UNCERTAINTY ANALYSIS AS A FIRST STEP OF DEVELOPING A RISK-BASED APPROACH TO NONPOINT SOURCE MODELING OF FECAL COLIFORM POLLUTION FOR TOTAL MAXIMUM DAILY LOAD ESTIMATES



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List of acronyms	
Acronyms	Full expansion or description
AGWETP	Fraction of remaining potential ET which can be satisfied from active
	groundwater storage.
BASETP	Fraction of remaining potential ET which can be satisfied from
	baseflow.
DEEPFR	Fraction of groundwater inflow which will enter deep groundwater.
ET	Evapotranspiration.
FSTDEC	First-order decay rate for generalized water quality constituent. The
	generalized quality constituent could be any of the non-conservative
CO CENIDECAN	pollutant considered for simulation.
GQ-GENDECAY	This block contains the constants of the first order decay equation of the quality constituent modeled
ЦС	Dent of important lond surface
ILS IMDI ND	This block contains the date newtoining to all impossions land
IMPLIND	surfaces
INFII T	Index that is used to calculate the infiltration canacity of the soil
INTEW	Parameter that is used to compute the inflow to interflow component
IRC	Parameter that is used to compute the shape of interflow recession
inc	curve.
KVARY	Parameter which affects the behavior of groundwater recession flow.
LSUR	Length of the overland flow plane.
LZETP	Lower zone ET parameter. Lower zone is the lower layer of the two
	zones present below the land surface and above the ground water.
LZSN	Lower zone nominal storage.
MON-INTERCEP	Monthly interception storage capacity.
MON-LZETPARM	Monthly lower zone ET parameter.
NSUR	Manning's n for the overland flow plane.
PERLND	This block contains the data pertaining to all pervious land surfaces.
PLS	Part of pervious land surface.
QUAL-INPUT	This block contains all the parameters that are associated with the
	generalized water quality constituents modeled under the pervious
	land surface and impervious land surface.
RCHRES	This block contains the data pertaining to all reaches or stream
	considered for modeling.
REISC	Surface retention storage capacity that designates any retention of
	moisture, which does not contribute to overland flow
SLSUK	Slope of the overland flow plane.
SQULIM	This is maximum storage of quality constituent on the land surface.
1851	constituent.
TWAT	Water temperature in the stream.
UZSN	Upper zone nominal storage. Upper zone is the upper layer of the two
	zones present below the land surface and above the ground water.

WSQOP	The rate of surface runoff that will remove 90 percent of quality
	constituent from the land surface (in/hr).

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EXECUTIVE SUMMARY

Salado Creek in Bexar County, Texas is one of 65 streams listed as impaired water bodies for its high concentration of fecal coliform bacteria in the Clean Water Act's 303(d) list. The Hydrological Simulation Program-FORTRAN (HSPF) available in the Environmental Protection Agency's (EPA) Better Assessment Science Integrating point and Non-point Sources (BASINS) computer model was applied to the Salado Creek watershed for studying its applicability as a prediction tool for in-stream fecal coliform bacterial concentration from both point and nonpoint sources associated with different types of landuses in the watershed. In addition, the sensitivity of simulated peak values of in-stream fecal coliform concentrations to changes in parameters associated with the bacterial simulation was evaluated. The hydrology of the watershed was calibrated for a period from 1990 January 1 to 1993 December 31. The model was validated for hydrology for the year of 1995. The simulated peak value of in-stream fecal coliform concentrations was found to be most sensitive to parameters that represent the maximum storage of fecal coliform on the pervious land surface and surface runoff that removes 90 percent of fecal coliform from the pervious land surface. In-stream fecal coliform concentrations were also sensitive to stream water temperature, first-order decay rate of fecal coliform and a temperature correction coefficient for the first order decay rate. A First Order Analysis (FOA) was conducted to determine the fraction of the variance of the simulated peak in-stream fecal coliform concentration due to the uncertainty in these

most sensitive parameters. The result of the FOA showed that the major portion of the variance in simulated in-stream peak fecal coliform concentration was attributed to the maximum storage of fecal coliform on the pervious land surface. Thus, the current study emphasizes the fact that small errors in parameterizing the maximum storage of fecal coliform over a given landuse class may result in large errors in predicted coliform counts.

INTRODUCTION

The transmission of human pathogenic agents via source water and treated water has been reported extensively in the literature (Barwick et al, 2000; Cruz et al., 1990; Carter et al., 1987). It is reasonable to believe that human population growth and anthropogenic activities such as intensive animal rearing and feeding operations are partially responsible for the contamination of water bodies. Given that a variety of microbial pathogen contamination sources do occur and will probably continue to occur in the future, modern society has to identify those water bodies that are contaminated or potentially vulnerable to contamination, and develop management and remediation strategies for those systems. However, evidence is mounting that these microbial organisms survive and proliferate in some ecosystems under specific climatic conditions. A geographic information system (GIS)-based geophysical model of the range of conditions and rates of proliferation of E. coli and coliphages would be a valuable tool in water quality management and human health protection. The objective of this project was to evaluate the effectiveness of the Hydrological Simulation Program-FORTRAN (HSPF), a GIS-based model, as a prediction tool for fecal coliform bacterial concentration, and to determine the sensitivity of the model to parameters associated with bacterial persistence and growth simulation.

The US Environmental Protection Agency (EPA), under its Clean Water Action Plan of 1996, emphasizes the need for State, local and tribal authorities to carry out a watershed level study and management approach in order to address the issues of nonpoint source runoff and pollution and restore the health of impaired waters. The restoration of water quality of the impaired streams starts with acquiring knowledge

about the system, such as the amount and sources of pollutant loading and the sources that need to be controlled.

Bacteria and Water Quality

The primary sources of pollution to the waters of the US are urban and agricultural runoff (USEPA, 1998). The most common pollutants from these non-point sources are nutrients, bacteria, and silt (USEPA, 1998). Thus, the persistence of potential microbial pathogens from wastes in soil and water is a constant concern. The Texas Natural Resource Conservation Commission (TNRCC) listed 148 stream segments in Texas as not meeting their designated use under the Clean Water Act, subsection 303(d) (TNRCC, 1998). Designated uses of streams include fishing, swimming, boating, wildlife habitat, agriculture, and industry. Bacterial contamination was listed as a pollutant of concern in 65 of these segments. Salado Creek in Bexar County, Texas was one of the streams found out to be unfit for human and wildlife consumption due to elevated concentrations of nutrients, fecal coliform bacteria and violation of dissolved oxygen standards (TNRCC, 1998). Subsequently, these water bodies have been included in the Federal Clean Water Act Section 303 (d) listing of impaired water bodies for Texas.

