Bacterial Loadings Watershed Model in Copano Bay

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by

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Abstract

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Copano Bay currently exceeds fecal coliform Texas Surface Water Quality Standards for oyster water use. Aransas and Mission River Tidals currently exceed enterococci water quality standards for contact recreation use. The fecal coliform Copano Bay Bacterial Loadings Model will be used to support the TCEQ Total Maximum Daily Load (TMDL) program to develop the TMDLs for the three impaired water segments. The objectives of this research are to identify the major bacterial sources in the Copano Bay watershed, to calculate the total bacterial loadings (i.e., the TMDLs) from these sources, and to estimate the load reductions needed to bring each of the impaired segments into compliance with water quality standards.

The potential bacterial sources that were considered in the model were wastewater treatment plants (WWTPs), waterbirds, livestock, failing septic systems, and other non-point sources that originate from different types of land uses (e.g., urban, forest, etc.).

This thesis presents an analysis of the existing bacterial monitoring dataset for fecal coliform, including spatial and statistical analysis of the bacterial monitoring data, an estimation of fecal coliform loadings (the input into the models), including non-point and point source calculations, and a description of bacterial transport of fecal coliform from the sources in the watersheds, rivers, and Copano Bay using the model, including explanations for how the model parameters were determined. The main assumptions used in the model were that the fecal coliform bacteria decay (first-order reaction rate) in watersheds and along streams and channels, and Copano Bay is divided up into four Continuous Flow, Stirred Tank Reactors (CFSTRs).

The results of the research include the modeled median fecal coliform concentrations throughout the watershed, the impact of different bacterial sources on each of the water segments in Copano Bay watershed, and the load reductions needed (and from what sources) to meet fecal coliform water quality standards. Cattle were determined (based on model results) to be the largest fecal coliform contributor of fecal coliform in Copano Bay.

Table of Contents

CHAPTER 1: INTRODUCTION

CHAPTER 2: LITERATURE REVIEW

CHAPTER 3: DATA DESCRIPTION

CHAPTER 4: ANALYSIS OF MONITORING DATASET

CHAPTER 5: ESTIMATION OF LOADINGS

CHAPTER 6: MODELING OF BACTERIAL TRANSPORT - SCHEMATIC PROCESSOR

CHAPTER 7: MODELING OF BACTERIAL TRANSPORT - MONTE CARLO SIMULATION

CHAPTER 8: RESULTS

CHAPTER 9: CONCLUSIONS AND RECOMMENDATIONS

List of Tables

List of Figures

Chapter 1: Introduction

1.1 BACKGROUND

Section 303(d) of the 1972 Federal Clean Water Act (CWA) requires that each State identify water bodies that do not meet the State's water quality standards and create a priority ranking of the impaired waters based on the severity of pollution and the water body's intended use.

For the State of Texas, the Texas Commission on Environmental Quality (TCEQ) has identified three water segments that do not meet the Texas Surface Water Quality Standards. Segment 2472, Copano/Port/Mission Bay, exceeds fecal coliform bacteria water quality standards for oyster water use. Segment 2003, Aransas River Tidal, exceeds enterococci bacteria water quality standards for contact recreation use, and Segment 2001, Mission River Tidal, exceeds enterococci bacteria water quality standards for contact recreation use. The three water segments are located along Texas's southeastern coastline, which is shown in Figure 1.1.

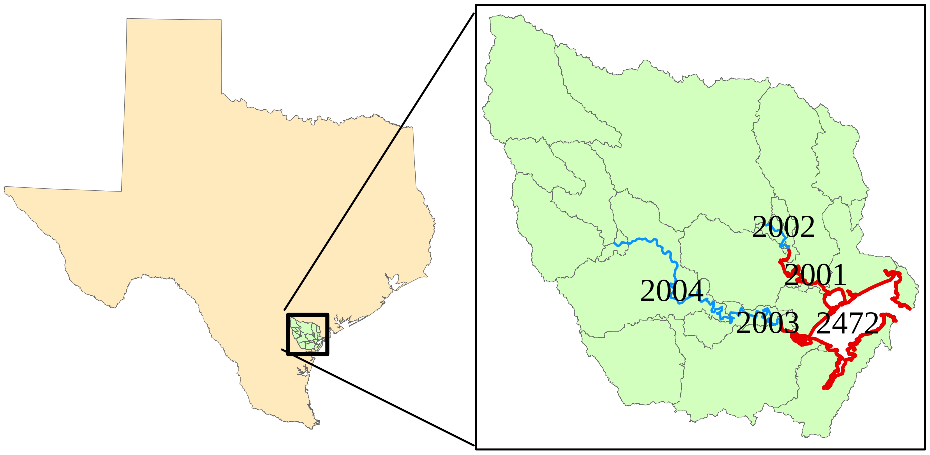

Figure 1.1 Impaired Water Segments in Copano Bay Watershed

1.1.1 Purpose and Objectives

The Copano Bay Bacterial Loadings Model will be used to support the TCEQ Total Maximum Daily Load (TMDL) program to develop the TMDLs for the three impaired water segments.

The objectives of this research are to identify the major bacterial sources in the Copano Bay watershed, to calculate the total bacterial loadings (i.e., the TMDLs) from these sources, and to estimate the load reductions needed to bring each of the impaired segments into compliance with water quality standards.

The primary bacterial indicator for recreational waters was fecal coliform until recently when the Environmental Protection Agency (EPA) began recommending *Escherichia coli* as a better freshwater indicator and enterococci as a better marine water indicator. Thus, the bacterial indicators for the Aransas and Mission River Tidals, which are classified as marine waters, were recently changed from fecal coliform to enterococci, and the bacterial indicators for the Aransas and Mission River Above Tidals, which are classified as freshwaters, were recently changed from fecal coliform to *E. coli*. However, fecal coliform is still the bacterial indicator for oyster water use standards in Copano Bay. Because the transition was more recent, there is not a significant amount of enterococci or *E. coli* monitoring data for the Tidals and Above Tidals as compared to fecal coliform monitoring data. For this reason, and because Copano Bay is the impaired water segment which motivates this study, fecal coliform bacterial loadings were modeled for this research. Thus, the TMDLs and estimate of total load reductions for each water segment were based on fecal coliform water quality standards. However, separate models will need to be created to model the other bacterial indicators (enterococci and *E. coli*) for the other water segments in subsequent studies.

1.1.2 Study Area

The geographic extent of the project includes the three previously mentioned water segments, which are all located in the Copano Bay watershed: Copano Bay (Segment 2472), Aransas River Tidal (Segment 2003), and Mission River Tidal (Segment 2001). The study area and impaired segments are shown in Figure 1.1. The Copano Bay watershed is located along the southeastern Texas coastline and has a drainage area, which all drains to Copano Bay, of 5,688 km^2. The Copano Bay watershed covers part of Aransas, Bee, Goliad, Karnes, Refugio, and San Patricio Counties as shown in Figure 1.2.

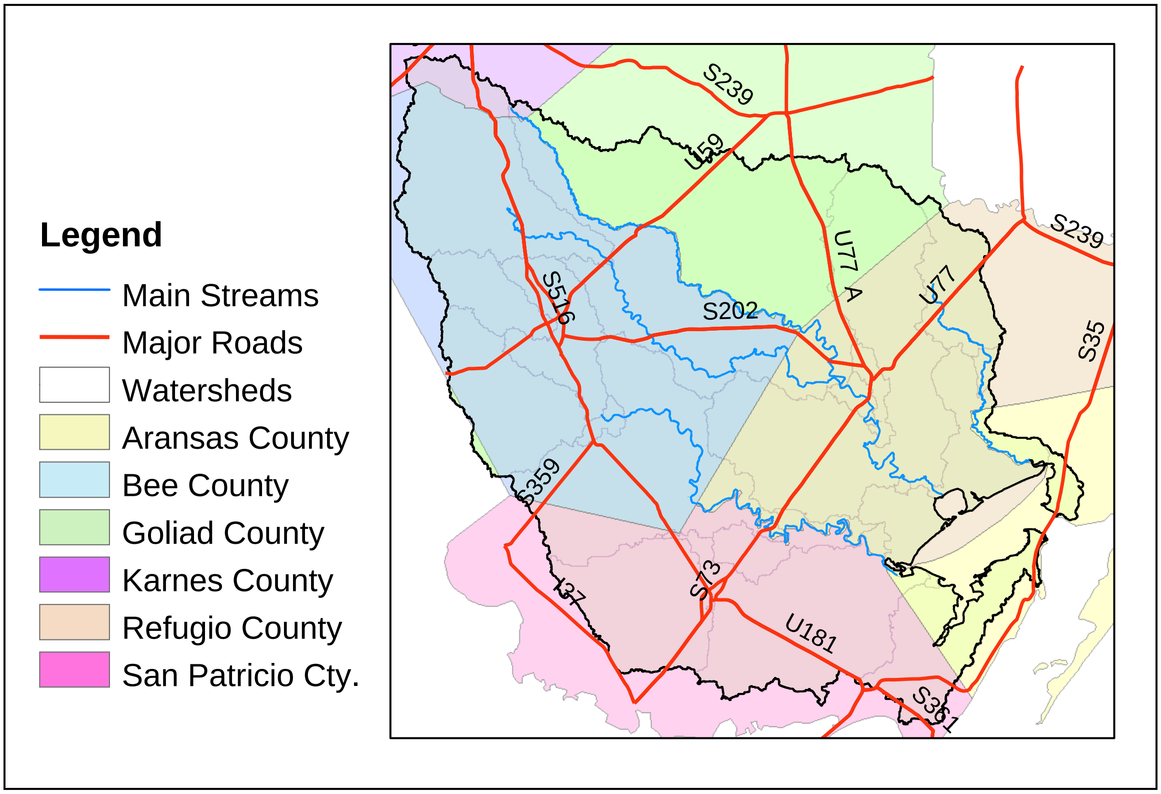

Figure 1.2 Major Highways and Counties in the Copano Bay Watershed

1.2 TEXAS SURFACE WATER QUALITY STANDARDS

The Texas Surface Water Quality Standards, which are found in the Texas Administrative Code (TAC), Title 30, Chapter 307 (TCEQ, 2005a) specify the water quality standards that must be met. Section §307.7 gives the site-specific uses and associated criteria. For this research, the fecal coliform water quality standards and criteria are given below since a fecal coliform loadings model was created.

The water uses that are of concern for these impaired water segments are contact recreation use (for Aransas and Mission River Tidals and Above Tidals) and oyster water use (for Copano Bay). Contact recreation includes recreational activities that involve a significant risk of ingestion of water, including wading by children, swimming, water skiing, diving, and surfing (TCEQ, 2005a). Oyster waters (Copano Bay, Segment 2472) are waters that produce edible species of clams, oysters, or mussels (TCEQ, 2005a).

The following are the criteria for fecal coliform in contact recreation waters in the state of Texas, §307.7(b)(1)(A):

(i) Fecal coliform content shall not exceed 200 colonies per 100 mL as a geometric mean based on a representative sampling of not less than five samples collected over not more than 30 days.

(ii) Fecal coliform content shall not equal or exceed 400 colonies per 100 mL in more than 10% of all samples, but based on at least five samples, taken during any 30-day period. If ten or fewer samples are analyzed, no more than one sample shall exceed 400 colonies per 100 mL.

The following are the criteria for fecal coliform in oyster waters in the state of Texas, §307.7(b)(3)(B):

(i) A 1,000 foot buffer zone, measured in the water from the shoreline at ordinary high tide, is established for all bay and gulf waters, except those contained in river or coastal basins as defined in §307.2 of this title (relating to Description of Standards). Fecal coliform content in buffer zones shall not exceed 200 colonies per 100 mL as a geometric mean of not less than five samples collected over not more than 30 days or equal or exceed 400 colonies per 100 mL in more than 10% of all samples taken during a 30-day period.

(ii) Median fecal coliform concentration in bay and gulf waters, exclusive of buffer zones, shall not exceed 14 colonies per 100 mL, with not more than 10% of all samples exceeding 43 colonies per 100 mL.

(iii) Oyster waters should be maintained so that concentrations of toxic materials do not cause edible species of clams, oysters, and mussels to exceed accepted guidelines for the protection of public health. Guidelines are provided by U.S. Food and Drug Administration Action Levels for molluscan shellfish.

1.3 TOTAL MAXIMUM DAILY LOAD PROGRAM

The TMDL program is a TCEQ program that is striving to improve water quality in the state of Texas. The program was created to fulfill the requirements of Section 303(d) of the Federal Clean Water Act.

The pathogen TMDL is the calculated allowable bacterial loadings that a waterbody can receive without exceeding water quality standards (EPA, 2005). The TMDL can be calculated by the following equation (EPA, 2005):

$$\text{TMDL} = \text{LC} = \text{WLA} + \text{LA} + \text{MOS}$$

Where: LC = Loading Capacity, or the greatest loading a waterbody can receive without exceeding water quality standards;

WLA = Wasteload Allocation, or the portion of the TMDL allocated to existing or future point sources;

LA = Load Allocation, or the portion of the TMDL allocated to existing or future non-point sources and natural background; and

MOS = Margin of Safety, or an accounting of uncertainty about the relationship between pollutant loads and receiving water quality. The margin of safety can be provided implicitly through analytical assumptions or explicitly by reserving a portion of loading capacity. Once the TMDL has been determined for each of the impaired water segments, an implementation plan can be developed to bring the segments' water quality into compliance with the water quality standards for a specific water use.

1.4 POTENTIAL SOURCES OF CONTAMINATION

1.4.1 Point Sources

Point sources are any sources that directly discharge pathogens into a water body (EPA, 2005). The potential point sources of pathogens in the Copano Bay watershed that are considered in the model are wastewater treatment plants (WWTPs), which may discharge fecal waste directly to the watershed due to bypass events, and waterbird colonies, which have known locations around the Bay.

1.4.2 Non-Point Sources

Non-point sources are indirect sources that are far enough away "…from waterbodies to allow attenuation of the pathogens in runoff, infiltrated water, or groundwater" (EPA, 2005). The major non-point source of bacteria is the feces of warm-blooded animals. The concentration of indicator bacteria (i.e., fecal coliform, *E. coli*, enterococci) in the impaired water segments suggests that pathogens may be entering the water body through improperly treated sewage or failing septic systems or from the feces of livestock, pets in urban areas, aquatic birds, and mammals (TCEQ, 2005b). The potential non-point sources in the Copano Bay watershed that are considered in the model are livestock, failing septic systems, and other non-point sources that originate from different types of land uses (e.g., urban, forest, etc.).

1.5 OUTLINE OF THESIS

Chapter 1 explains the objectives and purpose of this project, the study area, the current Texas Surface Water Quality Standards as well as the potential bacterial sources in the Copano Bay watershed and the outline of this paper.

Chapter 2 describes the different types of bacterial indicators that are measured in the Copano Bay water segments (fecal coliform, *E. coli*, and enterococci.) This project only models fecal coliform bacteria, but correlations are made in Chapter 2 between *E. coli*/enterococci and fecal coliform that can be used to convert the fecal coliform bacterial loadings into *E. coli*/enterococci bacterial loadings. Chapter 2 also describes the factors that can affect the decay rate of fecal coliform bacteria and presents studies that have been conducted to examine the effect of environmental factors and conditions on the survival rate of fecal coliform.

Chapter 3 provides descriptions of the datasets and sources that were used in this research to calculate the fecal coliform bacterial loadings, delineate watersheds, and for the Schematic Processor and Monte Carlo Simulation Models.

Chapter 4 analyzes the existing bacterial monitoring dataset for fecal coliform. This includes spatial and statistical analysis of the bacterial monitoring data, indicating the location and extent of exceedances of water quality standards in the Copano Bay watershed.

Chapter 5 estimates fecal coliform bacterial loadings (the input into the models), including non-point and point source calculations.

Chapter 6 models the bacterial transport of fecal coliform from the sources in the watersheds, rivers, and Copano Bay using the Schematic Processor Model, including how the model parameters were determined (Section 6.3.3). The results include the modeled median fecal coliform concentrations throughout the watershed and the impact of different bacterial sources on the Copano Bay watershed. The Schematic Processor Model was used to model average annual conditions, to calculate bacterial loadings in each of the water segments, and to determine the impact of the different bacterial sources on the concentrations of bacteria in the water segments.

Chapter 7 explains how the bacterial transport of fecal coliform from the sources is modeled using a Monte Carlo Simulation Model. The results indicate the load reductions needed (and from what sources) to meet fecal coliform water quality standards.

Chapter 8 summarizes the results from the calculations and procedures that were described in Chapters 6 and 7. The current loadings, allowable loadings, and amount the loads need to be reduced are presented for all the water segments in the Copano Bay watershed (Aransas River Above Tidal, Aransas River Tidal, Mission River Above Tidal, Mission River Tidal, and Copano Bay.)

Chapter 9 discusses the conclusions and recommendations from this research.

Chapter 2: Literature Review

2.1 BACTERIAL INDICATORS

Coliforms and fecal streptococci are measured in surface waters because they are indicators of pathogenic bacteria, viruses, and protozoans, all of which are typically found in human and animal feces (EPA, 2006). Bacterial indicators are typically not harmful themselves, but they indicate the possible presence of pathogenic microorganisms that could be harmful to human health. Testing for bacterial indicators is simpler, cheaper, and less time-consuming than testing specifically for all the different types of pathogens; thus, bacterial indicators are measured rather than the pathogenic microorganisms in surface waters (EPA, 2006).

Fecal coliforms, which are a subset of total coliform bacteria, have been used as the primary bacterial indicator for recreational waters. However, as described below, the Environmental Protection Agency (EPA) recently began recommending the use of *E. coli* and enterococci as better indicators. *E. coli* are fecal coliform bacteria, and enterococci are a subgroup of the fecal streptococci and have the ability to survive in salt water (EPA, 2006).

In 2001, the TCEQ collected 445 surface water samples from southeast Texas to compare the three different bacterial indicators that are measured in the Copano Bay watershed (TCEQ, 2006a): fecal coliform, *E. coli,* and enterococci. Based on the results of the study, EPA recommends measuring *E. coli* as the bacterial indicator in fresh waters and enterococci as the bacterial indicator in marine/salt waters (EPA, 2006).

The study also found that the number of samples exceeding the Texas Surface Water Quality Standards was greater for *E. coli* and enterococci than for fecal coliform. This also occurs in the Copano Bay watershed because none of the bacterial monitoring stations on the Mission and Aransas River Tidals and Above Tidals exceed fecal coliform water quality standards for contact recreation use (TCEQ, 2006b). Thus, Chapter 7 may underestimate the load reductions required to meet contact recreation use standards for *E. coli* and enterococci in the Tidal and Above Tidal reaches, which are recommended as the better indicators of pathogenic bacteria in fresh and salt waters, respectively.

The current bacterial indicators used for each water segment are given in Table 2.1.

Table 2.1 Bacterial Indicators for Water Segments

Environment	Water Segments	Water Use	Bacterial Indicator
Freshwater Stream	Aransas and Mission River Above Tidals	Contact Recreation Use	*E. coli*
Tidal Stream	Aransas and Mission River Tidals	Contact Recreation Use	Enterococcus
Bay	Copano Bay	Oyster Water Use	Fecal Coliform

2.1.1 Correlation between Fecal Coliform and Enterococci

Because fecal coliform is the current primary bacterial indicator for Copano Bay, all the bacterial loading calculations were calculated using fecal coliform for this research. However, to determine the TMDLs for the Tidal reaches, bacterial loading calculations for enterococci would need to be performed, and the resulting concentrations would then be compared to enterococci contact recreation use standards. However, it is difficult to find studies in which a direct or consistent correlation between fecal coliform and enterococci is found (TCEQ, 2006b). For this reason, different correlations will be used for different parts of the Copano Bay watershed.

The TCEQ bacterial monitoring data was analyzed for each of the Tidal reaches to compare the measurements made for fecal coliform and enterococci (when measurements of each were made at the same station and day) to determine if the concentrations of fecal coliform and enterococci are correlated in this study area.

For the Aransas River Tidal (Station 12948), fecal coliform and enterococci were both measured on 11 days (Table 2.2). The concentrations of fecal coliform and enterococci at Station 12948 versus time are shown in Figure 2.1, and the relationship between fecal coliform and enterococcus is shown in Figure 2.2.

Table 2.2 Fecal Coliform and Enterococcus Measurements at Station 12948: Aransas River Tidal

Date	**Fecal Coliform, (#/100mL)**	**Enterococcus (#/100mL)**
10/25/1999	12	47
1/19/2000	20	16
4/17/2000	3700	12200
7/11/2000	112	590
1/14/2002	94	1082
4/9/2002	94	1082
7/8/2002	1327	3400
10/15/2002	122	60
1/21/2003	58	29
4/22/2003	34	210
8/18/2003	28	44

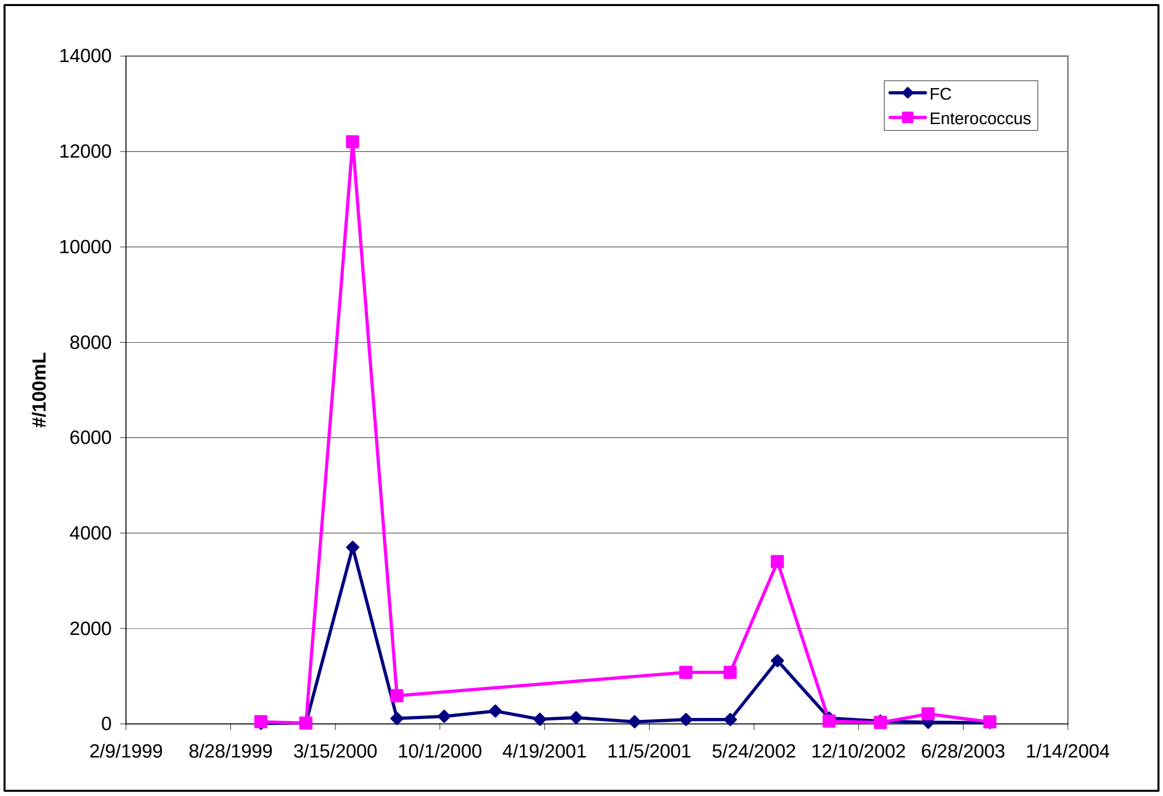

Figure 2.1 Fecal Coliform and Enterococcus Concentrations at Station 12948: Aransas River Tidal

There is a strong correlation between fecal coliform and enterococcus (shown in Figure 2.1), and the relationship between these two bacterial indicators is shown in Figure 2.2. This relationship can be used to convert the fecal coliform bacterial loadings (calculated in Chapter 5) to enterococci bacterial loadings for the Aransas River Tidal watersheds. However, this was not done for this report but is recommended for future work.

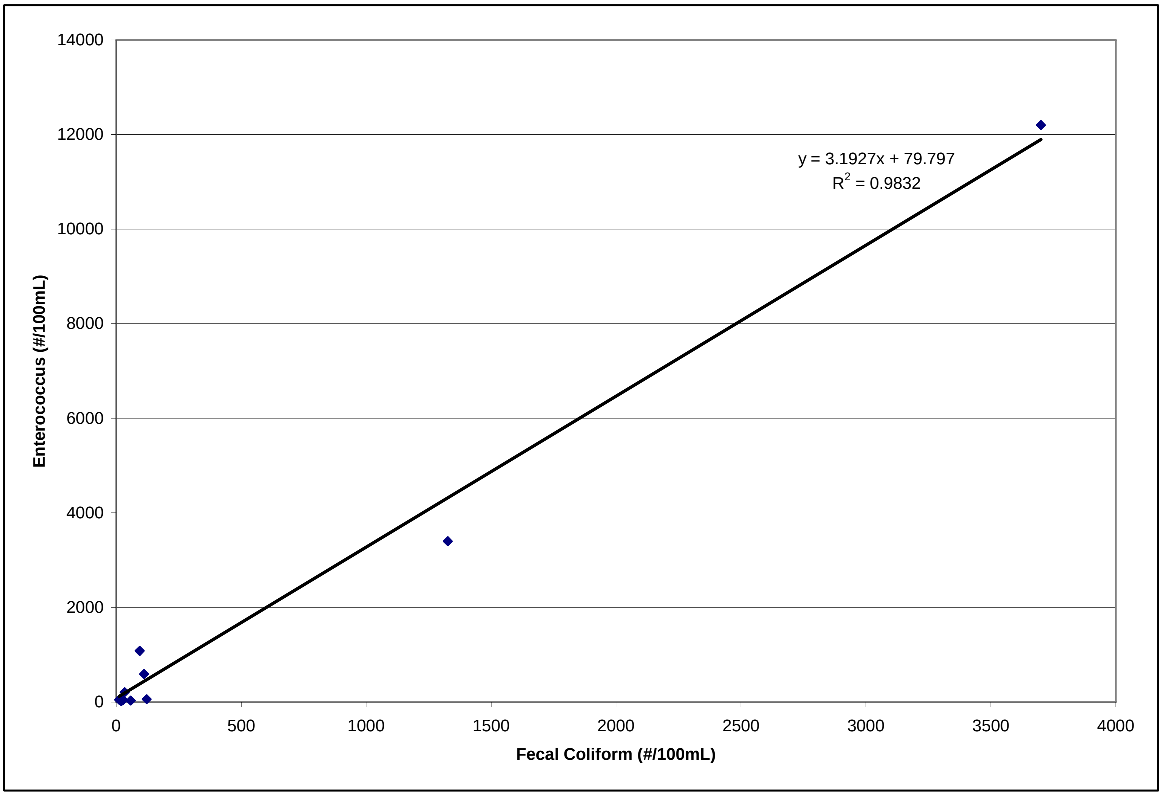

Figure 2.2 Relationship between Enterococcus and Fecal Coliform at Station 12948: Aransas River Tidal

For the Mission River Tidal (Station 12943), fecal coliform and enterococci were both measured on 16 days (Table 2.3). The concentrations of fecal coliform and enterococci at Station 12943 versus time are shown in Figure 2.3, and the relationship between fecal coliform and enterococcus is shown in Figure 2.4.

Table 2.3 Fecal Coliform and Enterococcus Measurements at Station 12943: Mission River Tidal

Date	Fecal Coliform, (#/100mL)	Enterococcus (#/100mL)
10/25/1999	32	98
1/19/2000	23	23
4/17/2000	52	31
7/11/2000	41	18
10/9/2000	3	13
1/15/2001	740	700
4/10/2001	37	68
6/18/2001	42	32
10/8/2001	22	84
1/14/2002	51	150
4/9/2002	51	150
7/8/2002	130	200
10/15/2002	21	250
1/21/2003	147	39
4/22/2003	270	74
8/18/2003	55	152

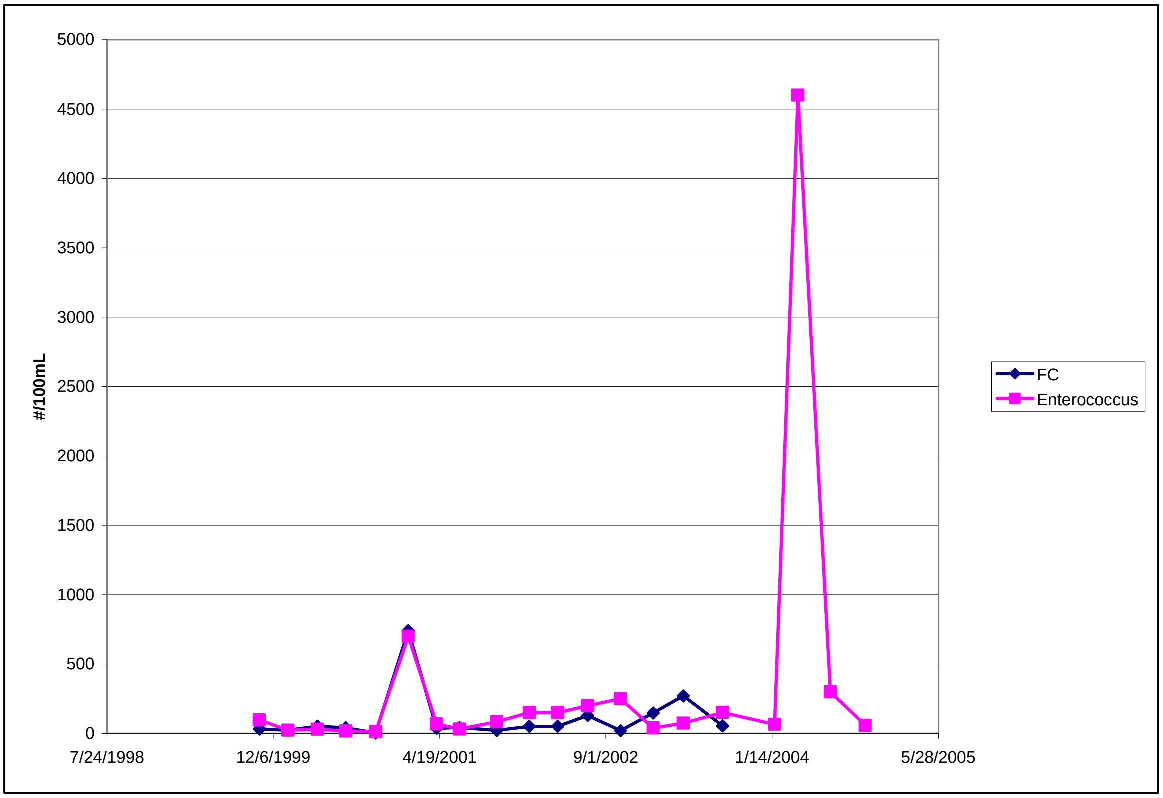

Figure 2.3 Fecal Coliform and Enterococcus Concentrations at Station 12943: Mission River Tidal

There appears to be a reasonable correlation between fecal coliform and enterococci concentrations for the field measurements (Figure 2.4). This relationship can be used to convert the fecal coliform bacterial loadings (calculated in Chapter 5) to enterococci bacterial loadings for the Mission River Tidal watersheds. However, this was not done for this report but is recommended for future work.

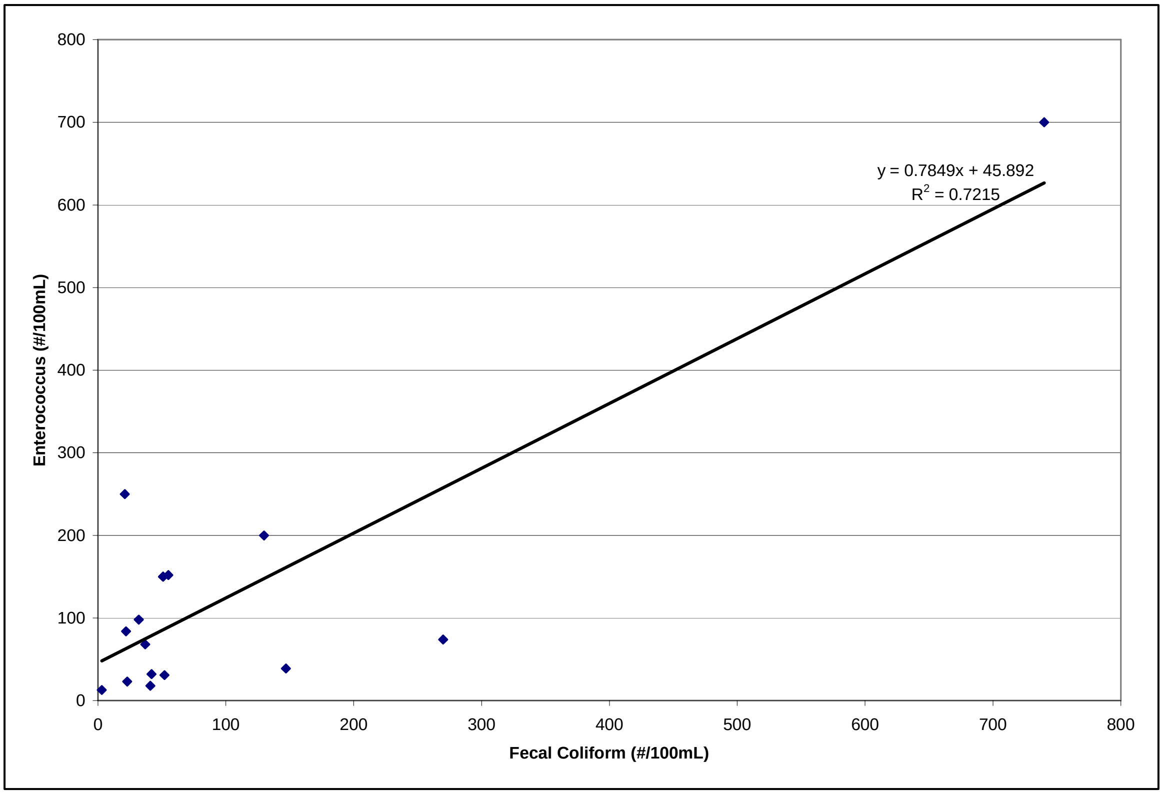

Figure 2.4 Relationship between Enterococcus and Fecal Coliform at Station 12943: Mission River Tidal

Comparing the monitoring data from the Aransas River Tidal to the Mission River Tidal (Figures 2.2 and 2.4), it can be seen that the correlations between fecal coliform and enterococcus vary greatly. The discrepancy shows how it is difficult to find a direct and consistent correlation between the two bacterial indicators. Thus, it is for this reason that different correlations should be used for different areas in the Copano Bay watershed.

2.1.2 Correlation between Fecal Coliform and *E. coli*

In order to determine the TMDLs for the Above Tidal reaches, bacterial loading calculations for *E. coli* would have to be performed and the results compared to *E. coli* contact recreation use standards because *E. coli* is the preferred bacterial indicator for these reaches. However, like with enterococci, it is difficult to find studies in which a direct or consistent correlation between fecal coliform and *E. coli* is found (TCEQ, 2006b). For this reason, different correlations will be used for different parts of the Copano Bay watershed.

The TCEQ bacterial monitoring data were analyzed for each of the Above Tidal reaches to determine if the concentrations of fecal coliform and *E. coli* are correlated.

For the Aransas River Above Tidal (Station 12952), fecal coliform and *E. coli* were both measured on 5 days (Table 2.4). The concentrations of fecal coliform and *E. coli* at Station 12952 versus time are shown in Figure 2.5, and the relationship between fecal coliform and *E. coli* is shown in Figure 2.6.

Table 2.4 Fecal Coliform and *E. coli* Measurements at Station 12952: Aransas River Above Tidal

Date	**Fecal Coliform, (#/100mL)**	***E. coli* (#/100mL)**
7/8/2002	836	400
10/15/2002	25	3
1/21/2003	72	3
4/22/2003	130	90
8/18/2003	58	56

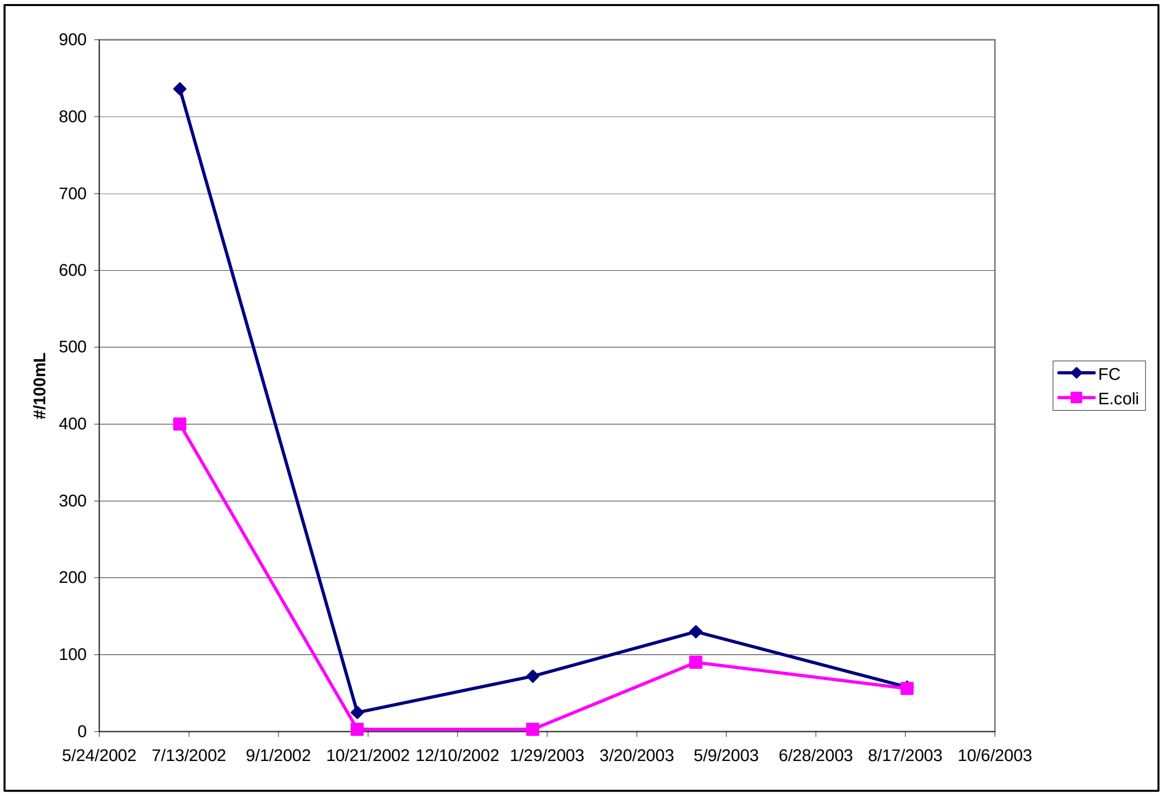

Figure 2.5 Fecal Coliform and *E. coli* Concentrations at Station 12952: Aransas River Above Tidal

There appears to be a strong correlation between fecal coliform and *E. coli* concentrations (Figure 2.6). This relationship can be used to convert the fecal coliform bacterial loadings (calculated in Chapter 5) to *E. coli* bacterial loadings for the Aransas River Above Tidal watersheds. However, this was not done for this report but is recommended for future work.

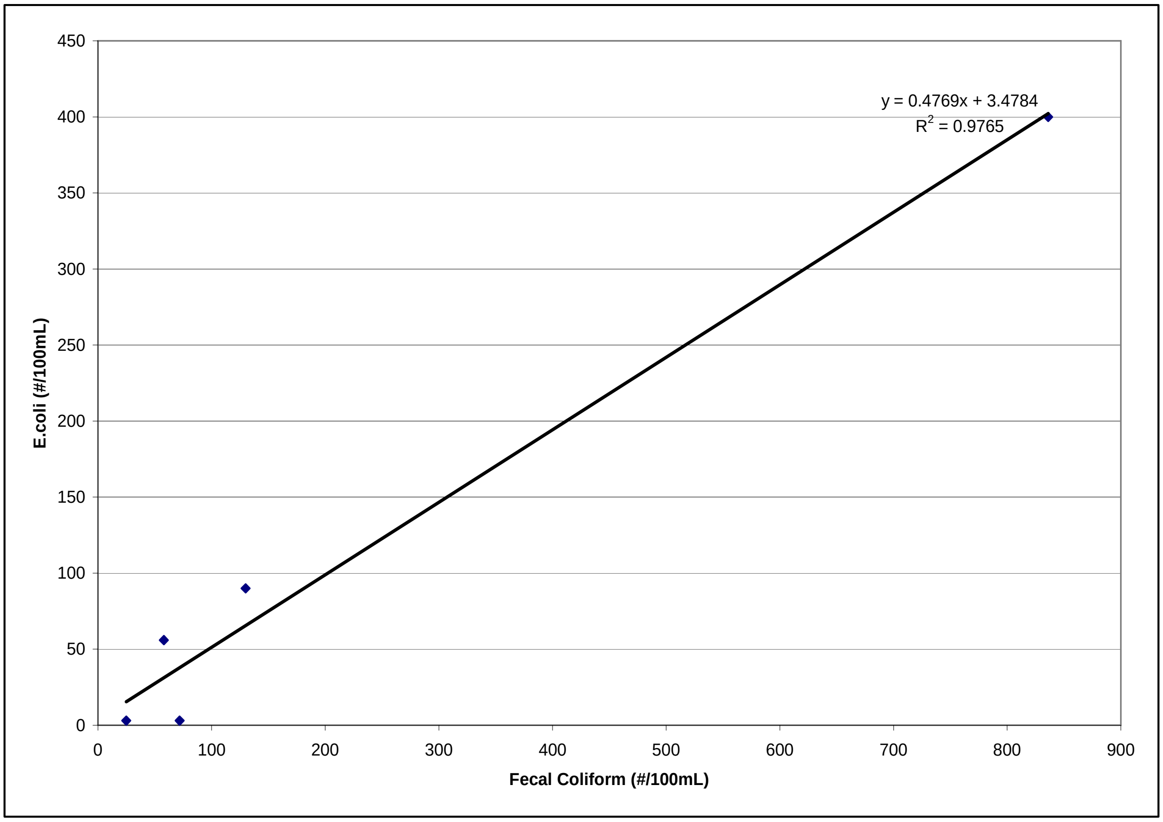

Figure 2.6 Relationship between *E. coli* and Fecal Coliform at Station 12952: Aransas River Above Tidal

For the Mission River Above Tidal (Station 12944), fecal coliform and *E. coli* concentrations were both measured on 17 days (Table 2.5). The concentrations of fecal coliform and *E. coli* at Station 12944 versus time are shown in Figure 2.7, and the relationship between fecal coliform and *E. coli* is shown in Figure 2.8.

Table 2.5 Fecal Coliform and *E. coli* Measurements at Station 12944: Mission River Above Tidal

Date	**Fecal Coliform, (#/100mL)**	***E. coli* (#/100mL)**
10/25/1999	58	52
1/19/2000	410	470
4/17/2000	112	74
7/11/2000	94	48
10/9/2000	1382	4200
1/15/2001	410	460
4/10/2001	320	62
6/18/2001	56	30
10/8/2001	157	55
1/14/2002	54	260
4/9/2002	54	260
7/8/2002	682	627
10/15/2002	46	92
1/21/2003	142	31
4/22/2003	120	132
5/12/2003	116	42
8/18/2003	54	10

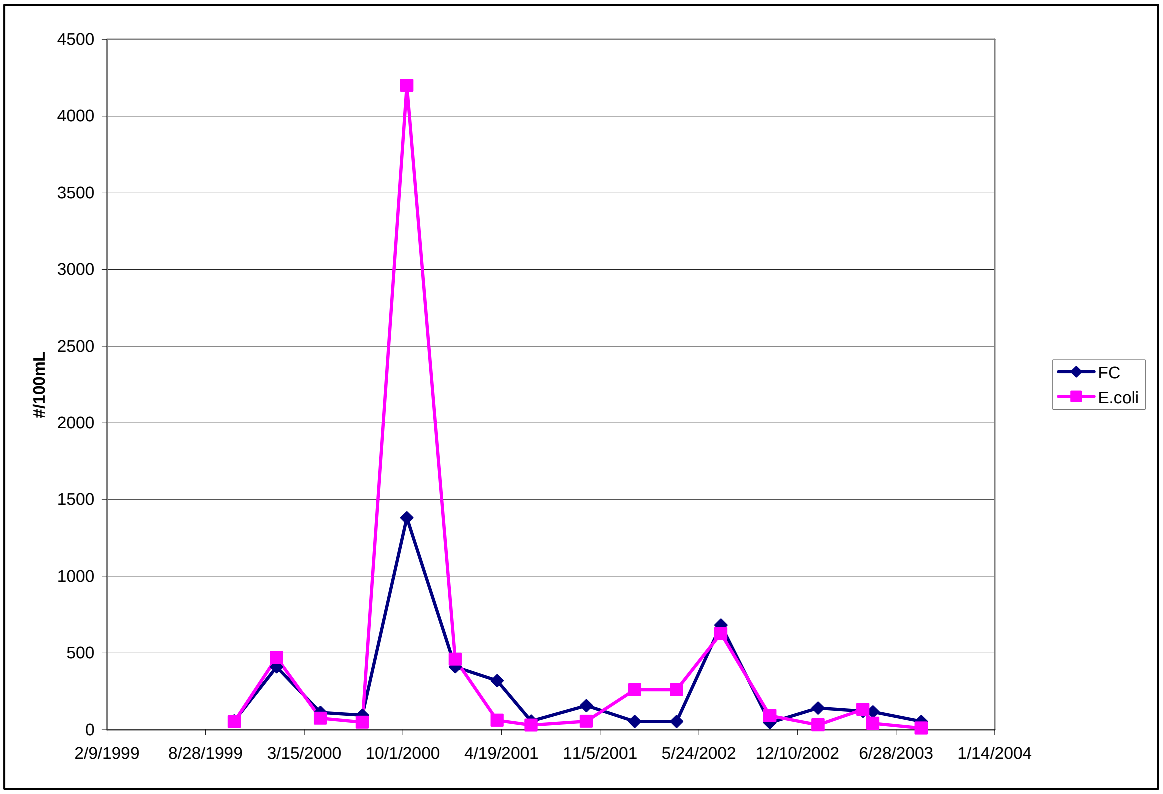

Figure 2.7 Fecal Coliform and *E. coli* Concentrations at Station 12944: Mission River Above Tidal

There appears to be a good correlation between fecal coliform and *E. coli* concentrations (Figure 2.8). This relationship can be used to convert the fecal coliform bacterial loadings (calculated in Chapter 5) to *E. coli* bacterial loadings for the Mission River Above Tidal watersheds. However, this was not done for this report but is recommended for future work.

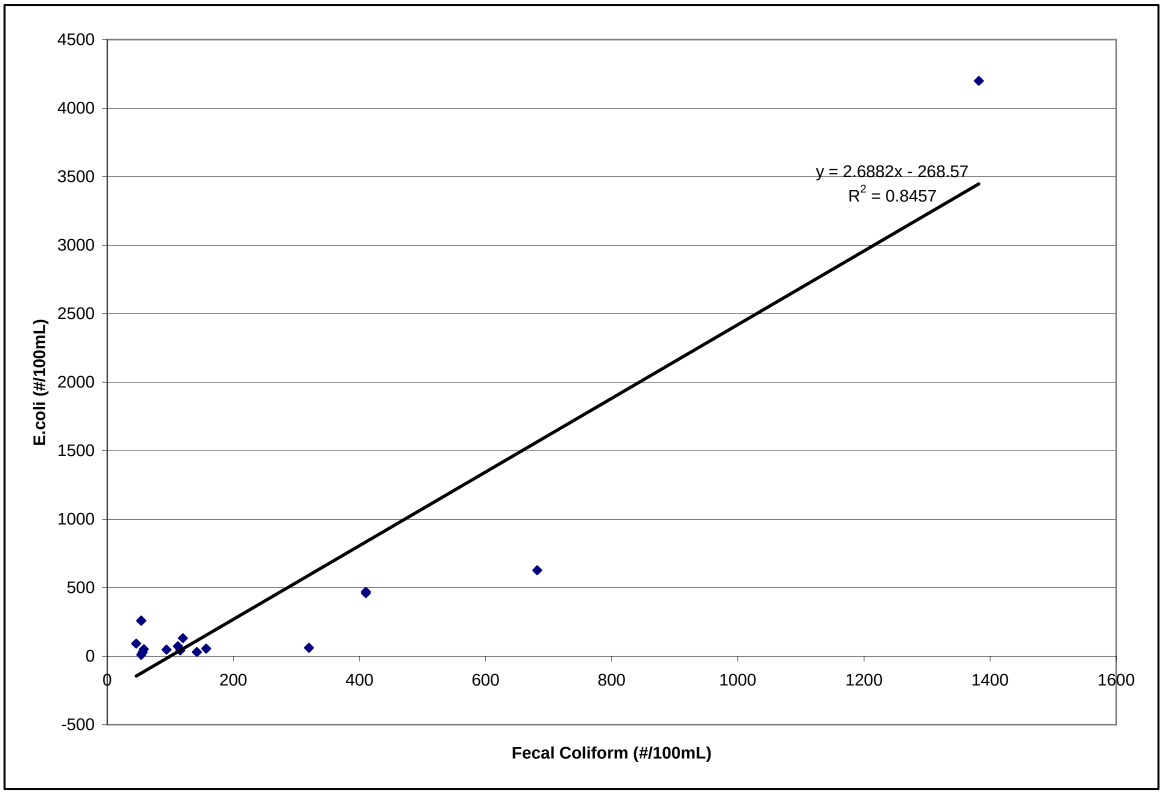

Figure 2.8 Relationship between *E. coli* and Fecal Coliform Concentrations at Station 12944: Mission River Above Tidal

Comparing the monitoring data from the Aransas River Above Tidal to the Mission River Above Tidal (Figures 2.6 and 2.8), it can be seen that the correlations between fecal coliform and *E. coli* vary greatly. The discrepancy shows how it is difficult to find a direct and consistent correlation between the two bacterial indicators. Thus, it is for this reason that different correlations should be used for different areas in the Copano Bay watershed.

2.2 DECAY RATE OF FECAL COLIFORM BACTERIA

2.2.1 Factors Affecting Decay Rate of Fecal Coliform

The fecal coliform bacteria are assumed to decay by a first-order decay process (van der Steen *et al*., 2000), so the decay of bacteria is modeled by the decay coefficient, k. The expression for first-order decay is given as follows:

$$c_t = c_o * \exp^{-kt} \tag{2.1}$$

Where: c_t = fecal coliform concentration after time t
c_o = initial fecal coliform concentration at t = 0
k = first-order decay coefficient
t = time

Many factors affect the decay rate of fecal coliform, including solar radiation intensity, temperature, salinity, pH, dissolved oxygen (DO), turbidity, presence of toxic agents, predation and parasitism, sedimentation, and nutrient concentrations (Davies *et al*., 1995). Some of the most critical factors have been identified as solar radiation intensity and temperature (Brissaud *et al.*, 2000; Burkhardt *et al*., 2000), and the decay constant, k, given in literature varies considerably, from 0.2 to 12 days^{-1} (Brissaud *et al*., 2000).

Many empirical equations have been formulated to model the effects of the various factors on fecal coliform decay. Canale *et al.* (1993) considered the combined effects of irradiance and temperature as well as sedimentation effects. However, there is an insufficient amount of data to apply this expression to the Copano Bay watershed.

2.2.1.1 pH

The fecal coliform decay rate is not significantly affected by pH when the pH is in the range of 7.2 and 9.1 (van der Steen *et al*., 2000). However, pH values above 9.0 increase the fecal coliform decay rate, especially under poor nutrient conditions; furthermore, increased temperatures exacerbate the pH effect (Pearson *et al.*, 1987). Curtis *et al.* (1992) showed that when pH > 9.0, the fecal coliform decay rate increases. However, looking at the water quality monitoring data from 1999-2005, the measured pH at all bacteria monitoring stations is less than 9.0, so pH is assumed not to be a significant factor on the decay rate of fecal coliform in the Copano Bay watershed.

The average measured pH (from 1999-2005) in the Copano Bay Segments[1] are given in Table 2.6 below.

Table 2.6 Average Measured pH in Copano Bay Segments

Copano Bay Segment[1]	**Average pH**
1	8.27
2	8.00
3	No Data
4	7.98

Since all the pH measurements are within the range of 7.2 and 9.1, pH was considered an insignificant factor on the decay rate of fecal coliform bacteria.

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[1] Copano Bay segmentation is defined in Section 6.3.1.1

2.2.1.2 Solar Radiation Intensity

Van der Steen *et al*. (2000) developed an empirical expression for the decay coefficient based on solar intensity and radiation in a solar-radiated pond environment. However, when the expression from this study was applied to the Copano Bay watershed using radiation intensities from the North American Regional Reanalysis (NARR) database, the fecal coliform decay coefficients were in the range of 35.5 days^{-1} to 44.5 days^{-1}, which are much greater than the typical range of 0.2 to 12 days^{-1} (Brissaud *et al.*, 2000). Thus, the empirical equation was not applied to Copano Bay.

Van der steen *et al*. (2000) exposed fecal coliform to solar radiation in batch reactors at 20°C and 30°C. The results showed that the temperature difference did not affect decay; the results also showed that fecal coliform decay is much more rapid under irradiated conditions than under dark conditions (van der Steen *et al.*, 2000).

Curtis *et al*. (1992) determined that fecal coliform decay by solar radiation is dependent on the dissolved oxygen concentration (i.e., photooxidation). Longer wavelengths (> 440 nm) could not kill fecal coliform when pH values are below 8.0. Thus, photooxidation is dependent on sunlight radiation, pH, and dissolved oxygen concentration.

2.2.1.3 Temperature

The literature is divided over the effect of temperature on fecal coliform decay. Van der Steen *et al.* (2000) conducted experiments with buffered effluents from Upflow Anaerobic Sludge Blanket (UASB) reactors, which treat domestic wastewater. Fecal coliform decay increased as temperature increased from 10 to 30°C. Two empirical expressions were developed in this study to calculate decay coefficients based on temperature. The expressions were applied to the Copano Bay watershed, and the calculated decay coefficients ranged from 0.53 to 2.93 days^{-1}. Auer and Niehaus (1993) measured fecal coliform in batch culture under dark conditions where the temperature ranged from 10-35°C. They concluded that there is no significant relationship between fecal coliform decay rate and temperature, and the great variation between temperature and die-off rate relationships may be due to other factors having an effect on the experiments (such as nutrients, sunlight radiation, etc.)

The average annual measured water temperature (from 1999-2005) in the Copano Bay Segments[2] are given in Table 2.7 below.

Table 2.7 Average Measured Temperature in Copano Bay Segments

Copano Bay Segment[2]	**Temperature (°C)**
1	19.6
2	20.0
3	17.8
4	18.9

2.2.1.4 Salinity

Estuarine waters have higher salinities than freshwaters; studies show that the decay rate of fecal coliform is greater in saltwater than in freshwater (Anderson *et al*., 2005).

The average measured salinities (from 1999-2005) in the Copano Bay Segments[2] are given in Table 2.8 below. Segments 1 and 4 have higher average salinity concentrations because they are closer to the Gulf of Mexico, which sea water typically has a salinity of approximately 35 ppt.

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[2] Copano Bay segmentation is defined in Section 6.3.1.1

Table 2.8 Average Measured Salinity in Copano Bay Segments

Copano Bay Segment	**Salinity (ppt)**
1	13.7
2	11.9
3	10.7
4	13.7

2.2.2 Summary

The fecal coliform decay rate is influenced by many environmental factors. Thus, it is critical that our model uses a variable decay rate to account for day and nighttime conditions, dry and wet weather conditions, and summer versus wintertime conditions, and so forth (Kashefipour *et al*., 2002). Because none of the empirically-derived decay coefficient equations (based on various environmental factors) could be applied to the Copano Bay watershed due to lack of data or resulting in values that were not within the range of literature values, the decay coefficients for the watershed were calculated by directly solving for k by using available monitoring data, and the procedure is described in Section 6.3.3.1. Thus, the range of decay coefficients is 2 to 2.5 days^{-1} for this study.

Chapter 3: Data Description

3.1 BACTERIAL MONITORING DATA

Bacterial monitoring data for all of the bacterial monitoring stations for the water segments in the Copano Bay watershed were used to observe and analyze the fecal coliform concentrations in the stream segments. The data were also used to calibrate the Schematic Processor Model (Chapter 6) and the Monte Carlo Simulation Model (Chapter 7) to ensure that the modeled fecal coliform concentrations agree with the existing monitoring concentrations at each bacterial monitoring station.

Bacterial monitoring data were obtained for the time period of January 1999 to October 2004 from Texas Department of Health (TDH) and TCEQ Regulatory Activities and Compliance System (TRACS) database for the Copano Bay watershed.

The TCEQ TRACS database stores surface water quality data from TCEQ water quality monitoring stations (TCEQ, 2006c). The monitoring data are organized by Station ID (the unique identifier for the bacteria monitoring station), the date the monitoring occurred, and the Storet code, which is a unique number that corresponds to the water quality parameter. The Storet codes associated with fecal coliform monitoring data are 79835 and 31616. Storet code 79835 describes fecal coliform concentrations in units of most probable number per 100 mL (MPN/100mL). MPN/100mL is measured using the multiple-tube fermentation technique. Approximately 84% of the fecal coliform concentrations in Copano Bay were measured using this technique. A Storet code of 31616 describes fecal coliform concentrations in units of number per 100 mL (#/100mL), which is the number of coliform bacteria per 100 mL of water and is measured using the membrane filtration method. Approximately 16% of the fecal coliform concentrations in Copano Bay and 100% of the fecal coliform samples in the Aransas and Mission Rivers were measured using this technique. Both of these measurements were used interchangeably in the bacterial analysis, and the units are defined as colony forming units per 100 mL of water (CFU/100mL) subsequently in this study.

Other parameter Storet codes that are used in our analysis are 31648 (*E. coli*, #/100mL) and 31649 (enterococcus, #/100mL). *E. coli*, which is a freshwater bacterial indicator, is the indicator for the Aransas and Mission Above Tidal reaches; enterococcus, which is a marine water bacterial indicator, is the indicator for the Aransas and Mission Tidal reaches. A correlation between *E. coli*/enterococcus and fecal coliform was found (described in Section 2.1) to create models that can determine the bacteria load reductions needed in the Above Tidal and Tidal reaches (TCEQ, 2006d).

3.2 DATASETS REQUIRED FOR LOADING ESTIMATION

3.2.1 Datasets Required for Non-Point Source Loads

To create a model to calculate bacterial loadings, Geographic Information Systems (GIS) data layers were compiled. The basic relationship that was used to calculate non-point source bacterial loadings for the model is

$$L = Q * C \tag{3.1}$$

Where: L = Bacterial Loading
Q = Runoff
C = Concentration

GIS data layers were prepared to calculate Runoff (Q) and Concentration (C).

3.2.1.1 Runoff Dataset

As explained in Section 5.1.2, several GIS data layers were used to calculate the runoff in the Copano Bay watershed. Runoff calculations were made using previously generated empirical equations (Quenzer, 1997). These runoff equations were developed by using the Microsoft Excel 5.0 Regression Tool, which was used to base the equations on a relationship among streamflow depth, precipitation depth, and percent land use in each of the nine watersheds in the Corpus Christi Bay system, which includes the Copano Bay watershed. These equations are given in Section 5.1.2.4.

3.2.1.1.1 Precipitation Data

The National Resources Conservation Service (NRCS) and the Spatial Climate Analysis Service (SCAS) at Oregon State University (OSU) developed PRISM (Parameter-elevation Regressions on Independent Slopes Model), which gives the average annual precipitation from 1961-1990. These data were downloaded for the state of Texas in shapefile format and were used to calculate runoff in the Copano Bay watershed.

3.2.1.1.2 Land Use / Land Cover Dataset

The National Land Cover Characterization project developed a national land cover data set from Multi-Resolution Land Characterization (MRLC) data called National Land Cover Data 1992 (NLCD 92). The National Land Cover Dataset is based on 30-meter Thematic Mapper data. NLCD data also exists for 2001; however, the data do not currently exist for the geographic area of interest (i.e., the Copano Bay watershed). The 1992 dataset was used along with the average annual precipitation to calculate runoff for the Copano Bay watershed.

3.2.1.2 Event Mean Concentration (EMC) Dataset

As explained in Section 5.1.2.7, several GIS data layers were used to calculate bacteria concentrations in the Copano Bay watershed. The land use/land cover dataset was obtained from the United States Geographic Survey (USGS) (Section 3.2.1.1.2). The event mean concentration (EMC) values can be approximated for each type of land use. For this research, fecal coliform EMCs for each land use code were previously determined (Zoun, 2003) and are listed in Table 3.1, and the Source Code descriptions for the EMC values in Table 3.1 are given in Table 3.2. The EMC values are average fecal coliform concentrations during an entire storm event associated with different types of land use in the Galveston Bay watershed, not the Copano Bay watershed. For this reason, we decided to find a more accurate way to account for animal fecal waste based on the numbers and types of animals in the Copano Bay watershed. Thus, the fecal coliform EMC values for land use classifications 51 (Shrubland), 71 (Grasslands/Herbaceous), and

81 (Pasture/Hay) were modified to zero in the non-point source calculations so that bacteria from livestock waste were not accounted for twice.

Table 3.1 Fecal Coliform EMC Values Based on Land Use Classifications (Zoun, 2003)

Land Use Code	Land Use Category	Fecal Coliform EMCs (CFU/ 100 mL)	Source Code
11	Open Water	0	NPS, Judgment
21	Low Intensity Residential	22,000	NPS
22	High Intensity Residential	22,000	NPS
23	Commercial/Industrial/Transportation	22,000	Inferred from NPS
31	Bare Rock/Sand/Clay	0	Judgment
32	Quarries/Strip Mines/ Gravel Pits	0	Judgment
41	Deciduous Forest	1,000	Judgment
42	Evergreen Forest	1,000	Judgment
43	Mixed Forest	1,000	Inferred, Judgment
51	Shrubland	0	Livestock
61	Orchards/Vineyards/Other	2,500	Inferred from NPS
71	Grasslands/Herbaceous	0	Livestock
81	Pasture/Hay	0	Livestock
82	Row Crops	2,500	NPS
83	Small Grains	2,500	NPS
85	Urban/Recreational Grasses	22,000	NPS
91	Woody Wetlands	200	Judgment
92	Emergent Herbaceous Wetlands	200	Judgment

Table 3.2 Description of Source Codes for EMC Values

Source Code	Description
NPS (Zoun, 2003)	Galveston Bay National Estuary Program Non-point Source Characterization (NPS) study
CCBNEP (Zoun, 2003)	Corpus Christi Bay National Estuary Program (CCBNEP) Study
Inferred (Zoun, 2003)	Value inferred from observed data for similar land use category in Galveston Bay area due to lack of data for the specific land use category in Galveston Bay area
Judgment (Zoun, 2003)	Professional judgment by Dr. George Ward, Professor, University of Texas at Austin
Livestock	Land use codes where livestock animals are assumed to be present. (Note: values are assumed to be zero, so that animal feces are only accounted for once in model. Livestock fecal coliform concentrations are accounted for in Section 5.2.)

3.2.1.3 Livestock Data

Livestock data (annual count per county) were obtained from the 2002 Census of Agriculture, National Agricultural Statistics Service (NASS), and the 2004 Texas Livestock Inventory and Production, United States Department of Agriculture (USDA), NASS, Texas Statistical Office. The animals that were considered in the calculations (due to census data availability) were cattle, goats, horses, sheep, hen, hogs, and chickens.

3.2.1.4 Septic System Data

The number of septic systems per county was obtained from the 1990 U.S. Census of Bureau for the Copano Bay watershed[3]. However, the exact locations of the septic systems were not given, nor is information available regarding the number of

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[3] The 2000 Census does not include questions regarding sewage disposal, so the number of septic systems per county is unknown since 1990.

malfunctioning septic systems. Other data from the U.S. Census of Bureau that was used in calculating the bacterial loadings from septic systems (see Section 5.5) were the occupied housing units per county (1990 and 2002), and the population per county (2004).

The Texas Department of Health (TDH) regulated septic systems prior to 1990. However, in 1991, the TCEQ was given the authority to regulate on-site sewage facilities (OSSFs), which includes authority over location, design, construction, installation, and proper functioning of OSSFs (Niemann, 2006). Thus, the number of installed septic systems from 1990 – 2004 per county was obtained from the TCEQ.

The types of soil in the watershed are also important for the determination of bacterial loadings from septic systems. The State Soil Geographic (STATSGO) Database, which gives soil maps with a mapping scale of 1:250,000, was used to identify the hydrologic soil groups throughout the Copano Bay watershed (Groups A, B, C, D). For example, Group A consists of soils that have low runoff potential and high infiltration rates and typically consist of USDA soil textures of sand, loamy sand, and sandy loam. The transmission rate is typically greater than 0.76 cm/hr (Maidment, 1992). Septic systems with soils classified in Group A are more likely than Groups B, C, and D to contaminate the groundwater and surface waters.

The number of malfunctioning septic systems in the other soil groups (B, C, D) in the Copano Bay watershed was estimated by looking at the Authorized Agents (AA) Monthly Reports that are submitted to the TCEQ Compliance Support Division OSSF Program. These reports are available on the TCEQ website and are called OSSF Activity Reports. The relevant information from this site is that it lists the monthly “Complaints Investigated” and “Court Cases Filed” per county for OSSFs.

The *Comprehensive Sanitary Survey of the Shellfish Producing Waters of Copano Bay* (TDH, 2000) gives approximate locations of septic systems around the Copano Bay area and reports only one malfunctioning septic system in the area around the Bay. This report was used to approximate the location of septic systems around Copano Bay.

3.2.2 Datasets Required for Point Source Loads

3.2.2.1 Bird Data

Approximately 30 different types of colonial waterbird species live along the Texas coastline. The Texas Colonial Waterbird Census, using bird population data collected by volunteers from state, federal, non-profit organizations, and professional organizations, gives the number of breeding pairs of colonial waterbirds along the Texas Coast. As detailed in Section 5.3, these data were used to calculate annual waste loadings from colonial waterbirds.

3.2.2.2 Industrial/Municipal Wastewater Outfalls Data

The locations of industrial/municipal wastewater outfalls were obtained from the Permitted Wastewater Outfalls shapefile provided by the TCEQ. Descriptions of the permitted facilities were obtained from Sandra Alvarado from the TCEQ TRACS database.

Permit monitoring data (including fecal coliform and flow measurements) of water discharge permits (discharge monitoring reports) were obtained from the Permit Compliance System (PCS) Database from the U.S. Environmental Protection Agency (EPA).

Wastewater treatment plant (WWTP) bacterial loadings are calculated in Section 5.4.

3.2.2.3 Concentrated Animal Feedlot Operations (CAFOs) Data

A shapefile that contains CAFOs within the Copano Bay watershed was obtained from the TCEQ. However, there is only one permitted facility, and it was not recently renewed because the company is no longer operating (Alvarado, 2005). Thus, there are no CAFOs within the Copano Bay watershed at this time.

3.2.3 Water Rights Analysis Package (WRAP) Hydro Watershed Delineation Dataset

Before calculating the bacterial loadings, watersheds must be delineated because the bacterial loading per watershed is needed for the Schematic Processor Model. Watershed delineation requires a Digital Elevation Model (DEM), river network, and Critical Points, which is a feature class that contains points where the fecal coliform concentration can be examined. Critical Points were determined to be USGS gauge stations, bacterial monitoring stations (so modeled values can be compared to existing monitoring data), and water segment endpoints. This process is described in Section 5.1.2.1.

3.2.3.1 DEM and Terrain Preprocessing

The DEM was obtained from the National Elevation Dataset (NED) from USGS, which provides seamless coverage of the United States, providing a 1:24,000-scale DEM. The DEM, along with the National Hydrography Dataset and critical points of interest (feature class called “CriticalPoints”), provides the necessary data to conduct Terrain Preprocessing (Appendix 5.1) in Arc Hydro to determine the drainage patterns for the basin. The drainage patterns determine the pathway by which the bacteria reach the impaired water segments.

3.2.3.2 National Hydrography Dataset (NHD)

The National Hydrography Dataset (NHD) provides digital spatial data about surface water features such as lakes, ponds, streams, rivers, springs and wells. This dataset is based on the USGS Digital Line Graph (DLG) hydrography data and on information from the EPA Reach File Version 3 (RF3). However, there were missing data in the NHD dataset (feature class called “NHDFlowline”) for the Copano Bay watershed (e.g., random gaps in the river segments at multiple locations). Using the Editor Toolbar in ArcGIS, new features were created in the NHDFlowline feature class to ensure that all the river segments were connected within the river network.

3.2.3.3 Critical Points (USGS Gauge Stations, Bacterial Monitoring Stations, Water Segment Endpoints)

The locations of the USGS gauge stations were obtained from Better Assessment Science Integrating Point and Non-point Sources (BASINS). BASINS is an environmental analysis system developed by the U.S. EPA that can be used to perform watershed and water quality studies. BASINS allows a user to evaluate point and non-point source data in an easy-to-use format. To use BASINS, a user specifies a geographic area of interest, and the system downloads data from EPA, USGS, and other GIS data internet sources.

The locations of the water segment endpoints and bacterial monitoring stations were received from Sandra Alvarado from the TCEQ.

3.2.4 Datasets Required for Schematic Processor Model

3.2.4.1 USGS Stream Gauge Data

USGS stream gauge data were used to compare the modeled average annual runoff to existing average annual flowrates at the gauge stations as well as to find the residence time distributions (Section 6.3.3.2) associated with the various river segments in the Copano Bay watershed.

USGS stream gauge data was downloaded for the USGS gauge stations located in the Copano Bay watershed. The USGS station names in the watershed as well as the periods of records of the available data are given below:

- USGS 08189200 Copano Ck nr Refugio, TX (1970-2004)
- USGS 08189300 Medio Ck nr Beeville, TX (1962-2004)
- USGS 08189500 Mission Rv at Refugio, TX (1939-2004)
- USGS 08189700 Aransas Rv nr Skidmore, TX (1964-2004)

The data that are used for the Schematic Processor Model are the historical available daily streamflow data and streamflow measurements, which specify measurements of the width, streamflow, and area of the channel at the USGS gauge station locations.

3.2.4.2 Bathymetry Data

Bathymetry data give the water depth of water bodies. A hard copy bathymetry map, shown in Figure 3.1, (Ward, 2005) was available for Copano Bay, but not for the upstream rivers. The bathymetry map was used to calculate the volumes of each of the four Copano Bay water segments.

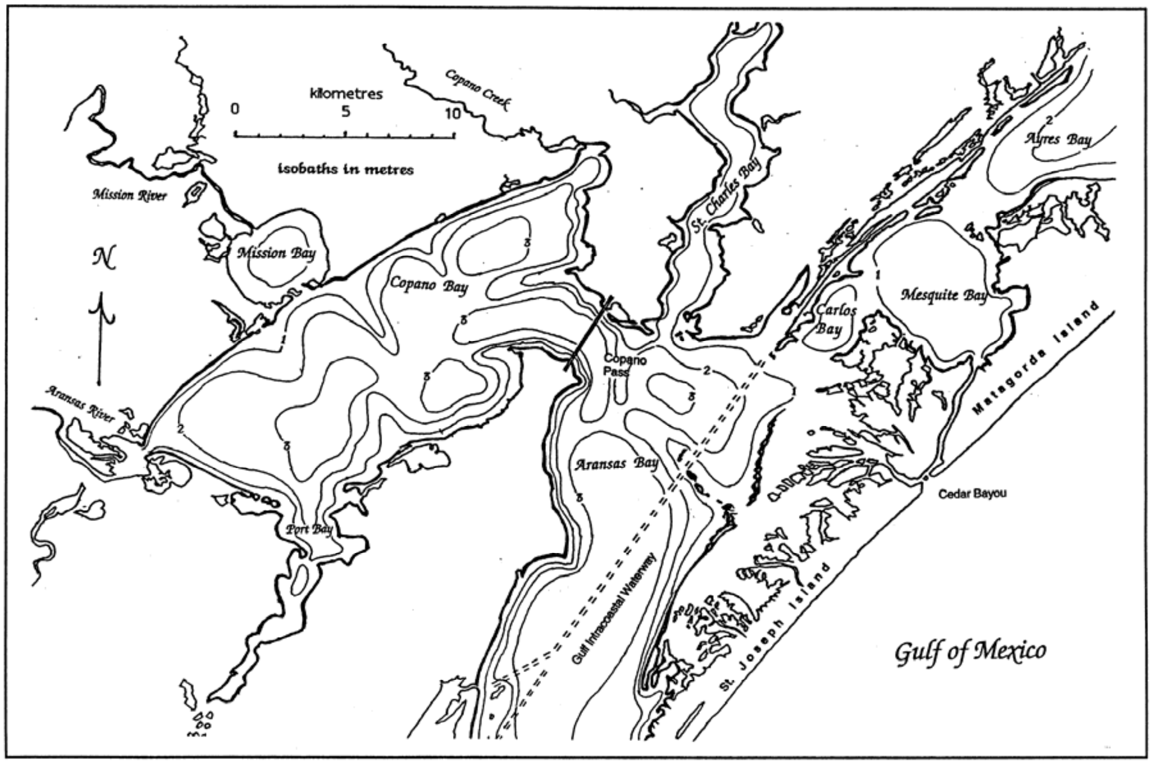

Figure 3.1 Bathymetry Map of Copano Bay

3.3 MAP PROJECTION AND COORDINATE SYSTEMS

All the datasets used for this project (described in Section 3.2) were retrieved from sources that may have had different map projection and coordinate systems. For GIS analysis and processes, it is critical to have all the datasets in the same coordinate system; thus, all the datasets for this project were projected into the same coordinate system.

The map projection that was used in the analyses of this project was Albers Conical Equal Area, and the geographic coordinate system that was used is North America Datum of 1983 (NAD 83). The projected coordinate system name is NAD_1983_Texas_Centric_Mapping_System_Albers, and the geographic coordinate system name is GCS_North_American_1983. The parameters for this projection are given in Table 3.3.

Table 3.3 Parameters for NAD_1983_Texas_Centric_Mapping_System_Albers

Projection	Albers Conical Equal Area
Datum	North American Datum of 1983 (NAD83)
Standard Parallel #1 (degrees)	27.5
Standard Parallel #2 (degrees)	35.0
Longitude of Central Meridian (degrees)	-100.0
Latitude of Projection Origin (degrees)	18.0
False Easting (meters)	1,500,000
False Northing (meters)	6,000,000
Units of Measure	Meters

Chapter 4: Analysis of Monitoring Dataset

4.1 SPATIAL DISTRIBUTION OF FECAL COLIFORM

4.1.1 Methodology

The bacterial monitoring data for fecal coliform was analyzed for this project because the bacterial indicator for oyster water use in Copano Bay is fecal coliform, and the most data exists for this bacterial indicator. The spatial distribution of fecal coliform concentrations was analyzed in the Copano Bay watershed at the locations of the bacterial monitoring stations.

The fecal coliform monitoring data came from the TCEQ TRACS database and is from the time period of January 1999 to May 2005. Fecal coliform bacteria are measured quarterly throughout the year, such that seasonal variations can be observed.

The fecal coliform standards that apply to the rivers and Copano Bay are given in Table 4.1.

Table 4.1 Fecal Coliform Water Quality Standards for Water Segments

Water Segment	Water Use	Geometric Mean (CFU/100mL)	Percent greater than Single Sample of 400 CFU/100mL (%)
Aransas River Above Tidal	Contact Recreation Use	< 200	< 25
Aransas River Tidal			
Mission River Above Tidal			
Mission River Tidal			
Water Segment	**Water Use**	**Median (CFU/100mL)**	**90th-Percentile (CFU/100mL)**
Copano Bay	Oyster Water Use	< 14	< 43

4.1.2 Procedure of Application

The minimum, maximum, geometric mean, arithmetic mean, and median of the existing fecal coliform concentrations (from 1999-2005) at each bacterial monitoring station are calculated and displayed using graduated symbols in ArcMap to convey the spatial variation of fecal coliform bacteria.

4.1.3 Result

The arithmetic mean, geometric mean, median, minimum, and maximum fecal coliform data (TCEQ TRACS database from 1999-2005) are shown in Figures 4.1 - 4.5 at each of the TCEQ bacterial monitoring stations in the Copano Bay watershed. The mean of all existing monitoring data is shown in Figure 4.1.

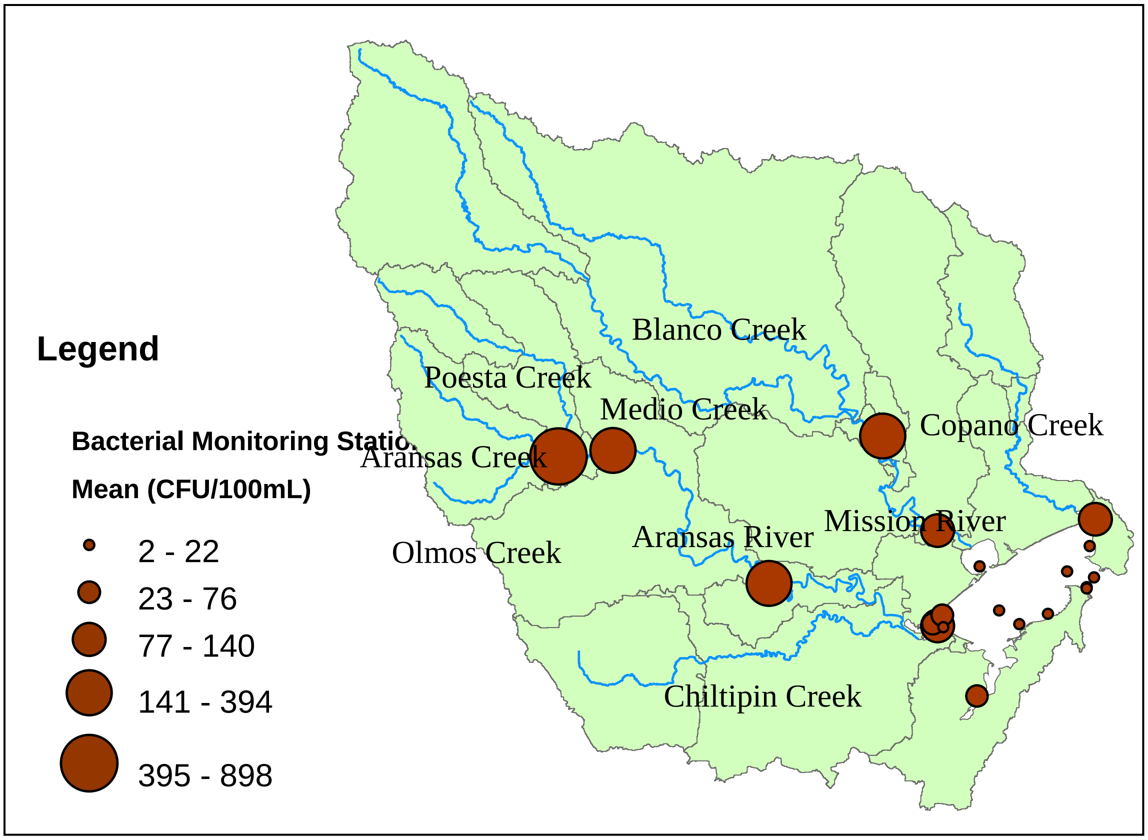

Figure 4.1 Mean of Fecal Coliform Concentrations at TCEQ Bacterial Monitoring Stations (1999-2005)

The mean fecal coliform concentrations are lower at stations that are closer to Copano Bay (Figure 4.1). Thus, water quality decreases the further upstream from the Bay. This trend can be explained by the effects that various environmental factors (e.g., solar radiation intensity, temperature, and salinity) have on bacterial decay. The lower concentrations in the Bay as compared to the upstream rivers and streams are also indicative of the dilution effects and higher salinity of Copano Bay. Note that higher mean fecal coliform concentrations occur in Copano Bay at locations where rivers and streams discharge into the Bay, but the lowest mean fecal coliform concentrations in the Bay occur at locations where no rivers discharge.

The highest mean fecal coliform concentrations are measured near where Olmos Creek enters Aransas Creek, where Poesta and Aransas Creeks merge to become Aransas River, and where Blanco and Medio creeks merge to become Mission River.

The geometric means and median concentrations of the existing data at the monitoring stations are shown in Figures 4.2 and 4.3, respectively. Use of the geometric mean and median concentrations reduces the effects of the high fecal coliform concentrations.

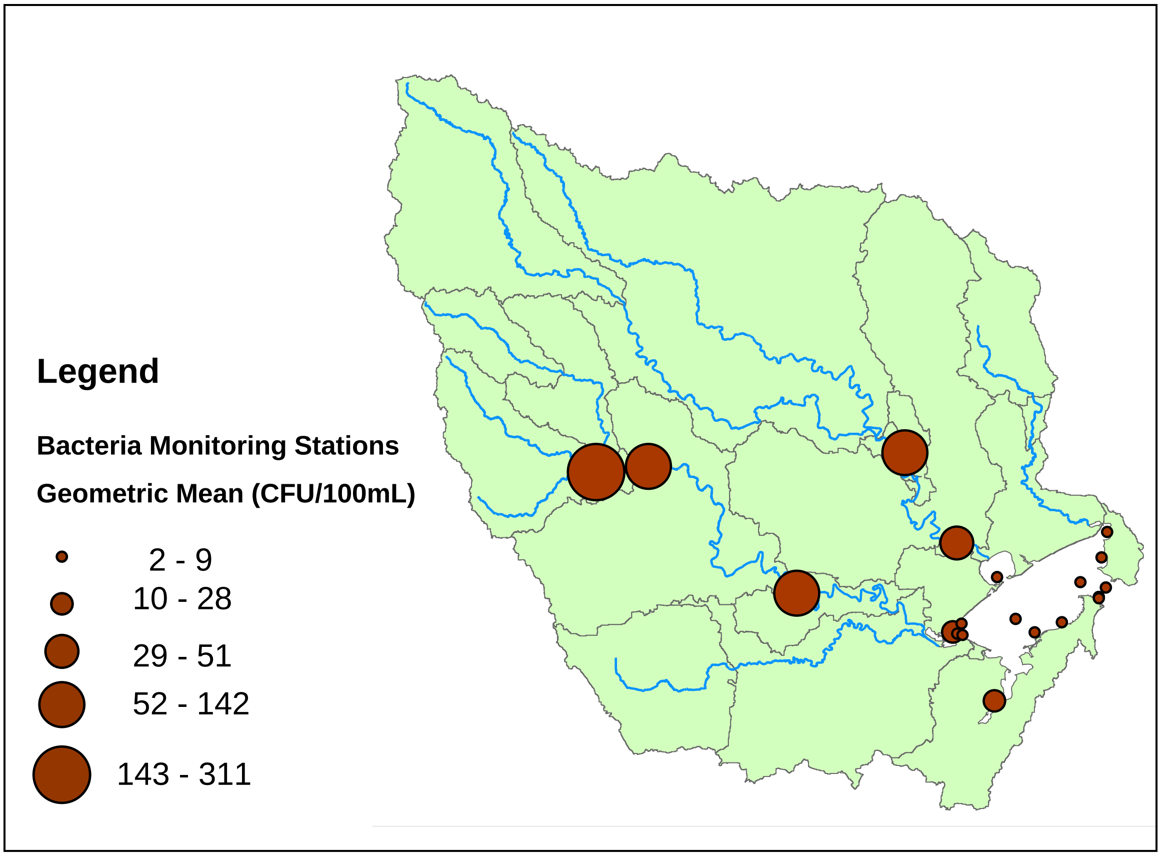

Figure 4.2 Geometric Mean of Fecal Coliform Concentrations at TCEQ Bacterial Monitoring Stations (1999-2005)

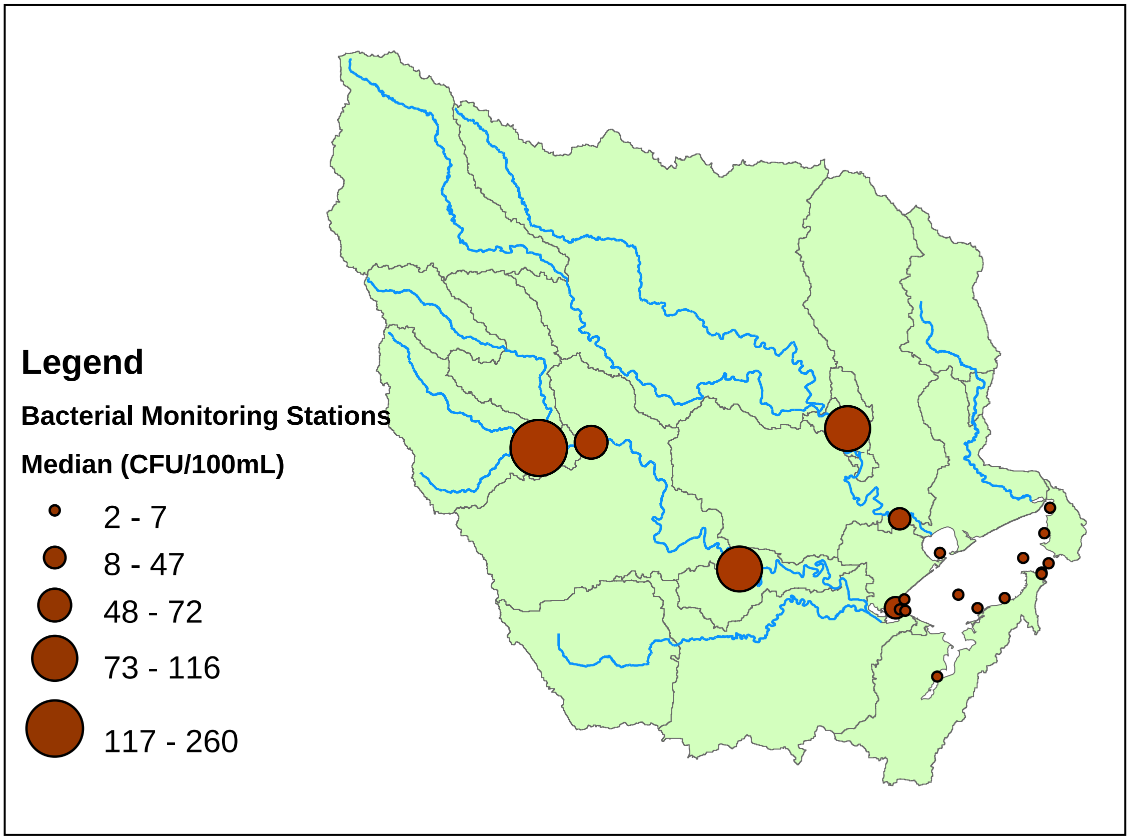

Figure 4.3 Median of Fecal Coliform Concentrations at TCEQ Bacterial Monitoring Stations (1999-2005)

Ignoring the high storm events that would skew the mean fecal coliform concentration values, the highest geometric mean/median fecal coliform concentrations are also in the upstream rivers and streams (as shown in Figures 4.2 and 4.3). However, the oyster water use standards that apply to Copano Bay are more stringent than the contact recreation use standards that apply to the river segments (Table 4.1). The highest geometric mean/median FC concentrations are measured where Olmos Creek enters Aransas Creek, and where Blanco and Medio Creeks merge to become Mission River. The measured median fecal coliform concentrations in the Bay comply with oyster water use fecal coliform water quality standards (median < 14 CFU/100mL.)

The minimum and maximum fecal coliform concentrations of the existing data at monitoring stations are shown in Figures 4.4 and 4.5, respectively.

