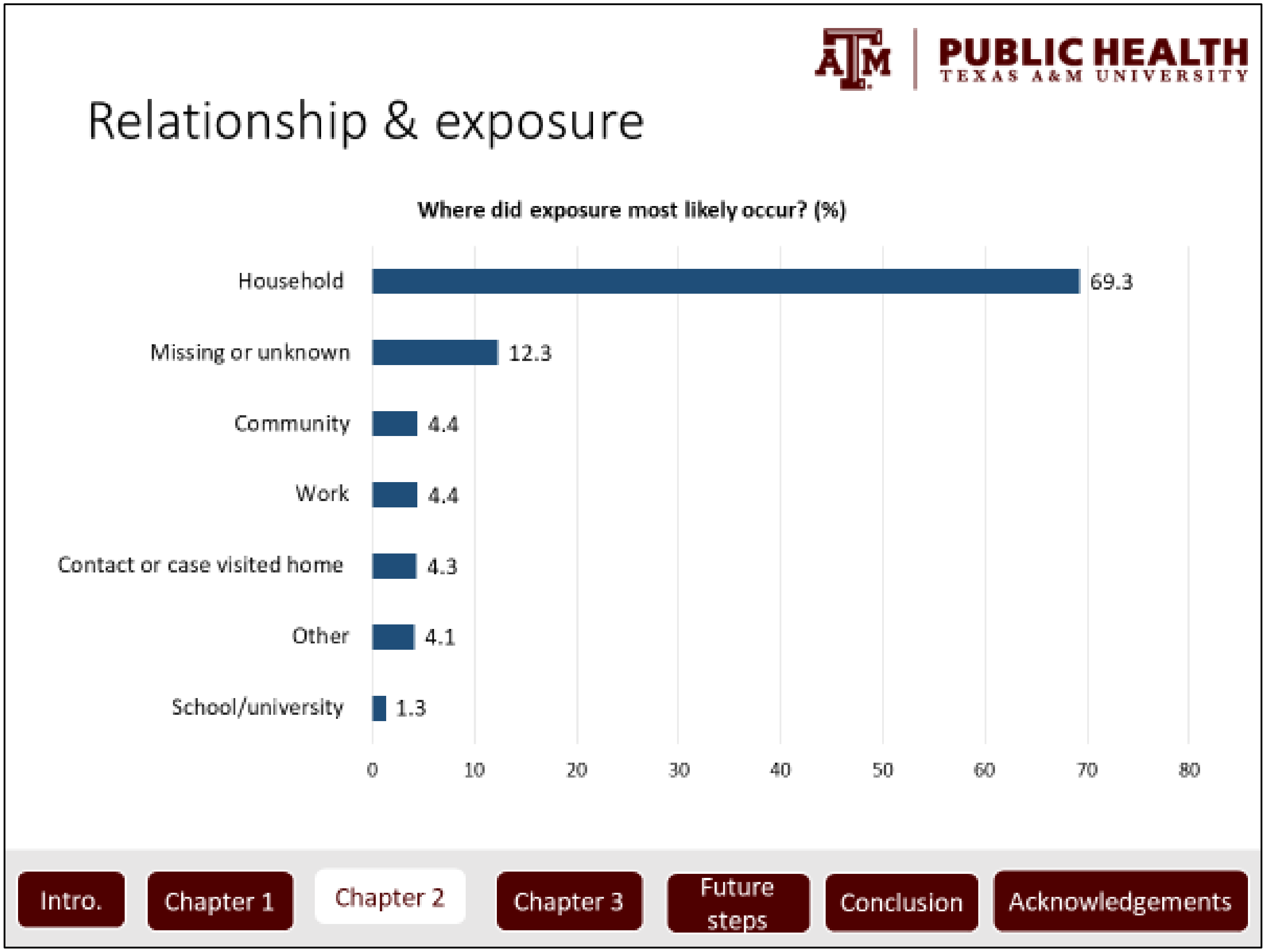
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Relationship & exposure
Where did exposure most likely occur? (%)
Household 69.3
Missing or unknown 12.3
Community 4.4
Work 4.4
Contact or case visited home 4.3
Other 4.1
School/university 1.3
0 10 20 30 40 50 60 70 80
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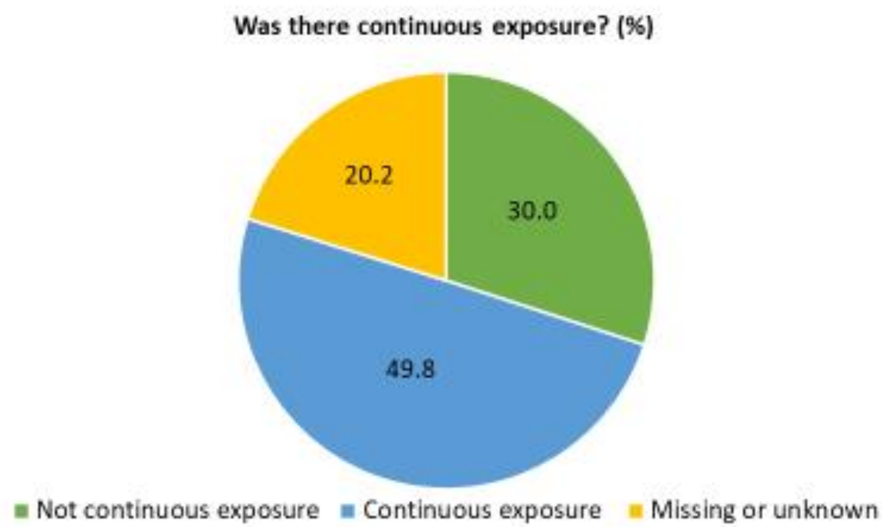
Relationship & exposure



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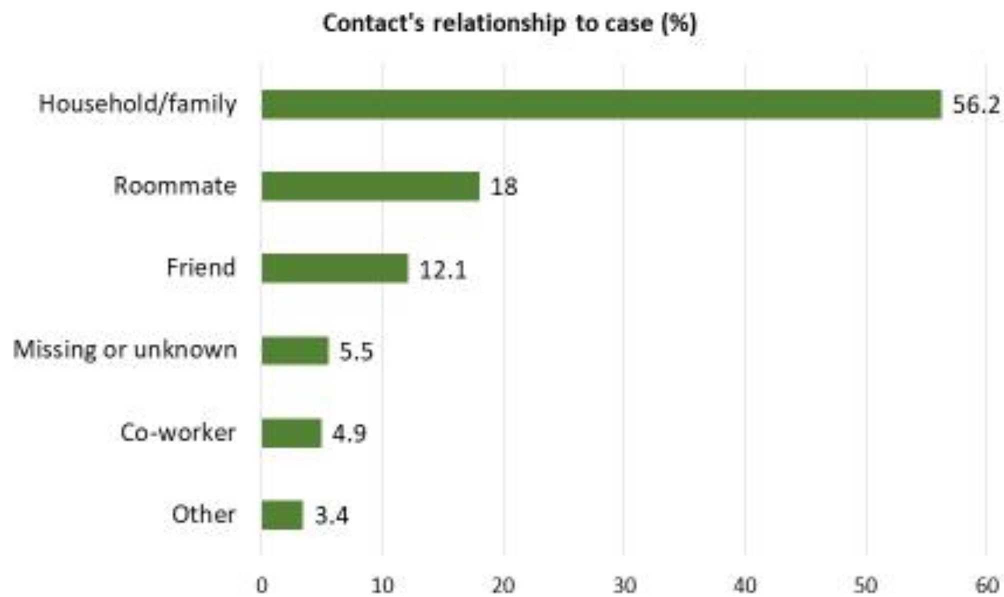
Relationship & exposure



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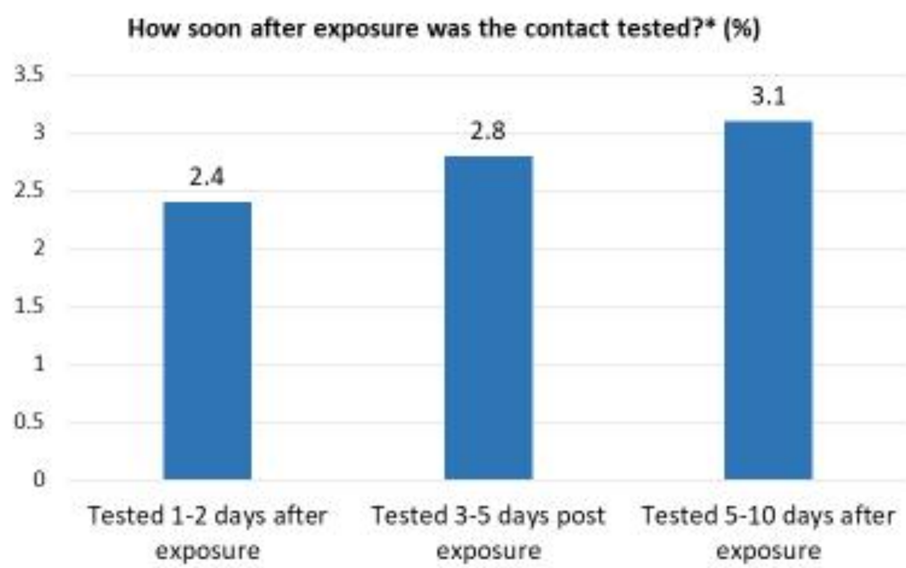
Testing