Fecal coliforms are a group of bacteria that primarily live in the lower intestines of warm-blooded animals, including humans. Many water-borne diseases, like dysentery and cholera, are associated with certain strains of E. Coli, which is but one category of fecal coliforms. Because of the serious potential health threat associated with certain strains of this general type of bacteria, the fecal coliform test is very important as an indicator of the health risk associated with human contact with a body of water. Fecal

coliforms are rare or absent in unpolluted waters because they are associated with warmblooded mammals.

Coliform Terminology and Measurement

Coliform bacteria are a collection of relatively harmless microorganisms that live in large numbers in the intestines of animals. Fecal coliforms, a subgroup of these bacteria, can grow at elevated temperature, and include bacteria such as *E. coli*. US EPA and TNRCC use the presence of fecal coliform bacteria in aquatic environments as an indicator that water bodies have been contaminated with fecal material and other pathogens. This contamination may result in exposure of humans and wildlife to harmful pathogens causing typhoid fever, hepatitis A, and other adverse health effects. The methods used to measure fecal coliform bacteria are prone to interferences, but continue to be used because they are the most cost-effective and practical methods currently available (APHA, 1997).

The detection of specific pathogenic microorganisms (bacteria, viruses, protozoa) is an extremely time consuming and expensive approach. For certain pathogens such as the caliciviruses (eg Norwalk virus) tissue culture systems are yet unavailable, which precludes an accurate estimation of pathogen loads in environmental samples. To overcome some of the limitations associated with the detection of specific microbial pathogens, the use of indicators to detect fecal contamination have been proposed. The rationale behind this approach is that if a particular water sample is fecally contaminated, then the probability that the sample contains pathogens is greater. A number of different microbial and chemical indicators of fecal contamination have been proposed. These

include total coliforms, *E. coli*, male specific coliphages, *Bacteroides fragilis* phages, fecal streptococci, sulfate-reducing clostridia, H₂S producers, and fecal sterols.

Total Coliforms. Total coliforms are defined as a heterogeneous group of Gram negative, non-spore-forming bacteria that are rod shaped, and ferment lactose with the production of acid and gas within 24 to 48 hours at 35°C. The coliform group has been used as the standard for assessing fecal contamination of recreational and drinking waters for most of the past century (Gerba, 2000). There are a number of limitations associated with the use of total coliforms as indicators. Studies have shown that there is significant regrowth in aquatic environments in both source and treated water (Gleeson and Cray, 1997). Additionally, the die-off rate of this organism is strongly influenced by the presence of organic matter and temperature. Other studies have shown that these organisms can originate from non-enteric sources such as wastes from the wood industry (Toranzos and McFeters, 1997) and epilithic algal mat communities in pristine streams. A primary limitation of total coliforms as an index of fecal contamination is that they are capable of regrowth even within distribution systems in the presence of free chlorine (LeChevallier et al., 1988). In water bodies rainfall events would cause a proliferation of these cells.

Fecal Coliforms. The fecal coliform group of organisms can be considered to be a subset of the larger "total coliform" group. Fecal coliforms are defined as Gramnegative, non-spore-forming, rod shaped bacteria that are able to ferment lactose with the production of acid and gas within 24 hours at an elevated temperature ($44.5\pm0.2^{\circ}$ C). Studies have shown that for the most part, fecal coliforms show strong correlation with fecal contamination from warm-blooded animals (Pourcher et al., 1991). The rationale

for the elevated temperature criterion is the elevated temperature found in mammalian enteric tracts. Though the incubation conditions are meant to select for those organisms that are indicative of fecal contamination, it does not distinguish human and animal contamination. There have been reports that fecal coliforms including *E. coli* have been detected in pristine tropical waters (Hazen and Toranzos, 1990; Toranzos, 1991; Solo-Gabriele et al., 2000) and that they can possibly proliferate outside the intestines of warm-blooded animals. Recent studies have also shown that fecal coliforms do not correlate positively with the presence of infectious enteric viruses. There have been studies that have documented viral infections from water samples that have been negative for fecal coliforms and *E. coli*.

E. coli. Escherichia coli, a member of the fecal coliform group of organisms, has been shown to be a useful microbiological indicator of water quality. A major drawback for their use, however, is the isolation of *E. coli* from tropical regions and the recent findings suggesting natural proliferation of the cells in subtropical coastal waterways (Hazen and Toranzos, 1990; Solo-Gabriele et al., 2000).

The Total Maximum Daily Load (TMDL) Process

A TMDL determination is an analysis used to calculate the maximum pollutant load a water body can receive (loading capacity) without violating water quality standards (Hession et al., 1995; Hession et al., 1996b). TMDLs establish waste load allocations (WLAs) for point sources, load allocations (LAs) for non-point sources, background loadings from natural sources, and a margin of safety to ensure achievement of the water quality goal (USEPA, 1991). The TMDL process has five distinct steps (USEPA, 1991):

- 1. Identify pollutants of concern
- 2. Estimate the waterbody's assimilative capacity for those pollutants
- 3. Estimate the pollution loading from all sources to the waterbody
- 4. Determine the total allowable pollutant load to the waterbody
- 5. Allocate pollutant loading limits to each source, including a margin of safety.

The difficulty with applying this approach to fecal coliform bacteria is that the units of measure, colony forming units (CFU), per 100 ml do not consider time or growth and reproduction based on source. The assumption is that fecal coliform bacteria, or those indicated on the American Society for Testing and Materials (ASTM) test method as fecal coliform bacteria do not grow *ex situ*. However, bacteria pathogenic to humans are known to survive in soil for defined periods of time. These bacteria may in fact persist and reproduce in warm, southern streams with high sediment and organic carbon loading (Jones and Mathews, 1975; Ginnivan et al., 1980; Kudva et al., 1998; Kunte et al., 1998). Recently Solo-Gabriele et al. (2000) have shown that *E. coli* could proliferate in subtropical waterways in Florida.

Factors affecting fecal coliform kinetics

There are a number of factors, which affect the fate of bacteria in general and fecal coliform in particular. These factors can be divided into physical, physicochemical and biochemical and biological factors. Some of the important factors and the way they affect the fate of fecal coliform are given in Table 1.