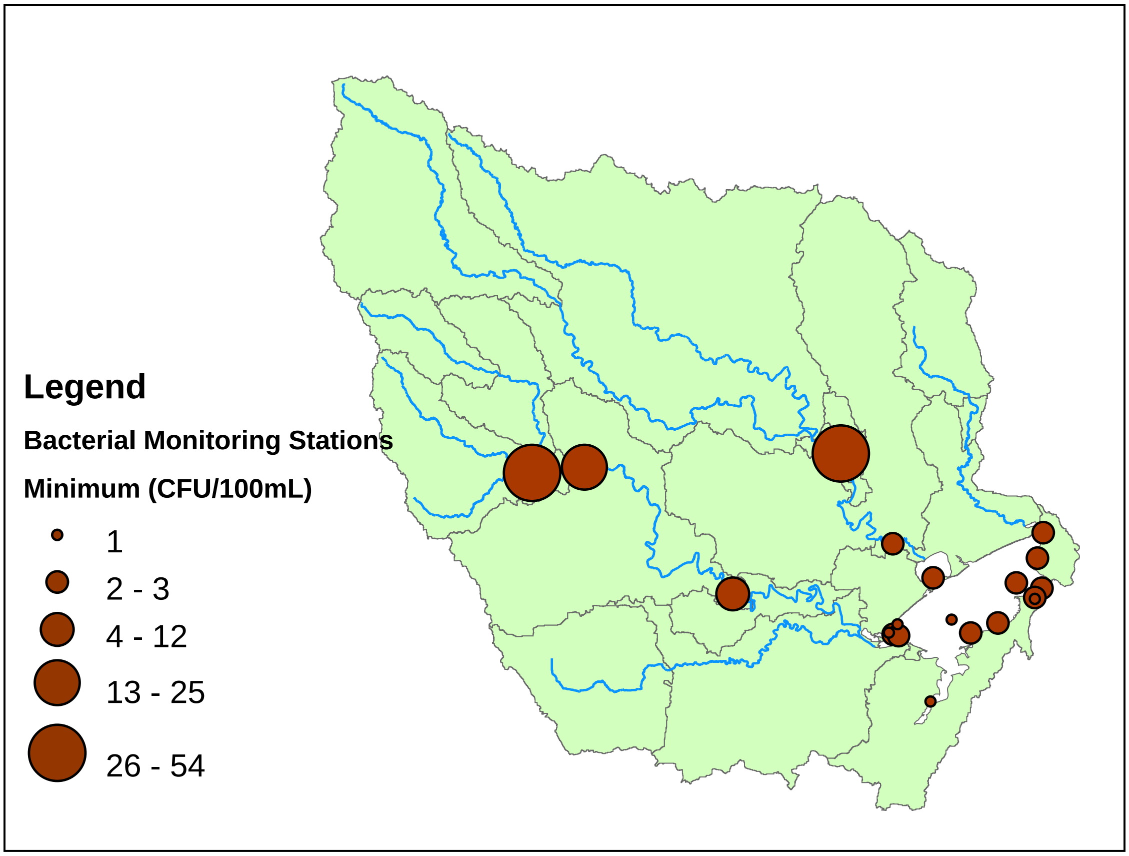

Figure 4.4 Minimum of Fecal Coliform Concentrations at TCEQ Bacterial Monitoring Stations (1999-2005)

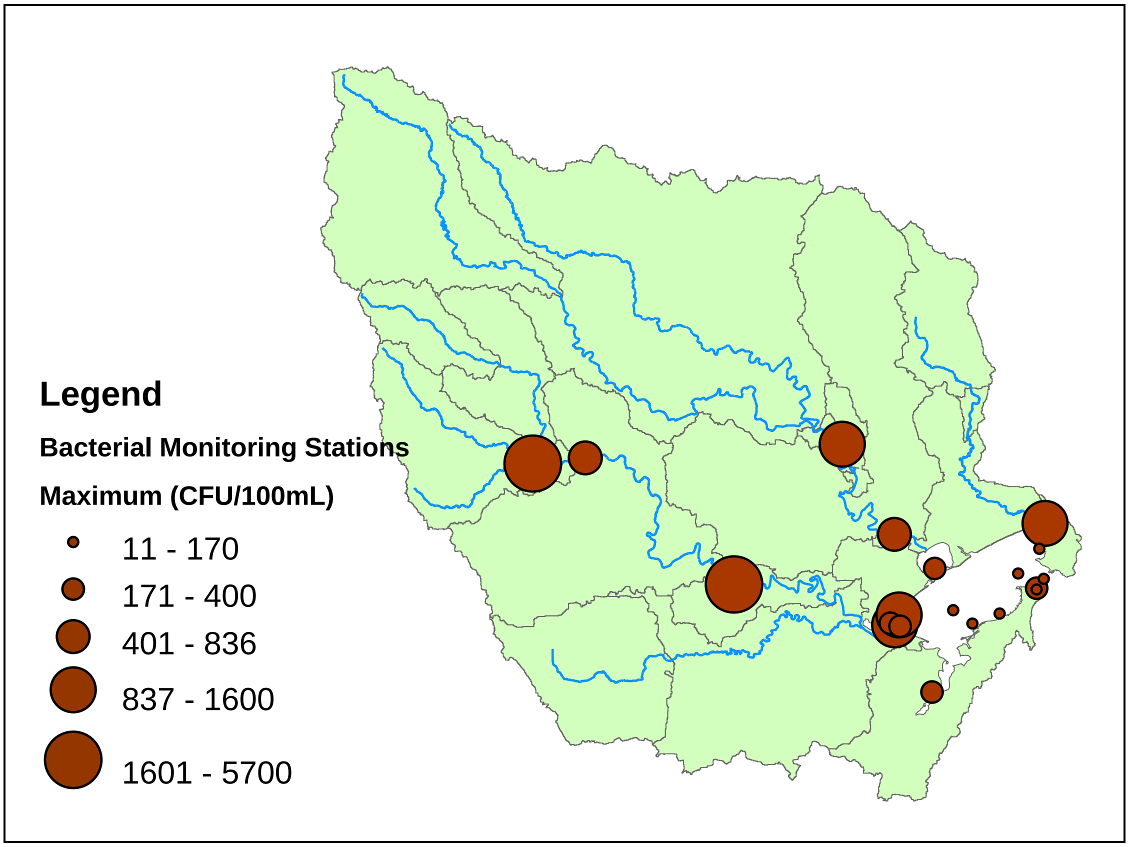

Figure 4.5 Maximum of Fecal Coliform Concentrations at Bacterial Monitoring Stations (1999-2005)

Very high fecal coliform concentrations are measured at the Aransas River and Copano Creek outlets in Copano Bay (Figure 4.5). These high fecal coliform concentrations can be attributed to storm events. It is these storm events that cause portions of Copano Bay to exceed oyster water use fecal coliform water quality standards (90th-percentile > 43 CFU/100mL).

The fecal coliform monitoring data from these bacterial stations are compared to modeled results in Chapters 6 and 7.

The bacterial monitoring stations associated with each water segment in the Copano Bay watershed are identified in Table 4.2.

Table 4.2 Water Segment Locations of Bacterial Monitoring Stations

Copano Bay Water Segment	Segment ID	Segment Name	Bacterial Monitoring Stations
N/A	2001	Mission River Tidal	12943
N/A	2002	Mission River Above Tidal	12944
N/A	2003	Aransas River Tidal	12948
N/A	2004	Aransas River Above Tidal	12952
1	2472	Copano Bay	13405, 14782, 14784, 14790
2			12945, 14783, 14787, 14788
3			14797
4			13404, 14779, 14780, 14785, 14792, 14793

The summary of the fecal coliform data for the water body segments (TCEQ segments) in the Copano Bay watershed can be found in Table 4.3. The summary of the fecal coliform monitoring data for the Copano Bay water segments (defined in Section 6.3.1.1) can be found in Table 4.4.

Table 4.3 Summary of TCEQ Fecal Coliform Monitoring Data for Water Segments

TCEQ Segment ID	Segment Name	Number of Stations	Arithmetic Mean (CFU/100mL)	Median (CFU/100mL)	Minimum (CFU/100mL)	Maximum (CFU/100mL)	Number of Data Points
2001	Mission River Tidal	1	107	47	3	740	16
2002	Mission River Tidal	1	251	116	46	1382	17
2003	Aransas River Tidal	1	394	96	12	3700	16
2004	Aransas River Above Tidal	1	224	72	25	836	5
2472	Copano Bay	15	33	2	1	1600	497

Table 4.4 Summary of TCEQ Fecal Coliform Monitoring Data for Copano Bay Water Segments

Segment ID	Segment Name	Number of Stations	Arithmetic Mean (CFU/100mL)	Median (CFU/100mL)	Minimum (CFU/100mL)	Maximum (CFU/100mL)	Number of Data Points
1	Watershed JunctionID 45405 Outlet	4	17	2	1	390	113
2	Aransas River Outlet	4	68	2	1	1600	121
3	Mission River Outlet	1	22	2	2	240	31
4	Copano Creek Outlet	6	25	2	1	1600	232

4.2 STATISTICAL DISTRIBUTION OF FECAL COLIFORM

4.2.1 Methodology

Two criteria need to be met for fecal coliform oyster water use standards: 1) the median of measured data needs to be less than 14 CFU/100mL, and 2) 90% of the measured concentrations need to be less than 43 CFU/100mL. The water quality of the four water segments of Copano Bay needs to comply with these oyster water use standards.

Two criteria need to be met for fecal coliform contact recreation use standards: 1) the geometric mean of measured data needs to be less than 200 CFU/100mL, and 2) 75% of the measured concentrations need to be less than 400 CFU/100mL. The water qualities of Aransas and Mission River Tidals and Aransas and Mission River Above Tidals need to comply with these contact recreation use standards.

To compare the monitoring data to water quality standards (also summarized in Table 4.1), the fecal coliform data at each bacterial monitoring station in the upstream rivers and segments and the monitoring data in each of the Copano Bay water segments (Segments 1, 2, 3, and 4) are plotted on a log scale versus the probability of exceedance. The two criteria (contact recreation use and oyster water use) are indicated on each plot in Section 4.2.3.

4.2.2 Procedure of Application

Blom's plotting formula was used to plot the probability distributions of the existing bacterial monitoring data, and a lognormal distribution was assumed (Zoun, 2003).

$$P = 100\ \% * (m - 3/8) / (n + 1/4) \qquad (4.1)$$

Where: P = probability of exceedance (%)

m = rank; (m = 1 for largest FC concentration)

n = number of data values

After calculating the probability of exceedance for each measured fecal coliform concentration using Equation 4.1., the measured fecal coliform concentrations were plotted on a log-scale versus the probability of exceedance.

The measured data of all of the bacterial monitoring stations for each Copano Bay water segment (Segments 1, 2, 3, and 4) are grouped together (the monitoring station data that were applied to each segment is shown in Table 4.2) for the probability distribution plots.

The measured data of the bacterial monitoring stations along the rivers are shown at each bacterial monitoring station.

These probability plots are used to calibrate the Monte Carlo Simulation Model at each bacterial monitoring station location (in Chapter 7).

4.2.3 Result

4.2.3.1 Aransas River Above Tidal

There is only one bacterial monitoring station on the Aransas River Above Tidal reach, but there is another bacterial monitoring station with fecal coliform monitoring data that is upstream of the Above Tidal reach and must also comply with contact recreation use standards. The latter station, Station 17592 (HydroID 61), was analyzed first because it is the most upstream station. The bacterial monitoring data from Station 17592 (from 1999-2004), the rank, probability of exceedance, and the geometric mean of the measured data are shown in Table 4.5.

Table 4.5 Bacterial Monitoring Data for Station 17592 (1999-2004)

Date	Fecal Coliform Concentration (CFU/100mL)	Rank	Probability of Exceedance, %
6/18/2001	5700	1	6.10
4/10/2001	1373	2	15.85
1/14/2002	500	3	25.61
4/9/2002	500	4	35.37
10/8/2001	270	5	45.12
7/11/2000	250	6	54.88
1/19/2000	147	7	64.63
1/15/2001	106	8	74.39
4/17/2000	76	9	84.15
10/25/1999	54	10	93.90
Geometric Mean (CFU/100mL)			**311** > 200
Percent > 400 CFU/100mL (%)			**~ 40** > 25

As shown in Table 4.5, both contact recreation use standards are exceeded at this bacterial monitoring station because the geometric mean is greater than 200 CFU/100mL, and more than 25% of the samples are greater than 400 CFU/100mL. However, this station is not along a TCEQ-defined water segment, and fecal coliform monitoring data have not been collected since April 2002. *E. coli* has recently been chosen as the bacterial indicator for the Aransas River Above Tidal; therefore, fecal coliform concentrations are no longer measured at this station. The probability distribution of the measured fecal coliform concentrations at Station 17592, which is a plot of the data given in Table 4.5, and the two fecal coliform contact recreation use standards are shown in Figure 4.6.

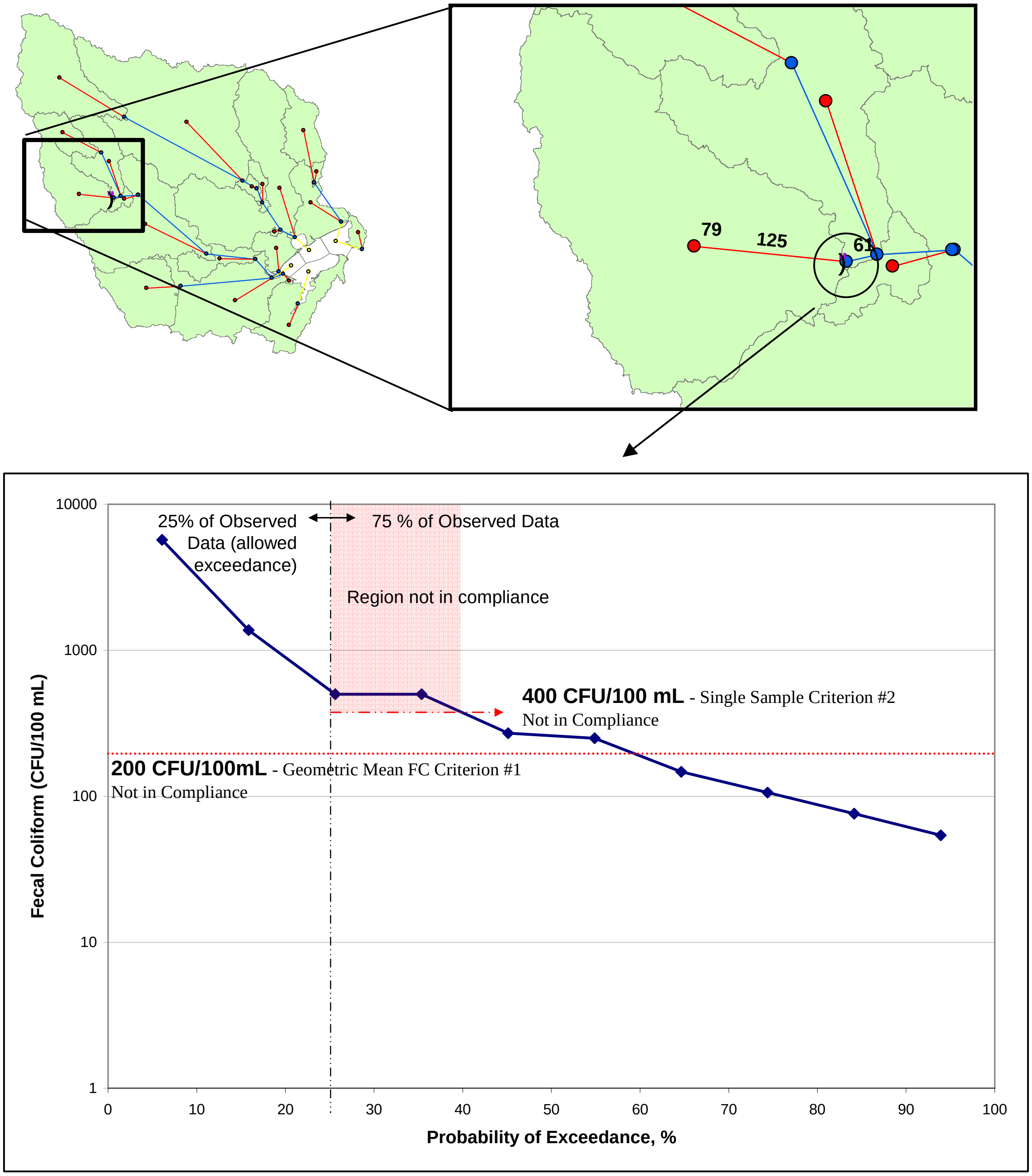

Figure 4.6 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Station 17592

Station 12952 (HydroID 68) is the bacterial monitoring station on the Aransas River Above Tidal (downstream of Station 17592.) The bacterial monitoring data that exist at Station 12952 (from 1999-2004), the rank, probability of exceedance, and the geometric mean of the measured data are shown in Table 4.6.

Table 4.6 Bacterial Monitoring Data for Station 12952 (1999-2004)

Date	**Fecal Coliform Concentration (CFU/100mL)**	**Rank**	**Probability of Exceedance, %**
7/8/2002	836	1	11.90
4/22/2003	130	2	30.95
1/21/2003	72	3	50.00
8/18/2003	58	4	69.05
10/15/2002	25	5	88.10
Geometric Mean (CFU/100mL)			103 < 200
Percent > 400 CFU/100mL (%)			~23 < 25

Both contact recreation use standards are met at this bacterial monitoring station (as shown in Table 4.6). However, fecal coliform monitoring data have not been collected since August 2003 because *E. coli* is now the primary bacterial indicator for the Aransas River Above Tidal. The probability distribution of the measured fecal coliform concentrations at Station 12952, which is a plot of the data given in Table 4.6, is shown in Figure 4.7. The two fecal coliform contact recreation use standards are also shown in Figure 4.7.

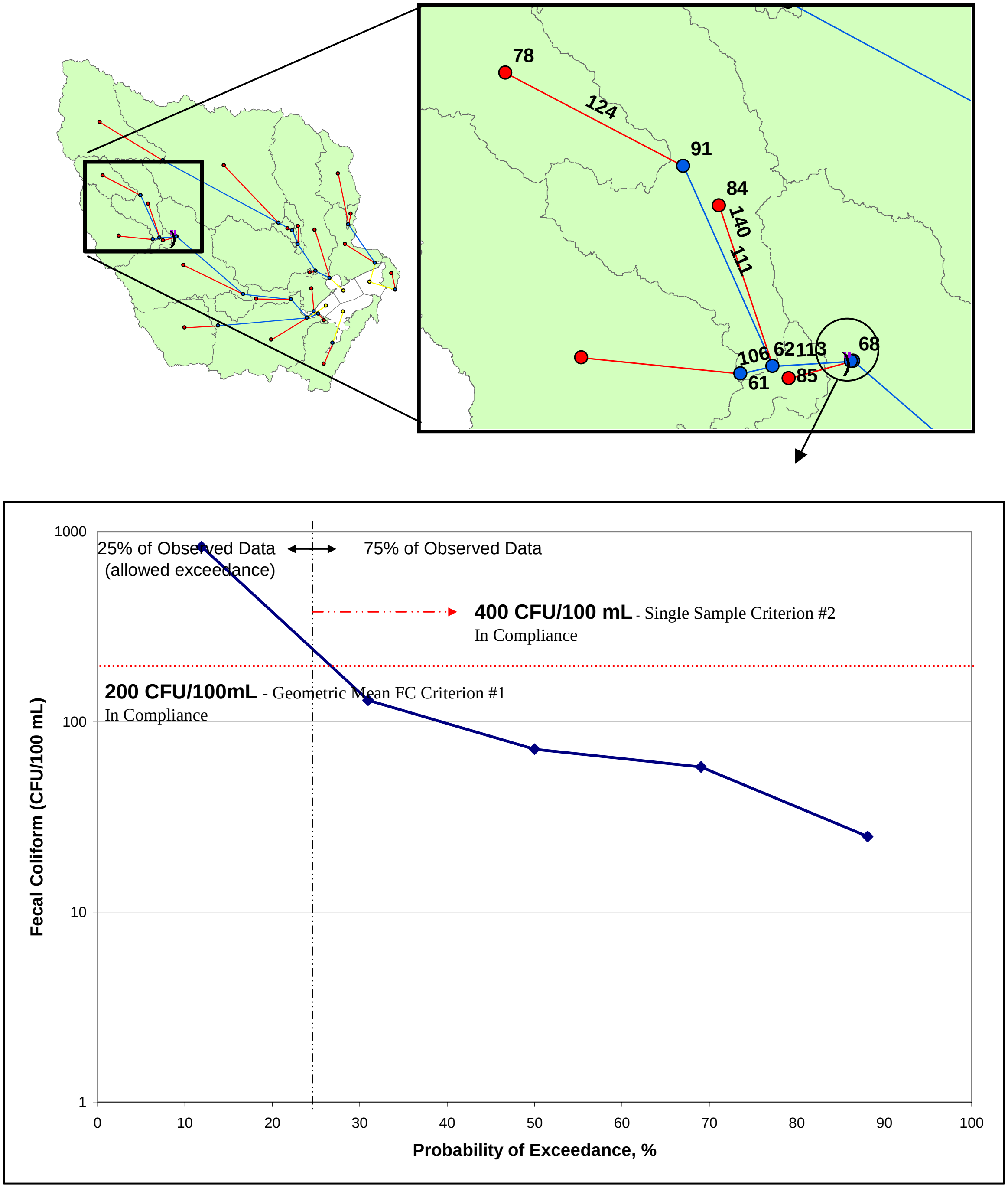

Figure 4.7 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Station 12952

4.2.3.2 Aransas River Tidal

Station 12948 (HydroID 75) is the only bacterial monitoring station on the Aransas River Tidal, and this segment must meet contact recreation use fecal coliform standards. The bacterial monitoring data that exists at Station 12948 (from 1999-2004), the rank, probability of exceedance, and the geometric mean of the measured data, are shown in Table 4.7.

Table 4.7 Bacterial Monitoring Data for Station 12948 (1999-2004)

Date	**Fecal Coliform Concentration (CFU/100mL)**	**Rank**	**Probability of Exceedance, %**
4/17/2000	3700	1	3.85
7/8/2002	1327	2	10.00
1/15/2001	270	3	16.15
10/9/2000	162	4	22.31
6/18/2001	131	5	28.46
10/15/2002	122	6	34.62
7/11/2000	112	7	40.77
4/10/2001	98	8	46.92
1/14/2002	94	9	53.08
4/9/2002	94	10	59.23
1/21/2003	58	11	65.38
10/8/2001	48	12	71.54
4/22/2003	34	13	77.69
8/18/2003	28	14	83.85
1/19/2000	20	15	90.00
10/25/1999	12	16	96.15
Geometric Mean (CFU/100mL)			105 < 200
Percent > 400 CFU/100mL (%)			~15 < 25

As shown in Table 4.7, both contact recreation use standards are met at this bacterial monitoring station. However, fecal coliform monitoring data have not been collected since August 2003 because enterococcus is now the primary bacterial indicator for the

Aransas River Tidal. As discussed in Section 2.1, enterococcus is a better bacterial indicator in marine waters. The probability distribution of the measured fecal coliform concentrations at Station 12948, which is a plot of the data given in Table 4.7, is shown in Figure 4.8. The two fecal coliform contact recreation use standards are also shown in Figure 4.8.

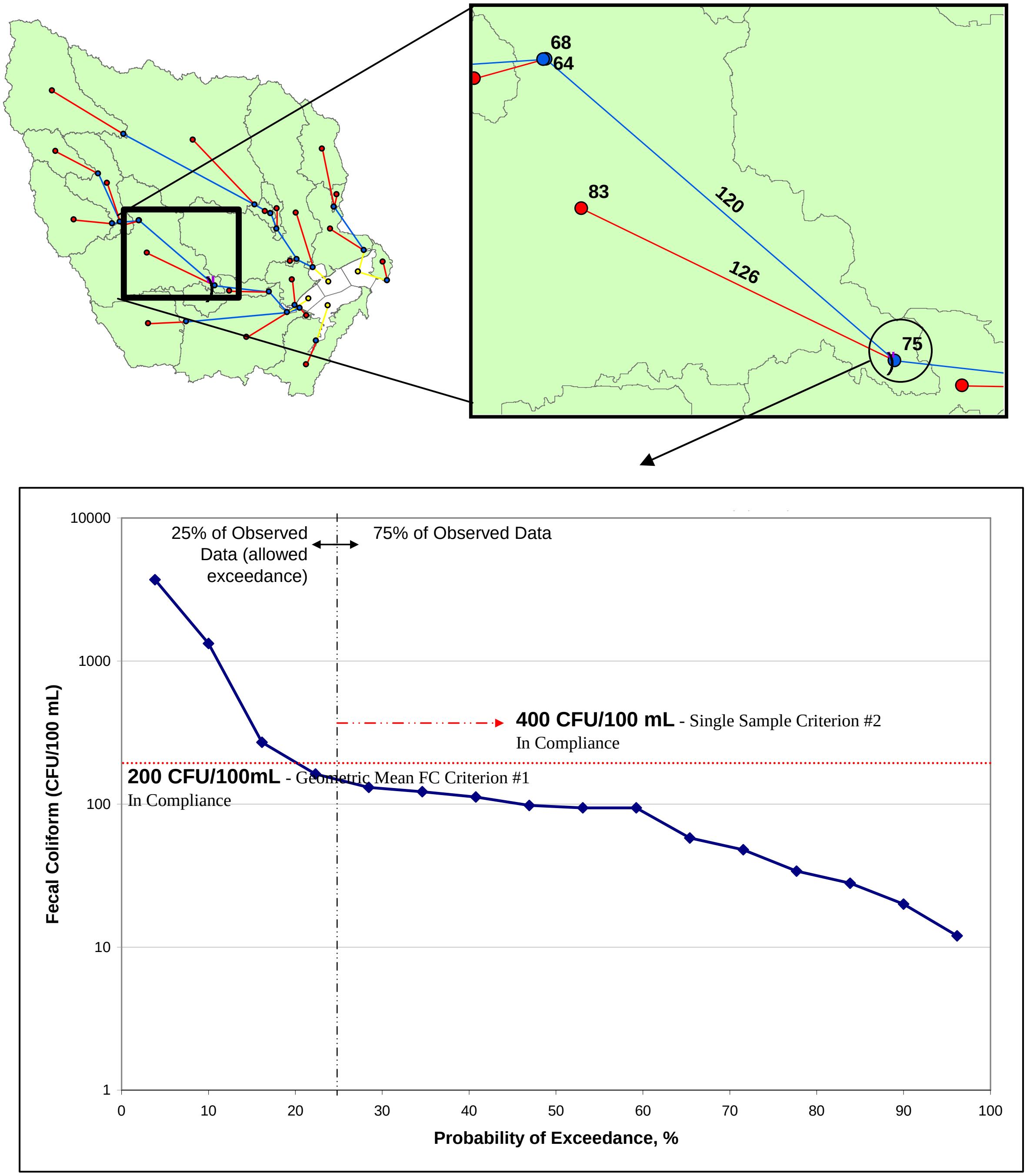

Figure 4.8 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Station 12948

4.2.3.3 Mission River Above Tidal

Station 12944 (HydroID 74) is the only bacterial monitoring station on the Mission River Above Tidal, and this segment must meet contact recreation use fecal coliform standards. The bacterial monitoring data that exists at Station 12944 (from 1999-2004), the rank, probability of exceedance, and the geometric mean of the measured data are shown in Table 4.8.

Table 4.8 Bacterial Monitoring Data for Station 12944 (1999-2004)

Date	**Fecal Coliform Concentration (CFU/100mL)**	**Rank**	**Probability of Exceedance, %**
10/9/2000	1382	1	3.62
7/8/2002	682	2	9.42
1/19/2000	410	3	15.22
1/15/2001	410	4	21.01
4/10/2001	320	5	26.81
10/8/2001	157	6	32.61
1/21/2003	142	7	38.41
4/22/2003	120	8	44.20
5/12/2003	116	9	50.00
4/17/2000	112	10	55.80
7/11/2000	94	11	61.59
10/25/1999	58	12	67.39
6/18/2001	56	13	73.19
1/14/2002	54	14	78.99
4/9/2002	54	15	84.78
8/18/2003	54	16	90.58
10/15/2002	46	17	96.38
Geometric Mean (CFU/100mL)			142 < 200
Percent > 400 CFU/100mL (%)			~21 < 25

As shown in Table 4.8, both contact recreation use standards are met at this bacterial monitoring station. However, fecal coliform monitoring data have not been collected since August 2003 because *E. coli* is now the primary bacterial indicator for the Mission River Above Tidal. The probability distribution of the measured fecal coliform concentrations at Station 12944, which is a plot of the data given in Table 4.8, is shown in Figure 4.9. The two fecal coliform contact recreation use standards are also shown in Figure 4.9.

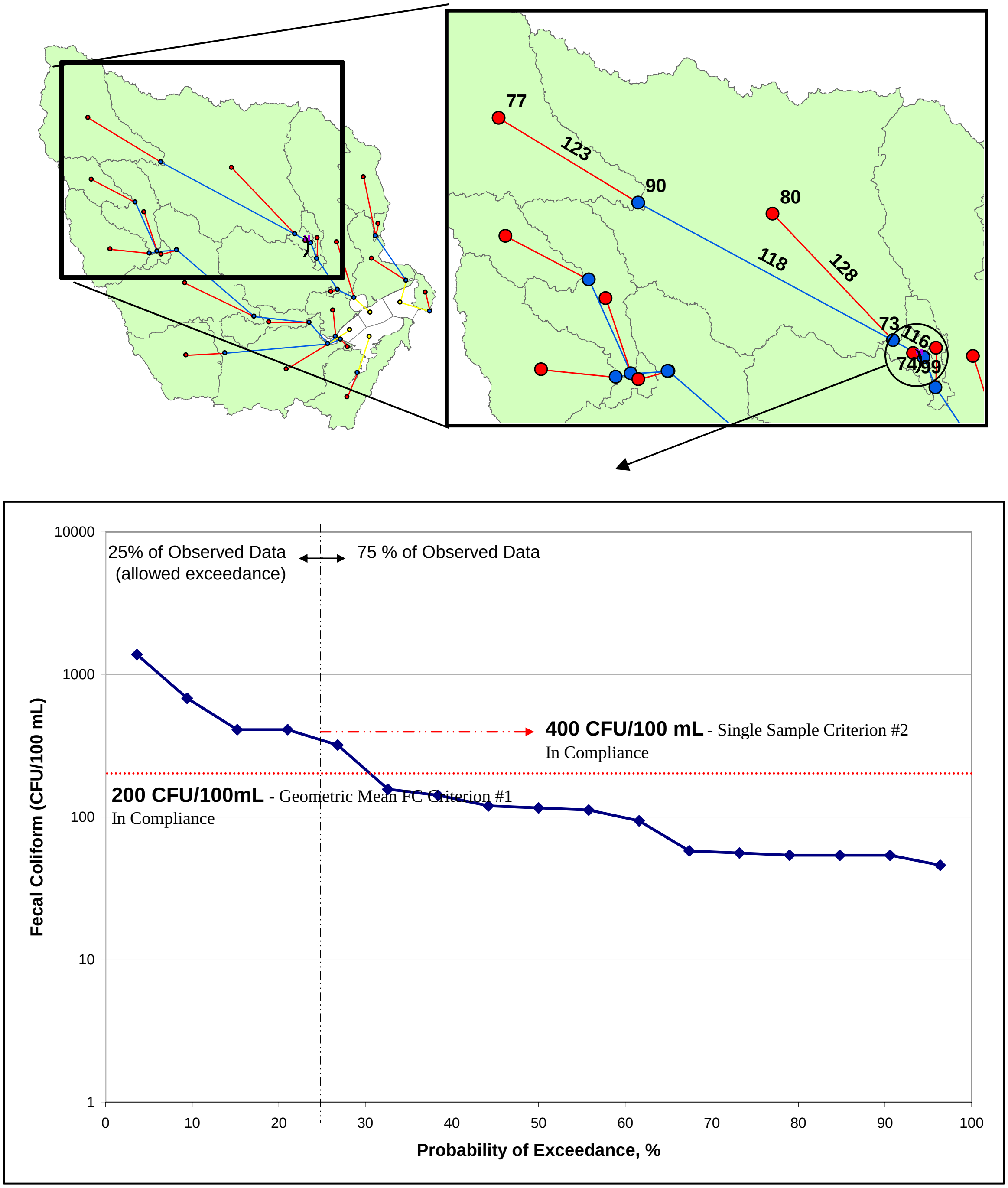

Figure 4.9 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Station 12944

4.2.3.4 Mission River Tidal

Station 12943 (HydroID 70) is the only bacterial monitoring station on the Mission River Tidal, and this segment must meet contact recreation use fecal coliform standards. The bacterial monitoring data that exists at Station 12943 (from 1999-2004), the rank, probability of exceedance, and the geometric mean of the measured data are shown in Table 4.9.

Table 4.9 Bacterial Monitoring Data for Station 12943 (1999-2004)

Date	**Fecal Coliform Concentration (CFU/100mL)**	**Rank**	**Probability of Exceedance, %**
1/15/2001	740	1	3.85
4/22/2003	270	2	10.00
1/21/2003	147	3	16.15
7/8/2002	130	4	22.31
8/18/2003	55	5	28.46
4/17/2000	52	6	34.62
1/14/2002	51	7	40.77
4/9/2002	51	8	46.92
6/18/2001	42	9	53.08
7/11/2000	41	10	59.23
4/10/2001	37	11	65.38
10/25/1999	32	12	71.54
1/19/2000	23	13	77.69
10/8/2001	22	14	83.85
10/15/2002	21	15	90.00
10/9/2000	3	16	96.15
Geometric Mean (CFU/100mL)			51 < 200
Percent > 400 CFU/100mL (%)			~10 < 25

As shown in Table 4.9, both contact recreation use standards are met at this bacterial monitoring station. However, fecal coliform monitoring data have not been collected since August 2003 because enterococcus is now the primary bacterial indicator for the Mission River Tidal. The probability distribution of the measured fecal coliform concentrations at Station 12943, which is a plot of the data given in Table 4.9, is shown in Figure 4.10. The two fecal coliform contact recreation use standards are also shown in Figure 4.10.

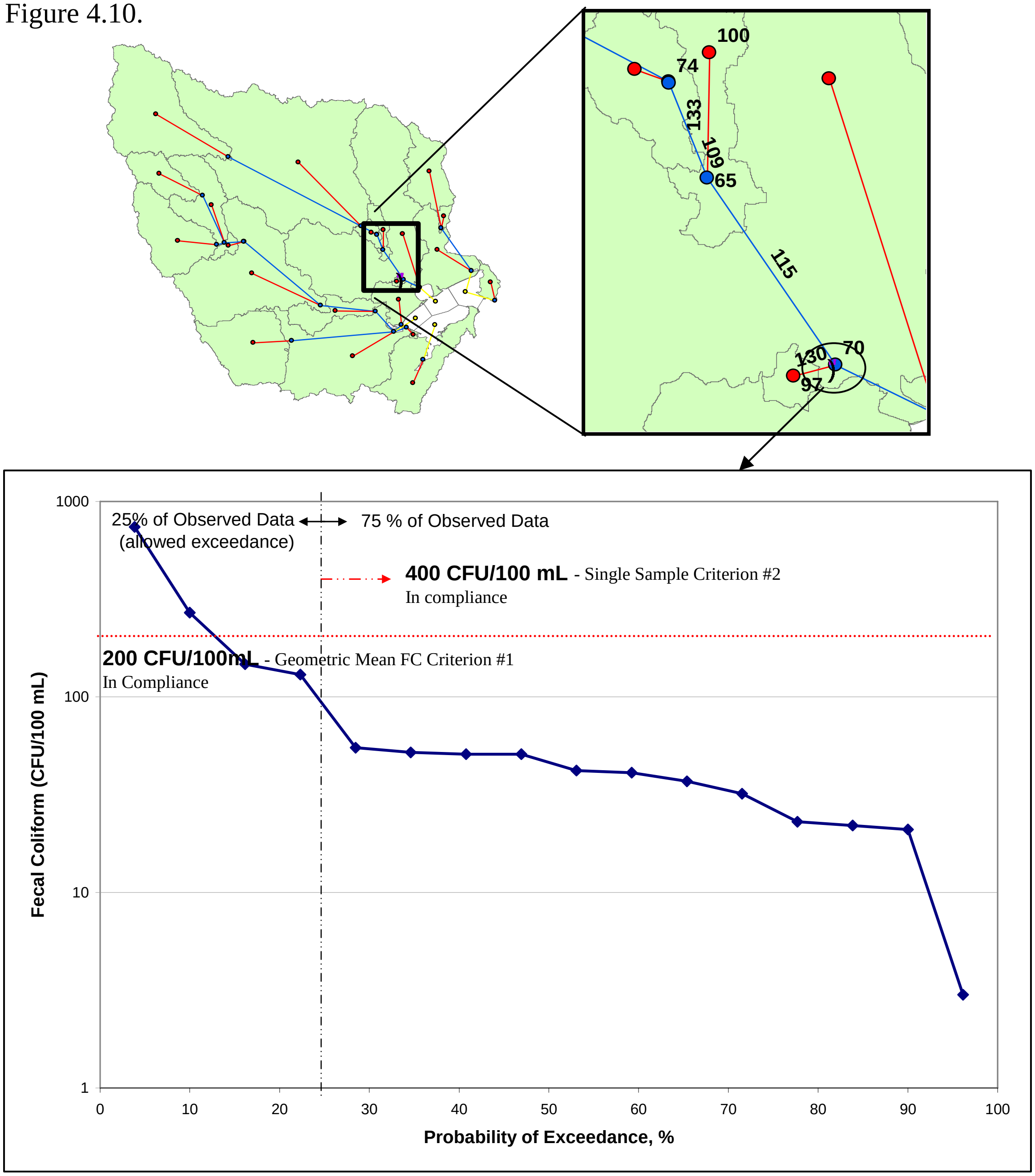

Figure 4.10 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Station 12943

4.2.3.5 Copano Bay

Bacterial monitoring data were analyzed at the four Copano Bay segments (Segments 1, 2, 3, and 4), which need to meet oyster water use fecal coliform standards. Fecal coliform remains the primary bacterial indicator in Copano Bay, so fecal coliform concentrations continue to be measured.

Watershed JunctionID 45405 drains into Segment 1 (SchemaNode 155). Bacterial monitoring stations 13405, 14782, 14784, and 14790 all measure fecal coliform concentrations in Copano Bay Segment 1. The median and 90th-percentile of the monitoring data (from 1999-2005) are shown in Table 4.10; all of the bacterial monitoring data that exists for Segment 1 (from 1999-2005) and the rank and the probability of exceedance for each measurement are given in Appendix 4.1.

Table 4.10 Statistics of Bacterial Monitoring Data for Stations in Segment 1 (1999-2005)

Median Fecal Coliform Concentration (CFU/100mL)	2
90th Percentile Fecal Coliform Concentration (CFU/100mL)	~ 15
Number of Measurements	113

As shown in Table 4.10, both oyster water use standards are met in Copano Bay Segment 1. The probability distribution of the measured fecal coliform concentrations at these stations is shown in Figure 4.11. The two fecal coliform oyster water use standards are also shown in Figure 4.11.

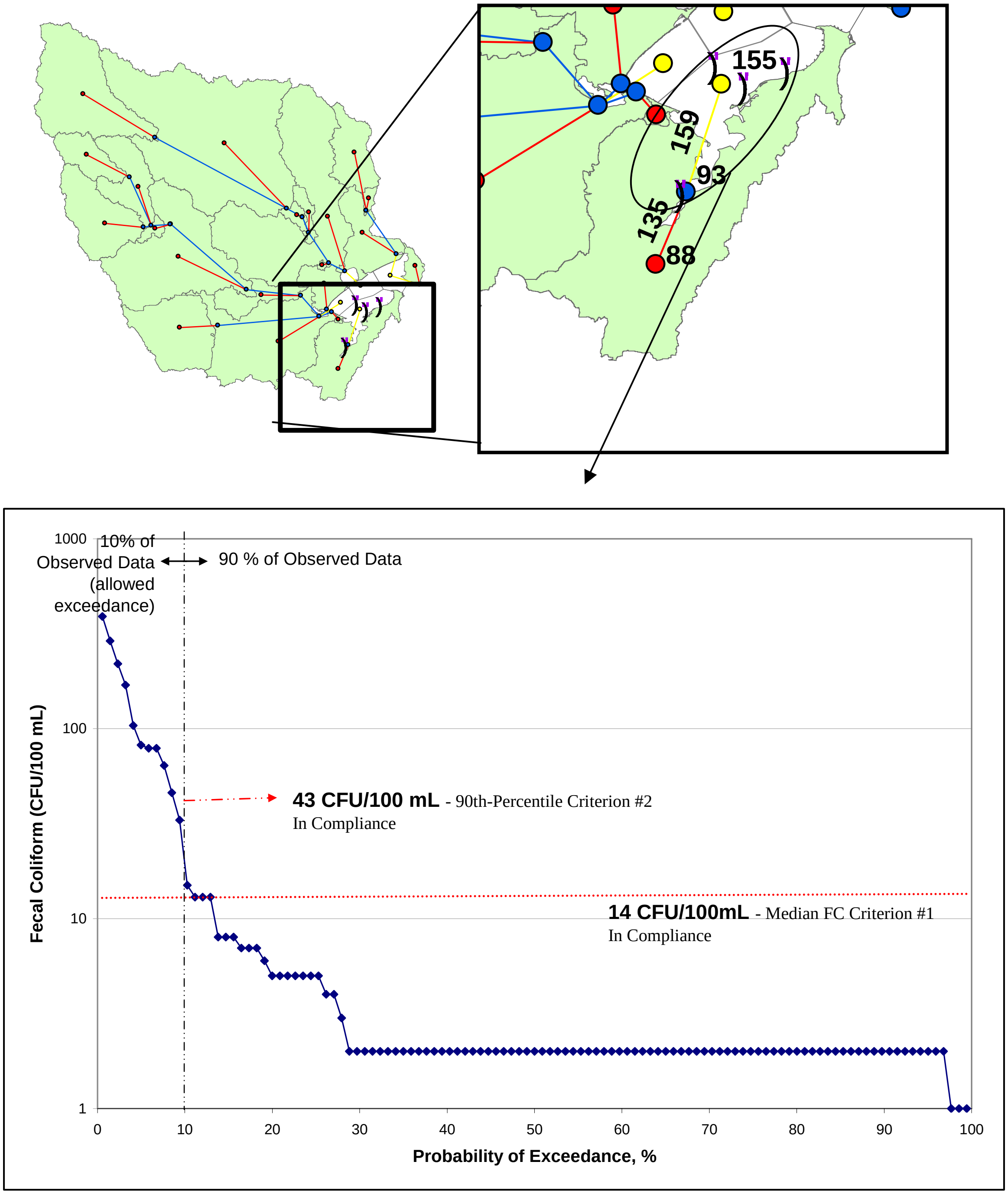

Figure 4.11 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Segment 1

Aransas River and Chiltipin Creek drain into Segment 2 (SchemaNode 154). Bacterial monitoring stations 12945, 14783, 14787, and 14788 measure fecal coliform concentrations in Copano Bay Segment 2. The median and 90th-percentile of the monitoring data (from 1999-2005) are shown in Table 4.11; all of the bacterial monitoring data that exists for Segment 2 (from 1999-2005) and the rank and the probability of exceedance for each measurement are given in Appendix 4.2.

Table 4.11 Statistics of Bacterial Monitoring Data for Stations in Segment 2 (1999-2005)

Median Fecal Coliform Concentration (CFU/100mL)	2
90th Percentile Fecal Coliform Concentration (CFU/100mL)	**~ 79**
Number of Measurements	121

As shown in Table 4.11, Copano Bay Segment 2 complies with the median fecal coliform standard (< 14 CFU/100mL) but exceeds the 90th-percentile fecal coliform standard of 43 CFU/100mL. The probability distribution of the measured fecal coliform concentrations at these stations is shown in Figure 4.12. The two fecal coliform oyster water use standards are also shown in Figure 4.12.

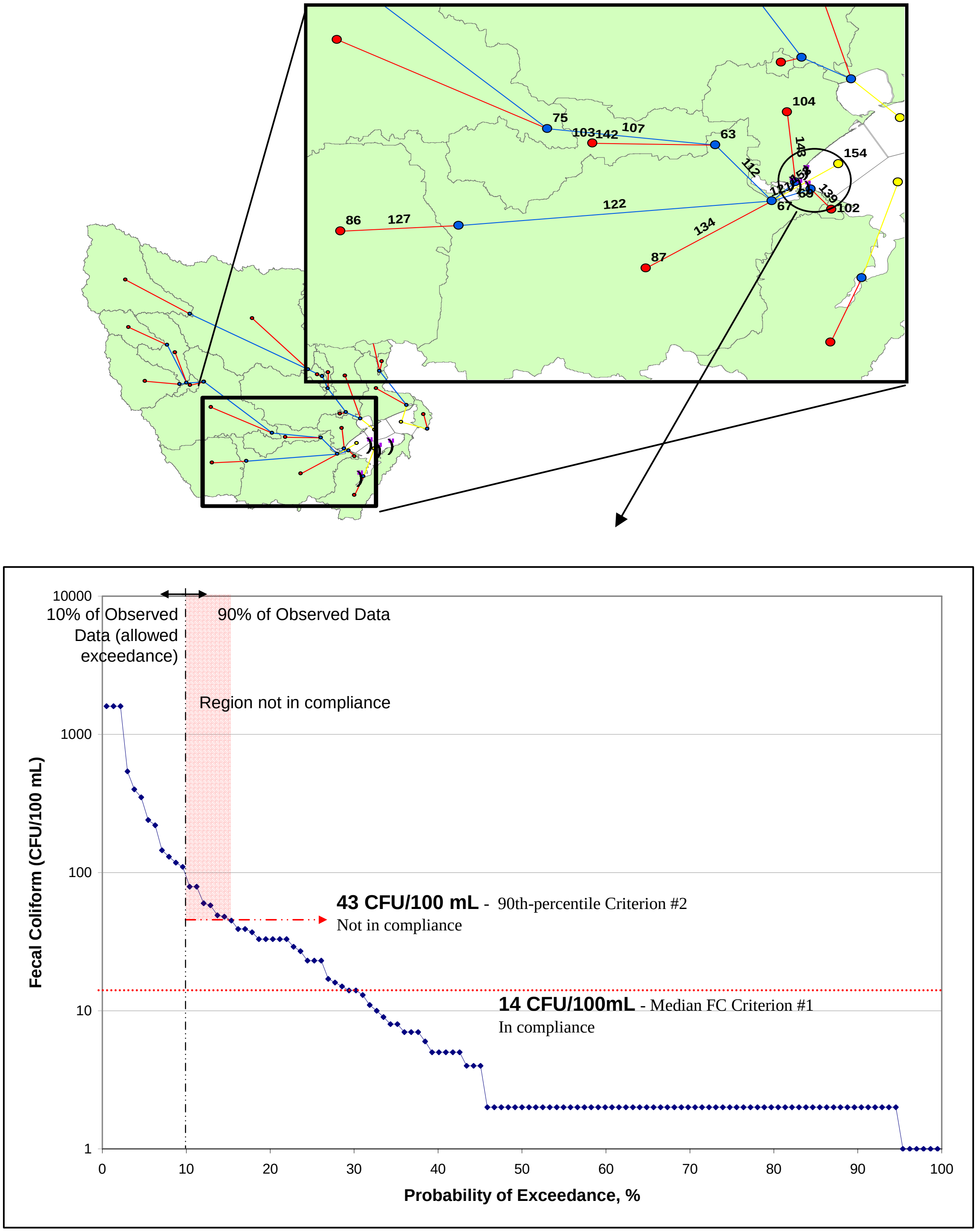

Figure 4.12 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Segment 2

The Mission River drains into Segment 3 (SchemaNode 153.) Bacterial monitoring station 14797 measures fecal coliform concentrations in Copano Bay Segment 3. The median and 90th-percentile of the monitoring data (from 1999-2005) are shown in Table 4.12; the bacterial monitoring data that exists for Segment 3 (from 1999-2005) and the rank and the probability of exceedance for each measurement are given in Appendix 4.3.

Table 4.12 Statistics of Bacterial Monitoring Data for Stations in Segment 3 (1999-2005)

Median Fecal Coliform Concentration (CFU/100mL)	2
90th Percentile Fecal Coliform Concentration (CFU/100mL)	**> 49**
Number of Measurements	31

As shown in Table 4.12, Copano Bay Segment 3 complies with the median fecal coliform standard (< 14 CFU/100mL) but exceeds the 90th-percentile fecal coliform standard of 43 CFU/100mL). The probability distribution of the measured fecal coliform concentrations at these stations is shown in Figure 4.13. The two fecal coliform oyster water use standards are also shown in Figure 4.13.

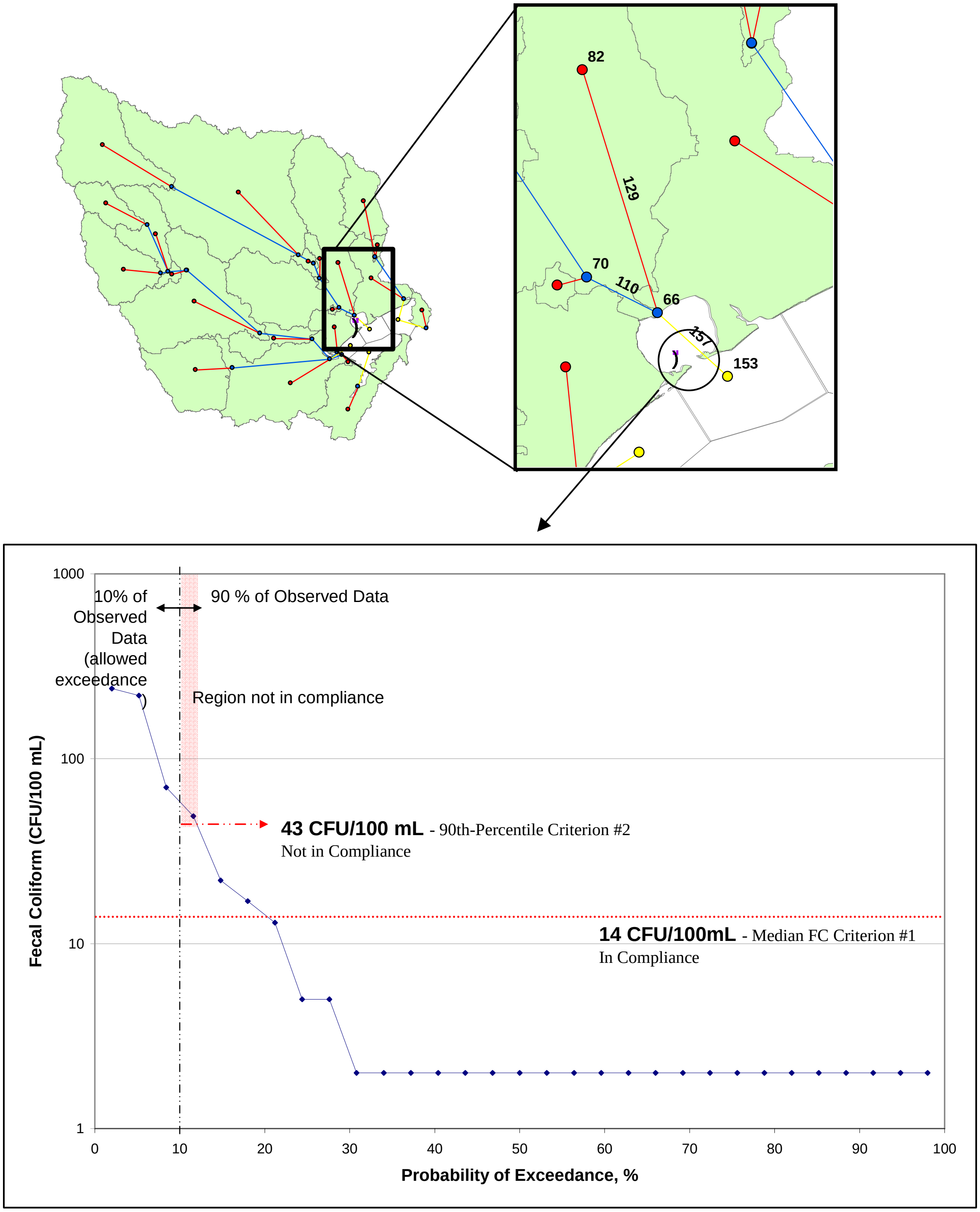

Figure 4.13 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Segment 3

Copano Creek drains into Segment 4. Bacterial monitoring stations 13404, 14779, 14780, 14785, 14792, and 14793 measure fecal coliform concentrations in Copano Bay Segment 4. The median and 90th-percentile of the monitoring data (from 1999-2005) are shown in Table 4.13; the bacterial monitoring data that exists for Segment 4 (from 1999-2005) and the rank and the probability of exceedance for each measurement are given in Appendix 4.4.

Table 4.13 Statistics of Bacterial Monitoring Data for Stations in Segment 4 (1999-2005)

Median Fecal Coliform Concentration (CFU/100mL)	2
90th Percentile Fecal Coliform Concentration (CFU/100mL)	~ 13
Number of Measurements	232

As shown in Table 4.13, Copano Bay Segment 4 complies with both fecal coliform oyster water use standards. The probability distribution of the measured fecal coliform concentrations at these stations is shown in Figure 4.14. The two fecal coliform oyster water use standards are also shown in Figure 4.14.

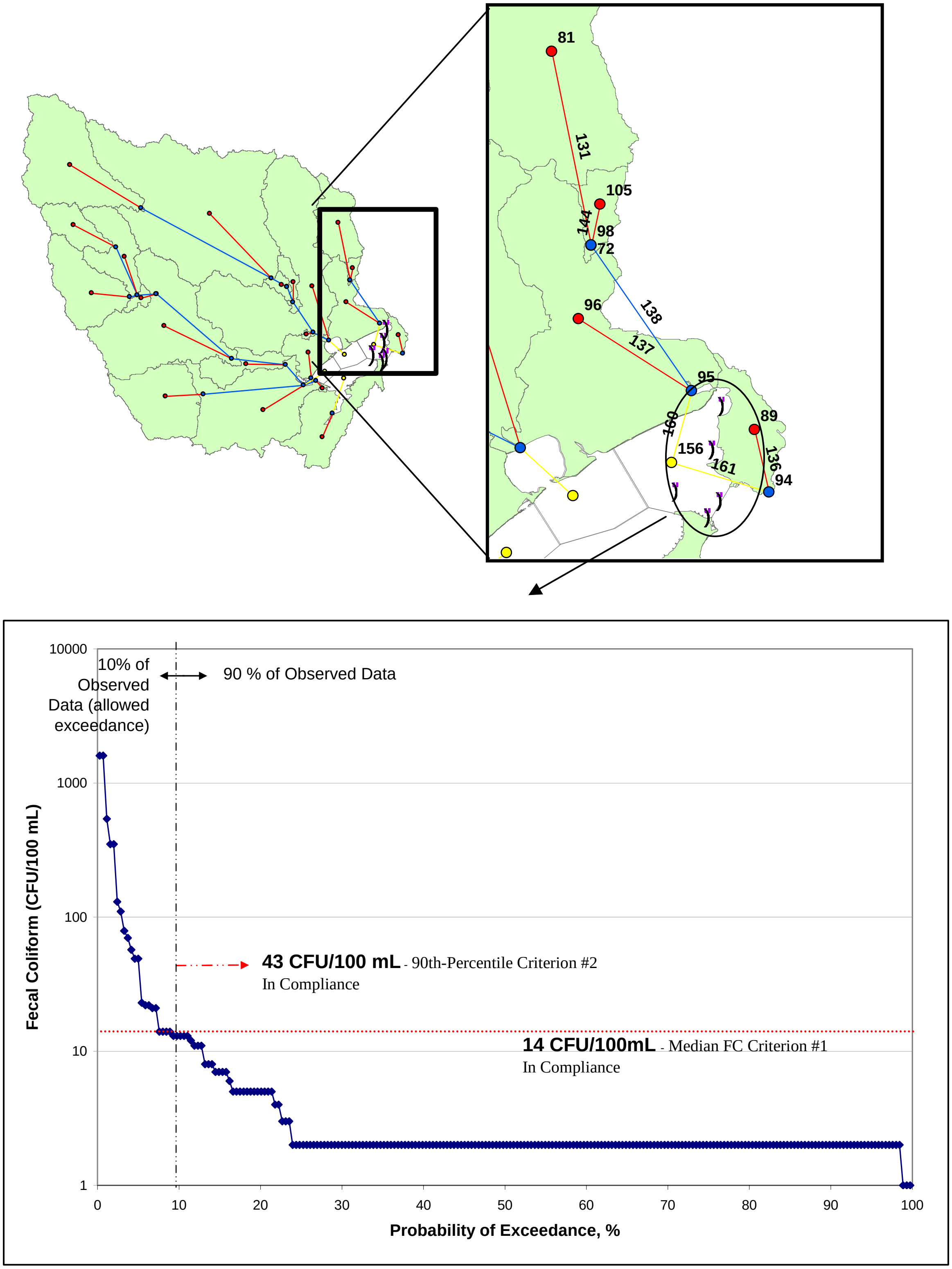

Figure 4.14 Existing Fecal Coliform Concentration Measurements versus Probability of Exceedance: Segment 4

Chapter 5: Estimation of Loadings

5.1 ESTIMATION OF NON-POINT BACTERIAL LOADINGS FROM WATERSHEDS

5.1.1 Methodology

The non-point bacterial loadings of fecal coliform flow into Copano Bay from adjacent watersheds directly into the Bay or from upstream watersheds into rivers/streams/channels that flow into Copano Bay. The Bacterial Loadings Model calculates the non-point bacterial loadings for each such watershed and models bacterial concentrations as the bacteria flow from the upstream watersheds to rivers/streams/channels to Copano Bay.

Non-point bacterial loadings are calculated as the product of runoff from each of the watersheds and Event Mean Concentration (EMC) of the corresponding land use land cover classifications within each watershed. The bacteria from the non-point sources (as well as the point sources) were decayed using the Schematic Processor (described in Chapter 6 of this report) as they travel from the watershed into rivers/channels and then into Copano Bay. The Bay was assumed to be completely mixed and acts as four Continuous Flow, Stirred Tank Reactors (CFSTRs)[4], and the inflow into each of the Bay segments equals the outflow.

The following steps were used to calculate the non-point bacterial loadings for each watershed:

1. Delineate watersheds to the Critical Points (USGS gauge stations, bacterial monitoring stations, and water segment endpoints) using the Digital Elevation Model (DEM), Arc Hydro's Terrain Preprocessing on the DEM, the National Hydrography Dataset (NHD), and Water Rights

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[4] See Section 6.3.1.1 for how and why Copano Bay was segmented.

Analysis Package (WRAP) Hydro, which is a toolbar located in Arc GIS that is used to delineate watersheds for the basin.

2. Collect mean annual precipitation data from PRISM in grid format and create a runoff grid using mathematical relationships between rainfall-runoff based on different land use characteristics.
3. Obtain the land use land cover dataset from USGS (in raster format) and convert it into an EMC grid based on the EMC associated with different land use classifications.
4. Multiply the runoff grid by the EMC grid to obtain the bacterial loading per grid cell in the watersheds.
5. Using the delineated watersheds and Spatial Analyst's Zonal Statistics, calculate the cumulative non-point bacterial loadings per watershed.

5.1.2 Procedure of Application

5.1.2.1 Watershed Delineation

Before conducting the runoff and concentration calculations and delineating the watersheds, Terrain Preprocessing (found in the Arc Hydro toolbar) was implemented on the DEM to determine the flow patterns in the basin. For this project (and in order to use WRAP Hydro), the only steps that were implemented from Terrain Preprocessing were DEM Reconditioning, Fill Sinks, and Flow Direction. The step-by-step process used to conduct Terrain Preprocessing is given in Appendix 5.1.

After completing Terrain Preprocessing, WRAP Hydro was used to delineate watersheds to the Critical Points (USGS gauge stations, bacterial monitoring stations, and water segment endpoints) for the basin (procedure described in Appendix 5.2.) The delineated watersheds for the basin are shown in Figure 5.1. The Critical Points are points at which the modeled fecal coliform loadings/concentrations need to be observed, analyzed, and/or compared to existing bacterial monitoring data.

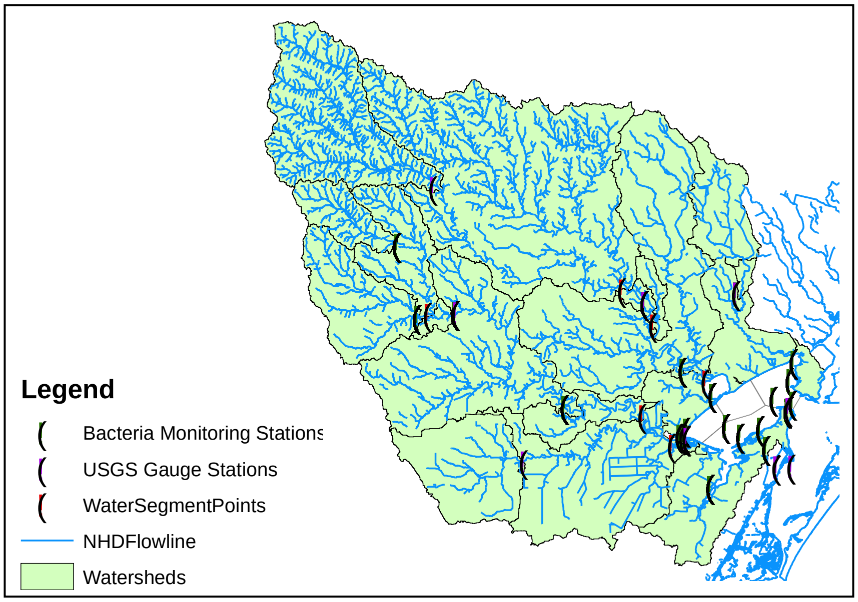


Figure 5.1 Watershed Delineation

5.1.2.2 Precipitation Data Preparation

The precipitation data were obtained from PRISM in polygon feature class format, which is shown in Figure 5.2. Using the "Feature to Raster" tool in Arc Toolbox, the polygon feature class was converted to a raster based on the field, "RANGE", which is the annual precipitation in inches. The annual precipitation was then converted to millimeters by using Spatial Analyst's Raster Calculator: [Precipitation in inches/year] * (25.4 mm/inch) = [Precipitation in mm/year] = **P**, where [] represents a raster.

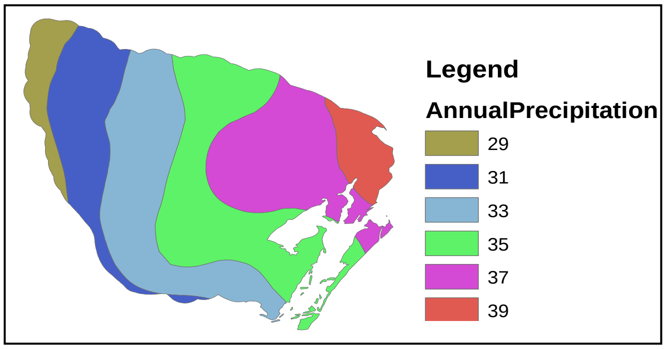


Figure 5.2 Precipitation Data (inches/year)

Rainfall-runoff relationships exist for four different land use categories to calculate runoff (Section 5.1.2.4). Thus, the precipitation grid was divided into four rasters based on the land use categories. This procedure is further described in Section 5.1.2.3 and Appendix 5.3.

5.1.2.3 Land Use Land Cover Data Preparation

The 1992 National Land Cover Dataset (NLCD), which comes in raster format, was converted to a polygon feature class using the "Raster to Polygon" tool in Arc Toolbox. There are rainfall-runoff relationships for four different land use categories to calculate runoff: "Agricultural Land"; "Rangeland, Forest, Barren, Other"; "Urban Land", and "Open Water"; (see Section 5.1.2.4 of this report for the equations.) Because the land use land cover dataset for Copano Bay has 18 different land use classifications, these classifications were grouped into four redefined land use categories that were used in the rainfall-runoff equations. The land use land cover classifications were reclassified into the corresponding four land use categories for this project (shown in Table 5.1).

Table 5.1 Reclassified Land Use Categories

Land Use Code (Gridcode)	**Land Use Category**	**Reclassified Land Use Category**
61	Orchards/Vineyards/Other	Agricultural Land
81	Pasture/Hay	
82	Row Crops	
83	Small Grains	
31	Bare Rock/Sand/Clay	Rangeland, Forest, Barren, Other
32	Quarries/Strip Mines/Gravel Pits	
41	Deciduous Forest	
42	Evergreen Forest	
43	Mixed Forest	
51	Shrubland	
71	Grasslands/Herbaceous	
91	Woody Wetlands	
92	Emergent Herbaceous Wetlands	
21	Low Intensity Residential	Urban Land
22	High Intensity Residential	
23	Commercial/Industrial/Transportation	
85	Urban/Recreational Grasses	
11	Open Water	Open Water

Thus, to calculate the runoff for each land use classification, the precipitation grid was divided into four different rasters based on these redefined land use classifications. The procedure on how to create precipitation rasters for different land use classifications is given in Appendix 5.3.

5.1.2.4 Rainfall-Runoff Relationships for Different Land Uses

Runoff calculations were made by using empirical equations from Quenzer (1997). These equations, shown below, relate runoff to precipitation and land use.

Agricultural Land:

$$\mathbf{Q} = 0.008312 * \exp(0.011415 * \mathbf{P}) \tag{5.1}$$

Rangeland, Forest, Barren, Other:

$$\mathbf{Q} = 0.0053 * \exp(0.010993 * \mathbf{P}) \tag{5.2}$$

Urban Land:

$$\mathbf{Q} = 0.24 * \mathbf{P} \tag{5.3}$$

Open Water:

$$\mathbf{Q} = 0 \tag{5.4}$$

Where: **Q** = Runoff (mm/year)
P = Precipitation (mm/year) – from PRISM

These equations were used to calculate runoff in the watersheds (see Section 5.1.2.5).

5.1.2.5 Developing Runoff Grid

After precipitation rasters, **P**, were created for each land use classification (see Section 5.1.2.3), Spatial Analyst’s Raster Calculator was used to calculate the runoff for each land use. An example calculation (Runoff raster for Agriculture) is shown in Figure 5.3:

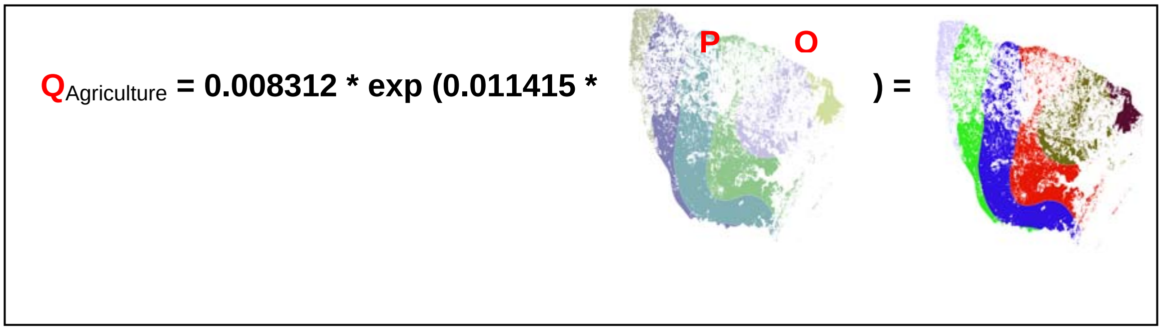


Figure 5.3 Calculation of Agricultural Runoff Grid

Once the four Runoff rasters were created for each land use, the “Mosaic” tool in Arc Toolbox was used to combine all four rasters into a single Runoff raster, which is shown in Figure 5.4.

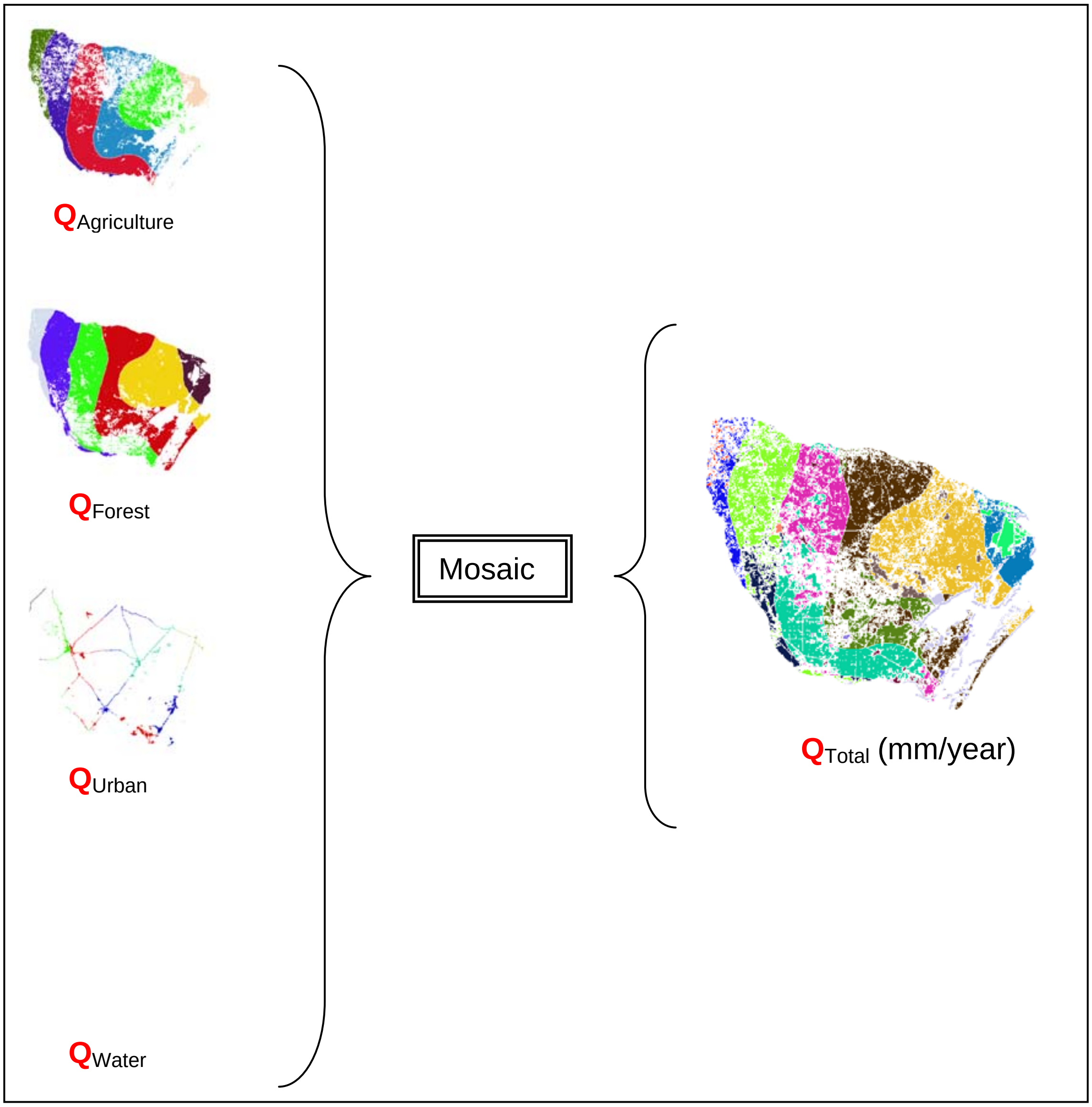


Figure 5.4 Creation of Runoff Grid

Once the total Runoff raster was created (Q_{total} in mm/year), the Raster Calculator was used to convert the runoff into m^3/year. Because the raster contains 30m by 30m grid cells, a conversion factor of 0.9 was used. [Runoff in mm/year] * 0.9 = [Runoff in m^3/year]. The final Runoff grid for the Copano Bay watershed is shown in Figure 5.5.

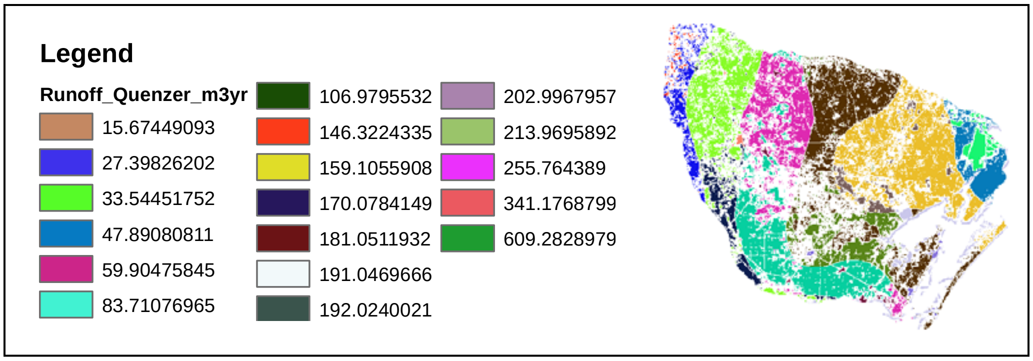
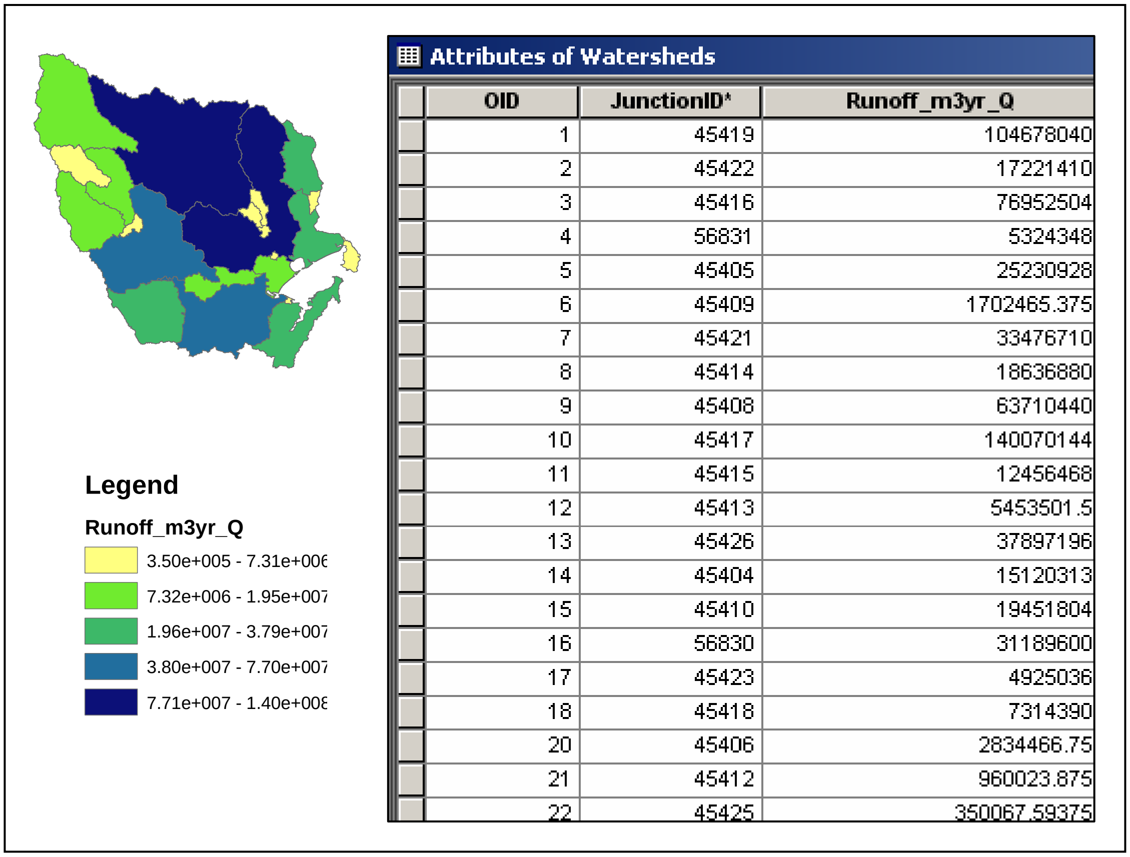


Figure 5.5 Runoff Grid (m^3/year)

5.1.2.6 Estimation of Flow from each Watershed

Using Zonal Statistics and the delineated watersheds (Figure 5.1), the cumulative runoff (summation of runoff grid cells in each watershed) was calculated for each watershed, and the results are shown in Figure 5.6.



OID	JunctionID*	Runoff_m3yr_Q
1	45419	104678040
2	45422	17221410
3	45416	76952504
4	56831	5324348
5	45405	25230928
6	45409	1702465.375
7	45421	33476710
8	45414	18636880
9	45408	63710440
10	45417	140070144
11	45415	12456468
12	45413	5453501.5
13	45426	37897196
14	45404	15120313
15	45410	19451804
16	56830	31189600
17	45423	4925036
18	45418	7314390
20	45406	2834466.75
21	45412	960023.875
22	45425	350067.59375

Figure 5.6 Runoff per Watershed (m^3/year)

5.1.2.7 Developing EMC Grid

The EMC (fecal coliform concentration) raster was created by using the relationship between fecal coliform concentrations and land use found in Section 3.2.1.2, Table 3.1. Once the EMC table (Table 3.1) was joined to the land use land cover feature class based on the land use codes (found in both the EMC Table and the Land Use Land Cover Polygon Feature Class), a raster was created based on the EMC field (now in the land use land cover feature class) using the "Feature to Raster" tool in Arc Toolbox. Raster Calculator was then used to convert CFU/100mL to CFU/m^3. [CFU/100mL] *

10,000 = [CFU/m^3]. The EMC grid for the Copano Bay watershed is shown in Figure 5.7.

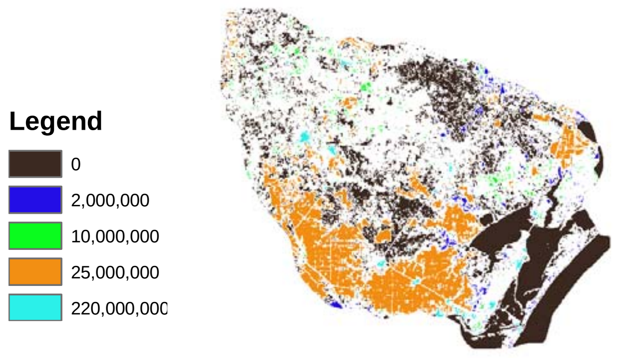


Figure 5.7 EMC Grid (CFU/m^3)

5.1.2.8 Estimation of Non-Point Bacterial Loading

Once the Runoff raster, **Q**, and the EMC raster, **C**, were created following the procedures given in Sections 5.1.2.5 and 5.1.2.7, respectively, the bacterial load per grid cell was calculated by using Spatial Analyst's Raster Calculator and the following equation: **L** = **Q** * **C**. This calculation is shown in Figure 5.8.

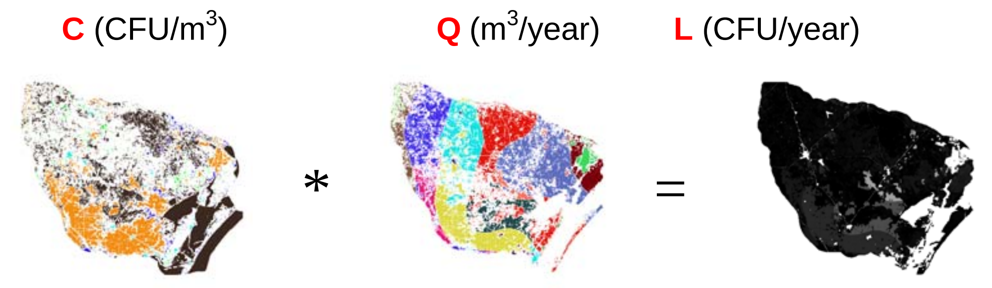
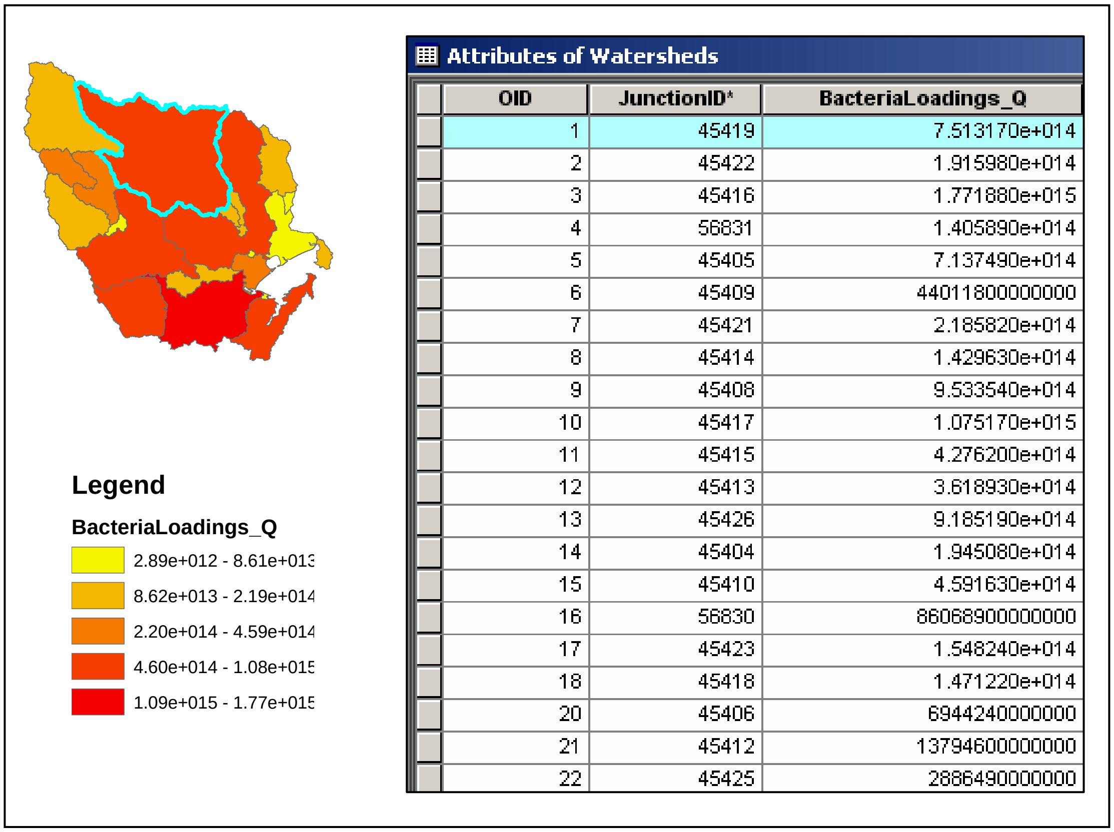


Figure 5.8 Creation of Bacterial Loading Grid (CFU/year)

Using Zonal Statistics and the delineated watersheds (Figure 5.1), the cumulative bacterial loadings were calculated for each watershed. The bacterial loading per watershed is shown in Figure 5.9.

5.1.3 Result

After completing the procedure described in Section 5.1.2, the cumulative non-point source bacterial loadings per watershed were calculated. The bacterial loading per watershed is shown in Figure 5.9.



OID	JunctionID*	BacterialLoadings_Q
1	45419	7.513170e+014
2	45422	1.915980e+014
3	45416	1.771880e+015
4	56831	1.405890e+014
5	45405	7.137490e+014
6	45409	44011800000000
7	45421	2.185820e+014
8	45414	1.429630e+014
9	45408	9.533540e+014
10	45417	1.075170e+015
11	45415	4.276200e+014
12	45413	3.618930e+014
13	45426	9.185190e+014
14	45404	1.945080e+014
15	45410	4.591630e+014
16	56830	86068900000000
17	45423	1.548240e+014
18	45418	1.471220e+014
20	45406	6944240000000
21	45412	13794600000000
22	45425	2886490000000

Figure 5.9 Non-Point Bacterial Loading per Watershed (CFU/year)

5.2 ESTIMATION OF LIVESTOCK LOADING

5.2.1 Methodology

Fecal coliform loadings (i.e., bacterial loadings) from livestock were not accounted for in the non-point bacterial loading calculations because the EMC values were determined from a Galveston Bay study and not for Copano Bay. Thus, we determined that using Census data (see Section 3.2.1.3) for livestock per county would be a more accurate way to estimate annual fecal waste from livestock animals in each watershed.

The fecal waste of the following seven animal species were accounted for in the bacterial loading model: cattle, horses, hogs, sheep, hens, goats, and chickens.

The annual bacterial loadings per watershed from livestock were calculated by finding the annual number of each livestock species per watershed on the following types of land: Shrubland (land use code 51), Grasslands/Herbaceous (land use code 71), and Pasture/Hay (land use code 81)[5] and multiplying the livestock counts by the amount of fecal waste produced per year per species (CFU/year-animal).

The following steps were used to calculate the livestock bacterial loadings for each watershed:

1. Determine the annual livestock count of each species per county from the 2002 Census of Agriculture (NASS) and 2004 Texas Livestock Inventory and Production (USDA, NASS, Texas Statistical Office.)
2. Calculate the area (m^2) of the land use classifications of 51, 71, and 81 in each county in the Copano Bay watershed.

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[5] These are the land use classifications that have an EMC value of zero for the non-point bacterial loading calculations (Table 3.1).

3. Find the density of each animal per county (count/$m^2_{\text{of Shrubland/Grasslands/Herbaceous/Pasture/Hay}}$). The following equation would be used where the number in the parentheses indicates the step in which the value was determined: (1)/(2)
4. Calculate the area of land use classifications 51, 71, and 81 of each county within each watershed (watersheds may have multiple counties.)
5. Multiply the area (m^2) of each county within each watershed by the animal density (count/m^2) to find the livestock count of each species that each county has in each watershed. (4)*(3)
6. Sum the livestock count of each type of species in each watershed to obtain the total number of each species per watershed.
7. Multiply the count of each species in each watershed by the fecal coliform typically produced each year (CFU/year-animal) that is found from the literature.
8. Sum the CFU/year for each species to get a cumulative CFU/year per watershed.

5.2.2 Procedure of Application

5.2.2.1 Finding Livestock per County

Livestock data (annual count per county) were obtained from the 2002 Census of Agriculture, NASS, and the 2004 Texas Livestock Inventory and Production, United States Department of Agriculture (USDA), NASS, Texas Statistical Office. The animals that were considered in the calculations were cattle, goats, horses, sheep, hens, hogs, and chickens. The livestock data that were used for the point source calculations is given in Table 5.2.