*91.7% of values were missing in this question

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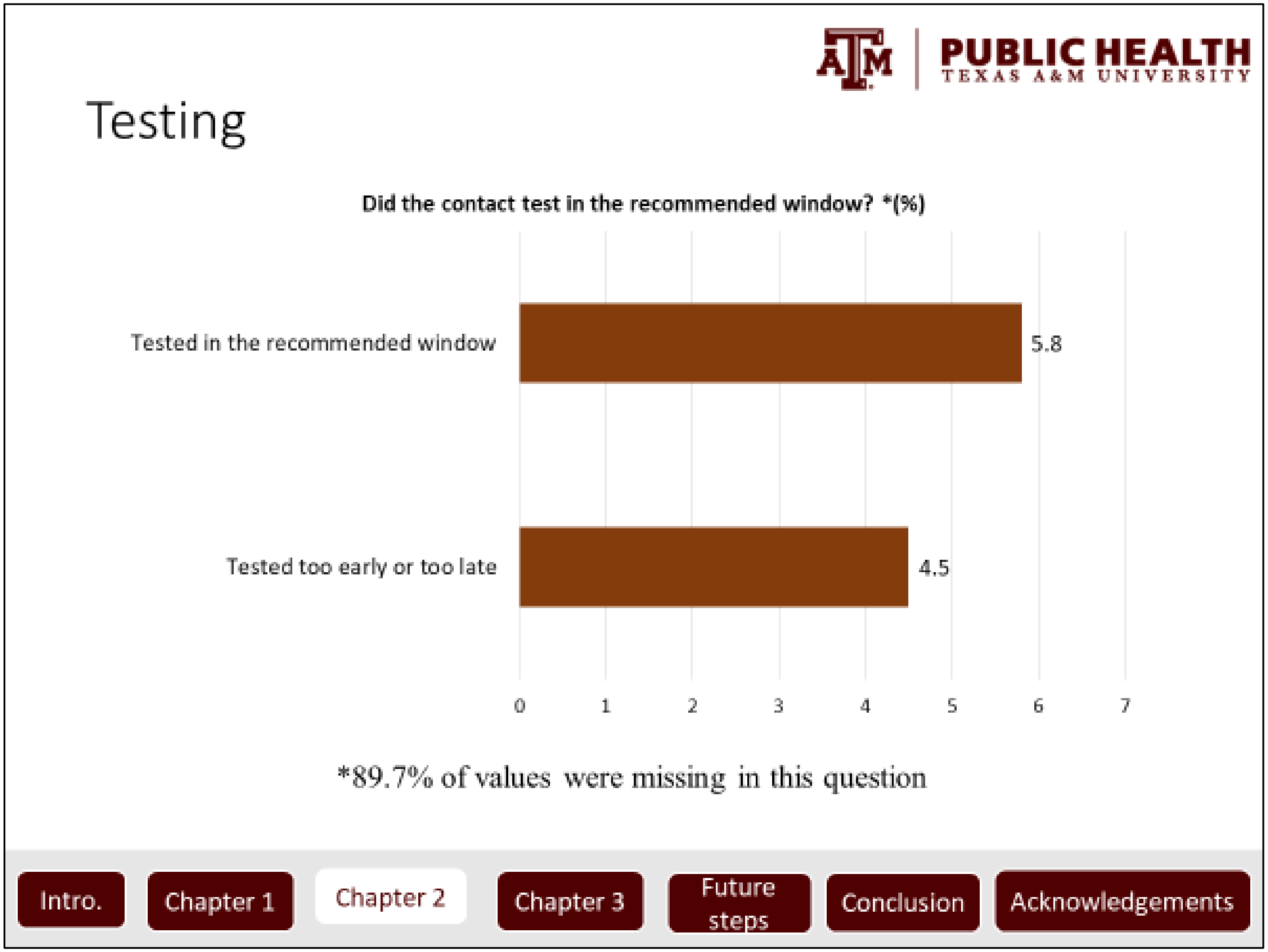
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Testing
Did the contact test in the recommended window? *(%)
Tested in the recommended window
5.8
Tested too early or too late
4.5
0
1
2
3
4
5
6
7
*89.7% of values were missing in this question
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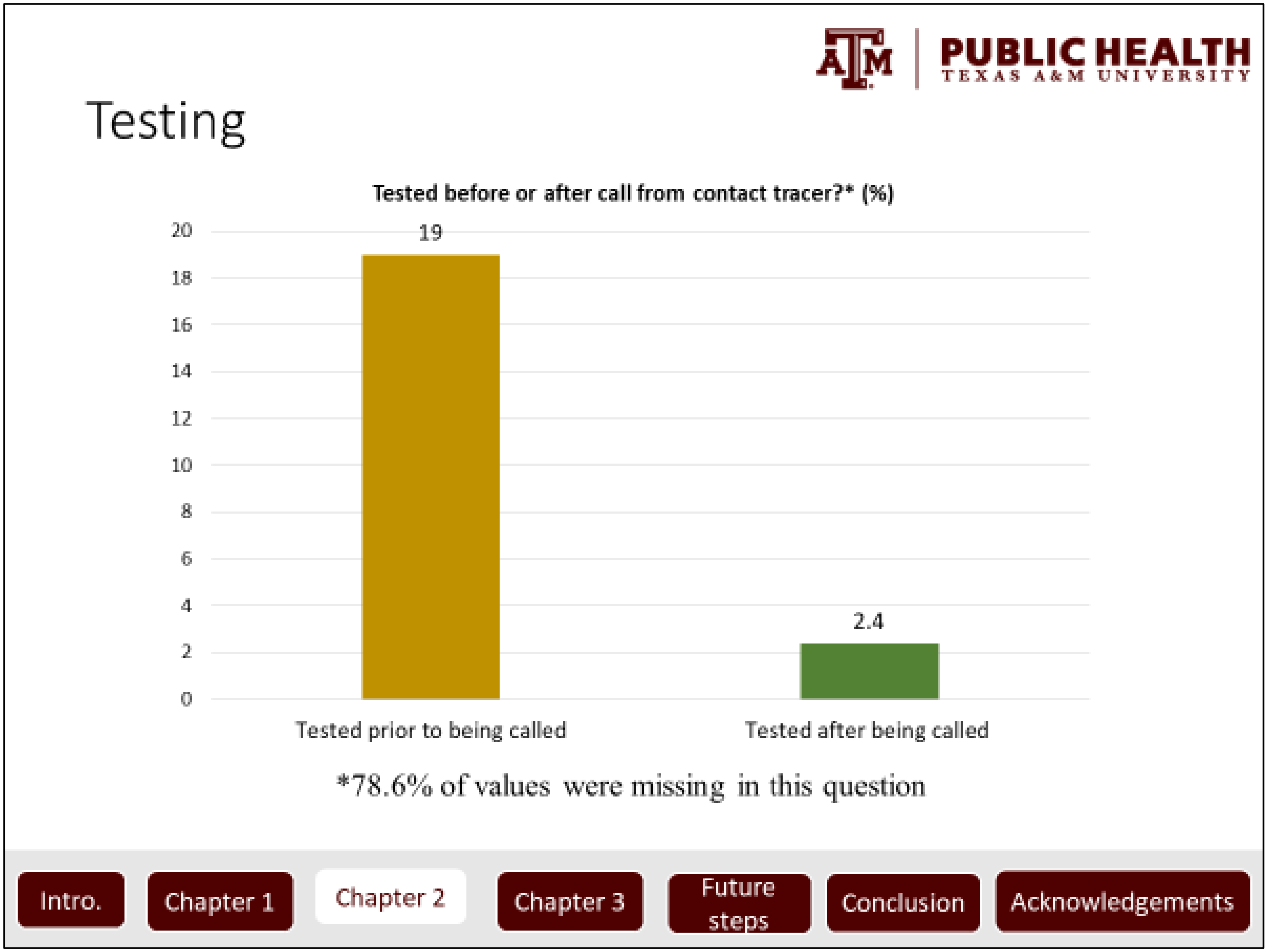
PUBLIC HEALTH
TEXAS A&M UNIVERSITY
Testing
Tested before or after call from contact tracer?* (%)
20
18
16
14
12
10
8
6
4
2
0
19
2.4
Tested prior to being called
Tested after being called
*78.6% of values were missing in this question
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What predicted someone more likely to test before or after a call from a contact tracer?