Category	Factors	Effect		
	Photo-oxidation	Light increases the mortality of fecal coliform		
	Adsorption	Affects fecal coliform mortality, but		
		inconclusive data available		
	Flocculation	Affects fecal coliform mortality, but		
		inconclusive data available		
	Coagulation	Affects fecal coliform mortality, but		
		inconclusive data available		
	Sedimentation	May decrease the mortality rate by depositing		
Physical		the fecal coliforms to the bottom of the stream		
		bed		
	Temperature	This is the most important factor affecting the		
		fate of bacteria. Other than directly affecting		
		the mortality rate, temperature affects other		
		factors which affect the mortality rate of		
		bacteria		
	Osmotic effects	Salinity is an important factor in the case of E. Coli.		
	рН	Generally E. Coli survives longer in lower pH		
	Chemical toxicity	In general the presence of heavy metals		
		reduces the bacterial concentration		
Physicochemical	Redox potential	The higher the redox potential the higher is		
		the mortality rate of bacteria		
	Nutrient level	Increase in nutrient level may increase amount		
		of in-stream fecal coliform		
	Presence of	May decrease mortality rate		
	organic substance			
Biochemical-	Predators	May increase the mortality rate		
biological	Algae	In general, detrimental to bacteria because of		
g		production of toxic substance along with algal		
		boom.		
	Presence of fecal	Increase the concentration of fecal coliform.		
	matter			

Table 1. Factors affecting the fecal coliform die-off rate

Modeling of Fecal Coliform

There are a number of models available for the modeling of fecal coliform. Some of the models used are Agricultural Runoff Management II: Animal Waste Version (ARM II) model (Overcash et al., 1983); the Utah State (UTAH) model (Springer et al., 1983); the MWASTE model (Moore et al., 1988); the COLI model (Walker et al., 1990); and HSPF model (Bricknell et al., 1993). All of these models calculate the bacterial dieoff using the first order exponential decay expressed as Chick's Law (Moore et al., 1988) directly or with some modifications.

According to Chick's law, the die-off of fecal coliform bacteria follows a first order decay rate given by the equation,

$$C_t = C_0 e^{-kt} \tag{1}$$

where $C_0 = initial \ colliform \ concentration, \ (count/100ml)$

 C_t = coliform concentration at time t, (count/100ml)

 $k = first order decay rate, (day^{-1})$

and t = exposure time, (days)

The MWASTE model modifies Chick's Law by adjusting the die-off rate constant based on temperature, manure application method and soil pH. The COLI model combines the Modified Universal Soil Loss Equation (MUSLE), Chick's Law, a cell density factor and a temperature adjustment equation (Walker et al., 1990) to determine the amount of bacteria lost from land-applied waste. The HSPF model allows both accumulated and fresh manure to contribute to bacterial losses from land-applied manure.

The main drawback of these models is that they all are highly dependent on the first order decay equation. None of them take into consideration the chance of re-growth of fecal bacteria under feasible conditions. Though HSPF is capable of handling the processes under urban conditions, most of the models mentioned earlier are suitable for agricultural and pasture lands but do not take into account the processes under urban conditions.

Uncertainty in Modeling

In recent years US EPA recognized the importance of incorporating the variability and uncertainty in risk assessment (USEPA, 1997). They pointed out that probability analysis techniques like Monte Carlo analysis are useful tools in adequately quantifying variability and uncertainty (Chang, 1999).

In most watershed-level assessment and management activities the only thing we are sure of is that we are "in doubt" (Hession et al., 1996a, 1996b, 1996c). There are many uncertainties inherent in such activities including: monitoring/measurement error, model error, model input parameter errors, spatial variability, errors in spatial data layers within a GIS, the effects of aggregation of spatial data when modeling watersheds, and temporal variability. These different errors or uncertainties may or may not be additive.

The importance of incorporating uncertainty analysis into ecological models has been emphasized by many authors (Beck, 1987; Reckhow, 1994; Haan et al., 1995; Kumar and Heatwole, 1995; Hession et al., 1996a, 1996b, 1996c). Rejeski (1993) referred to "modeling honesty" as the truthful representation of model limitations and uncertainties. Beven (1993) and Haan (1995) suggested that the inclusion of uncertainty analysis in modeling activities can be interpreted as intellectual honesty. Reckhow (1994) suggested that all scientific uncertainties must be estimated and included in modeling activities. However, few, if any, existing pollutant transport and fate models include thorough uncertainty analyses (Suter, 1993; Reckhow, 1994).

Many types of uncertainties have been identified in the literature utilizing various taxonomic breakdowns (Morgan and Henrion, 1992). Haan (1989), in discussing uncertainty in hydrologic models, classified uncertainty into three categories: the inherent variability in natural processes, model uncertainty, and parameter uncertainty. Similarly,

Suter et al. (1987) proposed a taxonomy of uncertainty identifying three sources of analytical uncertainty: 1) errors resulting from our conceptualizations of the world (model error), 2) stochasticity in the natural world, and 3) uncertainties in measuring model parameters (parameter error).

MacIntosh et al. (1994) defined the major types of uncertainty as knowledge uncertainty and stochastic variability. Knowledge uncertainty is due to incomplete understanding or inadequate measurement of system properties. This uncertainty is a property of the analyst and can also be considered subjective uncertainty (Helton, 1994). Knowledge uncertainty can be further partitioned into model and parameter uncertainty. Stochastic variability is due to unexplained random variability of the natural environment and is a property of the system under study. Stochasticity can be further subdivided into temporal and spatial variability.

Uncertainty is not a desirable aspect of modeling investigations for watershedlevel assessment and management. However, uncertainty and stochasticity are ubiquitous in such analyses and must not be ignored. In the past, the incorporation of a quantitative uncertainty analysis into modeling activities required special expertise and computing power. However, the accessibility of powerful personal computers and spreadsheetbased Monte Carlo analysis software make it possible for most assessors and managers to "honestly" incorporate uncertainty analysis into their analysis, thereby allowing for more knowledgeable decision making.

The current study was aimed at analyzing the HSPF model to find out its applicability as a prediction tool for fecal coliform bacterial concentration, to evaluate the sensitivity of the parameters associated with the bacterial simulation and to determine the

fraction of the variance in peak in-stream fecal coliform concentrations due to the uncertainty of these most sensitive parameters.

METHODOLOGY

Overview

The study was conducted using the tools available in BASINS system framework. The main steps involved are:

- 1. Calibration of the watershed hydrology component of HSPF.
- 2. Validation of the fecal coliform component of HSPF.
- 3. Sensitivity analysis of HSPF to identify parameters that may have the most effect on variability in peak in-stream fecal coliform concentration predictions.
- 4. Uncertainty analysis using the First Order Analysis technique to identify which parameters contribute the most to output variability.

Model Description

BASINS was developed by the US EPA's Office of Water to support environmental and ecological studies in a watershed context (USEPA, 2001). BASINS works within a GIS framework and comprises various components including (1) national databases (2) assessment tools (3) a watershed delineation tool (4) classification utilities (5) characterization reports (6) an in-stream water model, *QUAL2E* (7) watershed loading and transport models, *HSPF* and Soil and Water Assessment Tool, (*SWAT*); and (9) a simplified GIS based model, *PLOAD* that estimates annual average nonpoint source pollutant loads. Different programs employed in the current study and their interactions are shown in Figure 1.