Table 5.2 Livestock Count per County

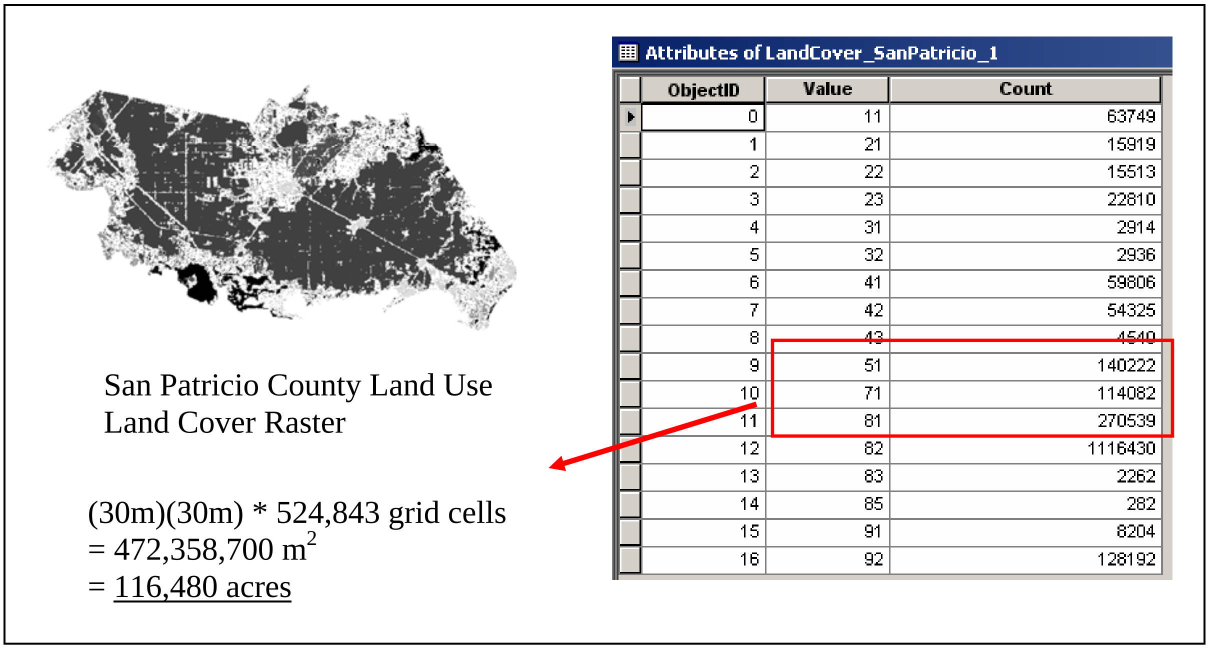
County	Livestock	2002 Data	2004 Data
Aransas	Cattle	2,878	2,000
	Goats	75	Unavailable
	Horses	46	Unavailable
	Sheep	0	Unavailable
	Hens	0	Unavailable
	Hogs	0	Unavailable
	Chickens	0	Unavailable
Bee	Cattle	49,950	49,000
	Goats	2344	2100
	Horses	1391	Unavailable
	Sheep	670	Unavailable
	Hens	793	Unavailable
	Hogs	0	Unavailable
	Chickens	0	Unavailable
Goliad	Cattle	63,398	66,000
	Goats	795	Unavailable
	Horses	887	Unavailable
	Sheep	0	Unavailable
	Hens	859	Unavailable
	Hogs	0	Unavailable
	Chickens	252	Unavailable
Karnes	Cattle	74,623	74,000
	Goats	2288	2100
	Horses	973	Unavailable
	Sheep	327	Unavailable
	Hens	0	Unavailable
	Hogs	0	Unavailable
	Chickens	0	Unavailable
Refugio	Cattle	41,239	36,000
	Goats	200	Unavailable
	Horses	692	Unavailable
	Sheep	71	Unavailable
	Hens	63	Unavailable
	Hogs	0	Unavailable
	Chickens	0	Unavailable
San Patricio	Cattle	22,253	20,000
	Goats	773	Unavailable
	Horses	662	Unavailable
	Sheep	0	Unavailable
	Hens	464	Unavailable
	Hogs	741	Unavailable
	Chickens	0	Unavailable

5.2.2.2 Calculating Density of Livestock per County

The density of livestock per county (acres/animal) was calculated for each animal by using the following equation: [Area in acres where the animals would be located within county] / [Total annual count of each animal]. The area where animals would be located was assumed to be from the land use land cover classifications 51 (Shrubland), 71 (Grasslands/Herbaceous), and 81 (Pasture/Hay). To find the area, the land use land cover dataset was masked by each county, and the corresponding grid cells (for land use codes 51, 71, and 81) were summed. For example, in San Patricio County (calculation shown in Figure 5.10), the total area where animals are located is 472,358,700 m^2 = 116,480 acres**.** Thus, the density of cattle in San Patricio county is 22,253 cattle/472,358,700 m^2 = 0.0000471 cattle/m^2 = 122 cattle/mi^2 = 5 acres per cow. The density of each livestock animal in each county is given in Table 5.3.

Table 5.3 Animal Density per County (Acres per Animal)

County	Area (acres)	Livestock	2002 Density	2004 Density
Aransas	51,200	Cattle	18	26
		Goats	640	Unavailable
		Horses	640	Unavailable
		Sheep	0	Unavailable
		Hen	0	Unavailable
		Hogs	0	Unavailable
		Chickens	0	Unavailable
Bee	341,760	Cattle	7	7
		Goats	160	160
		Horses	213	Unavailable
		Sheep	640	Unavailable
		Hen	640	Unavailable
		Hogs	0	Unavailable
		Chickens	0	Unavailable
Goliad	361,600	Cattle	6	6
		Goats	640	Unavailable
		Horses	320	Unavailable
		Sheep	0	Unavailable
		Hen	320	Unavailable
		Hogs	0	Unavailable
		Chickens	0	Unavailable
Karnes	318,080	Cattle	4	4
		Goats	32	160
		Horses	320	Unavailable
		Sheep	640	Unavailable
		Hen	0	Unavailable
		Hogs	0	Unavailable
		Chickens	0	Unavailable
Refugio	282,240	Cattle	7	8
		Goats	0	Unavailable
		Horses	320	Unavailable
		Sheep	0	Unavailable
		Hen	0	Unavailable
		Hogs	0	Unavailable
		Chickens	0	Unavailable
San Patricio	116,480	Cattle	5	6
		Goats	160	Unavailable
		Horses	160	Unavailable
		Sheep	0	Unavailable
		Hen	213	Unavailable
		Hogs	160	Unavailable
		Chickens	0	Unavailable



Attributes of LandCover_SanPatricio_1

ObjectID	Value	Count
0	11	63749
1	21	15919
2	22	15513
3	23	22810
4	31	2914
5	32	2936
6	41	59806
7	42	54325
8	43	4540
9	51	140222
10	71	114082
11	81	270539
12	82	1116430
13	83	2262
14	85	282
15	91	8204
16	92	128192

San Patricio County Land Use
Land Cover Raster

(30m)(30m) * 524,843 grid cells
= 472,358,700 m^2
= 116,480 acres

Figure 5.10 Determination of Area (Acres) of Animals in San Patricio County

5.2.2.3 Calculating Livestock Count per Watershed

The area (mi^2) of each county within each delineated watershed (Figure 5.1) was determined and then multiplied by each livestock's density in each corresponding county to find each livestock count.

$$\text{Livestock count} = \text{Area (mi}^2\text{)} * \text{Density (Count/mi}^2\text{)}$$

All the calculations for this procedure are given in Appendix 5.4. For example, Watershed JunctionID 45422 has two counties overlapping it, so there are two different areas and cattle densities to account for in the calculation. The cattle calculation for Watershed JunctionID 45422 is shown in Figure 5.11. 149 cattle/mi^2 is the cattle density in Karnes County, and 92 cattle/mi^2[6] is the density of cattle in Bee County. Approximately 17.6 mi^2 is the area in Watershed JunctionID that is a part of Karnes

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[6] The densities are per square mile of land where animals would be located based on land use classifications.

County (the area of land use types 51, 71, and 81 where animals would be located). Approximately 110.6 mi^2 is the area in Watershed JunctionID that is a part of Bee County. Thus, there are approximately 12,778 cattle in Watershed JunctionID 45422. This procedure was performed for all livestock species in each watershed.

149 cattle/mi^2 * 17.6 mi^2 = **2,625 cattle**

+

92 cattle/mi^2 * 110.6 mi^2 = **10,152 cattle**

Total = **12,778 cattle**

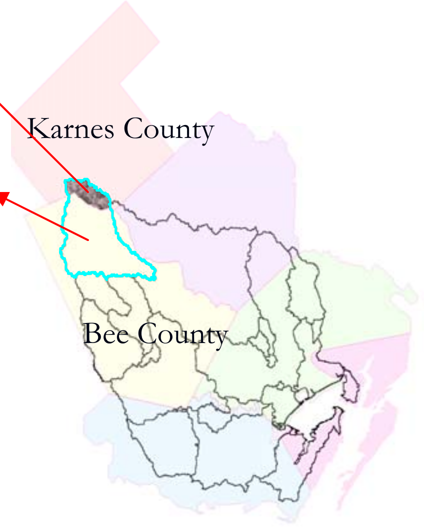

Figure 5.11 Determination of Cattle Count in Watershed JunctionID 45422[7]

5.2.2.4 Calculating Livestock Bacterial Loading (CFU/year) per Watershed

After determining the count of each animal within each watershed (see Section 5.2.2.3), the count was multiplied by the fecal coliform produced annually (CFU/year) by each animal. The CFU/year produced by each animal considered in this model is shown in Table 5.4. Information regarding fecal coliform production by hens and goats was not found in the literature, so estimations were made from similar animals. Since goats generally have a similar body mass to sheep, the production of fecal coliform was

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[7] The densities and areas were rounded, so the exact total cattle count is accurate, but it may not agree exactly when carrying out the multiplication.

assumed to be the same. The production of fecal coliform by hens was calculated by using a mass ratio based on chickens (0.66 hen:chicken mass ratio), with the assumption fecal coliform production is proportional to body mass.

Table 5.4 Annual Fecal Coliform Production from Livestock Animals (EPA, 2005)

Livestock	**CFU/year**	**Reference**
Sheep	1.10×10^{13}	Metcalf and Eddy, 1991 ASAE, 1998
Goat	1.10×10^{13}	(Assumed same as sheep)
Hog	3.63×10^{12}	Metcalf and Eddy, 1991 ASAE, 1998
Cattle	1.97×10^{12}	Metcalf and Eddy, 1991
Horse	1.53×10^{11}	ASAE, 1998
Chicken	1.39×10^{11}	Metcalf and Eddy, 1991 ASAE, 1998
Hen	4.61×10^{10}	Calculated from fecal coliform production of chicken (CFU/year) multiplied by hen:chicken body mass ratio

For example, in Watershed JunctionID 45422: 12,778 cattle * (1.97×10^{12} CFU/year-head of cattle) = 2.52×10^{16} CFU/year from cattle. The CFU/year needs to be summed for all species within each watershed to find the total CFU/year excreted from livestock species, which is shown below in Figure 5.12.

5.2.3 Result

After completing the procedure described in Section 5.2.2, the cumulative livestock bacterial loadings per watershed were calculated. The livestock bacterial loading per watershed is shown in Figure 5.12.

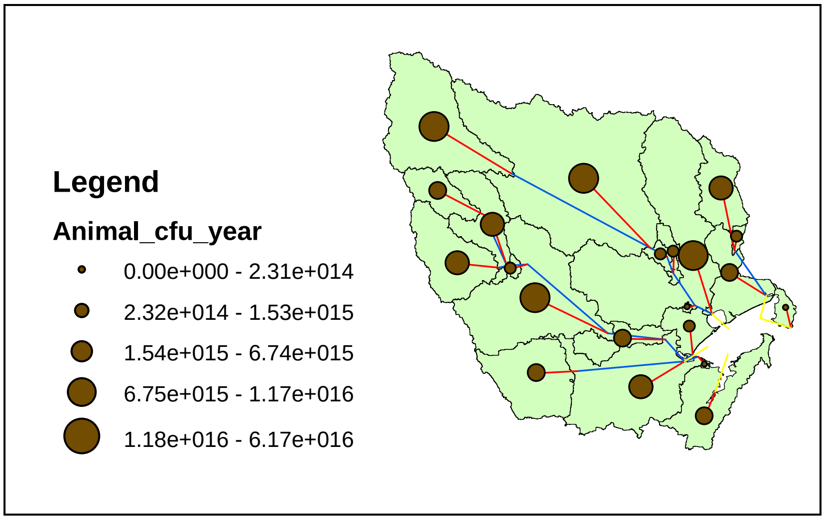

Figure 5.12 Livestock Bacterial Loading (CFU/year) per Watershed

Comparing Figure 5.12 (livestock bacterial loading) to Figure 5.9 (non-point bacterial loading from different land use types excluding livestock), livestock bacterial loadings are orders of magnitude greater than non-point bacterial loadings.

Figure 5.13 shows the percent distribution of bacterial loadings from each livestock species in the upstream watersheds.

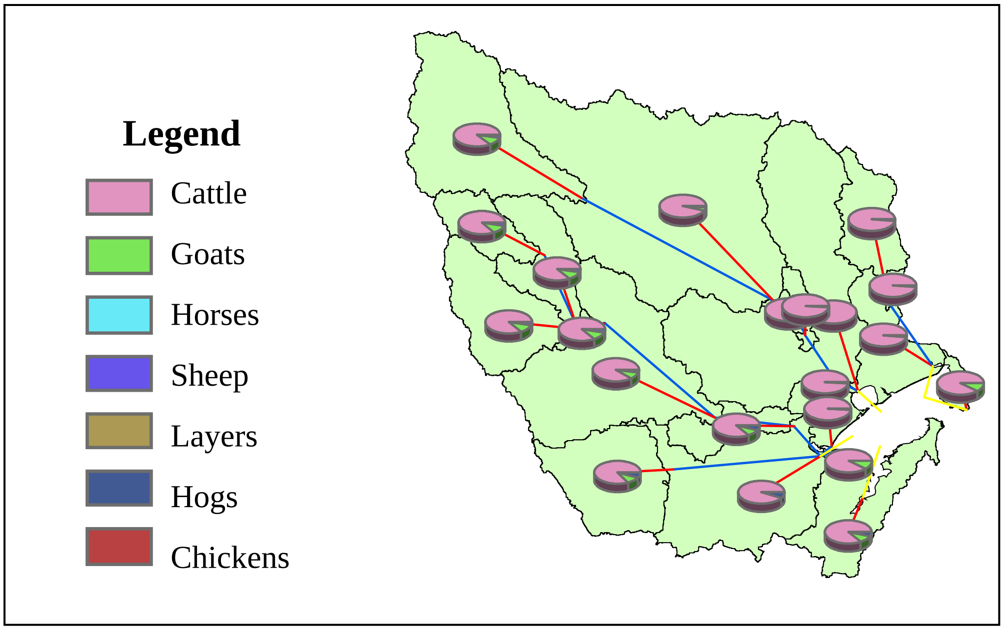

Figure 5.13 Percent Distribution of Bacterial Loadings from Livestock Species at Watersheds

As shown in Figure 5.13, cattle are the major livestock contributor to bacterial loading based on the model assumptions and calculations. Summing the total counts of each of the livestock species for the entire Copano Bay watershed, there are 111,433 cattle followed by 2,561 horses. Thus, there are significantly more cattle and cattle bacterial loadings than from any other species.

5.3 ESTIMATION OF AVIAN LOADING

5.3.1 Methodology

Fecal coliform loadings (i.e., bacterial loadings) from colonial waterbirds were determined by obtaining data from the Texas Colonial Waterbird Census (TCWC). There are approximately 30 different types of colonial waterbird species along the Texas coastline, and the TCWC gives the number of breeding pairs of different waterbird species from 1973-2003. The total fecal coliform from waterbirds was calculated and applied to the Copano Bay water segments by finding the average count of each waterbird species from 1973-2003, the annual fecal coliform production by each type of bird, and the approximate percentage of load reaching the Bay. The loading was calculated based on the following equation:

Avian Loading (CFU/year) = [Number of Breeding Pairs] x [2 Birds per Breeding Pair] x [Amount of Excretion per Bird (g/bird)] x [Fecal Coliform Concentration in Excretion (CFU/g)] x [Percent of Fecal Coliform that Reaches Copano Bay]

The following waterbird species were included in this model: Laughing Gull, Tricolored Heron, Black Skimmer, Neotropic Cormorant, Least Tern, Great Blue Heron, Great Egret, Snowy Egret, Roseate Spoonbill, Cattle Egret, Reddish Egret, American Oystercatcher, Fulvous Whistling Duck, Forster’s Tern, and Little Blue Heron.

The following steps were used to calculate the avian bacterial loadings for each Copano Bay water segment or watershed in which waterbird colonies are present:

1. Determine the average count for each species from 1973-2003 at each location from TCWC.

2. Find the daily excretion (g/bird) for each species in literature.
3. Find the fecal count per excretion (CFU/g) in literature.
4. Determine the percent of bacterial loading that reaches the bay, based on the amount of time that each waterbird species spends on bay year-round.
5. Multiply CFU/bird by the number of species for each location (water segment or watershed) and sum all species' CFU/year. This yields the total annual CFU/year contributed by colonial waterbirds to each segment/watershed.

5.3.2 Procedure of Application

5.3.2.1 Determining the Average Count of Waterbird Species

Waterbird data were obtained from the TCWC. An annual count of each type of waterbird breeding pair was tabulated by volunteers from State, Federal, Non-Profit Organizations, and Professional Organizations for each year from 1973-2003. For each type of waterbird species, an average annual count was found by averaging all the counts from 1973-2003. The average waterbird count at each location is given in Table 5.5. However, these counts do not include the number of waterbirds that are not breeding pairs.

Table 5.5 Average Waterbird Count (1973-2003)

Waterbird Species	Average Breeding Pair Count	Number of Locations
Laughing Gull	367	1
Tricolored Heron	158	1
Cattle Egret	87	2
Neotropic Cormorant	84	3
Black Skimmer	59	1
Great Blue Heron	54	3
Least Tern	45	4
Snowy Egret	14	2
Great Egret	13	1
Roseate Spoonbill	9	1
American Oystercatcher	3	1
Fulvous Whistling Duck	2	1
Forster’s Tern	1	1
Little Blue Heron	1	1

There are eight waterbird colony locations surrounding Copano Bay. The bacterial loadings produced from these colonies are applied to either a Copano Bay segment or watershed. The locations of the breeding pairs on the Copano Bay watershed and on the portion of the model to which the bacterial loadings will be applied are shown in Figure 5.14.

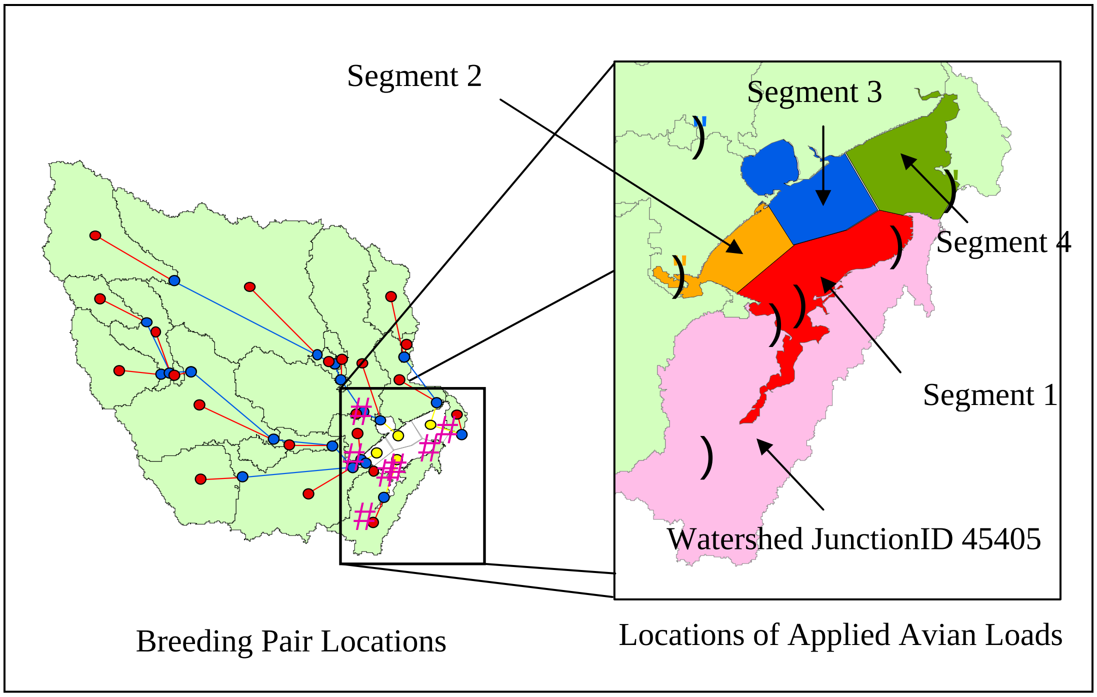

Figure 5.14 Locations of Breeding Pairs and Applied Loads

The colony codes, which correspond to each breeding pair location, and the Copano Bay segment or watershed that the bacterial loadings will be applied to are given in Table 5.6.

Table 5.6 Colony Codes and Watersheds/Segments to which Loads are Applied

Copano Bay Segment/Watershed	**Waterbird Colony Code**
1	609-460
	609-461
	609-480
2	614-295
3	614-296
4	609-380
JunctionID 45405	614-293
	614-294

Table 5.7 Number of Waterbird Species Applied to each Segment/Watershed

	Copano Bay				Watershed JunctionID
Species	**1**	**2**	**3**	**4**	**45405**
Laughing Gull	367				
Tricolored Heron	158				
Black Skimmer	59				
Neotropic Cormorant	44				40
Least Tern	23	6	4	12	
Great Blue Heron	14			40	22
Great Egret	13				
Snowy Egret	11				3
Roseate Spoonbill	9				
Cattle Egret	7				80
Reddish Egret	5				
American Oystercatcher	3				
Fulvous Whistling Duck	2				
Forster's Tern	1				
Little Blue Heron	0				1

5.3.2.2 Determining Excretion (g/bird) from Waterbirds

The fecal mass produced by each type of bird was found based on the excretion of the Adult Herring Gull that was determined by Reem Zoun in her thesis, *Estimation of Fecal Coliform Loadings to Galveston Bay* (Zoun, 2003). She found from literature that the daily fecal mass of an Adult Herring Gull is 15 g (dry weight)/bird. The fecal mass (g/bird) for the other types of waterbirds was calculated based on the different body masses of each type of bird compared to the Adult Herring Gull. For example, the Adult Herring Gull has a mass of approximately 1225 g (Percevia, 2005a) and the Laughing Gull has a mass of approximately 325 g (USGS, 2005a); thus, assuming a constant ratio between fecal mass and bird body mass, Laughing Gull excretion (g/bird) = {15 g fecal mass/Adult Herring Gull * 325 g/Laughing Gull} / {1225 g/Adult Herring Gull} = 3.98 g fecal mass per Laughing Gull.

The body mass (g) and the calculated daily fecal mass (g/bird) for each type of bird is given in Table 5.8.

Table 5.8 Estimated Daily Fecal Mass (g/bird)

Waterbird Species	Body Mass (g/bird)	Fecal Mass (g/bird)
Laughing Gull	325 (USGS, 2005a)	3.98
Tricolored Heron	374.5 (USGS, 2005b)	4.59
Cattle Egret	337 (Percevia, 2005b)	4.13
Neotropic Cormorant	1270 (Gil de Weir, 2005)	15.55
Black Skimmer	301.5 (USGS, 2005c)	3.69
Great Blue Heron	2400 (USGS, 2005d)	29.39
Least Tern	28 (CDEP, 2005a)	0.35
Snowy Egret	371 (USGS, 2005e)	4.54
Great Egret	1021 (CDEP, 2005b)	12.50
Roseate Spoonbill	1497 (Percevia, 2005c)	18.33
Reddish Egret	451 (Percevia, 2005d)	5.52
American Oystercatcher	602.5 (USGS, 2005f)	7.38
Fulvous Whistling Duck	670 (USGS, 2005g)	8.20
Forster's Tern	160	1.96
Little Blue Heron	366 (Percevia, 2002)	4.48
Adult Herring Gull	1225 (Percevia, 2002)	15

5.3.2.3 Estimation of Loadings (CFU/bird)

The bacterial loadings from waterbirds was calculated by accounting for the number of breeding pairs at each location, the fecal mass produced per bird, the fecal coliform concentration in the fecal material, and the percent of fecal coliform loading that discharged to the Bay (based on how much time each type of bird spends on Copano Bay annually.)

Based on the data of Zoun (2003), the fecal coliform concentration of avian excrement was estimated to be 10^8 CFU/g of fecal material for the fecal coliform loading calculations. Furthermore, the waterbirds spend an estimate of 50% of their time on the Bay, so 50% of the total fecal coliform loading from the waterbirds is assumed to reach

Copano Bay; this is a conservative estimate but would account for the fecal coliform loadings from some of the non-breeding pairs of waterbirds. The estimated fecal coliform loading for each type of waterbird is given in Table 5.9.

Table 5.9 Annual Fecal Coliform Loading per Bird

Waterbird Species	**Bacterial Loading Reaching Bay**	
	CFU/bird	**TCFU/bird**
Laughing Gull	1.99E+08	0.000199
Tricolored Heron	2.29E+08	0.000229
Cattle Egret	2.06E+08	0.000206
Neotropic Cormorant	7.78E+08	0.000778
Black Skimmer	1.85E+08	0.000185
Great Blue Heron	1.47E+09	0.000147
Least Tern	1.74E+07	0.000174
Snowy Egret	2.27E+08	0.000227
Great Egret	6.25E+08	0.000625
Roseate Spoonbill	9.17E+08	0.000917
Reddish Egret	2.76E+08	0.000276
American Oystercatcher	3.69E+08	0.000369
Fulvous Whistling Duck	4.10E+08	0.000410
Forster's Tern	9.80E+07	0.000980
Little Blue Heron	2.24E+08	0.000224

To find the CFU/year from waterbirds for each water segment and/or watershed, the values from Table 5.9 were multiplied by the number of each corresponding bird species over each water segment or watershed (given in Table 5.7).

5.3.3 Result

The total CFU/year excreted by the breeding pairs of different waterbirds for each water segment and watershed is tabulated in Table 5.10 and is shown in Figure 5.15.

Table 5.10 Annual Fecal Coliform Avian Loadings

Segment/Watershed	Bacterial Loading	
	CFU/yr	TCFU/yr
1	3.96E+11	0.39600
2	2.22E+09	0.00222
3	1.48E+09	0.00148
4	1.22E+11	0.12200
JunctionID 45405	2.75E+11	0.27500

As shown in Table 5.10 and Figure 5.15, the bacterial loadings from waterbirds are significantly smaller than non-point (Figure 5.9) and livestock bacterial loadings (Figure 5.12). However, these loadings are applied directly to Copano Bay, so there is no travel time for bacterial decay. The effects of this direct loading (compared to the upstream loadings) are analyzed and evaluated in Chapter 6, where the discussion of modeling bacterial transport is discussed.

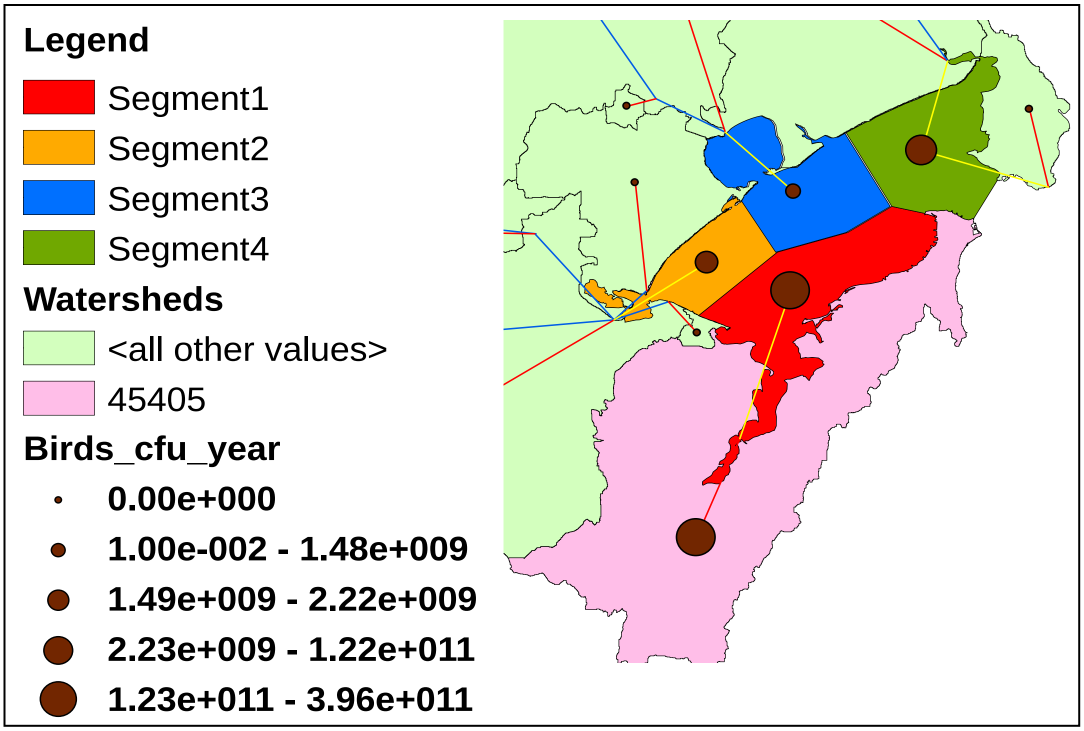

Figure 5.15 Avian Loadings (CFU/yr) on Copano Bay Water Segments and Watersheds

5.4 ESTIMATION OF WASTEWATER TREATMENT PLANT (WWTP) LOADINGS

5.4.1 Methodology

Fecal coliform loadings (i.e., bacterial loadings) from wastewater treatment plants (WWTPs) were calculated based on discharge monitoring data obtained from the Permit Compliance System (PCS) Database from the U.S. Environmental Protection Agency (EPA). The locations of the WWTPs and their corresponding permit numbers are shown in Figure 5.16.

WWTPs are required to disinfect their water (with chlorine, ozone, UV radiation, etc.) and meet Texas Surface Water Quality Standards before discharging into the receiving water bodies. However, fecal coliform bacteria are not one of the water quality characteristics that are monitored regularly because it does not require a water quality permit. Looking at the discharge monitoring reports (DMRs) of the permitted facilities in the Copano Bay watershed, some of the WWTPs have no fecal coliform monitoring data while some WWTPs only have one annual measurement (that may or may not meet water quality standards.) Thus, if fecal coliform monitoring data exist for a facility, the maximum fecal coliform concentration is used for the bacterial loading calculations (by multiplying by the average flow rate from the monitoring reports). If fecal coliform data do not exist for a facility, then fecal coliform counts from the literature were used.

The following steps were used to calculate the WWTP bacterial loadings for the watershed model:

1. Calculate the average fecal coliform concentration (CFU/100mL) for each WWTP facility in the Copano Bay watershed (either from monitoring data or literature values).

2. Calculate the average flow rate (m^3/year) from monitoring data for each WWTP facility in Copano Bay watershed.
3. Find the annual bacterial loading (CFU/year) for each WWTP by multiplying fecal coliform concentration (CFU/100mL) by average flow rate (m^3/year) and 10,000 (factor for converting CFU/100mL to CFU/m^3). The following equation would be used where the number in the parentheses indicates the step in which the value was determined: (1) * (2) * 10,000
4. Derive relationship that calculates residence time based on mean flow length in the watershed to calculate residence time from WWTPs to mainstreams[8].

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[8] Ernest To of the Center for Research in Water Resources (CRWR) derived this relationship for this project.

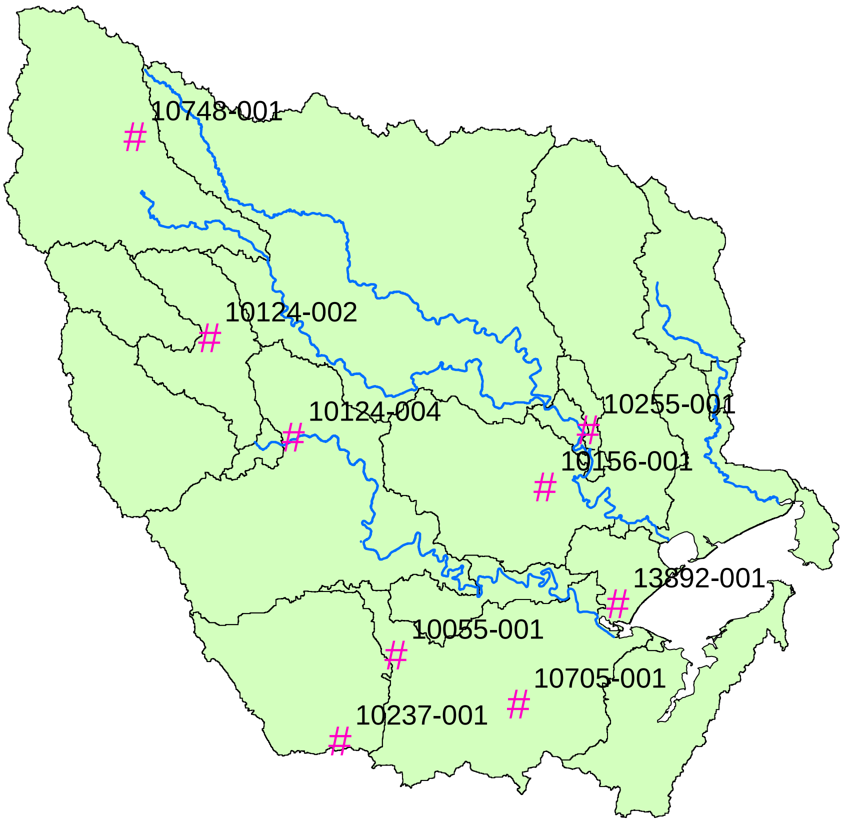

Figure 5.16 WWTP Locations and Permit Numbers

5.4.2 Procedure of Application

5.4.2.1 Determining the Fecal Coliform Concentration (CFU/100mL) from WWTPs

Fecal coliform concentrations from WWTPs were determined from DMRs obtained from the PCS Database from the EPA.

If fecal coliform monitoring data exist, then the maximum fecal coliform concentration was used. The fecal coliform concentrations used to calculate the average annual bacterial loading from WWTPs are given in Table 5.11.

If fecal coliform monitoring data do not exist, then the literature value of 84,000 CFU/100mL (Khan and Kamal, 2001) was used. This value is the fecal coliform count at a wastewater treatment plant discharge.

Table 5.11 Fecal Coliform Concentrations of WWTPs Applied to Model[9]

Permit Number	Facility Description	Maximum Fecal Coliform Concentration (CFU/100mL)
10124-002	City of Beeville, Moore Street WWTP	144,819
10156-001	Woodsboro WW Treatment Facility	126,388
10237-001	City of Odem WWTP	10
10255-001	Town of Refugio WW Treatment Facility	560
10705-001	City of Taft, Baird WWTP	< 1
10055-001	City of Sinton Main WWTP	84,000
10124-004	Chase Field WWTP	84,000
10748-001	Pettus Municipal Utility District WWTP	84,000
13892-001	Water Reclamation Facility	84,000

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[9] See Chapter 9 for details of the WWTP loading overestimation issue.

It was recently discovered during the finishing of this report that WWTP fecal coliform concentrations of treated effluent are reported on permit renewal files, which are only available in hard copy format; however, the fecal coliform concentration of treated effluent is not reported on the DMRs. The fecal coliform concentrations that are presented in Table 5.11 are actually sludge concentrations in CFU/g of total solids, so the fecal coliform concentrations that were used in the model for WWTPs are much larger than the actual fecal coliform concentrations of treated effluent reported on the renewal permit files. However, the WWTP bacterial loading results (in subsequent chapters) are based on the concentrations that are presented in Table 5.11. See Chapter 9 for details on how to re-adjust the WWTP loading for future work.

5.4.2.2 Determination of Average Flow (m^3/yr) from WWTPs

Average flows from the WWTPs were determined from DMRs obtained from the PCS Database from the EPA. The DMRs record flow rates once a month.

Flow is monitored regularly at all WWTPs within the Copano Bay watershed, so the average of all measured flows was used in the bacterial loading calculations. The flows used to calculate the average bacterial loading from WWTPs are given in Table 5.12.

Table 5.12 Flow Rates of WWTPs

Permit Number	**Facility Description**	**Average Flow Rate (m^3/yr)**	**Average Flow Rate (MGD)**
10124-002	City of Beeville, Moore Street WWTP	3,086,069[10]	2.23
10156-001	Woodsboro WW Treatment Facility	175,141	0.13
10237-001	City of Odem WWTP	207,256	0.15
10255-001	Town of Refugio WW Treatment Facility	466,003	0.34
10705-001	City of Taft, Baird WWTP	622,277	0.45
10055-001	City of Sinton Main WWTP	830,607	0.60
10124-004	Chase Field WWTP	569,976	0.41
10748-001	Pettus Municipal Utility District WWTP	88,334	0.06
13892-001	Water Reclamation Facility	11,586	0.01

5.4.2.3 Calculating Annual Bacterial Loading (CFU/year) from WWTPs

The annual bacterial loading from WWTPs was calculated by multiplying the fecal coliform concentration (Section 5.4.2.1 and listed in Table 5.11) by the average flow rate (determined in Section 5.4.2.2 and listed in Table 5.12). The annual bacterial loading from each WWTP (based on measured flow rates and estimated bacteria concentrations) is given in Table 5.13.

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[10] Error in the permit files (missing decimal points) were discovered late in the analysis. For all calculations, a flow rate of 155,283,858 m^3/year was used, but this is a conservative flow rate.

Table 5.13 Annual Bacterial Loadings from WWTPs

Permit Number	**Facility Description**	**Bacterial Loading**	
		CFU/yr	**TCFU/yr**
10055-001	City of Sinton Main WWTP	6.98E+14	698
10124-002	City of Beeville, Moore Street WWTP	4.47E+15[11]	4,470
10124-004	Chase Field WWTP	4.79E+14	479
10156-001	Woodsboro WW Treatment Facility	2.21E+14	221
10237-001	City of Odem WWTP	2.04E+10	0.02
10255-001	Town of Refugio WW Treatment Facility	2.61E+13	26.1
10705-001	City of Taft, Baird WWTP	1.24E+11	0.12
10748-001	Pettus Municipal Utility District WWTP	7.42E+13	74.2
13892-001	Water Reclamation Facility	9.73E+12	9.73

5.4.2.4 Calculating Residence Time to Mainstreams Based on Flow Length

Because the WWTPs are located at various distances from the mainstreams that are modeled for the Copano Bay watershed, the residence times from each WWTP to the downstream main river was calculated.

Ernest To of CRWR derived a relationship between residence time and mean flow length of the watersheds[12]. He isolated one portion of the model to calculate the overland flow velocity. Overland velocity can be calculated from the following equation:

$$v = L/\tau \qquad (5.5)$$

Where: L = mean flow length

τ = residence time

v = overland flow velocity

---

[11] For all subsequent calculations, a bacterial loading of 2.25E+17 was used (based on the conservative flow rate).

[12] The mean flow length of each watershed is the average flow length from each watershed to the watershed drainage outlet.

The overland flow velocity was estimated from two Schemalink feature classes along the Aransas River (Schemalink 120 and 125) that have the most available data. The overland flow velocity was then extrapolated to the entire watershed. The methodology is described as follows:

The relationship between the upstream and downstream loads is given by the equation:

$$Lds = Lus * \exp(-k*tau) \tag{5.6}$$

Where: Lds = downstream load

Lus = upstream load

k = decay rate

tau = watershed residence time

At both Schemalinks 120 and 125, Lds and Lus are known, therefore k*tau can be directly calculated. By assuming that k ~ 1.5 days^{-1}, tau can be calculated. With tau and mean_flow_length (mean flow length from watershed to the watershed drainage outlet) available for the two Schemalinks, linear regression can be applied to find the overland flow velocity for the watershed.

The following equation (derived by Ernest To, CRWR) relates flow length to residence time in the Copano Bay watershed:

$$\tau = 2 \text{ x } 10^{-5} * L + 1.6717 \tag{5.7}$$

Where: τ = residence time (d)

L = mean flow length (m)

Appendix 5.5 explains the procedure for determining the mean flow length for watersheds (which was used in deriving Equation 5.7), and Appendix 5.6 provides the procedure that was used in determining the mean flow length (based on Equation 5.7) from each WWTP to the downstream main river channels, which 3d models of the river channels were created.

Table 5.14 gives the calculated flow length from each of the WWTPs to the main river channels (determined from the flow length raster that was created in Appendix 5.6) as well as the decayed bacterial loading that is applied to the model.

Table 5.14 WWTP Bacterial Loading Applied to Model (See Chapter 6)

	(A)	(B)	(C)	(D)	(E)
Permit Number	Bacterial Loading (CFU/year)	Mean Flow Length, L (m)	Residence Time, τ (days)	Decayed Bacterial Loading (CFU/year)	Apply to IncVal SchemaNode HydroID
10055-001	6.98E+14	0	0	6.98E+14	92
10124-002	4.47E+15	20338.7	2.47[1]	3.20E+13	62
10124-004	4.79E+14	0	0	4.79E+14	64
10156-001	2.21E+14	3572.5	2.74[2]	9.17E+11	70
10237-001	2.04E+10	12258.3	1.92	4.42E+08	92
10255-001	2.61E+13	3662.87	1.74	7.96E+11	65
10705-001	6.22E+05	9844.47	1.87	1.48E+04	67
10748-001	7.42E+13	10080.6	1.87	1.75E+12	90
13892-001	9.73E+12	482.132	1.68	3.37E+11	69

[1] Residence time was calculated (based on Equation 5.7) to be 2.08 days, but the residence time was adjusted to allow more decay in order to match the median fecal coliform concentration at the downstream bacterial monitoring station.

[2] Residence time was calculated as 1.74 days, but one day was added since bacteria are flowing in stream before being applied to model.

Column A is the bacterial loading (CFU/year) that was calculated in Section 5.4.2.3 and shown in Table 5.12. Column B is the mean flow length from WWTPs to the next downstream main channel (or Copano Bay) that was determined (as described in Appendix 5.6.) Column C is the residence time calculated using Equation 5.7 from the mean flow length in Column B. Column D is the decayed bacterial loading from using the first-order decay equation and assuming a decay coefficient of 2 days$^{-1;}$ (see Section 6.3.3.1 for how decay coefficient was determined). (D) = (A) * exp (-2 days^{-1}*(C)). Column E is the SchemaNode to which the bacterial loading is applied (described in further detail in Chapter 6.)

5.4.3 Result

The total annual bacterial loadings from WWTPs applied to the model are shown below in Figure 5.17.

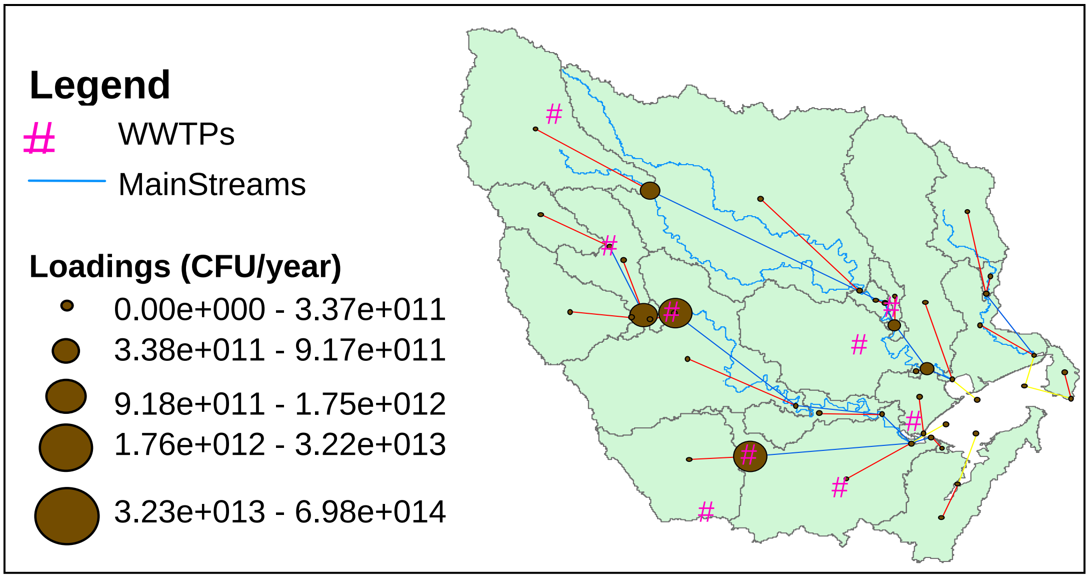


Figure 5.17 Annual WWTP Bacterial Loadings (CFU/year)

5.5 ESTIMATION OF LOADINGS FROM SEPTIC SYSTEMS

5.5.1 Methodology

Due to lack of data for septic systems, it was very difficult to quantify the fecal coliform bacterial loading that could be potentially contaminating certain areas of Copano Bay. There are many factors that affect whether or not bacteria from septic systems reach surface waters: type of soil, height of the water table, etc.

Fecal coliform loadings from septic systems were estimated using data from a variety of sources (given in Section 3.2.1.4).

The annual bacterial loadings per watershed from septic systems were calculated by finding the annual number of septic systems in use per watershed on the following types of land: Low and High Intensity Residential (land use codes 21 and 22, respectively.)

The following steps were used to calculate the bacterial loadings from septic systems for the watershed model:

1. Determine the number of septic systems in use, number of complaints, population, and housing units per county in 2004 from U.S. Census of Bureau and TCEQ data.
2. Find the area (m^2) of the land use classifications of 21 and 22 in each county in the Copano Bay watershed.
3. Calculate the density of septic systems in use, complaints, population, and housing units per county ($\text{count}/m^2_{\text{of High/Low Residential}}$) in 2004. The following equation would be used where the number in the parentheses indicates the step in which the value was determined: (1)/(2)

4. Find the area of land use classifications 21 and 22 of each county within each watershed, recognizing that watersheds may be part of multiple counties.
5. Find the area of each Soil Group (A, B, C, D) within each watershed in land use classifications 21 and 22.
6. Multiply the area (m^2) of each county within each watershed (for each soil group) by the septic system density and complaint density (count/m^2) to find the septic system count and complaint count per soil group for each watershed. (5) * (3)
7. Multiply the area (m^2) of each county within each watershed to find the population and housing count per watershed. (4) * (3)
8. Find the number of people per housing unit per watershed (from calculations made in step 7).
9. Apply the criteria given in Section 5.5.2.5 to find the number of impacting septic systems per watershed; these criteria account for the number of complaints and hydrologic soil groups in each of the watersheds.
10. Multiply the number of impacting septic systems per watershed by the number of people per housing unit (in corresponding watershed) to find the number of people that may be contaminating ground and surface waters. (9) * (8)
11. Multiply the number of humans (Step 10) by the number of fecal coliform excreted per year (CFU/year-human) to find the total CFU/year from impacting/malfunctioning septic systems per watershed.

5.5.2 Procedure of Application

5.5.2.1 Finding Septic Systems, Complaints, Population and Housing Units per County in 2004

Septic system data (annual count per county) were obtained from the 1990 U.S Census of Bureau, and the TCEQ provided the number of septic systems installed from 1990 - 2004. These data are given in Table 5.15.

Table 5.15 Septic System Data from 1990 U.S. Census and TCEQ Applications (1990-2004)

County	**Sewage Disposal: Septic Tank or Cesspool (1990 Census)**	**Applications for Septic Systems (TCEQ, 1990-2004)**
Aransas	6,456	2,931
Bee	3,859	616
Goliad	1,898	982
Karnes	1,765	269
Refugio	1,033	229
San Patricio	5,722	1,687

The number of complaints investigated for each county was also reported to the TCEQ. Assuming that the rate of complaint was constant, the number of complaints investigated from 1990-2004, and the complaint percentage per year was calculated. The TCEQ data (columns A-C) and the calculated data (columns D-F) are given in Table 5.16. Column D (Complaints Investigated per Year) is calculated by dividing Column B by the number of years, Column C. (D) = (B)/(C). Column E is calculated by multiplying Column D by 14 years (1990-2004). (E) = (D) * 14 years. Column F is calculated by dividing Column D (Complaints Investigated per Year) by the total number of septic system applications from TCEQ (Table 5.15) and multiplying by 100 to get the units in percent.

Table 5.16 Annual Septic System Complaint Percentage by County

(A)	(B)	(C)	(D)	(E)	(F)
County	**Complaints Investigated**	**Corresponding Years of Investigation**	**Complaints Investigated per Year**	**Complaints Investigated (1990-2004)**	**Complaint Percentage per Year (%)**
Aransas	398	1993-2003	39.8	557	1.36
Bee	123	1992-2003	11.2	157	1.82
Goliad	12	1998-2003	2.4	34	0.24
Karnes	2	1998-2003	0.4	6	0.15
Refugio	18	1992-2003	1.6	23	0.71
San Patricio[1]	321	1990-2004	23	321	1.36

[1] No complaint investigation data was available for San Patricio County. Number of complaints was found by applying ratio of septic systems installed from Aransas County.

The number of housing units per county for 2004 was determined by using the 1990 and 2002 U.S. Census data. The housing unit data available from U.S. Census are given in Table 5.17 (Columns A, B, and E.)

Table 5.17 Housing Unit Data by County

	(A)	(B)	(C)	(D)	(E)	(F)
	Housing Units		**Housing Units per Year**	**Projected Housing Units**	**Occupied Housing Units**	**Occupancy Rate (%)**
County	**1990**	**2002**	**1990-2002**	**2004**	**1990**	**1990/2004**
Aransas	10,889	13,258	197	13,653	6,938	64
Bee	10,208	11,043	70	11,182	8,592	84
Goliad	2,835	3,480	54	3,588	2,208	78
Karnes	5,117	5,523	34	5,591	4,337	85
Refugio	3,739	3,660	-7	3,647	2,937	79
San Patricio	22,126	25,650	294	26,237	18,776	85

Column C is calculated by finding the difference between Column A and B and dividing by the number of years (1990-2002). (C) = {(B) – (A)}/(2002 – 1990). Column D (Projected Housing Units) is calculated by multiplying the housing units per year by 2 years (2004-2002) and adding it to the number of housing units in 2002. (D) = (C) * 2 years + (B). Column F (Occupancy Rate %) is calculated by dividing the Occupied Housing Units in 1990 (Column E) by the Housing Units in 1990 (Column A) and multiplying by 100 to get the units in percent. (F) = (E) / (A) * 100%.

The number of septic systems in use (by county) can be found by assuming that the occupancy rate (%) is the same in 1990 as in 2004, and the number of complaints in 2004 is found by multiplying the number of septic systems in use by the complaint percentage per year (given in Table 5.16, Column F). The number of septic systems in use in 2004, the number of complaints in 2004, the population (from 2004 U.S. Census), and projected housing units in 2004 (from Table 5.17, Column D) are summarized in Table 5.18. When a complaint is filed for a house, it is usually a complaint that could apply to a whole neighborhood rather than just one house, so the number of complaints filed and investigated is used more as a qualitative assessment to identify areas that may have more malfunctioning septic systems.

Table 5.18 Septic Systems in Use, Complaints Investigated, Housing Units, and Population in 2004

County	Septic Systems in Use	Complaints Investigated	Housing Units	Population
Aransas	5,981	81	13,653	24,041
Bee	3,767	68	11,182	33,046
Goliad	2,243	5	3,588	7,104
Karnes	1,724	3	5,591	15,458
Refugio	991	7	3,647	7,640
San Patricio	6,287	85	26,237	68,187

5.5.2.2 Calculating Density of Septic Systems, Complaints Investigated, Housing Units, and Population per County in 2004

The density of septic systems, complaints investigated, housing units, and population per county in 2004 (count/m^2) were calculated by using the following equation: [Total annual count] / [Area in m^2 where the residences would be located within each county]. The area where septic systems, housing units, and populations would be located was assumed to be in the land use land cover classifications 21 and 22 (Low and High Density Residential). The low and high density residential land use areas in the Copano Bay watershed and the specified locations of septic systems around Copano Bay (TDH, 2000) are shown in Figure 5.18. Residential areas are greatly outnumbered by areas for agriculture, pasture, and shrubland (areas where livestock animals would be grazing), as shown in Figure 5.18. In order to find the residential area, the land use land cover dataset was masked by each county, and the corresponding grid cells (for land use codes 21 and 22) were summed. For example, in San Patricio County (calculation shown in Figure 5.19), the total area where septic systems, housing units, and people are located is 28,288,800 m^2**.** Thus, the density of septic systems in San Patricio county is 6,287 septic systems/28,288,800 m^2 = 0.00022 septic/m^2 = 576 septic/mi^2 = 222 septic/km^2. The density of septic systems, complaints investigated, housing units, and population per county in 2004 is given in Table 5.19.

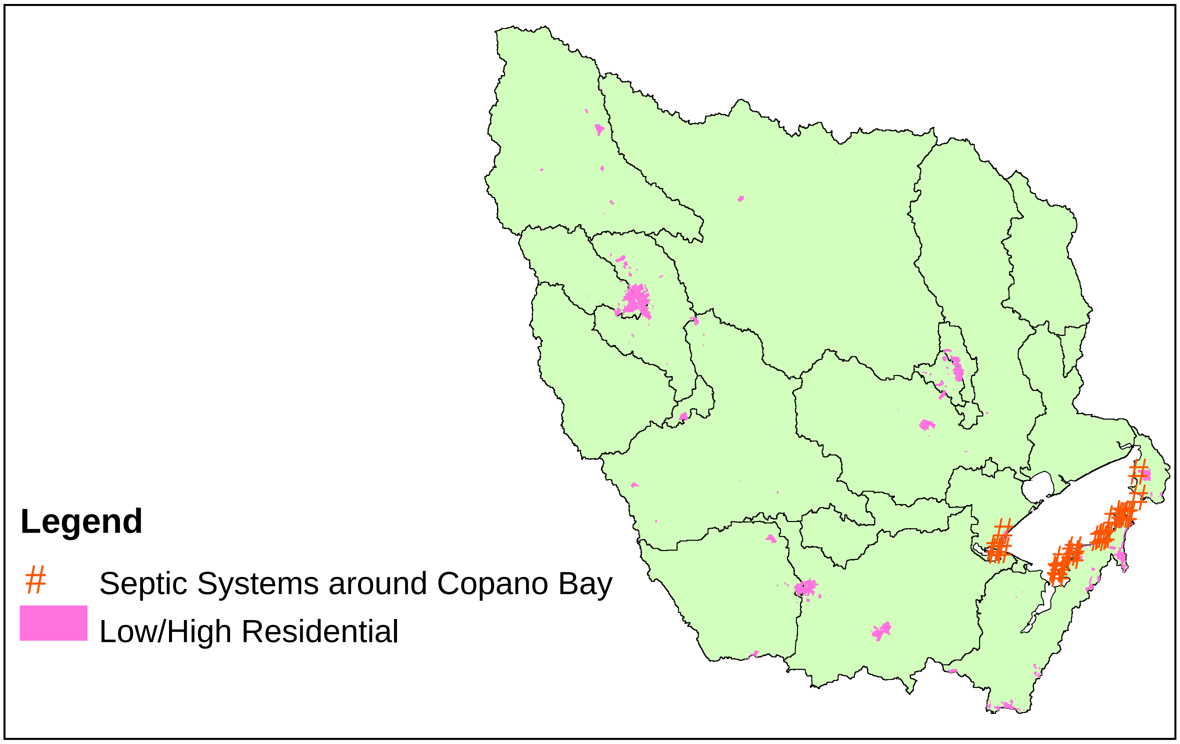
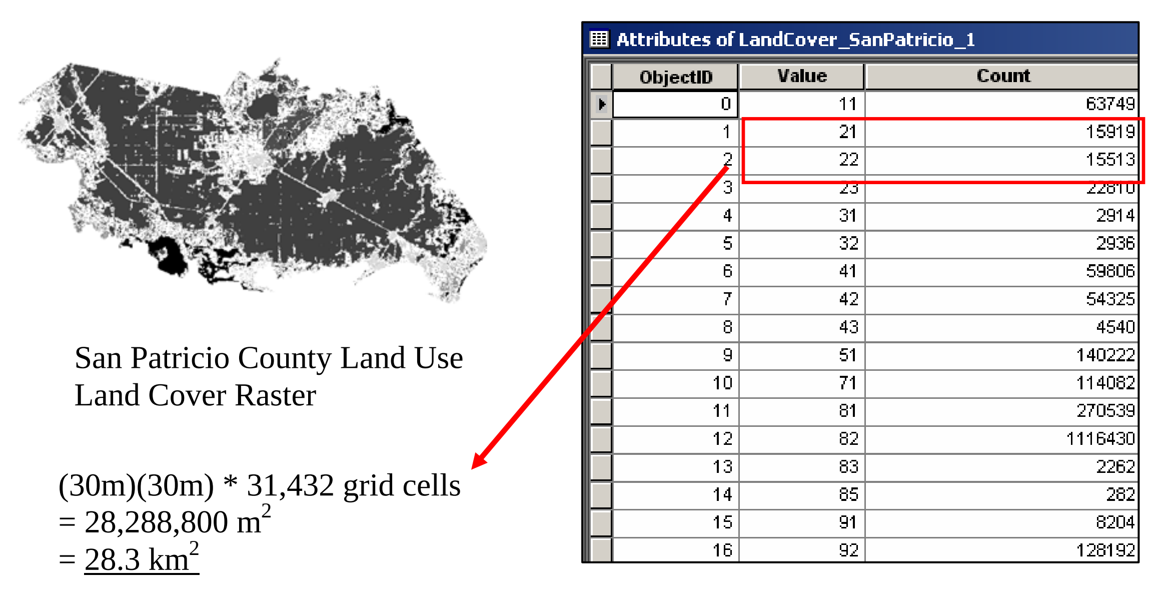


Figure 5.18 Low and High Residential Land Use Areas and Septic System Locations around Bay

Table 5.19 Septic Systems, Complaints Investigated, Housing Units, and Population per County (Count per km^2)

County	Residential Area (km^2)	Description	Density (Count/km^2)
Aransas	14.1	Septic Systems	424
		Complaints Investigated	6
		Occupied Housing Units	967
		Population	1,700
Bee	14.0	Septic Systems	269
		Complaints Investigated	5
		Occupied Housing Units	799
		Population	2,360
Goliad	2.4	Septic Systems	952
		Complaints Investigated	2
		Occupied Housing Units	1,520
		Population	3,010
Karnes	7.1	Septic Systems	244
		Complaints Investigated	0
		Occupied Housing Units	791
		Population	2,190
San Patricio	28.3	Septic Systems	222
		Complaints Investigated	3
		Occupied Housing Units	927
		Population	2,410



San Patricio County Land Use
Land Cover Raster

(30m)(30m) * 31,432 grid cells
= 28,288,800 m^2
= 28.3 km^2

Attributes of LandCover_SanPatricio_1

ObjectID	Value	Count
0	11	63749
1	21	15919
2	22	15513
3	23	22810
4	31	2914
5	32	2936
6	41	59806
7	42	54325
8	43	4540
9	51	140222
10	71	114082
11	81	270539
12	82	1116430
13	83	2262
14	85	282
15	91	8204
16	92	128192

Figure 5.19 Determination of Area (km^2) of Septic Systems and Residences in San Patricio County

5.5.2.3 Calculating Total Septic Systems, Complaints Investigated, Housing Units, and Population per Watershed

The area of low and high residential land use classifications (m^2) of each county within each delineated watershed (Figure 5.1) was determined and then multiplied by each density in each corresponding county. Appendix 5.7 shows the calculations and results for this procedure. For example, Watershed JunctionID 45422 has two counties overlapping it (Bee and Karnes Counties), so there are two different areas and densities for which to account. The calculation of how many septic systems are in Watershed JunctionID 45422 is shown in Figure 5.20. 632 septic/mi^2 is the density of septic systems in Karnes County, and 697 septic/mi^2 is the density of septic systems in Bee County; these densities are per square mile of land where septic systems are assumed to be located based on land use classifications. Approximately 1.4 km^2 (0.537 mi^2) is the area in Watershed JunctionID 45422 that is a part of Bee County (the area of land use types 21 and 22 where septic systems and residences are assumed to be located). Approximately 0 m^2 (0 mi^2) is the area in Watershed JunctionID that is a part of Karnes County[13]. Thus, there are approximately 374 septic systems in Watershed JunctionID 45422. This procedure was replicated for the population, housing units, and number of complaints investigated in each watershed.

632 septic/mi^2 * 0 mi^2 = **0 septics**

+

697 septic/mi^2 * 0.537 mi^2 = **374 septics**

Total = 374 septic systems

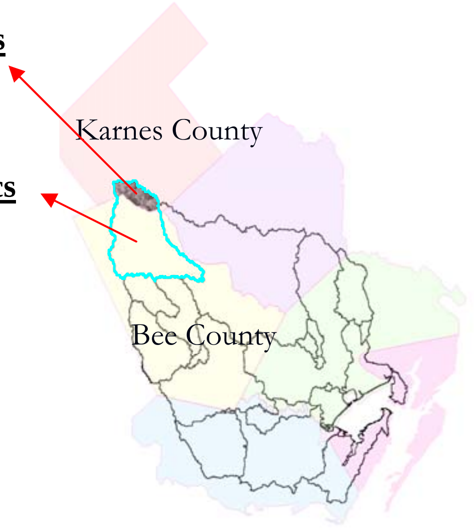


Figure 5.20 Determination of Septic System Count in Watershed JunctionID 45422

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[13] There are no areas of low and high residential land use in Watershed JunctionID 45422 in Karnes County.

Table 5.20 Total Septic Systems, Complaints Investigated, Population, Housing Units per Watershed, and People/Housing Unit per Watershed

Watershed JunctionID	Septic Systems	Complaints	Population	Housing Units	People/Housing Unit
45422	374.36	6.80	3,284	1111.39	2.96
45408	183.25	3.19	1,668	578.96	2.88
45426	471.66	6.40	5,115	1968.30	2.60
45414	0.00	0.00	0.00	0.00	0.00
45416	1,230.96	16.72	13,350	5136.95	2.60
45405	2,256.85	30.65	11,996	5961.68	2.01
45421	0.00	0.00	0.00	0.00	0.00
45417	293.00	2.09	2,258	1077.91	2.09
45404	0.97	0.02	8.00	2.88	2.96
45409	190.81	3.46	1,674	566.48	2.96
45415	1,271.99	23.09	11,160	3776.27	2.96
45419	257.58	0.74	857	422.56	2.03
45413	1,790.42	32.50	15,708	5315.39	2.96
56830	0.00	0.00	0.00	0.00	0.00
56831	823.81	11.19	3,311	1880.51	1.76
45425	0.00	0.00	0.00	0.00	0.00
45418	224.24	1.60	1,728	824.94	2.09
45423	245.60	1.75	1,893	903.51	2.09
45406	0.00	0.00	0.00	0.00	0.00
45412	0.00	0.00	0.00	0.00	0.00
45410	82.14	0.59	633	302.18	2.09

As shown in Table 5.20, there are approximately 74,645 people that live in the Copano Bay drainage area. To find the number of people that are on septic systems, the number of people per housing unit was multiplied by the number of septic systems in each corresponding watershed and summed for the entire drainage area; people/housing unit and number of septic systems per watershed is given in Table 5.20. Approximately, 23,912 people (out of 74,645 people) are on septic while the remaining people are assumed to have their wastewater treated by WWTPs.

5.5.2.4 Calculating Septic Systems and Complaints Investigated in Soil Groups A, B, C, and D per Watershed

After determining the density of septic systems and complaints in each county (see Section 5.5.2.2), the number of septic systems and complaints (in land use codes 21 and 22) in each Soil Group was found within each watershed. The hydrologic soil group data was retrieved from STATSGO. Soil data were downloaded for the state of Texas and then clipped to the Copano Bay watershed. A dbf table called "COMP.dbf" contains the hydrologic soil group data under the field, "Hydgrp". "COMP.dbf" can be joined to the soil polygon feature class based on the field "MUID" that is found in each attribute table. The hydrologic soil groups in the Copano Bay watershed are shown in Figure 5.21.

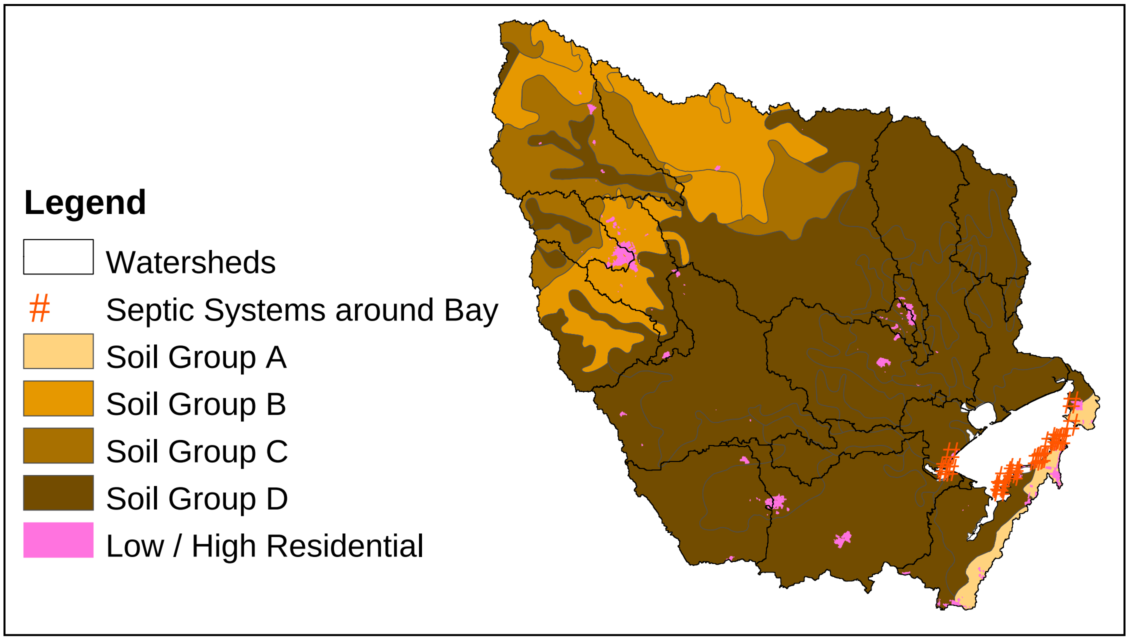


Figure 5.21 Hydrologic Soil Group Classifications

Soil group A consists of soils that have low runoff potential and high infiltration rates and typically consist of USDA soil textures of sand, loamy sand, and sandy loam. The transmission rate is typically greater than 0.76 cm/hr (Maidment, 1992). Thus, septic systems with soils classified in Group A are more likely to allow contamination of and infiltration into the groundwater and surface waters than other soil classifications. These types of soils (as seen in Figure 5.21) are only found around the South portion of Copano Bay.

Soil group B consists of soils that have moderate infiltration rates when the soil is thoroughly wetted and typically consist of USDA soil textures of silt loam and loam. The transmission rate is usually between 0.38 and 0.76 cm/h.

Soil group C consists of soils that have low infiltration rates when the soil is thoroughly wetted and typically consists of USDA soil textures of sandy clay loam. The transmission rate is usually between 0.13 and 0.38 cm/h.

Soil group D consists of soils that have high runoff potential and have very low infiltration rates when the soil is thoroughly wetted and typically consist of USDA soil textures of clay loam, silty clay loam, sandy clay, silty clay, and clay. The transmission rate is usually between 0 and 0.13 cm/h.

The area (m^2) of each soil group within each watershed (and land use codes 21 and 22) was found and then multiplied by the corresponding densities (of each overlapping county). The procedure for determining the area of each soil group within each watershed (and land use codes 21 and 22) is described in Appendix 5.8.

Table 5.21 Number of Septic Systems and Complaints per Watershed in Soil Groups A, B, C, and D

	Soil Group A			**Soil Group B**		
JunctionID	**Septic Systems**	**Complaints**	**%**	**Septic Systems**	**Complaints**	**%**
45422	0	0		23	0.4	1.8
45408	0	0		0	0	
45426	0	0		0	0	
45414	0	0		0	0	
45416	0	0		0	0	
45405	1543	21	1.4	0	0	
45421	0	0		0	0	
45417	0	0		0	0	
45404	0	0		0	0	
45409	0	0		0	0	
45415	0	0		1234	22.4	1.8
45419	0	0		254	0.7	0.3
45413	0	0		1787	32.4	1.8
56830	0	0		0	0	
56831	419	6	1.4	0	0	
45425	0	0		0	0	
45418	0	0		0	0	
45423	0	0		0	0	
45406	0	0		0	0	
45412	0	0		0	0	
45410	0	0		0	0	
	Soil Group C			**Soil Group D**		

JunctionID	Septic Systems	Complaints	%	Septic Systems	Complaints	%
45422	300	5.5	1.8	51	0.9	1.8
45408	0	0		183	3.2	1.7
45426	0	0		472	6.4	1.4
45414	0	0		0	0	
45416	0	0		1231	16.7	1.4
45405	0	0		697	9.5	1.4
45421	0	0		0	0	
45417	0	0		293	2.1	0.7
45404	0	0		1	0.0	
45409	0	0		191	3.5	1.8
45415	0	0		38	0.7	1.8
45419	0	0		4	0.0	
45413	4	0.1	1.8	0	0	
56830	0	0		0	0	
56831	0	0		397	5.4	1.4
45425	0	0		0	0	
45418	0	0		224	1.6	0.7
45423	0	0		246	1.8	0.7
45406	0	0		0	0	
45412	0	0		0	0	
45410	0	0		82	0.6	0.7

5.5.2.5 Calculating Septic System Bacterial Loading (CFU/year) per Watershed

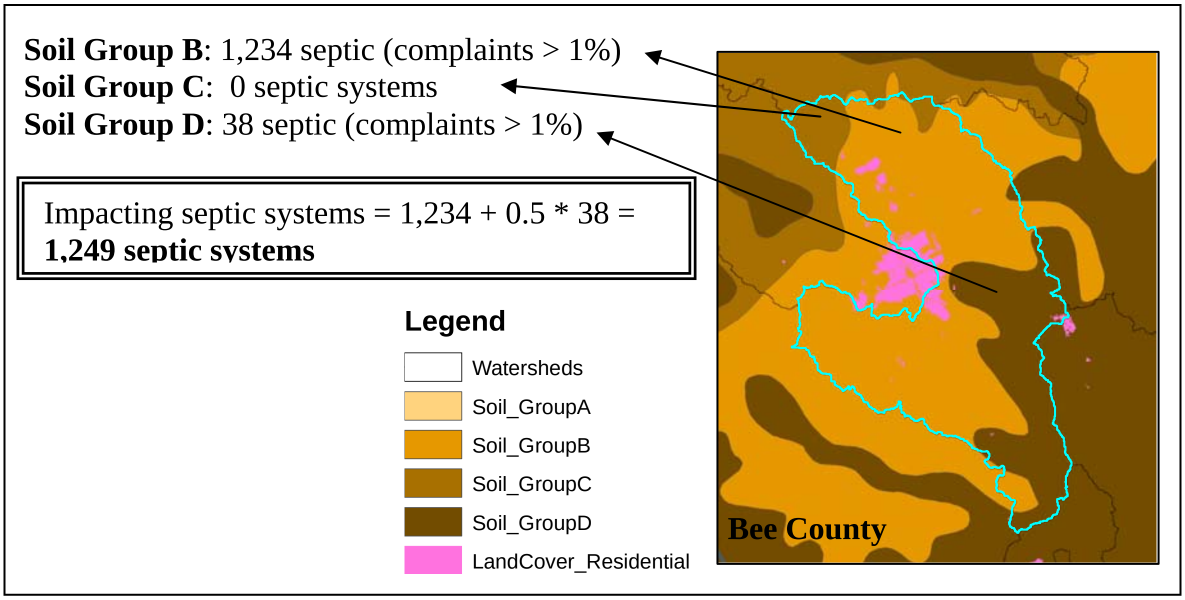
After determining the count of each septic system and complaints investigated within each soil group (see Section 5.5.2.4) and finding the population and occupied housing unit count in each watershed in low and high residential land use zones (see Section 5.5.2.3), an approximation of bacterial loadings from septic systems per watershed was found.

It was assumed that all of the septic systems found in hydrologic soil group A provide little to no removal of fecal coliform bacteria before reaching groundwater and surface waters. An approximation of the bacterial loadings from septic systems in hydrologic soil groups B, C, and D was made while considering the number of complaints (complaint percentage) in the corresponding watershed as well as the soil characteristics.

These basic assumptions were applied to all bacterial loading calculations for each soil group:

- Hydrologic soil group A: 100% of loading from septic systems flows directly into surface waters.
- Hydrologic soil group B: 100% of loading from septic systems flows directly into surface waters if complaint percentage is greater than 1%.
- Hydrologic soil group C: 50% of loading from septic systems flows directly into surface waters if complaint percentage is greater than 1%.
- Hydrologic soil group D: 50% of the loading from septic systems flows directly into surface waters if complaint percentage is greater than 1%.

The number of impacting septic systems (considering the above criteria) calculated for Watershed JunctionID 45415 is shown in Figure 5.22. The number of septic systems and complaints in Figure 5.22 are given in Table 5.21.



Soil Group B: 1,234 septic (complaints > 1%)
Soil Group C: 0 septic systems
Soil Group D: 38 septic (complaints > 1%)

Impacting septic systems = 1,234 + 0.5 * 38 =
1,249 septic systems

Figure 5.22 Determination of Number of Impacting Septic Systems in Watershed JunctionID 45415

Once the number of impacting septic systems was found for each watershed, the bacterial loadings from septic systems were calculated. For example, for Watershed JunctionID 45415, the number of impacting septic systems is 1,249 septic systems (Figure 5.22), and the number of people per housing unit is 2.96 people/housing unit (Table 5.20). Assuming that the annual human production of fecal coliform is 7.3 x 10^{11} CFU/year (EPA, 2005), then the total bacterial loading for Watershed JunctionID is (1,249 septic systems) * (2.96 people/housing unit) * (7.3 x 10^{11} CFU/year-person) = 2.70 x 10^{15} CFU/year.

The same procedure was repeated for all watersheds. The total fecal coliform bacterial loadings contributed by septic systems in the Copano Bay watershed are shown in Figure 5.23.

5.5.3 Result

After completing the procedure described in Section 5.5.2, the cumulative septic system bacterial loadings per watershed was calculated (following the procedure described in Section 5.5.2.5.) The septic system bacterial loading per watershed is shown in Figure 5.23.

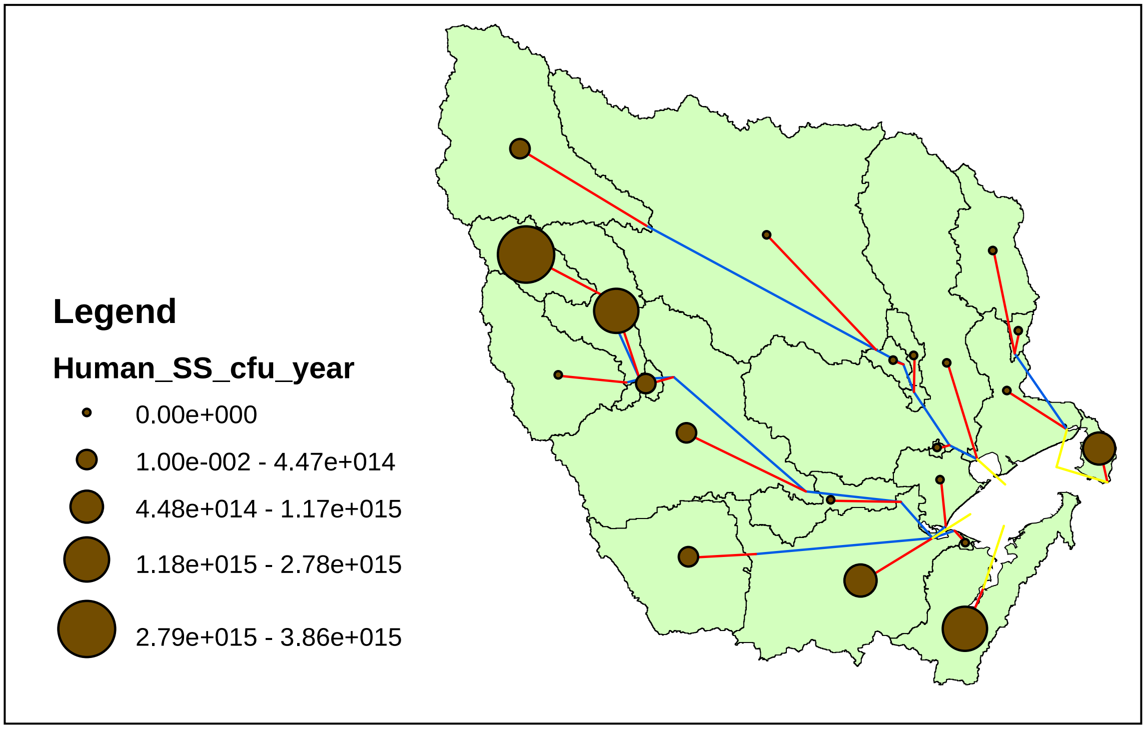


Figure 5.23 Septic System Annual Bacterial Loading (CFU/year)

5.6 ESTIMATION OF TOTAL LOADING

The total bacterial loadings from the watersheds (and in the Copano Bay water segments) were calculated by summing the non-point bacterial loadings (Section 5.1), livestock loadings (Section 5.2), avian loadings (Section 5.3), WWTP loadings (Section 5.4), and septic system loadings (Section 5.5). Figure 5.24 shows the total bacterial loadings for all the watersheds and water segments in the Copano Bay watershed.

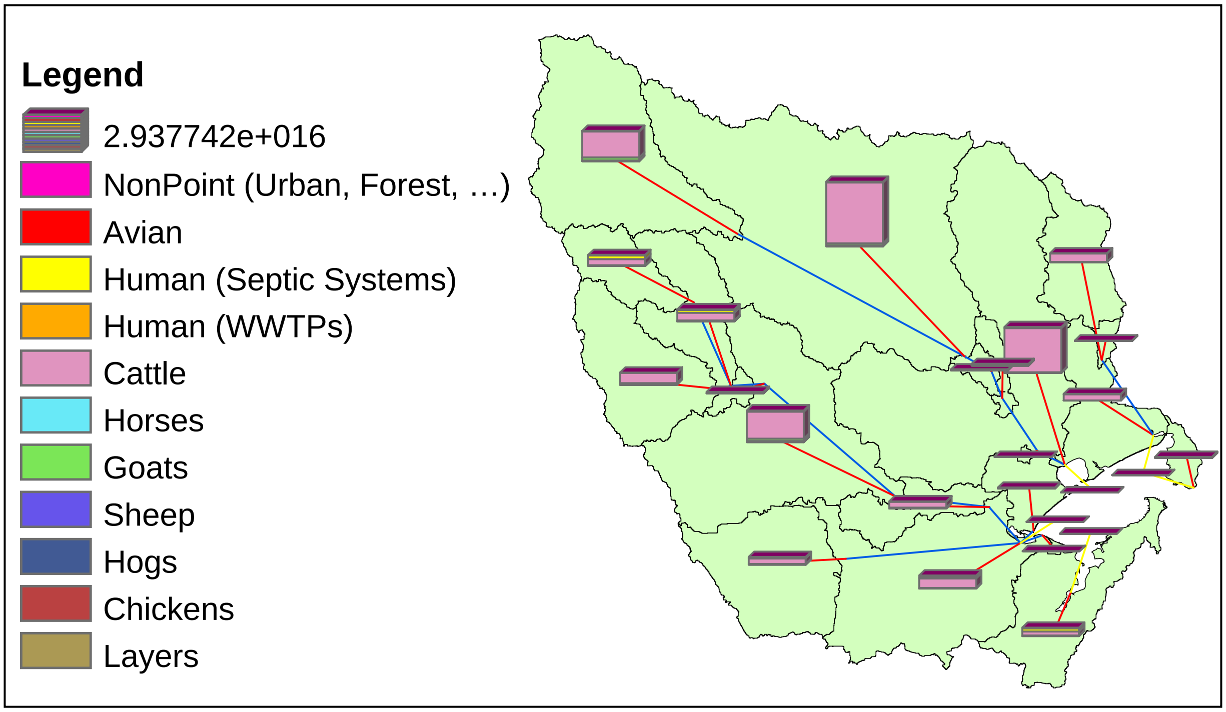


Figure 5.24 Total Annual Watershed/Segment Bacterial Loadings (CFU/year)

The watersheds' bacterial loadings from cattle are significantly larger than the bacterial loadings from any other point or non-point bacteria source (as shown in Figure 5.24.)

The percent distribution of bacterial loadings for the Copano Bay watersheds and water segments is shown in Figure 5.25, such that the relative difference of sources of bacterial loadings can be observed.

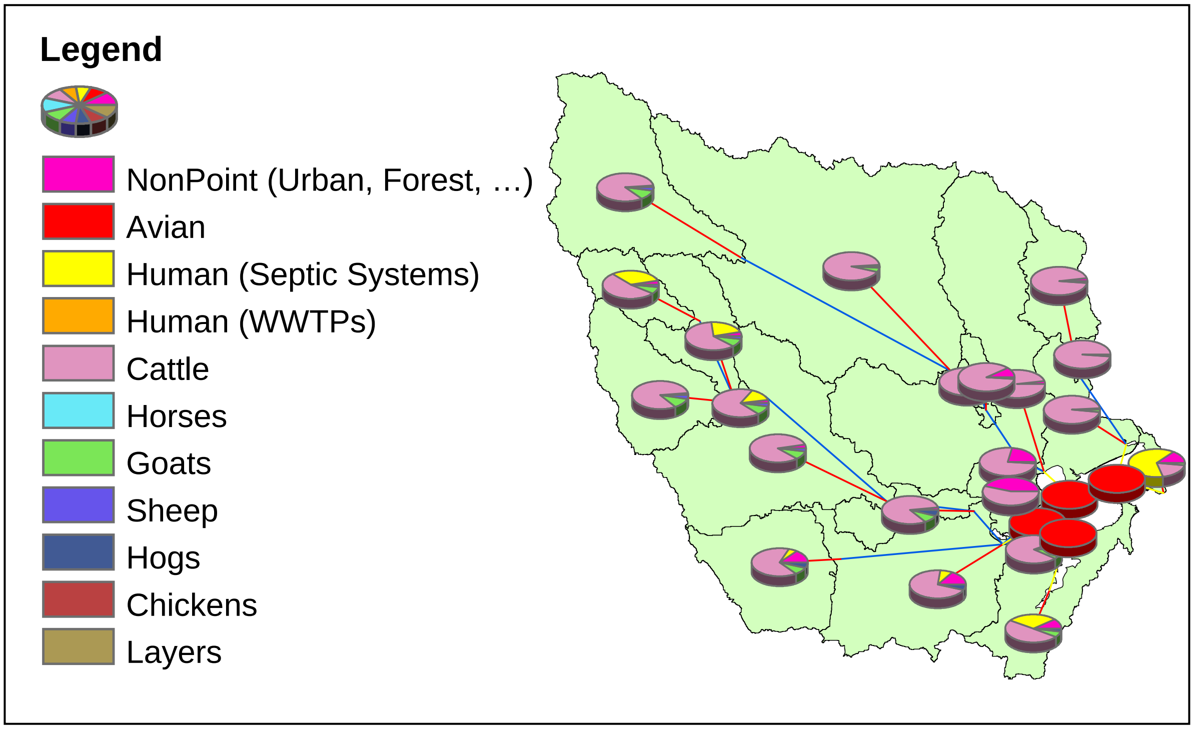


Figure 5.25 Percent Distribution of Bacterial Loading Sources

Cattle are the predominant source of fecal coliform at most upstream watersheds (as shown in Figure 5.25.) At the one watershed (where septic system bacterial loadings dominate) where cattle are not the major contributor, the bacterial loadings are significantly lower than the other upstream watersheds (see Figure 5.24). It can also be seen that the livestock bacterial loadings are significantly larger than the non-point, WWTP, septic system, and avian bacterial loadings. However, avian loads are applied directly on Copano Bay, and the bacterial loadings that would affect the quality of the Bay the greatest are the watersheds directly adjacent.

Table 5.22 summarizes the total bacterial loadings for the entire Copano Bay watershed from the major bacterial contributors.

Table 5.22 Annual Bacterial Loadings (TCFU/yr) from Major Bacterial Sources in Entire Copano Bay Watershed

Bacterial Source	**Number of Units**	**Bacterial Loading (TCFU/yr)**
Cattle	111,433	219,635
Goats	2,299	12,589
Human (Septic Systems)	23,912	12,576
Non-Point (Urban, Forest, etc.)	N/A	8,777
Sheep	659	3,607
Hogs	486	1,765
Human (WWTP)	50,733	1,213

These bacterial loadings are the input into the Schematic Processor and Monte Carlo Simulation Models. Thus, the bacteria transport (what happens to the bacteria as they flow from watersheds to rivers, along rivers, and into the Bay) was modeled to see how the bacterial loadings impact the quality of the rivers and Bay in the Copano Bay watershed. Bacteria transport is described in Chapter 6 and is modeled using the Schematic Processor.

Chapter 6: Modeling of Bacteria Transport – Schematic Processor

6.1 BACKGROUND

Once point and non-point bacterial loadings were calculated per watershed (described in Chapter 5), the transport of bacteria from the watersheds to Copano Bay was modeled. To simulate bacterial load transport, “Process Schematic”, a script tool that was developed by Jon Goodall and Tim Whiteaker in 2003, was used to implement dynamic linked libraries (DLLs). The two processing engines (DLLs) that were used in this bacteria watershed model were *clsDecay.dll*, which accounts for first-order decay of bacteria along water segments, and *clsCFSTR.dll*, which calculates the increase in bacteria concentration in Copano Bay due to bacterial loadings from the upstream watersheds. Goodall and Whiteaker submitted a journal article describing the Schematic Processor and Schematic Network in more detail (Goodall and Whiteaker, 2006).

6.2 METHODOLOGY

“Process Schematic”, also referred to as the Schematic Processor, can be used to model bacterial transport once the following steps have been completed:

1. Bacterial loadings have been calculated (Chapter 5).
2. Schematic Network of the Copano Bay watershed has been created.
3. The parameters of each SchemaNode and SchemaLink have been determined (through calculations and/or calibration).

6.3 PROCEDURE OF APPLICATION

6.3.1 Creation of Schematic Network

To implement the "Process Schematic" tool, a Schematic Network of the Copano Bay watershed was created, and the procedure is described in detail in Appendix 6.1. The Schematic Network is made up of two feature classes: SchemaNode and SchemaLink. SchemaNode represents the nodes in the watershed (a watershed, drainage point, or Copano Bay.) SchemaLinks connect the SchemaNodes and are a way to model what happens to the bacteria as they travel to Copano Bay. The Schematic Network was created for the Copano Bay watershed; the Schematic Network, as well as the parameters (inputs), necessary to run the model are shown in Figure 6.1 and explained in more detail in Appendix 6.1 and Section 6.3.2. The Bay was segmented into four water segments, and the segmentation of the Bay is described in Section 6.3.1.1.

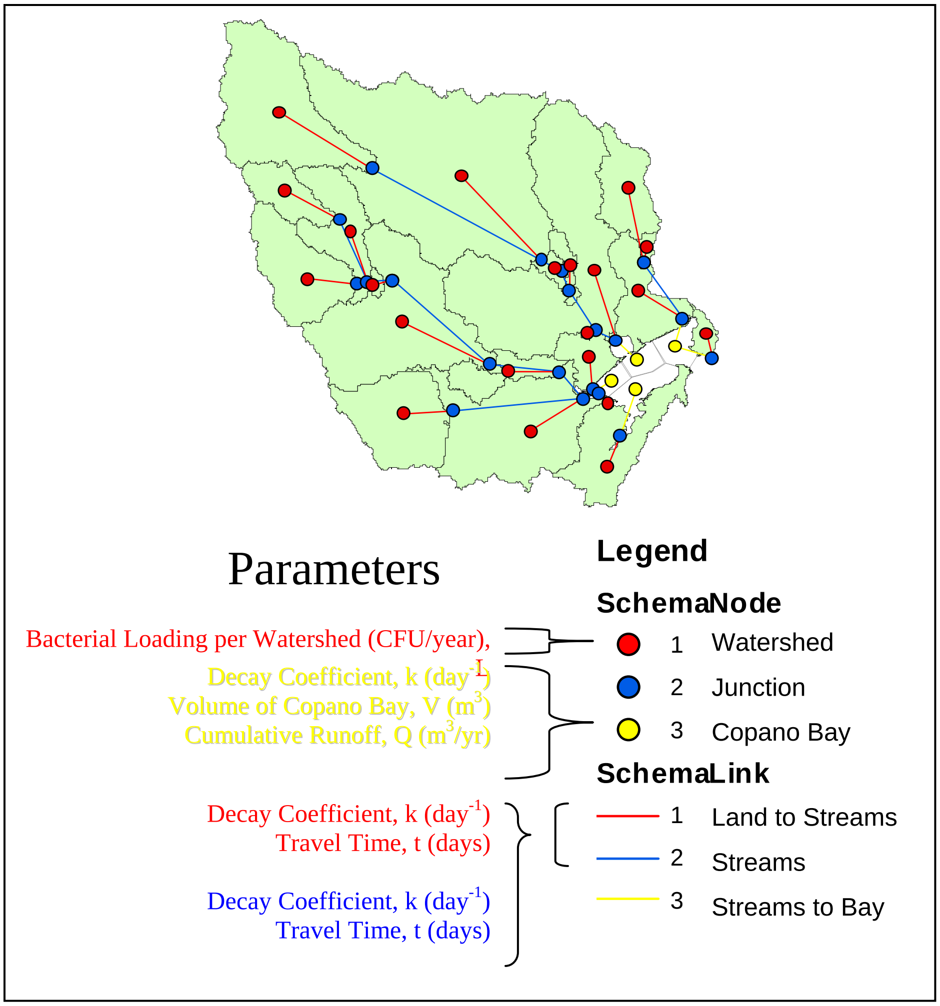


Figure 6.1 Schematic Network and Parameters

6.3.1.1 Copano Bay Segmentation

Ward and Armstrong (1997) segmented Copano Bay into water segments based on water quality parameter trends in the bay. Their study was a trends analysis on the Corpus Christi Bay system, which includes Copano Bay, in which the spatial variation of water quality monitoring data was used to segment the Bay system. Their segmentation allows the parameters to be representative by geographical location.