- Prior known contact with a positive case
  - People who knew their index case had higher odds of testing before being called by a contact tracer when compared to those who did not know their index case
  - OR: 0.2 (p=0.004; 95% CI: [0.1-0.6])

What predicted someone testing in the recommended window?

- Ages 10-19 years of age
  - People in these ages had lower odds of testing in the recommended window than testing too early/too late when compared to those ages 40-49 (referent group)
  - OR: 0.7 (p=0.033; 95% CI: [0.56-0.99])

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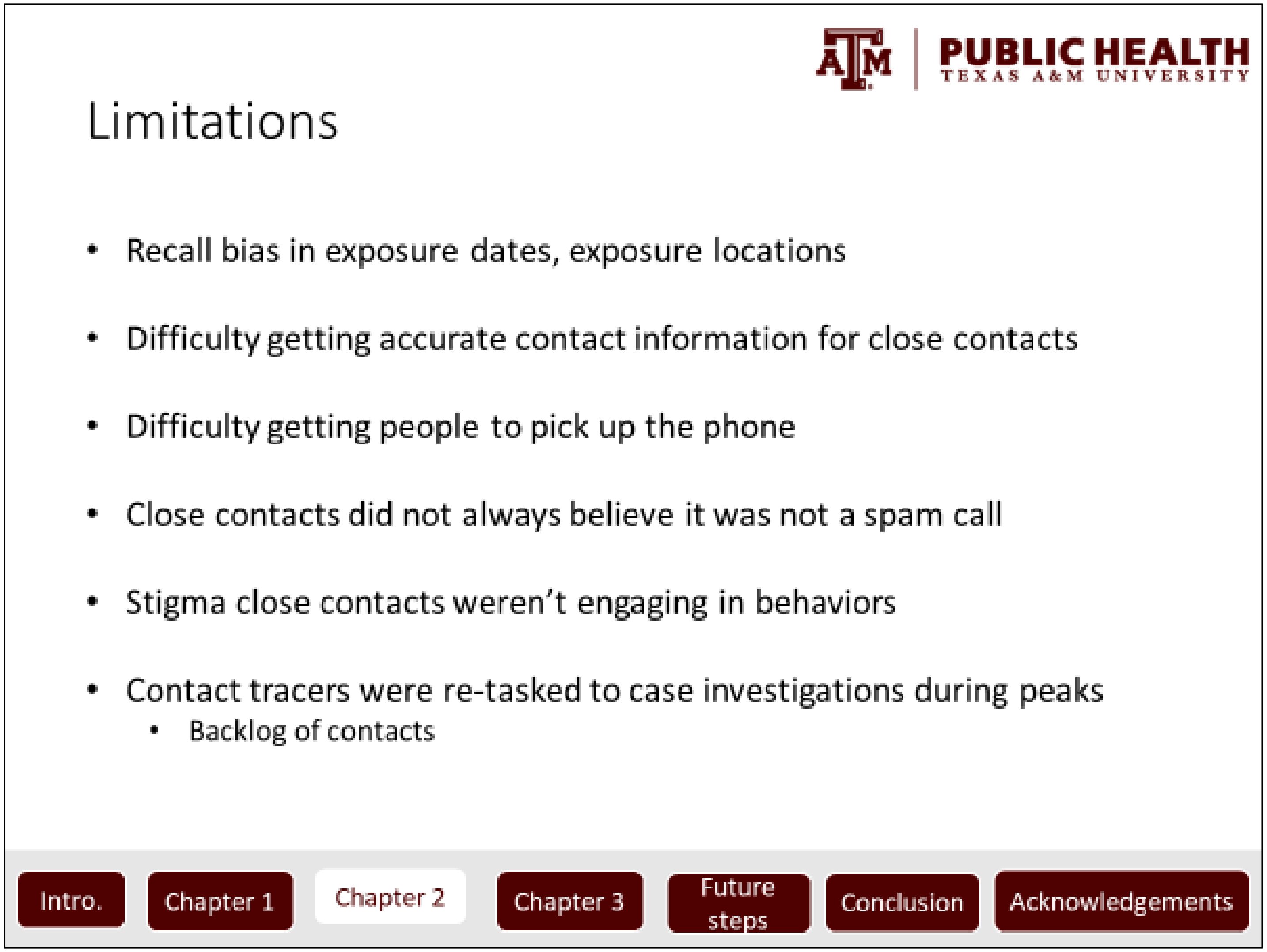
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Limitations
Recall bias in exposure dates, exposure locations
Difficulty getting accurate contact information for close contacts
Difficulty getting people to pick up the phone
Close contacts did not always believe it was not a spam call
Stigma close contacts weren't engaging in behaviors
Contact tracers were re-tasked to case investigations during peaks
Backlog of contacts
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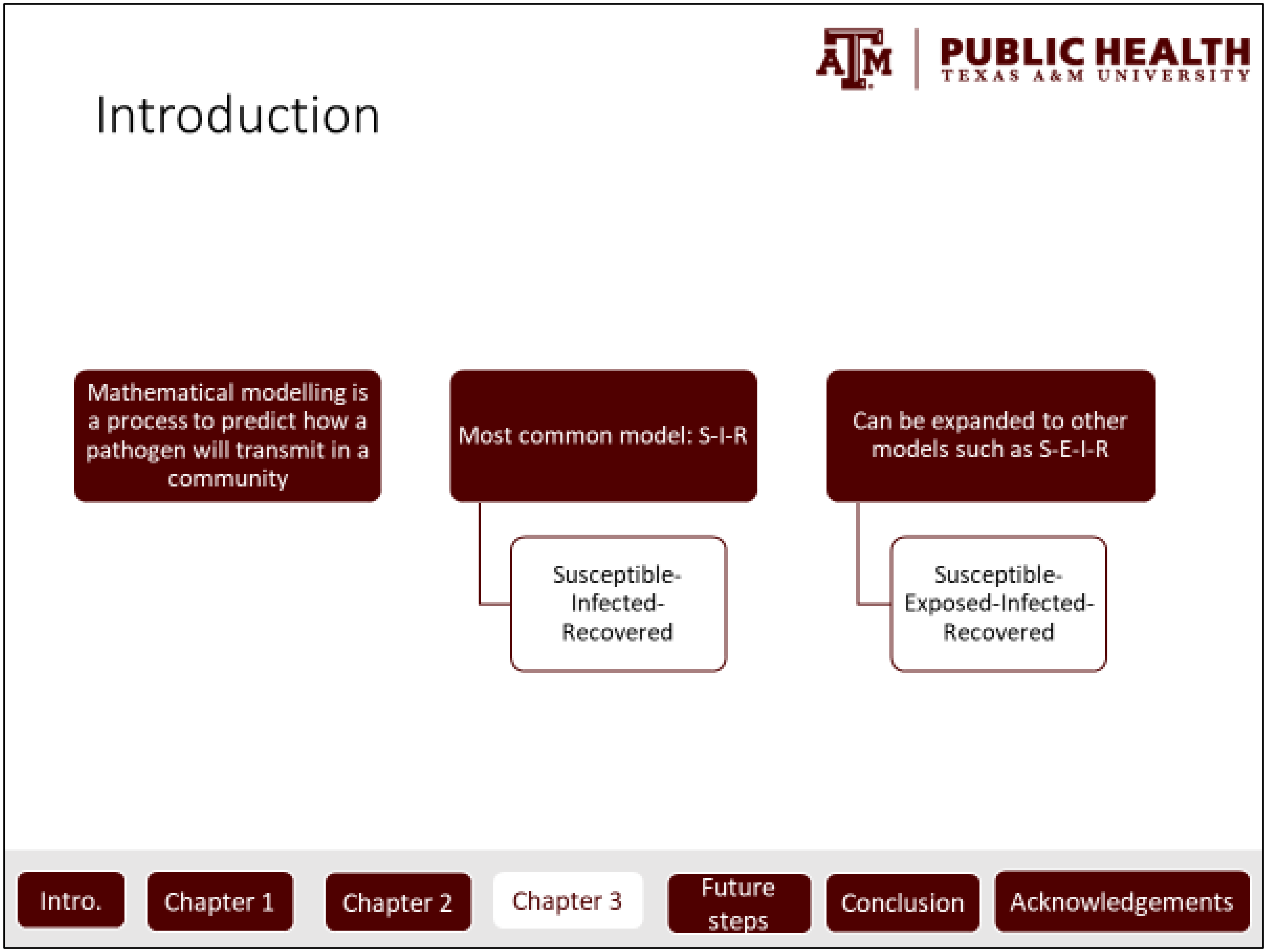
Conclusions