Figure 1. Computer programs employed in the project

HSPF is a continuous hydrological modeling software that can be used to simulate a comprehensive range of hydrologic and water quality processes. HSPF has a modular structure and the watershed is divided into three groups: pervious land, impervious land and channels or reaches. The modules PERLND, IMPLND and RCHRES in HSPF simulate the processes that occur in a pervious land segment, an impervious land segment and a single reach respectively. The spatial distribution of different land segments within a particular watershed is not considered in HSPF. Though HSPF is a versatile model, it is WinHSPF (Windows interface to HSPF), which provides the user an interactive graphical user interface (GUI). WinHSPF was created for the BASINS 3.0 system replacing the earlier program called Non Point Source Model (NPSM) used in combination with BASINS 1.0 and BASINS 2.0. WinHSPF helps the user to create a new HSPF input sequence or to modify an existing HSPF input sequence. WinHSPF also makes it easier to modify the input sequence for HSPEXP, an expert system developed by United States Geological Survey (USGS) for assisting users in calibrating HSPF. Figure 2 shows an HSPF project opened with the WinHSPF interface.



Figure 2. Graphical User Interface of WinHSPF opened with an HSPF project

The required meteorological data for the HSPF program is stored in a Watershed Data Management (WDM) file format. The WDMUtil program allows users to import available meteorological data into WDM files. The new WDMUtil 2.0 allows importing of data sets of various time steps and formats.

GENeration and analysis of model simulation SceNarios (GenScn) is a GUI based program for creating simulation scenarios, analyzing the results and comparing scenarios. The program can be used to run the HSPF model after changing the input sequence interactively and to view the results graphically for further analysis. Some of the plots that can be obtained from GenScn are a standard time-series plot, a residual time-series plot versus another time-series, a cumulative differences time-series plot and a scatter plot of two time-series including an optional 45-degree line and regression line. Three statistical analyses available in GenScn are comparing two time-series over a range of class intervals, constituent duration analysis, and frequency analysis.

HSPEXP, an Expert system for calibration of HSPF interactively allows the user to edit the input sequences of HSPF, simulates with HSPF, plots the output from the HSPF against different observed values and computes error statistics. Using a set of over 35 rules and 80 conditions, the system advises the users of necessary changes on different parameters to improve the calibration.

Study Area

The location of the Salado Creek study area is between latitudes 29.735 N and 29.147 N and longitudes 98.649W and 98.221 W. Salado Creek is one of the major tributaries of the San Antonio River with a total length of approximately 32 miles (Figure 3). The creek originates in the north central region of the San Antonio River basin and

flows in the eastern region of the San Antonio metropolitan area and joins the San Antonio River at the south end. The total area of the delineated watershed is 123,155 acres.

Climatic Data Used

Climatic data stored in WDM file corresponding to Texas (tx.wdm) was used. The weather station used was located at the San Antonio International Airport.

GIS Data Layers for Salado Creek

The Salado Creek Watershed is located within the Hydrologic Unit Code (HUC) 12100301. BASINS core data corresponding to HUC 12100301 was obtained from EPA's BASINS data web site. This includes GIS data layers required to create the BASINS project. These data sets include different data layers such as Land Use/ Land Cover, STATSGO Soils data, and Reach Network Version 1, all of which are at 1:250,000 scale.

The Digital Elevation Model (DEM) at 1:24,000 scale with a spatial resolution of 30m was obtained from Texas Natural Resources Information System (TNRIS). These are grids covering a full 7.5-minute USGS quadrangle. The DEMs for the entire Bexar County were obtained from TNRIS and mosaiced together for the current study.



Figure 3. Salado Creek Watershed, Bexar County, Texas

The detailed stream network for the HUC was obtained from National Hydrography Dataset (NHD) using the NHD download tool available with BASINS 3.0. NHD is based upon the content of USGS Digital Line Graph (DLG) hydrography data integrated with reach-related information from the EPA Reach File Version 3 (RF3). It is a comprehensive set of digital spatial data that contains information about surface water features such as lakes, ponds, streams, rivers, springs and wells. NHD is an improvement of DLG and RF3 without replacing them. It is based on 1:100,000-scale data.

The Salado Creek main watershed was sub-divided into hydrologically connected sub-watersheds using the DEMs and the Automatic Watershed Delineation tool available

with BASINS 3.0. The NHD stream network for HUC 12100301 was used to obtain the correct path of the streams (Figure 4).



Figure 4. Sub-Watersheds of Salado Creek Watershed, Bexar County, Texas

The Geographic Information Retrieval and Analysis System (GIRAS) Landuse/ Land Cover theme was obtained from EPA's web site. GIRAS data uses the Anderson Level II classification scheme. Some Anderson Level II classes were consolidated to obtain HSPF landuse classes. Figure 5 shows the landuse distribution for the study area with the reclassified groups. Appendix A gives the map projections used for different GIS layers.



Figure 5. Landuses of the Salado Creek Watershed, Bexar County, Texas

Data for Calibration

Historical daily mean stream flow data for USGS gauging stations 08178800 and 08178700 were obtained from the USGS web site for the simulation period. Historical water quality data for fecal coliform at different water quality stations were obtained from both the San Antonio River Authority and also from EPA's STORET (short for

STOrage and RETrieval) system. The location of the USGS gauging stations and the water quality stations are shown in Figure 6.



Figure 6. Locations of USGS gage stations and water quality observation

Sensitivity Analysis

Sensitivity analysis determines the sensitivity of model outputs to changes in model parameters, or, how much variation in the output is attributed to a particular input parameter. Two types of sensitivity coefficients, absolute sensitivity and relative sensitivity can be calculated (Haan, 1995a). The absolute sensitivity, S is calculated as:

$$S = \frac{fO}{fP} \tag{2}$$

where, O is the output value corresponding to the parameter value P. The absolute sensitivity is the absolute change in the output for a unit change in the input value. The relative sensitivity, S_r is calculated as:

$$S_r = \frac{fO}{fP} * \frac{P}{O}$$
(3)

The relative sensitivity is the percent change in the output for a unit percent change in the input. In the current project the relative sensitivity term is used to compare across parameters to select those parameters that when changed cause the greatest change in model outputs. The sensitivity of simulated peak in-stream fecal coliform concentrations at the main outlet of the Salado Creek to changes in model parameters was evaluated. Since the model was calibrated for the hydrology, only the parameters that affect the water quality modules in HSPF were selected for the sensitivity analysis.

Uncertainty Analysis

There are various techniques available for propagating the uncertainty of a model. Some of the popular techniques are Monte Carlo Simulation, Latin Hypercube Sampling and First Order Approximation. These techniques vary in their conceptual approach and the effort required for computation. First Order Approximation was used for propagation of uncertainty in this study.

First Order Analysis (FOA)

According to FOA the estimate of the variance of the output is given by (Haan, 1995a):

$$Var(O) = \int_{i=1}^{p} S_i^2 Var(P_i)$$
(4)

where S_i is the absolute sensitivity of the model output O with respect to parameter P_i . Also the fraction of the total variance attributed to a particular parameter is given by:

$$F_{i} = \frac{S_{i}^{2} Var(P_{i})}{\sum_{i=1}^{p} S_{i}^{2} Var(P_{i})}$$
(5)

where P is the number of sensitive parameters.