The water segments determined by Ward and Armstrong are shown in Figure 6.2. Their 15 water segments were dissolved into four Copano Bay water segments, each supporting the drainage of the upstream watersheds. The segments were clipped to the Copano Bay watershed to calculate a surface area for each segment, which can be seen in Figure 6.3 and Table 6.1.

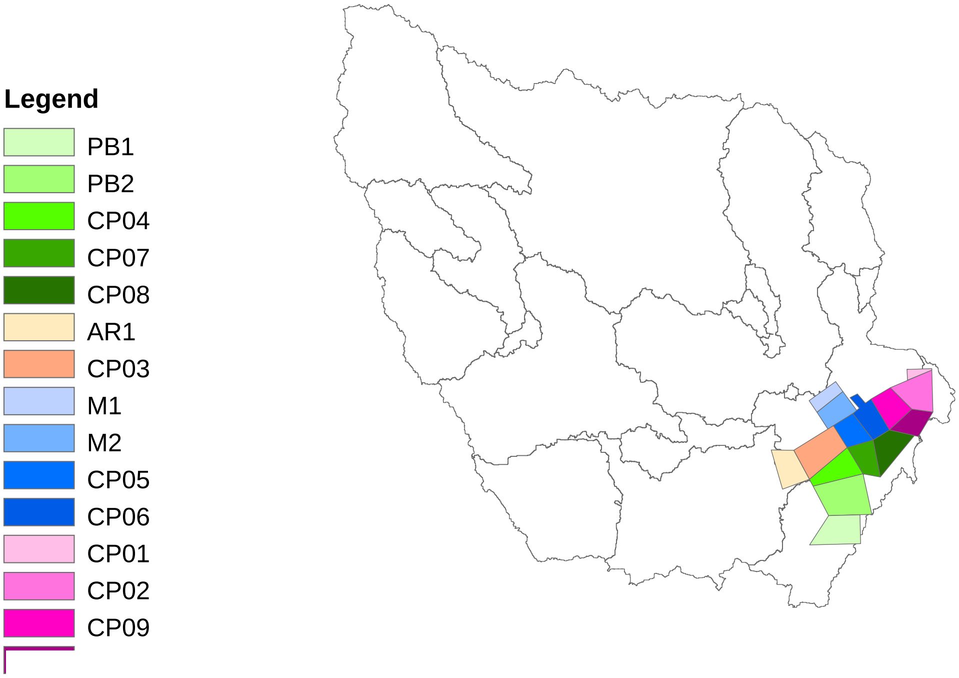


Figure 6.2 Copano Bay Initial Water Segments

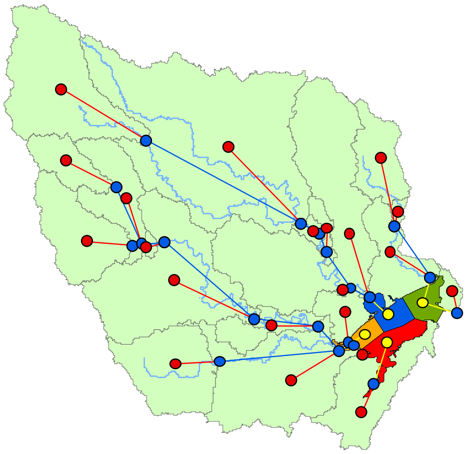


Figure 6.3 Copano Bay Segmentation

Table 6.1 Dissolving of Copano Bay Segments (New Labeling)

Initial Bay Segmentation Labels	**Copano Bay Segmentation Labels**
PB1	1
PB2	
CP04	
CP07	
CP08	
AR1	2
CP03	
M1	3
M2	
CP05	
CP06	
CP01	4
CP02	
CP09	
CP10	

6.3.2 Use of Dynamic Linked Libraries (DLLs)

6.3.2.1 First-order Decay: clsDecay.dll

clsDecay.dll simulates the decay of bacteria along stream segments (shown in Figure 6.4) and assumes first-order decay:

$$\mathrm{load}_{\mathrm{passed}} = \mathrm{load}_{\mathrm{received}} * e^{-k\tau} \qquad (6.1)$$

Where: k = first-order decay coefficient (day^{-1}), which is stored as an attribute in SchemaLink.

τ = residence time along streams (days), which is stored as an attribute in SchemaLink.

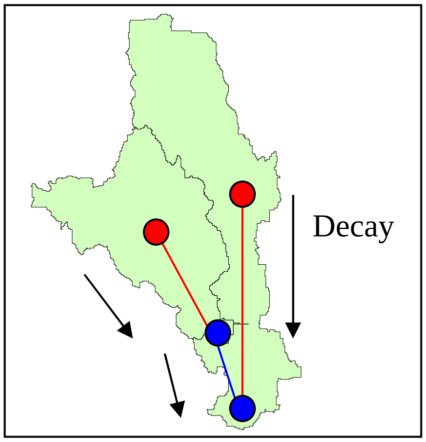


Figure 6.4 Simulation of Decay

6.3.2.2 Continuous Flow Stirred Tank Reactor: clsCFSTR.dll

clsCFSTR.dll calculates the increase in fecal coliform concentration in the Bay due to bacterial loadings. The Bay is assumed to be completely mixed and acts as four Continuous Flow, Stirred Tank Reactors (CFSTRs), which are shown in Figure 6.5; furthermore, the inflow into the Bay equals the outflow. The following equation calculates the fecal coliform concentration in the Bay:

$$c = L / (Q + kV) \qquad (6.2)$$

Where: c = concentration in bay (CFU/m^3)

L = bacterial load entering bay (CFU/year)

Q = total flow (m^3/year), which is stored as an attribute in SchemaNode

k = first-order decay coefficient ($year^{-1}$), which is stored as an attribute in SchemaNode

V = Volume of bay (m^3), which is stored as an attribute in SchemaNode

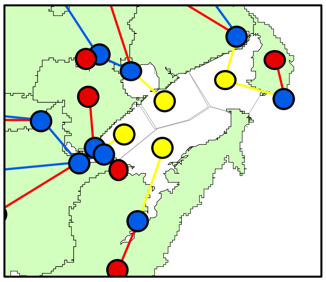


Figure 6.5 CFSTRs

6.3.3 Determination of Model Parameters

The DLLs described in Section 6.3.2 have many parameters that need to be determined before implementing the Schematic Processor. Each SchemaLink and SchemaNode in Figure 6.1 has parameters associated with the feature class that need to be determined. The following sections describe how the parameters were determined for each SchemaLink and SchemaNode in the Schematic Network.

6.3.3.1 Decay Coefficient

Section 2.2 describe the research that was conducted to quantify the decay coefficients that would be representative of different parts of the Copano Bay watershed.

From the literature review, the decay coefficient typically ranges between 0.5 and 3 days^{-1} for a typical system. However, due to lack of data on the Copano Bay watershed, these values are still inconclusive.

To determine a decay coefficient distribution for the Copano Bay watershed, one portion of the model was analyzed that contains the most available data, so that the decay coefficient could be calculated. The portion of the model that was segregated is shown in Figure 6.6. The data available for this portion of the model are from one USGS gauge flow data (USGS station 08189700) and two bacterial monitoring stations (Stations 12952 and 12948.)

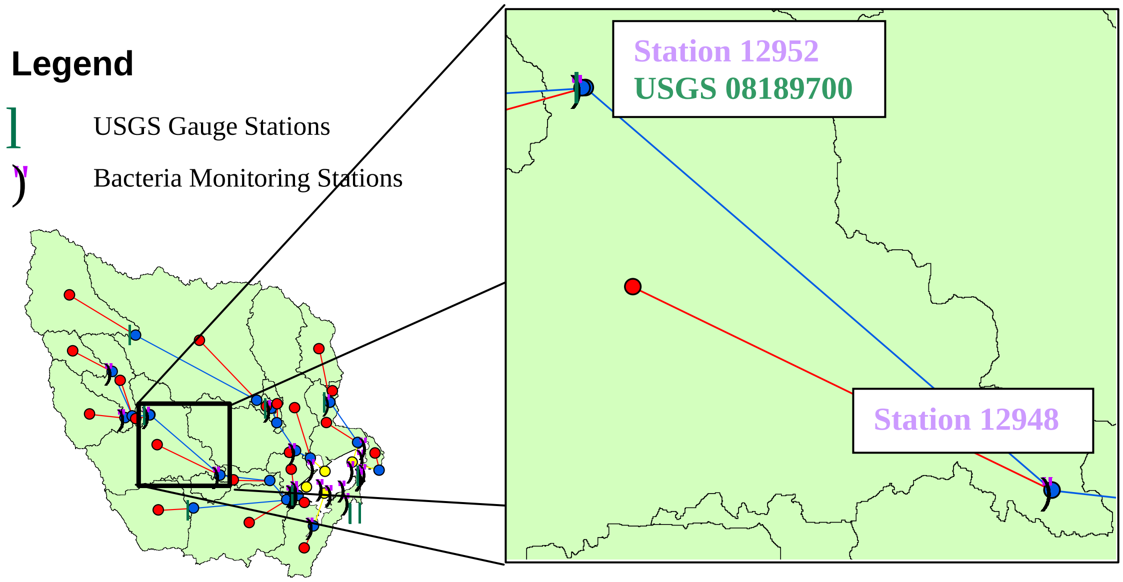


Figure 6.6 Segregated Portion of Model to Calculate Decay Coefficient Distribution

From 1999-2005, bacterial monitoring station 12952 only has five measurements (quarterly measurements taken between 2002 and 2003), and bacterial monitoring station 12948 has sixteen measurements. Thus, five days of data (corresponding to the dates from bacterial monitoring station 12952) were used in this analysis. The data from the bacterial monitoring stations and the USGS gauge station for these five days are given in Table 6.2. The data in this table were used to calculate a decay coefficient for each corresponding day (using Equation 6.1), so a distribution of five decay coefficients could be calculated.

Table 6.2 Available Data for Segregated Model on Aransas River Segment 2

Date	**Sta. 12952, Upstream (CFU/100mL)**	**Sta. 12948, Downstream (CFU/100mL)**	**USGS 08189700 Daily Flow (m^3/s)**
7/8/2002	836	1327	1.22
10/15/2002	25	122	0.19
1/21/2003	72	58	0.28
4/22/2003	130	34	0.21
8/18/2003	58	28	0.14

The bacterial concentrations were converted into bacterial loadings according to the following relationship:

$$L = Q * c \tag{6.3}$$

Where: L = bacteria loading (CFU/year)

Q = flow rate (m^3/year)

c = fecal coliform concentration (CFU/m^3)

The upstream bacterial loading (located at Station 12952) was calculated by multiplying the bacterial concentration at Station 12952 by the measured daily flow rate at the USGS gauge station (USGS 08189700), which is given in Table 6.2. The downstream bacterial loading (located at Station 12948) was calculated by multiplying the downstream daily flow rate by the downstream bacterial concentration (located at Station 12948). Since there is no USGS gauge station at the downstream location, the downstream flow rate was calculated according to the following equation:

$$q_{ds} = (q_{us}/q_{mean,us}) * q_{mean,\ ds} \tag{6.4}$$

Where: q_{ds} = downstream flow rate at Station 12948

q_{us} = upstream flow rate at Station 12952

$q_{mean,us}$ = median flow rate at upstream station (from USGS data) = 0.12 m^3/s

$q_{mean,ds}$ = mean downstream flow rate (from modeled flow rates, see Figure 6.18) = 2.11 m^3/s

The residence times between the upstream and downstream bacterial monitoring stations (segment referred to as Aransas River Segment 2 in Section 6.3.3.2.2) were determined by applying the equation derived in Section 6.3.3.2.2, which relates residence time and flow rate (see Figure 6.13). This equation is repeated below for convenience.

$$\tau = -0.4374*\ln Q + 1.7584 \tag{6.5}$$

Where: τ = residence time (days)

Q = upstream or downstream flow rate (m^3/s)

The residence time was found for each day for both the corresponding upstream and downstream flow rates, and then the residence time was averaged. The residence time of the watershed was assumed to be 1.5 times longer than the residence time of the stream (Aransas River Segment 2).

The parameters and the assumptions for calculating the decay coefficient distribution are shown in Figure 6.7.

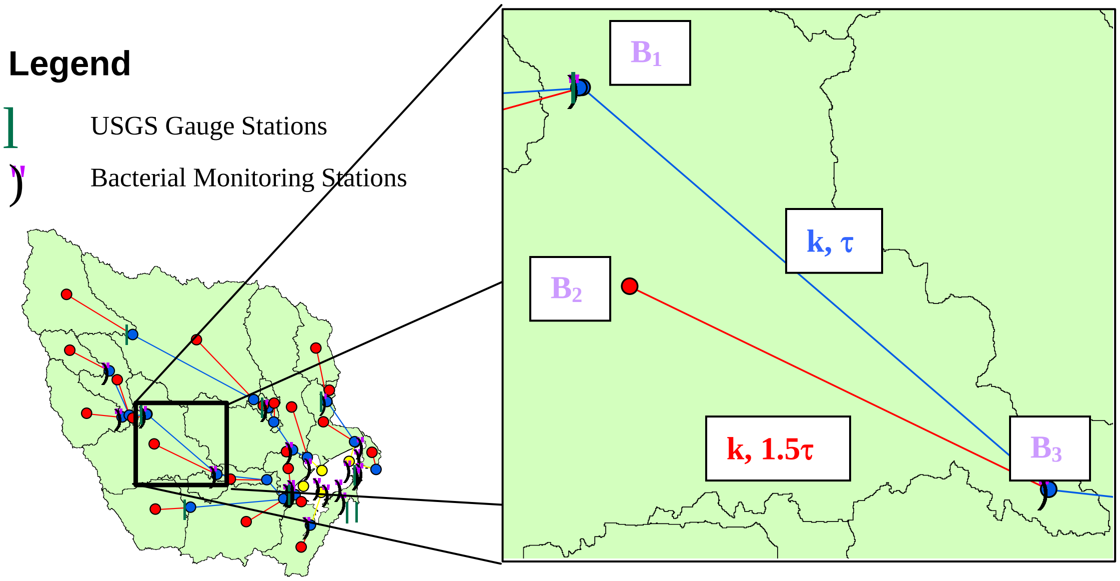


Figure 6.7 Assumptions and Derivation of k-distribution

In Figure 6.7, B_1 and B_3 are the bacterial loadings calculated from the measured fecal coliform concentrations and USGS flow data (Equation 6.3). B_2 is the bacterial loading for Watershed JunctionID 45408 that was calculated in Chapter 5 (3.07×10^{16} CFU/year). Thus, for all five days, B_2 remains constant. The decay coefficient was assumed to be constant for the Aransas River and the watershed travel due to lack of data availability. The relationships among the parameters/values, taking into account first-order decay, are shown below (Equation 6.6).

$$B_1 * \exp^{-k\tau} + B_2 * \exp^{-k(1.5\tau)} = B_3 \tag{6.6}$$

For each of the five days, all the values are known except for k, so k was calculated for each day; the results are given in Table 6.3.

Table 6.3 Calculation of Decay Coefficient for Segregated Model

Date	**B_1 (CFU/year)**	**B_2 (CFU/year)**	**B_3 (CFU/year)**	**τ (days)**	**1.5*τ (days)**	**k (days^{-1})**
7/8/2002	3.21E+14	3.07E+16	8.96E+15	1.05	1.57	0.80
10/15/2002	1.50E+12	3.07E+16	1.28E+14	1.86	2.79	1.96
1/21/2003	6.37E+12	3.07E+16	9.02E+13	1.69	2.53	2.30
4/22/2003	8.59E+12	3.07E+16	3.95E+13	1.81	2.72	2.44
8/18/2003	2.49E+12	3.07E+16	2.11E+13	2.00	3.01	2.42

The range of k values is from 0.80 to 2.42 days^{-1}, which are all in between the typical range of 0.5 to 3 days^{-1}. As can be inferred from the flow rate data in Table 6.2, calculation of the 7/8/2002 k value was based on a storm event. The other four k values are more similar to each other than to the first k value because the flow rates on 10/15/2002 – 8/18/2003 were more similar. From the calculated k-distribution, an average decay coefficient of k = 2 days^{-1} was used for all the SchemaNodes and SchemaLinks in the Schematic Processor Model.

6.3.3.2 Residence Time

One of the most critical input parameters in the model is the hydraulic residence time, τ, of the bacteria for each of the water segments. Residence time is the amount of time the bacteria remain in a specific water segment; thus, the residence time corresponds to the amount of time that the bacteria decay in a specific environment (e.g., watershed, river, or bay). Residence time can be calculated according to the following relationship:

$$\tau = V/Q \tag{6.7}$$

Where: V = volume of the water segment

Q = flow rate of the water segment

Before determining the volume and flow going through each water segments, 3d representations of each of the main river channels were created using Venkatesh Merwade's River Channel Morphology Model (RCMM) Toolbar (Merwade and Maidment, 2006), which is described in Section 6.3.3.2.1.

6.3.3.2.1 3d Channel Morphology (RCMM Toolbar)

Using the National Hydrography Dataset (NHD in high resolution), a mainstream network was created (shown in Figure 6.8) to generate 3d models of the main channels in HEC-RAS. Only the main channels were modeled due to data availability. Following is a list of the criteria used to determine which river segments are main channels:

- River segments that have "GNIS_Name", which is a field in the NHD feature class.
- River segments with streamflow greater than 30 cfs (based on Reach File, RF1).

- River segments that have a USGS gauge station measuring the streamflow.

Before the toolbar can be used, specific information and shapefiles are needed. The RCMM toolbar requires the NHD centerline of the river and at least two points on the river where the width, depth, and bank elevation are known. For this project, the width, depth, and bank elevation were determined at the USGS gauge station on each river segment, and other available sources were used to determine the most downstream river segment cross-section.

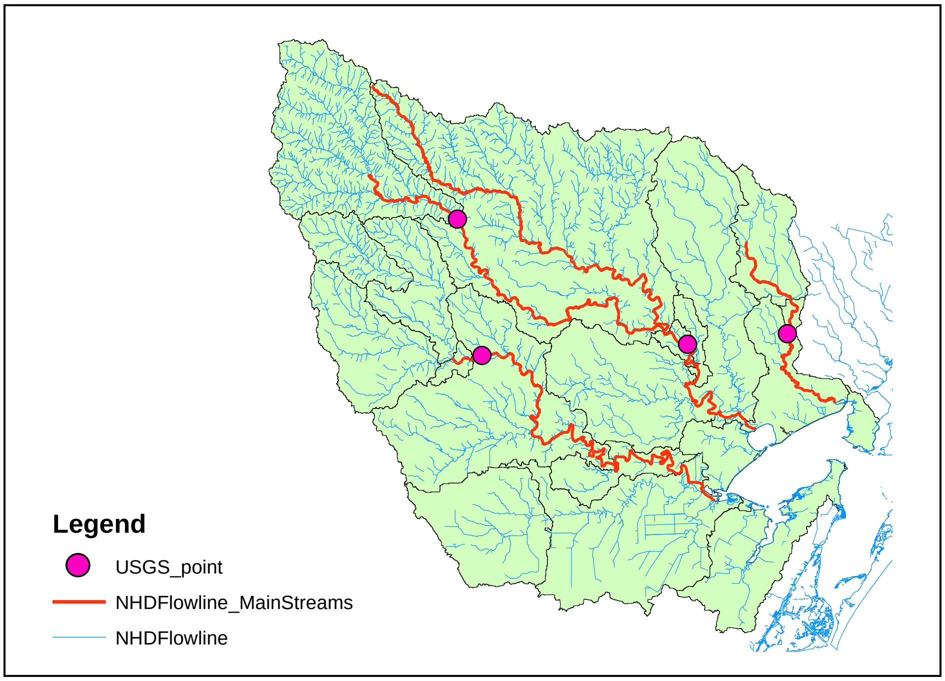


Figure 6.8 Mainsteam Network for RCMM

6.3.3.2.2 3d Model of Aransas River: Residence Time Determination

In order to find the cross-sectional area at the USGS gauge station, USGS gauge data (for USGS station 08189700) were downloaded from the USGS website from

"Surface-Water Measurements", which includes width, area, and stream flow measurements. The flow and width were then plotted for all the data available from 1987 to 2005 (Figure 6.9**)**.

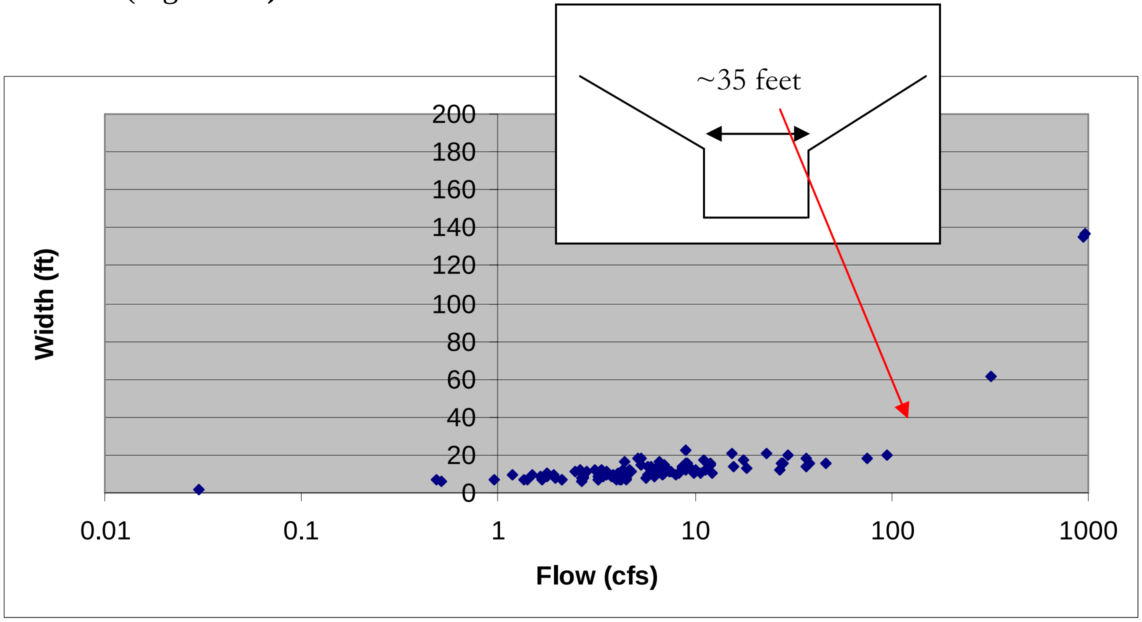


Figure 6.9 Flow versus Width for USGS Station 08189700

The width of the channel was approximated to be 35 feet, which is the width of the channel before the width dramatically increases at higher flowrates. The channel was assumed to have a square cross-section; thus, the depth can be calculated for each USGS measurement by dividing the measured area by the measured width for each stream flow. The depth and width of the channel were plotted for all available measurements in Figure 6.10, and a best-fit line was determined. The best-fit line was then used to find the depth at the width of 35 feet. Hence, the depth at USGS gauge station 08189700 was estimated to be 1.24 feet.

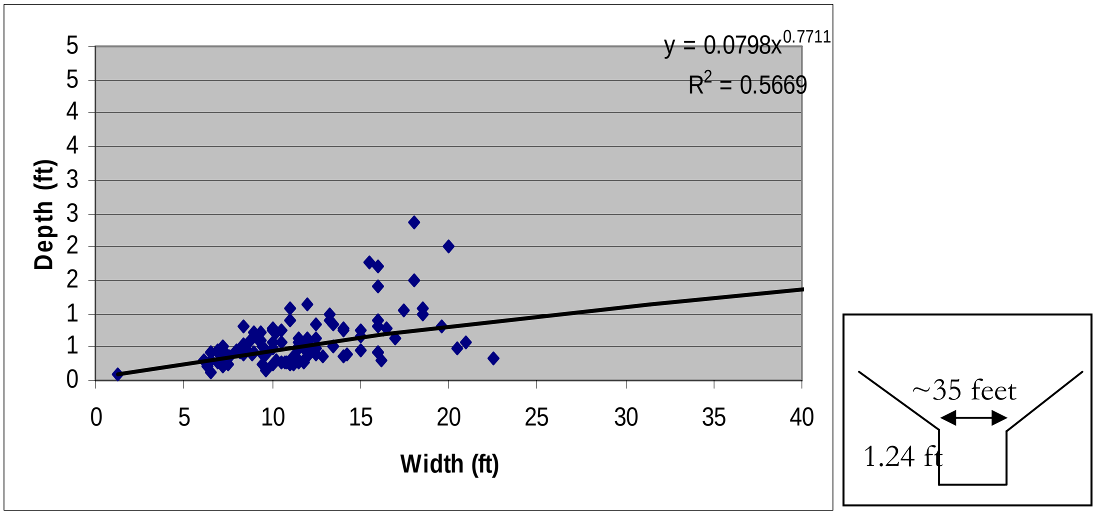


Figure 6.10 Width versus Depth (Square Cross-Section) for USGS Station 08189700

The bank elevation is given for the USGS gauge station on the USGS website in “Surface-Water Measurements”, and is 72.37 feet above sea level for Station 08189700.

Because there is only one USGS gauge station along the Aransas River, other sources were used to estimate the cross-section at the most downstream point of the Aransas River. The other sources that were used were aerial photographs and the Reach File (RF1) Database. First, the sources were compared to the USGS approximation at the USGS gauge station location to see the percent difference (Table 6.4).

Table 6.4 Upstream Cross-Section Data Comparison (Aransas River; USGS 08189700)

			Percent Error (%)	
	Width (ft)	**Depth (ft)**	**Width**	**Depth**
RF1	17.77	0.44	49.22	64.46
Aerial	31.00	-	11.42	-
USGS/RCMM Input	35.00	1.24	-	-

The aerial photograph seems to be closest to the USGS approximation for width (as shown in Table 6.4). The RF1 file is the only known data source to approximate depth since the available bathymetric maps do not cover the rivers in the Copano Bay watershed. The downstream dimensions using the available sources are given in Table 6.5.

Table 6.5 Downstream Cross-Section Data (Aransas River)

	Width (ft)	Depth (ft)
RF1	39.54	0.71
Aerial	205.38	-

The width of the channel was approximated (taking into account the 11.42% error) to be 184.33 feet while the depth was approximated (taking into account the 64.46% error) to be 2.00 feet, which seems too low since this location is at the discharge point into Copano Bay. Thus, using the same width-to-depth ratio that exists at the USGS gauge station, the depth was approximated to be 6.52 feet. The bank elevation at the most downstream point was determined using the Digital Elevation Model (DEM). A summary of all the data that are needed for the RCMM toolbar is shown in Figure 6.11.

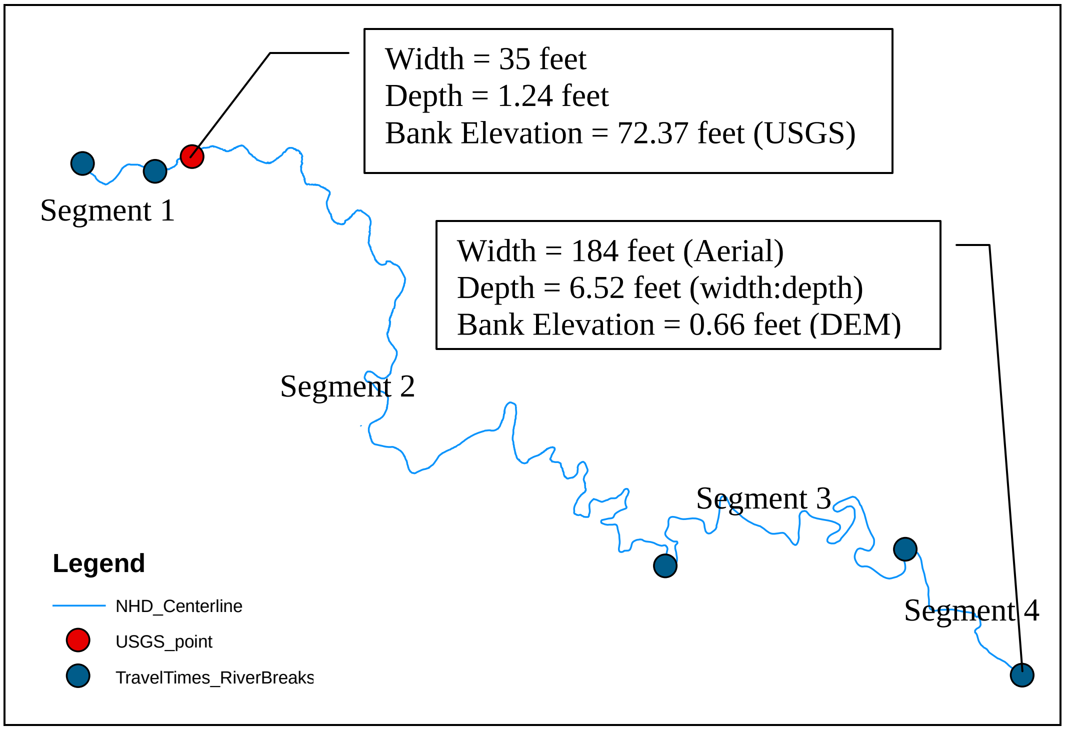


Figure 6.11 Summary of RCMM Toolbar Data Requirements (Aransas River)

After obtaining the NHD centerline feature class, USGS gauge station feature class, and the cross-section dimensions at two points, Merwade's RCMM toolbar was used to generate a 3d model of the Aransas River (Merwade and Maidment, 2006). However, the river was divided into four 3d segments (shown in Figure 6.11) because the residence time was needed for each of these four segments. The division of these segments was based on the watershed delineations. Each of the points represents when the river crosses a watershed; the watersheds and Schematic Network were based on Critical Points: USGS gauge stations, bacterial monitoring stations, and water segment endpoints.

Using the 3d Aransas River model (HEC-RAS), a relationship was found between residence time and flow rate for each of the four segments (Figure 6.11). The relationships between residence time and flow rate are shown in Figures 6.12 - 6.15.

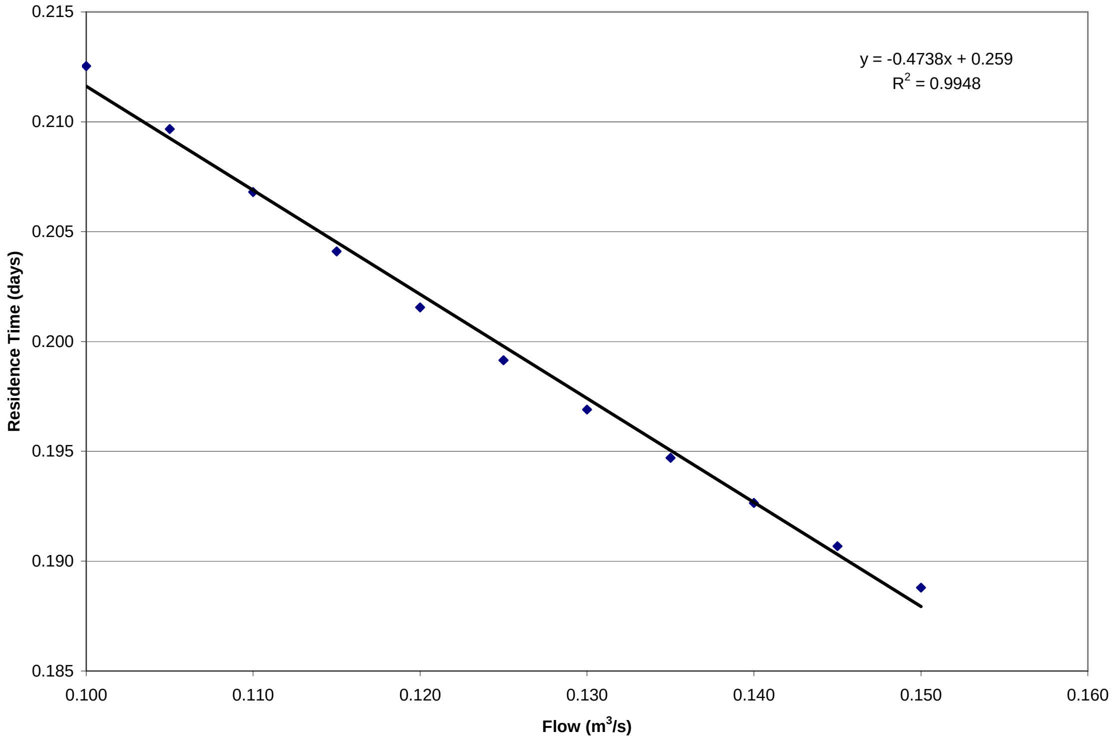


Figure 6.12 Flow versus Residence Time for Aransas River Segment 1

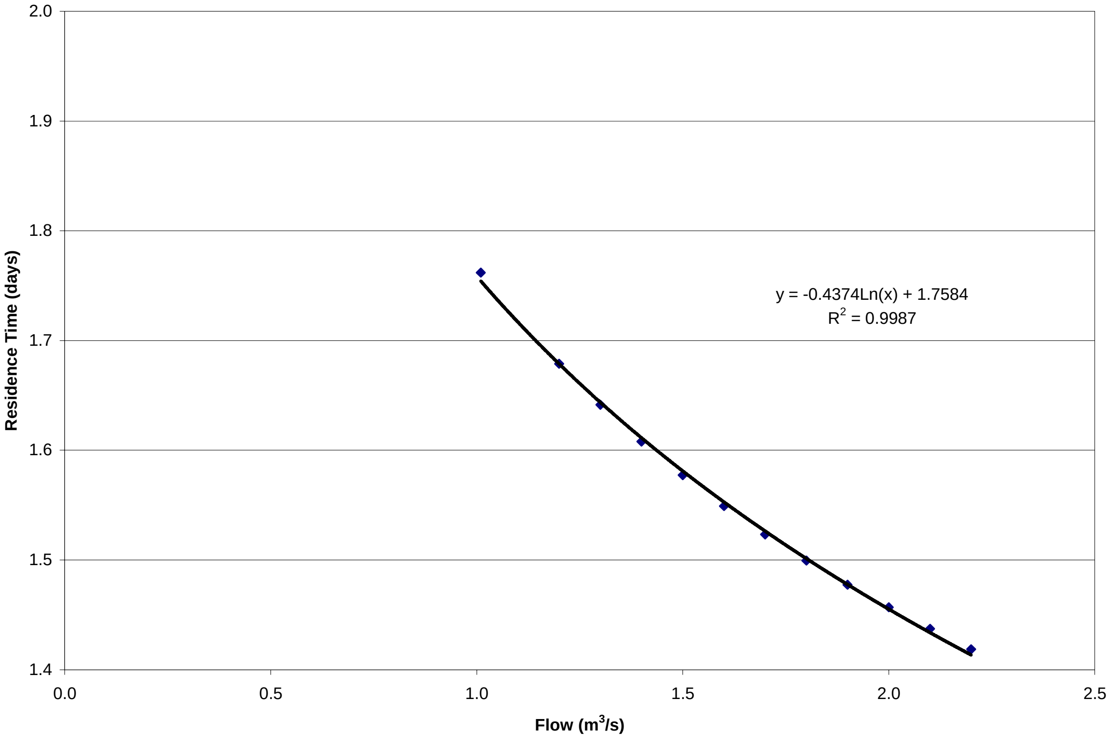


Figure 6.13 Flow versus Residence Time for Aransas River Segment 2

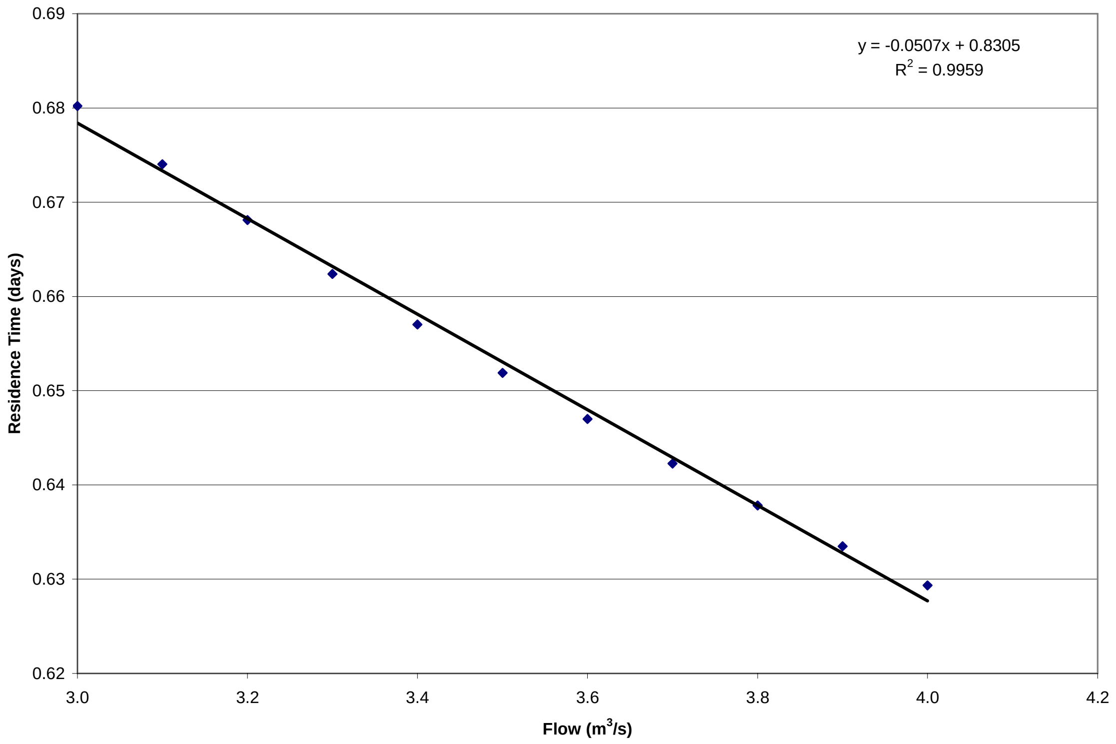


Figure 6.14 Flow versus Residence Time for Aransas River Segment 3

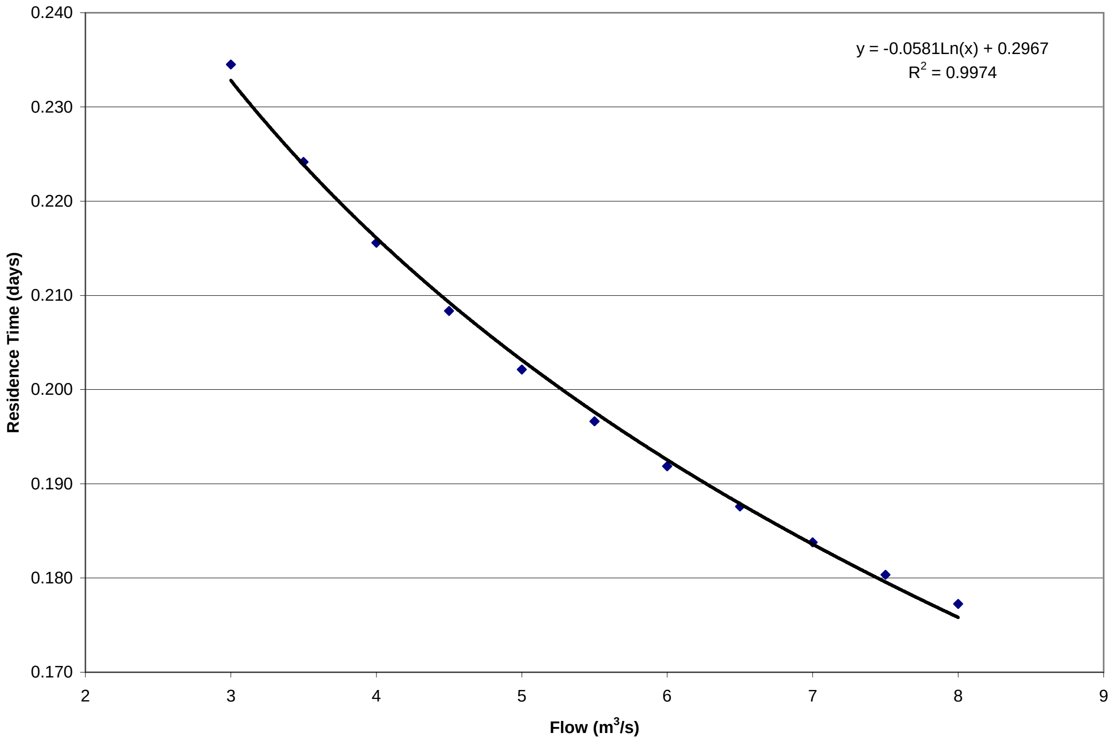


Figure 6.15 Flow versus Residence Time for Aransas River Segment 4

A flow cumulative distribution function (CDF) plot was created for each segment. The flow CDF was based on USGS gauge daily mean streamflow data (from 1964-2004). USGS gauge station 08189700 is on Aransas River Segment 1, so a flow CDF was found directly for Segment 1. The flow CDF for Segment 1 is shown in Figure 6.16.

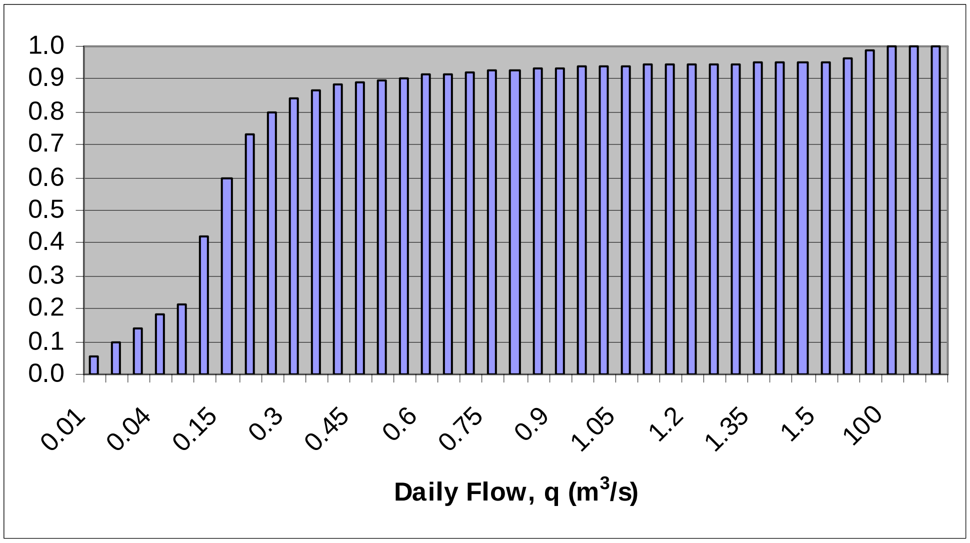


Figure 6.16 Flow Cumulative Distribution Function for Aransas River Segment 1

Because there is only one USGS gauge station on the Aransas River, the flow CDF of Segment 1 was used to find the flow CDF for Segments 2, 3, and 4. The median flow for Segment 1 was determined by finding the flow when the flow CDF equals 0.5, which is approximately 0.12 m^3/s (see Figure 6.16.) A dimensionless CDF was then found for Segment 1 by dividing the flow by the median flow (Figure 6.17).

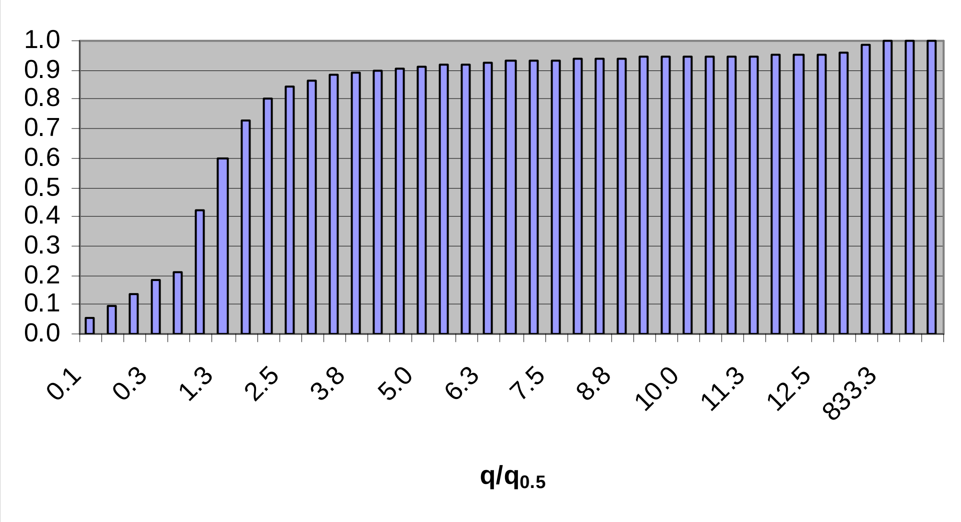


Figure 6.17 Cumulative Distribution Function, $q/q_{0.5}$ for Segment 1

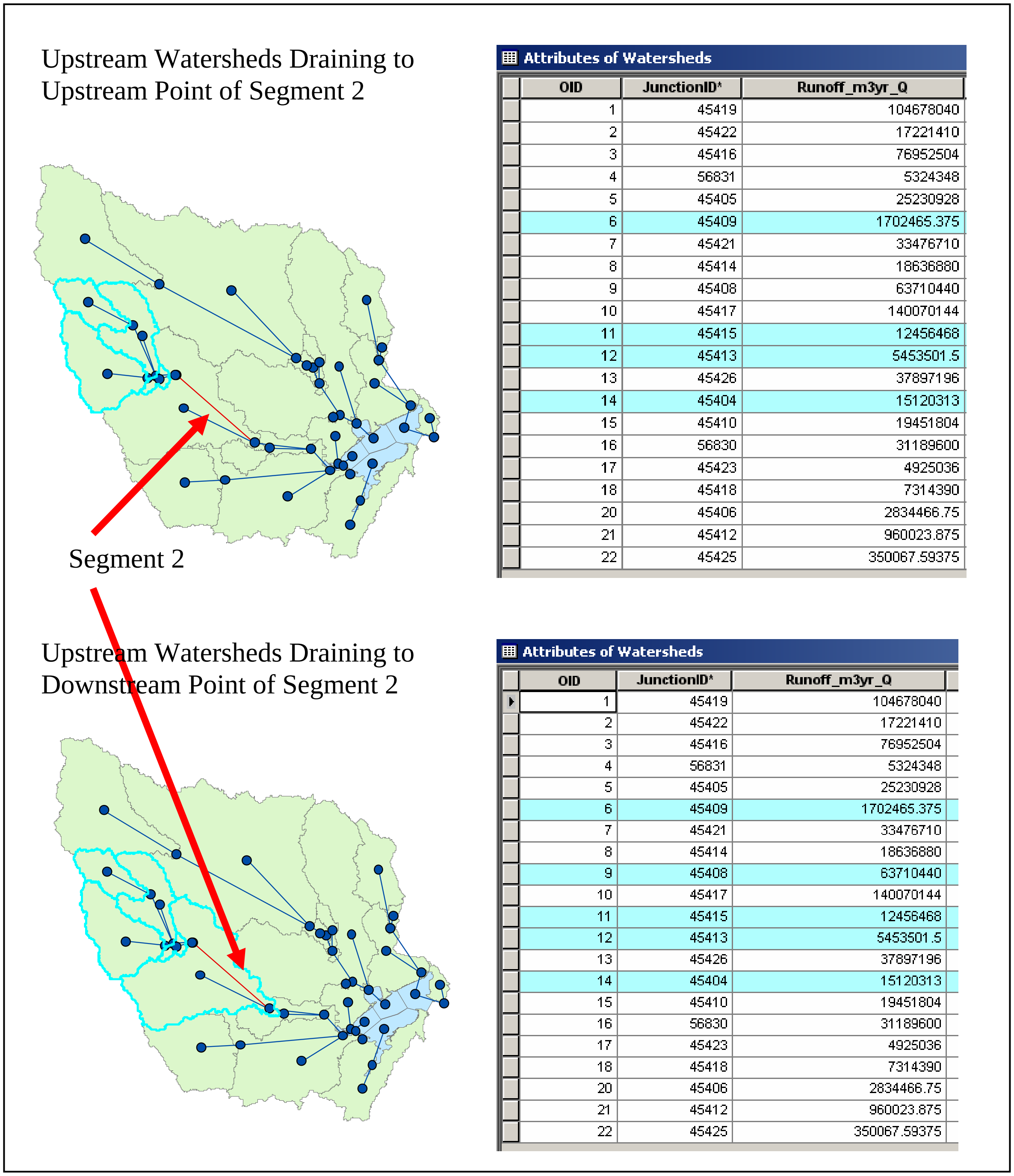
The flows for Segments 2, 3, and 4 were determined according to the following relationship:

$$q = (q/q_{0.5}) * q_{mean} \tag{6.8}$$

Where: $(q/q_{0.5})$ = dimensionless value obtained from Segment 1

q_{mean} = mean flow of Segments 2, 3, or 4 from water quality model

Each watershed has an annual mean flow that was calculated using the runoff equations derived by Quenzer (2003), which are given in Section 5.1.2.4. The mean flow was calculated by averaging the cumulative flow at the upstream point of the segment (the sum of flow of all upstream watersheds) and the cumulative flow at the downstream point of the segment. The mean flow to Aransas River Segment 2 was calculated and is shown in Figure 6.18.



Attributes of Watersheds

OID	JunctionID*	Runoff_m3yr_Q
1	45419	104678040
2	45422	17221410
3	45416	76952504
4	56831	5324348
5	45405	25230928
6	45409	1702465.375
7	45421	33476710
8	45414	18636880
9	45408	63710440
10	45417	140070144
11	45415	12456468
12	45413	5453501.5
13	45426	37897196
14	45404	15120313
15	45410	19451804
16	56830	31189600
17	45423	4925036
18	45418	7314390
20	45406	2834466.75
21	45412	960023.875
22	45425	350067.59375

Attributes of Watersheds

OID	JunctionID*	Runoff_m3yr_Q
1	45419	104678040
2	45422	17221410
3	45416	76952504
4	56831	5324348
5	45405	25230928
6	45409	1702465.375
7	45421	33476710
8	45414	18636880
9	45408	63710440
10	45417	140070144
11	45415	12456468
12	45413	5453501.5
13	45426	37897196
14	45404	15120313
15	45410	19451804
16	56830	31189600
17	45423	4925036
18	45418	7314390
20	45406	2834466.75
21	45412	960023.875
22	45425	350067.59375

Figure 6.18 Calculating Mean Flow to Aransas River Segment 2

After finding the mean flow for each segment, the flow CDF was calculated for each segment by using the relationship in Equation 6.8. The results for Segments 2, 3, and 4 are shown in Figures 6.19 - 6.21.

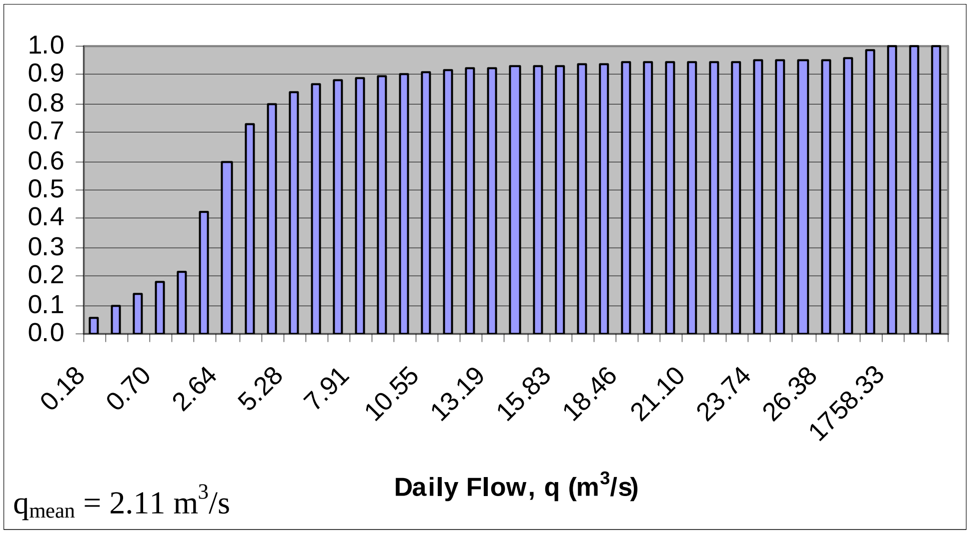


Figure 6.19 Flow Cumulative Distribution Function for Aransas River Segment 2

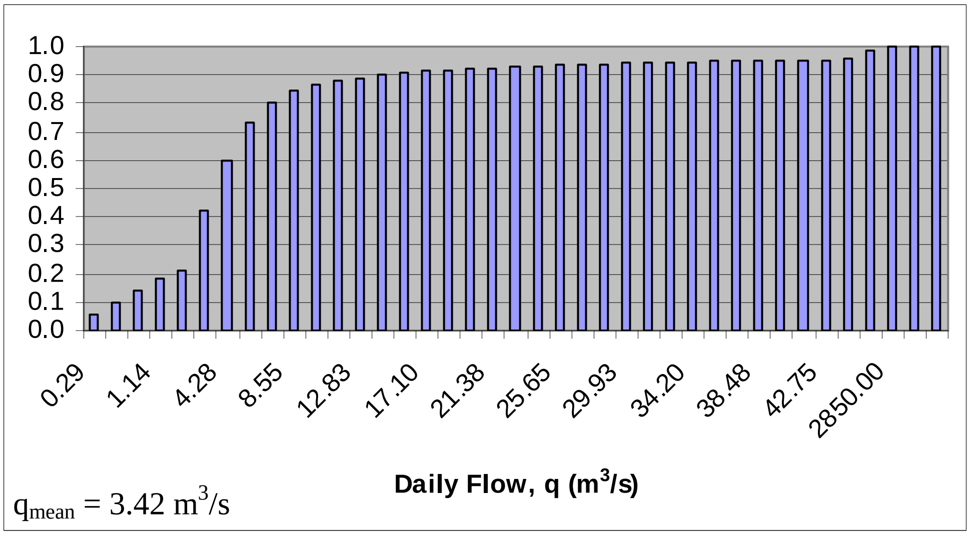
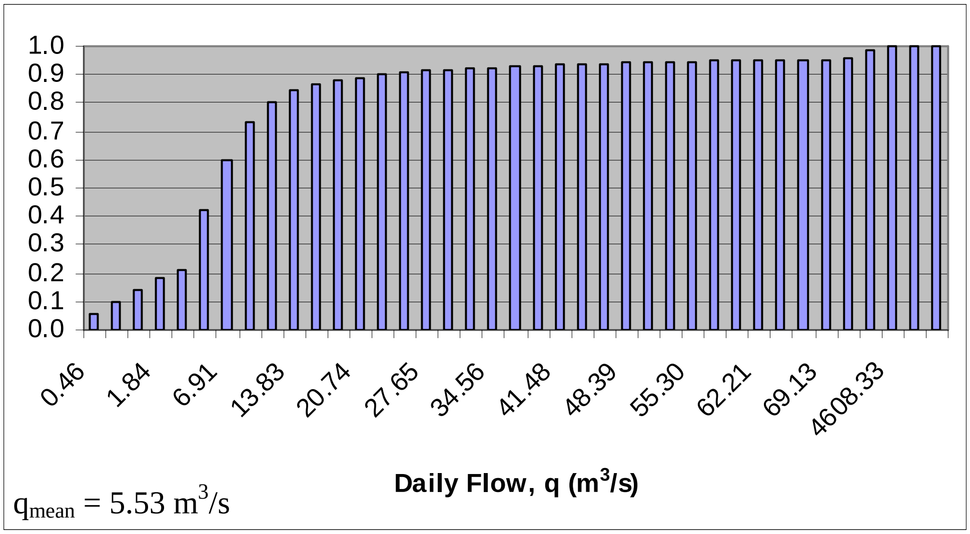


Figure 6.20 Flow Cumulative Distribution Function for Aransas River Segment 3



$q_{mean} = 5.53\ m^3/s$

Figure 6.21 Flow Cumulative Distribution Function for Aransas River Segment 4

Once the flow CDF was found for the four segments, the Residence Time Distribution (RTD) was determined for each segment using the relationships between residence time and flow that are shown in Figures 6.12 - 6.15. The RTD for Segments 1, 2, 3, and 4 are shown in Figures 6.22 - 6.25.

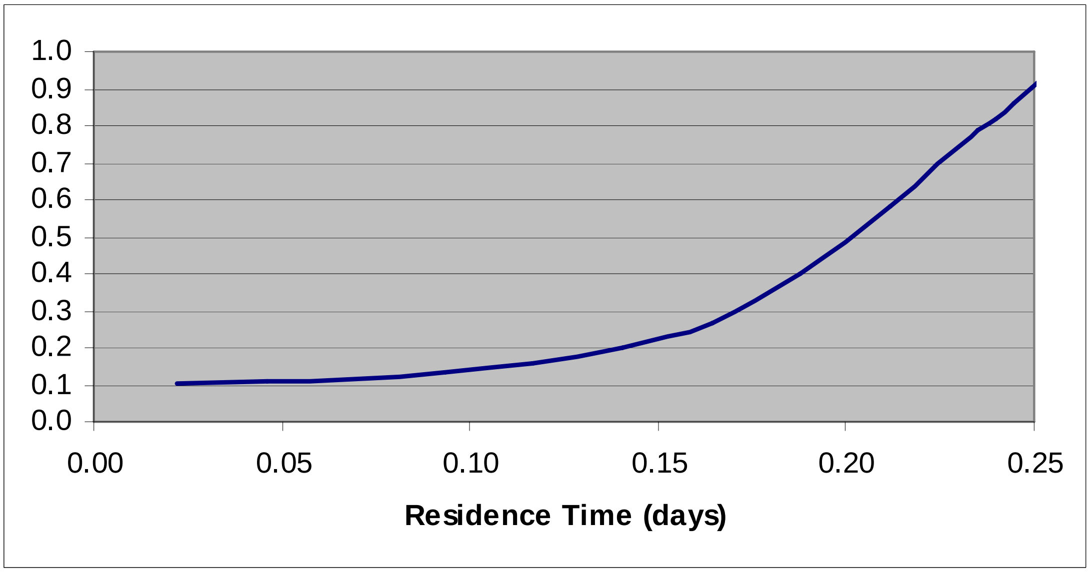


Figure 6.22 Residence Time Distribution for Aransas River Segment 1

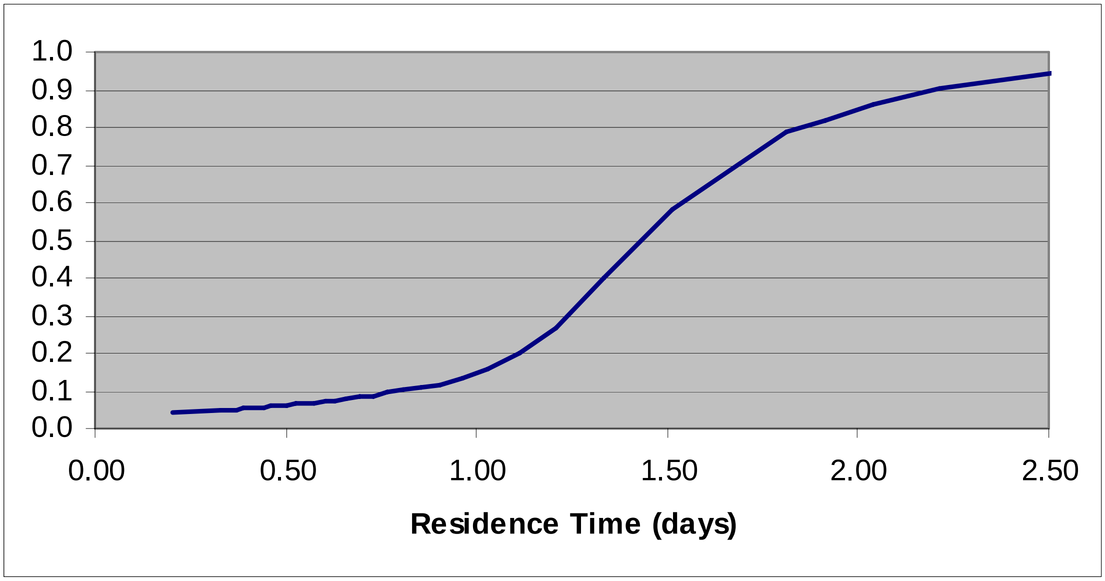


Figure 6.23 Residence Time Distribution for Aransas River Segment 2

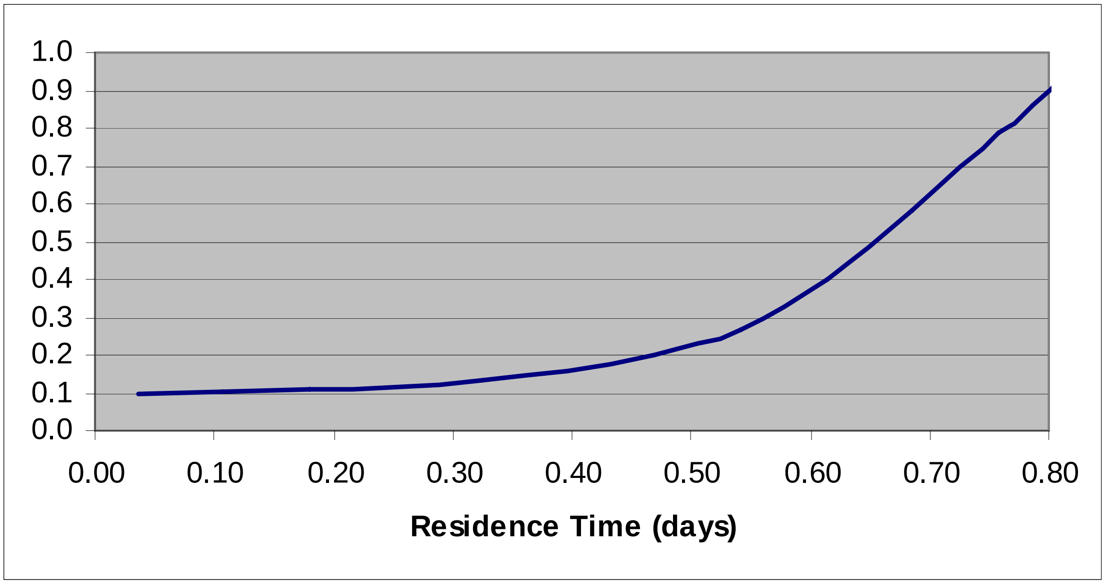


Figure 6.24 Residence Time Distribution for Aransas River Segment 3

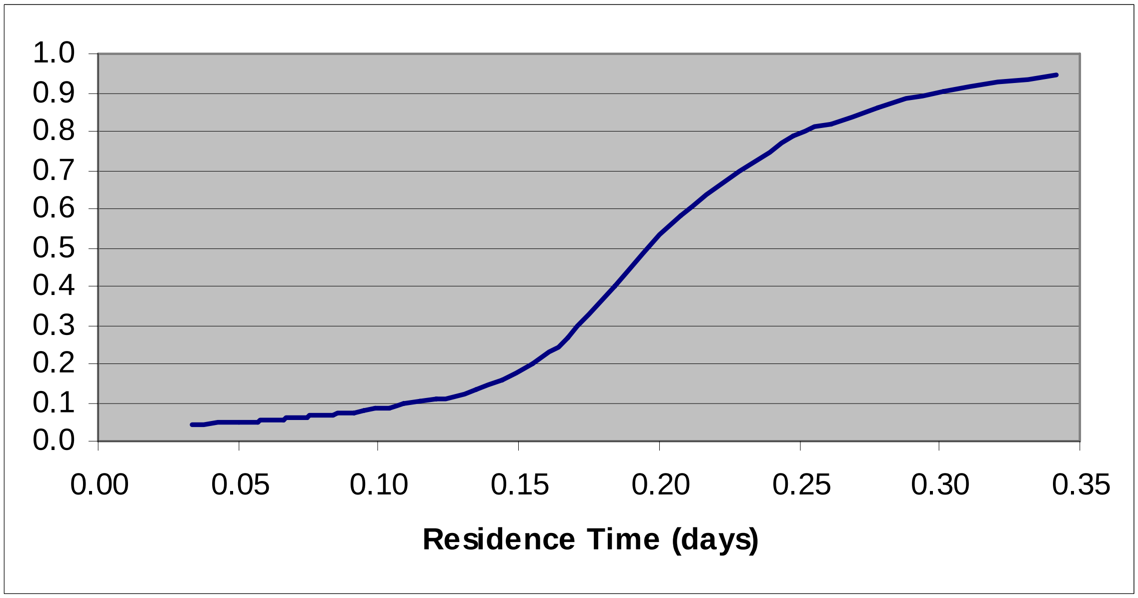


Figure 6.25 Residence Time Distribution for Aransas River Segment 4

The probability distributions were also found for the residence times of all the segments along the Aransas River and are shown in Figures 6.26 - 6.29.

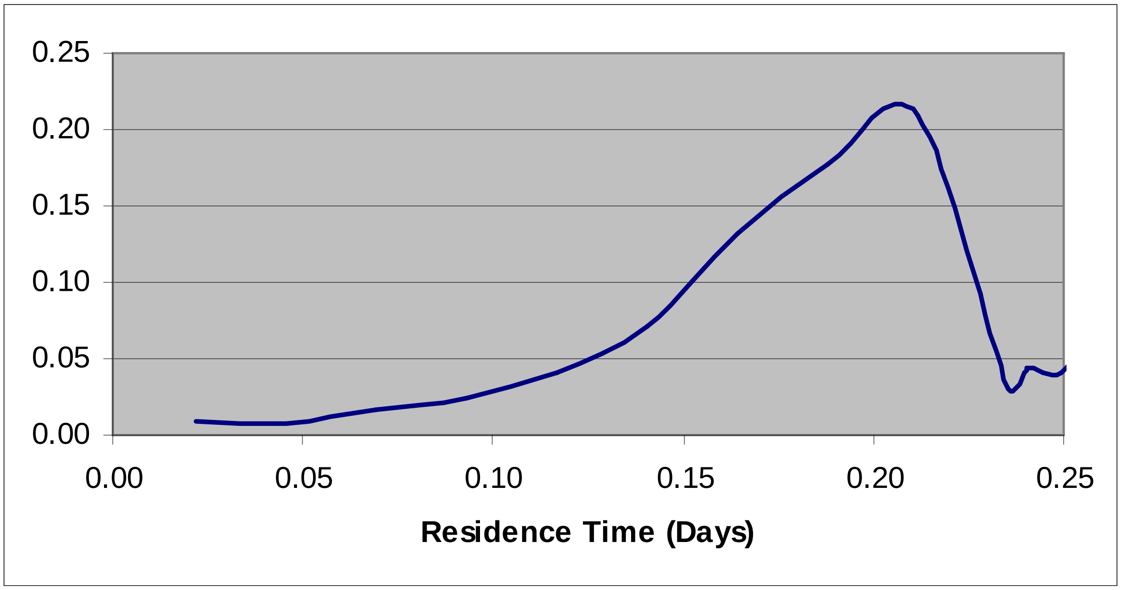


Figure 6.26 Probability Distribution of Residence Time for Aransas River Segment 1

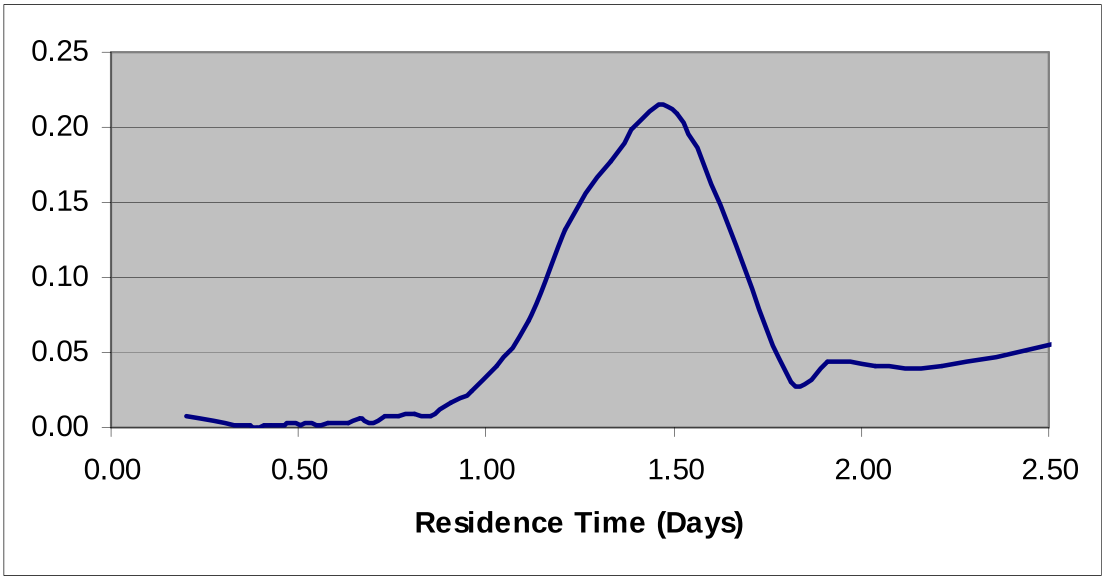


Figure 6.27 Probability Distribution of Residence Time for Aransas River Segment 2

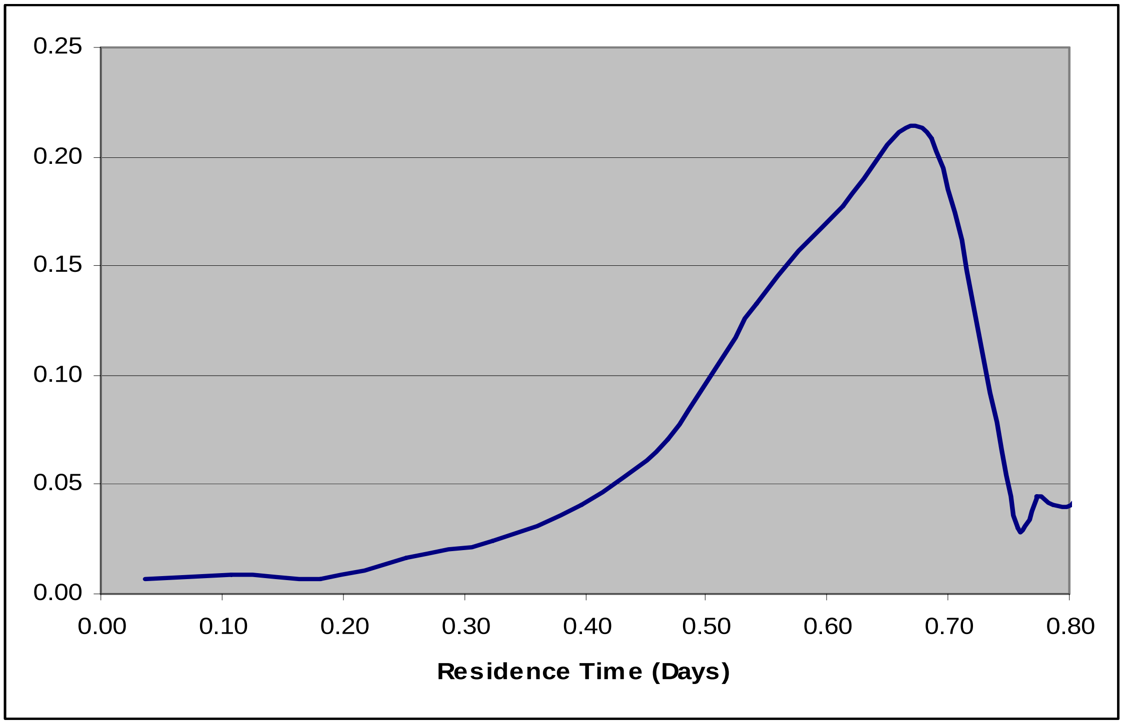


Figure 6.28 Probability Distribution of Residence Time for Aransas River Segment 3

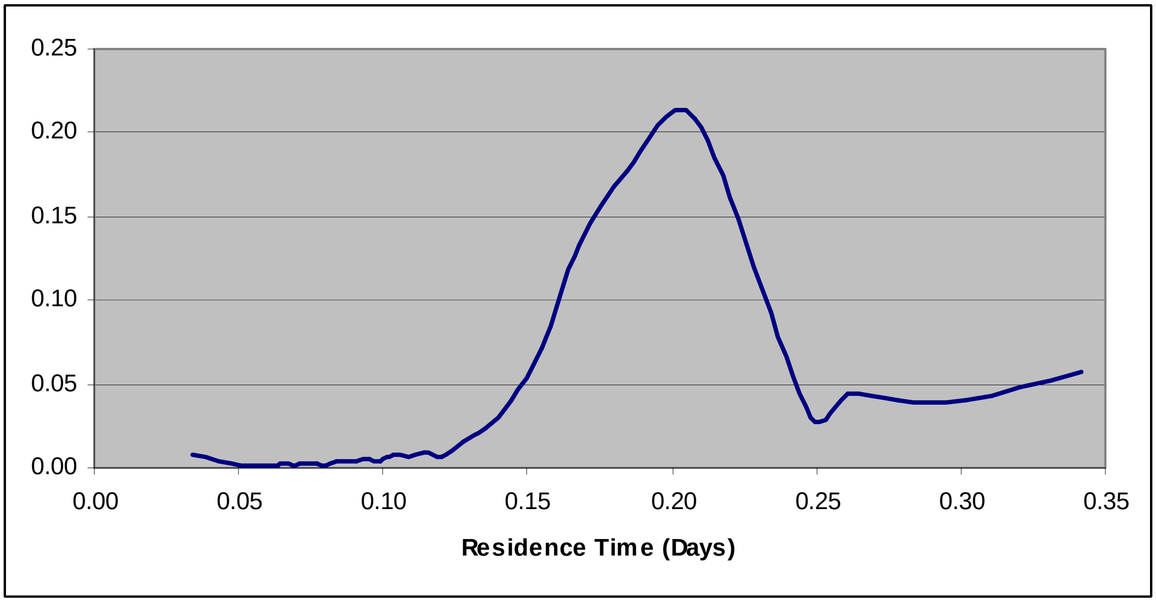


Figure 6.29 Probability Distribution of Residence Time for Aransas River Segment 4

The RTDs were used as approximations for the corresponding SchemaLinks' residence times in the Schematic Processor Model. Aransas River Segments 1, 2, 3, and 4 correspond to SchemaLink HydroIDs 113, 120, 107, 112, respectively, which are shown in Figure 6.30. For this Schematic Processor Model, the most frequent residence time (from the probability and residence time distributions) is the residence time associated with the corresponding SchemaLinks, and these residence times are given in Table 6.6.

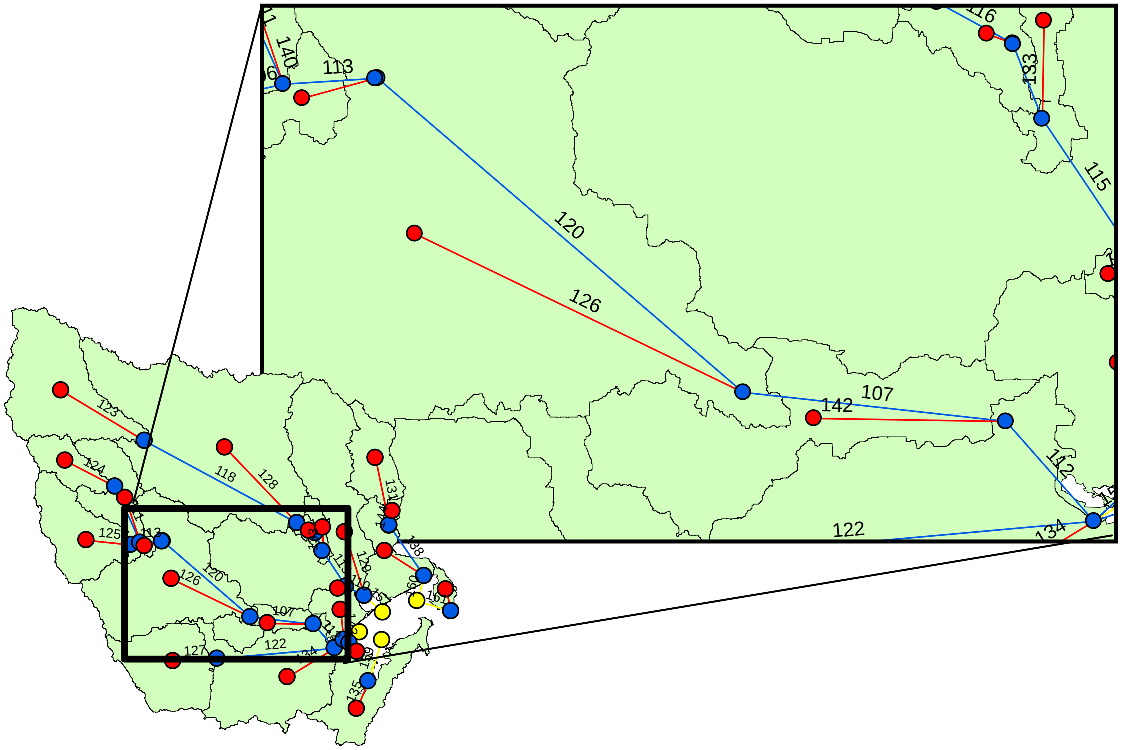


Figure 6.30 SchemaLinks of Corresponding Aransas River Segments

Table 6.6 Residence Times of Aransas River Segments for Schematic Processor Model

Aransas River Segment	SchemaLink HydroID	Residence Time (days)
1	113	0.212
2	120	1.51
3	107	0.686
4	112	0.208

6.3.3.2.3 3d Model of Mission River: Residence Time Determination

The two USGS gauge stations along the Mission River were used to create a 3d model of Mission River in HEC-RAS (USGS gauge stations 08189300 and 08189500). The same methodology that was used to find the RTD of the Aransas River segments was used.

To find the cross-sectional dimensions at the USGS gauge station, USGS gauge data (for USGS stations 08189300 and 08189500) were downloaded from the USGS website from “Surface-Water Measurements”, which includes width, area, and stream flow measurements. The flow and width were then plotted for all available data (Figures 6.31 and 6.32). “Surface-Water Measurements” were available from 2001-2005 for USGS 08189300 and from 1971-2005 for USGS 08189500.

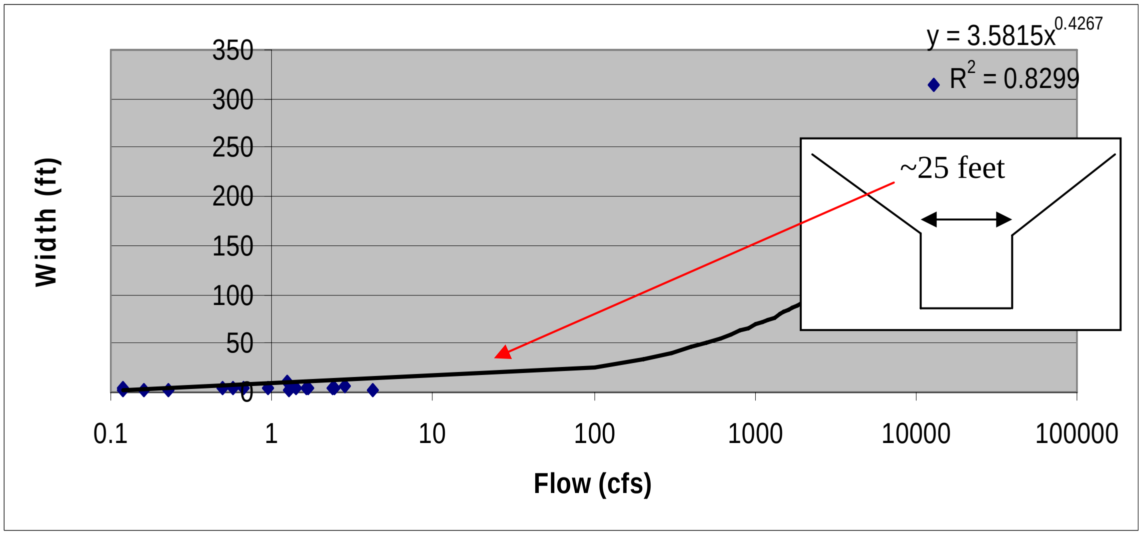


Figure 6.31 Flow versus Width for USGS Station 08189300

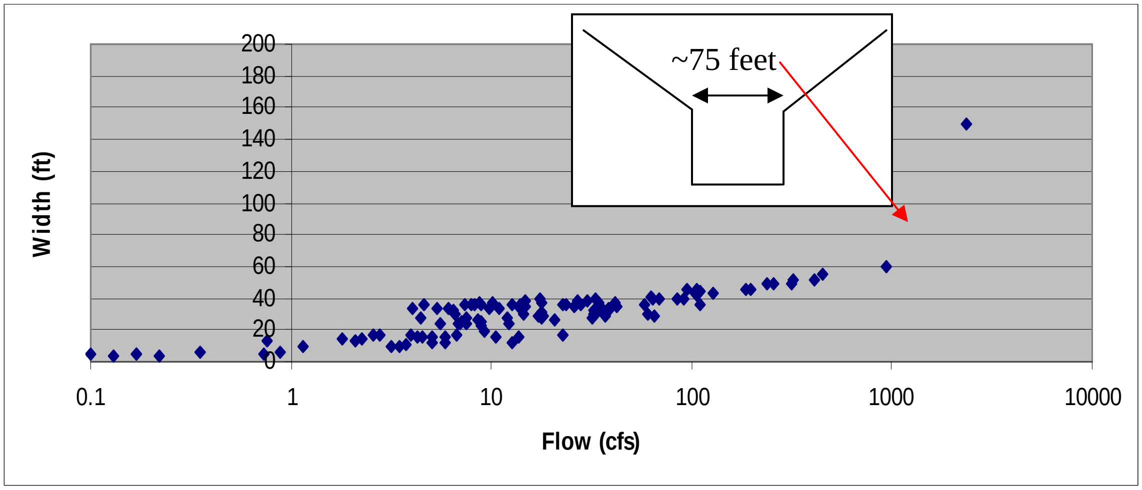


Figure 6.32 Flow versus Width for USGS Station 08189500

The width of the channel at USGS gauge station 08189300 (on Medio Creek), Figure 6.31, was approximated to be 25 feet. The width of the channel at USGS gauge station 08189500 (on Mission River), Figure 6.32, was approximated to be 75 feet. The channels were assumed to have square cross-sections; thus, the depth was calculated for each USGS measurement by dividing the measured area by the measured width for each stream flow. The depth and width of each channel were then plotted for all available measurements in Figures 6.33 and 6.34. The best-fit line (given in Figure 6.33) was used to find the depth in Medio Creek at the width of 25 feet. The approximate depth at USGS gauge station 08189300 is 1.69 feet. Similarly, using the data in Figure 6.34, the depth at USGS gauge station 08189500 at a width of 75 feet was approximated to be 8.20 feet.

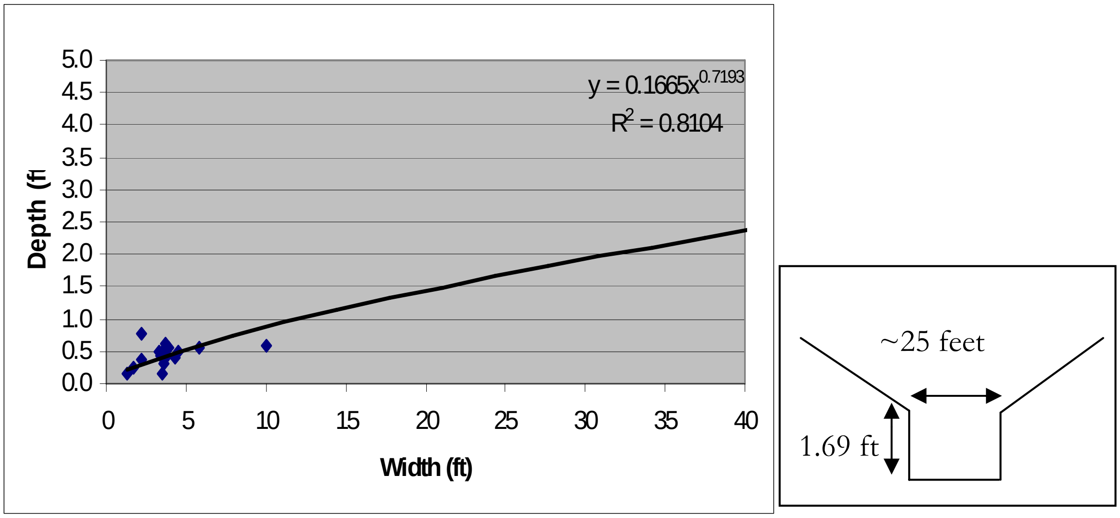


Figure 6.33 Width versus Depth (Square Cross-Section) for USGS Station 08189300

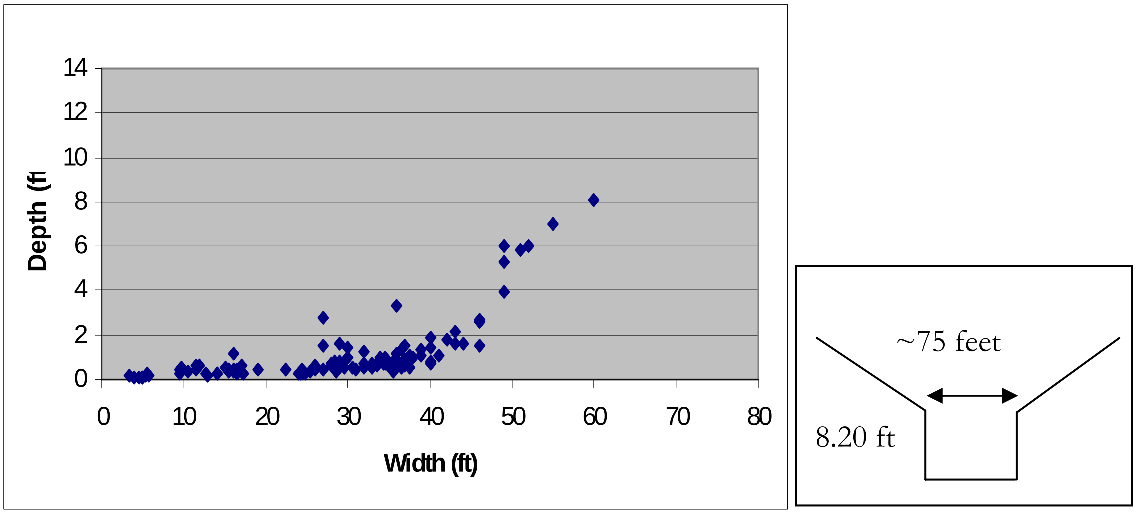


Figure 6.34 Width versus Depth (Square Cross-Section) for USGS Station 08189500

The bank elevations are given for USGS gauge stations on the USGS website (in “Surface-Water Measurements”) and are 163.00 feet above sea level for USGS 08189300 and 1.00 feet above sea level for USGS 08189500.

Because there is only one USGS gauge station along Medio Creek, other sources were used to estimate the cross-section at the most downstream point of Medio Creek where it drains into Mission River. The other sources that were used were aerial photographs and the RF1 Database. First, the sources were compared to the USGS approximation at the USGS gauge station location to see the percent difference. The percentage differences are shown below in Table 6.7.

Table 6.7 Upstream Cross-Section Data Comparison (Medio Creek; USGS 08189300)

			Percent Error (%)	
	Width (ft)	**Depth (ft)**	**Width**	**Depth**
RF1	14.96	0.13	40.16	92.24
Aerial	21.03	-	15.88	-
USGS/RCMM Input	25.00	1.69	-	-

The aerial photograph is closer to the USGS approximation for width (Table 6.7); and the RF1 file is the only known data source to approximate depth because the available bathymetric maps do not cover the rivers in the Copano Bay watershed. The downstream dimensions using the available sources are shown in Table 6.8.