- Close contacts who provided a test date most often reported testing before a call from a contact tracer
  - Speaks to limitations of contact tracing
- Include guidance in case investigations to let the public health professionals give testing information
- Request health district provide statements to school districts on recommended testing

Chapter 3: Mathematical Modelling of COVID-19 in a university city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Introduction
Mathematical modelling is a process to predict how a pathogen will transmit in a community
Most common model: S-I-R
Susceptible-Infected-Recovered
Can be expanded to other models such as S-E-I-R
Susceptible-Exposed-Infected-Recovered
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Goals

1. Present difference of changing vaccination rates in a susceptible population
2. Highlight the effect earlier vaccination can have on mitigating an outbreak
3. Demonstrate importance of using appropriate models for an objective

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Intro to the S-E-I-R model

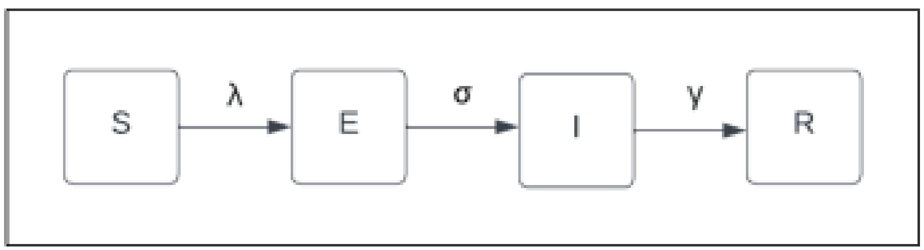
- Population size: $N = S + E + I + R$
- Transmission rate: $\beta = c * p$
- Force of infection: $\lambda = \frac{\beta * I}{N}$
- Recovery rate: $\gamma = \frac{1}{D}$
- Basic reproductive number: $R_0 = \frac{\beta}{\gamma}$

Basic parameters:

- Population size (N)
- Number of contacts per unit time (C)
- Pathogen infectivity (p)
- Duration of illness (D)
- Incubation period
- Basic reproduction number (R_0)

Intro to the S-E-I-R model cont'd

- Once you have the parameters, how do you get the compartments?
  - $\frac{dS}{dt} = -\lambda S$
  - $\frac{dE}{dt} = \lambda S - \sigma E$
  - $\frac{dI}{dt} = \sigma E - \gamma I$
  - $\frac{dR}{dt} = \gamma I$
- This basic model assumes a static population – no death



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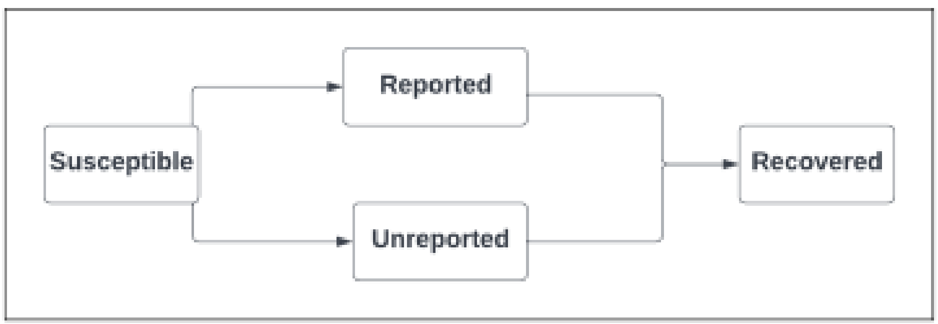
S-Re-U-R model

- Susceptible – Reported – Underreported – Recovered
- Main difference from previous models is it looks at infected/reported and infected/not reported



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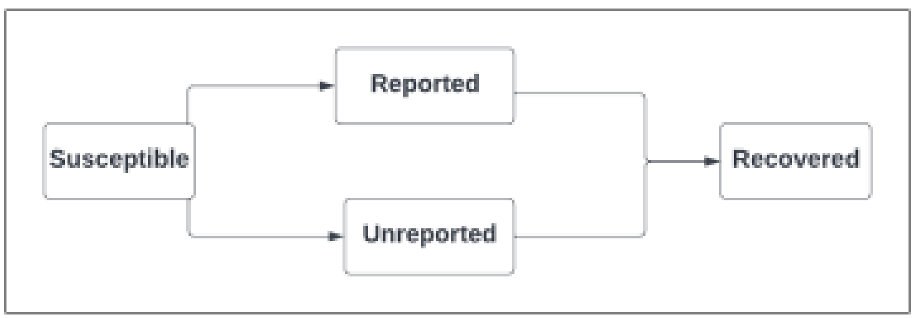
S-Re-U-R model

- S-Re-U-R specific equations:
  - Susceptible: $\frac{dS}{dt} = \frac{(-\beta * S * (Re + \varepsilon * U))}{N} + \lambda * R$
  - Reported: $\frac{dRe}{dt} = \frac{pr * (\beta * S * (Re + \varepsilon * U))}{N} - \gamma S * Re$
  - Unreported: $\frac{dU}{dt} = \frac{(1 - pr) * (\beta * S * (Re + \varepsilon * U))}{N} - \gamma U * U$
  - Recovered: $\frac{dR}{dt} = \gamma U * U + \gamma S * Re - \lambda * R$



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Methods

- Using the S-Re-U-R model and Matlab software
- Data was extracted from the case and contact databases
- Data used was from September 1, 2020-March 31, 2021
- Serial interval was calculated by matching close contacts to their associated cases.
- R software package EpiEstim was used to calculate R_t using parametric serial interval method
- R code produced R_t over time, the mean, median, standard deviation, and quantiles

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Methods – cont'd

- S-Re-U-R model created to match the data
- R_t derived from the model using the following equation:
  - $R_t = \frac{pr * \beta(t)}{\gamma_{Re}} + \frac{(1-pr) * \varepsilon * \beta(t)}{\gamma_U}$
- Where, $\beta(t) = q * c(t)$
  - q = probability of infection per contact
  - c(t) = contact rate

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Methods – cont'd

Parameter definition	Parameter symbol	Parameter values
Population	N	233849
Number of contacts per unit time	c	Derived from model
Transmission risk per contact	q	0.75
Relative infectivity of symptomatic to pre-symptomatic	ε	0.55
Recovery rate	γ	1/8
Proportion of symptomatic cases reported	pr	0.25

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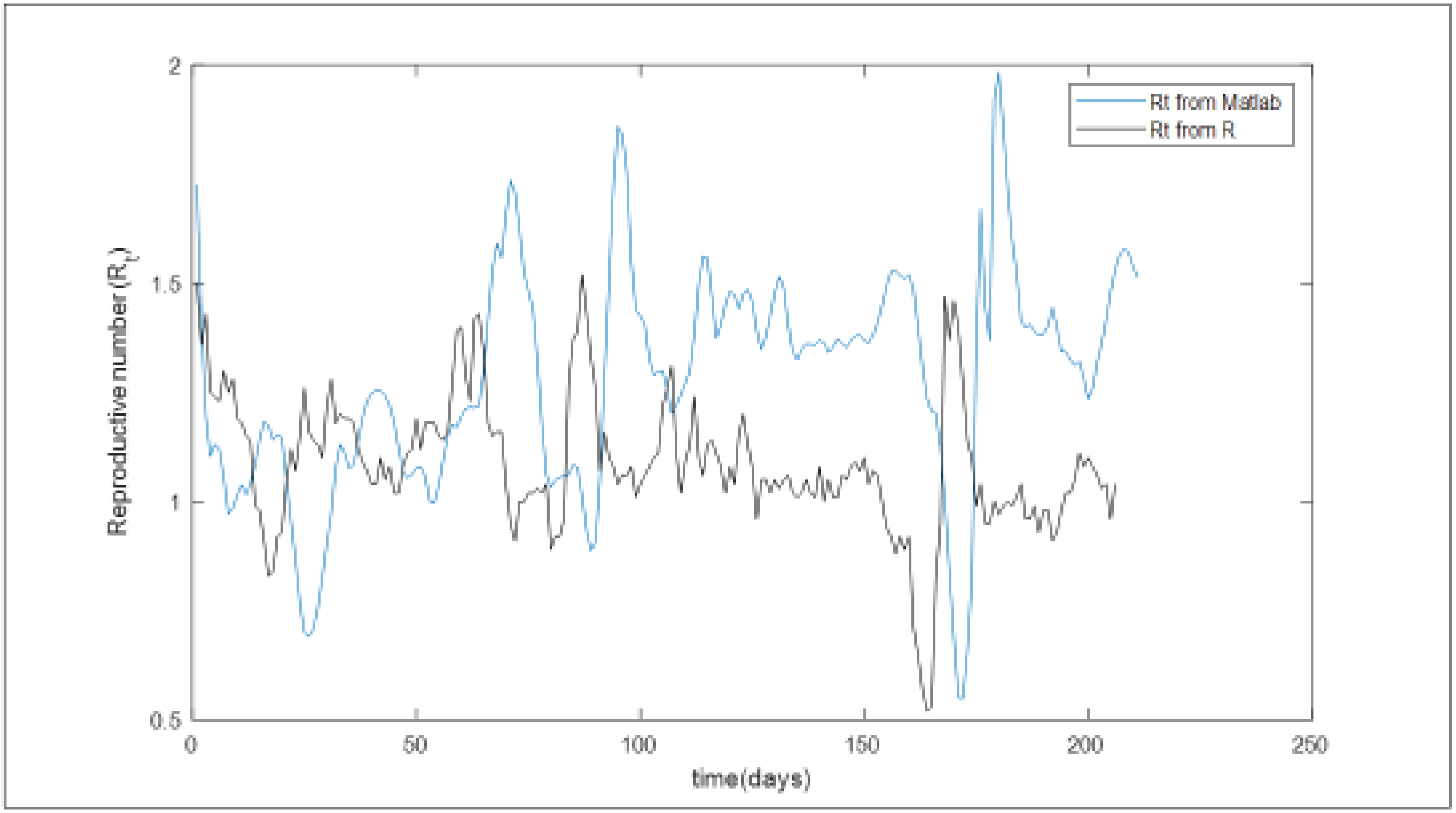
Methods