This study was aimed at obtaining the fraction of the variance of the simulated peak instream fecal coliform concentration due to the uncertainty in the most sensitive parameters determined by the sensitivity analysis.

RESULTS AND DISCUSSION

Model Calibration for Hydrology

The hydrology calibration of HSPF was done in four steps:

- Developing an overall water mass balance by adjusting precipitation, evapotranspiration, and loss to deep groundwater
- 2. Adjusting the high-flow/low-flow distribution by adjusting percolation rates, groundwater recharges, and re-emergence of water to streams
- 3. Matching peak storm volumes and adjusting the number of days required for flow to return to normal levels
- Fitting the seasonal distribution of flows considering the seasonal variation in evapotranspiration, soil moisture, and changes in groundwater recharge to streams.

The hydrology calibration was carried out using the expert system HSPEXP. For running HSPEXP, eight output time series, simulated total runoff (SIMQ), simulated surface runoff (SURO), simulated interflow (IFWO), simulated baseflow (AGWO), potential evapotranspiration (ET) (PETX), simulated actual ET (SAET), upper zone storage (UZSX), and lower zone storage (LZSX) were required. The input file for HSPF called as User's Control Input (UCI) was modified to incorporate these output time series. Following advice from the HSPEXP expert system and also in accordance with the four calibration steps, the input parameters were modified. To get an overall water balance the parameter that controls the loss of water to deep groundwater, DEEPFR in the pervious land segment (PLS) was increased considerably. Increasing DEEPFR decreases the runoff from the PLS. Lower zone nominal storage (LZSN), which controls evapotranspiration, was adjusted next. The other parameters adjusted during the first round of calibration were, monthly lower zone ET parameter (MON-LZETPARM), monthly interception storage capacity (MON-INTERCEP), fraction of potential ET that can be satisfied from baseflow (BASETP), and fraction of potential ET that can be satisfied from active groundwater storage (AGWETP).

The second step in the hydrology calibration was to match the high-flow/low-flow distribution in the monitoring data. This was achieved by adjusting model parameters representing infiltration (INFILT), interflow (INTFW), and groundwater recession (AGWRC).

The third step in the hydrology calibration was to match storm flow. The parameters in the PLS such as the interflow recession parameter (IRC), upper zone nominal storage (UZSN), and surface flow parameters such as the length of the overland flow plane (LSUR), Manning's n for the overland flow plane (NSUR), and slope of the overland flow plane (SLSUR) were adjusted to match observed and simulated storm flow.

The fourth and final step in the hydrology calibration was to match the seasonal distribution of flows. This was done by adjusting the parameters that control the seasonal characteristics of the model like MON-INTERCEP, MON-LZETPARM, UZSN, BASETP, and a parameter that affects the behavior of groundwater recession flow (KVARY).

Additional calibration was done to parameters like retention storage capacity (RETSC), length of the assumed overland flow plane (LSUR), and slope of the overland

flow plane (SLSUR) in the impervious land segment (ILS). After adjusting the above parameters the annual average observed flows and the simulated flows were found to have very good correlation with an R^2 above 0.90. However, the base flows were underpredicted throughout the simulation period. The seepage from the Edwards Aquifer beyond the extent of the Salado Creek Watershed caused an increase in observed base flows. In order to account for this additional flow, a point source of inflow was added at the middle of the watershed with a mean value of 5 cfs.

Hydrology calibration started with long term overall matching of observed and simulated flows. The model simulations were done for a time period of January 1, 1970 to December 31, 1993. Figure 7 shows observed flow at USGS gauging station 08178800 and the simulated flow at the main outlet of the Salado Creek corresponding to a long term calibration plotted against time. Also the comparison between the observed and simulated annual flows at the same stream location is given in Figure 8.



Figure 7. Analysis plot for yearly mean streamflow at the outlet of the Salado Creek



Figure 8. Scatter plot for yearly mean streamflow at the outlet of the Salado Creek

The model parameters were further adjusted to get a close correlation between the observed and simulated daily flows for three years, from 1991 through 1993. The comparison of the flows during this time period for the above gauging location is shown in Figure 9. The parameters values corresponding to the hydrology calibration of HSPF model are given in Appendices B, C, and D.



Figure 9. Scatter Plot for daily mean streamflow at the outlet of the Salado Creek Model Validation for Bacteria

Once the hydrology component of the model was properly calibrated for the study area, the next step was to simulate the in-stream fecal coliform concentrations and compare them with the observed data. Availability of observed water quality data was very limited, making it difficult to do a reasonable calibration. The current study aims only to quantify parameter uncertainty of the HSPF model, therefore, calibration of the bacterial model was not necessary. However, HSPF model was tested to observe how well the model can represent the dynamics of the fecal coliform in-stream. Figure 10 and 11 show simulated and observed in-stream concentrations of fecal coliform at the main outlet of the Salado Creek corresponding to years 1994 and 1996 respectively. The HSPF model produces a continuous output of in-stream fecal coliform concentration whereas the water quality observations correspond to grab samples obtained at discrete time periods.



Figure 10. Fecal coliform concentration at the outlet of the Salado Creek for 1994



Figure 11. Fecal coliform concentration at the outlet of the Salado Creek for 1996

Sensitivity Analysis

A sensitivity analysis of the HSPF model was done to determine which parameters, when changed, caused the greatest change in the peak in-stream concentrations of fecal coliform in at the outlet of the Salado Creek. Input parameters were varied by ±10% of P to observe the effect on the output parameter O. Table 2 shows the results of the sensitivity analysis. The peak concentration of fecal coliform at the outlet of Salado Creek was most sensitive to the maximum storage of fecal coliform on the land surface (SQOLIM), the rate of surface runoff that will remove 90 percent of fecal coliform from the land surface (WSQOP) of PLS, the temperature correction coefficient for first-order decay of fecal coliform (THFST), the in-stream water temperature (TWAT), and the first-order decay rate for fecal coliform (FSTDEC) of RCHRES. Further uncertainty analysis was concentrated on these parameters.