Table 6.8 Downstream Cross-Section Data (Medio Creek)

	Width (ft)	Depth (ft)
RF1	13.77	0.12
Aerial	22.97	-

The width of the channel was approximated (taking into account the 15.88% error) to be 27.30 feet while the depth was rounded up to 2.00 feet (taking into account the 92.24% error and in order to keep the depth deeper than the upstream depth). The bank elevation at the most downstream point was determined using the DEM. A summary of all the data needed for the RCMM toolbar for Medio Creek is shown in Figure 6.35.

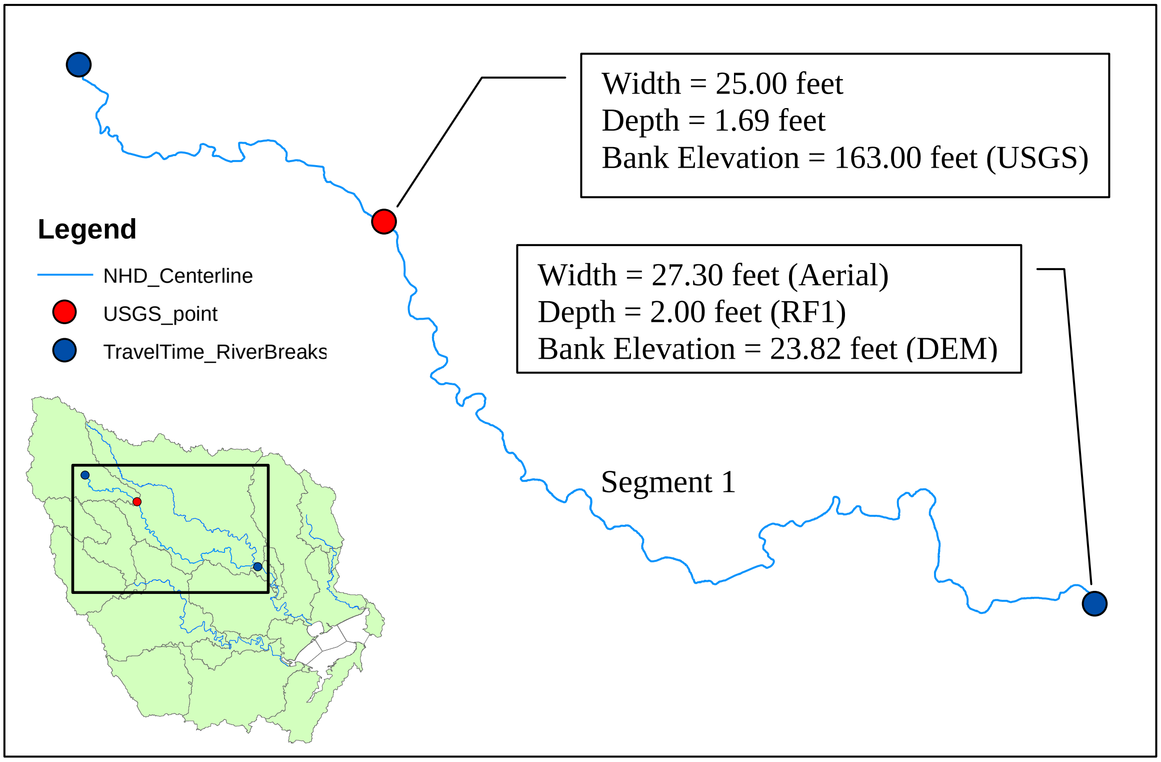


Figure 6.35 Summary of RCMM Toolbar Data Requirements (Medio Creek)

The cross-section at the most downstream point of Mission River, where it drains into Copano Bay, is determined using the same methodology as for Aransas River and Medio Creek. The other sources that were used were aerial photographs and the RF1 Database. First, the sources were compared to the USGS approximation at the USGS gauge station location to see the percentage difference. The percentage differences are shown below in Table 6.9.

Table 6.9 Upstream Cross-Section Data Comparison (Mission River; USGS 08189500)

			Percent Error (%)	
	Width (ft)	**Depth (ft)**	**Width**	**Depth**
RF1	35.59	0.26	52.54	96.86
Aerial	32.81	-	56.26	-
USGS/RCMM Input	75.00	8.20	-	-

The RF1 file seems is closer to the USGS approximation for width (Table 6.9); and the RF1 file is the only known data source to approximate depth because the available bathymetric maps do not cover the rivers in the Copano Bay watershed. The downstream dimensions using the available sources are shown in Table 6.10.

Table 6.10 Downstream Cross-Section Data (Mission River)

	Width (ft)	**Depth (ft)**
RF1	60.57	0.37
Aerial	125.66	-

The width of the channel was approximated (taking into account the 52.54% error) to be 264.76 feet while the depth (taking into account the 56.26% error) was 11.83 feet. The bank elevation at the most downstream point was determined using the DEM. A summary of all the data needed for the RCMM toolbar for Mission River is shown in Figure 6.36.

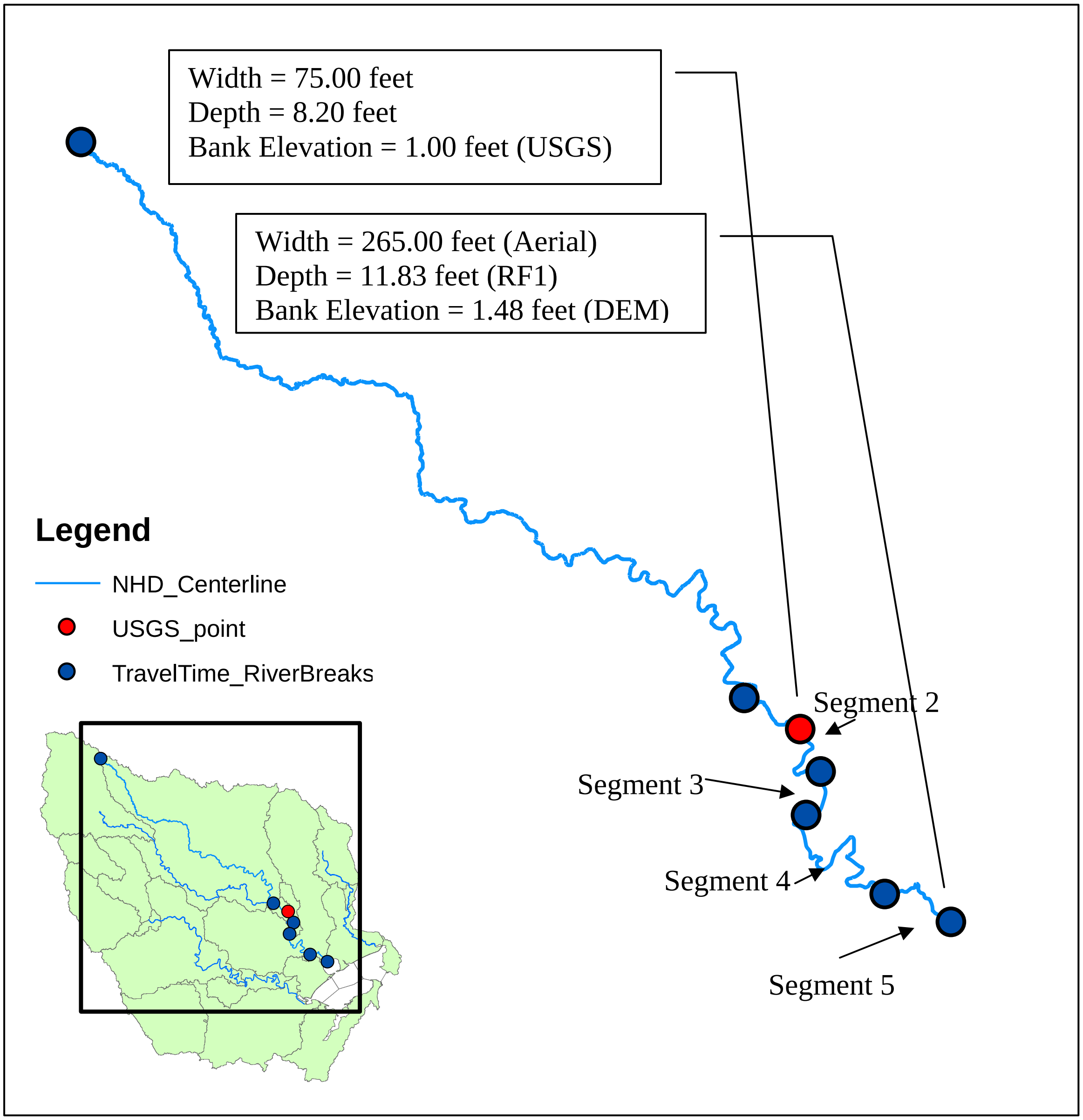


Figure 6.36 Summary of RCMM Toolbar Data Requirements (Mission River)

After obtaining the NHD centerline feature class, USGS gauge station feature class, and the cross-section dimensions at two points, Merwade’s RCMM toolbar was used to generate 3d models of Medio Creek and Mission River. Medio Creek was made into one 3d segment (Figure 6.35), and Mission River was divided into four 3d segments (Figure 6.36) because the residence time for each of these five segments was needed.

Using the 3d Medio Creek and Mission River models (HEC-RAS), a relationship was found between residence time and flow rate for each of the segments. The relationships between residence time and flow rate for Medio Creek and Mission River are shown in Figures 6.37 - 6.41.

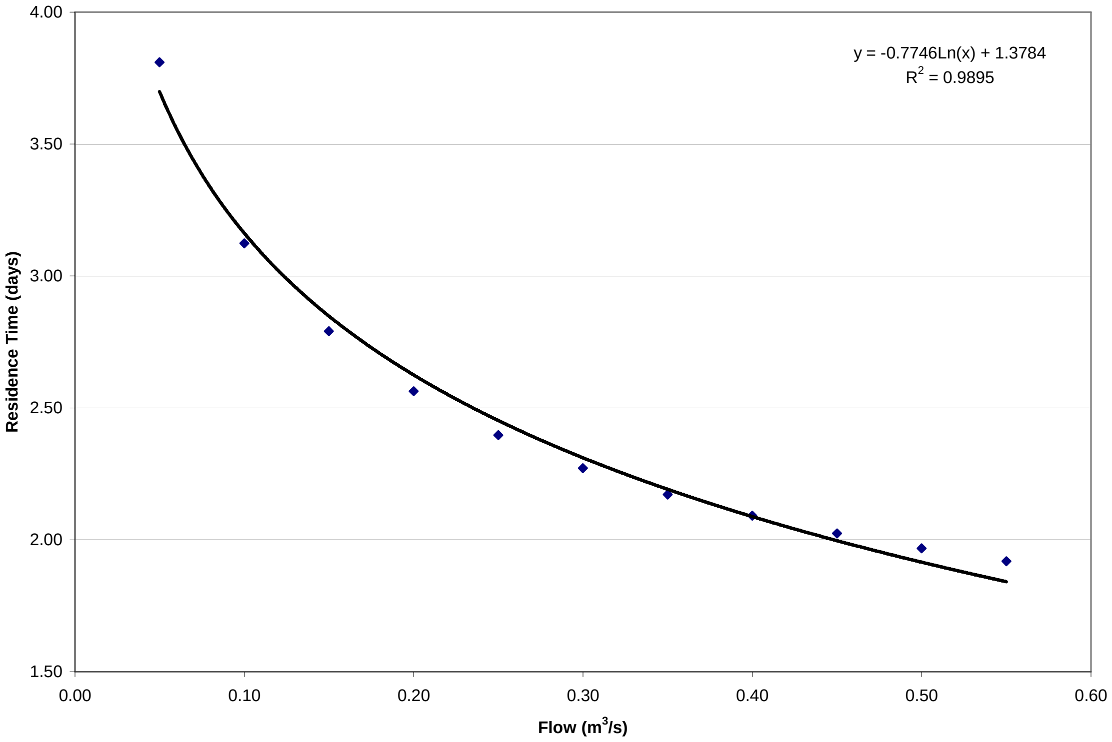


Figure 6.37 Flow versus Residence Time for Medio Creek Segment 1

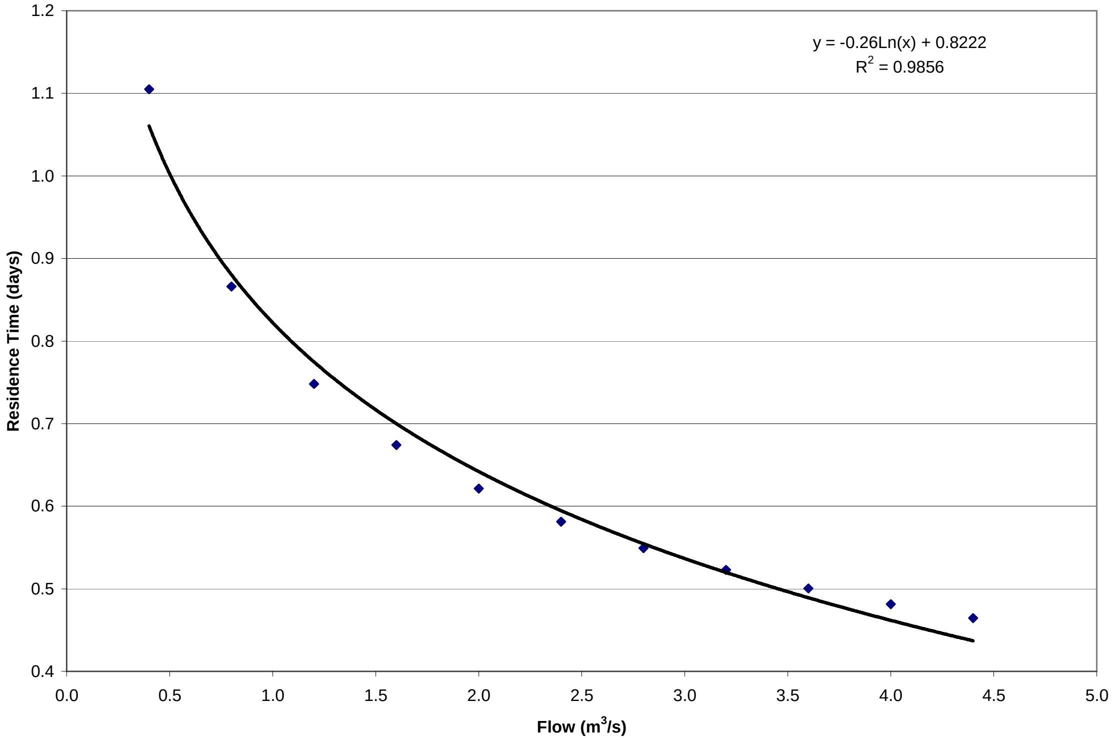


Figure 6.38 Flow versus Residence Time for Mission River Segment 2

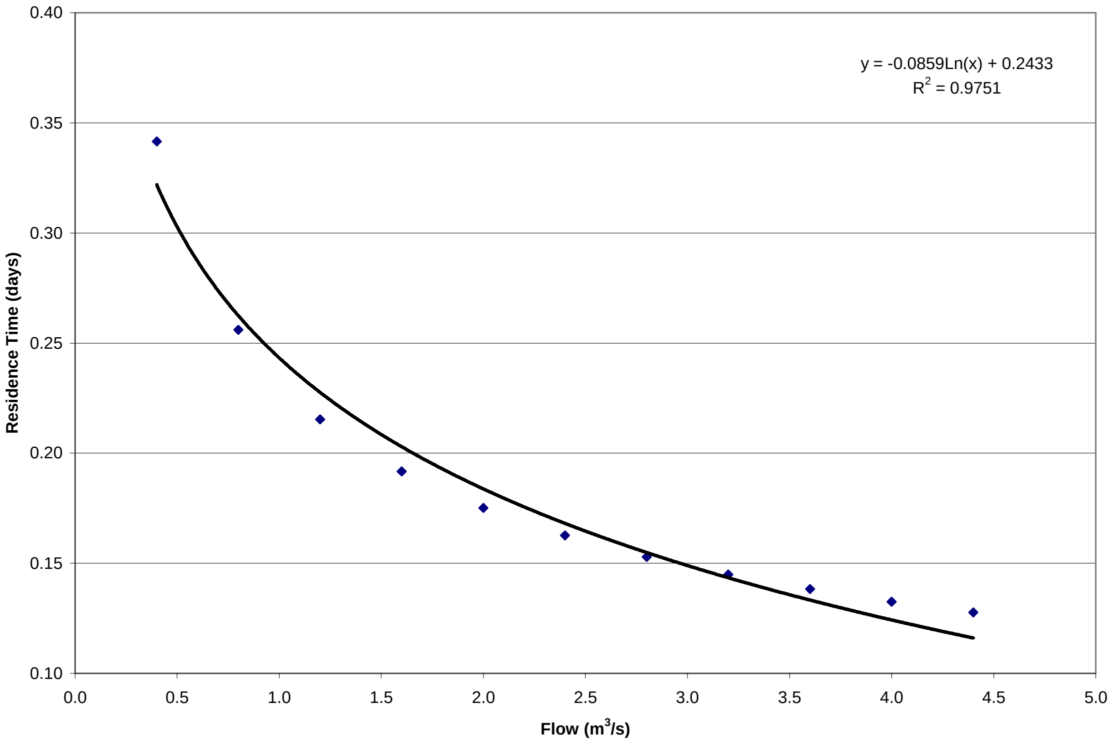


Figure 6.39 Flow versus Residence Time for Mission River Segment 3

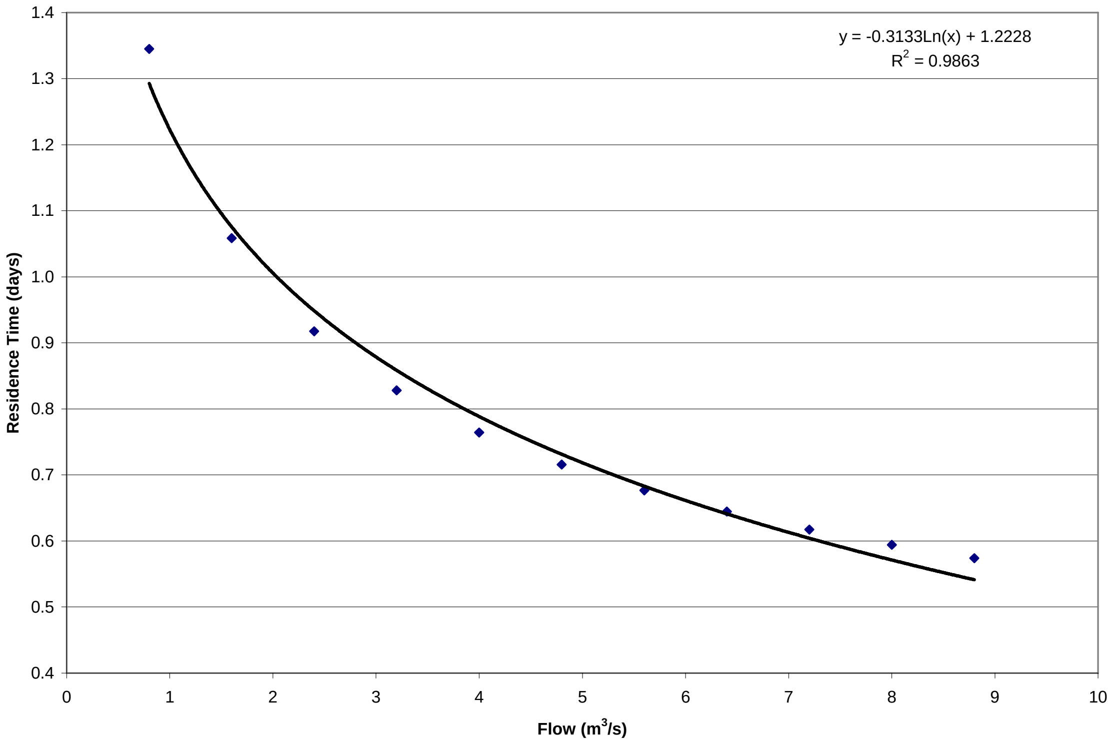


Figure 6.40 Flow versus Residence Time for Mission River Segment 4

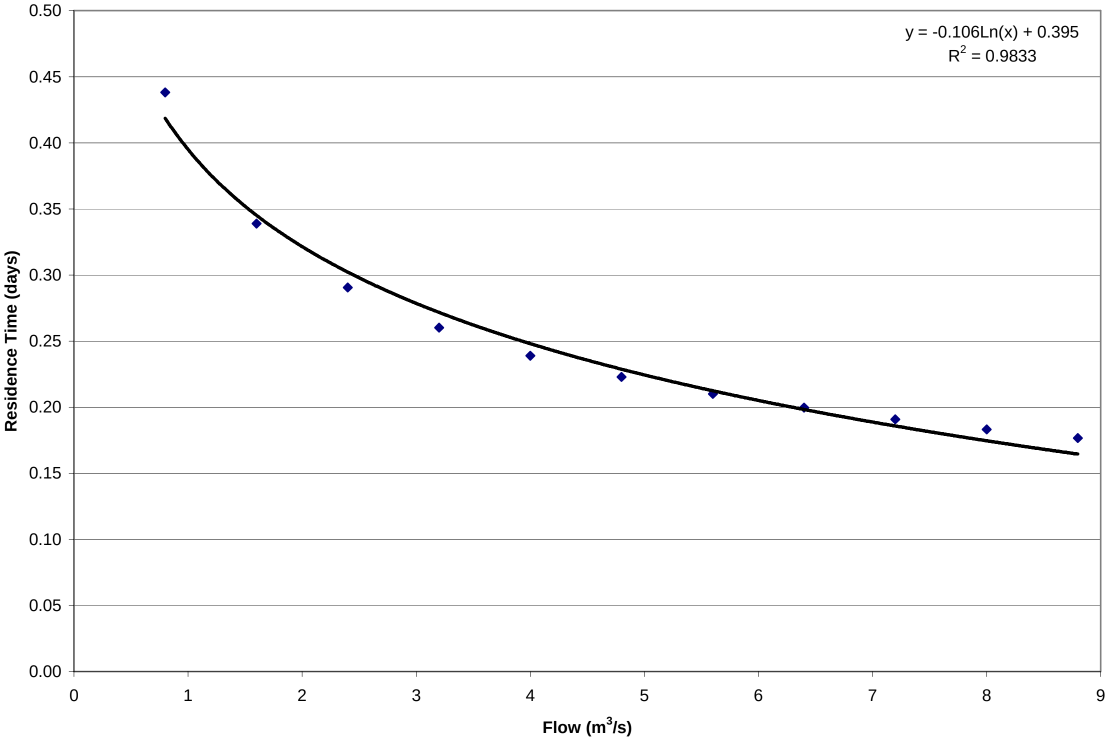


Figure 6.41 Flow versus Residence Time for Mission River Segment 5

A flow CDF plot was created for each segment. The flow CDF was based on USGS gauge daily mean streamflow data. The USGS gauge station 08189300 is on Medio Creek Segment 1, so a flow CDF was found directly for Segment 1, and daily mean streamflow data is available from 1962 to 2004. The flow CDF function for Medio Creek Segment 1 is shown in Figure 6.42.

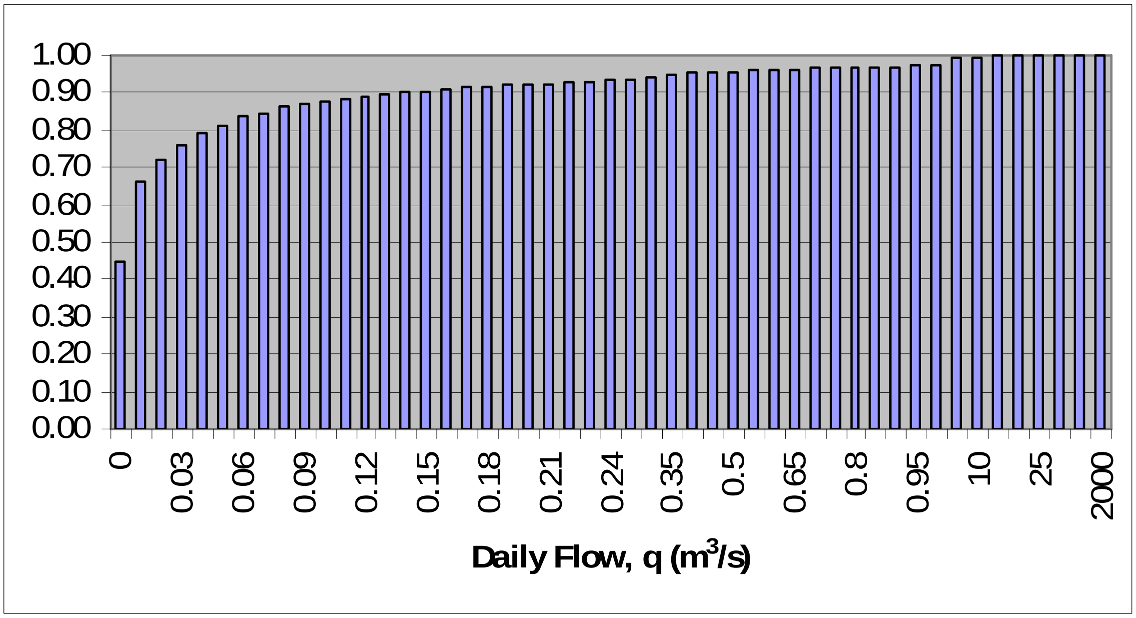


Figure 6.42 Flow Cumulative Distribution Function for Segment 1 (USGS Data; 1962-2004)

The flow CDF for Mission River Segment 2 is based on USGS gauge daily mean streamflow data that are available from 1939 to 2004. The USGS gauge station 08189500 is on Mission River Segment 2, so a flow CDF was found directly for Segment 2. The flow CDF for Mission River is shown in Figure 6.43.

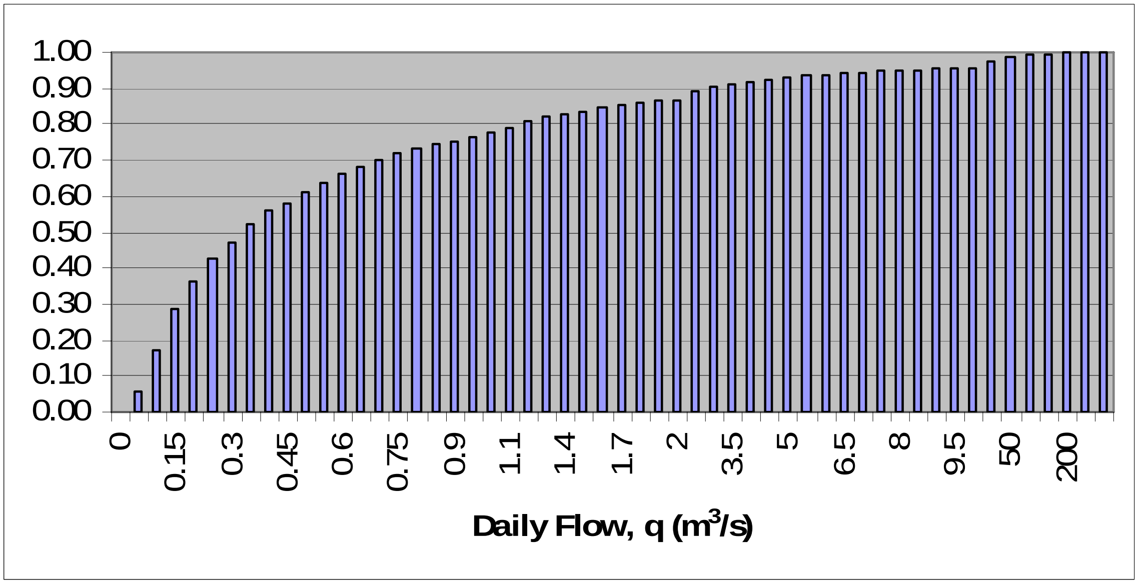


Figure 6.43 Flow Cumulative Distribution Function for Segment 2 (USGS Data; 1939-2004)

Because there is only one USGS gauge station on the Mission River, the flow CDF of Segment 2 was used to find the flow CDF for Segments 3, 4, and 5. The median flow for Segment 2 was found by finding the flow when the CDF equals 0.5, which is approximately 0.33 m^3/s (Figure 6.43). A dimensionless CDF was found for Segment 2 by dividing the flow by the median flow (Figure 6.44).

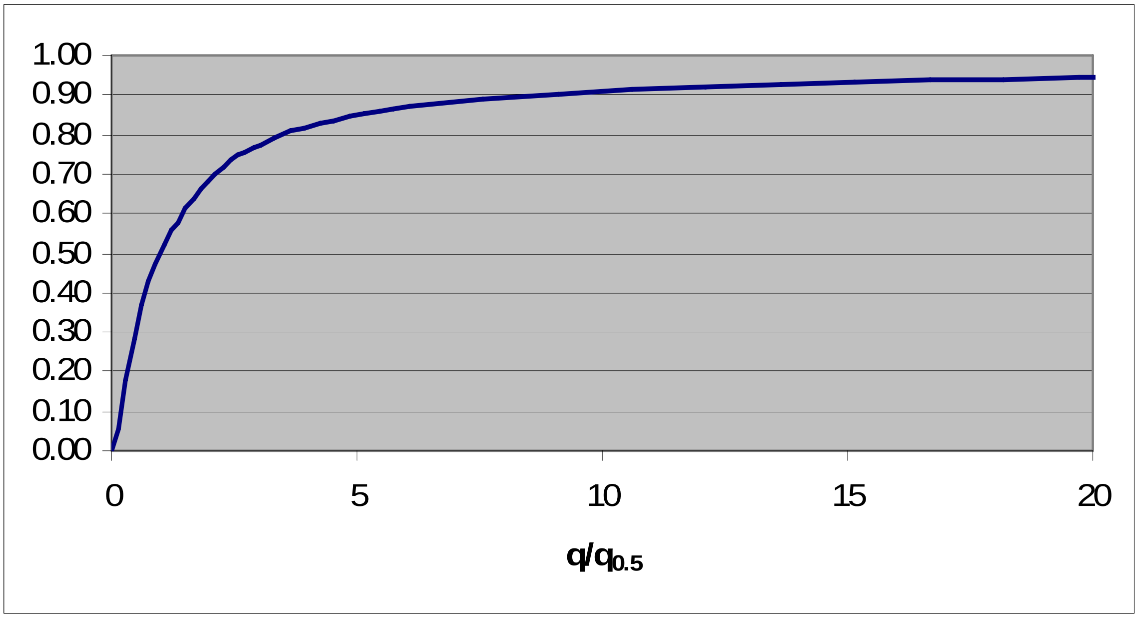


Figure 6.44 Cumulative Distribution Function, $q/q_{0.5}$ for Mission River Segment 2

The flow for Mission River Segments 3, 4, and 5 was determined by using the following relationship:

$$q = (q/q_{mean}) * q_{mean} \tag{6.9}$$

Where: (q/q_{mean}) = dimensionless value obtained from Segment 2

q_{mean} = mean flow of either Segment 3, 4, or 5 from water quality model

Each watershed has an annual mean flow that was calculated using the runoff equations derived by Quenzer (2003), which are given in Section 5.1.2.4. The mean flow was calculated by averaging the cumulative flow at the upstream point of each segment (the sum of flow of all upstream watersheds) and the cumulative flow at the downstream point of each segment. The mean flow to Aransas River Segment 2 was calculated (Figure 6.18), and the same process was used to calculate the mean flow for each of the Mission River segments.

After finding the mean flow for each segment, the flow CDF was calculated for each segment with Equation 6.9. The results for Segments 3, 4, and 5 are shown in Figures 6.45 - 6.47**.**

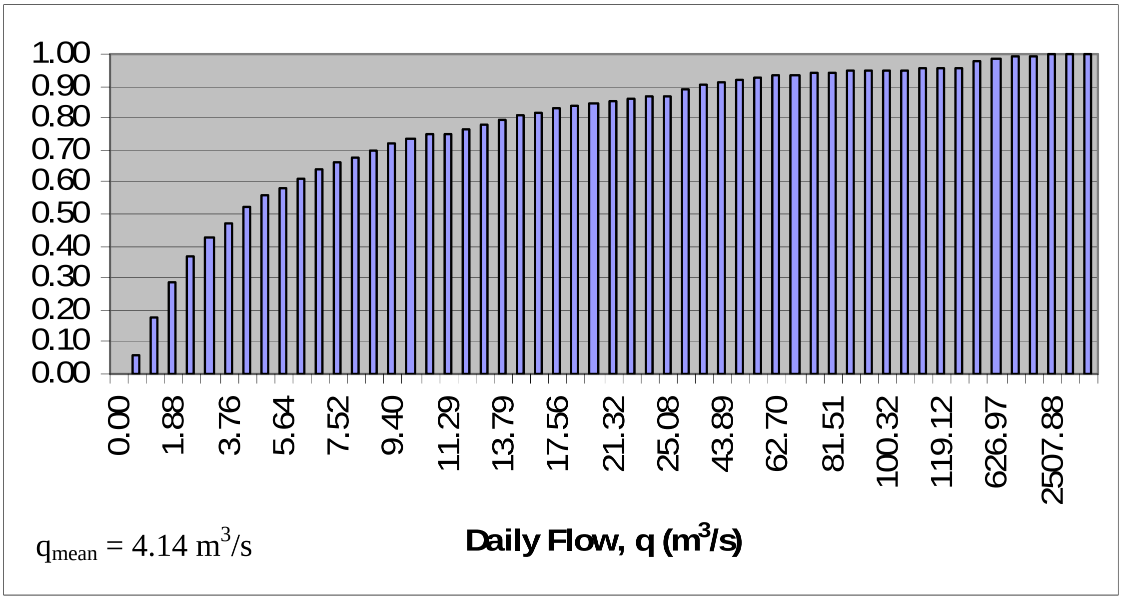


Figure 6.45 Flow Cumulative Distribution Function for Mission River Segment 3

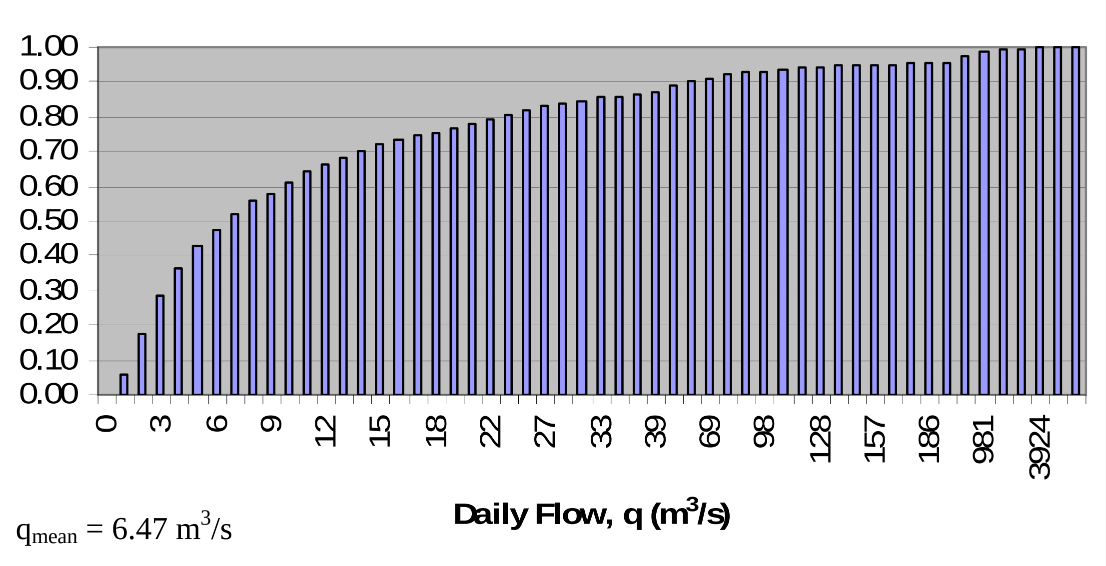


Figure 6.46 Flow Cumulative Distribution Function for Mission River Segment 4

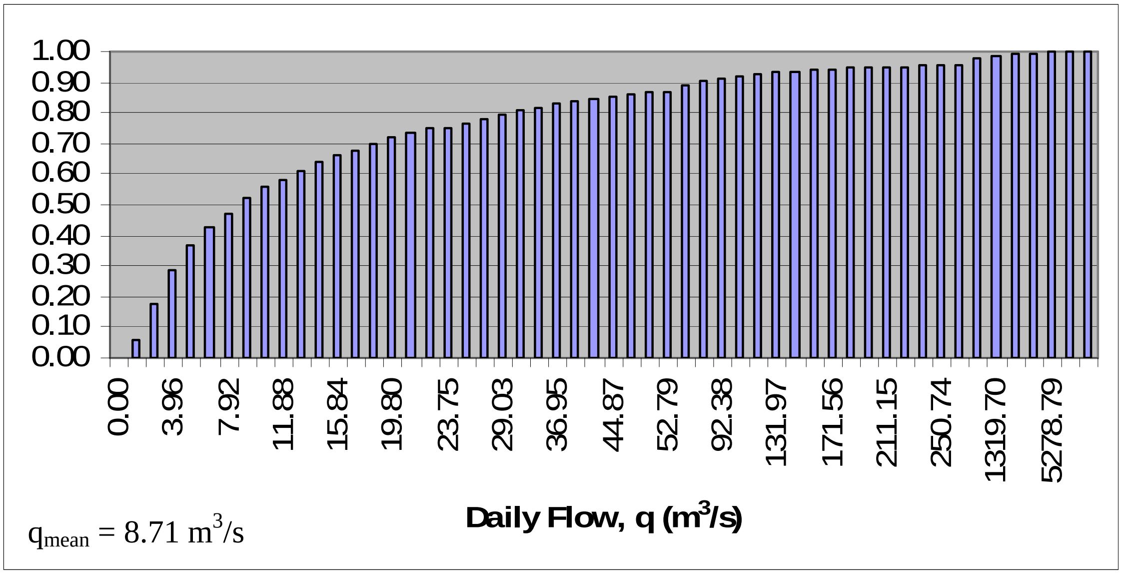


Figure 6.47 Flow Cumulative Distribution Function for Mission River Segment 5

Once the flow CDF was determined for all five segments, the RTD was found for each segment using the relationships between residence time and flow (Figures 6.37 - 6.41). The RTDs for Segments 1, 2, 3, 4, and 5 are shown in Figures 6.48 - 6.52.

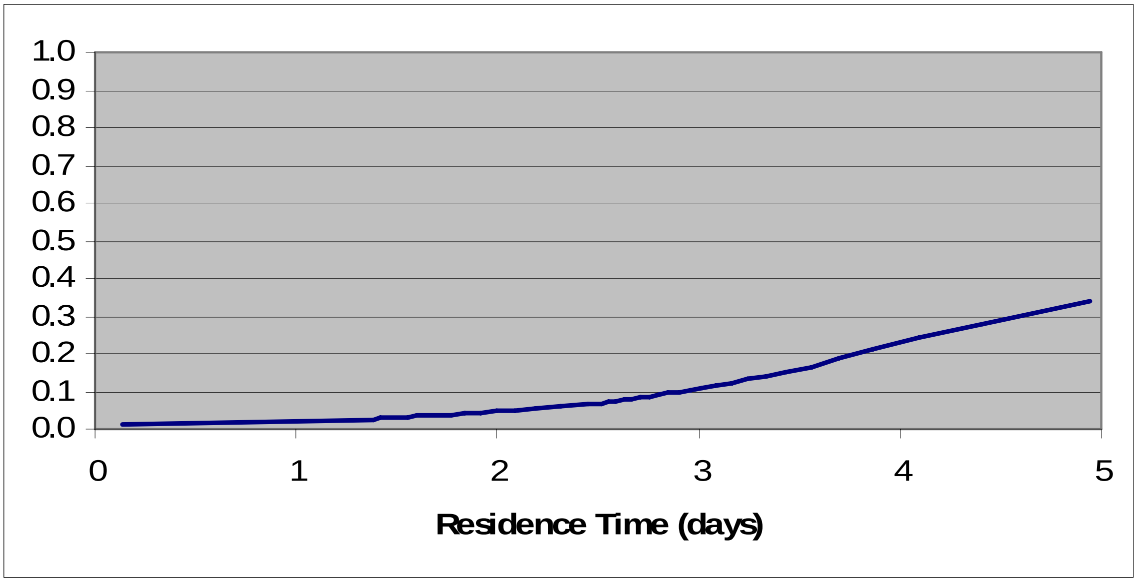


Figure 6.48 Residence Time Distribution for Medio Creek Segment 1

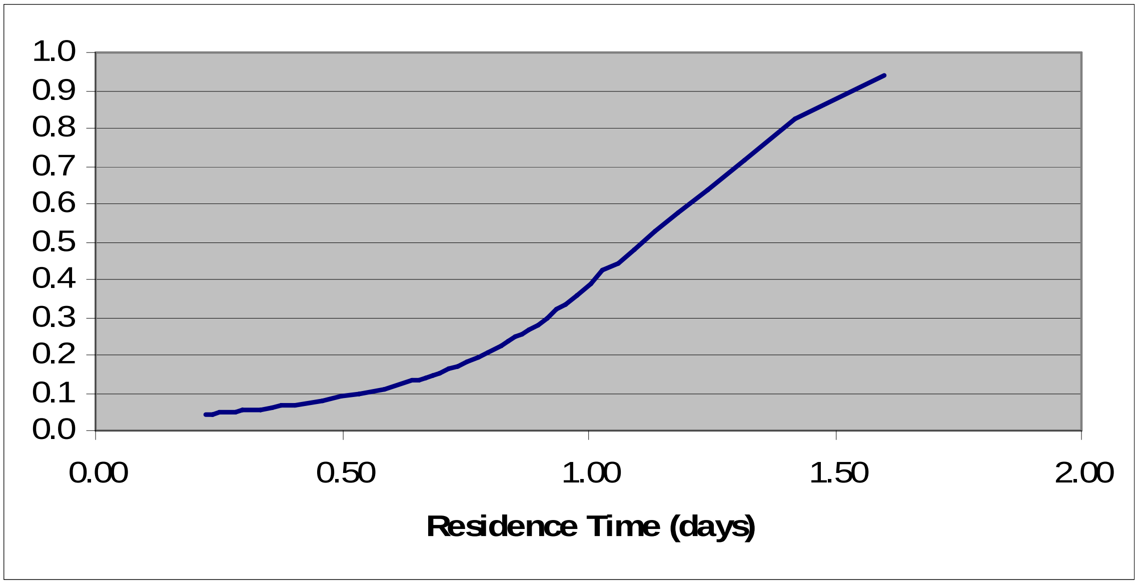


Figure 6.49 Residence Time Distribution for Mission River Segment 2

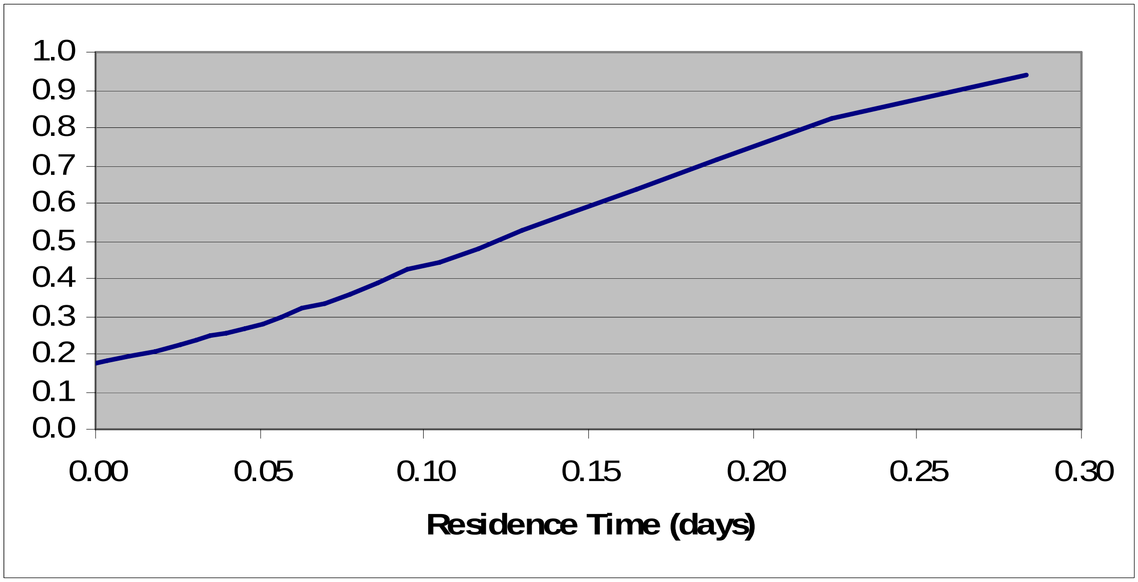


Figure 6.50 Residence Time Distribution for Mission River Segment 3

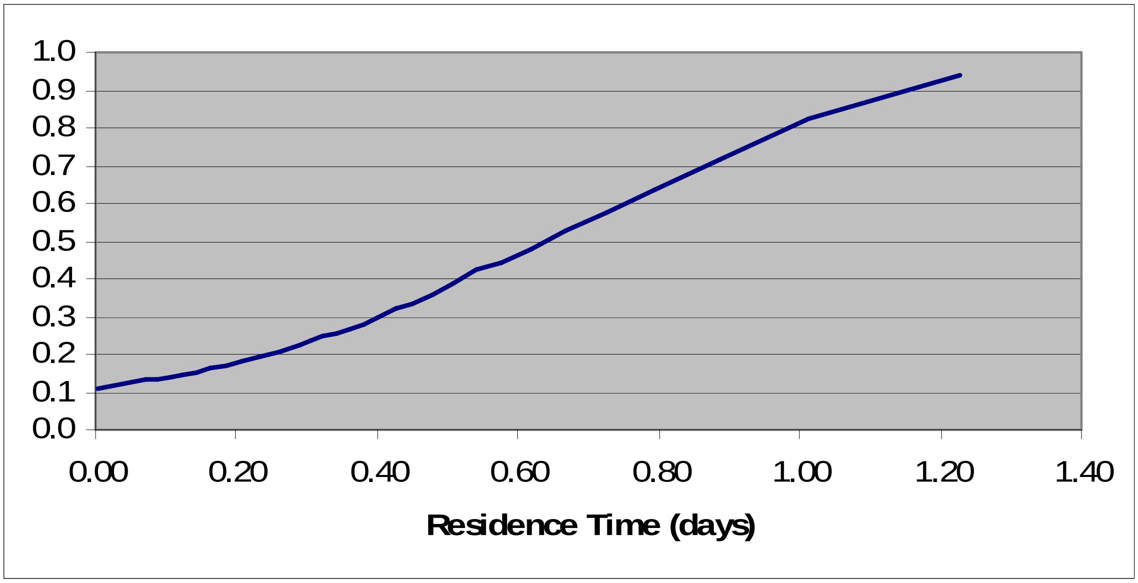


Figure 6.51 Residence Time Distribution for Mission River Segment 4

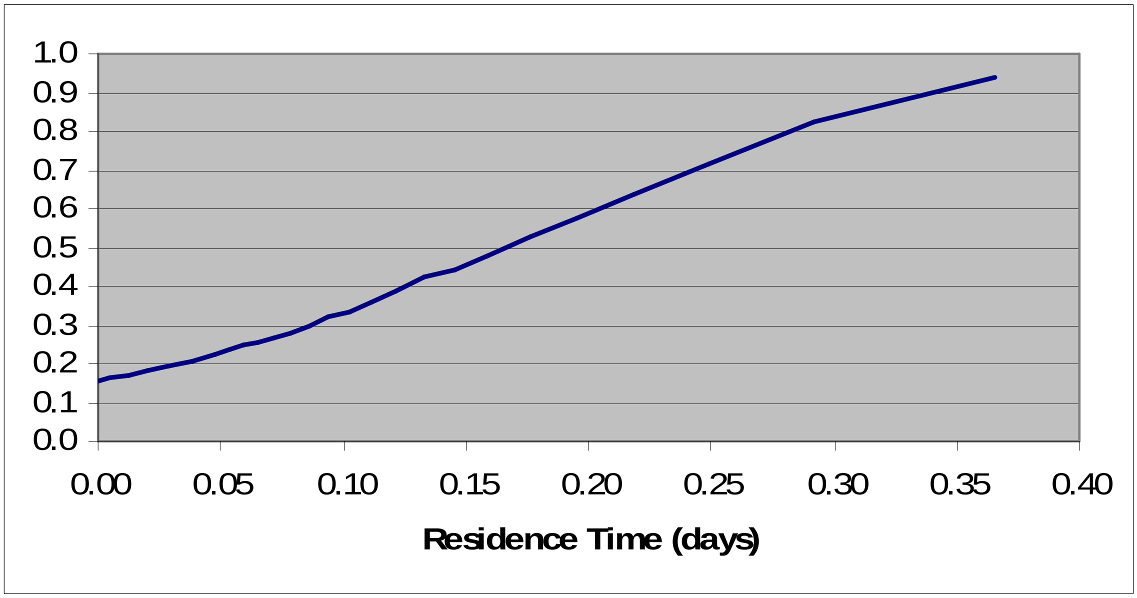


Figure 6.52 Residence Time Distribution for Mission River Segment 5

The probability distributions were also found for the residence times of all segments along the Mission River and are shown in Figures 6.53 - 6.57.

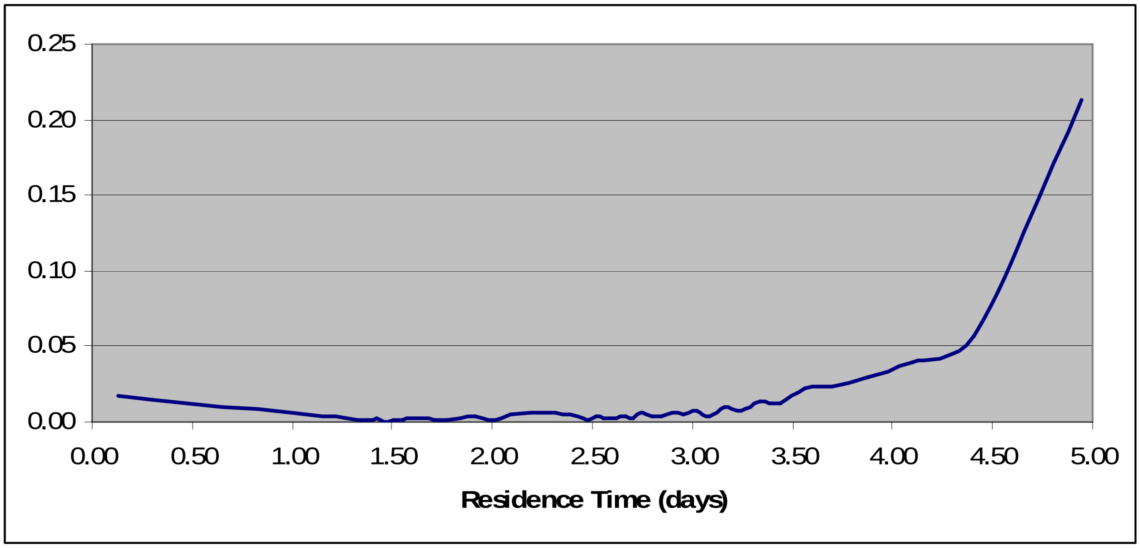


Figure 6.53 Probability Distribution of Residence Time for Medio Creek Segment 1

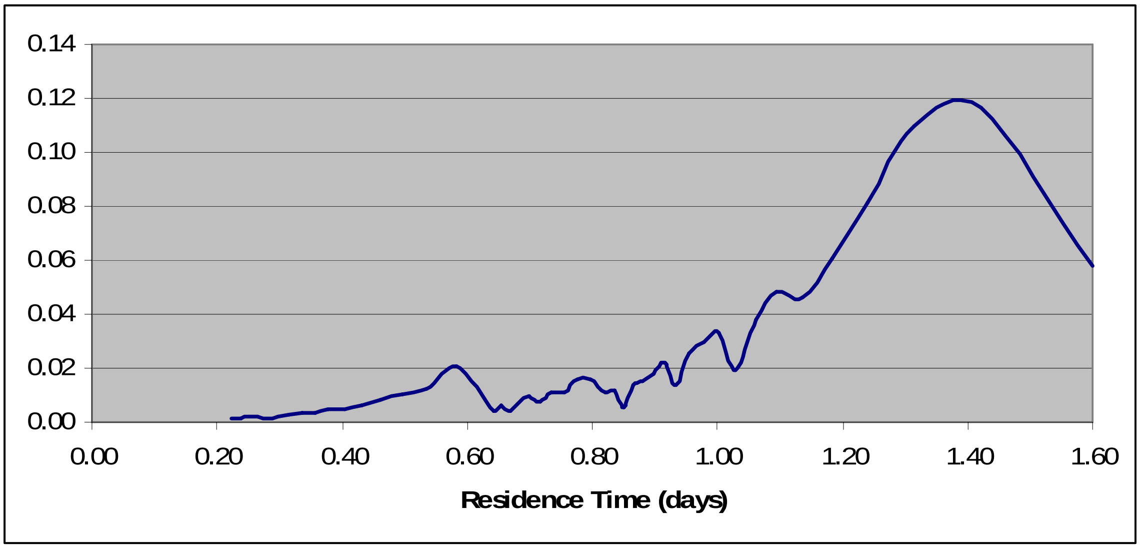


Figure 6.54 Probability Distribution of Residence Time for Mission River Segment 2

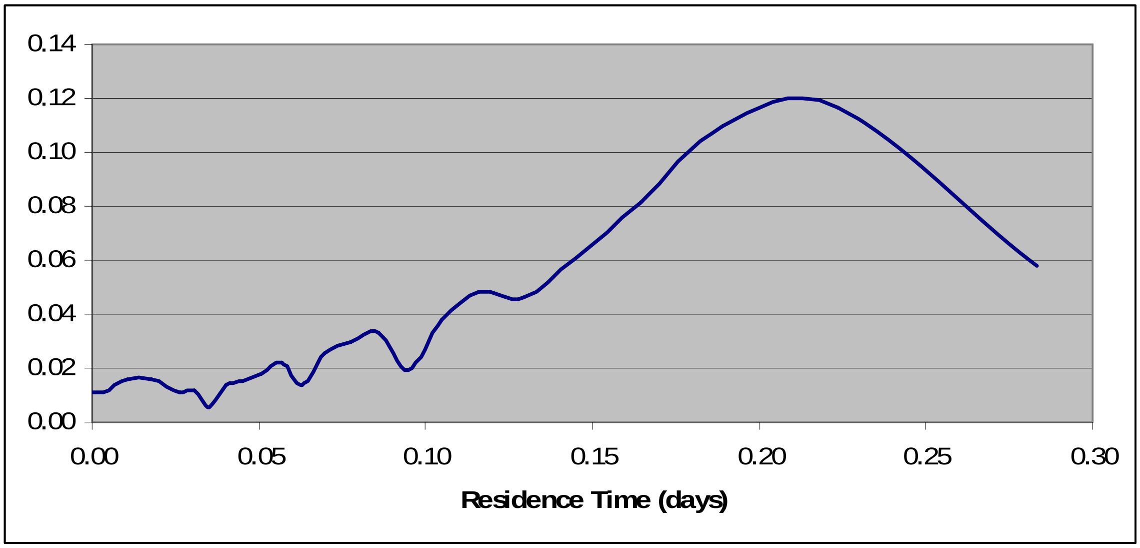


Figure 6.55 Probability Distribution of Residence Time for Mission River Segment 3

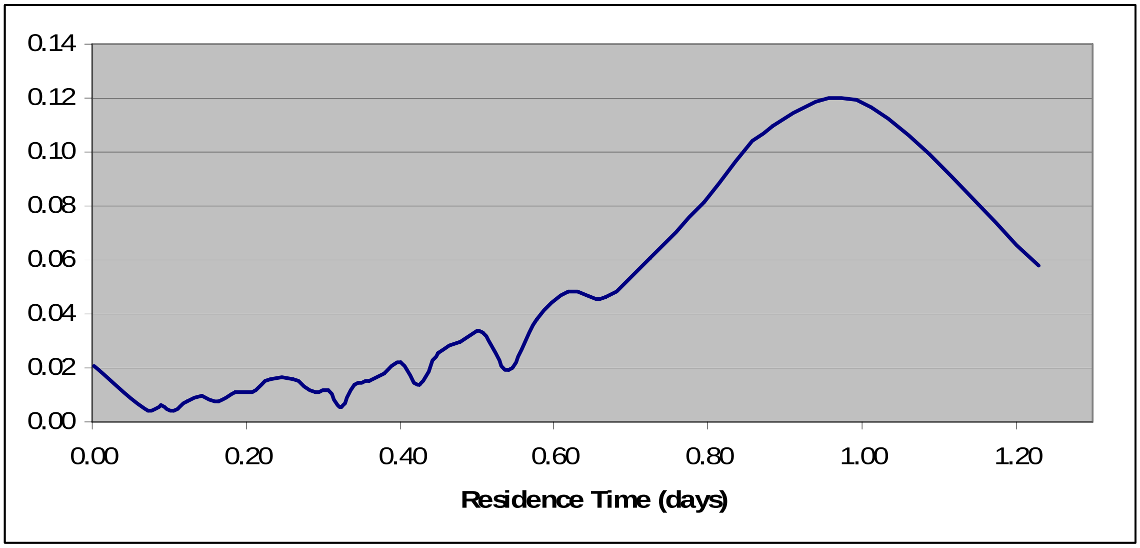


Figure 6.56 Probability Distribution of Residence Time for Mission River Segment 4

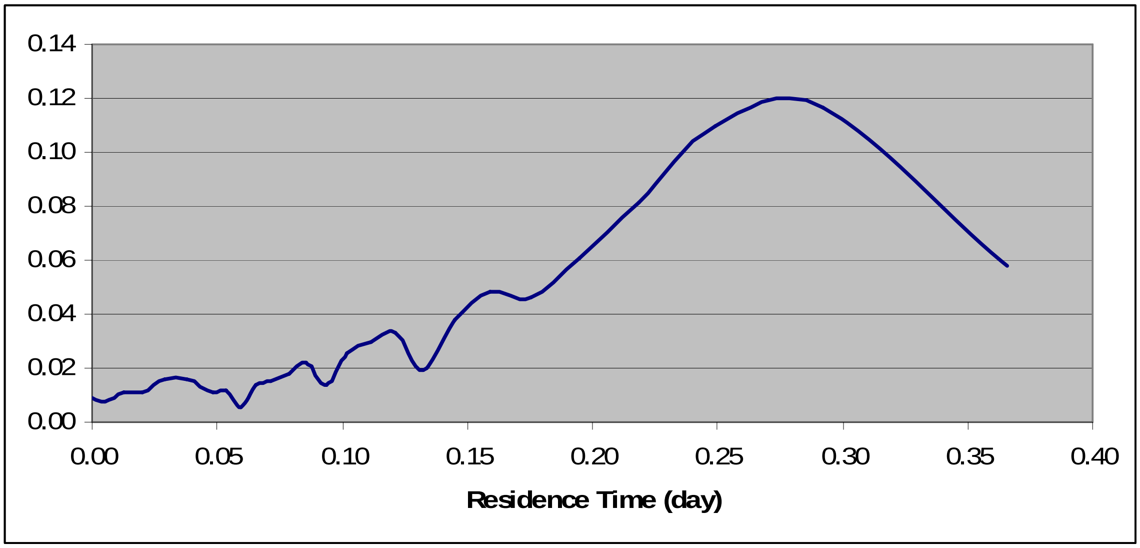


Figure 6.57 Probability Distribution of Residence Time for Mission River Segment 5

The RTDs were used as approximations for the corresponding SchemaLinks' residence times in the Schematic Processor Model. Medio Creek Segment 1 corresponds to SchemaLink HydroID 118 while Mission River Segments 2, 3, 4, and 5 correspond to SchemaLink HydroIDs 116, 109, 115, 110, respectively, which are shown in Figure 6.58[14]. For this Schematic Processor Model, the most frequent residence time from the probability and residence time distributions is the residence time associated with the corresponding SchemaLinks, and these residence times are given in Table 6.11.

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[14] SchemaLink 133 corresponds to the neighboring watershed link, not Segment 3.

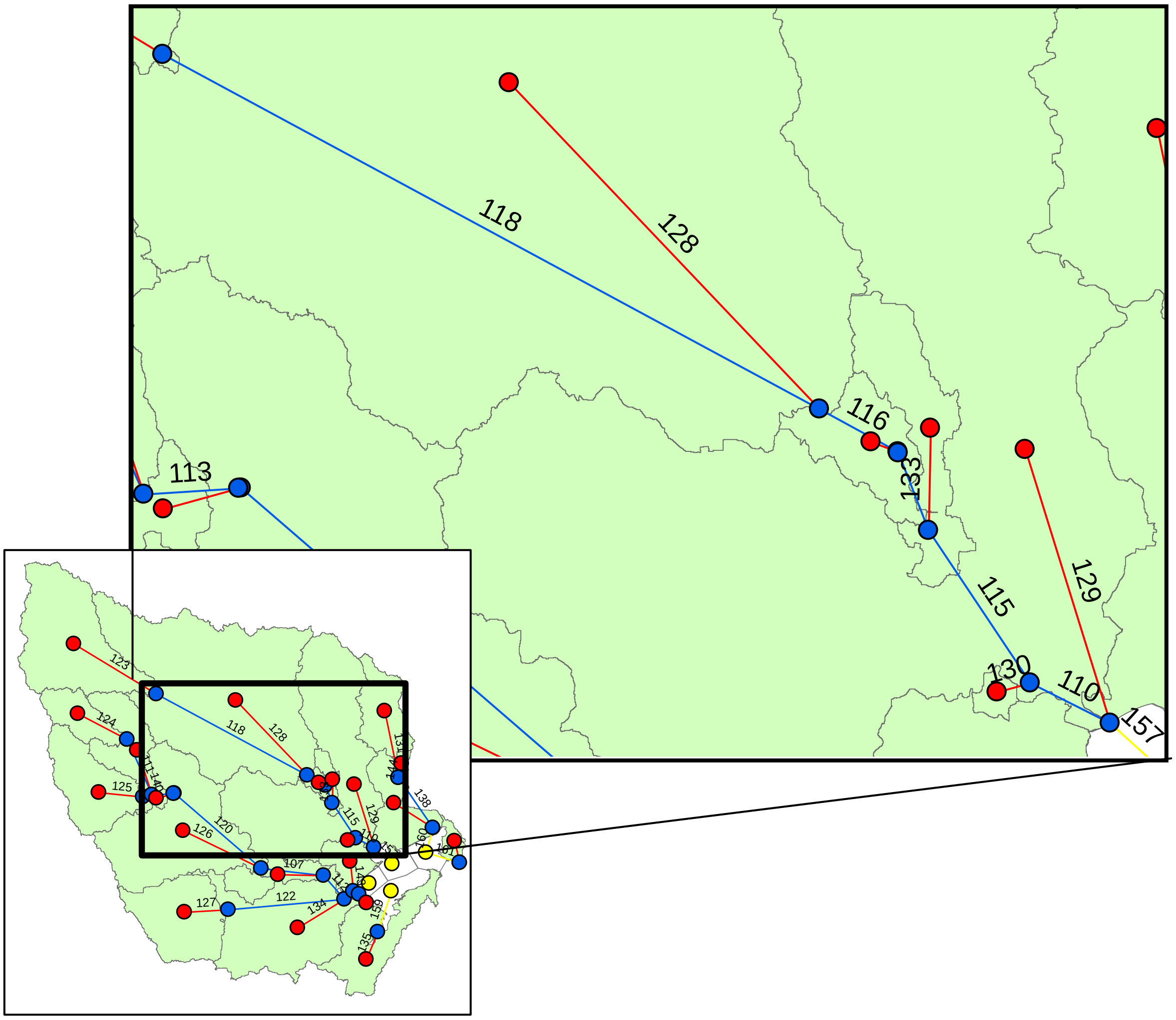

Figure 6.58 SchemaLinks of Corresponding Medio Creek and Mission River Segments

Table 6.11 Residence Times of Medio Creek and Mission River Segments for Schematic Processor Model

Medio Creek/Mission River Segment	SchemaLink HydroID	Residence Time (days)
1	118	4.95
2	116	1.42
3	109	0.22
4	115	1.01
5	110	0.29

6.3.3.2.4 3d Model of Copano Creek: Residence Time Determination

A 3d model of Copano Creek was created in HEC-RAS (USGS gauge stations 08189200) using the one USGS gauge station along the creek. The same methodology that was used to find the RTDs of the Aransas and Mission River segments was applied.

To find the cross-section at the USGS gauge station, USGS gauge data (for USGS station 08189200) were downloaded from the USGS website from “Surface-Water Measurements”, which includes width, area, and stream flow measurements. The relationship between flow and width (Figure 6.59) was plotted for all available data (1967-2005 at USGS 08189200).

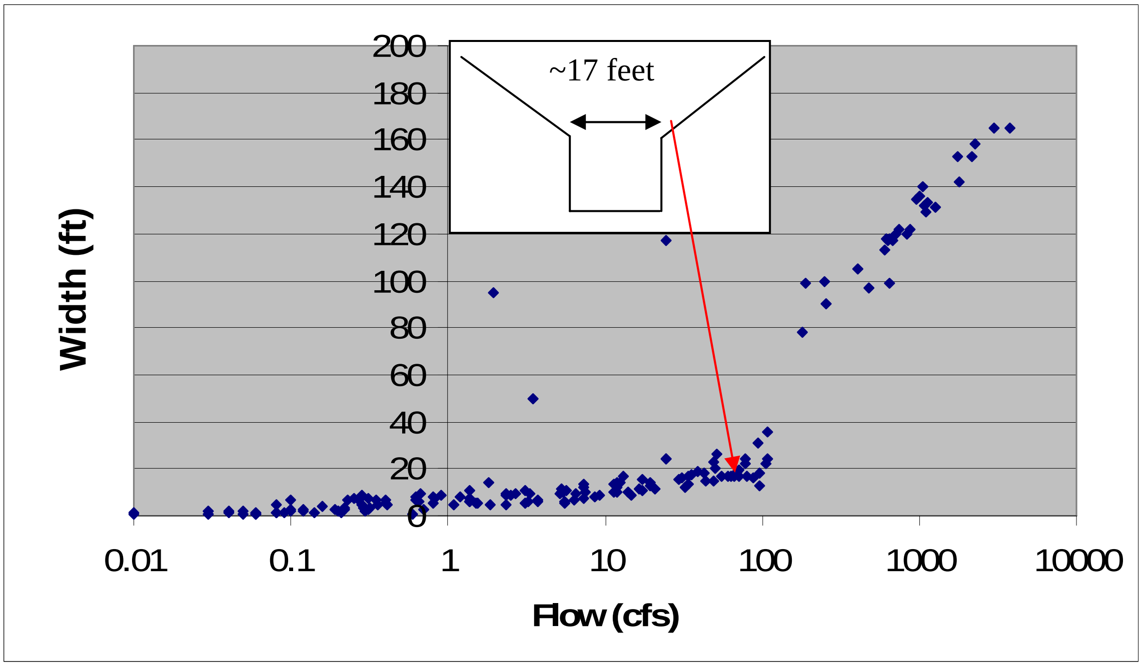

Figure 6.59 Flow versus Width for USGS Station 08189200

The width of the channel at USGS gauge station 08189200 on Copano Creek was approximated to be 17 feet (Figure 6.59). The channel was assumed to have a square cross-section at the USGS gauge station; thus, the depth was calculated for each USGS measurement by dividing the measured area by the measured width for each measured stream flow. In Figure 6.60, the depth and width of each channel were plotted for all available measurements, and these data were used to approximate the depth in Copano Creek at a width of 17 feet. The approximate depth at USGS gauge station 08189200 with a width of 17 feet is approximately 1.74 feet (the average depth of the seven 17-ft width measurements that were made from the available USGS data).

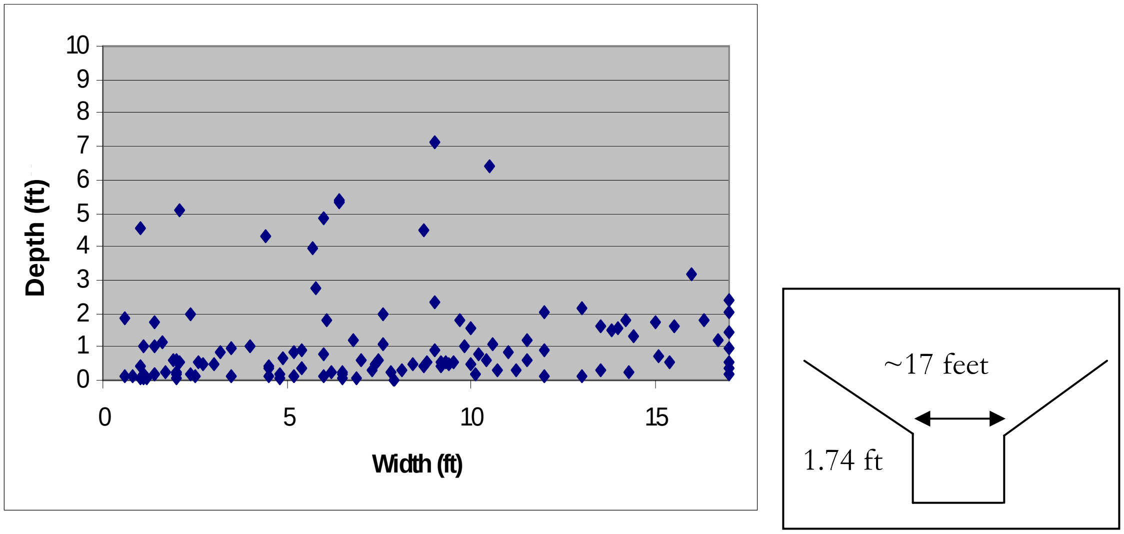

Figure 6.60 Width versus Depth (Square Cross-Section) for USGS Station 08189200

The bank elevations are given for USGS gauge stations on the USGS website in “Surface-Water Measurements”, and the bank elevation is 17.25 feet above sea level for USGS 08189200.

Because there is only one USGS gauge station along Copano Creek, other sources were used to estimate the cross-section at the most downstream point of Copano Creek where it drains into Copano Bay. The other sources that were used were aerial photographs and the RF1 Database. First, the sources were compared to the USGS approximation at the USGS gauge station location to see the percentage difference. The percentage differences are shown below in Table 6.12.

Table 6.12 Upstream Cross-Section Data Comparison (Copano Creek; USGS 08189200)

			Percent Error (%)	
	Width (ft)	**Depth (ft)**	**Width**	**Depth**
RF1	68.65	0.34	303.82	80.47
Aerial	65.60	-	285.88	-
USGS/RCMM Input	17.00	1.74	-	-

The aerial photograph is closer to the USGS approximation for width (Table 6.12); the RF1 file is the only known data source to approximate depth. The downstream dimensions using the available sources are shown in Table 6.13.

Table 6.13 Downstream Cross-Section Data (Copano Creek)

	Width (ft)	**Depth (ft)**
RF1	68.65	0.34
Aerial	101.68	-

The width of the channel was approximated (taking into account the 285.88% error) to be 26.35 feet, which was rounded to 50.00 feet (since the downstream width should be much wider than the upstream width) while the depth was approximated (taking into account the 80.47% error) to be 1.74 feet, which is the same depth as upstream at the USGS gauge station, which the depth should be larger downstream. Thus, the depth was approximated as 5.00 feet by assuming the same width:depth ratio that exists at the USGS gauge station. The bank elevation at the most downstream point was determined using the DEM. A summary of all the data needed for the RCMM toolbar for Copano Creek is shown in Figure 6.61.

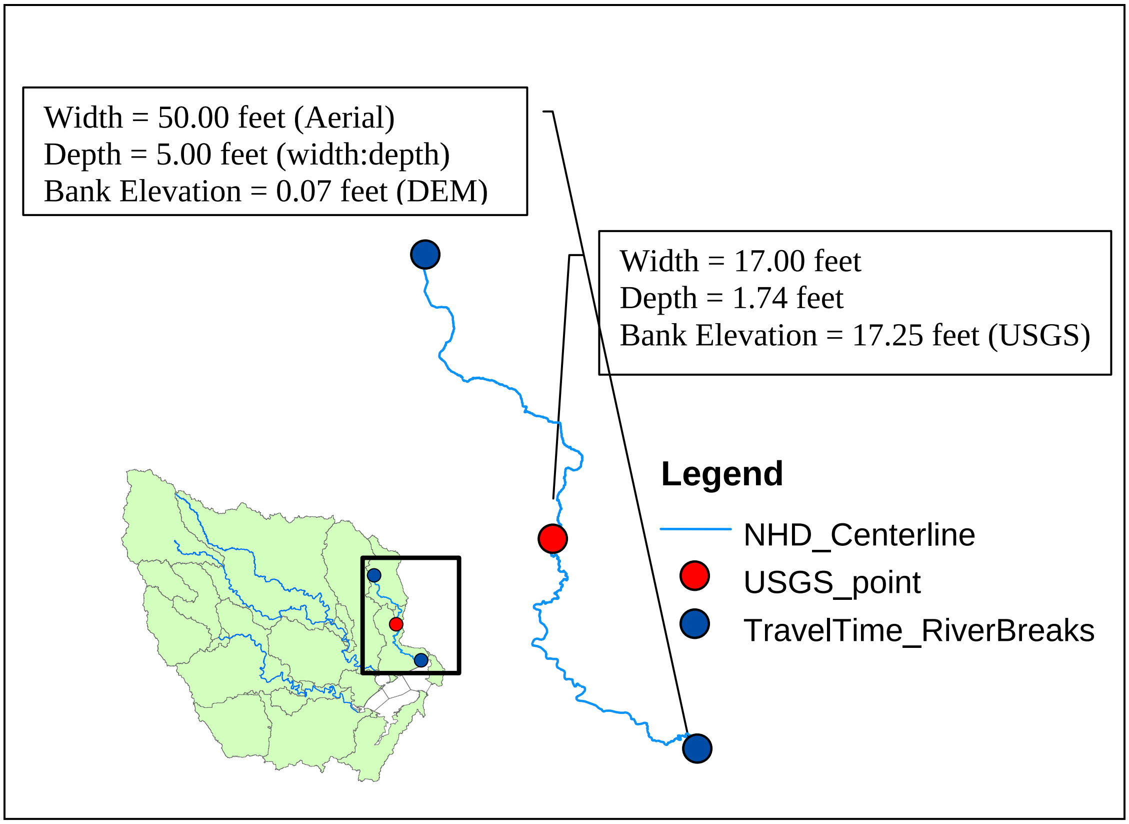

Figure 6.61 Summary of RCMM Toolbar Data Requirements (Copano Creek)

After obtaining the NHD centerline feature class, USGS gauge station feature class, and the cross-section dimensions at two points, Merwade's RCMM toolbar was used to generate a 3d model of Copano Creek[15]. Copano Creek was made into one 3d segment (Figure 6.61) because the residence time was needed for this one segment.

Using the 3d Copano Creek model (HEC-RAS), a relationship was found between residence time and flow rate for the one segment (Figure 6.62).

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[15] Merwade generated the 3d river models for this project.

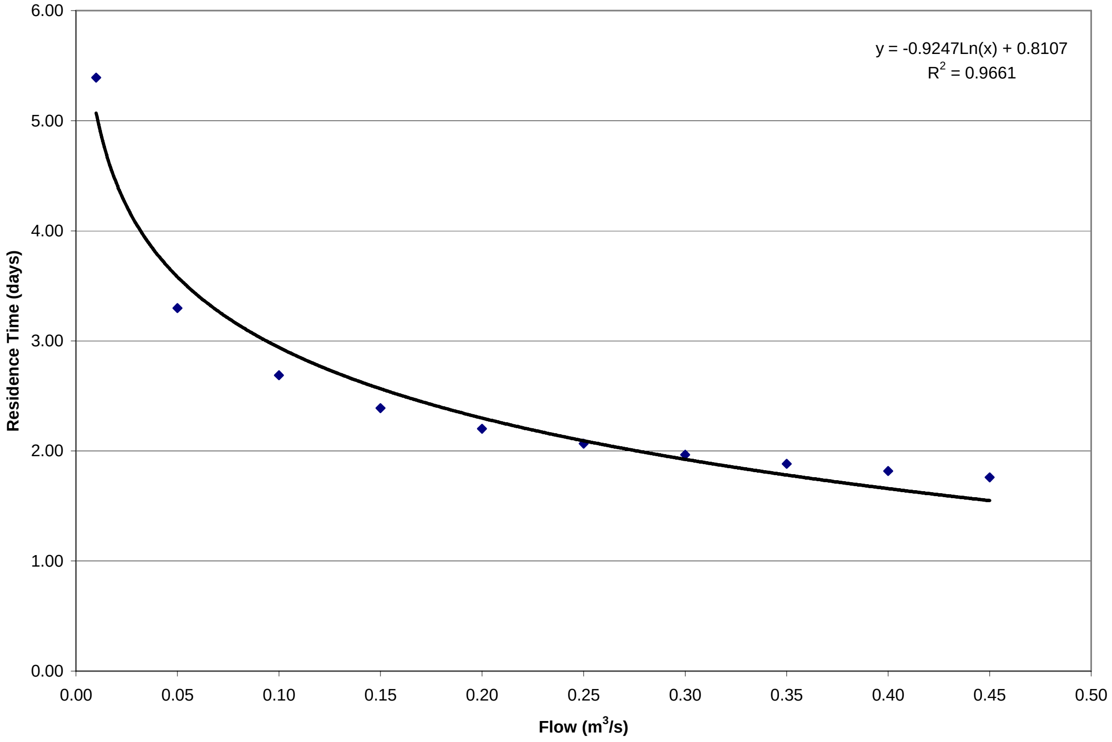


Figure 6.62 Flow versus Residence Time for Copano Creek

A flow CDF plot was created for the segment. The flow CDF was based on USGS gauge daily mean streamflow data that were available from 1970 to 2004. The USGS gauge station 08189200 is on Copano Creek, so a flow CDF was found directly for this segment (Figure 6.63).

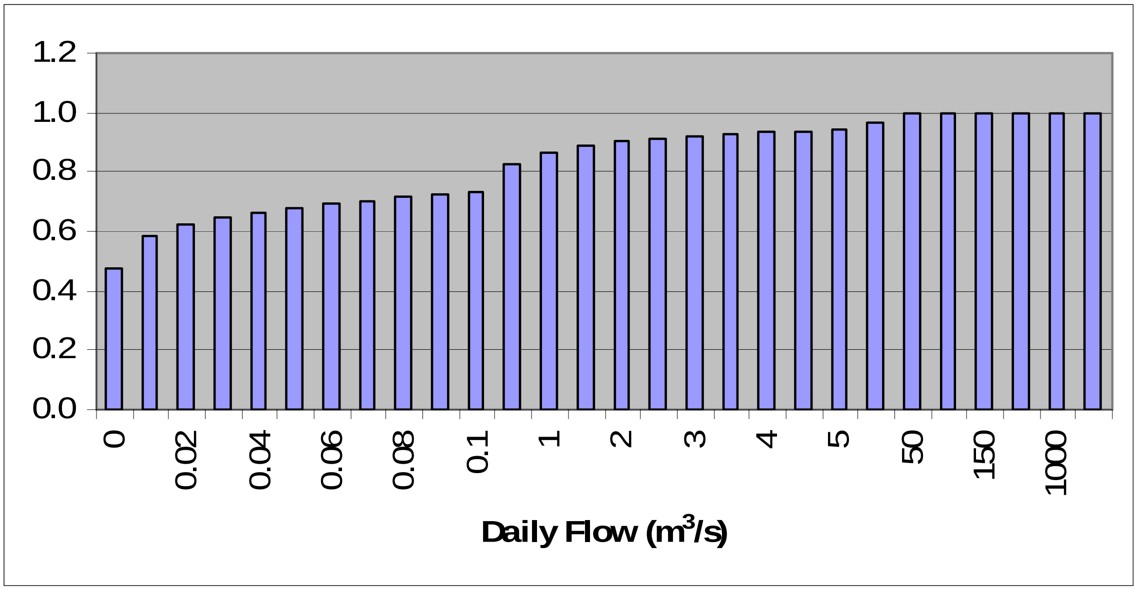


Figure 6.63 Flow Cumulative Distribution Function for Copano Creek (USGS Data; 1970-2004)

Once the flow CDF was found, the RTD was found for each segment using the relationship between residence time and flow from Figure 6.62. Figure 6.64 shows the RTD for Copano Creek.

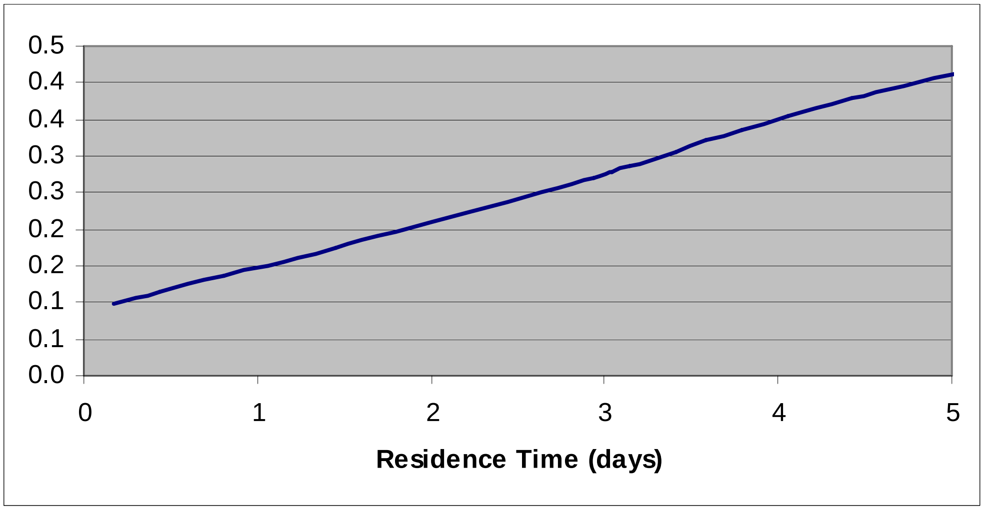


Figure 6.64 Residence Time Distribution for Copano Creek

The probability distribution was also found for the residence times of the Copano Creek segment and is shown in Figure 6.65.

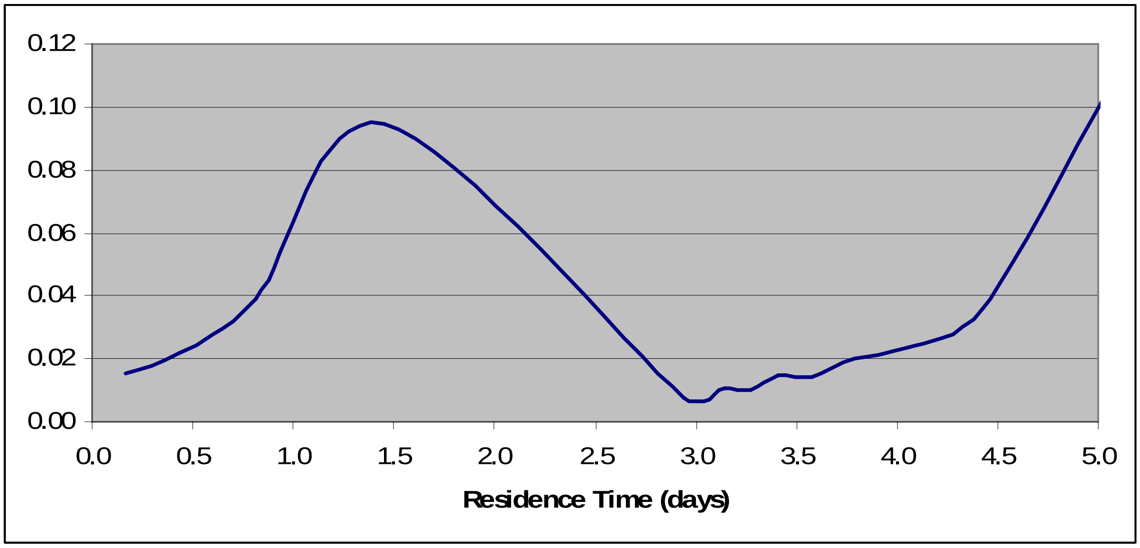


Figure 6.65 Probability Distribution of Residence Time for Copano Creek

The RTD was used as an approximation for the corresponding SchemaLink's residence time in the Schematic Processor Model. Copano Creek Segment 1 corresponds to SchemaLink HydroID 138. For this Schematic Processor Model, the most frequent residence time from the probability and residence time distributions is the residence time associated with the corresponding SchemaLink, and the residence time is given in Table 6.14.

Table 6.14 Residence Time of Copano Creek for Schematic Processor Model

Copano Creek River Segment	**SchemaLink HydroID**	**Residence Time (days)**
1	138	5.069

6.3.3.2.5 Determination of Residence Times of Remaining SchemaLinks (Calibration)

The preliminary residence times of the remaining SchemaLinks (i.e., those that were not modeled as 3d main river channels) were found by using the following relationship: Travel Time = Flow Length / Velocity. The procedure for calculating the initial residence time for each of the remaining river segments in the watershed is described in Appendix 6.2.

After the initial residence times of the SchemaLinks were found, the Schematic Processor Model was calibrated at each of the bacterial monitoring stations, adjusting the residence times of the SchemaLinks that were not represented by 3d HEC-RAS models. The Schematic Processor Model needs to be able to accurately model what is actually occurring in the Copano Bay watershed. The bacterial loadings and concentrations calculated from the model were compared to existing bacterial monitoring data to calibrate the model. The Schematic Processor Model is calibrated to the median fecal coliform bacteria concentrations of the bacterial monitoring data provided by TCEQ from 1999 to 2005.

Three bacterial monitoring stations (with fecal coliform monitoring data) exist along the Aransas River (Stations 12948, 12952, 17592) and four bacterial monitoring stations exist in Copano Bay Segment 2 (Stations 12945, 14783, 14787, 14788), which are shown in Figure 6.66. The watersheds that are shown in Figure 6.66 drain into Copano Bay Segment 2.

Two bacterial monitoring stations exist along the Mission River (Stations 12943, 12944), and one bacterial monitoring station exists in Copano Bay at the Mission River outlet (Station 14797), which are shown in Figure 6.67. The watersheds that are shown in Figure 6.67 drain into Copano Bay Segment 3.

Six bacterial monitoring stations are located in Copano Bay Segment 4 (Stations 14793, 14792, 14785, 14780, 14779, and 13404), which are shown in Figure 6.68.

Four bacterial monitoring stations are located in Copano Bay Segment 1 (Stations 14790, 14784, 14782, 13405), which are shown in Figure 6.68.