- Vaccination rates modeled:
  - No additional vaccination
  - 120 individuals vaccinated/day
  - 240 individuals vaccinated/day
  - 480 individuals vaccinated/day
  - 720 individuals vaccinated/day
- Vaccination dates modeled:
  - 1/8/2021
  - 12/13/2020
  - 12/1/2020
  - 10/30/2020
- Reporting changes modeled
  - Reporting 12% of cases and vaccinating 240 people/day
  - Baseline of reporting 25% of cases and vaccinating 240 people/day
  - Reporting 50% of cases and vaccinating 240 people/day

Results – calculating R_t



Results: S-Re-U-R model

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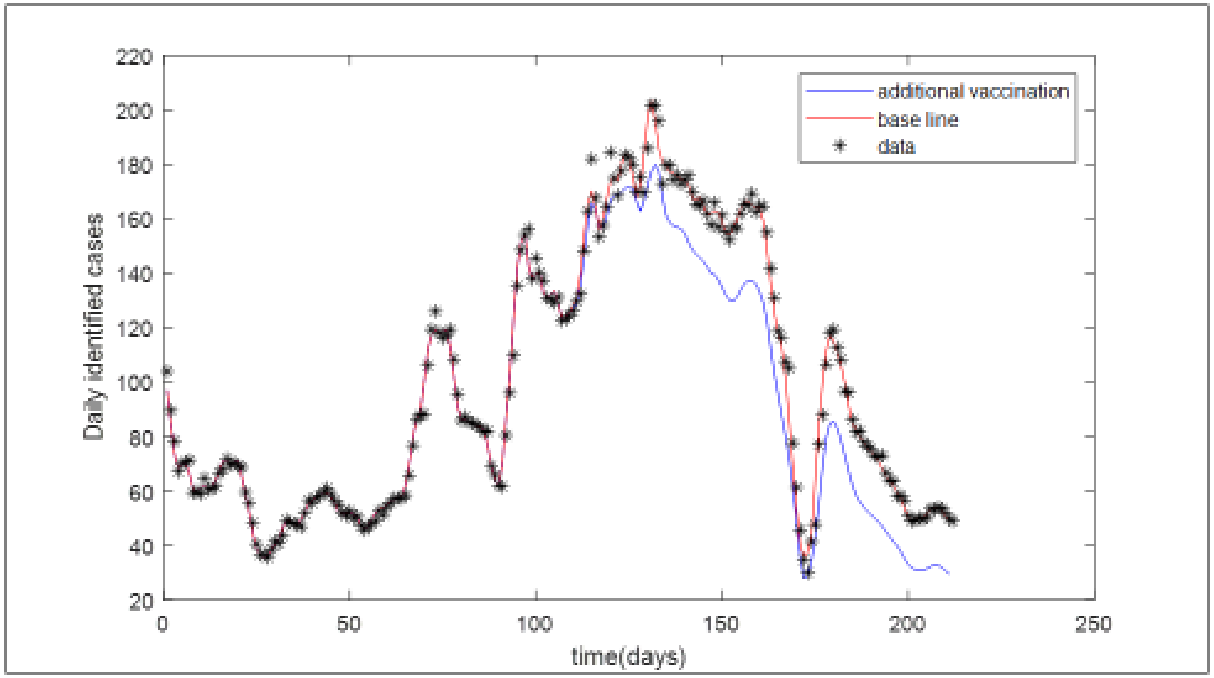

*Additional vaccination = constant 240 people vaccinated/day

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Results: S-Re-U-R model, different vaccination rates

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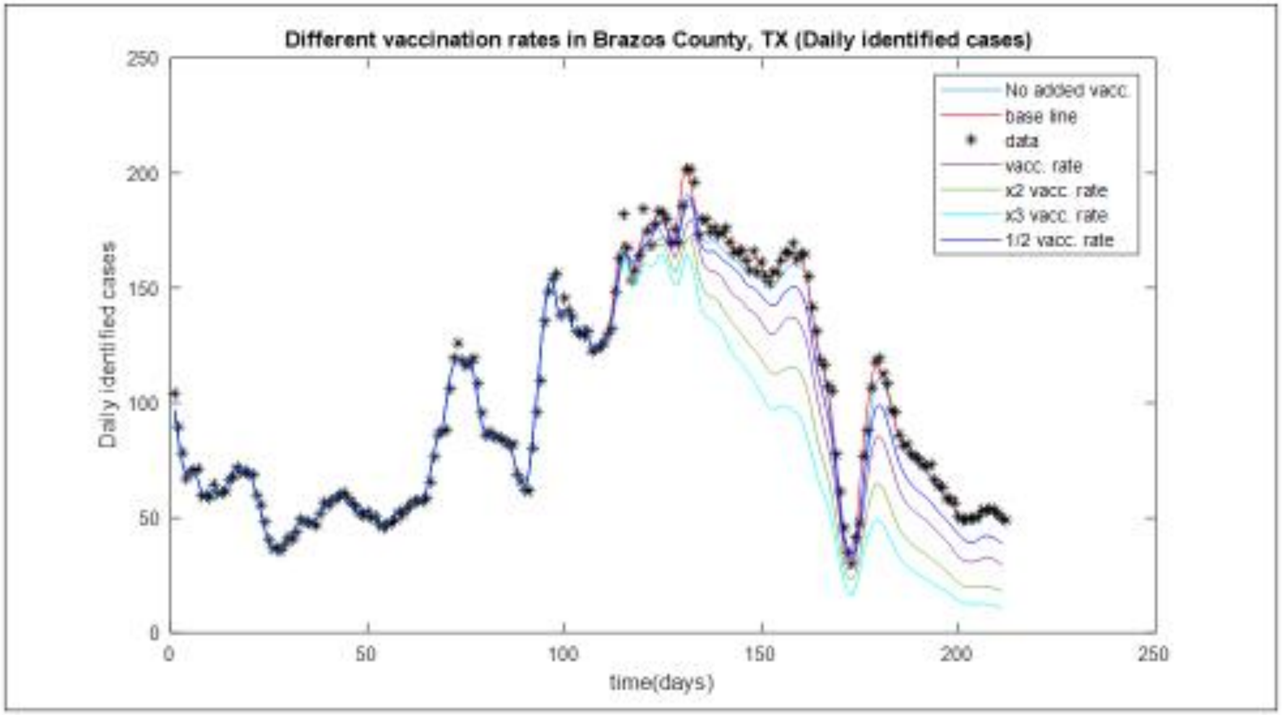

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Results: S-Re-U-R model, different vaccination rates

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No added Vacc.		½ Vacc. Rate		Vacc. Rate		x2 Vacc. Rate		x3 Vacc. Rate	
Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases
12426	1643	12426	1643	12426	1643	12426	1643	12426	1643
94753	1613	92088	1327	88544	1046	83627	676	79571	434
Averted cases		2665	285	6209	567	11126	936	15181	1178
% Averted		3	18	7	35	12	58	16	73