Table 2. Absolute sensitivity (S) and relative sensitivity (Sr) of peak in-stream fecal coliform concentrations (PFC, cfu /100 ml) to HSPF input parameters for the Salado Creek Watershed

		Parameter	PFC	P –	PFC	P +	PFC		
Group of activity in HSPF model	Parameter	Mean P	For P O	10%P P1	For P ₁ O ₁	10%P P2	For P ₂ O ₂	S	S_r
PERLND:QUAL-INPUT	SQOLIM	8.79E+12	428,000	7.91E+12	385,000	9.67E+12	470,000	4.84E-08	0.99
RCHRES:GQ-GENDECAY	THFST	1.05	428,000	1.00	409,000	1.15	458,000	3.23E+05	0.79
PERLND:QUAL-INPUT	WSQOP	1.64	428,000	1.48	473,000	1.80	390,000	-2.53E+05	-0.97
RCHRES:GQ-VALUES	TWAT	60.00	428,000	54.00	440,000	66.00	414,000	-2170.0	-0.30
RCHRES:GQ-GENDECAY	FSTDEC	0.40	428,000	0.36	436,000	0.44	419,000	-2.13E+05	-0.20
PERLND:QUAL-INPUT	SQO	8.79E+12	428,000	7.91E+12	428,000	9.67E+12	428,000	0.00	0.00
PERLND:QUAL-INPUT	ACQOP	5.84E+12	428,000	5.25E+12	428,000	6.42E+12	428,000	0.00	0.00
PERLND:QUAL-INPUT	IOQC	10,000	428,000	9,000	428,000	11,000	428,000	0.00	0.00
PERLND:QUAL-INPUT	AOQC	10,000	428,000	9,000	428,000	11,000	428,000	0.00	0.00
IMPLND:QUAL-INPUT	SQO	2.06E+07	428,000	1.86E+07	428,000	2.27E+07	428,000	0.00	0.00
IMPLND:QUAL-INPUT	ACQOP	1.29E+07	428,000	1.16E+07	428,000	1.42E+07	428,000	0.00	0.00
IMPLND:QUAL-INPUT	SQOLIM	2.06E+07	428,000	1.86E+07	428,000	2.27E+07	428,000	0.00	0.00
IMPLND:QUAL-INPUT	WSQOP	1.64	428,000	1.48	428,000	1.80	428,000	0.00	0.00

Data for Calculation of Parameter Statistics

The availability of historical values for storage of fecal coliform on the land surface (SQOLIM) was very limited. This parameter depends on the landuse distribution and the numbers of various animals present for each landuse. The parameter SQOLIM was calculated for a 26-year period from 1975 to 2000, using the landuse distribution for Bexar County and yearly population of livestock and wildlife. The statistics corresponding to temperature correction coefficient for first-order decay of fecal coliform (THFST), rate of surface runoff that will remove 90 percent of fecal coliform from the land surface (WSQOP) of PLS, and first-order decay rate for fecal coliform (FSTDEC) were obtained from literature (USEPA, 1985; USEPA, 2000). The statistic for water temperature in the stream (TWAT) was calculated using historical values available from EPA's STORET database and is given as Appendix F.

Livestock Data

Historical data for livestock counts for Bexar County were obtained from the National Agricultural Statistics Service (NASS) web site (NASS, 2002), (Table 4). The yearly data pertaining to Bexar County obtained from NASS include the number of beef cows, dairy cows, chickens (both commercial broilers and layers), goats, sheep and hogs. Most of the data were available for a period ranging from 1975 to 2000, except for the number of chickens. County data for chickens were available only for the period from 1975 to 1980. However, the number of chickens was available for the South Central District D81 (NASS, 2002) for a period of 1975-2000. These numbers were used to calculate the average ratio of chickens in Bexar County to the number of chickens in Bexar

County for the period from 1981 to 2000 was estimated by multiplying the number of chickens for the corresponding year in District D81 with the calculated ratio. Animal counts were not available for the period from 1988 to 1992 and hence those years were not considered for the calculation of the parameters.

	Numbers of Animals					
Year	BEEF	DAIRY	CHICKEN	HOG	SHEEP	
1975	34,000	6,600	275,000	9,400	3,500	
1976	33,000	6,200	272,000	10,500	3,000	
1977	32,000	6,100	357,000	9,900	2,500	
1978	31,000	5,200	343,000	11,100	2,700	
1979	31,000	4,800	372,000	12,500	2,400	
1980	24,000	5,000	297,000	11,300	2,000	
1981	20,000	4,000	358,974	8,700	1,200	
1982	35,000	3,600	310,464	7,500	2,500	
1983	41,000	3,300	282,744	8,500	2,600	
1984	34,000	3,000	287,109	5,400	1,800	
1985	26,000	3,500	295,190	4,500	1,800	
1986	21,000	4,000	303,984	4,900	2,000	
1987	22,000	2,900	332,536	5,613	1,500	
1993	28,000	700	313,832	3,330	1,900	
1994	28,000	800	441,946	2,730	2,500	
1995	25,000	700	464,545	1,798	2,500	
1996	26,000	600	485,370	2,331	3,000	
1997	26,000	0	484,739	2,331	1,100	
1998	25,000	0	518,260	2,131	5,900	
1999	22,000	0	530,061	1,864	6,100	
2000	25,000	0	485,370	1,864	5,000	

Table 4. Number of livestock in Bexar County, Texas 1975-2000

Wildlife Data

The information regarding the number of wildlife was downloaded from the Texas Parks and Wildlife (TPWD) website (TPWD, 2002). The information available was limited to the deer population. Wildlife data for Bexar County was available for four years, 1993, 1995, 1996 and 1997 and these are given in Table 5. For other periods, the bacterial loading from wildlife was calculated using the average number of wildlife for the above four-year period.

Table 5. Number of white-tailed deer in Bexar County, Texas

Year	1993	1995	1996	1997
Number	34,000	55,000	37,000	36,000

Historical Landuse

Since the calculation of the parameters depends not only on the number of different animals present on the watershed, but also the landuse distribution of the watershed it is important to consider the change in the landuse patterns over the period of study. Harris (2000) gives the landuse distribution corresponding to 1976, 1985, and 1991. Harris (2000) found that there was 57% decrease in cropland in Salado Creek watershed in Bexar County during the period from 1976 to 1991. For the same period there were considerable increase of area under forestland (394%) and commercial landuse (100%). For the current study, landuse distributions corresponding to 1976, 1985, and 1991 were assigned to periods 1975-1982, 1983- 1987 and 1988-2000 respectively. The landuse distribution data used for the calculation are given in Table 5.

I ou dugog	Periods						
Landuses	1975-1982	1983-1987	1988-2000				
COMMERCIAL AND							
SERVICES	14,074	20,913	28,640				
CROP	429,309	376,402	299,087				
FOREST	128,958	187,217	241,440				
INDUSTRIAL	1,319	1,878	2,510				
MIXED URBAN OR							
BUILT-UP LAND	1,766	2,565	3,467				
OTHER	25,309	31,753	31,753				
OTHER URBAN OR							
BUILT-UP LAND	8,397	13,169	18,561				
PASTURE	105,282	88,556	64,114				
RESERVOIR	6,718	6,718	6,718				
RESIDENTIAL	69,304	62,301	94,874				
TRANSPORTATION,							
COMMUNICATIONS							
AND UTILITIES	12,011	10,974	11,282				

 Table 6. The landuse areas (acres) distribution in Bexar County during different periods

Calculation of Parameter Statistics

Storage of fecal coliform on the land surface (SQOLIM) values were calculated based on the number of livestock and wildlife over a period from 1975 –2000. The calculation steps are given in Appendix E. The values for SQOLIM were calculated for four different landuses, cropland, forestland, pastureland, and urban or built-up land. Mean and standard deviation of SQOLIM for the different landuses are given in Table 7. The overall mean and standard deviation of SQOLIM are found out to be 24,770,000 and 86,240,000 Mfc/ac (million fecal coliform per acre) respectively.