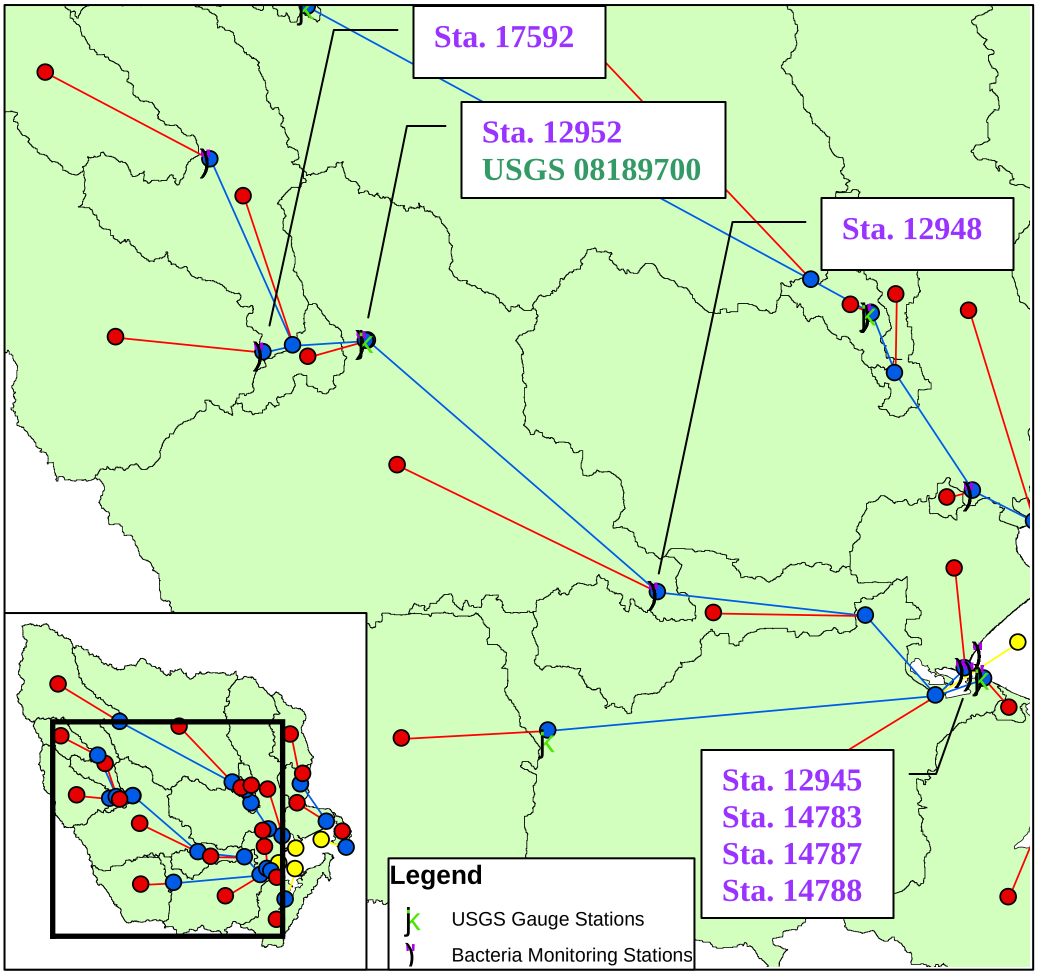


Figure 6.66 Bacterial Monitoring and USGS Stations along Aransas River

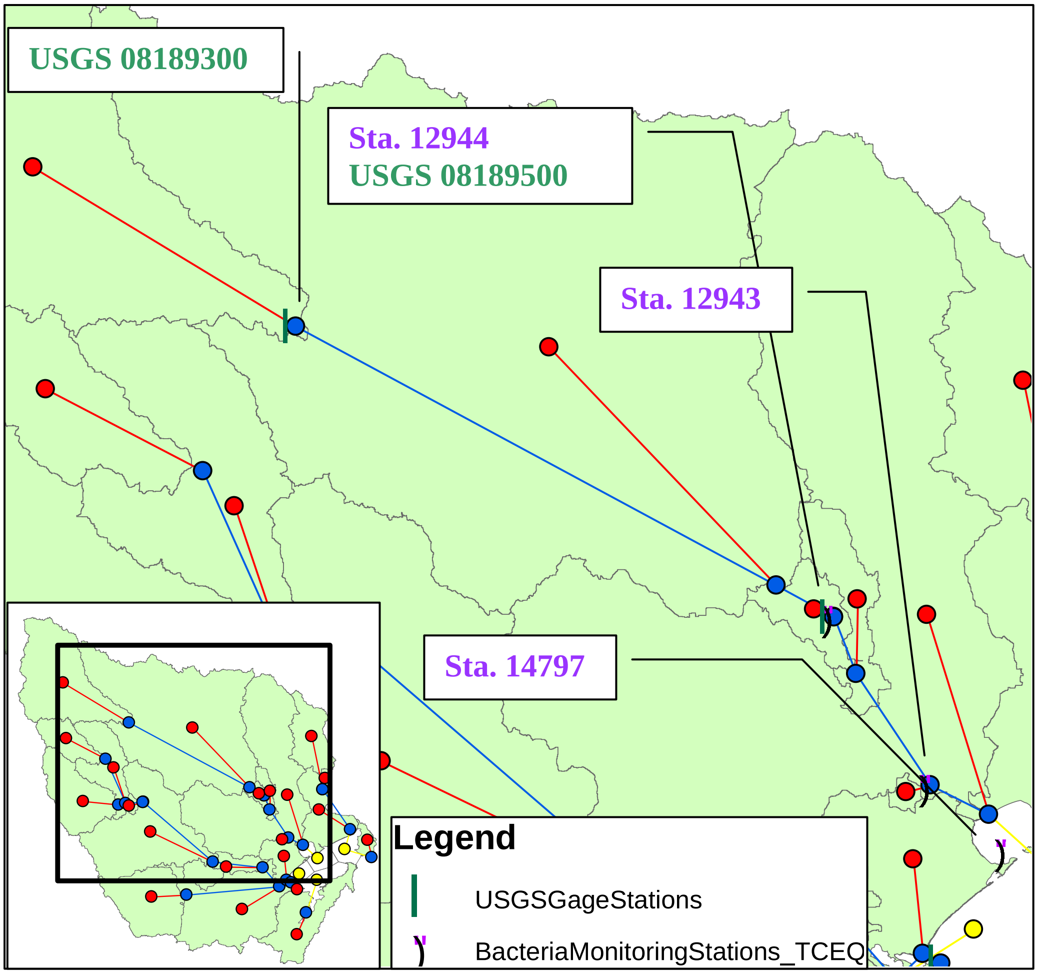


Figure 6.67 Bacterial Monitoring and USGS Stations along Mission River

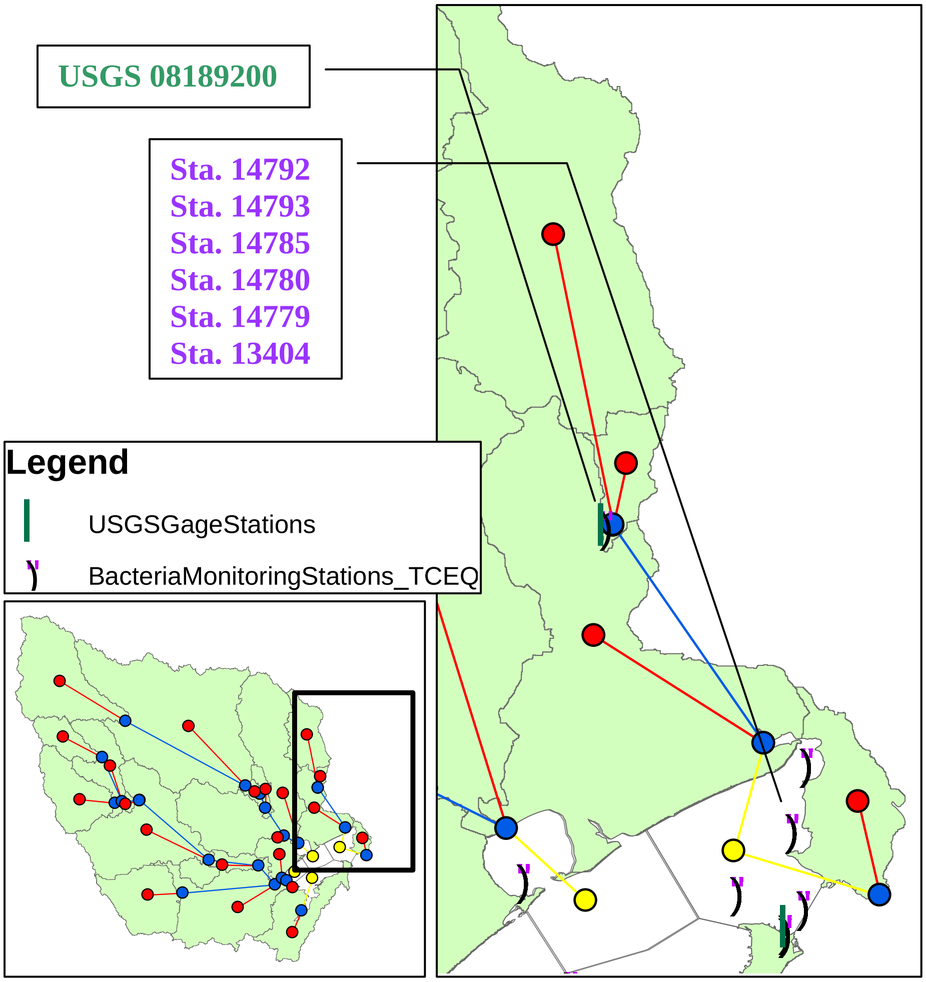


Figure 6.68 Bacterial Monitoring and USGS Station along Copano Creek

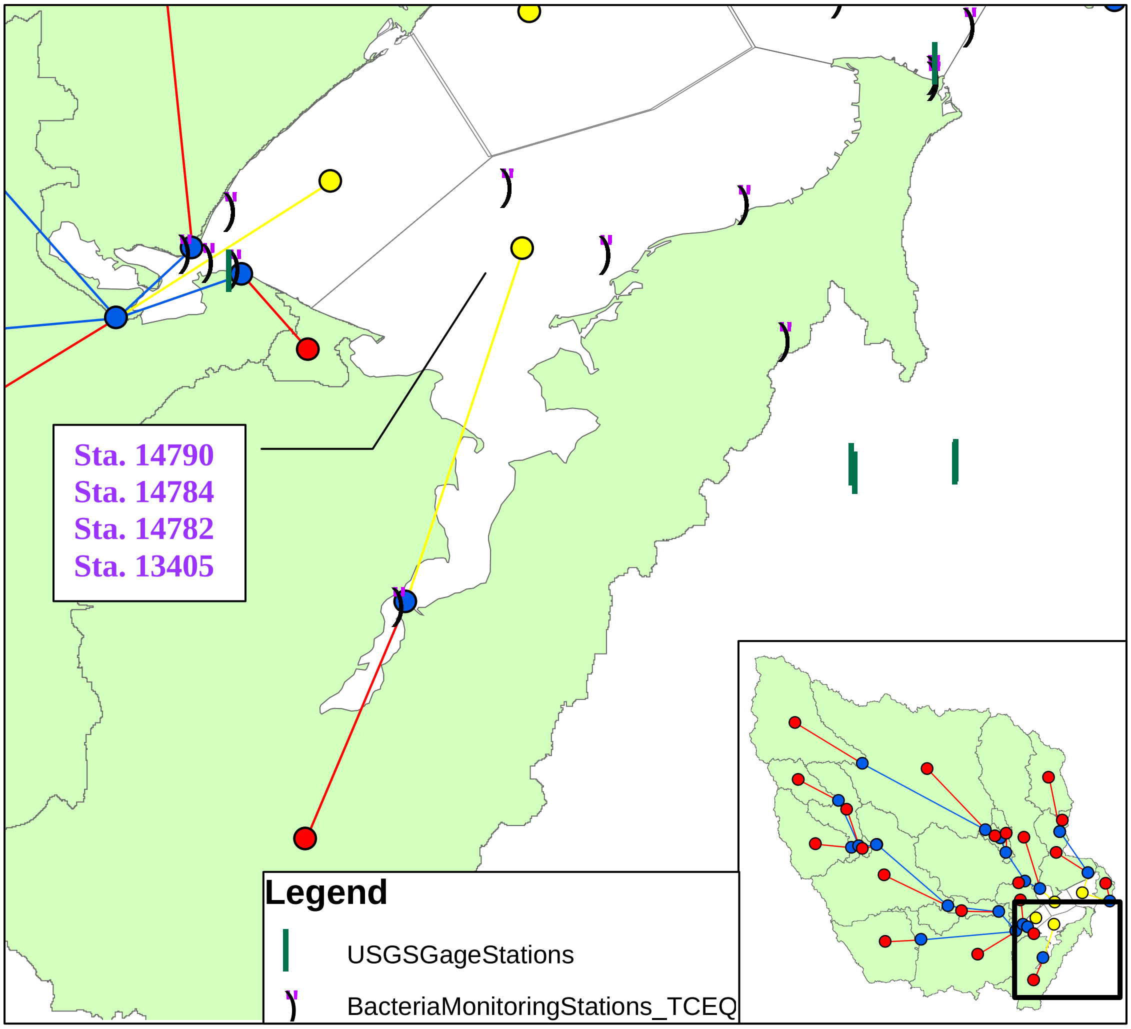


Figure 6.69 Bacterial Monitoring and USGS Stations along Copano Bay Segment 1

To calibrate the model for the Copano Bay watershed, the residence time, τ, parameter was adjusted for the river segments that were not considered main river channels to reflect the existing median fecal coliform monitoring data at each station labeled in Figures 6.66 - 6.69.

The bacterial loadings of the SchemaLinks (that transport the greatest bacterial loads) directly upstream of the bacterial monitoring station are most influential of the quality of the river water since the bacteria do not have a sufficient amount of time to decay.

For this calibration, a decay coefficient of 2 days^{-1} was assumed. A model was created in Microsoft Excel using the Solver add-in function and the calculated bacterial loadings; using this model, we solved for the residence time of the SchemaLink that most directly affects the bacterial concentration at the bacterial monitoring station.

The most upstream bacterial monitoring station locations were calibrated first; then, the next downstream bacterial monitoring station was calibrated, adjusting only those parameters that do not affect the calibration of the upstream bacterial monitoring stations. The SchemaLinks' parameters (i.e., residence time) that can be adjusted for each bacterial monitoring station along the Aransas River are shown in Figure 6.70. Each station has a corresponding color that identifies the SchemaLinks' parameters that can be adjusted. However, only the most influential SchemaLink (i.e., directly upstream of the bacterial monitoring station and transporting the greatest bacterial load) was adjusted at each station.

After calibration was complete at each bacterial monitoring station in the Copano Bay watershed, the Schematic Processor Model was used to model the median fecal coliform concentration at each station. The residence time of each SchemaLink is shown in Figure 6.71.

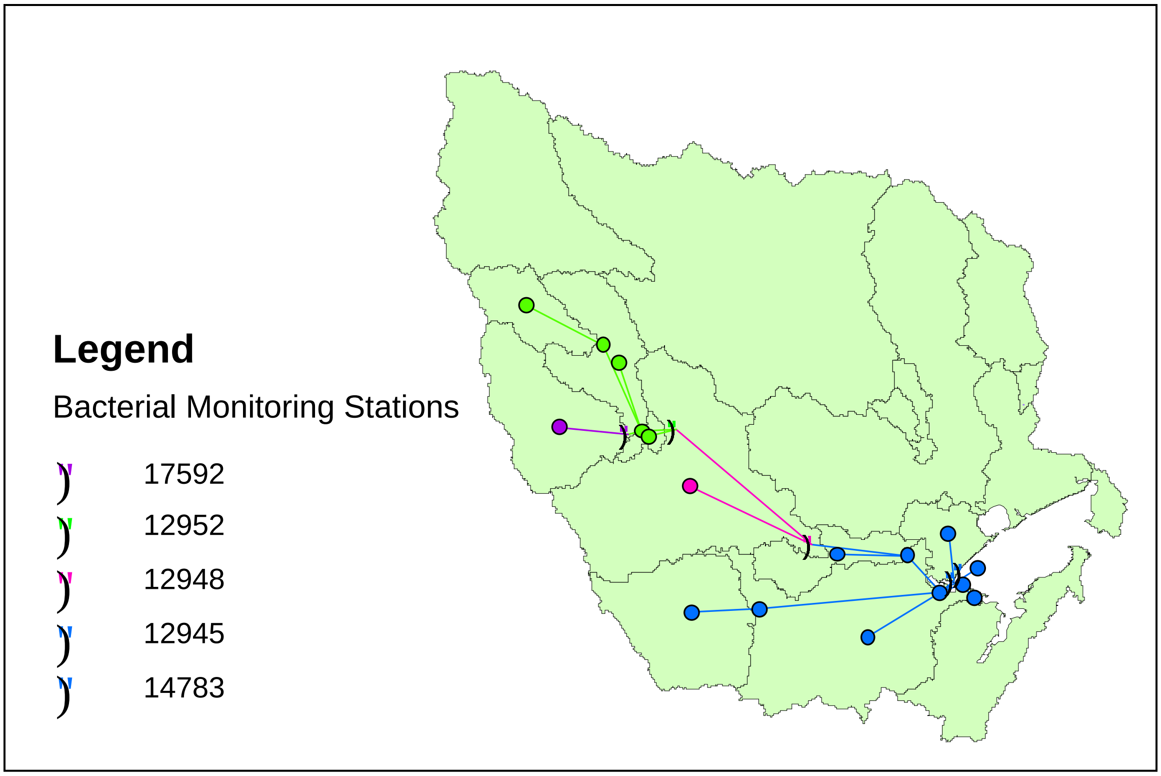


Figure 6.70 Nodes/Links' Parameters that can be Varied for Each Station along Aransas River

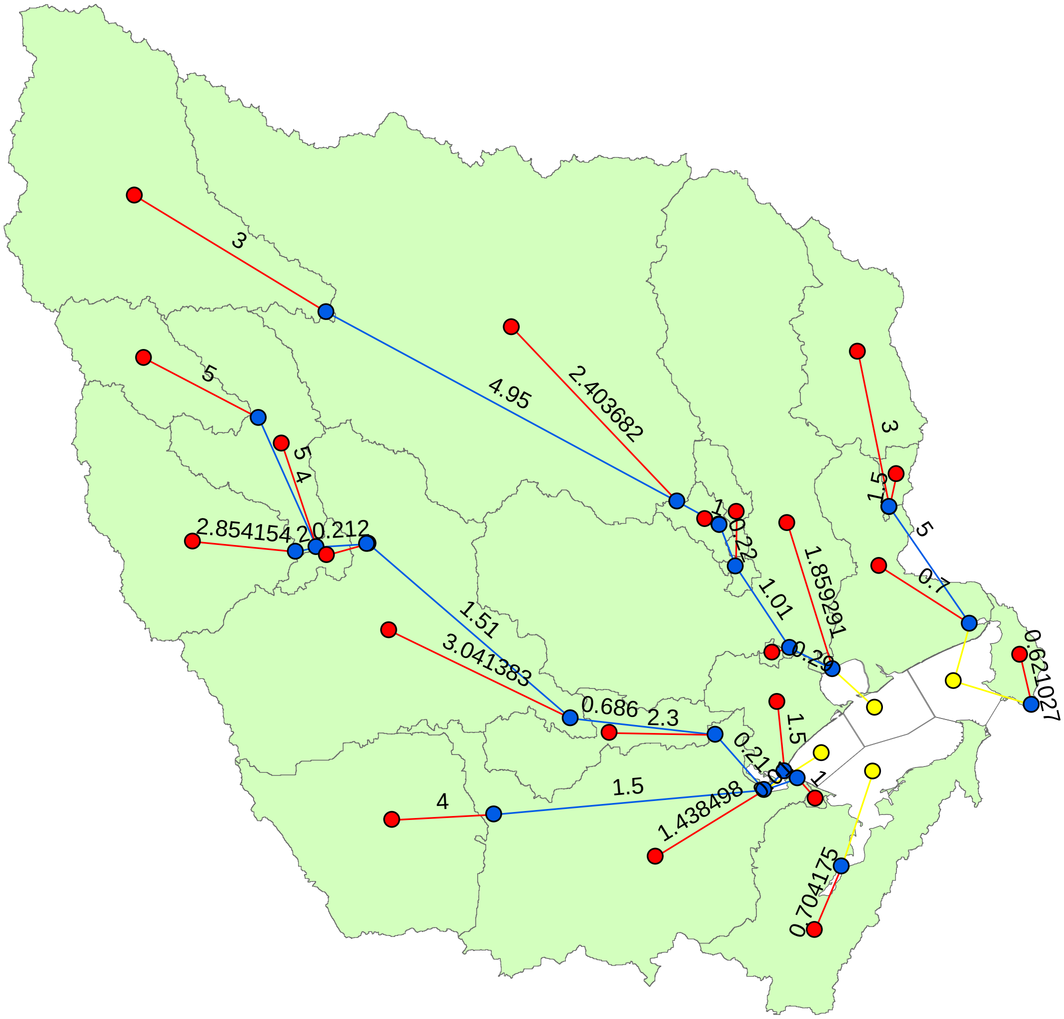


Figure 6.71 Residence Times (days) of SchemaLinks (k = 2 day^{-1}) for Schematic Processor Model

6.3.3.3 Volume of Copano Bay Segments

A rough approximation was made for calculating the individual volumes of the four Copano Bay segments that are shown in Figure 6.3. A bathymetry map, which shows the depth of different parts of the Bay, was used (Figure 6.72) to determine the average depth of each segment (Ward and Armstrong, 1997). The surface area of each of the water segments was found by opening the attribute table of each polygon feature class and looking under the field “ShapeArea”, which gives the area of the segment in square meters. For each of the four water segments (defined in Section 6.3.1.1), the depth was found by weighting the depth based on area covered by each of Ward’s segments that make up the segment. The volume was then calculated by multiplying the weighted depth by the surface area of each segment. The areas, depths, and volumes of each of the segments are given in Table 6.15.

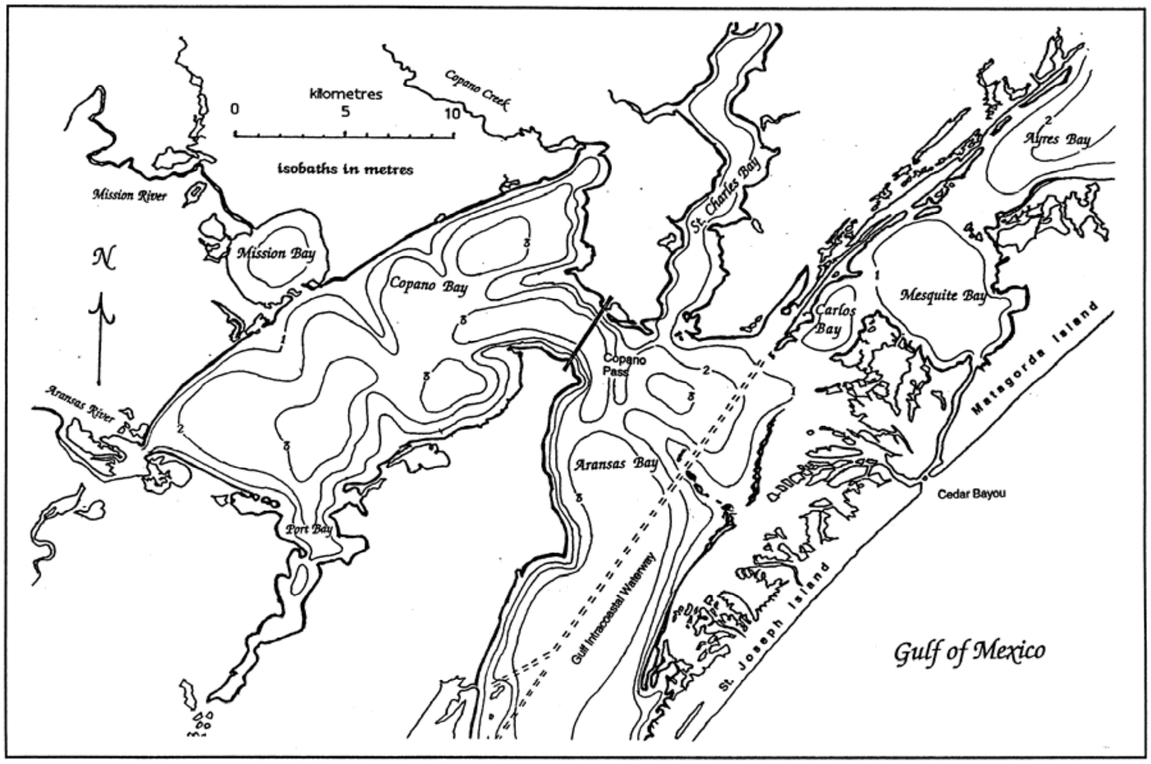


Figure 6.72 Bathymetry Map of Copano Bay

Table 6.15 Area, Depth, and Volume of Copano Bay Segments

Copano Bay Segment	**Original Segmentation**	**Area (m^2)**		**Depth (m)**		**Volume (m^3)**
1	PB1	3,078,276	69,062,585	1	1.98	136,843,257
	PB2	14,196,885		1		
	CP04	20,001,720		2.8		
	CP07	14,346,749		2		
	CP08	17,434,891		2		
2	AR1	4,524,570	31854530	1	1.86	59,184,474
	CP03	27,329,952		2		
3	M1	650,022	51,014,845	0.5	1.49	76,010,829
	M2	14,166,339		1		
	CP05	18,079,089		1.7		
	CP06	18,108,840		1.7		
4	CP01	846,994	52,170,162	0.5	2.55	132,923,219
	CP02	16,493,027		2		
	CP09	20,131,477		2.9		
	CP10	14,690,137		2.8		

6.3.3.4 Flow of Copano Bay Segments

The cumulative flow to each Copano Bay water segment was determined by finding the total annual upstream flow of the upstream watersheds to each Copano Bay segment. The cumulative annual runoff for each watershed was calculated using the runoff per watershed that was determined in Section 5.1.2.6 and runoff equations (Quenzer, 2003) that relate runoff to precipitation and land use. The cumulative runoff (m^3/year) to each Copano Bay segment is given in Table 6.16.

Table 6.16 Cumulative Annual Runoff to Copano Bay Segments

Copano Bay Water Segment	**Cumulative Annual Runoff (m^3/year)**
1	25,230,928
2	251,731,639
3	275,169,044
4	72,825,125

6.3.4 Implementation of Schematic Processor

Once the Schematic Network is created and the parameter values are input to the corresponding fields in the attribute tables of SchemaNode and SchemaLink, "Process Schematic" can be run. See Appendix 6.3 for the procedure on how to use "Process Schematic" and how to interpret the results.

All of the parameters and values of each corresponding SchemaNode in the Schematic Network are given in Table 6.17. "HydroID" is the unique identifier for each SchemaNode. "FeatureID" is the unique identifier for each watershed, so the SchemaNodes that have a FeatureID are nodes that represent watersheds. "SrcType" is the type of SchemaNode that the node represents; ("1" = watershed, "2" = drainage junction, "3" = Copano Bay.) "IncVal" is the sum of all the bacterial loadings from all sources (calculated in Section 5.6) that are input into the model at the specific SchemaNode. "Flow (m^3/yr)" is the cumulative annual runoff for each Copano Bay water segment (calculated in Section 6.3.3.4). "Volume (m^3)" is the volume of each Copano Bay water segment (calculated in Section 6.3.3.3). "Die-off rate (days^{-1})" is the decay coefficient associated with each node. "Cumulative Runoff (m^3/yr)" is the cumulative runoff of all the upstream watersheds that drain to the node of interest.

The HydroIDs of each of the SchemaNodes in the Schematic Network are shown in Figure 6.73.

Table 6.17 SchemaNode Attribute Table (Calibrated to Median Fecal Coliform Concentrations)

Hydro ID	Feature ID	Src Type	IncVal	Flow (m^3/yr)	Volume (m^3)	Die-off Rate (d^{-1})	Cumulative Runoff (m^3/yr)
61	0	2	0.00E+00	0	0	2	1.51E+07
62	0	2	3.22E+13	0	0	2	3.30E+07
63	0	2	0.00E+00	0	0	2	1.17E+08
64	0	2	4.79E+14	0	0	2	3.47E+07
65	0	2	7.96E+11	0	0	2	1.34E+08
66	0	2	0.00E+00	0	0	2	2.75E+08
67	0	2	1.48E+04	0	0	2	2.52E+08
68	0	2	0.00E+00	0	0	2	3.47E+07
69	0	2	3.37E+11	0	0	2	1.95E+07
70	0	2	9.17E+11	0	0	2	1.35E+08
71	0	2	0.00E+00	0	0	2	1.27E+08
72	0	2	0.00E+00	0	0	2	3.63E+07
73	0	2	0.00E+00	0	0	2	1.22E+08
74	0	2	0.00E+00	0	0	2	1.27E+08
75	0	2	0.00E+00	0	0	2	9.84E+07
77	45422	1	2.95E+16	0	0	2	0.00E+00
78	45413	1	1.09E+16	0	0	2	0.00E+00
79	45404	1	1.18E+16	0	0	2	0.00E+00
80	45419	1	6.25E+16	0	0	2	0.00E+00
81	45421	1	8.60E+15	0	0	2	0.00E+00
82	45417	1	4.45E+16	0	0	2	0.00E+00
83	45408	1	3.07E+16	0	0	2	0.00E+00
84	45415	1	1.17E+16	0	0	2	0.00E+00
85	45409	1	1.58E+15	0	0	2	0.00E+00
86	45426	1	7.67E+15	0	0	2	0.00E+00
87	45416	1	1.27E+16	0	0	2	0.00E+00
88	45405	1	8.17E+15	0	0	2	0.00E+00
89	56831	1	1.16E+15	0	0	2	0.00E+00
90	0	2	1.75E+12	0	0	2	1.72E+07
91	0	2	0.00E+00	0	0	2	5.45E+06
92	0	2	6.98E+14	0	0	2	3.79E+07
93	0	2	0.00E+00	0	0	2	2.52E+07
94	0	2	0.00E+00	0	0	2	5.32E+06
95	0	2	0.00E+00	0	0	2	6.75E+07
96	56830	1	6.51E+15	0	0	2	0.00E+00
97	45412	1	6.42E+13	0	0	2	0.00E+00

98	0	2	0.00E+00	0	0	2	3.63E+07
99	45423	1	9.81E+14	0	0	2	0.00E+00
100	45418	1	1.67E+15	0	0	2	0.00E+00
101	0	2	0.00E+00	0	0	2	3.50E+05
102	45425	1	4.02E+13	0	0	2	0.00E+00
103	45414	1	6.89E+15	0	0	2	0.00E+00
104	45410	1	1.02E+15	0	0	2	0.00E+00
105	45406	1	7.40E+14	0	0	2	0.00E+00
153	0	3	1.48E+09	2.75E+08	7.60E+07	2	2.75E+08
154	0	3	2.22E+09	2.52E+08	5.92E+07	2	2.52E+08
155	0	3	3.96E+11	2.52E+07	1.37E+08	2	2.52E+07
156	0	3	1.22E+11	7.28E+07	1.33E+08	2	7.28E+07

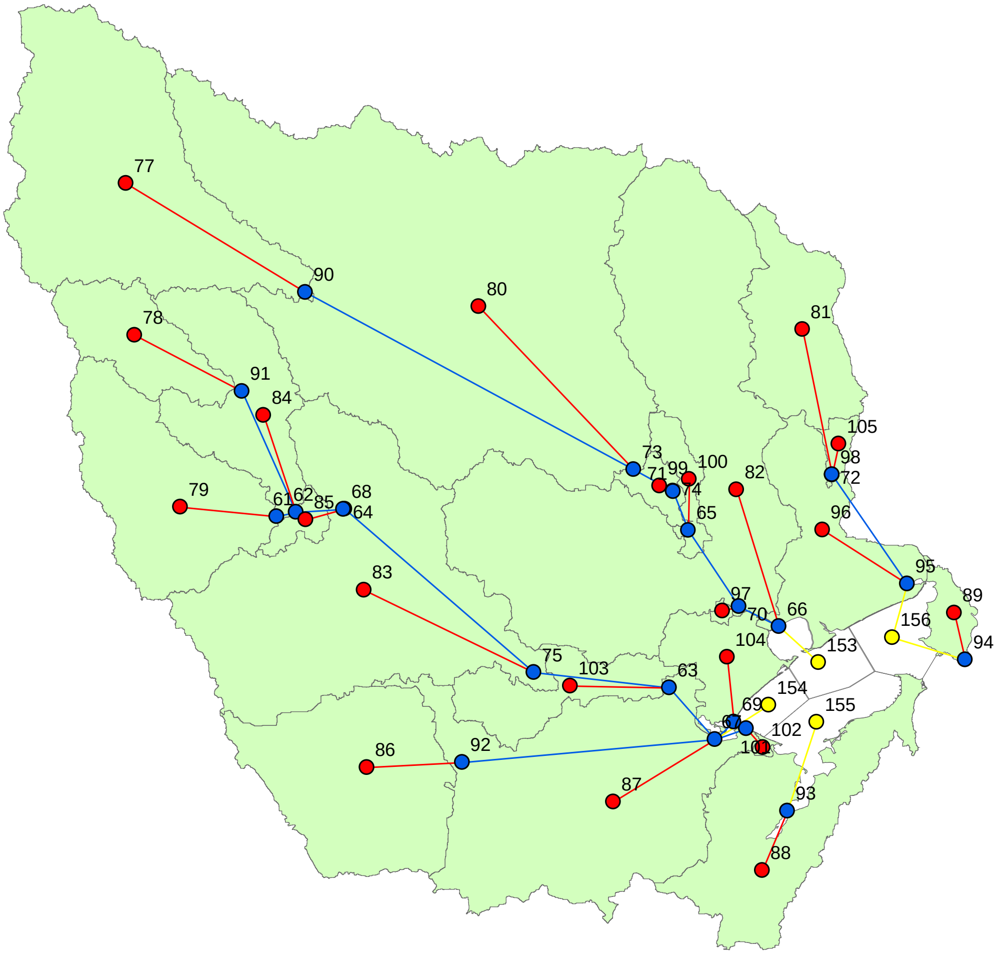


Figure 6.73 HydroIDs of SchemaNodes

All of the parameters and values of each corresponding SchemaLink in the Schematic Network are shown in Table 6.18. “HydroID” is the unique identifier for each SchemaLink. “FromNodeID” is the HydroID of the upstream SchemaNode, and “ToNodeID” is the HydroID of the downstream SchemaNode. “LinkType” is the type of SchemaLink that the link represents; (“1” = watershed travel, “2” = river, “3” = Copano Bay.) “Die-off rate (days^{-1})” is the decay coefficient associated with each link. “Residence Time (days)” is the amount of time the bacteria are allowed to decay in each water segment (SchemaLink), which was determined in Section 6.3.3.2.

The HydroID of each of the SchemaLinks in the Schematic Network is shown in Figure 6.74.

Table 6.18 SchemaLink Attribute Table (Calibrated to Median Fecal Coliform Concentrations)

HydroID	**FromNodeID**	**ToNodeID**	**LinkType**	**Die-off Rate (days^{-1})**	**Residence Time (days)**
106	61	62	2	2	2.00
107	75	63	2	2	0.69
108	68	64	2	2	0.05
109	74	65	2	2	0.22
110	70	66	2	2	0.29
111	91	62	2	2	4.00
112	63	67	2	2	0.21
113	62	68	2	2	0.21
114	69	67	2	2	0.01
115	65	70	2	2	1.01
116	73	71	2	2	1.42
117	98	72	2	2	0.05
118	90	73	2	2	4.95
119	71	74	2	2	0.05
120	64	75	2	2	1.51
121	101	67	2	2	0.01
122	92	67	2	2	1.50
123	77	90	1	2	3.00

124	78	91	1	2	5.00
125	79	61	1	2	2.85
126	83	75	1	2	3.04
127	86	92	1	2	4.00
128	80	73	1	2	2.40
129	82	66	1	2	1.86
130	97	70	1	2	0.18
131	81	98	1	2	3.00
132	99	71	1	2	1.00
133	100	65	1	2	2.00
134	87	67	1	2	1.44
135	88	93	1	2	0.70
136	89	94	1	2	0.62
137	96	95	1	2	0.70
138	72	95	2	2	5.00
139	102	101	1	2	1.00
140	84	62	1	2	5.00
141	85	68	1	2	3.12
142	103	63	1	2	2.30
143	104	69	1	2	1.50
144	105	72	1	2	1.50
157	66	153	3	2	0.00
158	67	154	3	2	0.00
159	93	155	3	2	0.00
160	95	156	3	2	0.00
161	94	156	3	2	0.00

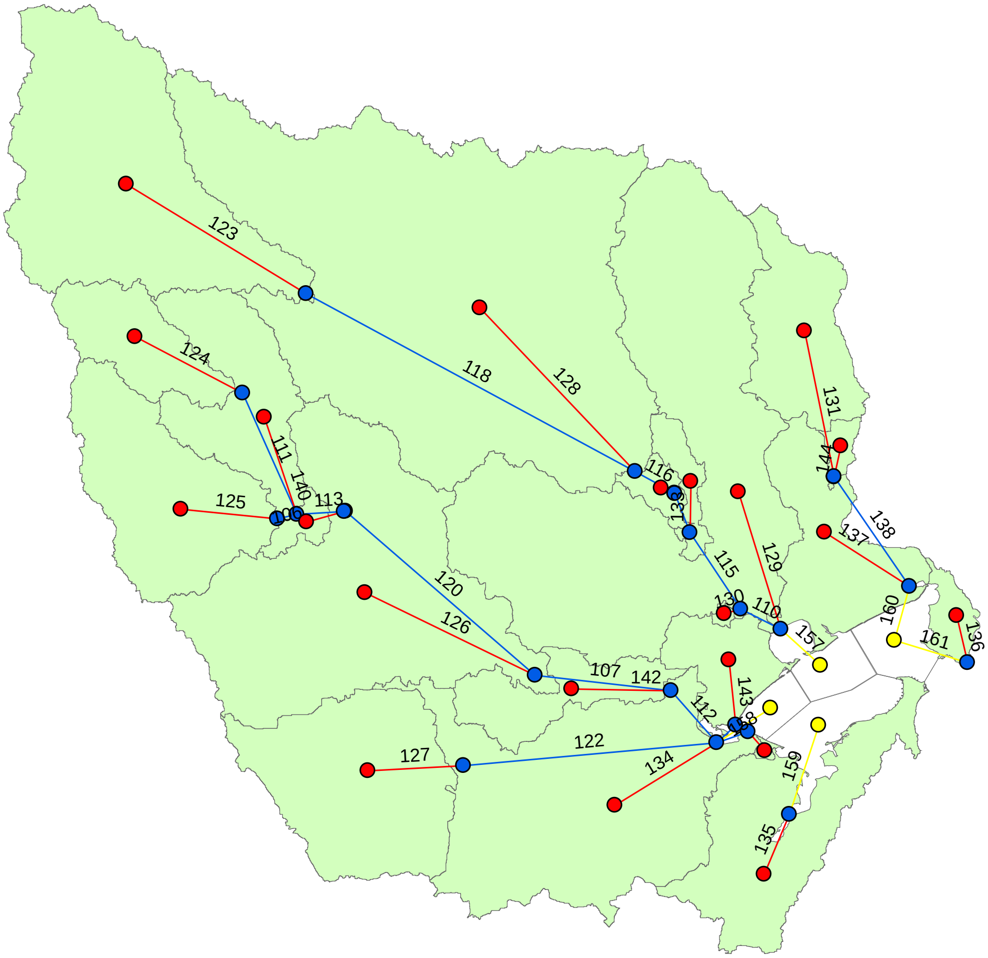


Figure 6.74 HydroIDs of SchemaLinks

6.4 RESULTS

The current loadings to each of the water segments (Aransas River Tidal, Mission River Tidal, and Copano Bay) are given in Chapter 8 of this report.

After one simulation of the Schematic Processor was run, the bacterial loading was converted to bacterial concentration (CFU/100mL) at each of the SchemaNodes. The modeled fecal coliform concentration at each SchemaNode is shown in Figure 6.75.

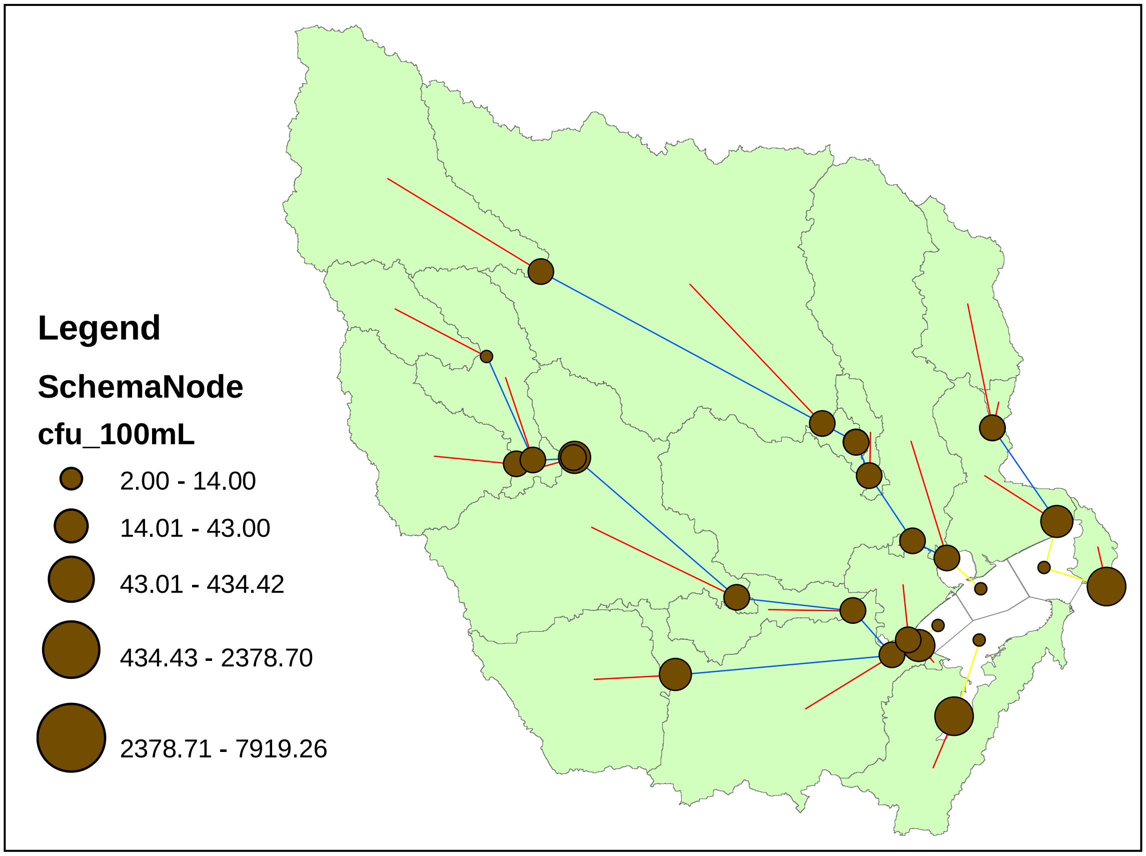


Figure 6.75 Fecal Coliform Concentrations (CFU/100mL) – Schematic Processor Results

The fecal coliform concentrations of SchemaNode Src Types 2 and 3 and the modeled concentrations versus the measured median fecal coliform concentrations at the bacterial monitoring station locations are shown in Table 6.19.

Table 6.19 Modeled versus Existing Fecal Coliform Concentrations: Schematic Processor Model

SchemaNode HydroID	**Bacterial Monitoring Station ID**	**Modeled Fecal Coliform Concentration (CFU/100mL)**	**Measured Median Fecal Coliform Concentration (CFU/100mL)**
61	17592	**260.00**	**260**
62		101.27	
63		79.60	
64		1444.23	
65		94.09	
66		405.26	
67		345.32	
68	12952	**71.98**	**72**
69		262.88	
70	12943	**46.57**	**47**
71		128.20	
72		154.59	
73		418.77	
74	12944	**116.00**	**116**
75	12948	**96.01**	**96**
90		434.42	
91		9.04	
92		1847.85	
93		7919.26	
94		6318.24	
95		2378.70	
98		58.72	
101		1555.86	
153	14797	**2.00**	**2**
154	12945, 14783, 14787, 14788	**2.00**	**2**
155	13405, 14782, 14784, 14790	**2.00**	**2**
156	13404, 14779, 14780, 14785, 14792, 14793	**2.00**	**2**

As shown in Table 6.19, the modeled fecal coliform concentrations from the Schematic Processor Model match up very well with the existing median fecal coliform concentrations.

This is one simulation of the Schematic Processor model (Figure 6.75 and Table 6.19), and this simulation is supposed to be representative of average annual conditions. That is why the modeled concentrations are compared to the median fecal coliform concentrations of monitoring data from 1999 to 2005.

The concentrations in all segments of the Bay are constant as modeled (at 2 CFU/100mL.) This is consistent with the monitoring data in each portion of the Bay. All segments of the Bay are currently meeting the median fecal coliform standards for oyster harvesting use (< 14 CFU/100mL). Thus, the Schematic Processor Model was not used to determine the load reductions necessary to meet water quality standards because it does not generate a probability distribution (the criterion of 90th-percentile < 43 CFU/100mL is exceeded in two Copano Bay segments.) The Monte Carlo Simulation Model (described in Chapter 7) is used to determine load reductions.

Thus, the results of the Schematic Processor model were used to explore the impact of the different bacteria sources on the four segments of Copano Bay. The bacterial loading from each source, as calculated in Chapter 5, was input to the Schematic Processor model (bacterial loading of a source = "IncVal", Schematic Processor is run, and then the "PassedVal" and "TotVal" fields were stored as the bacterial loading impact from that particular source).

The effects of bacterial decay along the SchemaLinks as the bacteria travel from the upstream watersheds (bacterial loadings not shown), along the rivers, and to Copano Bay are shown in Figure 6.76.

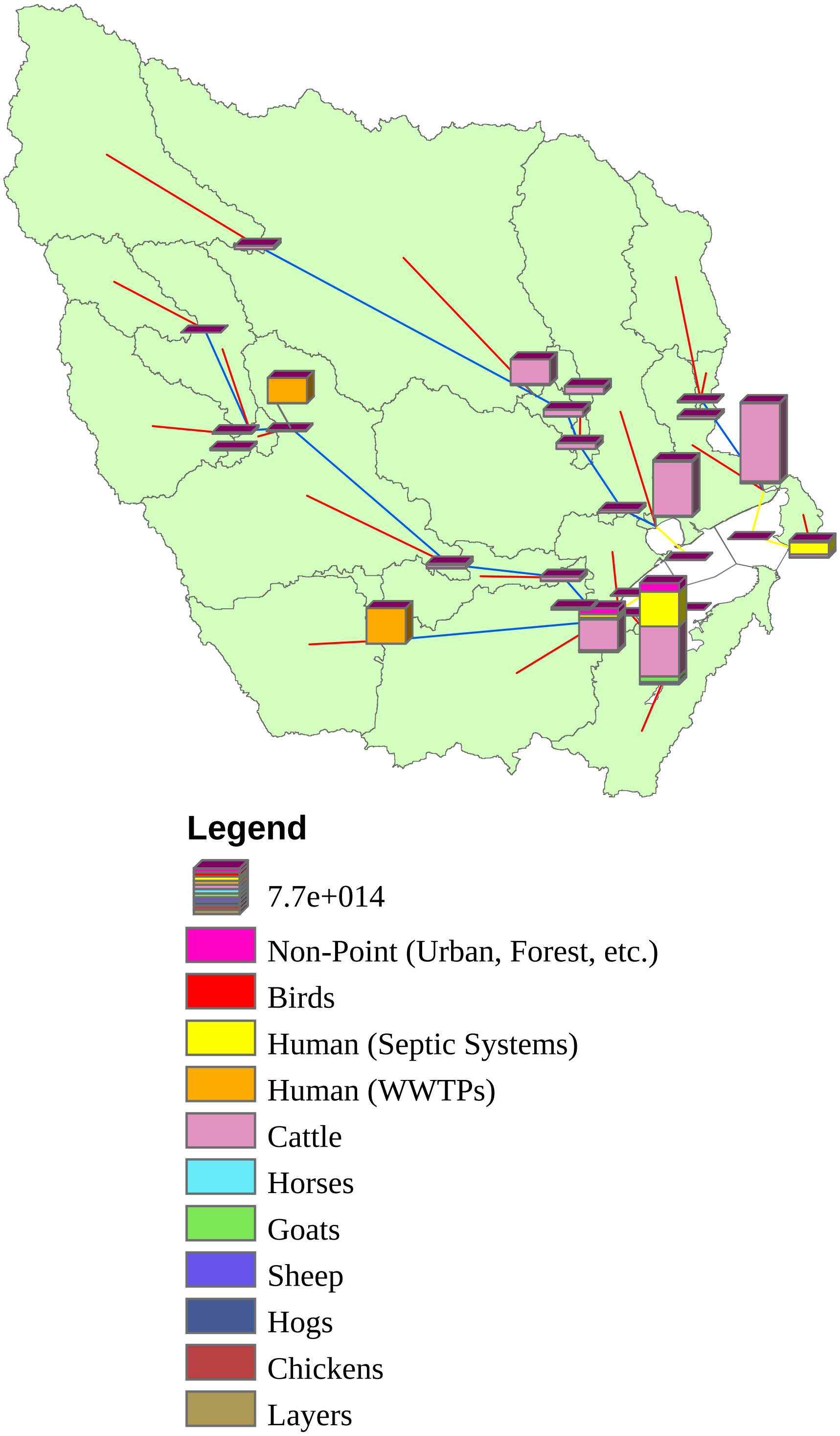


Figure 6.76 Bacterial Loadings (from Sources) to SchemaNodes SrcTypes 2 and 3

The watersheds that will most influence the quality of the Bay are the watersheds directly upstream and adjacent to the Bay because the bacteria have not had as long to decay as the bacteria from watersheds farther upstream of the Bay. Looking at the watersheds directly adjacent to the Bay (Figure 6.76), it can be seen that cattle are the greatest bacteria contributors to all Copano Bay segments.

The total bacterial loadings (CFU/year) to each of the Copano Bay water segments after decay and mixing in the CFSTRs are modeled, are shown in Figure 6.77.

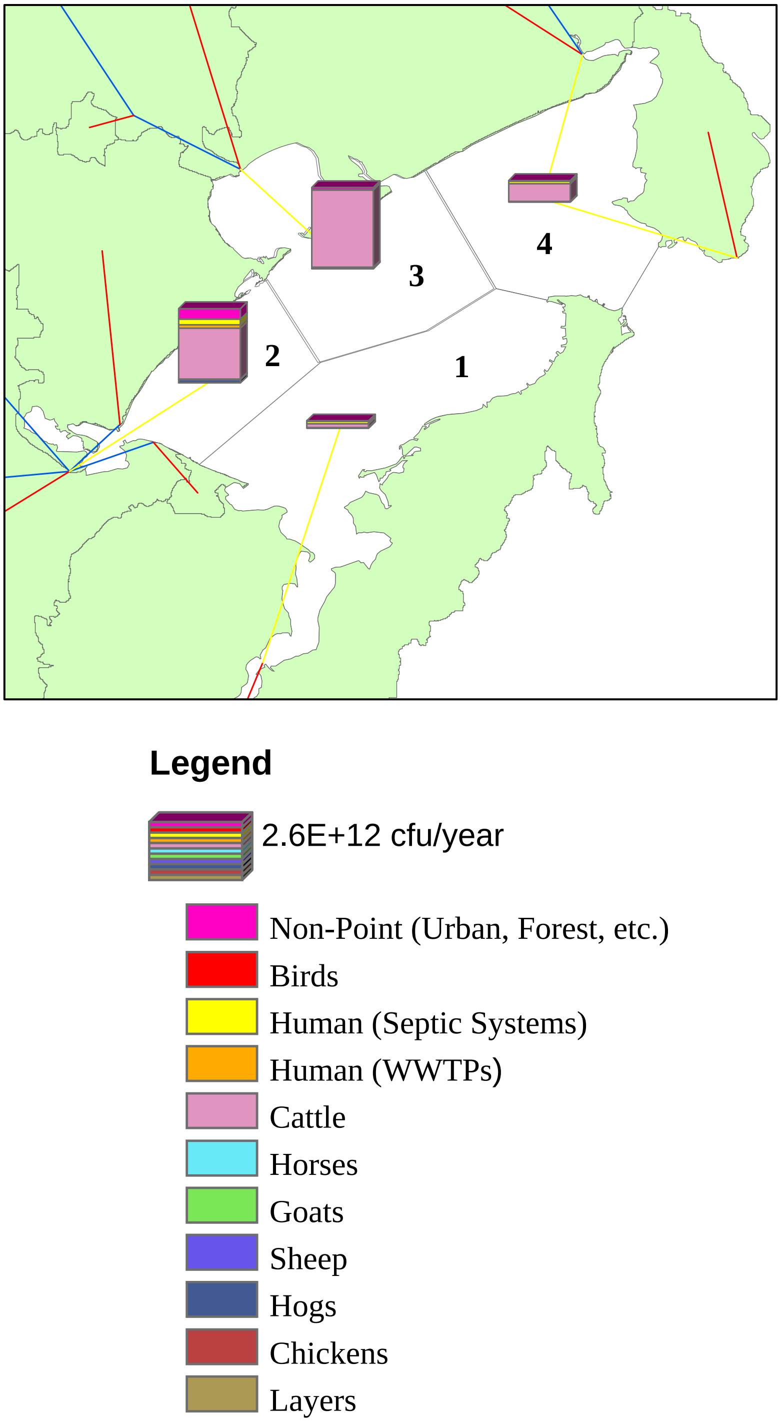


Figure 6.77 Bacterial Loading (from Sources) to Copano Bay (CFU/year)

As shown in Figure 6.77, Copano Bay Segments 2 and 3 have the highest bacterial loads compared to the other segments. However, due to the larger cumulative flow in these portions of the Bay and an increased number of upstream watersheds draining to these portions of the Bay, the median fecal coliform concentration is the same in each segment. Recall that Equation 6.2 is used to calculate the concentration of fecal coliform in each segment of the Bay.

The percent distribution of the bacterial loadings to all four segments of Copano Bay is shown in Figure 6.78. In all four Copano Bay segments, cattle are the dominant bacterial loading contributor based on the model and bacterial loading calculations.

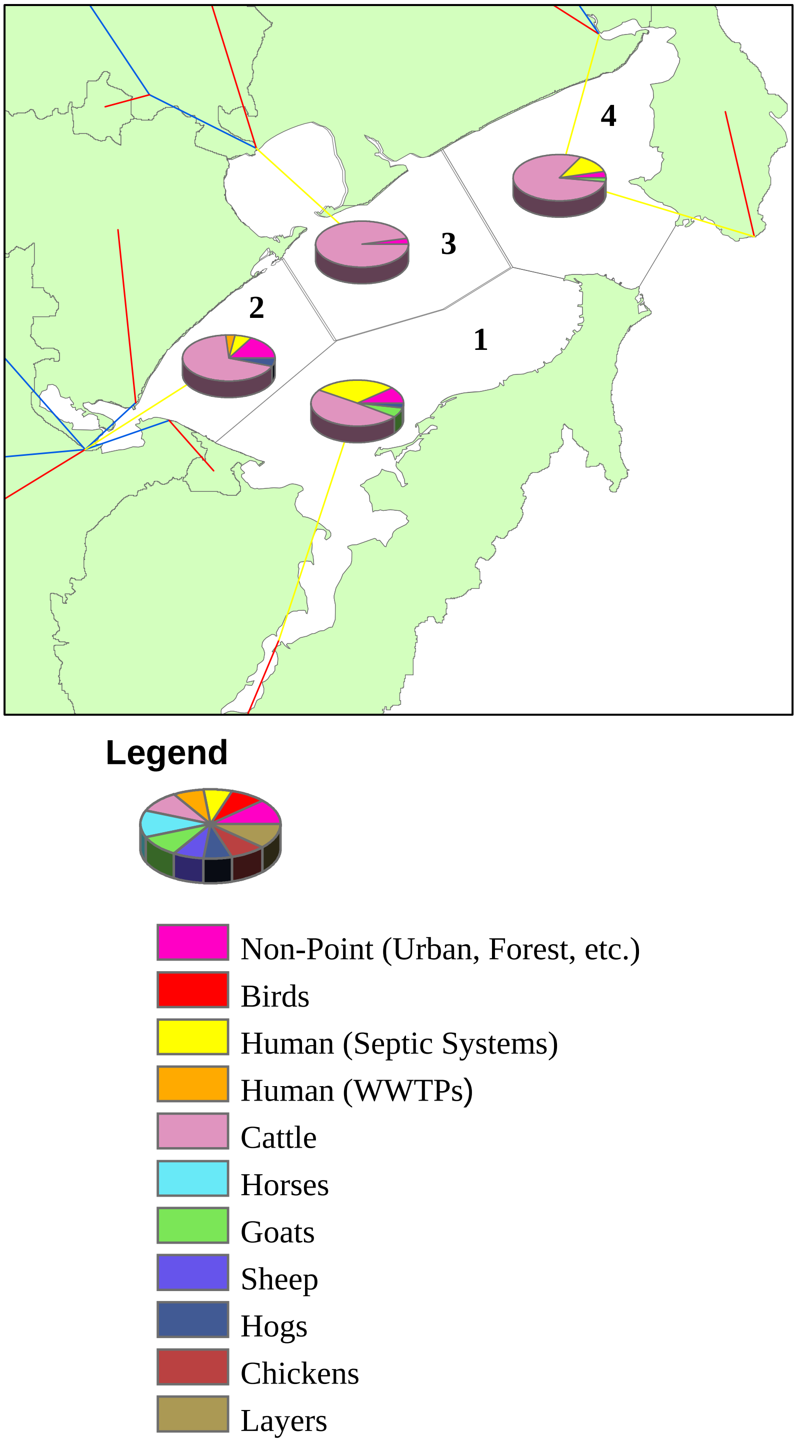


Figure 6.78 Percent Distribution of Bacterial Loading Sources (Output)

In Section 5.6, the total bacterial loadings input into the model are described; with this information, the effects of the bacterial loadings from different sources on the fecal coliform concentration in the Bay can be examined (since the effects of bacterial transport have been implemented). For instance, the avian loading, which is the only source load that is applied directly to the Bay, does not have as great an impact on the Bay; (see Figure 5.25). This seems reasonable since the magnitudes of the bacterial loadings from avian sources (Section 5.3.3) are so much less than the magnitudes of the bacterial loadings from cattle (Section 5.2.3). Thus, even though avian loads are applied directly to the Bay and one upstream watershed, the effects of these loadings are negligible compared to other sources (see Figure 6.78).

One of the watersheds that drains into Copano Bay Segment 4 (Figure 6.76) contains fecal coliform predominantly from human sources (i.e., septic systems), as shown in Figure 5.25. However, after we account for the effects of bacterial transport and the loadings from the other upstream watersheds that drain to Segment 4, the bacterial loadings from cattle dominate. Septic system bacterial loading of one of the upstream watersheds of Segment 4 dominates (as shown in Figure 6.76), but the magnitude of the bacterial loading is significantly smaller than the other upstream watersheds that also drain into Segment 4 (where cattle is the main contributor). Thus, even though the loadings from one of the upstream watersheds is predominantly from malfunctioning septic systems, the overall bacterial load from that particular watershed is significantly lower than the bacterial loads from other contributing upstream watersheds. Malfunctioning septic systems appear to have an impact on Segments 1 and 4. However, Segments 1 and 4 are currently not exceeding Texas Surface Water Quality Standards for fecal coliform oyster harvesting use.

The other results from the Schematic Processor Model are discussed in Chapter 8.

Chapter 7: Modeling of Bacterial Transport – Monte Carlo Simulation

7.1 BACKGROUND

The 90th-percentile fecal coliform concentration needs to be less than 43 CFU/100mL to meet oyster water use standards in Copano Bay. A second model was created to predict probability distributions of fecal coliform since the Schematic Processor Model does not have this capability. The second model (created by Ernest To, CRWR) conducts a Monte Carlo simulation analysis for the Copano Bay watershed and models bacterial transport the same as the Schematic Processor Model (applying first-order decay and treating the Bay as four CFSTRs).

Monte Carlo analysis picks random numbers from a probability distribution associated with uncertain parameters to simulate random behavior based on the parameter distributions. Conducting Monte Carlo simulations generates multiple outcomes (i.e., fecal coliform concentrations) by repeatedly sampling values from probability distributions of uncertain parameters and plotting the results as a probability distribution. If the model accurately represents what is occurring in the watershed, then the output distribution (i.e., modeled fecal coliform concentrations) should match the actual distribution (i.e., measured fecal coliform concentrations) at the specific point of interest (i.e., bacterial monitoring station).

A schematic diagram was created to show how the Monte Carlo simulation analysis works for this project and is shown in Figure 7.1. Shown are the parameters and inputs associated with one output location (i.e., bacterial monitoring station 17592). Because only one SchemaLink and SchemaNode exist upstream of Station 17592, there is only one k-distribution, one bacterial loading distribution, and one residence time upstream of this location. The more SchemaLinks and SchemaNodes that are upstream of a bacterial monitoring station, the more inputs and parameters can affect the output distribution results.

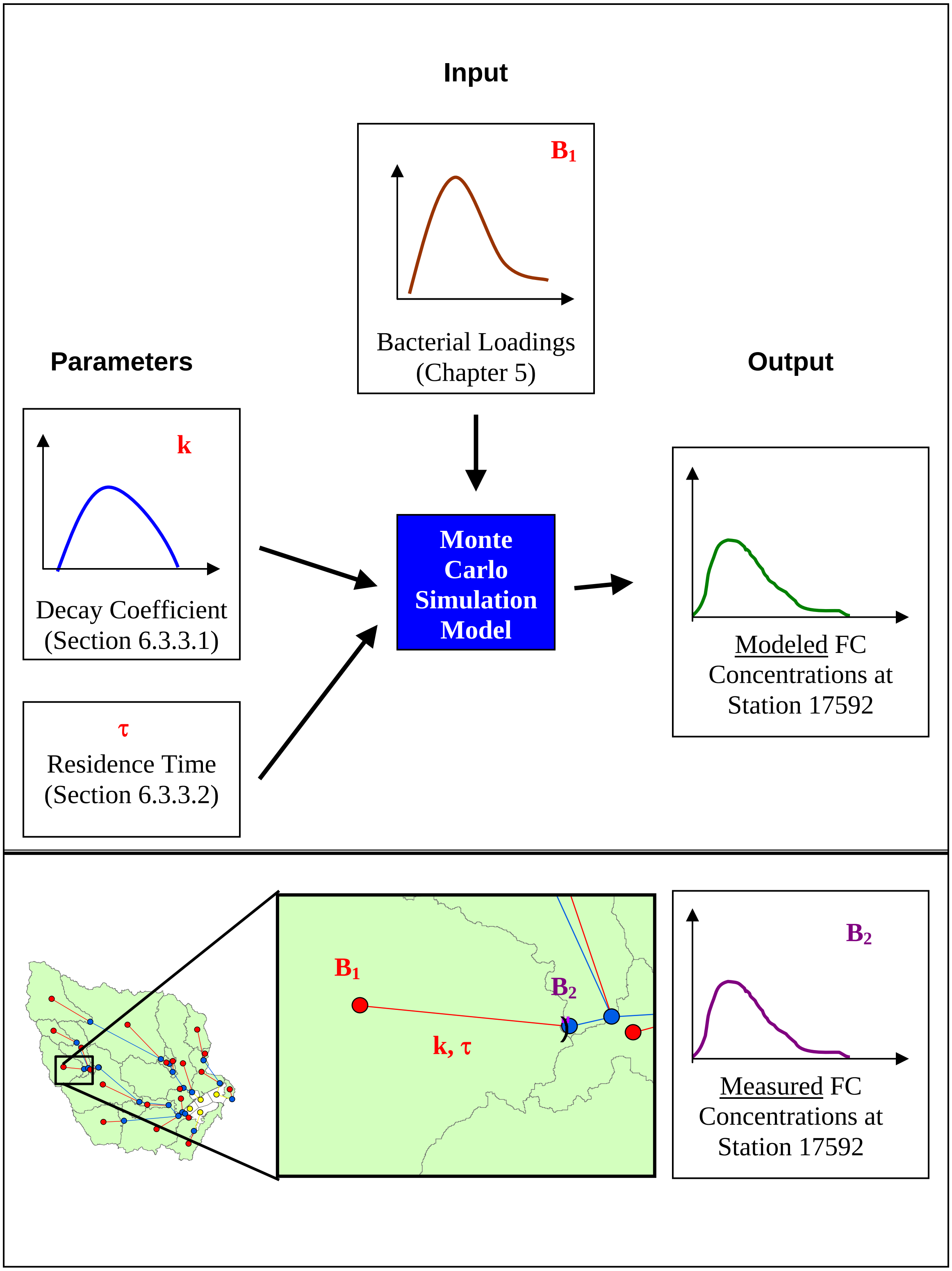


Figure 7.1 Monte Carlo Simulation Conceptual Diagram

The output distribution (shown in Figure 7.1) is then compared to the measured distribution from the bacterial monitoring station to determine if the model accurately characterizes the Copano Bay system, which it does in this situation. The schematic diagram (shown in Figure 7.1) is cited in the following sections to clarify the implementation of the model.

The Monte Carlo Simulation Model was created in Microsoft Excel 2003. The original intention was to perform the Monte Carlo analysis in ArcGIS Model Builder. However, Excel was chosen instead because it has built-in procedures that can sample from different probability distributions, it has built-in graphing capabilities, and the analysis takes a shorter amount of time to run because it is faster to update spreadsheets than to access and update databases (To, 2005).

This chapter discusses how the Monte Carlo Simulation Model was applied and used for the Copano Bay project. However, the procedure for creating the Monte Carlo Simulation Model and the programming code and macros behind the model will not be discussed in this report. The user interface of the Monte Carlo Simulation Model, which are all of the worksheets used in Microsoft Excel, and explanations of the important features and parameters used in running the model are shown in Appendix 7.1.

For the Copano Bay project, the Monte Carlo Simulation Model was used to model existing bacterial concentration conditions at all SchemaNode locations as well as to determine the load reductions necessary to reduce the fecal coliform bacteria concentrations to meet Texas Surface Water Quality Standards.

7.2 METHODOLOGY

To use the Monte Carlo Simulation Model, the following steps were completed:

1. Schematic Network of the Copano Bay watershed was created (Section 6.3.1).
2. Annual average bacterial loadings were calculated (Chapter 5).
3. The parameters (or parameter distributions) of each SchemaNode and SchemaLink were determined through calculations and/or calibration.

The Monte Carlo Simulation Model was calibrated at each bacterial monitoring station to match the existing bacterial monitoring data (from 1999-2005). Once the model was calibrated, the model was used to determine the load reductions required from various bacterial sources to attain fecal coliform water quality standards in each of the water segments.

7.3 PROCEDURE OF APPLICATION

7.3.1 Determination of Parameters

The following sections describe how the parameters were determined for each SchemaLink and SchemaNode in the Schematic Network for the Monte Carlo Simulation Model.

7.3.1.1 Bacterial Loading

Recall that the bacterial loading was calculated by using the following equation: L = Q * C, where L = bacterial loading, Q = flow rate, and C = fecal coliform concentration. Based on this equation, it can be seen that the bacterial loading to all of the water segments is going to vary throughout the year. There are many factors (e.g., precipitation and runoff), which would affect the bacterial loadings (the input into the model) in the watershed. For example, when the precipitation and runoff in the watershed are very high, then the bacterial loadings dramatically increase and affect the quality of the receiving waters.

The calculations of the average annual bacterial loadings from the point and non-point bacteria sources in the watershed are described in Chapter 5. From the data analysis in Chapter 4, the measured bacterial concentrations at the bacterial monitoring stations are very similar to a lognormal distribution; thus, the bacterial loadings for the Monte Carlo Simulation Model are assumed to be log normally distributed.

At each SchemaNode in which bacteria are input into the model (e.g. SchemaNodes SrcType =1, which are watersheds), a lognormal distribution of the bacterial loadings was determined. While running a simulation of the Monte Carlo Simulation Model, the model randomly selects a bacterial loading at each SchemaNode based on these lognormal distributions. For example, looking at Figure 7.1, there is only one SchemaNode that has a bacterial loading input into the model that would affect the water quality at Station 17592; thus, the Monte Carlo Simulation Model randomly selects one bacterial loading, B_1, from the lognormal distribution and then simulates the decay of bacterial transport by randomly selecting one decay coefficient from the k-distribution (described in Section 7.3.1.2) and the given residence time for the upstream SchemaLink (described in Section 7.3.1.3) to obtain one output fecal coliform concentration by applying the equation: $[B_1 * \exp(-k\tau)]/Q$ = modeled fecal coliform bacterial concentration[16]. To get a distribution of modeled fecal coliform concentrations in the output, the model is run multiple times.

Two main parameters are used to create the lognormal distributions at each bacterial loading source (e.g., watershed or drainage point): the *median* of the bacterial loadings and a *multiplication factor* that is associated with the standard deviation and spread of the distribution. The median of each lognormal distribution was assumed to be the average annual bacterial loading that was calculated in Chapter 5, and the multiplication factor is described in the following[17]. Microsoft Excel cannot directly sample from a lognormal distribution with a given mean and standard deviation, but Excel can sample from a unit normal distribution (a.k.a, z-curve). As a result, the lognormal distribution has to undertake a series of transformations to create a unit normal distribution in which the mean = 0 and the standard deviation = 1. The bacterial load distributions are modeled as lognormal distributions (Figure 7.2).

---

[16] Q is the cumulative annual runoff upstream of the point of interest, and the calculation of Q for each watershed is described in Section 5.1.2.6.

[17] Ernest To, CRWR, provided the information necessary to describe the Excel process and define the multiplication factor.

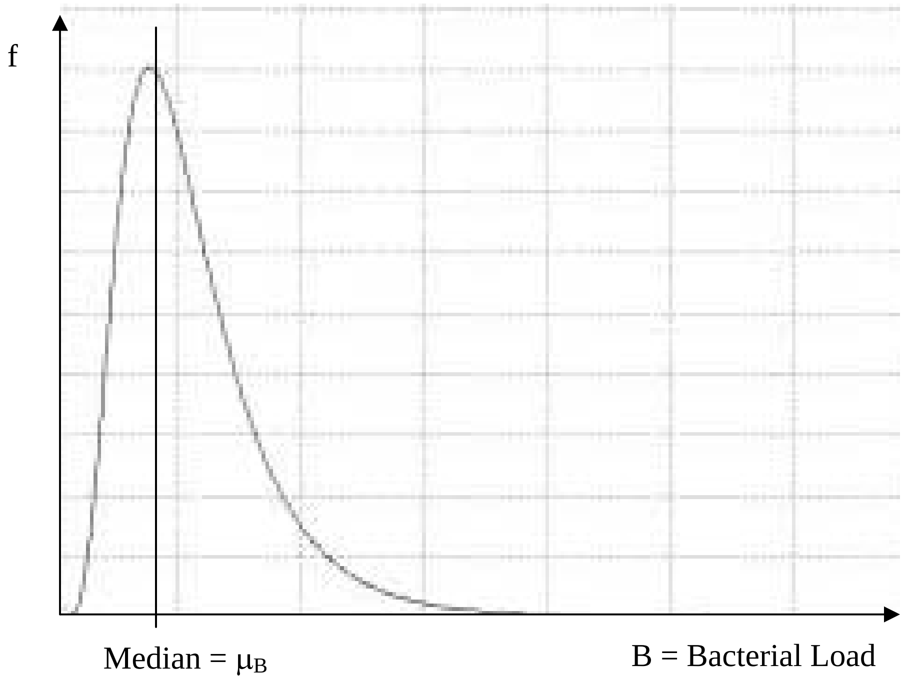


Figure 7.2 Bacterial Load Distribution Modeled as Lognormal Distribution

The step-by-step procedure for the transformation of the lognormal distribution (Figure 7.2) into a unit normal distribution is described below:

1. Normalize the lognormal distribution with the median to obtain a lognormal distribution with a median of 1 (Figure 7.3).

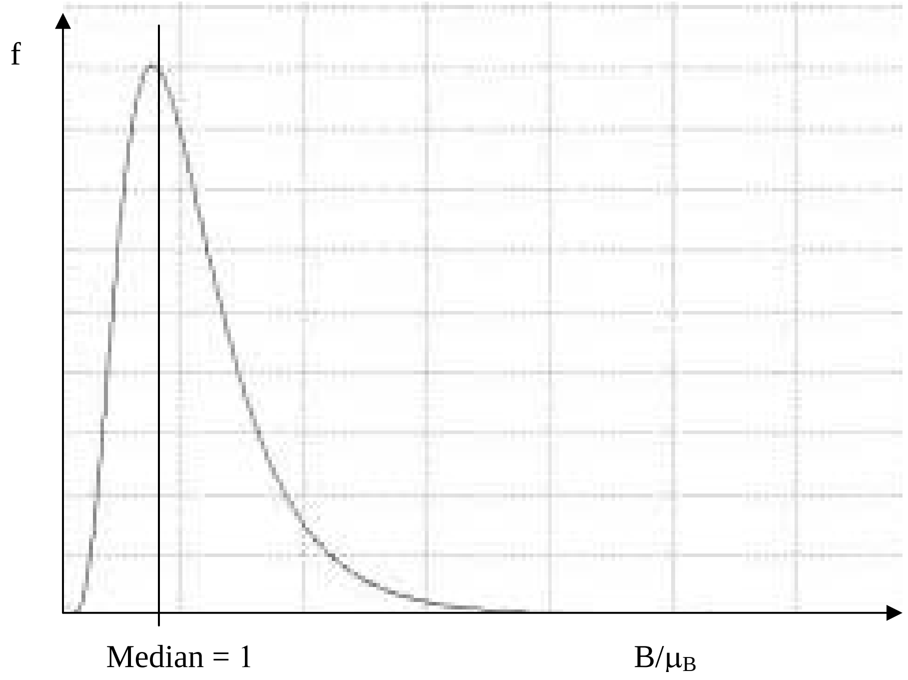


Figure 7.3 Lognormal Distribution with Median = 1 (Normalized Lognormal Distribution by μ_B)

2. Take the natural-log, ln( ), of the lognormal distribution (Figure 7.3) to transform the distribution into a normal distribution with mean = median = 0 and standard deviation, $\sigma_{\ln(B/\mu B}$ (Figure 7.4). The standard deviation of this normal distribution is also referred to as the *multiplication factor*. Thus, the multiplication factor = $\sigma_{\ln(B/\mu B).}$

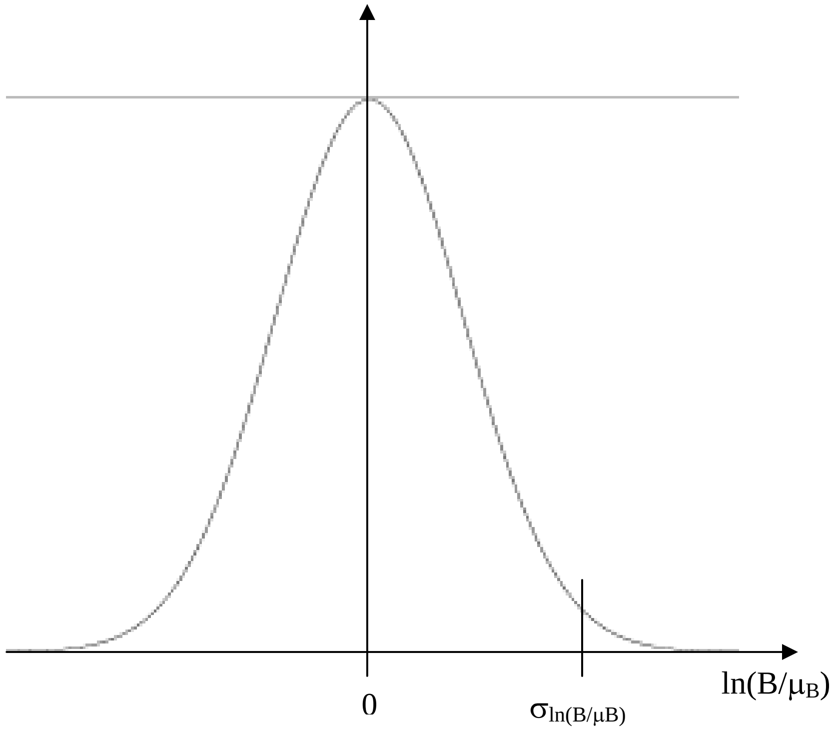


Figure 7.4 Normal Distribution with Mean = Median = 0 and Standard Deviation, $\sigma_{\ln(B/\mu B)}$

3. Normalize the normal distribution (Figure 7.4) by the multiplication factor, $\sigma_{\ln(B/\mu B)}$, to obtain a unit normal distribution with standard deviation of 1 (a.k.a, the z-curve).

Microsoft Excel can randomly sample from a unit normal distribution (Figure 7.4), so to obtain the fecal coliform bacterial loading from the original lognormal distribution (Figure 7.2), Excel needs to work backwards (through Steps #1-3) from the normal distribution (Figure 7.4). The formula used in Excel to find the sampled bacterial loading from the original lognormal distribution (Figure 7.2), B_1, is given below:

$$B_1 = \mu_B \text{ x EXP (} \sigma \ln (B/\mu_B) \text{ x NORMINV (ABS (RAND( ),0,1))}$$

The multiplication factor can be related to the coefficient of variation, which is the standard deviation divided by the mean. Thus, the greater the multiplication factor the greater the spread of the distribution of bacterial loadings.

The multiplication factor was one of the parameters that were adjusted to try to match the modeled output fecal coliform distributions to the measured fecal coliform distributions at each bacterial monitoring station. The results of the calibration are given in Section 7.3.2.

7.3.1.2 Decay Coefficient

The procedure for how a k-distribution was determined for a portion of the model is described in Section 6.3.3.1. Due to lack of data and studies in the Copano Bay watershed with regard to bacterial decay, the k-distribution given in Table 6.3 was used for all the SchemaLinks in the Schematic Network.

The k-distribution varies from approximately 2 to 2.5 days^{-1}. A beta distribution was used to represent the k-distribution for the Monte Carlo Simulation Model as explained in Appendix 7.1. The beta distribution that was chosen for the analysis was $\alpha = 2$ and $\beta = 2$, which is shown in Figure 7.5 (Wikipedia, 2006). The lower and upper limits are 2 and 2.5 days^{-1}, respectively. Ignoring the large storm event (see Table 6.3; k = 0.8 days^{-1}), the average of the remaining four decay coefficients is approximately 2.25 days^{-1}. Thus, instead of skewing the distribution, it was assumed that the likelihood of the decay coefficient being 2.25 days^{-1} is higher than the probability of the decay coefficient being either 2 or 2.5 days^{-1}. Thus, the probability of the decay coefficient being 2.25 days^{-1} was assumed highest, and the probability of the decay coefficient being 2 or 2.5 days^{-1} was lowest. Each simulation the Monte Carlo Simulation Model randomly selects a decay coefficient for each SchemaLink based on this probability distribution in the Copano Bay watershed.

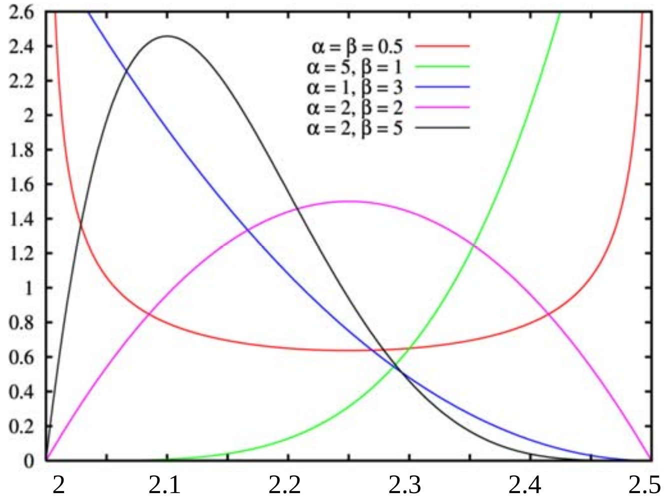


Figure 7.5 Beta Distribution

7.3.1.3 Residence Time

The initial residence times, which are shown in Figure 6.71, for the SchemaLinks in the Monte Carlo Simulation Model were the residence times that were used in the Schematic Processor Model. The reason that a distribution was not found for the residence time of each SchemaLink (particularly since precipitation and flow vary greatly throughout the year) was because the bacterial loadings have lognormal distributions associated with them. Running a Monte Carlo simulation on both parameters may counteract the intended effect. For instance, in one simulation a high bacterial loading may be randomly selected from the upstream SchemaNode (Figure 7.1), which would indicate a high flow event; however, if there is a probability distribution associated with the residence time of the SchemaLink, then the model may select a longer residence time, which would indicate a low flow event. Thus, the effects of a large storm event with high bacterial loadings would be minimal and non-realistic if the residence time was relatively large because the bacteria would have a significant amount of time to decay. In an actually large storm event, the residence time should be much smaller, allowing minimal amount of time for decay. To eliminate this ‘counteracting’ effect, each SchemaLinks’ residence time was held constant for all simulations.

Some of the residence times were adjusted in an attempt to match the modeled fecal coliform distribution to the measured fecal coliform concentration distribution at each bacterial monitoring station. As in the Schematic Processor Model, only the residence times of the most influential SchemaLinks (i.e., those directly upstream of a bacterial monitoring station and transporting the highest bacterial load) were adjusted at each station. The results of the calibration are given in Section 7.3.2.

It should be mentioned that residence time distributions (RTDs) for the mainstreams were determined in Section 6.3.3.2. A separate Monte Carlo analysis was conducted in which the bacterial loadings (calculated in Chapter 5) were held constant, and the RTDs of the corresponding SchemaLinks were applied to the model. In this analysis, the bacterial loadings were held constant to eliminate the ‘counteracting’ effect while distributions were applied to the residence times. However, this Monte Carlo analysis did not model the existing conditions as well as the Monte Carlo analysis in which the bacterial loadings were varied and the residence times remained constant, so this model was not used in our research.

7.3.1.4 Other Parameters

In this Monte Carlo Simulation Model, the bacterial loadings and decay coefficients have probability distributions associated with them (as shown in Figure 7.1 and described in Sections 7.3.1.1 and 7.3.1.2.) The residence times of the SchemaLinks are held constant (Section 7.3.1.3.)

However, the remaining parameters, which are only associated with SchemaNode SrcType 3 (i.e., flow, volume, and decay coefficient) were held constant during all the analyses. Thus, for the Copano Bay segments, the parameters of flow (Section 6.3.3.4), volume (Section 6.3.3.3), and decay coefficient (2 days^{-1}) are the same values that were determined in Chapter 6.

7.3.2 Calibration of Model

The only two parameters of the model that were adjusted for calibration purposes (i.e., to match the modeled with the measured fecal coliform concentrations at each bacterial monitoring station) were the multiplication factor (described in Section 7.3.1.1) and the residence time of the SchemaLinks (described in Section 7.3.1.3.) This section describes how each portion of the model, based on water segment, was calibrated and shows the results of the calibration.

The residence time of the SchemaLink transporting the highest bacterial load to the bacterial monitoring station greatly influences the median of the modeled concentrations. The residence time of the most influential SchemaLink was adjusted such that the modeled median matched the median of the measured data.

The multiplication factor influences the shape of the curve (fecal coliform versus probability of exceedance) and 90th-percentile modeled concentrations. The multiplication factor was adjusted such that the shape of the curve and the 90th-percentile values matched between the model and the measured data.

Thus, the combination of adjusting the residence times and multiplication factors in the model was conducted to match the modeled fecal coliform distributions to the measured fecal coliform distributions at each bacterial monitoring station.

7.3.2.1 Aransas River Above Tidal

There is only one bacterial monitoring station along the Aransas River Above Tidal, but there is a bacterial monitoring station, Station 17592, with fecal coliform monitoring data upstream of the Above Tidal that will be analyzed first.

The parameters of the SchemaNodes and SchemaLinks that were adjusted at Station 17592 are given in Tables 7.1 and 7.2, respectively. The locations of the SchemaNodes, SchemaLinks, Station 17592, and the results of the calibration are shown in Figure 7.3.

Table 7.1 SchemaNode Adjusted Parameters for Calibration of Station 17592

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
79	1.5

Table 7.2 SchemaLink Adjusted Parameters for Calibration of Station 17592

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
125	2.93	2.55

Only 9 fecal coliform concentration measurements were made at Station 17592 from 1999-2005 (Figure 7.6), and these measurements were used to calibrate the model at this location.

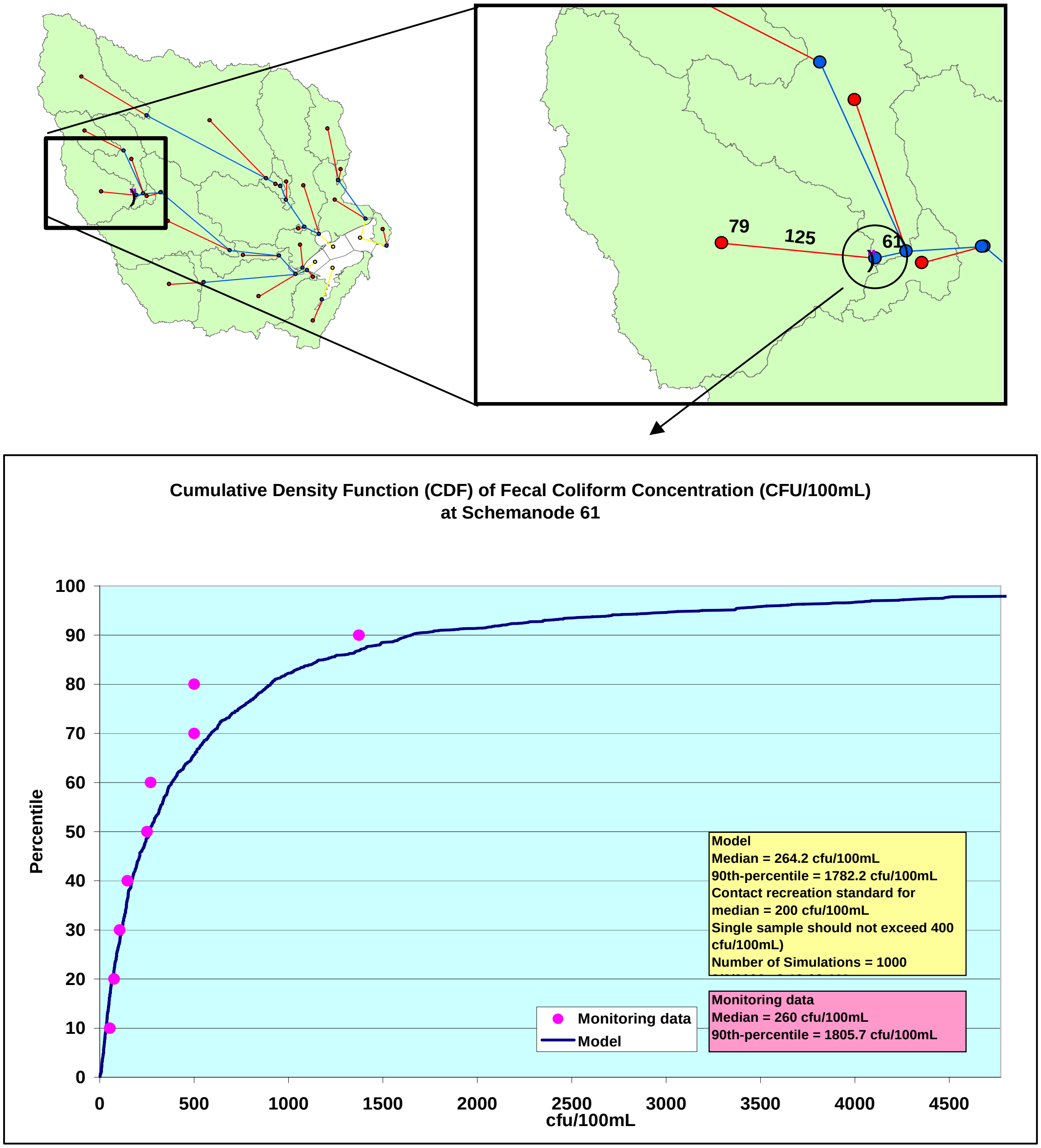


Figure 7.6 Modeled versus Measured Fecal Coliform Concentrations at Station 17592

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Station 12952, which is the next downstream bacterial monitoring station along the Aransas River Above Tidal, are given in Tables 7.3 and 7.4, respectively. The locations of the SchemaNodes, SchemaLinks, Station 12952, and the results of the calibration are shown in Figure 7.7.