Results: S-Re-U-R model, earlier vaccination

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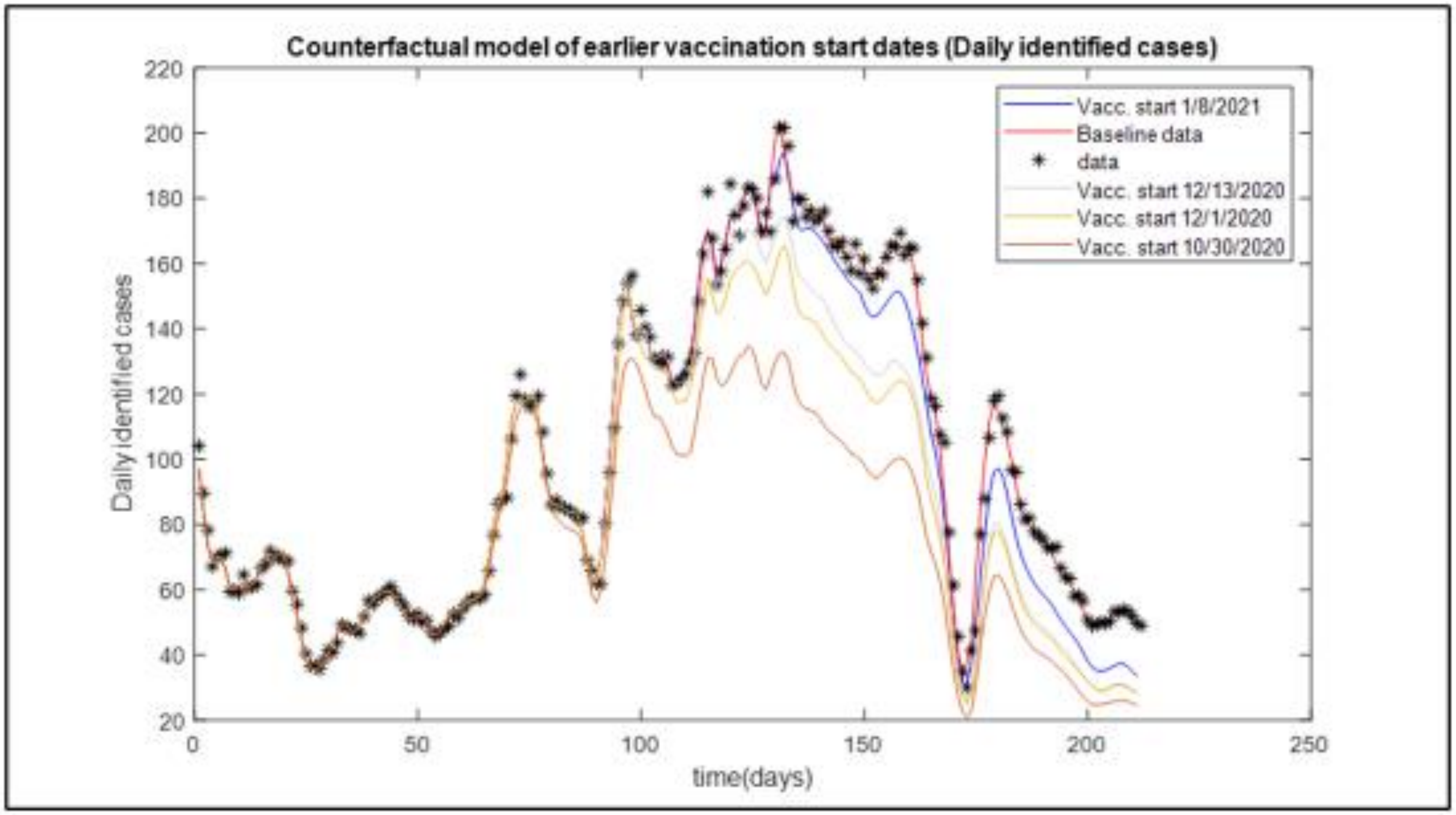

Results: S-Re-U-R model, earlier vaccination

Day 130		Day 104		Day 92		Day 60	
1/8/2021 Vacc. Start		12/13/2020 Vacc. Start		12/1/2020 Vacc. Start		10/30/2020 Vacc. Start	
Total cases	Active cases	Total cases	Active cases	Total cases	Active cases	Total cases	Active cases
12426	1643	12426	1643	12426	1643	12426	1643
92169	1192	87125	1000	84697	980	76220	835
Averted cases		5044	193	7472	212	15949	358
% Averted cases		5	16	8	18	17	30

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Results: S-Re-U-R model, reporting changes

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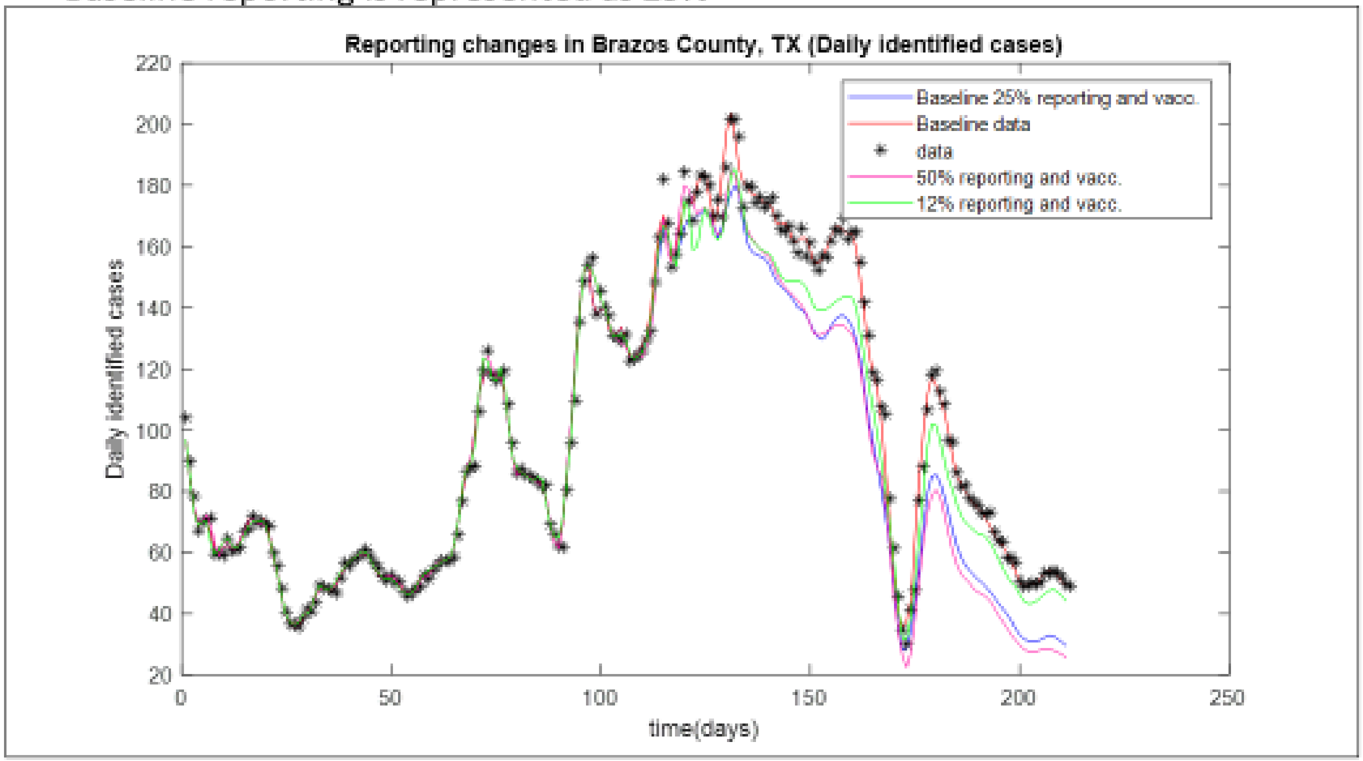
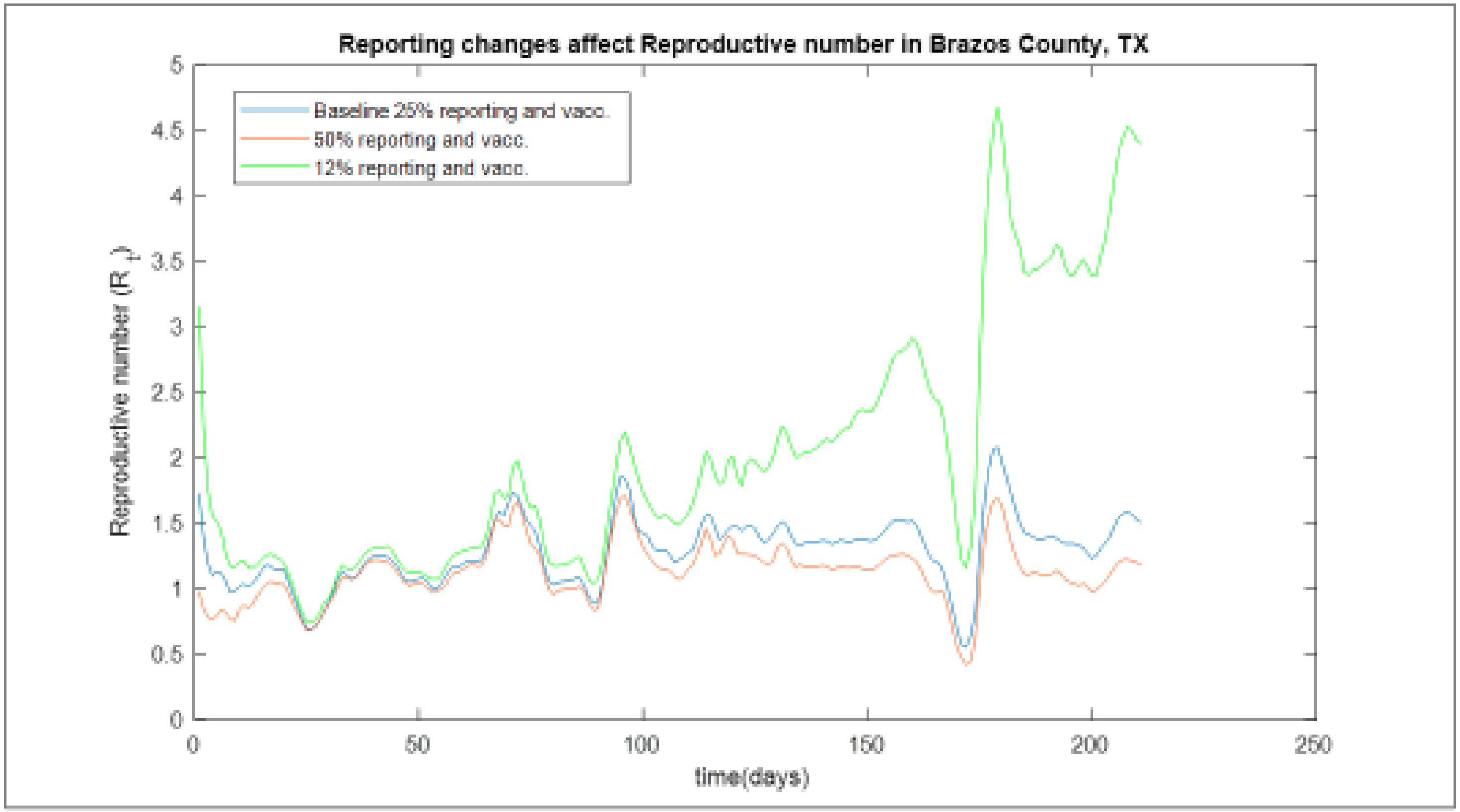
- Per CDC, on average, 1 in 4 or 25% of COVID-19 cases are reported.
- Baseline reporting is represented as 25%