Landuse	Mean (million fecal coliform per acre)	Standard deviation (million fecal coliform per acre)		
Cropland	1,514	1,459		
Pastureland	99,101,993	149,814,130		
Urban or built-up land	21	2		
Forestland	43	14		

Table 7. Mean and standard deviation of SQOLIM for the different landuses

The first-order decay rate for fecal coliform (THFST), values were obtained from the literature (USEPA, 1985). Based on the values given in literature, THFST was assumed to have a uniform distribution ranging from 0.95 to 1.1. The mean and variance of THFST are 1.025 and 0.00188 respectively.

The temperature correction coefficient for first-order decay of water quality constituent (FSTDEC) was based on the literature (USEPA, 1985). Values obtained were assumed to have a uniform distribution ranging from 0.1 to 1.0. The mean and variance of FSTDEC are 0.55 and 0.0675 respectively.

The rate of surface runoff per hour that will remove 90 percent of the water quality constituent stored over the land surface (WSQOP) was assumed to have a uniform distribution ranging from 0.5 to 2.0 based on limited information. The mean and variance are 1.25 and 0.1875 respectively.

The historical water temperature data for the Salado Creek were obtained from the US EPA's STORET database. The data were analyzed to find out mean and standard deviation. The mean and variance of TWAT are 70.99 and 75.08 respectively.

Results of First Order Approximation

The availability of historical values for SQOLIM was very limited. This parameter depends on the landuse distribution and the numbers of animals present for each landuse. The parameter SQOLIM was calculated for a 26-year period from 1975 to 2000, using the landuse distribution for Bexar County (Harris, 2000) and yearly population of livestock (NASS, 2000) and wildlife (TPWD, 2002). The values corresponding to THFST, WSQOP and FSTDEC were obtained from USEPA (1985, 2000). Based on the recommended values found in USEPA (1985, 2000a, 2001b) THFST, WSQOP and FSTDEC were assumed to have uniform distributions with intervals [0.95, 1.1], [0.5, 2.0], and [0.1, 1.0] respectively. The mean and the variance of TWAT were calculated using historical values available from EPA's STORET database. Table 8 shows the means and variances of the five parameters.

The five parameters that the maximum value of in-stream fecal coliform concentrations at the outlet of the Salado Creek showed the most sensitivity to were used in a First Order Approximation. The First Order Approximation was used to determine which of these sensitive parameters contributed the most to the variance of in-stream fecal coliform concentration. The results of the FOA are given in Table 8. The FOA showed that 99.9% of the variance in simulated peak concentration of fecal coliform concentration in-stream was contributed by the parameter that represents the maximum storage of fecal coliform over the pervious land segment. This is due to the very large variability in this parameter. Small portions of the variance were attributed to WSQOP

(0.07%) and FSTDEC (0.02%). There were negligible contributions from THFST and TWAT to the output variance.

Parameter	Mean	Variance	Sensitivity S	S ² _Var	Fraction of Model Variance	% of variance
SQOLIM	2.477E+07	7.44 E+27				
	¹ Mfc/ac		4.84E+08	1.74E+13	9.99E-01	99.91
THFST	1.025 (/day)	0.00188	3.23E+05	1.96E+08	1.13E-05	0.00
FSTDEC	0.55	0.0675	-2.53E+05	1.20E+10	6.89E-04	0.07
TWAT	70.99 (F)	75.08	-2.13E+05	3.05E+09	1.75E-04	0.02
WSQOP	1.25 (in/hr)	0.1875	-2.17E+03	3.52E+08	2.02E-05	0.00

 Table 8. First Order Analysis of HSPF for Fecal Coliform

¹Million fecal coliform colony forming units/ac

CONCLUSION

The Salado Creek watershed in Bexar County, Texas was modeled using the HSPF model in BASINS. The model was calibrated for hydrology. A sensitivity analysis and first order approximation were performed to determine the parameters that most influence the in-stream fecal coliform concentration predictions. The specific findings from the study include:

- The parameters that peak in-stream fecal coliform concentrations are most sensitive to are those that represent the maximum storage of fecal coliform bacteria over the pervious land segment (SQOLIM), and surface runoff that removes 90 percent of quality constituent from pervious land segment (WSQOP) of PERLND section (corresponding to pervious land segment) of HSPF model.
- Other parameters in-stream fecal coliform concentration predictions are sensitive to are stream water temperature (TWAT), first-order decay rate of quality constituent (FSTDEC) and temperature correction coefficient for the first order decay rate (THFST) of RCHRES section.
- 3. Though the model is highly sensitive to the parameters listed above, results of the First Order Analysis showed that a major portion of the model output variance is caused by the variation in the parameter representing the maximum storage of fecal coliform bacteria over the pervious land segment.

These results point out the importance of parameterization in modeling with any complex, process-based watershed model. Small errors in assigning values to the

maximum storage of fecal coliform over a given landuse class may result in large errors in predicted coliform counts.

Further study is recommended using Monte Carlo Simulation techniques to evaluate the risk of exceeding some TMDL based on current land-use practices. This will provide us a better understanding of the system and thereby helps us in reducing the uncertainty associated with bacterial loading into the streams.

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APPENDIX

Appendix A Map Projection The projection information of the GIS layers used for the current study

Category	Value
Projection	UTM - 1983 ; Zone 14
Spheroid	GRS 80
Central Meridian	-99
Reference Latitude	0
Northing	0
Easting	500000
Scale Factor	0.9996

Appendix B

HSPF HYDROLOGY PARAMETERS AND CALIBRATED VALUES FOR PERVIOUS LAND SEGMENT

NAME	DEFINITION	UNITS	CALIBRATED VALUES
PWAT - PARM2			
FOREST	Fraction forest cover	none	1 for forest landuse, 0 for others
LZSN	Lower Zone Nominal Soil Moisture Storage	inches	9.0000
INFILT	Index to Infiltration Capacity	in/hr	0.3000
LSUR	Length of overland flow	feet	300.0000
SLSUR	Slope of overland flow plane	ft/ft	0.0564
KVARY	Variable groundwater recession	1/inches	0.0000
AGWRC	Base groundwater recession	none	0.9200
PWAT - PARM3			
PETMAX	Temp below which ET is reduced	deg. F	40.0000
PETMIN	Temp below which ET is set to zero	deg. F	35.0000
INFEXP	Exponent in infiltration equation	none	2.0000
INFILD	Ratio of max/mean infiltration capacities	none	2.0000
DEEPFR	Fraction of GW inflow to deep recharge	none	0.7000
BASETP	Fraction of remaining ET from baseflow	none	0.0200
AGWETP	Fraction of remaining ET from active GW	none	0.0020
PWAT - PARM4			
CEPSC	Interception storage capacity	inches	0.1000
UZSN	Upper zone nominal soil moisture storage	inches	2.0000
NSUR	Manning's n (roughness) for overland flow	none	0.3000
INTFW	Interflow inflow parameter	none	8.0000
IRC	Interflow recession parameter	none	0.9990
LZETP	Lower zone ET parameter	none	0.1000