Table 7.3 SchemaNode Adjusted Parameters for Calibration of Station 12952

SchemaNode (HydroID)	**Bacteria Loading Multiplication Factor**
61	1.7
62	1.7
78	1.7
84	1.7
85	1.7
91	1.7

Table 7.4 SchemaLink Adjusted Parameters for Calibration of Station 12952

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
106	2	2
111	4	4
113	0.212	0.212
124	5	5
140	5	5
141	3	3.3*

* Parameters that were adjusted for calibration

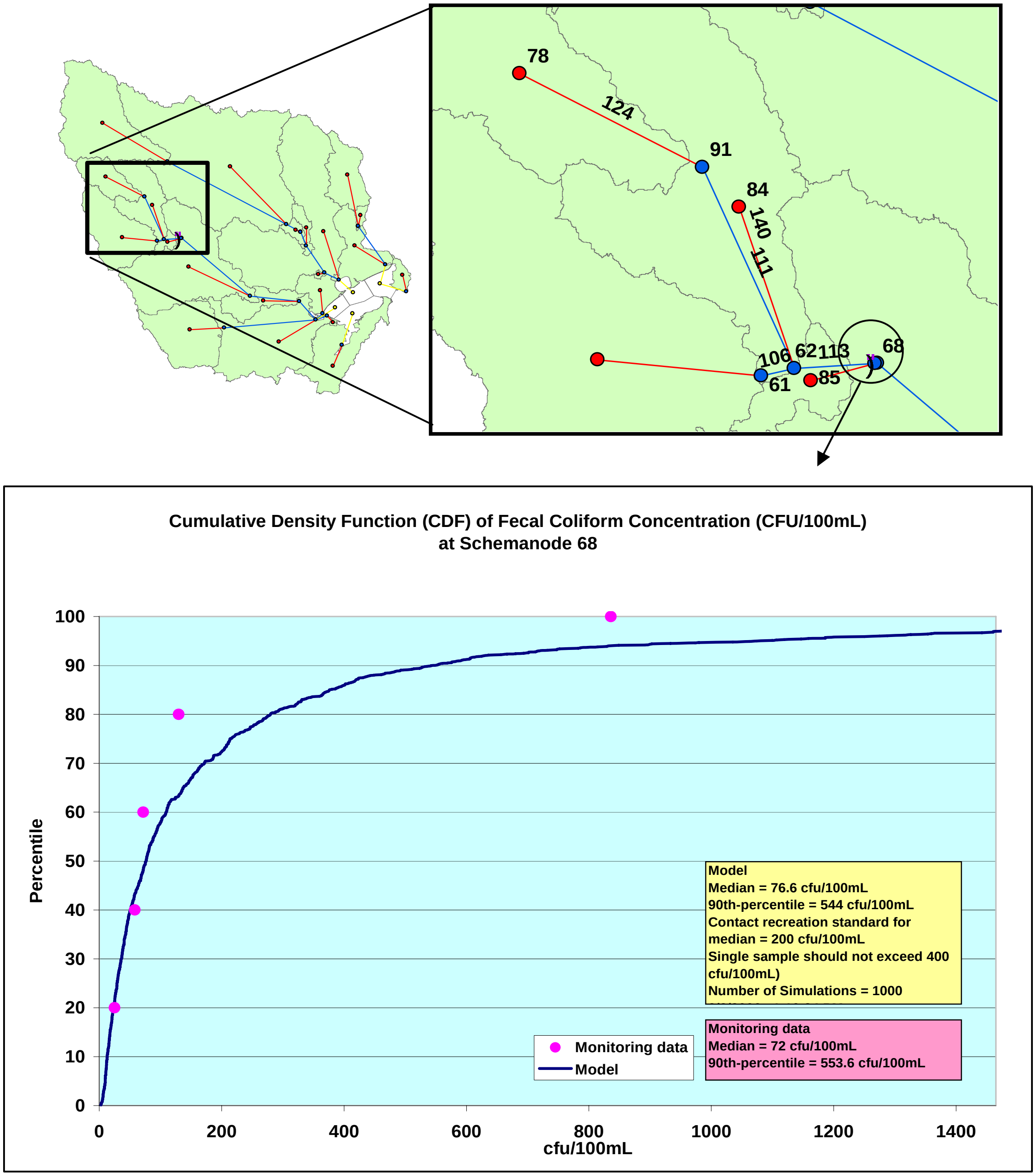


Figure 7.7 Modeled versus Measured Fecal Coliform Concentrations at Station 12952

7.3.2.2 Aransas River Tidal

Station 12948 is the only bacterial monitoring station along the Aransas River Tidal.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Station 12948 are given in Tables 7.5 and 7.6, respectively. The locations of the SchemaNodes, SchemaLinks, Station 12948, and the results of the calibration are shown in Figure 7.8.

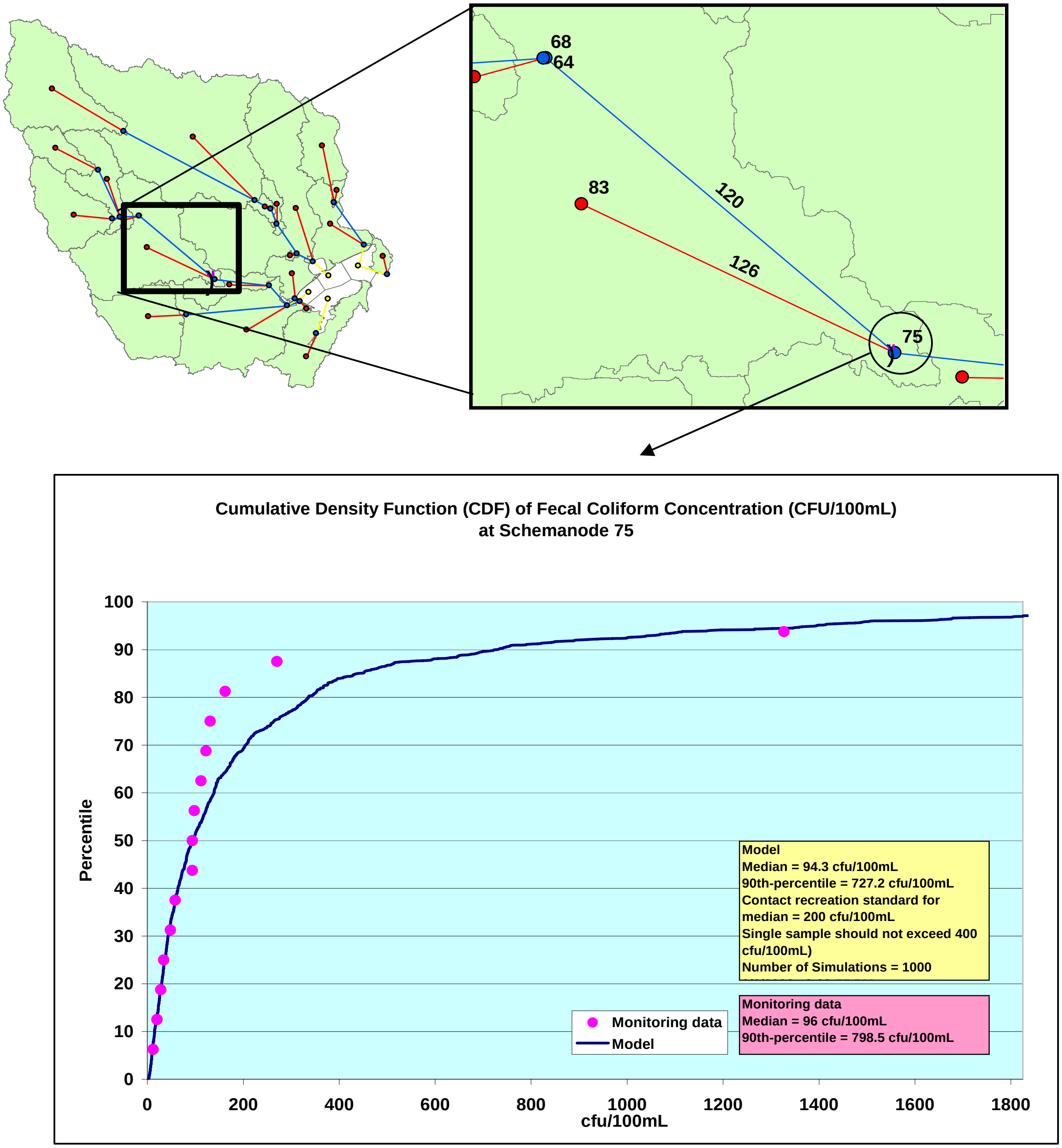
Table 7.5 SchemaNode Adjusted Parameters for Calibration of Station 12948

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
64	1.9
68	1.9
83	1.9

Table 7.6 SchemaLink Adjusted Parameters for Calibration of Station 12948

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
108	0.05	0.05
120	1.51	1.51
126	3.2	2.95*

* Parameters that were adjusted for calibration



Model
Median = 94.3 cfu/100mL
90th-percentile = 727.2 cfu/100mL
Contact recreation standard for median = 200 cfu/100mL
Single sample should not exceed 400 cfu/100mL)
Number of Simulations = 1000

Monitoring data
Median = 96 cfu/100mL
90th-percentile = 798.5 cfu/100mL

Figure 7.8 Modeled versus Measured Fecal Coliform Concentrations at Station 12948

7.3.2.3 Mission River Above Tidal

Station 12944 is the only bacterial monitoring station along the Mission River Above Tidal.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Station 12944 are given in Tables 7.7 and 7.8, respectively. The locations of the SchemaNodes, SchemaLinks, Station 12944, and the results of the calibration are shown in Figure 7.9.

Table 7.7 SchemaNode Adjusted Parameters for Calibration of Station 12944

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
71	1.6
73	1.6
77	1.6
80	1.6
90	1.6
99	1.6

Table 7.8 SchemaLink Adjusted Parameters for Calibration of Station 12944

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
116	1.42	1.36*
118	4.95	4.95
119	0.05	0.05
123	3	3
128	2.29	2.29
132	1	1

* Parameters that were adjusted for calibration

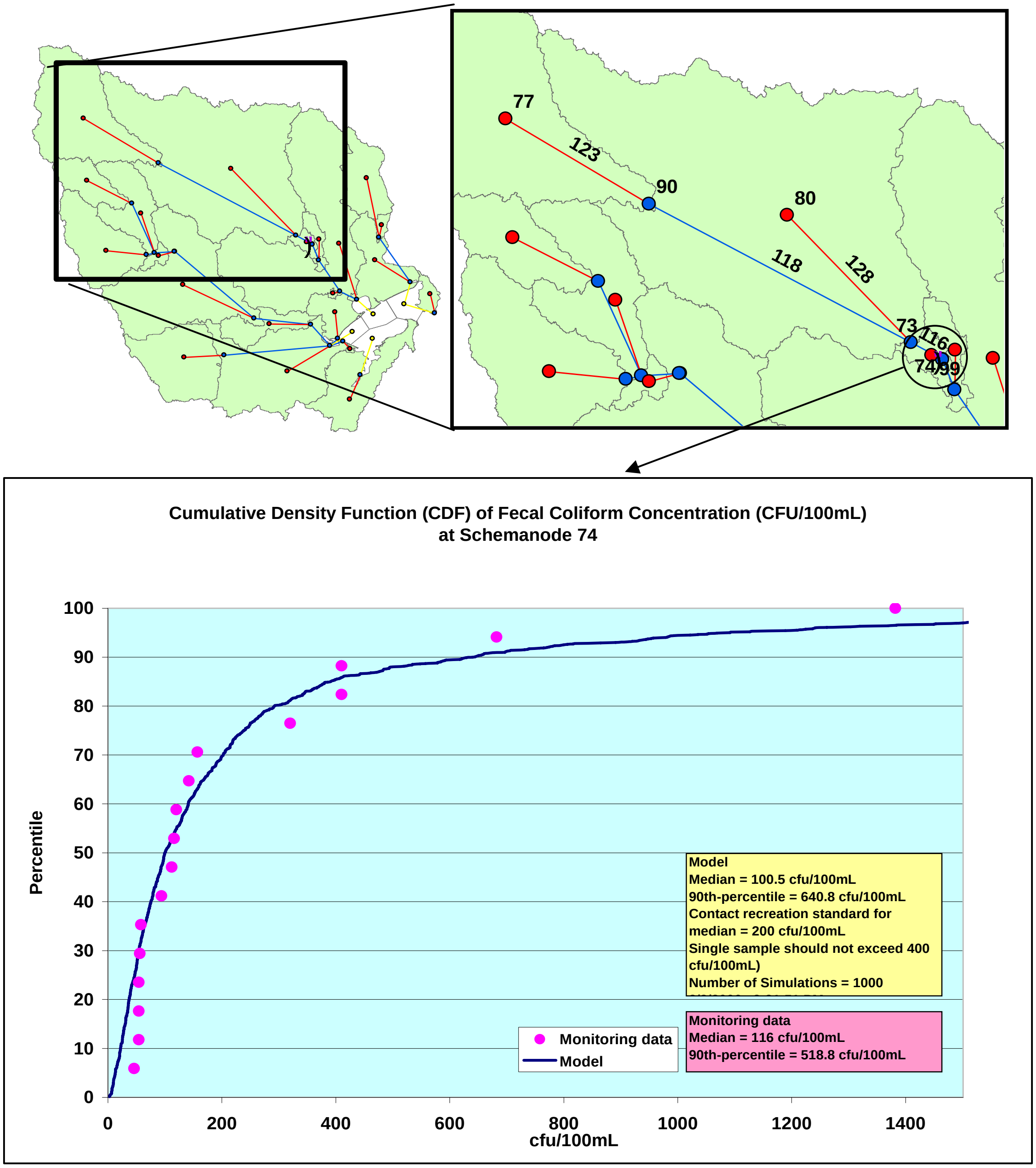


Figure 7.9 Modeled versus Measured Fecal Coliform Concentrations at Station 12944

7.3.2.4 Mission River Tidal

Station 12943 is the only bacterial monitoring station along the Mission River Tidal.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Station 12943 are given in Tables 7.9 and 7.10, respectively. The locations of the SchemaNodes, SchemaLinks, Station 12943, and the results of the calibration are shown in Figure 7.10.

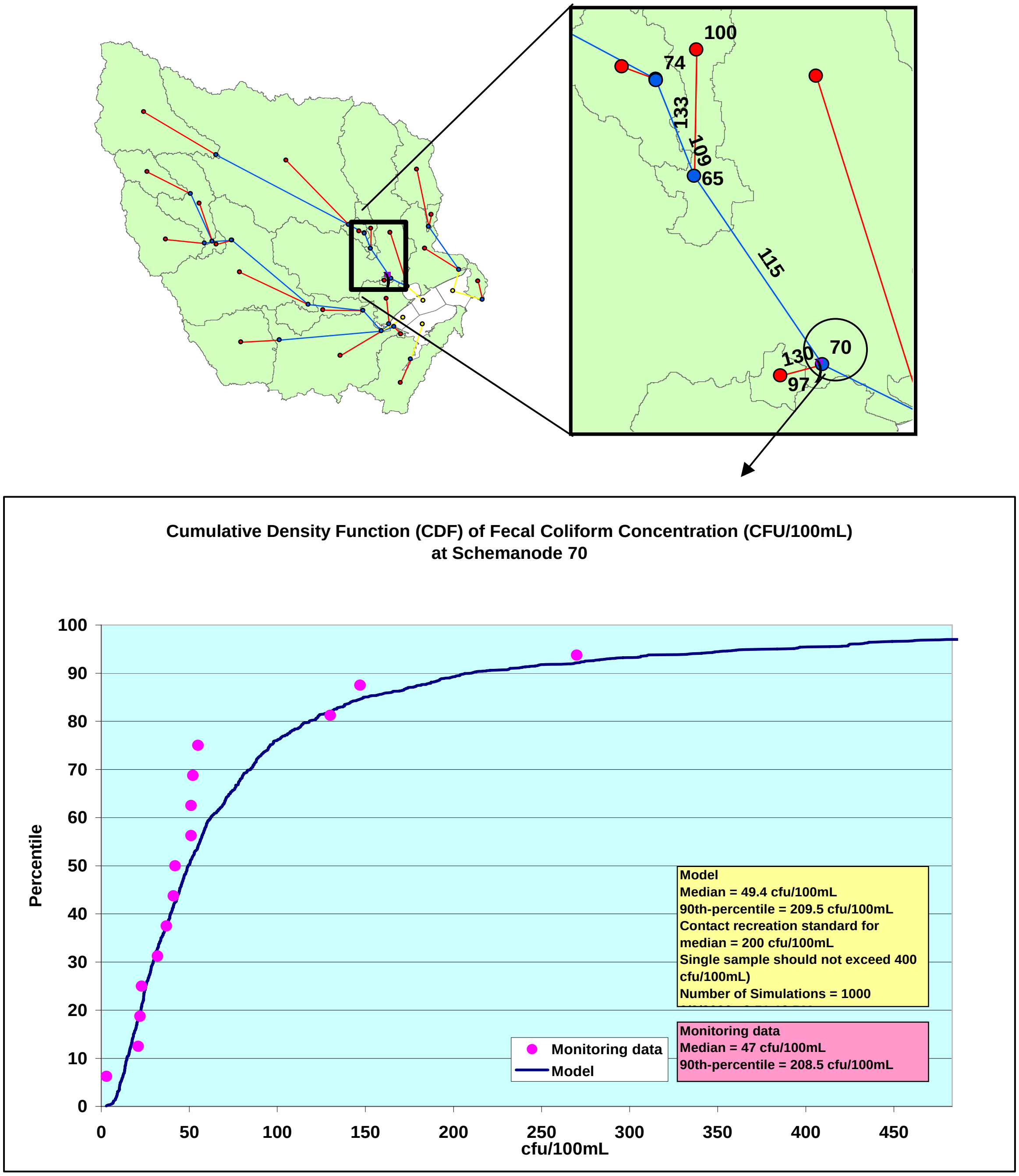
Table 7.9 SchemaNode Adjusted Parameters for Calibration of Station 12943

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
65	1.4
74	1.4
97	1.4
100	1.4

Table 7.10 SchemaLink Adjusted Parameters for Calibration of Station 12943

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
109	0.22	0.22
115	1.01	1.1*
130	0.19	0.19
133	2	2

* Parameters that were adjusted for calibration



Cumulative Density Function (CDF) of Fecal Coliform Concentration (CFU/100mL)
at Schemanode 70

Model
Median = 49.4 cfu/100mL
90th-percentile = 209.5 cfu/100mL
Contact recreation standard for
median = 200 cfu/100mL
Single sample should not exceed 400
cfu/100mL)
Number of Simulations = 1000

Monitoring data
Median = 47 cfu/100mL
90th-percentile = 208.5 cfu/100mL

Figure 7.10 Modeled versus Measured Fecal Coliform Concentrations at Station 12943

7.3.2.5 Copano Bay

The four Copano Bay segments (Segments 1, 2, 3, and 4) were calibrated.

Watershed JunctionID 45405 drains into Segment 1. Bacterial monitoring stations 13405, 14782, 14784, and 14790 measure fecal coliform concentrations in Copano Bay Segment 1.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Segment 1 are given in Tables 7.11 and 7.12, respectively. The locations of the SchemaNodes, SchemaLinks, the bacterial monitoring stations, and the results of the calibration are shown in Figure 7.11.

Table 7.11 SchemaNode Adjusted Parameters for Calibration of Segment 1

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
88	2
93	2
155	1.6

Table 7.12 SchemaLink Adjusted Parameters for Calibration of Segment 1

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
135	0.487	0.6*
159	-	-

* Parameters that were adjusted for calibration

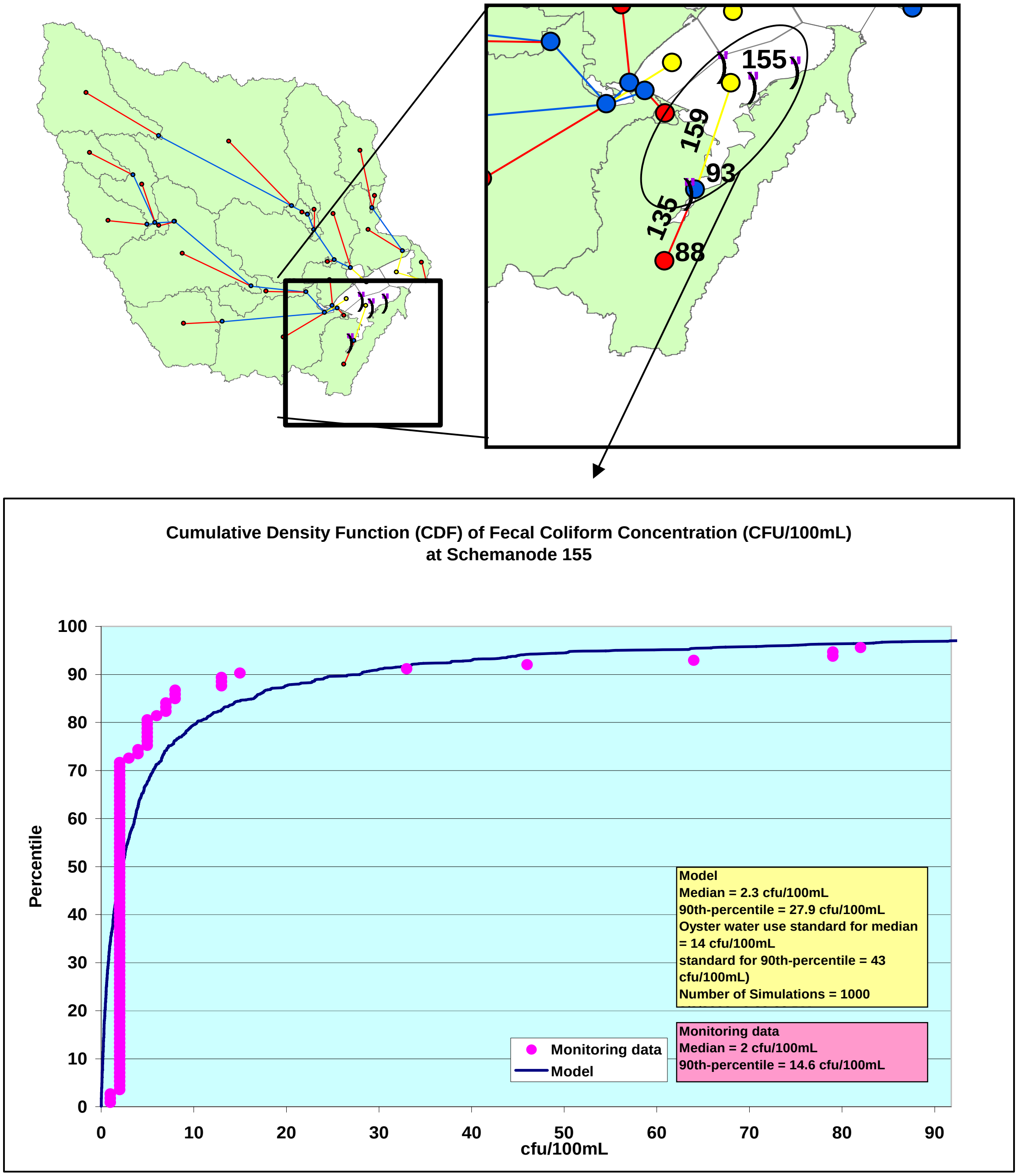


Figure 7.11 Modeled versus Measured Fecal Coliform Concentrations at Segment 1

Aransas River and Chilipitin Creek drain into Segment 2. Bacterial monitoring stations 12945, 14783, 14787, and 14788 measure fecal coliform concentrations in Copano Bay Segment 2.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Segment 2 are given in Tables 7.13 and 7.14, respectively. The locations of the SchemaNodes, SchemaLinks, the bacteria monitoring stations, and the results of the calibration are shown in Figure 7.12.

Table 7.13 SchemaNode Adjusted Parameters for Calibration of Segment 2

SchemaNode (HydroID)	Bacterial Loading Multiplication Factor
63	1.1
67	3.5
69	1.1
75	1.1
86	1.1
87	3.5
101	1.1
102	1.1
103	1.1
104	3.5
154	3.5

Table 7.14 SchemaLink Adjusted Parameters for Calibration of Segment 2

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
107	0.686	0.686
112	0.21	0.21
114	0.01	0.01
121	0.01	0.01
122	1.5	1.5
127	4	4
134	2.31	2.6*
139	1	1
142	2.3	2.3
143	1.5	1.5
158	-	-

* Parameters that were adjusted for calibration

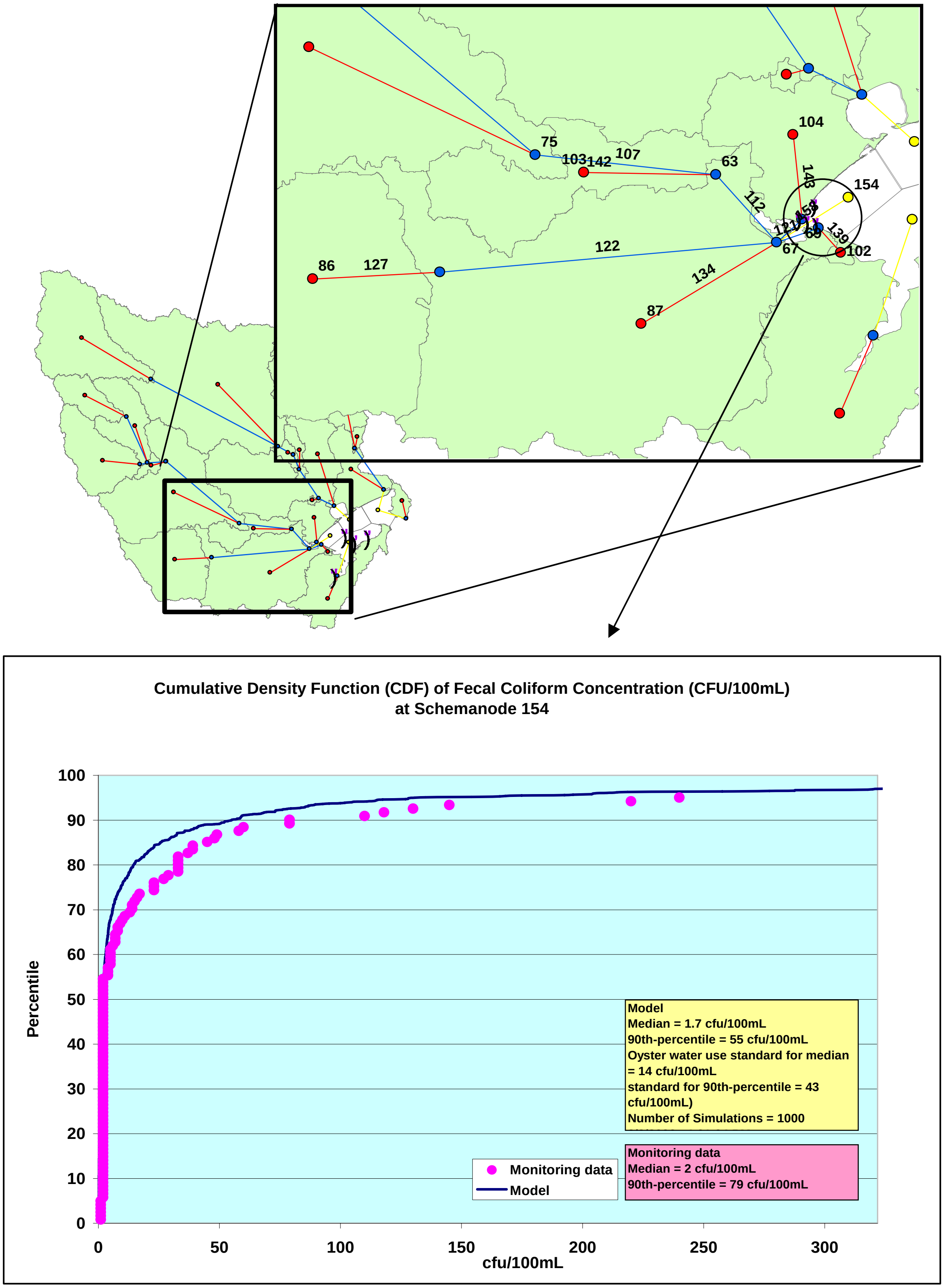


Figure 7.12 Modeled versus Measured Fecal Coliform Concentrations at Segment 2

Mission River drains into Segment 3. Bacterial monitoring station 14797 measures fecal coliform concentrations in Copano Bay Segment 3.

The parameters of the SchemaNodes and SchemaLinks that could have been and/or were adjusted at Segment 3 are given in Tables 7.15 and 7.16, respectively. The locations of the SchemaNodes, SchemaLinks, the bacterial monitoring stations, and the results of the calibration are shown in Figure 7.13.

Table 7.15 SchemaNode Adjusted Parameters for Calibration of Segment 3

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
66	2.5
70	1.4
82	2.5
153	1.4

Table 7.16 SchemaLink Adjusted Parameters for Calibration of Segment 3

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
110	0.29	0.29
129	2.18	1.7*
157	-	-

* Parameters that were adjusted for calibration

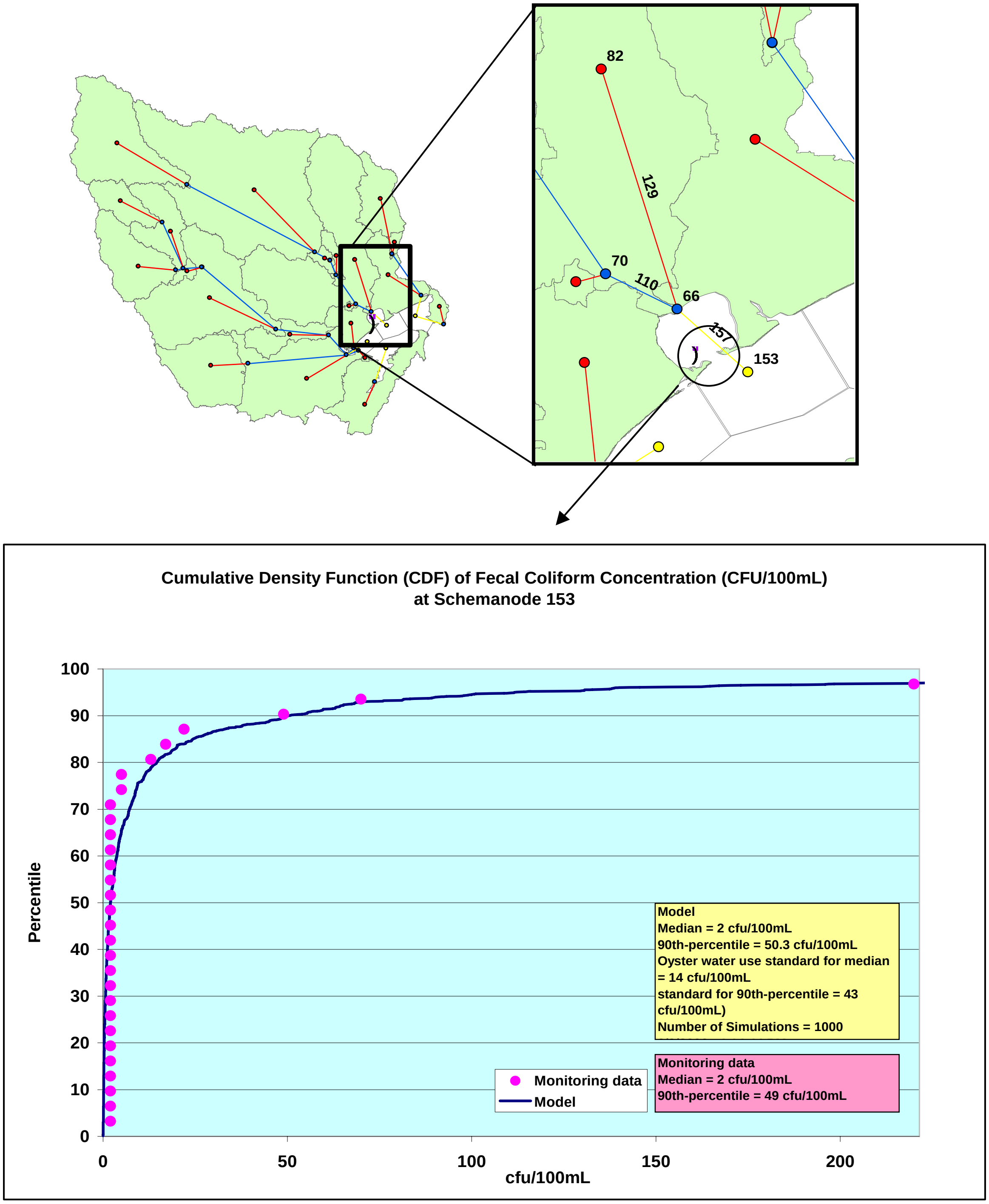


Figure 7.13 Modeled versus Measured Fecal Coliform Concentrations at Segment 3

Copano Creek drains into Segment 4. Bacterial monitoring stations 13404, 14779, 14780, 14785, 14792, and 14793 measure fecal coliform concentrations in Copano Bay Segment 4.

The parameters of the SchemaNodes and SchemaLinks that were adjusted at Segment 4 are given in Tables 7.17 and 7.18, respectively. The locations of the SchemaNodes, SchemaLinks, the bacterial monitoring stations, and the results of the calibration are shown in Figure 7.14.

Table 7.17 SchemaNode Adjusted Parameters for Calibration of Segment 4

SchemaNode (HydroID)	**Bacterial Loading Multiplication Factor**
72	1.2
81	1.2
89	2
94	1.2
95	1.2
96	2
98	1.2
105	1.2
156	1.2

Table 7.18 SchemaLink Adjusted Parameters for Calibration of Segment 4

SchemaLink (HydroID)	**Residence Time (days)**	
	Initial (Schematic Processor Model)	Final (Monte Carlo Simulation Model)
117	0.05	0.05
131	3	3
136	1.5	1.5
137	1.15	0.9*
138	5	5
144	1.5	1.5
160	-	-
161	-	-

* Parameters that were adjusted for calibration

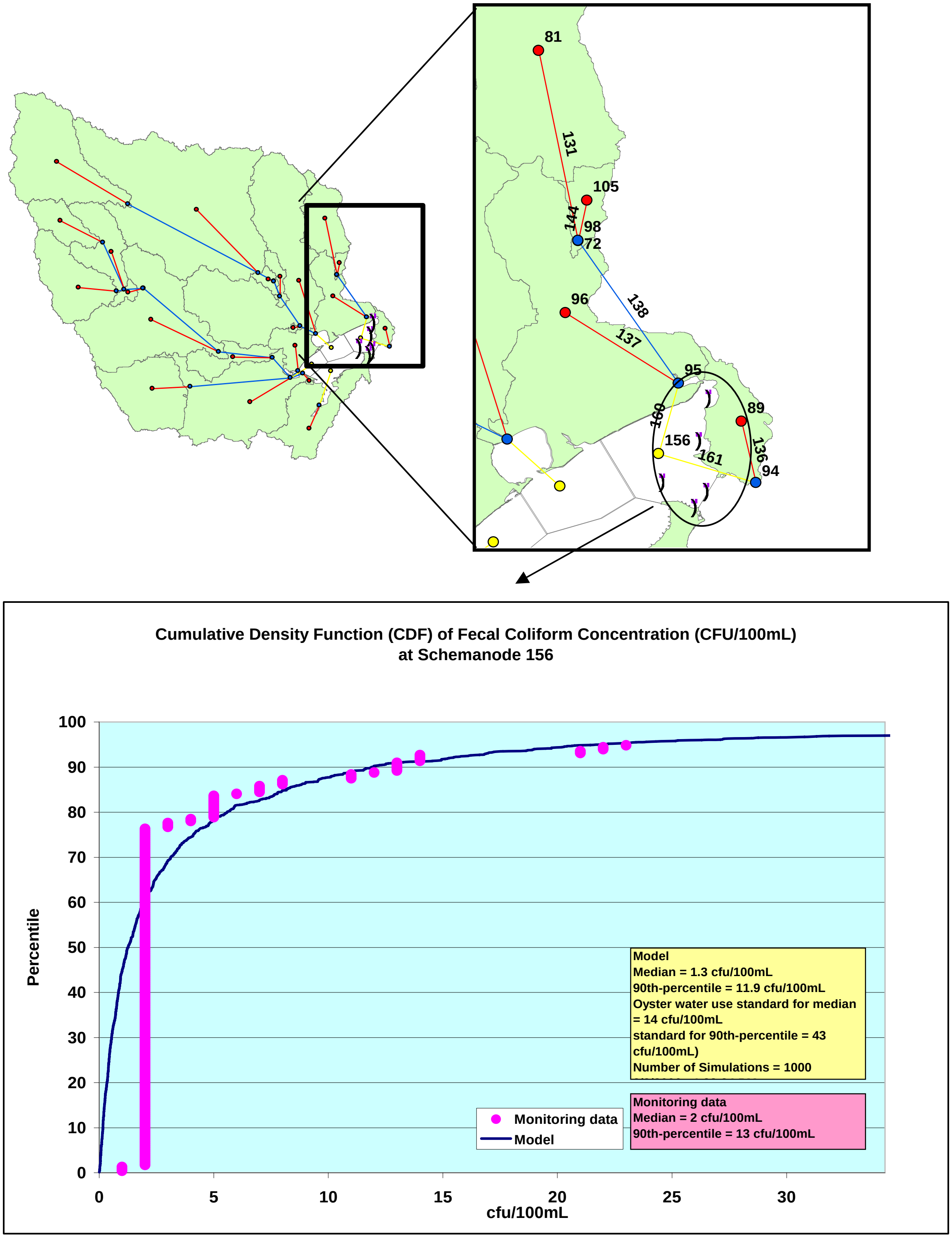


Figure 7.14 Modeled versus Measured Fecal Coliform Concentrations at Segment 4

7.3.3 Calculation of Load Allocations

Once the model was calibrated (see Section 7.3.2), the parameters of the model were not re-adjusted because the calibrated model well-represented the measured fecal coliform concentrations at each of the bacterial monitoring stations.

Fecal coliform water quality standards are currently being exceeded in Copano Bay segments 2 and 3. Because this is a fecal coliform model, only the fecal coliform water quality standards were considered in the load reduction determinations. However, three indicator bacteria are used in the Copano Bay watershed (enterococci for Aransas and Mission River Tidals, *E. coli* for Aransas and Mission River Above Tidals, and fecal coliform for Copano Bay), so we recommend that a model be created for each indicator bacteria to determine the appropriate load reductions in the water segments using those indicators.

To ensure compliance with the fecal coliform water quality standards, the model was used to investigate fecal coliform concentrations at the upstream and downstream portions of the Above Tidals and Tidals, the locations of the bacterial monitoring stations, and the Copano Bay water segments. Like the calibration of the model, load reduction determinations started at the upstream locations and proceeded toward the downstream locations because upstream load reductions affect what downstream reductions are necessary.

If load reduction was necessary for a segment, the loadings at controlled point sources (e.g., WWTPs) were reduced first. If that reduction was not sufficient to meet the water quality standards, then loadings from non-point sources (e.g., livestock) were reduced until the water quality standards were met.

Two scenarios of load reductions were found for each water segment. Load Reduction Scenario #1 is the load reduction necessary to meet fecal coliform water quality standards for all water segments (Aransas and Mission River Tidals, Aransas and Mission River Above Tidals, and Copano Bay) at each location in the model that was analyzed. However, each portion of the model that was analyzed that did not meet fecal coliform water quality standards was not always verified by existing monitoring data; thus, the results from Load Reduction Scenario #1 are inconclusive due to lack of monitoring data and are presented in Appendix 7.2. Load Reduction Scenario #2 is the load reductions necessary to meet fecal coliform water quality standards for all water segments at each monitoring station location. Only the fecal coliform bacterial load reductions for Copano Bay are presented in this chapter because fecal coliform is the primary bacterial indicator for Copano Bay.

7.3.3.1 Copano Bay

Copano Bay must meet oyster harvesting use standards for fecal coliform. The median of the samples (within a two-year period) must be less than 14 CFU/100mL, and the 90th-percentile of the samples must be less than 43 CFU/100mL (i.e., 10% of the samples are allowed to exceed 43 CFU/100mL.)

Four Copano Bay segments (Segments 1, 2, 3, and 4) were analyzed (shown in Figure 7.15). Considering all the fecal coliform monitoring data from 1999-2005, Segments 1 and 4 are currently meeting water quality standards. Segments 2 and 3 (Aransas and Mission River outlets, respectively) are currently exceeding water quality standards. Thus, only load reductions for Segments 2 and 3 must be determined.

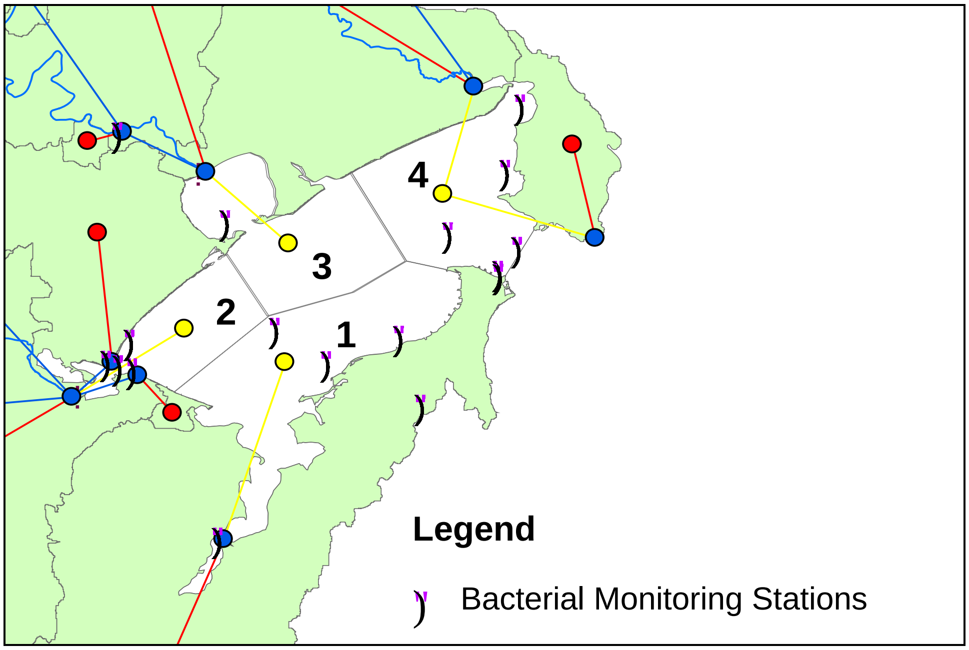


Figure 7.15 Copano Bay Segments 1, 2, 3, 4

Without any load reductions in the upstream watersheds of Copano Bay Segment 2, two runs of 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 simulation runs, the median and 90th-percentile CFU/100mL are shown in Table 7.19.

Copano Bay Segment 2 exceeds the fecal coliform water quality standard 90th-percentile > 43 CFU/100mL based on modeled results and monitoring data (shown in Table 7.19).

WWTP and livestock bacterial loadings were reduced in an attempt to meet water quality standards. The bacterial loadings were reduced at all three upstream WWTPs, and livestock bacterial loadings were reduced at the adjacent upstream watersheds to Copano Bay; these watersheds are shown in Figure 7.16.

The number of runs of simulations and the modeled results at SchemaNode 154 with various load reductions of WWTP and livestock bacterial loadings are also shown in Table 7.19.

Table 7.19 Modeled Results at SchemaNode 154 with Various WWTP/Livestock Load Reductions

Run #	**Load Reduction (%)**	**Bacteria Source**	**Median (CFU/100mL)**	**90th-Percentile > 43 CFU/100mL**
1	0	N/A	1.8	**54.89**
2	0	N/A	1.69	**46.29**
1	50	WWTP	1.6	**46.05**
2	0	Livestock	1.48	**46.58**
1	50	WWTP	1.45	41.62
2			1.24	30.81
3	10	Livestock	1.38	25.27
4			1.38	37.31
1	50	WWTP	1.53	38.79
2	15	Livestock	1.30	33.84
3			1.40	32.88
Simulations			100	1000

Reducing the WWTP bacterial loadings[18] by 50% and livestock bacterial loadings by 15% in the adjacent upstream watersheds allows the 90th-percentile to be approximately 35 CFU/100mL, which is less than the 43 CFU/100mL standard and results in a median less than 14 CFU/100mL (shown in Table 7.19). The reductions necessary to meet fecal coliform oyster water use standards at Copano Bay Segment 2 based on modeled results are shown in Figure 7.16. Reduction of livestock bacterial loadings would require implementations of agricultural BMPs, and reduction of WWTP bacterial loadings would require proper disinfection before discharging into surface waters. The existing monitoring data from 1999-2005 and the probability distribution when the load reductions are implemented are shown in Figure 7.17. Both criteria are met when the reductions are implemented.

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[18] The WWTP load reductions were based on the overestimated bacterial loadings from WWTPs (explained in Section 5.4.2).

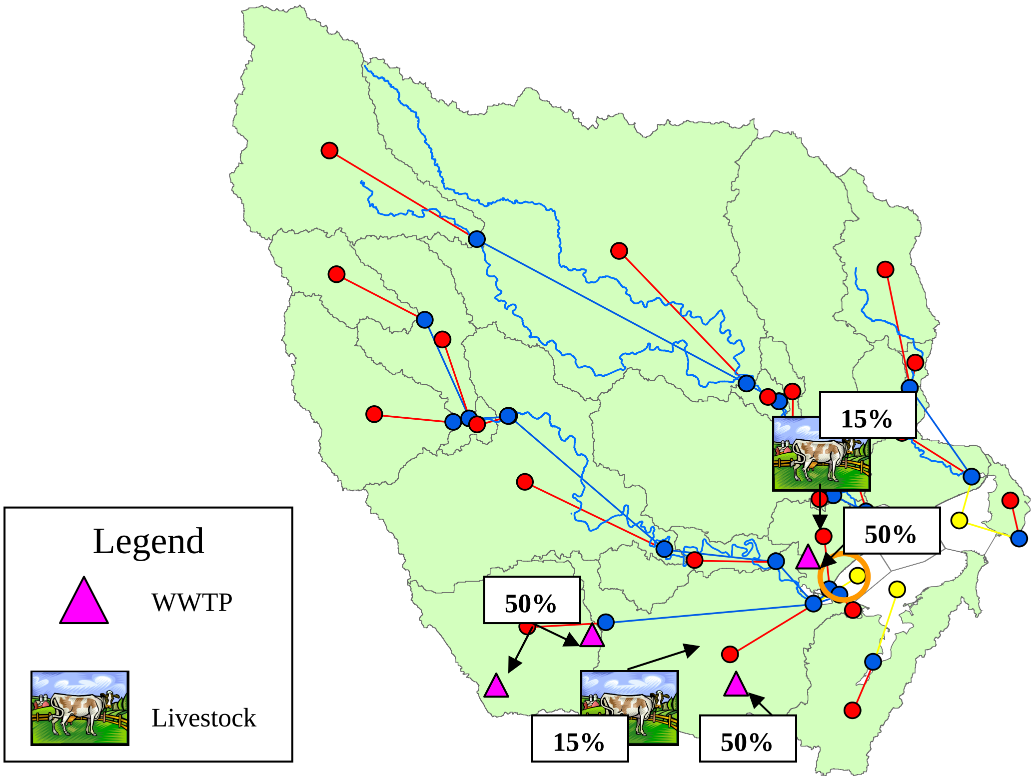


Figure 7.16 Load Reductions for SchemaNode 154: Copano Bay

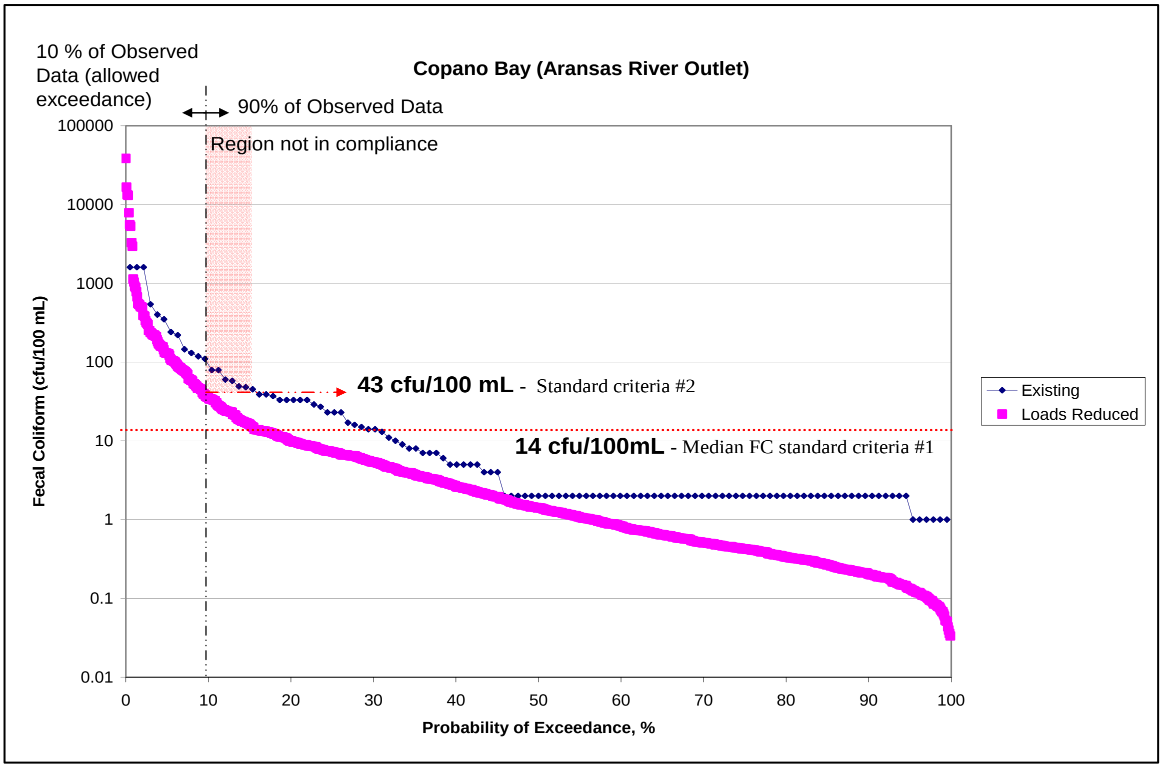


Figure 7.17 Existing versus Reduced Loads in Copano Bay Segment 2

Without any load reductions in the upstream watersheds of Copano Bay Segment 3, two runs of 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 simulation runs, the median and 90th-percentile CFU/100mL are shown in Table 7.20.

Table 7.20 shows that Copano Bay Segment 3 exceeds the fecal coliform water quality standard 90th-percentile > 43 CFU/100mL based on modeled results and monitoring data when no load reductions are applied.

Livestock bacterial loadings were reduced (in the upstream watershed adjacent to the Bay, shown in Figure 7.18) in an attempt to meet water quality standards; septic systems, WWTPs, and avian loadings do not discharge directly to Copano Bay, and non-point bacterial loadings are significantly less than livestock loadings.

The number of runs of simulations and the modeled results at SchemaNode 153 with various load reductions of livestock bacterial loadings are also shown in Table 7.20.

Table 7.20 Modeled Results at SchemaNode 153 with Various Livestock Load Reductions

Run #	**Load Reduction (%)**	**Bacteria Source**	**Median (CFU/100mL)**	**90th-Percentile < 43 CFU/100mL**
1	0	N/A	1.9	**47.2**
2	0	N/A	2.2	**53.4**
1	10	Livestock	1.59	42.6
1	15	Livestock	1.54	33.0
2			2.02	**46.1**
3			1.61	42.2
1	20	Livestock	1.49	33.7
2			1.74	28.0
Simulations			100	1000

Reducing the livestock bacterial loadings by 20% in the adjacent upstream watersheds allows the 90th-percentile to be approximately 30.85 CFU/100mL, which is less than the 43 CFU/100mL standard and results in a median less than 14 CFU/100mL (shown in Table 7.20). The load reductions necessary to meet fecal coliform oyster water use standards at Copano Bay Segment 3 based on modeled results are shown in Figure 7.18. Reduction of livestock bacterial loadings would require implementations of agricultural BMPs.

The existing monitoring data from 1999-2005 and the probability distribution when the load reductions are implemented for the Mission River outlet into Copano Bay are shown in Figure 7.19.

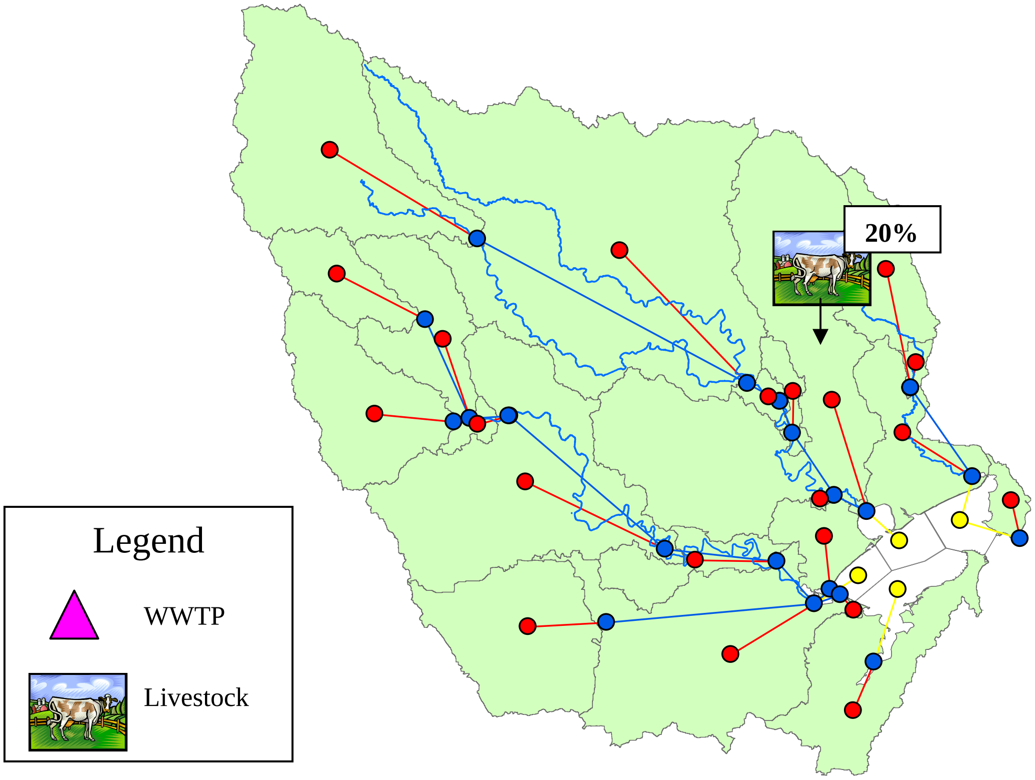


Figure 7.18 Load Reductions for SchemaNode 153: Copano Bay

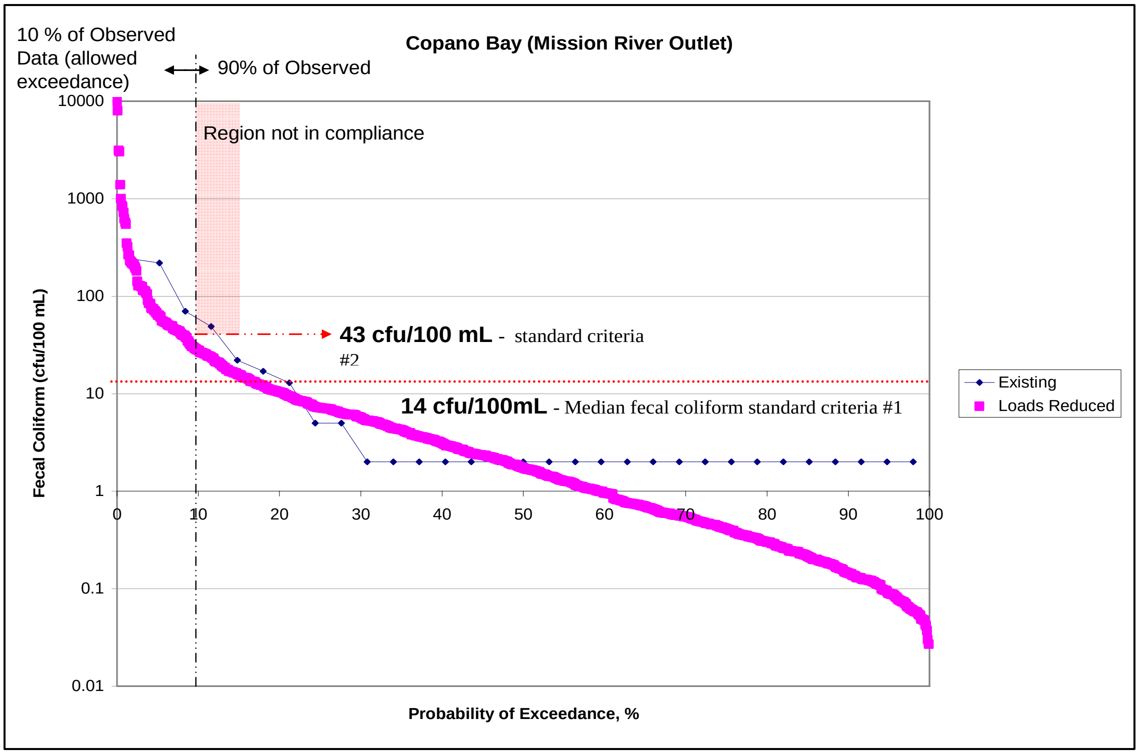


Figure 7.19 Existing versus Reduced Loads in Copano Bay Segment 3

7.4 RESULTS

The current loadings and load allocations from each source to each of the water segments (i.e., Aransas River Above Tidal, Aransas River Tidal, Mission River Above Tidal, Mission River Tidal, and Copano Bay) for the Monte Carlo Simulation Model are given in Chapter 8 of this report.

Considering only fecal coliform water quality standards, the load reductions required to satisfy the standards for all portions of the model where bacterial monitoring stations indicate exceedances are shown in Figure 7.20. This load reduction scenario is referred to as Load Reduction Scenario #2. Thus, based on fecal coliform monitoring data from 1999-2005, only Copano Bay Segments 2 and 3 exceed fecal coliform water quality standards.

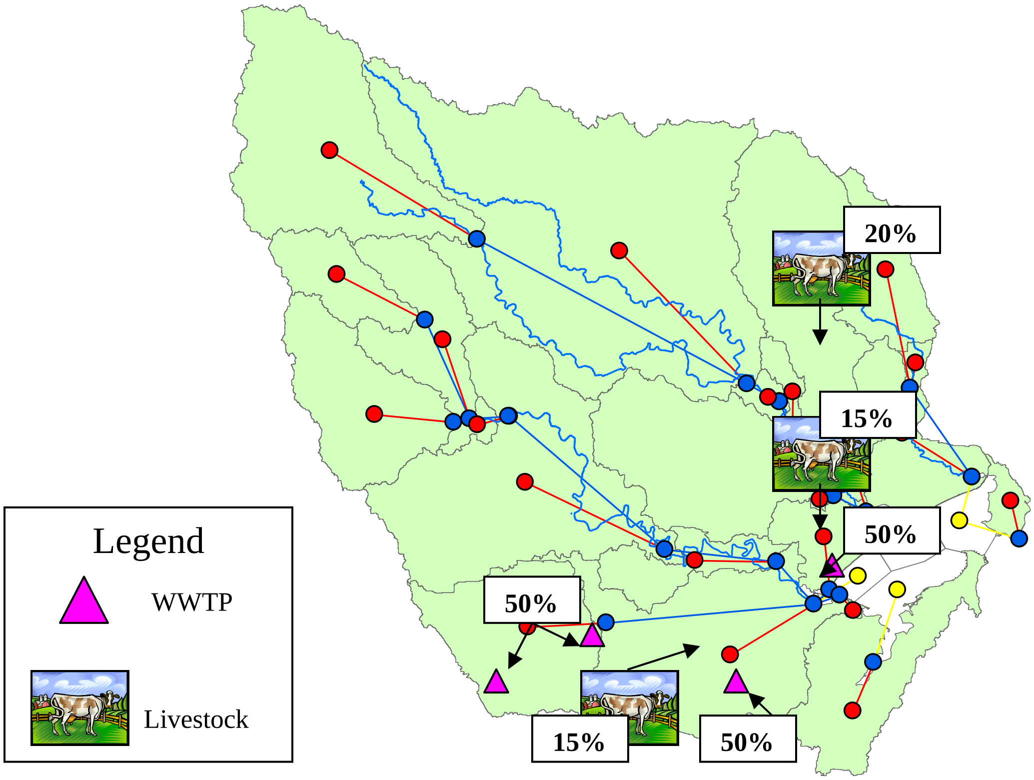


Figure 7.20 Load Reductions to Satisfy Fecal Coliform Standards for Monitored Conditions

Results are described in more detail in Chapter 8 of this report, and Chapter 9 discusses recommendations on how to reduce these bacterial loadings.

Chapter 8: Results

8.1 ESTIMATION OF LOADINGS

The current loadings to the water segments in the Copano Bay watershed are presented in this section using the Schematic Processor Model and Monte Carlo Simulation Model.

8.1.1 Schematic Processor

The current loadings to each of the water segments (Aransas River Above Tidal, Mission River Above Tidal, Aransas River Tidal, Mission River Tidal, and Copano Bay) are presented in this section. Other results from the Schematic Processor Model are given in Section 6.4.

These loadings are based on the annual bacterial loadings that were calculated in Chapter 5 and the simulation of bacterial transport (with the calibrated Schematic Processor Model) that is described in Chapter 6. Because bacterial loadings are only input into the model at locations of SchemaNodes, the upstream and downstream bacterial loadings of each of the water segments were found. These loadings are the “PassedVal” and “TotVal” in the attribute table of the SchemaNode feature class after the Schematic Processor (“Process Schematic” script) was run under calibrated conditions (described in Section 6.3.4).

The bacterial loadings at the upstream and downstream nodes of the Aransas River Above Tidal (segment 2004) are shown in Table 8.1. The bacterial loadings from the major bacterial sources (identified in Section 6.4) are shown in Table 8.2.

Table 8.1 Schematic Processor Bacterial Loadings to Aransas River Above Tidal (Segment 2004)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	62	3.345E+13
Downstream	75	9.452E+13

Table 8.2 Schematic Processor Bacterial Loadings (from Major Sources) to Aransas River Above Tidal (Segment 2004)

Bacteria Source	Upstream, Node 62 (CFU/year)	Downstream, Node 75 (CFU/year)
Cattle	9.463E+11	5.961E+13
WWTP	3.220E+13	2.431E+13
OSSF	1.228E+11	4.611E+11
Birds	0.000E+00	0.000E+00
Non-point (Urban, Forest, etc.)	3.124E+10	2.180E+12
Total Load	3.345E+13	9.452E+13

The bacterial loadings increase from the upstream to the downstream portions of the Aransas River Above Tidal (shown in Tables 8.1 and 8.2), which can be explained by the large upstream watershed draining to the Aransas River Above Tidal. The major bacterial source at the upstream portion of the Aransas River Above Tidal is the WWTP (City of Beeville Moore Street WWTP) based on the results of the Schematic Processor Model. However, as explained in Section 5.4.2, the WWTP bacterial loading is largely overestimated for our research. The major bacterial source at the downstream of the Aransas River Above Tidal is cattle.

The bacterial loadings at the upstream and downstream nodes of the Aransas River Tidal (segment 2003) are shown in Table 8.3. The bacterial loadings from the major bacterial sources (identified in Section 6.4) are shown in Table 8.4.

Table 8.3 Schematic Processor Bacterial Loadings to Aransas River Tidal (Segment 2003)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	75	9.452E+13
Downstream	67	8.693E+14

Table 8.4 Schematic Processor Bacterial Loadings (from Major Sources) to Aransas River Tidal (Segment 2003)

Bacteria Source	Upstream, Node 75 (CFU/year)	Downstream, Node 67 (CFU/year)
Cattle	5.961E+13	5.961E+14
WWTP	2.431E+13	3.912E+13
OSSF	4.611E+11	6.583E+13
Birds	0.000E+00	0.000E+00
Non-point (Urban, Forest, etc.)	2.180E+12	1.239E+14
Total Load	9.452E+13	8.693E+14

The bacterial loadings increase from the upstream to the downstream portions of the Aransas River Tidal (shown in Tables 8.3 and 8.4). The major bacterial source at the upstream portion of the Aransas River Tidal is cattle, which is about double the bacterial loadings from the upstream WWTPs (Water Reclamation Facility, City of Taft Baird WWTP, City of Sinton Main WWTP, City of Odem WWTP) based on the results of the Schematic Processor Model. The major bacterial source downstream of the Aransas River Tidal is cattle, followed by non-point bacterial sources (land uses of urban, forest, etc.), and then septic systems.

The bacterial loadings at the upstream and downstream nodes of the Mission River Above Tidal (segment 2002) are shown in Table 8.5. The bacterial loadings from the major bacterial sources (identified in Section 6.4) are shown in Table 8.6.

Table 8.5 Schematic Processor Bacterial Loadings to Mission River Above Tidal (Segment 2002)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	73	5.105E+14
Downstream	65	1.262E+14

Table 8.6 Schematic Processor Bacterial Loadings (from Major Sources) to Mission River Above Tidal (Segment 2002)

Bacteria Source	Upstream, Node 73 (CFU/year)	Downstream, Node 65 (CFU/year)
Cattle	4.800E+14	1.074E+14
WWTP	2.431E+13	7.960E+11
OSSF	4.611E+11	1.815E+06
Birds	0.000E+00	0.000E+00
Non-point (Urban, Forest, etc.)	2.180E+12	1.511E+13
Total Load	5.105E+14	1.262E+14

The bacterial loading decreases from the upstream to the downstream portions of the Mission River Above Tidal (shown in Tables 8.5 and 8.6). This can be explained by the major upstream watersheds draining to the upstream portion of the Mission River Above Tidal and very small watersheds draining along the Mission River Above Tidal. The major bacterial source at the upstream portion of the Mission River Above Tidal is cattle based on the results of the Schematic Processor Model. The major bacterial source at the downstream of the Mission River Above Tidal is also cattle, followed by non-point bacterial sources (land uses of urban, forest, etc.).

The bacterial loadings at the upstream and downstream nodes of the Mission River Tidal (segment 2001) are shown in Table 8.7. The bacterial loadings from the major bacterial sources (identified in Section 6.4) are shown in Table 8.8.

Table 8.7 Schematic Processor Bacterial Loadings to Mission River Tidal (Segment 2001)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	65	1.262E+14
Downstream	66	1.115E+15

Table 8.8 Schematic Processor Bacterial Loadings (from Major Sources) to Mission River Tidal (Segment 2001)

Bacteria Source	Upstream, Node 65 (CFU/year)	Downstream, Node 66 (CFU/year)
Cattle	1.074E+14	1.062E+15
WWTP	7.960E+11	5.726E+11
OSSF	1.815E+06	1.348E+05
Birds	0.000E+00	0.000E+00
Non-point (Urban, Forest, etc.)	1.511E+13	3.266E+13
Total Load	1.262E+14	1.115E+15

The bacterial loadings increase from the upstream to the downstream portions of the Mission River Tidal (shown in Tables 8.7 and 8.8.) The major bacterial source at the upstream portion of the Mission River Tidal is cattle based on the results of the Schematic Processor Model. The major bacterial source downstream of the Mission River Tidal is also cattle, followed by non-point bacterial sources (land uses of urban, forest, etc.).

The bacterial loadings to each of the Copano Bay segments (Segments 1, 2, 3, and 4) and the total current annual bacterial loading to Copano Bay are shown in Table 8.9. The bacterial loadings were calculated by multiplying the “TotVal” by the “CumRunoff_m3_yr”, fields in the SchemaNode attribute table. Recall, that “TotVal” is the concentration of a SchemaNode SrcType 3 in CFU/m^3, and “CumRunoff_m3_yr” is the cumulative runoff of all the upstream watersheds that drain to that particular

Schemanode SrcType 3. The bacterial loading was calculated for each of the four Copano Bay segments (of the four SchemaNodes SrcType 3). The bacterial loadings from the major bacterial sources for each of the Copano Bay segments (identified in Section 6.4) are shown in Table 8.10.

Table 8.9 Schematic Processor Bacterial Loadings to Copano Bay (Segment 2472)

Copano Bay Segment	SchemaNode HydroID	Load (CFU/year)
Watershed 45405 (Segment 1)	155	5.062E+10
Aransas River Outlet (Segment 2)	154	5.036E+12
Mission River Outlet (Segment 3)	153	5.503E+12
Copano Creek Outlet (Segment 4)	156	1.457E+12
Total		1.205E+13

Table 8.10 Schematic Processor Bacterial Loadings from Major Sources to Copano Bay (Segment 2472) in CFU/year

Bacteria Source	Segment 1 (Node 155)	Segment 2 (Node 154)	Segment 3 (Node 153)	Segment 4 (Node 156)	Total
Cattle	2.491E+11	3.453E+12	5.243E+12	1.202E+12	1.015E+13
WWTP	0.000E+00	2.266E+11	2.826E+09	0.000E+00	2.294E+11
OSSF	1.716E+11	3.813E+11	6.650E+02	1.718E+11	7.247E+11
Birds	1.169E+08	1.283E+07	7.287E+06	9.148E+07	2.285E+08
Non-point (Urban, Forest, etc.)	4.407E+10	7.176E+11	1.611E+11	4.637E+10	9.692E+11
Total Load	5.062E+10	5.036E+12	5.503E+12	1.457E+12	1.205E+13

Bacterial loading is greatest at the Mission River outlet (Copano Bay Segment 3) and the Aransas River outlet (Copano Bay Segment 2), which is shown in Table 8.9. Cattle are the major bacterial source based on Schematic Processor Model results (Table 8.10) for all Copano Bay segments.

8.1.2 Monte Carlo Simulations

The current loadings to each of the water segments (Aransas River Above Tidal, Mission River Above Tidal, Aransas River Tidal, Mission River Tidal, and Copano Bay) are presented in this section using the Monte Carlo Simulation Model. Other results from the Monte Carlo Simulation Model are given in Section 7.4.

The difficulty with calculating the current loadings to each water segment using the Monte Carlo Simulation Model is that 1000 simulations (user-defined) are implemented per run, so this means that each SchemaNode in the Schematic Network has 1000 bacterial concentrations/loadings associated with it (i.e., a probability distribution of concentrations/loadings). On the other hand, the Schematic Processor Model implements one simulation (that represents average annual conditions), so only one bacterial loading/concentration is associated with each SchemaNode in the Schematic Network at calibrated conditions. Thus, the median of the 1000 simulations for each SchemaNode is used to represent the 'current loading' to each SchemaNode (and each water segment). These values should be similar to the current loadings calculated by the Schematic Processor Model in Section 8.1.1 since the bacterial loading distributions (at input locations) were based on the assumption that the median equals the annual average bacterial loadings that were calculated in Chapter 5. However, separate runs were not implemented for each bacterial source, so only the total current loadings to each water segment were determined using the Monte Carlo Simulation Model.

The Monte Carlo Simulation Model outputs fecal coliform concentrations in CFU/100mL, so the median concentration was multiplied by the cumulative flow (of the upstream watersheds that were calculated in Section 5.1.2.6) and multiplied by 10,000 to convert from CFU/100mL to CFU/m^3 to find the bacterial loading in CFU/year.

The bacterial loadings at the upstream and downstream nodes of the Aransas River Above Tidal (segment 2004) are shown in Table 8.11.

Table 8.11 Monte Carlo Simulation Model Loadings to Aransas River Above Tidal (Segment 2004)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	62	3.712E+13
Downstream	75	9.680E+13

The bacterial loading increases from the upstream to the downstream portions of the Aransas River Above Tidal (shown in Table 8.11).

The bacterial loadings at the upstream and downstream nodes of the Aransas River Tidal (segment 2003) are shown in Table 8.12.

Table 8.12 Monte Carlo Simulation Model Loadings to Aransas River Tidal (Segment 2003)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	75	9.680E+13
Downstream	67	8.418E+14

The bacterial loadings increase from the upstream to the downstream portions of the Aransas River Tidal (shown in Table 8.12).

The bacterial loadings at the upstream and downstream nodes of the Mission River Above Tidal (segment 2002) are shown in Table 8.13.

Table 8.13 Monte Carlo Simulation Model Loadings to Mission River Above Tidal (Segment 2002)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	73	3.645E+14
Downstream	65	1.397E+14

The bacterial loadings decrease from the upstream to the downstream portions of the Mission River Above Tidal (shown in Table 8.13). This can be explained by the fact that major upstream watersheds drain to the upstream portion of the Mission River Above Tidal, and very small watersheds drain along the Mission River Above Tidal.

The bacterial loadings at the upstream and downstream nodes of the Mission River Tidal (segment 2001) are shown in Table 8.14.

Table 8.14 Monte Carlo Simulation Model Loadings to Mission River Tidal (Segment 2001)

Location on Segment	SchemaNode HydroID	Load (CFU/year)
Upstream	65	1.397E+14
Downstream	66	1.123E+15

The bacterial loadings increase from the upstream to the downstream portions of the Mission River Tidal (shown in Table 8.14).

The bacterial loadings to each of the Copano Bay segments (Segments 1, 2, 3, and 4) and the total current annual bacterial loading to Copano Bay are shown in Table 8.15. The bacterial loading was calculated for each of the four Copano Bay segments (i.e., the four SchemaNodes SrcType 3).

Table 8.15 Monte Carlo Simulation Model Loadings to Copano Bay (Segment 2472)

Copano Bay Segment	SchemaNode HydroID	Load (CFU/year)
Watershed 45405 (Segment 1)	155	6.504E+10
Aransas River Outlet (Segment 2)	154	4.868E+12
Mission River Outlet (Segment 3)	153	4.995E+12
Copano Creek Outlet (Segment 4)	156	8.354E+11
Total		1.076E+13

The bacterial loading is greatest at the Mission River outlet (Copano Bay Segment 3) and the Aransas River outlet (Copano Bay Segment 2), which is shown in Table 8.15.

8.2 ESTIMATION OF LOAD ALLOCATION

The percent load reductions necessary to meet fecal coliform water quality standards were determined using the Monte Carlo Simulation Model, and the Schematic Processor Model was used to quantify the load reductions required (as well as the allowable load) for each water segment in the Copano Bay watershed.

8.2.1 Monte Carlo Simulations

The percent load reductions from the point and non-point source loadings (and the locations in the watershed) were determined in Chapter 7, and the final results are given in Section 7.4. These percent load reductions, which have a margin of safety incorporated, ensure that the water segments would be in compliance with fecal coliform bacterial water quality standards.

There were two scenarios of load reductions presented (in Section 7.4 and Appendix 7.2). Load Reduction Scenario #1 looked at the upstream and downstream SchemaNodes of all river segments (Aransas and Mission River Above Tidals, and Aransas and Mission River Tidals), the SchemaNodes of all the bacterial monitoring stations, as well as the SchemaNodes of the four Copano Bay segments (Segments 1, 2, 3, and 4). Load reductions for this scenario were calculated to ensure that contact recreation and oyster water use fecal coliform standards were being met at all analyzed locations (Appendix 7.2). Load Reduction Scenario #2 looked at the SchemaNodes of where bacterial monitoring stations are located in the Monte Carlo Simulation Model to ensure that contact recreation and oyster water use fecal coliform standards are being met; thus, percent reductions were determined for locations where monitoring data indicated problems with complying with fecal coliform water quality standards (Section 7.4).

These percent load reductions (determined using the Monte Carlo Simulation Model in Chapter 7) were used with the Schematic Processor Model (the current loadings using the calibrated conditions at the average annual conditions) to determine the load reduction requirements and the allowable load (in CFU/year) for each of the water segments.

8.2.2 Applied to Schematic Processor Model

The percent load reductions from the point and non-point sources of SchemaNodes in the Copano Bay watershed were applied to the SchemaNode where the bacterial loading from the source was applied to the model. However, the load reduced at the source (where the bacterial loading is applied to the model) is not necessarily the load that would need to be reduced at the downstream water segment of interest (e.g., Aransas River Above Tidal). The bacterial loadings from sources may be further upstream from the water segment of interest. Thus, these bacterial loadings were reduced at the source and then decayed by the corresponding residence times (determined in Section 6.3.3.2) of the SchemaLinks that the bacteria travel down (either watershed travel and/or river travel) between the source and the water segment. Thus, the corresponding load reduction at the water segments was found for each of the sources in the watershed.

Load Reduction Scenario #1 contains the load reductions necessary to satisfy (including a margin of safety) fecal coliform water quality standards for all portions of the model that were analyzed (upstream/downstream SchemaNodes of water segments and bacterial monitoring stations). The results for Load Reduction Scenario #1 are presented in Appendix 8.1. Load Reduction Scenario #2 are the load reductions necessary to satisfy (including a margin of safety) fecal coliform water quality standards for the portions of the model that correspond to bacterial monitoring stations, where problems are proven to exist by bacterial monitoring data. The results for Load Reduction Scenario #2 are presented in the following sections.

8.2.2.1 Aransas River Above Tidal

The load reduction necessary for the Aransas River Above Tidal was determined for both load reduction scenarios. Load Reduction Scenario #1 is presented in Appendix 8.1, and Load Reduction Scenario #2 is presented below.

No load reductions were necessary to meet water quality standards at the bacterial monitoring stations (Load Reduction Scenario #2). Thus, the current loadings and allowable loadings (given in Table 8.1) for the upstream and downstream portions of the Aransas River Above Tidal are the allowable loads to the segment.

8.2.2.2 Aransas River Tidal

The load reduction necessary for the Aransas River Tidal was determined for both load reduction scenarios. Load Reduction Scenario #1 is presented in Appendix 8.1, and Load Reduction Scenario #2 is presented below.

The recommended load reductions to comply with water quality standards at the bacterial monitoring station were from upstream WWTPs and livestock bacterial sources. The percent of reductions from the corresponding sources (determined in Section 7.3.3) and the SchemaNodes and SchemaLinks of interest are shown in Figure 8.1.

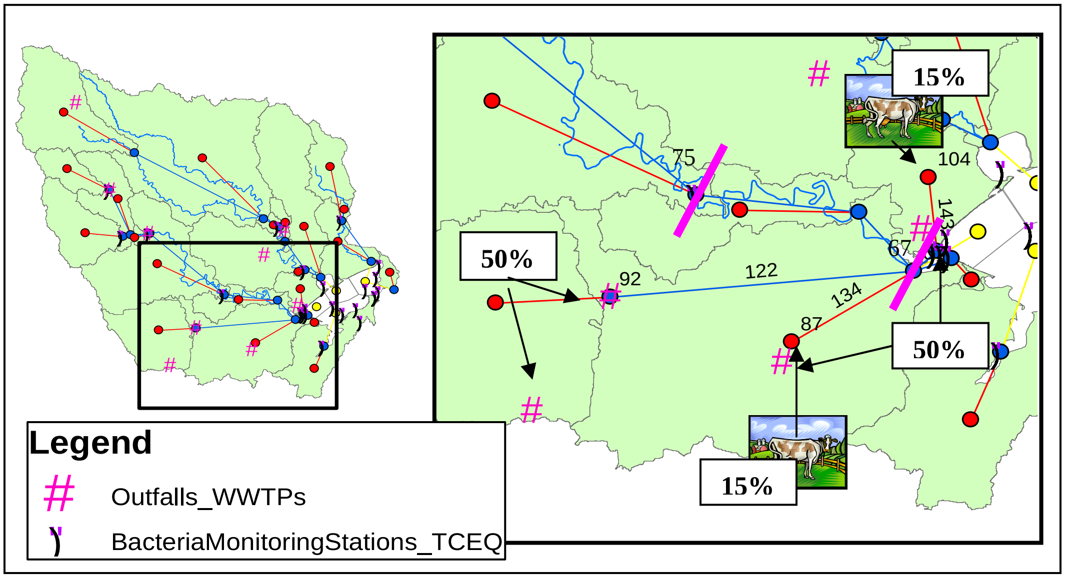


Figure 8.1 Load Reduction Scenario #2: Aransas River Tidal

The load reductions and allowable loads to the upstream portion of the Aransas River Tidal are the same as the load reductions and allowable loads to the downstream portion of the Aransas River Above Tidal because it is the same SchemaNode (HydroID 75) in the Schematic Network. Since there are no load reductions in the downstream portion of the Aransas River Above Tidal, there are no load reductions in the upstream portion of the Aransas River Tidal. Thus, the allowable load equals the current load of the upstream portion of the Aransas River Tidal, which is given in Table 8.3. Table 8.16 shows the load reductions at the bacterial sources for the downstream portion of the Aransas River Tidal (SchemaNode 67).

Table 8.16 Load Reduction Scenario #2 at Downstream Node of Aransas River Tidal

Schema-Node	Source	Current Loading (CFU/yr)	Load Reduction at Source (CFU/yr)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/yr)
67	WWTP	1.48E+04	7.40E+03	0.00	7.40E+03
69	WWTP	3.37E+11	1.69E+11	0.01	1.65E+11
87	Livestock	9.81E+15	1.47E+15	1.44	8.28E+13
92	WWTP	6.98E+14	3.49E+14	1.50	1.74E+13
104	Livestock	5.61E+14	8.42E+13	1.51	4.11E+12
Total Load Reduction (CFU/year)					1.05E+14
Current Loading (CFU/year), Table 8.3					8.69E+14
Allowable Load (CFU/year)					7.65E+14

8.2.2.3 Mission River Above Tidal

The load reduction necessary for the Mission River Above Tidal was determined for both load reduction scenarios. Load Reduction Scenario #1 is presented in Appendix 8.1, and Load Reduction Scenario #2 is presented below.

No load reductions were needed to meet water quality standards at the bacterial monitoring station. Thus, the current loads of the upstream and downstream portions of the Mission River Above Tidal are the allowable loads to the segment; see Table 8.5 for current upstream/downstream bacterial loadings.

8.2.2.4 Mission River Tidal

The load reduction necessary for the Mission River Tidal was determined for both load reduction scenarios. Load Reduction Scenario #1 is presented in Appendix 8.1, and Load Reduction Scenario #2 is presented below.

The recommended load reductions to comply with water quality standards at the bacterial monitoring station were from upstream livestock bacterial sources. The percent of reductions (determined in Section 7.3.3), the corresponding sources, and the SchemaNodes and SchemaLinks of interest are shown in Figure 8.2.

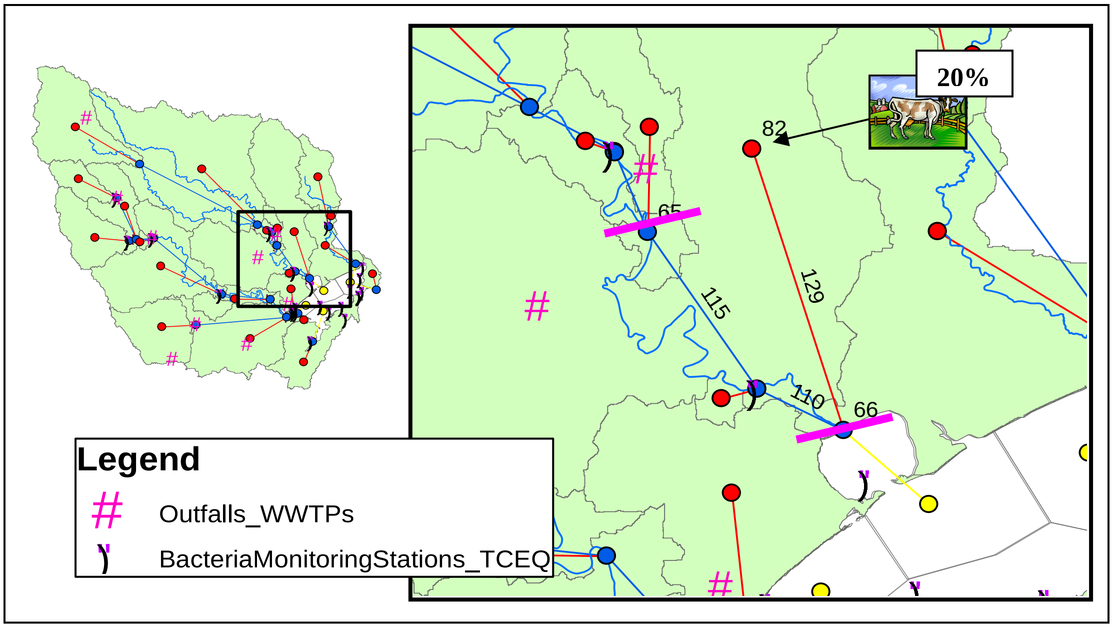


Figure 8.2 Load Reduction Scenario #2: Mission River Tidal

The load reductions and allowable loads to the upstream portion of the Mission River Tidal are the same as the load reductions and allowable loads to the downstream portion of the Mission River Above Tidal because it is the same SchemaNode (HydroID 65) in the Schematic Network. Since there are no load reductions in the downstream portion of the Mission River Above Tidal, there are no load reductions in the upstream portion of the Mission River Tidal. Thus, the allowable load equals the current load of the upstream portion of the Mission River Tidal, which is given in Table 8.7. The load reductions at the bacterial sources for the downstream portion of the Mission River Tidal (SchemaNode 66) are shown in Table 8.17.

Table 8.17 Load Reduction Scenario #2 at Downstream Node of Mission River Tidal

Schema-Node	Source	Current Loading (CFU/yr)	Load Reduction at Source (CFU/yr)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/yr)
82	Livestock	4.34E+16	8.68E+15	1.86	2.11E+14
Total Load Reduction (CFU/year)					2.11E+14
Current Loading (CFU/year), Table 8.7					1.16E+15
Allowable Load (CFU/year)					9.04E+14

8.2.2.5 Copano Bay

The load reduction necessary for Copano Bay was determined for both load reduction scenarios. Load Reduction Scenario #1 is presented in Appendix 8.1, and Load Reduction Scenario #2 is presented below.

No load reductions were necessary for Copano Bay Segments 1 and 4 in either scenario; however, load reductions were necessary for the Aransas River outlet (Copano Bay Segment 2) and the Mission River outlet (Copano Bay Segment 3.) The load reductions and allowable loads (CFU/year) for each Copano Bay Segment were determined first, and then the total load reductions and allowable loads for Copano Bay were determined.

The recommended load reductions to comply with water quality standards at the bacterial monitoring stations were from upstream WWTPs/livestock bacterial sources (shown in Figure 7.20).

The load reductions that are accounted for at the Aransas River outlet (Copano Bay Segment 2) are shown in Figure 8.1. The Aransas River Tidal drains directly into Copano Bay Segment 2, and the only additional loadings to this portion of the Bay are avian. Since the avian loading cannot be reduced, the total load reduction applied at

Segment 2 is the same load reduction that was found for the downstream portion of the Aransas River Tidal, which is given in Table 8.16. The load reduction needed at the Copano Bay Aransas River outlet (Copano Bay Segment 2) is shown in Table 8.18. Note that these load reductions are the reductions necessary to meet fecal coliform water quality standards in Copano Bay.

Table 8.18 Load Reduction Scenario #2 at Copano Bay Aransas River Outlet, Segment 2

SchemaNode	**Source**	**Equivalent Load at Tidal (CFU/yr)**	**Concentration in Bay (CFU/m^3)**	**Load in Bay (CFU/yr)**
67	WWTP	7.40E+03	1.70E-07	4.29E+01
69	WWTP	1.65E+11	3.80E+00	9.57E+08
87	Livestock	8.28E+13	1.91E+03	4.80E+11
92	WWTP	1.74E+13	4.00E+02	1.00E+11
104	Livestock	4.11E+12	9.45E+01	2.38E+10
Cumulative Runoff. Q (m^3/yr), Section 6.3.3.4				2.52E+08
Volume of Copano Bay Segment, V (m^3), Section 6.3.3.3				5.92E+07
Decay Coefficient of Segment, k ($years^{-1}$), Section 6.3.3.1				7.30E+02
Total Load Reduction (CFU/year)				6.05E+11
Current Loading (CFU/year), Table 8.9				5.04E+12
Allowable Load (CFU/year)				4.43E+12

The load reductions that are accounted for at the Mission River outlet (Copano Bay Segment 3) are shown in Figure 8.2. The Mission River Tidal drains directly into Copano Bay Segment 3, and the only additional loadings to this portion of the Bay are avian. Since the avian loading is not reduced, the total load reduction applied at Segment 3 is the same load reduction that was found for the downstream portion of the Mission River Tidal, which is given in Table 8.17. The load reduction needed at the Copano Bay Mission River outlet (Copano Bay Segment 3) is shown in Table 8.19. Note that these load reductions are the reductions necessary to meet fecal coliform water quality standards in Copano Bay.