Results: S-Re-U-R model, reporting changes



Discussion: R_t methods

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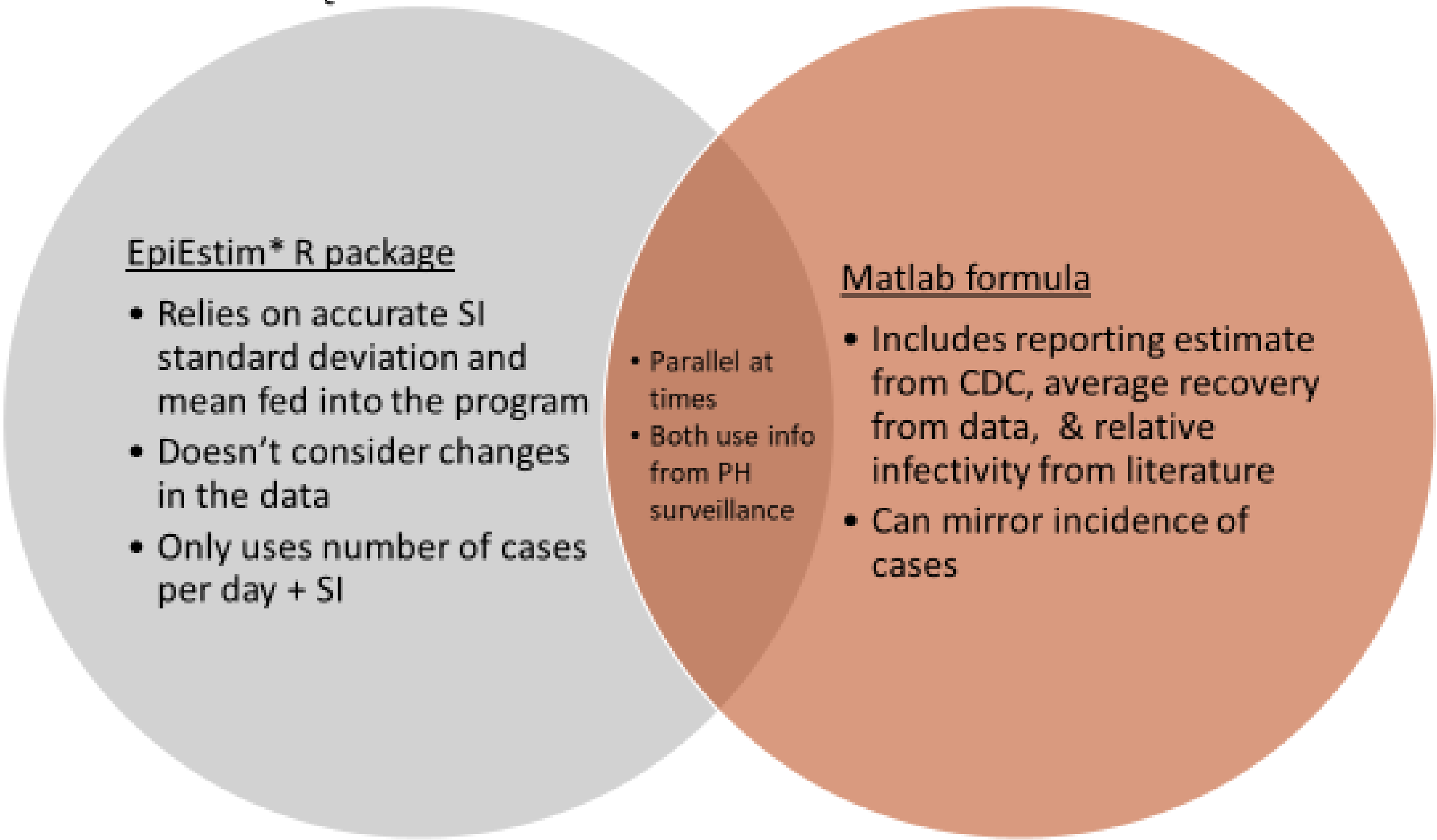

*Only applies to parametric method within the EpiEstim R package

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Discussion: S-Re-U-R model

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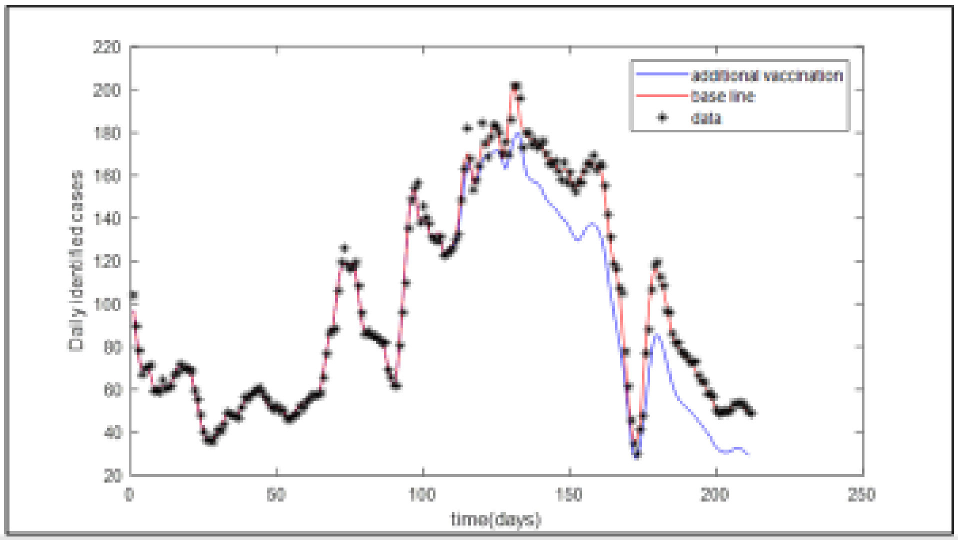
- Model matched to historical data alongside vaccination introduced on January 8, 2021
- Does not match actual vaccination in the area.
- Demonstrates need for true vaccination rates over time to model its effect on a population