Appendix C

HSPF HYDROLOGY PARAMETERS AND CALIBRATED VALUES FOR IMPERVIOUS LAND SEGMENT

NAME	DEFINITION	UNITS	CALIBRATED VALUES	
IWAT - PARM2				
LSUR	Length of overland flow	feet	500.0000	
SLSUR	Slope of overland flow plane	ft/ft	0.0600	
NSUR	Manning's n (roughness) for overland flow	none	0.0900	
RETSC	Retention storage capacity	inches	0.4000	
IWAT - PARM3				
РЕТМАХ	Temp below which ET is reduced by half	deg. F	40.0000	
PETMIN	Temp below which ET is set to zero	deg. F	35.0000	

Appendix D

HSPF HYDRAULIC PARAMETERS AND VALUE RANGES

NAME	DEFINITION	UNITS	CALIBRATED VALUES	
HYDR - PARM2				
FTBDSN	WDM data set number for FTABLE	none		
FTABNO	FTABLE number in UCI file	none	0.0000	
LEN	Stream reach (RCHRES) length	miles	Values obtained from BASINS	
DELTH	Stream reach length change in elevation	feet	Values obtained from BASINS	
STCOR	Stage correction factor	feet	3.2000	
ĸs	Routing weighting factor	none	0.5000	
DB50	Bed sediment diameter	inches	0.0100	
ADCALC - DATA				
CRRAT	Ratio of maximum to mean flow velocity	none	1.5000	
VOL	Initial stream channel water volume	acre-feet	10.000	

Appendix E

Calculation of SQOLIM

SQOLIM is the maximum storage of fecal coliform over the land surface. The calculation of the parameter followed the procedures outlined in Protocol for Developing Pathogen TMDLs (USEPA, 2001) and also in a fecal coliform TMDL case study published by USEPA (USEPA, 2000c).

1. Cropland:

Sources of fecal coliform on cropland are mainly wildlife, hog manure, cattle manure (both dairy and beef cows), and poultry litter.

Loading from wildlife

$$Wild_{crop,bact} = \frac{\left(N_{deer} * LR_{deer}\right)}{Area_{crop}}$$

where, Wild_{crop, bact} = fecal coliform contribution from wildlife over cropland, #cfu/day/acre

 N_{deer} = Total number of deer on cropland

Area_{crop} = area under cropland, acres

LR_{deer} = fecal coliform bacteria production rate of deer, #cfu/day

Loading from hog manure

$$Hog_{crop,bact,i} = \frac{365 * N_{hog} * LR_{hog} * MF_i * FR_{hog,i}}{ND_i * Area_{crop}}$$

where, $Hog_{crop, bact,i}$ = fecal coliform contribution from hog manure over cropland in ith month, #cfu/day/acre

 $N_{hog} = Total$ number of hogs/swine on cropland

LR_{hog} = fecal coliform bacteria production rate of hog, #cfu/day

 MF_i = fraction of annual manure applied in ith month

 $FR_{hog,i}$ = fraction of hog manure available for runoff in ith month

 ND_i = number of days in ith month

Loading from poultry litter

FC contribution of poultry over cropland (# cfu/day/acre) = FCPD / CLA

= $(NC * FCL_{poul} * 365 * PM_i * WashP_i) / (NumDays* CLA)$

 $Poultry_{crop,bact,i} = \frac{365 * N_{chicken} * LR_{chicken} * MF_i * FR_{chicken,i}}{ND_i * Area_{crop}}$

where, $Poultry_{crop, bact,i} = fecal coliform contribution from poultry litter over cropland in ith month, #cfu/day/acre$

N_{chicken} = total number of chicken on cropland

 $LR_{chicken} =$ fecal coliform bacteria production rate of chicken, #cfu/day

 $FR_{chicken,i}$ = fraction of poultry litter available for runoff in ith month

Loading from cattle manure

$$Cattle_{crop,bact,i} = \frac{365*N_{dairy}*LR_{dairy}*MF_i*FR_{dairy,i} + (365 - ND_{grazing})*N_{beef}*LR_{beef}*MF_i*FR_{bee_i}}{ND_i*(Area_{crop} + Area_{pasture})}$$

where, $Cattle_{crop, bact,i}$ = fecal coliform contribution from cattle manure over cropland in

 i^{th} month, #cfu/day/acre

N_{dairy} = total number of dairy cows on cropland

 N_{beef} = total number of beef cows on cropland

Area_{pasture} = area under pastureland, acres

 $FR_{dairy,i}$ = fraction of dairy manure available for runoff in ith month

 $FR_{beef,i} = fraction of beef manure available for runoff in ith month$

LR_{dairy} = fecal coliform bacteria production rate of dairy cows, #cfu/day

LR_{beef} = fecal coliform bacteria production rate of beef cows, #cfu/day

$ND_{grazing}$ = number of grazing days for beef cows

2. Pastureland:

Sources of fecal coliform on pastureland are mainly wildlife, cattle manure (both dairy and beef cows) and from grazing beef cattle.

$$Cattle_{pasture,bact,i} = \frac{365 * N_{dairy} * LR_{dairy} * MF_i * FR_{dairy,i} + (365 - ND_{grazing}) * N_{beef} * LR_{beef} * MF_i * FR_{beef,i}}{ND_i * (Area_{crop} + Area_{pasture})} + \frac{N_{beef} * LR_{beef} * (1 - FT_{confine})}{Area_{pasture}}$$

where, Cattle_{pasture, bact,i} = fecal coliform contribution from cattle manure over

pastureland in ith month, #cfu/day/acre

 $FT_{confined}$ = fraction of time beef cows are in confinement

3. Forestland:

Only source of fecal coliform on forestland is wildlife.

Wild forest, bact =
$$\frac{(V_{deer, forest} * LR_{deer})}{Area_{forest}}$$

where, Wild_{forest,bact} = fecal coliform contribution from wildlife over forest land,

 $N_{deer,forest} = total number of deer over forest land,$

 $Area_{forest} = area under the forestland$

4. Urban/built-up land:

Accumulation rate in urban/built-up land was calculated as the weighted average of background concentrations of fecal coliform for four different types of built-up lands,