Discussion: S-Re-U-R model, changing vaccination rates

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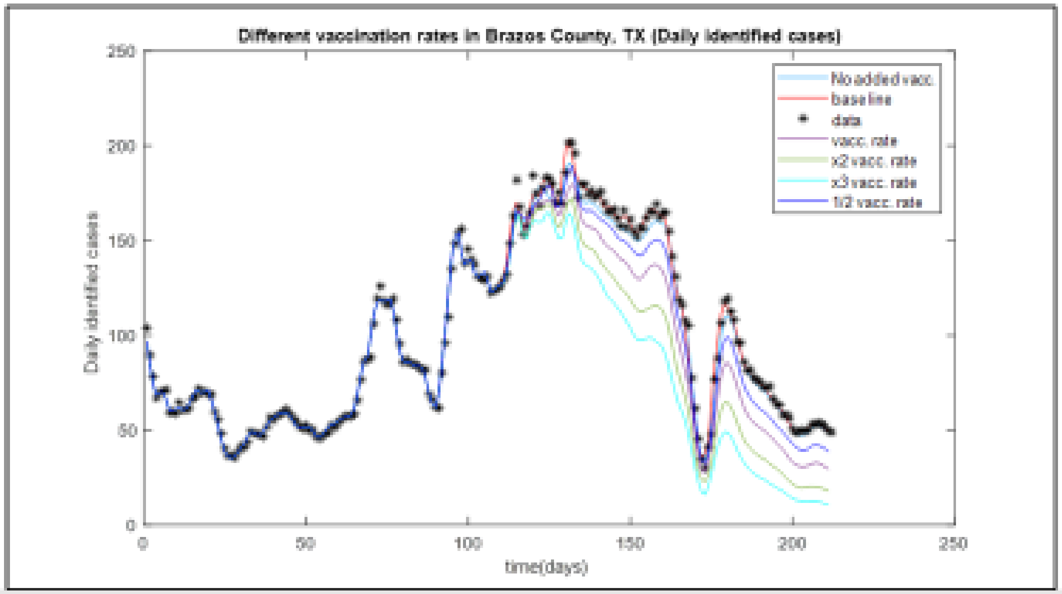
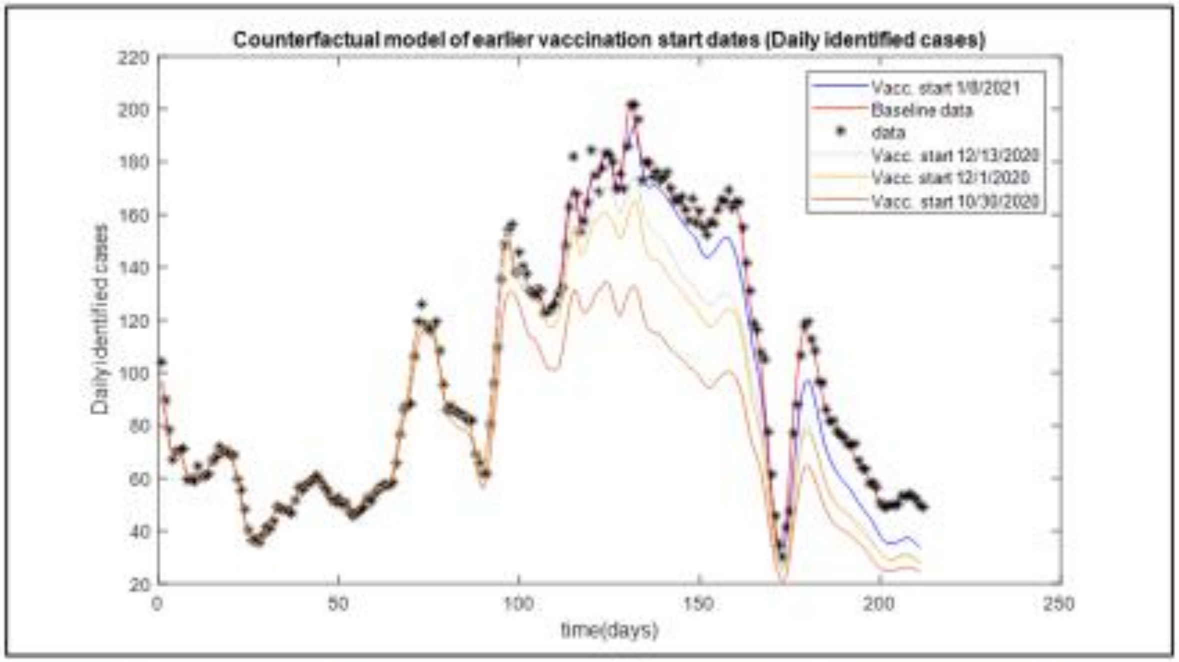
- Depicts how the epidemic curve would decrease with increase in vaccination rate.
- With only 120 people vaccinated/day, 3% of people may have avoided illness
- With up to 720 people vaccinated/day, 16% of people may have avoided illness
- Any increase in vaccination may have decreased the burden on healthcare
- There was inconsistent messaging, may have hindered vaccination rates



Discussion: S-Re-U-R model, earlier vaccination

- If vaccination began with TX DSHS phase 1A, would have averted 5% of cases
- Demonstrates how starting vaccine campaign at any earlier date would have avoided illnesses



Discussion: S-Re-U-R model, change in reporting

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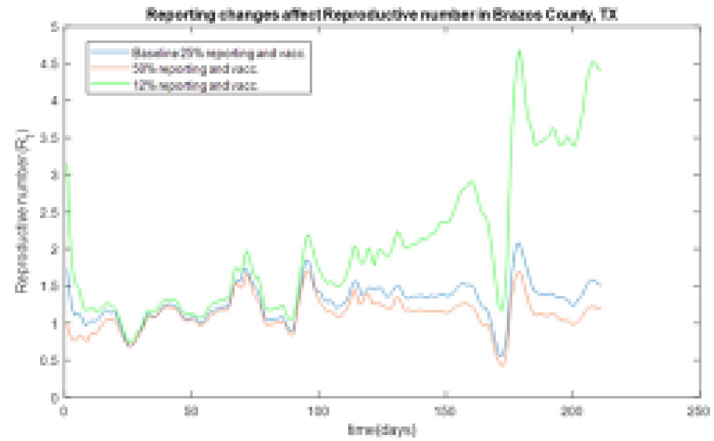
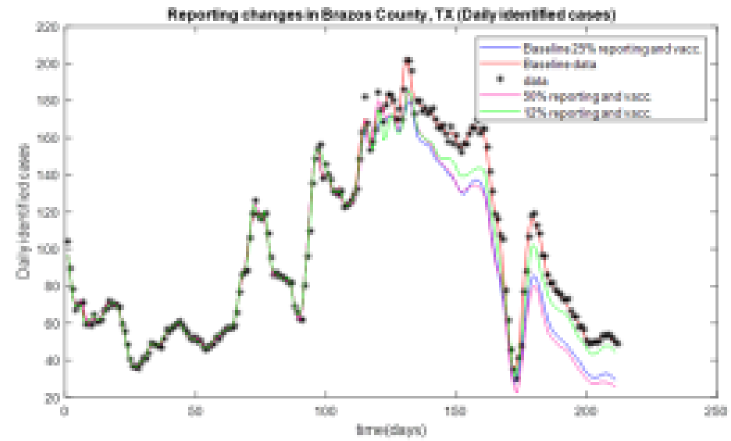
- Counterintuitive results
- Relationship due to set-up of equations in the model
- Suggests modeling reporting changes should be designed for that express purpose.





Policy implications

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- Earlier vaccination = mitigated spread
- Politicians were aware of anticipated vaccine release but may not have been informed of distribution challenges
- Recommended to begin developing vaccine distribution plan as soon as anticipated release is known

Future steps

Future steps

- More mapping!
- Compare clinical presentation for different variants
- Look at data past July 31, 2021
- Work on manuscripts

Conclusion

Conclusion

- Limitations on case investigations and contact tracing provide information on ways to improve
- Community transmission was present, but most transmission was in households, families & friends
  - They quickly tested for the virus, without waiting for public health guidance
- Some transmission and testing burden may have been avoided had vaccination begun earlier

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Questions?