Table 8.19 Load Reduction Scenario #2 at Copano Bay Mission River Outlet, Segment 3

SchemaNode	**Source**	**Equilavent Load at Tidal (CFU/yr)**	**Concentration in Bay (CFU/m^3)**	**Load in Bay (CFU/yr)**
82	Livestock	2.11E+14	3.78E+03	1.04E+12
Cumulative Runoff. Q (m^3/yr), Section 6.3.3.4				2.75E+08
Volume of Copano Bay Segment, V (m^3), Section 6.3.3.3				7.60E+07
Decay Coefficient of Segment, k (years^{-1}), Section 6.3.3.1				7.30E+02
Total Load Reduction (CFU/year)				1.04E+12
Current Loading (CFU/year), Table 8.9				5.50E+12
Allowable Load (CFU/year)				4.46E+12

The total load reduction and allowable loading to Copano Bay were found by summing all the load reductions and current loadings for all four Copano Bay Segments. The load reductions, current loadings, and allowable loads to meet fecal coliform standards for Load Reduction Scenario #2 are shown in Table 8.20.

Table 8.20 Load Reduction Scenario #2 at Copano Bay

Portion of Bay	**Current Load (CFU/yr)**	**Load Reductions (CFU/yr)**	**Allowable Load (CFU/yr)**
Aransas Outlet (Segment 2)	5.04E+12	6.05E+11	4.43E+12
Mission Outlet (Segment 3)	5.50E+12	1.04E+12	4.46E+12
Copano Creek Outlet (Segment 4)	1.46E+12	0.00E+00	0.00E+00
Watershed JunctionID Outlet (Segment 1)	5.06E+10	0.00E+00	0.00E+00
Total Load	1.20E+13	1.65E+12	8.89E+12

Chapter 9: Conclusions and Recommendations

9.1 CONCLUSIONS

Conclusions are presented based on the chapter from which the conclusions were drawn. All of these conclusions are based on the modeled results and the assumptions and calculations that are presented throughout this report.

In Chapter 4, the bacterial monitoring data were analyzed throughout the Copano Bay watershed. From the analyses, the highest fecal coliform concentrations are found in the upstream rivers and streams; however, the rivers and streams have less stringent standards (i.e., contact recreation use) than Copano Bay (i.e., oyster water use). Within Copano Bay, the highest fecal coliform concentrations occur at the outlets where rivers and streams discharge into the Bay. At all of the bacterial monitoring stations in Copano Bay (from 1999-2005), the median fecal coliform concentrations are less than 14 CFU/100mL (the median fecal coliform standard in the Bay).

In Section 4.2.3, all bacterial monitoring stations along the upstream rivers and streams meet fecal coliform contact recreation use standards based on available data from 1999-2004, except for station 17592. Station 17592 (upstream of Aransas River Above Tidal) does not comply with contact recreation use standards based on the available data from 1999-2004 and exceeds both criteria. However, this station does not monitor the water quality of TCEQ-defined water segments. In Copano Bay, Segments 2 and 3 exceed the fecal coliform oyster water use standard for the 90th-percentile fecal coliform concentration based on available data from 1999-2005; however, Segments 1 and 4 comply with these water quality standards.

In Chapter 5, the annual bacterial loading calculations were made for all the point and non-point sources included in the models, and these loadings are the ‘input’ into both models. Based on the model assumptions and calculations, cattle are the main livestock contributors and contribute the greatest bacterial loading (input) compared to all other bacterial sources considered in the models. The upstream watersheds contribute the greatest bacterial loading; however, the loadings do not directly impact Copano Bay unless directly upstream up or adjacent to the Bay. Also, it was discovered towards the end of the analyses of this report that the WWTP bacterial loadings were greatly overestimated, so the WWTP loadings are even less of a bacterial contributor than what was presented in this report.

Chapter 6 discusses the Schematic Processor Model and how it was calibrated to the median fecal coliform concentrations at each bacterial monitoring station. This Model models the average, annual conditions of the bacterial loadings in the Copano Bay watershed.

Section 6.4 gives the results from the calibrated Schematic Processor Model. In this section, it was shown that the bacterial loadings decay very quickly; thus, at a point of interest, the bacterial loading from the watershed directly upstream will have the greatest impact on the receiving water quality. Thus, the watersheds that will most influence the quality of Copano Bay are the watersheds directly upstream and adjacent to the Bay because the bacteria have not had sufficient time to decay due to environmental conditions.

After the modeling of bacterial transport (decay and CFSTRs simulated), cattle were found to be the greatest fecal coliform bacteria contributor to all Copano Bay segments based on model assumptions and calculations (shown in Figures 6.77 and 6.78). Note that Joanna Mott’s bacteria source tracking (BST) study (Mott, 2005) concluded that cattle and horses contribute to fecal contamination at many of the Copano Bay stations when there is rainfall and high river flow.

Wildlife (from non-point source calculations) and gulls (avian loading calculations) contribute relatively insignificant bacterial contamination to Copano Bay, which agrees with the findings from the BST study (Mott, 2005).

The greatest bacterial loadings impact Copano Bay Segments 2 and 3 (shown in Figure 6.77). WWTP bacterial loadings are insignificant compared to non-point bacterial loadings (e.g., livestock, septic systems, and urban, forest runoff).

Chapter 7 explains the Monte Carlo Simulation Model and how it was calibrated to the measured bacterial probability distributions at all of the bacterial monitoring stations. This Model models the variation in bacterial loadings throughout the year, accounting for seasonal, precipitation, runoff, bacterial loading, and temperature variations.

Section 7.3.3 presents the load reductions necessary to meet fecal coliform water quality standards at the bacterial monitoring stations. Because Copano Bay Segments 1 and 4 meet water quality standards, no load reductions are necessary from the watersheds that drain to these portions of the Bay. However, load reductions are necessary for Copano Bay Segments 2 and 3. To meet water quality standards in the Bay, bacterial loadings from WWTPs and livestock need to be reduced in the watersheds that drain to these portions of the Bay. The reduction of bacterial loadings from WWTPs alone is not sufficient to meet standards in the Bay.

Chapter 8 presents the current and allowable loadings to each of the water segments (Aransas River Above Tidal, Aransas River Tidal, Mission River Above Tidal, Mission River Tidal, and Copano Bay).

9.2 RECOMMENDATIONS

To conduct a TMDL study for the Aransas River Above Tidal, Aransas River Tidal, Mission River Above Tidal, and Mission River Tidal, it is critical to create bacterial models that model the chosen primary bacterial indicator for each of these water segments. Thus, *E. coli* and enterococci models must be created for the Copano Bay watershed. One option to create these models is to find correlations between fecal coliform and *E. coli* / enterococci (presented in Section 2.1).

One of the assumptions in the bacterial loading calculations (Chapter 5) was that all of the loading from livestock species was assumed to reach surface waters by either pasture runoff or direct discharge into the streams. There is a stakeholder concern that this overestimates livestock bacterial loadings. To see if these bacterial loadings are an overestimate, the event mean concentrations (EMCs) associated with land use types of agriculture, pasture, rangeland (land use classifications where bacterial loadings would come from primarily livestock species) of local studies should be compared to the livestock loadings calculated in these analyses. If there is a significant difference, then more research needs to be conducted to determine the fraction of the bacterial loadings that would reach surface waters from livestock species, taking into account location, time spent in water bodies, and survival rates of bacteria.

More fecal coliform (or the bacterial indicator of interest based on location in stream network) monitoring should occur at WWTPs to ensure compliance with Texas Surface Water Quality Standards. However, from the modeled results, WWTP loadings were significantly less than livestock/non-point bacterial loadings (though these loadings directly discharge into surface waters). Also, from the BST study, human and sewage are not always the primary bacterial source in Copano Bay (Mott, 2005), so reductions from

WWTPs alone will not eliminate the bacteria contamination in the Bay. The WWTP bacterial loadings need to be re-calculated with the monitoring data from renewal permit files.

The bacterial contribution from septic systems is very uncertain because it is difficult to quantify the bacterial loading that would reach surface and ground waters. Due to lack of data, it is recommended that a sensitivity analysis be conducted to determine the impact that the percentage of failing septic systems would have on Copano Bay.

Feral hogs were not included as one of the potential bacteria sources in the Copano Bay watershed, and thus were not included in the bacterial loading calculations (Chapter 5.) However, at the Stakeholder's Meeting in Refugio County on February 6, 2006, many stakeholders mentioned that feral hogs are prominent throughout the watershed and could be a major bacterial source directly impacting the quality of rivers, streams, and Copano Bay. Thus, bacterial loadings from feral hogs should be calculated and incorporated into the Schematic Processor and Monte Carlo Simulation Models.

In the BST study, the following bacterial sources were analyzed: human (sewage), cow, horse, duck, gull and wildlife (Mott, 2005). All of these bacterial sources were accounted for in the models of this report, except for the duck populations, which were not included in the avian loading calculations. Based on the BST study, there are large populations of migratory ducks that inhabit the marsh areas that surround TDH stations COP 00013 and 00014 (near Aransas River outlet) and in the Mission Bay area (Mott, 2005). Thus, bacterial loadings from ducks should be calculated and incorporated into the Schematic Processor and Monte Carlo Simulation Models since ducks were found to be the major bacterial contributors in some of the storm events and stations studied and analyzed (Mott, 2005).

More monitoring data should be collected along the Aransas and Mission River Tidals. In the downstream portions of these two Tidals in the Monte Carlo Simulation Model, livestock, non-point, and WWTP bacterial loadings need to be significantly reduced to meet contact recreation use standards according to fecal coliform modeled results (Appendix 7.2). However, there are no monitoring data to conclude that there is a problem with complying with standards at these two locations.

Monitoring data should be collected more frequently than quarterly. It is difficult to capture the variations and peaks in bacterial loadings with one bacteria measurement every three months. The more bacterial monitoring data that can be collected, the more measured data that can be used to ensure that the model is modeling what is occurring in the watershed.

Agricultural Best Management Practices (BMPs) need to be implemented to reduce livestock bacterial loadings (the major modeled bacterial contributor) in the Copano Bay watershed.

The final recommendation regards the Total Maximum Daily Load (TMDL) process in general. Useful information and feedback were obtained from each stakeholder meeting. Stakeholders are much more familiar with the occurrences in their watersheds than a modeler who does not live in the watershed. However, a majority of the work for the models was completed before the first stakeholder meeting. With each meeting, more useful information and feedback were given on how to improve the accuracy of the model. Since it is the stakeholders who end up being responsible for implementing BMPs, finding ways to reduce loads, and who must approve the plan and model before implementation, it is recommended that the stakeholders be involved throughout the entire process. If the stakeholders are involved from the beginning, I believe that the process will be more time and cost efficient since calculations would not need to be continually redone; stakeholders would be able to provide useful input and feedback throughout the TMDL process rather than final comments.

Appendix 4.1: Bacterial Monitoring Data (1999-2005) of Copano Bay Segment 1

Station	Date	Fecal Coliform Concentration (CFU/100mL)	Rank, m	Probability of Exceedance, P (%)
13405	1/16/2001	390	1	0.55
13405	7/9/2002	290	2	1.44
13405	8/19/2003	220	3	2.32
14790	11/5/2002	170	4	3.20
13405	10/10/2000	104	5	4.08
13405	1/22/2003	82	6	4.97
14782	11/5/2002	79	7	5.85
14784	2/19/2003	79	8	6.73
14782	4/8/2004	64	9	7.62
14790	4/8/2004	46	10	8.50
14784	4/8/2004	33	11	9.38
14782	2/24/1999	15	12	10.27
13405	10/26/1999	13	13	11.15
14790	3/2/2004	13	14	12.03
14790	1/20/2005	13	15	12.91
13405	1/18/2000	8	16	13.80
14790	3/22/1999	8	17	14.68
14790	12/20/2004	8	18	15.56
13405	4/23/2003	7	19	16.45
14784	5/1/2002	7	20	17.33
14790	3/28/2005	7	21	18.21
13405	10/17/2002	6	22	19.10
13405	6/19/2001	5	23	19.98
14782	2/19/2003	5	24	20.86
14784	11/5/2002	5	25	21.74
14784	1/8/2004	5	26	22.63
14790	2/24/1999	5	27	23.51
14790	10/28/2004	5	28	24.39
14790	2/15/2005	5	29	25.28
13405	1/16/2002	4	30	26.16
13405	4/10/2002	4	31	27.04
13405	10/10/2001	3	32	27.93
13405	4/18/2000	2	33	28.81
14782	3/22/1999	2	34	29.69

14782	4/27/1999	2	35	30.57
14782	10/11/1999	2	36	31.46
14782	11/8/1999	2	37	32.34
14782	12/29/1999	2	38	33.22
14782	1/31/2000	2	39	34.11
14782	2/8/2000	2	40	34.99
14782	3/9/2000	2	41	35.87
14782	3/20/2000	2	42	36.76
14782	3/28/2000	2	43	37.64
14782	4/26/2000	2	44	38.52
14782	12/20/2000	2	45	39.40
14782	2/1/2001	2	46	40.29
14782	5/1/2002	2	47	41.17
14782	10/21/2002	2	48	42.05
14782	12/11/2002	2	49	42.94
14782	1/6/2003	2	50	43.82
14782	2/27/2003	2	51	44.70
14782	1/8/2004	2	52	45.59
14782	2/17/2004	2	53	46.47
14782	2/26/2004	2	54	47.35
14782	3/2/2004	2	55	48.23
14782	10/28/2004	2	56	49.12
14782	11/8/2004	2	57	50.00
14782	12/20/2004	2	58	50.88
14782	1/20/2005	2	59	51.77
14782	2/15/2005	2	60	52.65
14782	3/28/2005	2	61	53.53
14784	2/24/1999	2	62	54.42
14784	3/22/1999	2	63	55.30
14784	4/27/1999	2	64	56.18
14784	10/11/1999	2	65	57.06
14784	11/8/1999	2	66	57.95
14784	12/29/1999	2	67	58.83
14784	1/31/2000	2	68	59.71
14784	2/8/2000	2	69	60.60
14784	3/9/2000	2	70	61.48
14784	3/20/2000	2	71	62.36
14784	3/28/2000	2	72	63.25
14784	4/26/2000	2	73	64.13
14784	12/20/2000	2	74	65.01
14784	2/1/2001	2	75	65.89
14784	10/21/2002	2	76	66.78

14784	12/11/2002	2	77	67.66
14784	1/6/2003	2	78	68.54
14784	2/27/2003	2	79	69.43
14784	2/17/2004	2	80	70.31
14784	2/26/2004	2	81	71.19
14784	3/2/2004	2	82	72.08
14784	10/28/2004	2	83	72.96
14784	11/8/2004	2	84	73.84
14784	12/20/2004	2	85	74.72
14784	1/20/2005	2	86	75.61
14784	2/15/2005	2	87	76.49
14784	3/28/2005	2	88	77.37
14790	4/27/1999	2	89	78.26
14790	10/11/1999	2	90	79.14
14790	11/8/1999	2	91	80.02
14790	12/29/1999	2	92	80.91
14790	1/31/2000	2	93	81.79
14790	2/8/2000	2	94	82.67
14790	3/9/2000	2	95	83.55
14790	3/20/2000	2	96	84.44
14790	3/28/2000	2	97	85.32
14790	4/26/2000	2	98	86.20
14790	12/20/2000	2	99	87.09
14790	2/1/2001	2	100	87.97
14790	5/1/2002	2	101	88.85
14790	10/21/2002	2	102	89.74
14790	12/11/2002	2	103	90.62
14790	1/6/2003	2	104	91.50
14790	2/19/2003	2	105	92.38
14790	2/27/2003	2	106	93.27
14790	2/17/2004	2	107	94.15
14790	1/8/2004	2	108	95.03
14790	2/26/2004	2	109	95.92
14790	11/8/2004	2	110	96.80
13405	7/12/2000	1	111	97.68
14784	1/5/2000	1	112	98.57
14784	6/22/2000	1	113	99.45

Appendix 4.2: Bacterial Monitoring Data (1999-2005) of Copano Bay Segment 2

Station	Date	Fecal Coliform Concentration (CFU/100mL)	Rank, m	Probability of Exceedance, P (%)
14788	4/27/1999	1600	1	0.52
14788	3/20/2000	1600	2	1.34
14783	4/8/2004	1600	3	2.16
14788	4/8/2004	540	4	2.99
12945	1/21/2003	400	5	3.81
14783	11/5/2002	350	6	4.64
14788	11/5/2002	240	7	5.46
14787	11/5/2002	220	8	6.29
12945	7/8/2002	145	9	7.11
14787	4/8/2004	130	10	7.94
12945	8/18/2003	118	11	8.76
14783	2/19/2003	110	12	9.59
14788	3/28/2000	79	13	10.41
14788	2/27/2003	79	14	11.24
12945	4/17/2000	60	15	12.06
12945	4/22/2003	58	16	12.89
14783	3/20/2000	49	17	13.71
14783	11/13/2002	48	18	14.54
14783	5/18/1999	45	19	15.36
12945	1/14/2002	39	20	16.19
12945	4/9/2002	39	21	17.01
12945	4/10/2001	37	22	17.84
14788	2/26/2004	33	23	18.66
14787	2/19/2003	33	24	19.48
14787	2/26/2004	33	25	20.31
14783	4/27/1999	33	26	21.13
14783	3/28/2005	33	27	21.96
12945	10/8/2001	29	28	22.78
14783	3/28/2000	27	29	23.61
14788	2/19/2003	23	30	24.43
14787	2/27/2003	23	31	25.26
14787	3/28/2005	23	32	26.08
14788	3/28/2005	17	33	26.91
12945	1/19/2000	16	34	27.73
12945	1/15/2001	15	35	28.56

12945	10/15/2002	14	36	29.38
12945	10/9/2000	14	37	30.21
14787	3/20/2000	13	38	31.03
14787	12/11/2002	11	39	31.86
12945	10/25/1999	10	40	32.68
14788	2/24/1999	9	41	33.51
14783	12/11/2002	8	42	34.33
14783	2/27/2003	8	43	35.15
14788	10/21/2002	7	44	35.98
14788	1/8/2004	7	45	36.80
14783	2/15/2005	7	46	37.63
12945	6/18/2001	6	47	38.45
14788	3/22/1999	5	48	39.28
14788	5/1/2002	5	49	40.10
14787	2/24/1999	5	50	40.93
14787	3/28/2000	5	51	41.75
14787	1/8/2004	5	52	42.58
14788	1/20/2005	4	53	43.40
14783	2/16/1999	4	54	44.23
14783	7/30/2002	4	55	45.05
14788	11/8/1999	2	56	45.88
14788	12/29/1999	2	57	46.70
14788	1/31/2000	2	58	47.53
14788	2/8/2000	2	59	48.35
14788	3/9/2000	2	60	49.18
14788	4/26/2000	2	61	50.00
14788	12/20/2000	2	62	50.82
14788	2/1/2001	2	63	51.65
14788	12/11/2002	2	64	52.47
14788	1/6/2003	2	65	53.30
14788	2/17/2004	2	66	54.12
14788	3/2/2004	2	67	54.95
14788	10/28/2004	2	68	55.77
14788	11/8/2004	2	69	56.60
14788	12/20/2004	2	70	57.42
14788	2/15/2005	2	71	58.25
14787	3/22/1999	2	72	59.07
14787	4/27/1999	2	73	59.90
14787	11/8/1999	2	74	60.72
14787	12/29/1999	2	75	61.55
14787	1/31/2000	2	76	62.37
14787	2/8/2000	2	77	63.20

14787	3/9/2000	2	78	64.02
14787	4/26/2000	2	79	64.85
14787	12/20/2000	2	80	65.67
14787	2/1/2001	2	81	66.49
14787	5/1/2002	2	82	67.32
14787	10/21/2002	2	83	68.14
14787	1/6/2003	2	84	68.97
14787	2/17/2004	2	85	69.79
14787	3/2/2004	2	86	70.62
14787	10/28/2004	2	87	71.44
14787	11/8/2004	2	88	72.27
14787	12/20/2004	2	89	73.09
14787	1/20/2005	2	90	73.92
14787	3/15/2005	2	91	74.74
14783	2/24/1999	2	92	75.57
14783	3/22/1999	2	93	76.39
14783	11/8/1999	2	94	77.22
14783	12/29/1999	2	95	78.04
14783	1/31/2000	2	96	78.87
14783	2/8/2000	2	97	79.69
14783	3/9/2000	2	98	80.52
14783	4/26/2000	2	99	81.34
14783	12/20/2000	2	100	82.16
14783	2/1/2001	2	101	82.99
14783	2/14/2002	2	102	83.81
14783	3/28/2002	2	103	84.64
14783	5/1/2002	2	104	85.46
14783	10/21/2002	2	105	86.29
14783	1/6/2003	2	106	87.11
14783	1/30/2003	2	107	87.94
14783	1/8/2004	2	108	88.76
14783	2/17/2004	2	109	89.59
14783	2/26/2004	2	110	90.41
14783	3/2/2004	2	111	91.24
14783	10/28/2004	2	112	92.06
14783	11/8/2004	2	113	92.89
14783	12/20/2004	2	114	93.71
14783	1/20/2005	2	115	94.54
14783	7/19/1999	1	116	95.36
14783	1/5/2000	1	117	96.19
14783	6/22/2000	1	118	97.01
14783	10/3/2000	1	119	97.84

14783	1/24/2001	1	120	98.66
12945	7/11/2000	1	121	99.48

Appendix 4.3: Bacterial Monitoring Data (1999-2005) of Copano Bay Segment 3

Station	Date	Fecal Coliform Concentration (CFU/100mL)	Rank, m	Probability of Exceedance, P (%)
14797	4/8/2004	240	1	2.00
14797	11/5/2002	220	2	5.20
14797	2/19/2003	70	3	8.40
14797	3/20/2000	49	4	11.60
14797	2/24/1999	22	5	14.80
14797	2/27/2003	17	6	18.00
14797	1/8/2004	13	7	21.20
14797	3/2/2004	5	8	24.40
14797	10/28/2004	5	9	27.60
14797	3/22/1999	2	10	30.80
14797	4/27/1999	2	11	34.00
14797	11/8/1999	2	12	37.20
14797	12/29/1999	2	13	40.40
14797	1/31/2000	2	14	43.60
14797	2/8/2000	2	15	46.80
14797	3/9/2000	2	16	50.00
14797	3/28/2000	2	17	53.20
14797	4/26/2000	2	18	56.40
14797	12/20/2000	2	19	59.60
14797	2/1/2001	2	20	62.80
14797	5/1/2002	2	21	66.00
14797	10/21/2002	2	22	69.20
14797	12/11/2002	2	23	72.40
14797	1/6/2003	2	24	75.60
14797	2/17/2004	2	25	78.80
14797	2/26/2004	2	26	82.00
14797	11/8/2004	2	27	85.20
14797	12/20/2004	2	28	88.40
14797	1/20/2005	2	29	91.60
14797	2/15/2005	2	30	94.80
14797	2/15/2005	2	31	98.00

Appendix 4.4: Bacterial Monitoring Data (1999-2005) of Copano Bay Segment 4

Station	Date	Fecal Coliform Concentration (CFU/100mL)	Rank, m	Probability of Exceedance, P (%)
14792	2/19/2003	1600	1	0.27
14792	2/26/2004	1600	2	0.70
14792	12/11/2002	540	3	1.13
14779	11/6/2002	350	4	1.56
14792	11/5/2002	350	5	1.99
14793	11/5/2002	130	6	2.42
14792	4/8/2004	110	7	2.85
14793	4/27/1999	79	8	3.28
13404	6/19/2001	70	9	3.71
13404	7/9/2002	57	10	4.14
14792	4/27/1999	49	11	4.57
14793	1/8/2004	49	12	5.01
14792	2/24/1999	23	13	5.44
14792	2/15/2005	22	14	5.87
14793	3/20/2000	22	15	6.30
13404	4/9/2001	21	16	6.73
13404	10/10/2001	21	17	7.16
13404	1/22/2003	14	18	7.59
13404	4/23/2003	14	19	8.02
14779	12/11/2002	14	20	8.45
14780	12/11/2002	14	21	8.88
13404	10/10/2000	13	22	9.31
14780	11/5/2002	13	23	9.74
14780	2/27/2003	13	24	10.17
14793	3/9/2000	13	25	10.60
14793	3/2/2004	13	26	11.03
14793	2/26/2004	12	27	11.46
13404	11/5/2002	11	28	11.89
13404	1/8/2004	11	29	12.33
14785	11/5/2002	11	30	12.76
14779	3/24/2005	8	31	13.19
14780	3/2/2004	8	32	13.62
14792	2/27/2003	8	33	14.05
13404	12/11/2002	7	34	14.48
14779	4/27/1999	7	35	14.91

14779	12/11/2002	7	36	15.34
14793	2/15/2005	7	37	15.77
13404	1/16/2001	6	38	16.20
14779	11/5/2002	5	39	16.63
14779	1/6/2003	5	40	17.06
14779	2/26/2004	5	41	17.49
14779	1/20/2005	5	42	17.92
14785	2/24/1999	5	43	18.35
14785	2/19/2003	5	44	18.78
14792	1/31/2000	5	45	19.21
14792	2/17/2004	5	46	19.64
14792	3/2/2004	5	47	20.08
14793	2/1/2001	5	48	20.51
14793	12/11/2002	5	49	20.94
14793	4/8/2004	5	50	21.37
14780	1/20/2005	4	51	21.80
14793	2/19/2003	4	52	22.23
13404	4/18/2000	3	53	22.66
13404	10/17/2002	3	54	23.09
14793	12/20/2004	3	55	23.52
13404	10/26/1999	2	56	23.95
13404	2/24/1999	2	57	24.38
13404	3/22/1999	2	58	24.81
13404	4/27/1999	2	59	25.24
13404	10/11/1999	2	60	25.67
13404	11/8/1999	2	61	26.10
13404	12/29/1999	2	62	26.53
13404	1/31/2000	2	63	26.96
13404	2/8/2000	2	64	27.40
13404	3/9/2000	2	65	27.83
13404	3/20/2000	2	66	28.26
13404	3/28/2000	2	67	28.69
13404	4/26/2000	2	68	29.12
13404	12/20/2000	2	69	29.55
13404	2/1/2001	2	70	29.98
13404	1/16/2002	2	71	30.41
13404	4/10/2002	2	72	30.84
13404	5/1/2002	2	73	31.27
13404	10/21/2002	2	74	31.70
13404	1/6/2003	2	75	32.13
13404	2/19/2003	2	76	32.56
13404	2/27/2003	2	77	32.99

13404	2/17/2004	2	78	33.42
13404	2/26/2004	2	79	33.85
13404	3/2/2004	2	80	34.28
13404	4/8/2004	2	81	34.71
13404	10/28/2004	2	82	35.15
13404	11/8/2004	2	83	35.58
13404	12/20/2004	2	84	36.01
13404	1/20/2005	2	85	36.44
13404	2/15/2005	2	86	36.87
14779	1/13/1999	2	87	37.30
14779	2/11/1999	2	88	37.73
14779	2/24/1999	2	89	38.16
14779	3/18/1999	2	90	38.59
14779	3/22/1999	2	91	39.02
14779	4/13/1999	2	92	39.45
14779	10/11/1999	2	93	39.88
14779	10/12/1999	2	94	40.31
14779	11/8/1999	2	95	40.74
14779	11/9/1999	2	96	41.17
14779	12/13/1999	2	97	41.60
14779	12/29/1999	2	98	42.03
14779	1/31/2000	2	99	42.47
14779	1/31/2000	2	100	42.90
14779	2/8/2000	2	101	43.33
14779	2/8/2000	2	102	43.76
14779	3/9/2000	2	103	44.19
14779	3/20/2000	2	104	44.62
14779	3/28/2000	2	105	45.05
14779	3/28/2000	2	106	45.48
14779	4/26/2000	2	107	45.91
14779	4/26/2000	2	108	46.34
14779	12/11/2000	2	109	46.77
14779	12/20/2000	2	110	47.20
14779	1/23/2001	2	111	47.63
14779	2/1/2001	2	112	48.06
14779	5/1/2002	2	113	48.49
14779	5/6/2002	2	114	48.92
14779	10/21/2002	2	115	49.35
14779	1/8/2003	2	116	49.78
14779	2/11/2003	2	117	50.22
14779	2/19/2003	2	118	50.65
14779	2/27/2003	2	119	51.08

14779	1/8/2004	2	120	51.51
14779	1/20/2004	2	121	51.94
14779	1/28/2004	2	122	52.37
14779	2/17/2004	2	123	52.80
14779	2/24/2004	2	124	53.23
14779	3/2/2004	2	125	53.66
14779	3/25/2004	2	126	54.09
14779	4/8/2004	2	127	54.52
14779	10/19/2004	2	128	54.95
14779	10/28/2004	2	129	55.38
14779	11/8/2004	2	130	55.81
14779	11/10/2004	2	131	56.24
14779	12/2/2004	2	132	56.67
14779	12/20/2004	2	133	57.10
14779	1/24/2005	2	134	57.53
14779	2/4/2005	2	135	57.97
14779	2/15/2005	2	136	58.40
14779	3/28/2005	2	137	58.83
14780	2/24/1999	2	138	59.26
14780	3/22/1999	2	139	59.69
14780	4/27/1999	2	140	60.12
14780	10/11/1999	2	141	60.55
14780	11/8/1999	2	142	60.98
14780	12/29/1999	2	143	61.41
14780	1/31/2000	2	144	61.84
14780	2/8/2000	2	145	62.27
14780	3/9/2000	2	146	62.70
14780	3/20/2000	2	147	63.13
14780	3/28/2000	2	148	63.56
14780	4/26/2000	2	149	63.99
14780	12/20/2000	2	150	64.42
14780	2/1/2001	2	151	64.85
14780	5/1/2002	2	152	65.29
14780	10/21/2002	2	153	65.72
14780	1/6/2003	2	154	66.15
14780	2/19/2003	2	155	66.58
14780	1/8/2004	2	156	67.01
14780	2/17/2004	2	157	67.44
14780	2/26/2004	2	158	67.87
14780	4/8/2004	2	159	68.30
14780	10/28/2004	2	160	68.73
14780	11/8/2004	2	161	69.16

14780	12/20/2004	2	162	69.59
14780	2/15/2005	2	163	70.02
14785	3/22/1999	2	164	70.45
14785	4/27/1999	2	165	70.88
14785	10/11/1999	2	166	71.31
14785	11/8/1999	2	167	71.74
14785	12/29/1999	2	168	72.17
14785	1/31/2000	2	169	72.60
14785	2/8/2000	2	170	73.04
14785	3/9/2000	2	171	73.47
14785	3/20/2000	2	172	73.90
14785	3/28/2000	2	173	74.33
14785	4/26/2000	2	174	74.76
14785	12/20/2000	2	175	75.19
14785	2/1/2001	2	176	75.62
14785	5/1/2002	2	177	76.05
14785	10/21/2002	2	178	76.48
14785	12/11/2002	2	179	76.91
14785	1/6/2003	2	180	77.34
14785	2/27/2003	2	181	77.77
14785	1/8/2004	2	182	78.20
14785	2/17/2004	2	183	78.63
14785	2/26/2004	2	184	79.06
14785	3/2/2004	2	185	79.49
14785	4/8/2004	2	186	79.92
14785	10/28/2004	2	187	80.36
14785	11/8/2004	2	188	80.79
14785	12/20/2004	2	189	81.22
14785	1/20/2005	2	190	81.65
14785	2/15/2005	2	191	82.08
14785	3/28/2005	2	192	82.51
14792	3/22/1999	2	193	82.94
14792	10/11/1999	2	194	83.37
14792	11/8/1999	2	195	83.80
14792	12/29/1999	2	196	84.23
14792	2/8/2000	2	197	84.66
14792	3/9/2000	2	198	85.09
14792	3/20/2000	2	199	85.52
14792	3/28/2000	2	200	85.95
14792	4/26/2000	2	201	86.38
14792	12/20/2000	2	202	86.81
14792	2/1/2001	2	203	87.24

14792	5/1/2002	2	204	87.67
14792	10/21/2002	2	205	88.11
14792	1/6/2003	2	206	88.54
14792	1/8/2004	2	207	88.97
14792	10/28/2004	2	208	89.40
14792	11/8/2004	2	209	89.83
14792	12/20/2004	2	210	90.26
14792	1/20/2005	2	211	90.69
14793	2/24/1999	2	212	91.12
14793	3/22/1999	2	213	91.55
14793	10/11/1999	2	214	91.98
14793	11/8/1999	2	215	92.41
14793	12/29/1999	2	216	92.84
14793	1/31/2000	2	217	93.27
14793	2/8/2000	2	218	93.70
14793	3/28/2000	2	219	94.13
14793	4/26/2000	2	220	94.56
14793	12/20/2000	2	221	94.99
14793	5/1/2002	2	222	95.43
14793	10/21/2002	2	223	95.86
14793	1/6/2003	2	224	96.29
14793	2/27/2003	2	225	96.72
14793	2/17/2004	2	226	97.15
14793	10/28/2004	2	227	97.58
14793	11/8/2004	2	228	98.01
14793	1/20/2005	2	229	98.44
13404	1/18/2000	1	230	98.87
13404	7/12/2000	1	231	99.30
13404	8/19/2003	1	232	99.73

Appendix 5.1: Terrain Preprocessing

For this project, and to allow the use of Water Rights Analysis Package (WRAP) Hydro, the only steps that were implemented from Terrain Preprocessing (located in the Arc Hydro Toolbar) were DEM Reconditioning, Fill Sinks, and Flow Direction. Before starting the process, the DEM was clipped to the watershed basin by going to **Spatial Analyst | Options** and changing the “Analysis Mask” to the subbasin feature class. Then I went to **Spatial Analyst | Raster Calculator** and evaluated the DEM to obtain the clipped DEM.

DEM Reconditioning

1. Select **Terrain Preprocessing | DEM Reconditioning.**
2. Select the clipped DEM as the “Raw DEM”.
3. Select the modified NHDFlowline (with all the river segments connected) as the “Agree Stream”.
4. Keep all the default settings, and the output will be “AgreeDEM”.
5. Press OK, and the “AgreeDEM” layer will be added to the map.

Fill Sinks

1. Select **Terrain Preprocessing | Fill Sinks.**
2. Select AgreeDEM as "DEM".
3. Keep all the default settings, and the output will be "Fil".
4. Press OK, and the "Fil" layer will be added to the map.

Flow Direction

1. Select **Terrain Preprocessing | Flow Direction**.
2. Select Fil as “Hydro DEM”.
3. Keep all the default settings, and the output will be “Fdr”.
4. Press OK, and the “Fdr” layer will be added to the map.

Appendix 5.2: WRAP Hydro Process

Water Rights Analysis Package (WRAP) Hydro, which is a toolbar located in Arc GIS, is used to delineate watersheds. The watersheds were delineated to the Critical Points (USGS gauge stations, water segment endpoints, and bacterial monitoring stations.)

Create Geometric Network

1. Using Arc Catalog, create a personal geodatabase called “WRAPHydro” within a chosen directory.
2. Create a feature dataset (called “WRAPHydro”) within the Geodatabase, and use the projection: NAD 1983 Texas Centric Mapping System Albers. This will maintain the area, which is crucial in maintaining drainage areas for non-point source calculations.
3. Import NHDFlowline (with all the river segments connected) into the feature dataset, and rename it “WRAPFlowline”.
4. Import “CriticalPoints”, which is the created feature class that contains the USGS gauge stations, bacteria monitoring stations, and water segment endpoints. (Note: before creating a geometric network, the Editor Toolbar in Arc GIS needs to be implemented to ensure that all the critical points are connected to the river network (WRAPFlowline). “Critical Points” is the target layer, and “Modify Feature” is the task. Go to **Editor | Snapping…** and check the box to allow the critical points to snap to the edge, WRAPFlowline. This allows one to move and snap the critical points to WRAPFlowline.
5. Right-click on the feature dataset in Arc Catalog, and go to **New | Geometric Network…**
6. Hit “Next”, and select “Build a geometric network from existing features.”
7. Select “WRAPFlowline” and “CriticalPoints”, name the geometric network, and hit “Next”.
8. Select “Yes”, so the complex edges will be in the network.
9. Keep all the default settings for the rest of the options, and hit “Finish”.

Assign HydroIDs to the Edges

1. In the Arc Hydro Toolbar in Arc Map, go to **Attribute Tools | Assign HydroID**.
2. Select the WRAPFlowline and CriticalPoints layers.
3. Say “Yes” to overwrite existing HydroIDs, apply to selected features, and press “OK”.

Delineate Watersheds

1. Make sure the WRAP Hydro Toolbar is open in Arc Map.
2. Set spatial extent.
3. Using the Spatial Analyst Toolbar, go to **Spatial Analyst | Options…**
4. Select the "Extent" tab, and make sure that the Fdr or DEM grid is selected for the Analysis Extent.
5. Set flow direction.
6. Using the Arc Hydro Toolbar, go to **Network Tools | Set Flow Direction…**
7. Select the WRAPFlowline layer and assign based on Fdr (flow direction grid that was created in Terrain Preprocessing) attribute, and press "OK".
8. Using the WRAPHydro Toolbar, go to **Settings | Layers**
9. Set "WRAPJunction" to CriticalPoints.
10. Set "HydroEdge" to WRAPFlowline.
11. Set "Flow Direction Raster" to Fdr.
12. Go to **Options | Delineate Watershed.**
13. Set "Source Layer" as WRAPFlowline.
14. Set "Source Attribute" as JunctionID.
15. Set the Drainage Area Units as square meters.
16. Click on "Batch Process WRAPJunctions" from the WRAP Hydro menu to delineate the watersheds.
17. Clip the watersheds, so that Copano Bay is excluded from the watershed areas.

Appendix 5.3: Precipitation Rasters for Land Use Classifications

To calculate the runoff for each land use classification, the precipitation grid was divided into four different rasters based on land use classifications.

Create Feature Classes of Different Land Uses

1. Use “Raster to Polygon” tool in Arc Toolbox to convert the land use land cover raster to a polygon feature class.
2. Right-click on land use land cover feature class (in Arc Map), go to **Properties | Definition Query**.
3. Select “Query Builder…”
4. Double-click on [GRIDCODE] (the field that contains the land use codes), “=” and select one of the grid code values that can be classified as either Agriculture, Forest, Urban, or Open Water. If there are multiple grid codes that could be Agriculture, Forest, Urban, or Open Water, click “AND”, and repeat step 4. (Note: what grid codes are associated with which land use classification is open to interpretation.)
5. After conducting a query for one of the land use classifications, then select all the polygons in the Arc Map view.
6. Right-click on the land use land cover polygon feature class, and **Data | Export Data…** and create a new feature class for that specific land use classification.
7. Repeat steps #4-6 until you have four new feature classes (Agriculture, Forest, Urban, and Open Water.)

Create Precipitation Rasters for Land Use Classifications

1. Go to **Spatial Analyst | Options…**
2. Set the “Analysis mask” to one of the land use classification feature classes (Agriculture, Forest, Urban, Open Water).
3. Set the “Extent” and “Cell Size” to the land use land cover raster.
4. Go to **Spatial Analyst | Raster Calculator…**
5. Double-click on the precipitation raster, **P,** and “Evaluate”.
6. Right-click on the Calculation raster and **Make Permanent**.
7. Repeat steps #1-6 for the other three land use classifications. (You will now have the original precipitation raster divided into four precipitation rasters based on the four different land use classifications.)

Appendix 5.4: Livestock Loading Calculations and Results

The calculations for bacterial loading due to livestock are shown in Table 5A.1, and the annual bacterial loadings due to livestock per watershed are given in Table 5A.2. Table 5A.1 includes the area of each county, the area of each county where animals were assumed to be located, and the census data for each county. The census data are from 2004 if these data existed; otherwise, the data are from 2002. The area of each watershed within each county (area where animals would be located) is also given, as well as the calculated livestock count and bacterial loading for each watershed. The locations of the Watershed JunctionIDs (used in Tables 5A.1 and 5A.2) are shown in Figure 5A.1.

Table 5A.1 Livestock Loading Calculations and Results

County	**Bee**	**San Patricio**	**Aransas**	**Refugio**	**Goliad**	**Karnes**
Area (m^2)	2344047042	1798057954	742112132	2016188169	2286808461	1965399713
Shrub./Pasture/Hay (m^2)	1382538600	472358700	207011700	1141603200	1462038300	1286240400
Cattle/Calves	49000	20000	2000	36000	66000	74000
Goats	2100	773	75	200	795	2100
Horses/Ponies	1391	662	46	692	887	973
Sheep/Lambs	670	0	0	71	0	327
Deer	0	0	0	0	0	0
Layers (20 weeks +)	793	464	0	63	859	0
Hogs and Pigs	0	741	0	0	0	0
Meat-type	0	0	0	0	252	0

Watershed Totals	
Cattle	111433
Horses	2561
Goat	2299
Sheep	659

Chickens								
Cattle/m^2	3.54E-05	4.23E-05	9.66E-06	3.15E-05	4.51E-05	5.75E-05		
Goats/m^2	1.52E-06	1.64E-06	3.62E-07	1.75E-07	5.44E-07	1.63E-06		
Horses/m^2	1.01E-06	1.40E-06	2.22E-07	6.06E-07	6.07E-07	7.56E-07		
Sheep/m^2	4.85E-07	0.00E+00	0.00E+00	6.22E-08	0.00E+00	2.54E-07		
Deer/m^2	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00		
Layers/m^2	5.74E-07	9.82E-07	0.00E+00	5.52E-08	5.88E-07	0.00E+00		
Hogs/m^2	0.00E+00	1.57E-06	0.00E+00	0.00E+00	0.00E+00	0.00E+00		
Chickens/m^2	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.72E-07	0.00E+00		
WATERSHEDS (JunctionID)								
45422								
Shrub./Pasture/Hay (m^2)	286448400					45632700	**Count**	**CFU/year**
Cattle	10152.32					2625.34	12777.66	2.52E+16
Goats	435.10					74.50	509.60	2.79E+15
Horses	288.20					34.52	322.72	4.95E+13
Sheep	138.82					11.60	150.42	8.24E+14
Layers	164.30					0.00	164.30	7.57E+12
Hogs	0.00					0.00	0.00	0.00E+00
Chickens	0.00					0.00	0.00	0.00E+00
45408								
Shrub./Pasture/Hay (m^2)	288088200	42202800		38923200			**Count**	**CFU/year**
Cattle	10210.44	1786.90		1227.43			13224.76	2.61E+16
Goats	437.59	69.06		6.82			437.59	2.40E+15
Horses	289.85	59.15		23.59			372.59	5.71E+13
Sheep	139.61	0.00		2.42			142.03	7.78E+14

Layers	165.24	41.46		2.15			208.85	9.62E+12
Hogs	0.00	66.20		0.00			66.20	2.40E+14
Chickens	0.00	0.00		0.00			0.00	0.00E+00
45426								
Shrub./Pasture/Hay (m^2)		64056600					**Count**	**CFU/year**
Cattle		2712.20					2712.20	5.35E+15
Goats		104.83					104.83	5.74E+14
Horses		89.77					89.77	1.38E+13
Sheep		0.00					0.00	0.00E+00
Layers		62.92					62.92	2.90E+12
Hogs		100.49					100.49	3.65E+14
Chickens		0.00					0.00	0.00E+00
45414								
Shrub./Pasture/Hay (m^2)		61632900		10715400			**Count**	**CFU/year**
Cattle		2609.58		337.91			2947.49	5.81E+15
Goats		100.86		1.88			102.74	5.62E+14
Horses		86.38		6.50			92.87	1.42E+13
Sheep		0.00		0.67			0.67	3.65E+12
Layers		60.54		0.59			61.13	2.82E+12
Hogs		96.68		0.00			96.68	3.51E+14
Chickens		0.00		0.00			0.00	0.00E+00
45416								
Shrub./Pasture/Hay (m^2)	5400	106298100	2049300	4218300			**Count**	**CFU/year**
Cattle	0.19	4500.74	19.80	133.02			4653.75	9.17E+15
Goats	0.01	173.95	0.74	0.74			0.01	4.49E+10
Horses	0.01	148.97	0.46	2.56			151.99	2.33E+13

Sheep	0.00	0.00	0.00	0.26			0.26	1.45E+12
Layers	0.00	104.42	0.00	0.23			104.65	4.82E+12
Hogs	0.00	166.75	0.00	0.00			166.75	6.06E+14
Chickens	0.00	0.00	0.00	0.00			0.00	0.00E+00
45405								
Shrub./Pasture/Hay (m^2)		35626500	55712700				**Count**	**CFU/year**
Cattle		1508.45	538.26				2046.71	4.03E+15
Goats		58.30	20.18				78.49	4.30E+14
Horses		49.93	12.38				62.31	9.55E+12
Sheep		0.00	0.00				0.00	0.00E+00
Layers		35.00	0.00				35.00	1.61E+12
Hogs		55.89	0.00				55.89	2.03E+14
Chickens		0.00	0.00				0.00	0.00E+00
45421								
Shrub./Pasture/Hay (m^2)				124290000	5258700		**Count**	**CFU/year**
Cattle				3919.44	237.39		4156.83	8.19E+15
Goats				21.77	2.86		24.63	1.35E+14
Horses				75.34	3.19		78.53	1.20E+13
Sheep				7.73	0.00		7.73	4.23E+13
Layers				6.86	3.09		9.95	4.58E+11
Hogs				0.00	0.00		0.00	0.00E+00
Chickens				0.00	0.91		0.91	6.29E+10
45417								
Shrub./Pasture/Hay (m^2)	51879600			409879800	152252100		**Count**	**CFU/year**
Cattle	1838.72			12925.40	6873.03		21637.15	4.26E+16
Goats	78.80			71.81	82.79		78.80	4.31E+14

Horses	52.20			248.45	92.37		393.02	6.03E+13
Sheep	25.14			25.49	0.00		50.63	2.77E+14
Layers	29.76			22.62	89.45		141.83	6.53E+12
Hogs	0.00			0.00	0.00		0.00	0.00E+00
Chickens	0.00			0.00	26.24		26.24	1.82E+12
45404								
Shrub./Pasture/Hay (m^2)	143850600						**Count**	**CFU/year**
Cattle	5098.36						5098.36	1.00E+16
Goats	218.50						218.50	1.20E+15
Horses	144.73						144.73	2.22E+13
Sheep	69.71						69.71	3.82E+14
Layers	82.51						82.51	3.80E+12
Hogs	0.00						0.00	0.00E+00
Chickens	0.00						0.00	0.00E+00
45409								
Shrub./Pasture/Hay (m^2)	16466400						**Count**	**CFU/year**
Cattle	583.60						583.60	1.15E+15
Goats	25.01						25.01	1.37E+14
Horses	16.57						16.57	2.54E+12
Sheep	7.98						7.98	4.37E+13
Layers	9.44						9.44	4.35E+11
Hogs	0.00						0.00	0.00E+00
Chickens	0.00						0.00	0.00E+00
45415								
Shrub./Pasture/Hay (m^2)	105787800						**Count**	**CFU/year**
Cattle	3749.34						3749.34	7.39E+15

Goats	160.69						160.69	8.80E+14
Horses	106.44						106.44	1.63E+13
Sheep	51.27						51.27	2.81E+14
Layers	60.68						60.68	2.79E+12
Hogs	0.00						0.00	0.00E+00
Chickens	0.00						0.00	0.00E+00
45419								
Shrub./Pasture/Hay (m^2)	254346300			66544200	406713600	5850900	**Count**	**CFU/year**
Cattle	9014.55			2098.44	18360.05	336.61	29809.66	5.88E+16
Goats	386.34			11.66	221.16	9.55	395.89	2.17E+15
Horses	255.90			40.34	246.75	4.43	547.41	8.39E+13
Sheep	123.26			4.14	0.00	1.49	128.89	7.06E+14
Layers	145.89			3.67	238.96	0.00	388.52	1.79E+13
Hogs	0.00			0.00	0.00	0.00	0.00	0.00E+00
Chickens	0.00			0.00	70.10	0.00	70.10	4.86E+12
45413								
Shrub./Pasture/Hay (m^2)	81936900						**Count**	**CFU/year**
Cattle	2904.01						2904.01	5.72E+15
Goats	124.46						124.46	6.81E+14
Horses	82.44						82.44	1.26E+13
Sheep	39.71						39.71	2.17E+14
Layers	47.00						47.00	2.16E+12
Hogs	0.00						0.00	0.00E+00
Chickens	0.00						0.00	0.00E+00
56830								
Shrub./Pasture/Hay (m^2)			18531000	94962600			**Count**	**CFU/year**

Cattle			179.03	2994.61			3173.64	6.26E+15
Goats			6.71	16.64			23.35	1.28E+14
Horses			4.12	57.56			61.68	9.46E+12
Sheep			0.00	5.91			5.91	3.23E+13
Layers			0.00	5.24			5.24	2.41E+11
Hogs			0.00	0.00			0.00	0.00E+00
Chickens			0.00	0.00			0.00	0.00E+00
56831								
Shrub./Pasture/Hay (m^2)			10971000				**Count**	**CFU/year**
Cattle			105.99				105.99	2.09E+14
Goats			3.97				3.97	2.18E+13
Horses			2.44				2.44	3.74E+11
Sheep			0.00				0.00	0.00E+00
Layers			0.00				0.00	0.00E+00
Hogs			0.00				0.00	0.00E+00
Chickens			0.00				0.00	0.00E+00
45425								
Shrub./Pasture/Hay (m^2)			1773900				**Count**	**CFU/year**
Cattle			17.14				17.14	3.38E+13
Goats			0.64				0.64	3.52E+12
Horses			0.39				0.39	6.04E+10
Sheep			0.00				0.00	0.00E+00
Layers			0.00				0.00	0.00E+00
Hogs			0.00				0.00	0.00E+00
Chickens			0.00				0.00	0.00E+00
45418								
Shrub./Pasture/Hay				24035400			**Count**	**CFU/year**

(m^2)								
Cattle				868.25			757.95	1.49E+15
Goats				4.21			4.21	2.31E+13
Horses				14.57			14.57	2.23E+12
Sheep				1.49			1.49	8.18E+12
Layers				1.33			1.33	6.11E+10
Hogs				0.00			0.00	0.00E+00
Chickens				0.00			0.00	0.00E+00
45423								
Shrub./Pasture/Hay (m^2)				13000500			**Count**	**CFU/year**
Cattle				469.63			409.97	8.08E+14
Goats				2.28			2.28	1.25E+13
Horses				7.88			7.88	1.21E+12
Sheep				0.81			0.81	4.43E+12
Layers				0.72			0.72	3.30E+10
Hogs				0.00			0.00	0.00E+00
Chickens				0.00			0.00	0.00E+00
45406								
Shrub./Pasture/Hay (m^2)				11534400			**Count**	**CFU/year**
Cattle				416.67			363.73	7.17E+14
Goats				2.02			2.02	1.11E+13
Horses				6.99			6.99	1.07E+12
Sheep				0.72			0.72	3.93E+12
Layers				0.64			0.64	2.93E+10
Hogs				0.00			0.00	0.00E+00
Chickens				0.00			0.00	0.00E+00
45412								

Shrub./Pasture/Hay (m^2)				793800			**Count**	**CFU/year**
Cattle				28.68			25.03	4.93E+13
Goats				0.14			0.14	7.61E+11
Horses				0.48			0.48	7.38E+10
Sheep				0.05			0.05	2.70E+11
Layers				0.04			0.04	2.02E+09
Hogs				0.00			0.00	0.00E+00
Chickens				0.00			0.00	0.00E+00
45410								
Shrub./Pasture/Hay (m^2)				8829900			**Count**	**CFU/year**
Cattle				318.97			278.45	5.49E+14
Goats				1.55			1.55	8.47E+12
Horses				5.35			5.35	8.21E+11
Sheep				0.55			0.55	3.01E+12
Layers				0.49			0.49	2.24E+10
Hogs				0.00			0.00	0.00E+00
Chickens				0.00			0.00	0.00E+00

Table 5A.2 Annual Livestock Bacterial Loading per Watershed

Watershed (JunctionID)	**CFU/year**
45422	2.89E+16
45408	2.95E+16
45426	6.30E+15
45414	6.74E+15
45416	9.81E+15
45405	4.68E+15
45421	8.38E+15
45417	4.34E+16
45404	1.17E+16
45409	1.33E+15
45415	8.57E+15
45419	6.17E+16
45413	6.64E+15
56830	6.43E+15
56831	2.31E+14
45425	3.74E+13
45418	1.53E+15
45423	8.26E+14
45406	7.33E+14
45412	5.04E+13
45410	5.61E+14

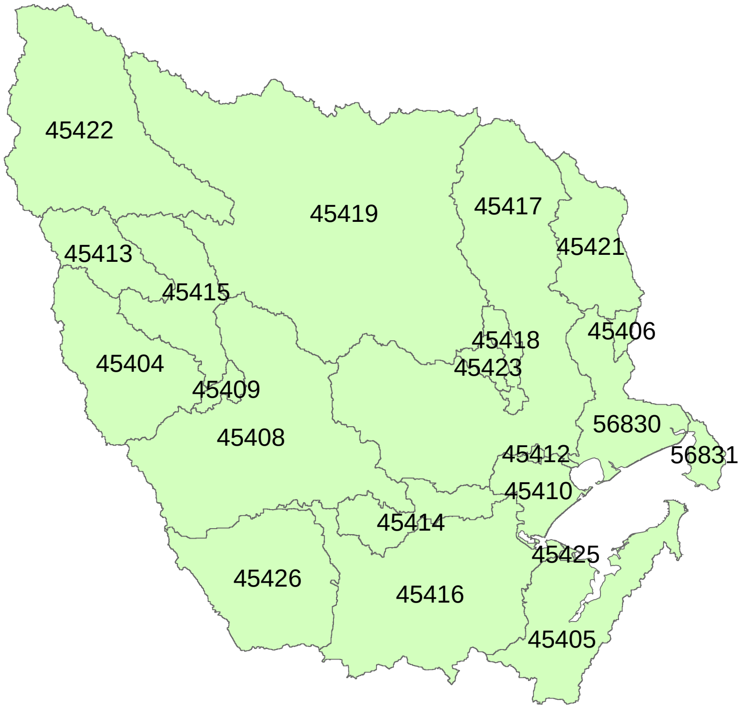


Figure 5A.1 Watershed JunctionIDs

Appendix 5.5: Mean Flow Length for Watersheds

In using Equation 5.7, the mean flow lengths for watersheds are needed. The mean flow lengths for watersheds were calculated as follows:

Creation of Flow Length Raster

1. Create Fdr (Flow Direction Raster that was created during Terrain Preprocessing, Appendix 5.1, with the Digital Elevation Model, DEM.)
2. In Arc Toolbox, go to the Spatial Analyst Tools, and open the tool “Flow Length”.
3. Select the Fdr raster as the “Input flow direction raster”.
4. Choose the name and directory for which the raster is to be placed.
5. Set the “Direction of measurement” to DOWNSTREAM, and press “OK”, and the flow length from each grid cell to the outlet in the Copano Bay watershed will be calculated.

Determination of Mean Flow Length in Watersheds

1. Go to “Zonal Statistics as Table”.
2. Select the delineated watersheds (Figure 5.1) as the “Input raster or feature zone data”.
3. Set the “Zone field” to JunctionID (the identifier for each watershed).
4. Set the “Input value raster” to the flow length raster that has already been created.
5. Choose the name and directory for which the table is to be placed.
6. Join table (Flow Length Statistics Table) to the watershed feature class.
7. Go to CRWR Attribute Tools in Arc Toolbox and use the tool: “Copy Field to Feature Class from Table” that was created by Nate Johnson (2004).
8. Join based on JunctionID (field in Watershed feature class) and VALUE_ (field in Flow Length Statistics Table that correlates with JunctionID) and add the field, MEAN, from the Statistics Table, which will give the mean of the flow length values within each delineated watershed. (Note: this is the mean flow length from the watershed to the outlet of the Copano Bay watershed.)
9. In order to calculate the mean flow length of each watershed (from the watershed to the drainage outlet of the watershed), the flow length (from the watershed to the outlet) was calculated by: {Mean flow length of the watershed} – {flow length at the drainage junction determined from FlowLength raster}.
10. Open the attribute table of the delineated watershed feature class.
11. Go to **Options… | Add Field**
    i. Name: “FlowLength”, Type: “Double”.

12. Go to **Editor | Start Editing…**, and edit within the Personal Geodatabase that contains the delineated watersheds (Figure 5.1).
13. Open the attribute table of delineated watershed feature class, and manually input the flow lengths for each of the watersheds as explained in the statement in step #9.
14. Go to **Editor | Stop Editing**, and save edits.

Appendix 5.6: Mean Flow Length from WWTPs to Mainstreams

Because the WWTPs are located at various distances from the mainstreams that are modeled for the Copano Bay watershed, the residence times from each WWTP to the downstream main river were calculated.

Creation of Flow Direction Raster (Fdr) with Copano Bay and Mainstreams Omitted

1. Create Fdr (Flow Direction Raster that was created during Terrain Preprocessing, Appendix 5.1, with the Digital Elevation Model, DEM.)
2. Create a 35-meter buffer around mainstream polyline feature class.
    a. Go to **Analysis Tools | Proximity | Buffer** to access the buffer tool.
    b. Under “Input Features”, select the mainstream feature class.
    c. Create a 35-meter buffer around the mainstream polyline feature class (under “Distance [value or field]”).
    d. Select OK, and a mainstream polygon feature class will be created.
3. Create polygon feature class of subbasin with Copano Bay and mainstreams omitted.
    a. Use “Union” tool under Analysis tools to combine the feature classes: Copano Bay, subbasin, and the mainstream channels.
    b. Using the Editor Toolbar, delete Copano Bay and the mainstream channels from the created feature class, and save edits.
4. Go to **Spatial Analyst | Options…**, and set the “Analysis Mask” to the feature class that was created in step 3.
5. Set the “Extent” and “Cell Size” to the Fdr raster.
6. Go to **Spatial Analyst | Raster Calculator…**
7. Double-click on the Fdr raster, and “Evaluate”.
8. Right-click on the Calculation raster and **Make Permanent**.

Creation of Flow Length Raster with Copano Bay and Mainstreams Omitted

1. In Arc Toolbox, go to the Spatial Analyst Tools, and open the tool “Flow Length”.
2. Select the Fdr raster (with Copano Bay and mainstreams omitted) as the “Input flow direction raster”.
3. Choose the name and directory for which the raster is to be placed.
4. Set the “Direction of measurement” to DOWNSTREAM, and press “OK”.

5. The flow length from each grid cell to either a mainstream or Copano Bay is then calculated and a flow length raster is created.
6. By using the identifier tool on the flow length raster that was just created, the distance (in meters) from the WWTP to either Copano Bay or a mainstream can be determined.

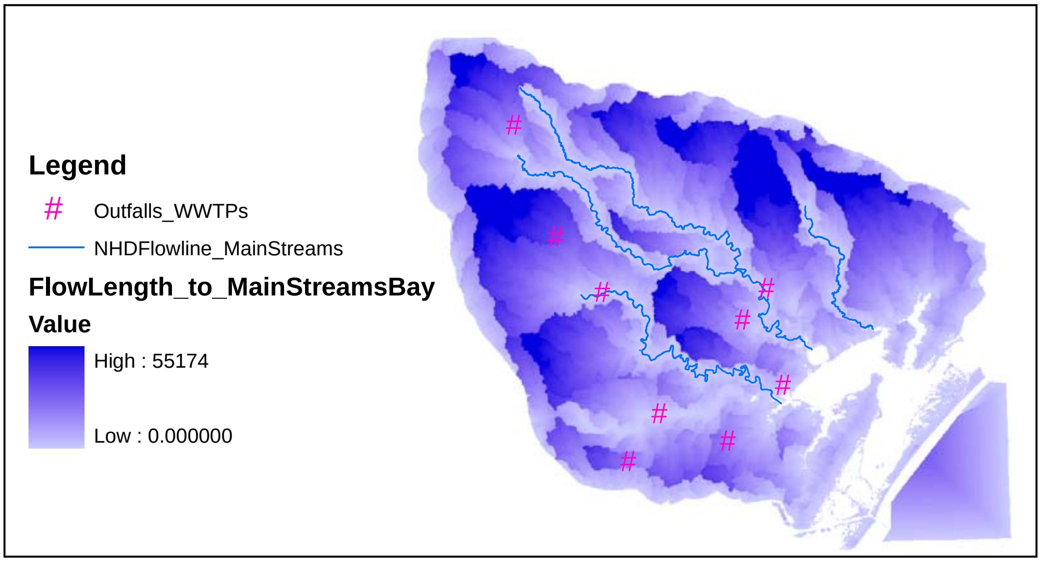


Figure 5A.2 Flow Length Raster to Mainstream and Copano Bay

Appendix 5.7: Septic System Loading Calculations and Results

The septic system loading calculations (how the bacterial loadings were calculated for each watershed) are shown in Table 5A.3, and the annual bacterial loadings per watershed due to septic systems are given in Table 5A.4. Table 5A.3 includes the area of each county, the area of each county classified as residential, and the area within each hydrologic soil group (within watershed and low/high residential areas), and the census data for each county. The septic system count (of each hydrologic soil group), human count, relative complaint count, number of housing units, and bacterial loadings for each watershed are also shown in Table 5A.3. The locations of the Watershed JunctionIDs (used in Tables 5A.3 and 5A.4) are shown in Figure 5A.1 in Appendix 5.4.

Table 5A.3 Septic System Loading Calculations and Results

County	**Bee**	**San Patricio**	**Aransas**	**Refugio**	**Goliad**	**Karnes**
Area (m^2)	2344047042	1798057954	742112132	2016188169	2286808461	1965399713
Low/High Res. (m^2)	13999500	28288800	14113800	7603200	2357100	7070400
Population, 2004 Estimate	33046	68187	24041	7640	7104	15458
Projected Housing Units, 2004	11182	26237	13653	3647	3588	5591
Septic Systems in use, 2004	3767	6287	5981	991	2243	1724
Complaints, 2004	68	85	81	7	5	3
Humans/m^2	0.00236	0.00241	0.00170	0.00100	0.00301	0.00219
Housing units/m^2	0.00080	0.00093	0.00097	0.00048	0.00152	0.00079
Septic Systems/m^2	0.00027	0.00022	0.00042	0.00013	0.00095	0.00024
Complaints/m^2	0.00000	0.00000	0.00001	0.00000	0.00000	0.00000
WATERSHEDS (JunctionID)						

7.3E+11 **CFU/year (Humans)**

45422									
Low/High Res. (m^2)	1391400					0	**Count**	**CFU/year**	
Soil Group A (m^2)	0					0	0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	85500					0	23		**Septic Systems in Soil Group B**
Soil Group C (m^2)	1116000					0	300		**Septic Systems in Soil Group C**
Soil Group D (m^2)	189900					0	51		**Septic Systems in Soil Group D**
Humans	3284					0	3284	2.40E+15	**Humans**
Housing Units	1111					0	1111		**Housing Units**
Septic Systems	374					0	374		**Septic Systems**
Complaints	7					0	7		**Complaints**
45408									
Low/High Res. (m^2)	573300	130500		0			**Count**	**CFU/year**	
Soil Group A (m^2)	0	0		0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	0	0		0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)	0	0		0			0		**Septic**

									Systems in Soil Group C
Soil Group D (m^2)	573300	130500		0			183		**Septic Systems in Soil Group D**
Humans	1353	315		0			1668	1.22E+15	**Humans**
Housing Units	458	121		0			579		**Housing Units**
Septic Systems	154	29		0			183		**Septic Systems**
Complaints	3	0		0			3		**Complaints**
45426									
Low/High Res. (m^2)		2122200					**Count**	**CFU/year**	
Soil Group A (m^2)		0					0		**Septic Systems in Soil Group A**
Soil Group B (m^2)		0					0		**Septic Systems in Soil Group B**
Soil Group C (m^2)		0					0		**Septic Systems in Soil Group C**
Soil Group D (m^2)		2122200					472		**Septic Systems in Soil Group D**
Humans		5115					5115	3.73E+15	**Humans**
Housing Units		1968					1968		**Housing Units**
Septic Systems		472					472		**Septic Systems**

Complaints		6					6		**Complaints**
45414									
Low/High Res. (m^2)		0		0			**Count**	**CFU/year**	
Soil Group A (m^2)		0		0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)		0		0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)		0		0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)		0		0			0		**Septic Systems in Soil Group D**
Humans		0		0			0	0.00E+00	**Humans**
Housing Units		0		0			0		**Housing Units**
Septic Systems		0		0			0		**Septic Systems**
Complaints		0		0			0		**Complaints**
45416									
Low/High Res. (m^2)	0	5538600	0	0			**Count**	**CFU/year**	
Soil Group A (m^2)	0	0	0	0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	0	0	0	0			0		**Septic Systems in Soil Group B**

Soil Group C (m^{2})	0	0	0	0			0		**Septic Systems in Soil Group C**
Soil Group D (m^{2})	0	5538600	0	0			1231		**Septic Systems in Soil Group D**
Humans	0	13350	0	0			13350	9.75E+15	**Humans**
Housing Units	0	5137	0	0			5137		**Housing Units**
Septic Systems	0	1231	0	0			1231		**Septic Systems**
Complaints	0	17	0	0			17		**Complaints**
45405									
Low/High Res. (m^{2})		1927800	4314600				**Count**	**CFU/year**	
Soil Group A (m^{2})		834300	3204000				1543		**Septic Systems in Soil Group A**
Soil Group B (m^{2})		0	0				0		**Septic Systems in Soil Group B**
Soil Group C (m^{2})		0	0				0		**Septic Systems in Soil Group C**
Soil Group D (m^{2})		1087200	1074600				697		**Septic Systems in Soil Group D**
Humans		4647	7349				11996	8.76E+15	**Humans**
Housing Units		1788	4174				5962		**Housing Units**

Septic Systems		428	1828				2257		**Septic Systems (total)**
Complaints		6	25				31		**Complaints**
45421									
Low/High Res. (m^2)				0	0		**Count**	**CFU/year**	
Soil Group A (m^2)				0	0		0		**Septic Systems in Soil Group A**
Soil Group B (m^2)				0	0		0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0	0		0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				0	0		0		**Septic Systems in Soil Group D**
Humans				0	0		0	0.00E+00	**Humans**
Housing Units				0	0		0		**Housing Units**
Septic Systems				0	0		0		**Septic Systems**
Complaints				0	0		0		**Complaints**
45417									
Low/High Res. (m^2)	0			2247300	0		**Count**	**CFU/year**	
Soil Group A (m^2)	0			0	0		0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	0			0	0		0		**Septic**

									Systems in Soil Group B
Soil Group C (m^2)	0			0	0		0		**Septic Systems in Soil Group C**
Soil Group D (m^2)	0			2247300	0		293		**Septic Systems in Soil Group D**
Humans	0			2258	0		2258	1.65E+15	**Humans**
Housing Units	0			1078	0		1078		**Housing Units**
Septic Systems	0			293	0		293		**Septic Systems**
Complaints	0			2	0		2		**Complaints**
45404									
Low/High Res. (m^2)	3600						**Count**	**CFU/year**	
Soil Group A (m^2)	0						0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	0						0		**Septic Systems in Soil Group B**
Soil Group C (m^2)	0						0		**Septic Systems in Soil Group C**
Soil Group D (m^2)	3600						1		**Septic Systems in Soil Group D**
Humans	8						8	6.20E+12	**Humans**

Housing Units	3						3		**Housing Units**
Septic Systems	1						1		**Septic Systems**
Complaints	0						0		**Complaints**
45409									
Low/High Res. (m^2)	709200						**Count**	**CFU/year**	
Soil Group A (m^2)	0						0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	0						0		**Septic Systems in Soil Group B**
Soil Group C (m^2)	0						0		**Septic Systems in Soil Group C**
Soil Group D (m^2)	709200						191		**Septic Systems in Soil Group D**
Humans	1674						1674	1.22E+15	**Humans**
Housing Units	566						566		**Housing Units**
Septic Systems	191						191		**Septic Systems**
Complaints	3						3		**Complaints**
45415									
Low/High Res. (m^2)	4727700						**Count**	**CFU/year**	
Soil Group A (m^2)	0						0		**Septic Systems in Soil Group A**

Soil Group B (m^2)	4588200						1234		**Septic Systems in Soil Group B**
Soil Group C (m^2)	0						0		**Septic Systems in Soil Group C**
Soil Group D (m^2)	139500						38		**Septic Systems in Soil Group D**
Humans	11160						11160	8.15E+15	**Humans**
Housing Units	3776						3776		**Housing Units**
Septic Systems	1272						1272		**Septic Systems**
Complaints	23						23		**Complaints**
45419									
Low/High Res. (m^2)	26100			3600	262800	0	**Count**	**CFU/year**	
Soil Group A (m^2)	0			0	0	0	0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	26100			0	259200	0	254		**Septic Systems in Soil Group B**
Soil Group C (m^2)	0			0	0	0	0		**Septic Systems in Soil Group C**
Soil Group D (m^2)	0			3600	3600	0	4		**Septic Systems in Soil Group D**

Humans	62			4	792	0	857	6.26E+14	**Humans**
Housing Units	21			2	400	0	423		**Housing Units**
Septic Systems	7			0	250	0	258		**Septic Systems**
Complaints	0			0	1	0	1		**Complaints**
45413									
Low/High Res. (m^2)	6654600						**Count**	**CFU/year**	
Soil Group A (m^2)	0						0		**Septic Systems in Soil Group A**
Soil Group B (m^2)	6641100						1787		**Septic Systems in Soil Group B**
Soil Group C (m^2)	13500						4		**Septic Systems in Soil Group C**
Soil Group D (m^2)	0						0		**Septic Systems in Soil Group D**
Humans	15708						15708	1.15E+16	**Humans**
Housing Units	5315						5315		**Housing Units**
Septic Systems	1790						1790		**Septic Systems**
Complaints	33						33		**Complaints**
56830									
Low/High Res. (m^2)			0	0			**Count**	**CFU/year**	
Soil Group A (m^2)			0	0			0		**Septic Systems in Soil Group**

									A
Soil Group B (m^2)			0	0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)			0	0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)			0	0			0		**Septic Systems in Soil Group D**
Humans			0	0			0	0.00E+00	**Humans**
Housing Units			0	0			0		**Housing Units**
Septic Systems			0	0			0		**Septic Systems**
Complaints			0	0			0		**Complaints**
56831									
Low/High Res. (m^2)			1944000				**Count**	**CFU/year**	
Soil Group A (m^2)			988200				419		**Septic Systems in Soil Group A**
Soil Group B (m^2)			0				0		**Septic Systems in Soil Group B**
Soil Group C (m^2)			0				0		**Septic Systems in Soil Group C**
Soil Group D (m^2)			936000				397		**Septic Systems in Soil Group**

									D
Humans			3311				3311	2.42E+15	**Humans**
Housing Units			1881				1881		**Housing Units**
Septic Systems			824				824		**Septic Systems**
Complaints			11				11		**Complaints**
45425									
Low/High Res. (m^2)			0				**Count**	**CFU/year**	
Soil Group A (m^2)			0				0		**Septic Systems in Soil Group A**
Soil Group B (m^2)			0				0		**Septic Systems in Soil Group B**
Soil Group C (m^2)			0				0		**Septic Systems in Soil Group C**
Soil Group D (m^2)			0				0		**Septic Systems in Soil Group D**
Humans			0				0	0.00E+00	**Humans**
Housing Units			0				0		**Housing Units**
Septic Systems			0				0		**Septic Systems**
Complaints			0				0		**Complaints**
45418									
Low/High Res. (m^2)				1719900			**Count**	**CFU/year**	
Soil Group A (m^2)				0			0		**Septic Systems in**

									Soil Group A
Soil Group B (m^2)				0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				1719900			224		**Septic Systems in Soil Group D**
Humans				1728			1728	1.26E+15	**Humans**
Housing Units				825			825		**Housing Units**
Septic Systems				224			224		**Septic Systems**
Complaints				2			2		**Complaints**
45423									
Low/High Res. (m^2)				1883700			**Count**	**CFU/year**	
Soil Group A (m^2)				0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)				0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				1883700			246		**Septic Systems in**

									Soil Group D
Humans				1893			1893	1.38E+15	**Humans**
Housing Units				904			904		**Housing Units**
Septic Systems				246			246		**Septic Systems**
Complaints				2			2		**Complaints**
45406									
Low/High Res. (m^2)				0			**Count**	**CFU/year**	
Soil Group A (m^2)				0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)				0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				0			0		**Septic Systems in Soil Group D**
Humans				0			0	0.00E+00	**Humans**
Housing Units				0			0		**Housing Units**
Septic Systems				0			0		**Septic Systems**
Complaints				0			0		**Complaints**
45412									
Low/High Res. (m^2)				0			**Count**	**CFU/year**	
Soil Group A (m^2)				0			0		**Septic**

									Systems in Soil Group A
Soil Group B (m^2)				0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				0			0		**Septic Systems in Soil Group D**
Humans				0			0	0.00E+00	**Humans**
Housing Units				0			0		**Housing Units**
Septic Systems				0			0		**Septic Systems**
Complaints				0			0		**Complaints**
45410									
Low/High Res. (m^2)				630000			**Count**	**CFU/year**	
Soil Group A (m^2)				0			0		**Septic Systems in Soil Group A**
Soil Group B (m^2)				0			0		**Septic Systems in Soil Group B**
Soil Group C (m^2)				0			0		**Septic Systems in Soil Group C**
Soil Group D (m^2)				630000			82		**Septic**

									Systems in Soil Group D
Humans				633			633	4.62E+14	**Humans**
Housing Units				302			302		**Housing Units**
Septic Systems				82			82		**Septic Systems**
Complaints				1			1		**Complaints**

Table 5A.4 Annual Septic System Bacterial Loading per Watershed

Watershed (JunctionID)	CFU/year
45422	4.29E+14
45408	1.93E+14
45426	4.47E+14
45414	0.00E+00
45416	1.17E+15
45405	2.78E+15
45421	0.00E+00
45417	0.00E+00
45404	0.00E+00
45409	2.06E+14
45415	2.70E+15
45419	0.00E+00
45413	3.86E+15
56830	0.00E+00
56831	7.93E+14
45425	0.00E+00
45418	0.00E+00

45423	8.26E+14
45406	7.33E+14
45412	5.04E+13
45410	5.61E+14

Appendix 5.8: Determination of Soil Group Areas within each Watershed and Land Use Classifications 21 and 22

To calculate the number of septic systems and the number of complaints investigated for each hydrologic soil group classification within each watershed in the land use classifications 21 and 22, the soil group areas within each watershed and land use classifications 21 and 22 were determined by the procedure given below. To find the total count of septic systems and complaints investigated, the area of each soil group was multiplied by each corresponding county's density.

Join Comp.dbf to Soil Polygon Feature Class (STATSGO data)

1. Right-click on soil polygon feature class, and go to **Joins and Relates | Join…**
2. Base the join on the field "MUID", which is found in both the soil polygon feature class and Comp.dbf.

Create Feature Classes of Different Hydrologic Soil Groups (A, B, C, D)

1. Right-click on the soil polygon feature class (in Arc Map), go to **Properties | Definition Query**.
2. Select "Query Builder…"
3. Double-click on [COMP.HYDGRP] (the field that contains the hydrologic soil groups), "=" and select one of the soil groups (either A, B, C, or D.)
4. After conducting a query for one of the soil groups, select all the polygons in the Arc Map view.
5. Right-click on the soil polygon feature class, and **Data | Export Data…** and create a new feature class for that specific soil group.
6. Repeat steps #3-5 until there are four new feature classes (Soil Group A, Soil Group B, Soil Group C, and Soil Group D.)

Create Land Use Land Cover Rasters for Each Hydrologic Soil Group

1. Go to **Spatial Analyst | Options…**
2. Set the "Analysis mask" to one of the soil group feature classes (A, B, C, or D).
3. Set the "Extent" and "Cell Size" to the land use land cover raster.
4. Go to **Spatial Analyst | Raster Calculator…**
5. Double-click on the land use land cover raster and "Evaluate".
6. Right-click on the Calculation raster and **Make Permanent**.
7. Repeat steps #1-6 for the other three soil group classifications. (There will now be land use land cover rasters for each of the different soil groups.)

Create Land Use Land Cover Rasters for each Soil Group in each Watershed

1. Go to **Spatial Analyst | Options…**
2. Set the “Analysis mask” to one of the watershed feature classes (each watershed needs to be exported into its own feature class).
3. Set the “Extent” and “Cell Size” to the land use land cover raster.
4. Go to **Spatial Analyst | Raster Calculator…**
5. Double-click on the land use land cover raster of a soil group found within that specified watershed (in step #2) and “Evaluate”.
6. Right-click on the Calculation raster and **Make Permanent**.
7. Repeat steps #5-6 until all the soil groups found within the watershed (specified in step #2) have been created into land use land cover rasters within the watershed.
8. Repeat steps #2-7 until the land use land cover rasters have been divided up into all the watersheds in the Copano Bay watershed.

Create Land Use Land Cover Rasters for each Soil Group in each Watershed within each County

1. Go to **Spatial Analyst | Options…**
2. Set the “Analysis mask” to one of the counties that is overlapping the watershed of interest (each county needs to be exported into its own feature class).
3. Set the “Extent” and “Cell Size” to the land use land cover raster.
4. Go to **Spatial Analyst | Raster Calculator…**
5. Double-click on the land use land cover raster that was created for a specified watershed in a specified soil group and “Evaluate”.
6. Right-click on the Calculation raster and **Make Permanent**.
7. Repeat steps #5-6 until all the soil groups found within the watershed (specified in step #2) have been created into land use land cover rasters within the watershed and overlapping county.
8. Repeat steps #2-7 until the land use land cover rasters (of soil groups) have been divided up into all the watersheds *and* counties in the Copano Bay watershed.

Calculate the Area of Low/High Residential within each Soil Group within each Watershed and each County.

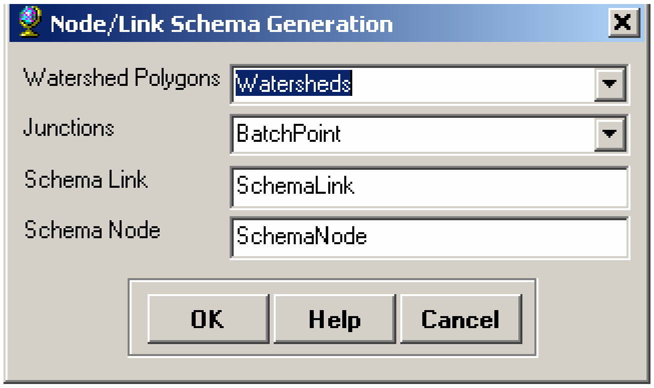
1. Add all the land use land cover rasters for a particular watershed (the land use land cover rasters for each soil group and county within the specified watershed) to Arc Map or preview each raster’s table in ArcCatalog.
2. Right-click on each raster, and open up the attribute table. The field, “Value”, is the land use land cover classification, and “Count” is the number of grid cells that correspond to each land use land cover classification.
3. Sum the grid cell count for the land use land cover classifications 21 and 22 (low/high residential) and multiply by 900 m^2 (the area of one grid cell) to find the total area corresponding to low/high residential for each soil group and county within each watershed.

Appendix 6.1: Schematic Network

To run the "Process Schematic", a Schematic Network of the Copano Bay watershed was created. The Schematic Network consists of two feature classes: SchemaNode and SchemaLink.

Creation of Automated Schematic Network

1. Go to Arc Hydro Toolbar, go to **Network Tools** | **Node/Link Schema Generation.**
2. Set the Watershed Polygons as the delineated watersheds, and the Junctions as BatchPoint (the feature class that contains the critical points: USGS gauge stations, bacteria monitoring stations, and water segment endpoints). (Note: the feature classes SchemaLink and SchemaNode will be automatically created.)



Watershed Polygons: Watersheds
Junctions: BatchPoint
Schema Link: SchemaLink
Schema Node: SchemaNode

Modify Automated Schematic Network

Because of the complex network (due to Copano Bay), the SchemaLink and SchemaNode attributes will need to be manually modified.

SchemaNode Modifications

1. Go to **Editor** | **Start Editing…**, and edit within the Personal Geodatabase that contains the SchemaLink and SchemaNode feature classes.
2. Set the Task as "Create New Feature" and the Target layer as "SchemaNode".
3. Add junctions in the middle of each of the watersheds, drainage points (BatchPoint), and four junctions in Copano Bay; (Copano Bay was divided into four segments.)

4. Open the attribute table of the SchemaNode feature class, and set the SrcType for each of the junctions (1 = Watershed, 2 = Junction watershed drains to, 3 = Copano Bay.)
5. Open the attribute table of the SchemaNode feature class, and set the FeatureID for each of the watershed junctions (SrcType = 1) to the JunctionID of the corresponding watershed.
6. Go to **Editor | Stop Editing**, and save edits.

SchemaLink Modifications

1. Go to **Editor | Start Editing…**, and edit within the Personal Geodatabase that contains the SchemaNode and SchemaLink feature classes.
2. Set the Task as “Create New Feature” and the Target layer as “SchemaLink”.
3. Add links, so that all the SchemaNode feature classes are connected by a SchemaLink. (Go to **Editor | Snapping…**, and select the Vertex, Edge, and End boxes of the SchemaNode feature class, so the endpoints of SchemaLink will snap to the SchemaNodes.)
4. Open the attribute table of the SchemaLink feature class, and set the LinkType for each of the links (1 = Connects watershed to drainage junction, 2 = Connects drainage junction to drainage junction, 3 = Connects drainage junction to Copano Bay.)
5. Go to **Editor | Stop Editing**, and save edits.
6. Go to the Arc Hydro toolbar, and go to **Attribute Tools | Assign HydroID**, and assign HydroIDs for the SchemaNode and SchemaLink feature classes.
7. Start the Editor, and edit the SchemaLink feature class.
8. Open the SchemaLink attribute table, and populate the fields FromNodeID and ToNodeID with the corresponding HydroIDs of the upstream and downstream SchemaNodes.
9. Go to **Editor | Stop Editing**, and save edits.

Schematic Network Parameters

Before the Schematic Network is complete, fields need to be added to the attribute tables of the SchemaNode and SchemaLink feature classes.

SchemaLink

1. Open the attribute table of the SchemaLink feature class, and go to **Options | Add Field…**
2. Repeat step #1 until all the following fields are added:
    a. Name: “DecayConst_day”, Type: “Double”
    b. Name: “TravelTime_day”, Type: “Double”
    c. Name: “TotVal”, Type: “Double”
    d. Name: “PassedVal”, Type: “Double”
    e. Name: “IncVal”, Type: “Double”

3. Using the Editor Toolbar, the following fields need to be populated for LinkTypes 1 and 2: “DecayConst_day” and “TravelTime_day”; see Section 6.3.3 to see how the parameters were determined for this project.

SchemaNode

1. Open the attribute table of the SchemaNode feature class, and go to **Options | Add Field…**
2. Repeat step #1 until all the following fields are added:
    a. Name: “DecayCoef_day”, Type: “Double”
    b. Name: “FLOW_m3_yr”, Type: “Double”
    c. Name: “Volume”, Type: “Double”
    d. Name: “TotVal”, Type: “Double”
    e. Name: “PassedVal”, Type: “Double”
    f. Name: “IncVal”, Type: “Double”
3. Using the Editor Toolbar, the following fields need to be populated for SrcType 1:
    a. “IncVal” – The values that should populate this field are the total bacterial loadings (or the loadings that effects of transport are desired) in cfu/year per watershed. (“IncVal” = cfu/year of corresponding SchemaNode in Schematic Network.)
4. Using the Editor Toolbar, the following field needs to be populated for SrcType 2:
    a. “IncVal” – The values that should populate this field are the total bacterial loadings (or loadings that effects of transport are desired) in cfu/year for each node.
4. Using the Editor Toolbar, the following fields need to be populated for SrcType 3:
    a. “DecayCoef_day” – see Section 6.3.3.1 to see how this parameter was determined for this project.
    b. “Volume” – see Section 6.3.3.3 to see how this parameter was determined for this project.
    c. “FLOW_m3_year” – see Section 6.3.3.4 to see how this parameter was determined for this project.

Appendix 6.2: Travel Time Calculations

The travel times for Link types 1 and 2 were determined as input to the Schematic Processor. The following equation was used to calculate the initial travel time (before calibration) for the segments that were not made into 3d river models:

Travel Time = Flow Length / Velocity

Flow Length Calculations

1. Create Fdr (Flow Direction Raster that was created during Terrain Preprocessing, Appendix 5.1, with the Digital Elevation Model, DEM) that does not include Copano Bay.
2. Create polygon feature class of subbasin with Copano Bay omitted.
    a. Use "Union" tool under Analysis tools to combine the feature classes: Copano Bay and the subbasin.
    b. Using the Editor Toolbar, delete Copano Bay from the created feature class, and save edits.
3. Go to **Spatial Analyst | Options…**, and set the "Analysis Mask" to the feature class that was created in step a.
4. Set the "Extent" and "Cell Size" to the Fdr raster.
5. Go to **Spatial Analyst | Raster Calculator…**
6. Double-click on the Fdr raster, and "Evaluate".
7. Right-click on the Calculation raster and **Make Permanent**.
8. Create flow length raster.
9. In Arc Toolbox, go to the Spatial Analyst Tools, and open the tool "Flow Length".
10. Select the Fdr raster (with Copano Bay omitted) as the "Input flow direction raster".
11. Choose the name and directory for which the raster is to be placed.
12. Set the "Direction of measurement" to DOWNSTREAM, and press "OK".
13. The flow length from each grid cell to Copano Bay is then calculated.
14. Determine mean flow length in each delineated watershed.
15. Go to "Zonal Statistics as Table".
16. Select the delineated watersheds as the "Input raster or feature zone data".
17. Set the "Zone field" to JunctionID (the identifier for each watershed).
18. Set the "Input value raster" to the flow length raster that was created in steps #8-13.
19. Choose the name and directory for which the table is to be placed.
20. Join table that was created in steps #15-19 (Flow Length Statistics Table) to the watershed feature class.
21. Go to CRWR Attribute Tools in Arc Toolbox and use the tool: "Copy Field to Feature Class from Table" that was created by Nate Johnson (2004).

22. Join based on JunctionID (field in Watershed feature class) and VALUE_ (field in Flow Length Statistics Table that correlates with JunctionID) and add the field, MEAN, from the Statistics Table, which will give the mean of the flow length values within each delineated watershed.
23. For SchemaLink (Link type 1), the flow length (from the watershed to the stream) was calculated by: {Mean flow length of the watershed} – {flow length at the drainage junction (SchemaNode Srctype 2) determined from FlowLength raster}.
24. Open the attribute table of the delineated watershed feature class.
25. Go to **Options… | Add Field**
    i. Name: “FlowLength”, Type: “Double”.
26. Go to **Editor | Start Editing…**, and edit within the Personal Geodatabase that contains the delineated watersheds.
27. Open the attribute table of delineated watershed feature class, and manually input the flow lengths for each of the links (LinkType 1) as explained in the statement in step #23.
28. Go to **Editor | Stop Editing**, and save edits.
29. For SchemaLink (Link type 2), the flow length along the streams was calculated by: {Flow length at upstream SchemaNode} – {Flow length at downstream SchemaNode}.
30. Go to **Editor | Start Editing…**, and edit within the Personal Geodatabase that contains the delineated watersheds.
31. Open the attribute table of delineated watershed feature class, and manually input the flow lengths for each of the links (LinkType 2) as explained in the statement in step #29.
32. Go to **Editor | Stop Editing**, and save edits.

Velocity Calculations

For preliminary work, velocities of the streams were determined using flow – velocity relationships similar to Zoun (2003). The relationship between flow and velocity was derived from the EPA Reach File 1 (RF1) database, which documents flow and velocity for the entire United States. A regression line was fitted to the flow and velocity data for the Copano Bay watershed area (same method Zoun used to derive flow and velocity relationship in Galveston Bay area). These following equations were used to calculate the velocity for each of the stream segments (SchemaLinks).

$$V = 63.252 * Q^{0.3132}$$

Where: V = velocity in m/day

Q = flow in m^3/year

The cumulative runoff at each upstream and downstream SchemaNode were averaged for each SchemaLink, and then entered into the above equation.

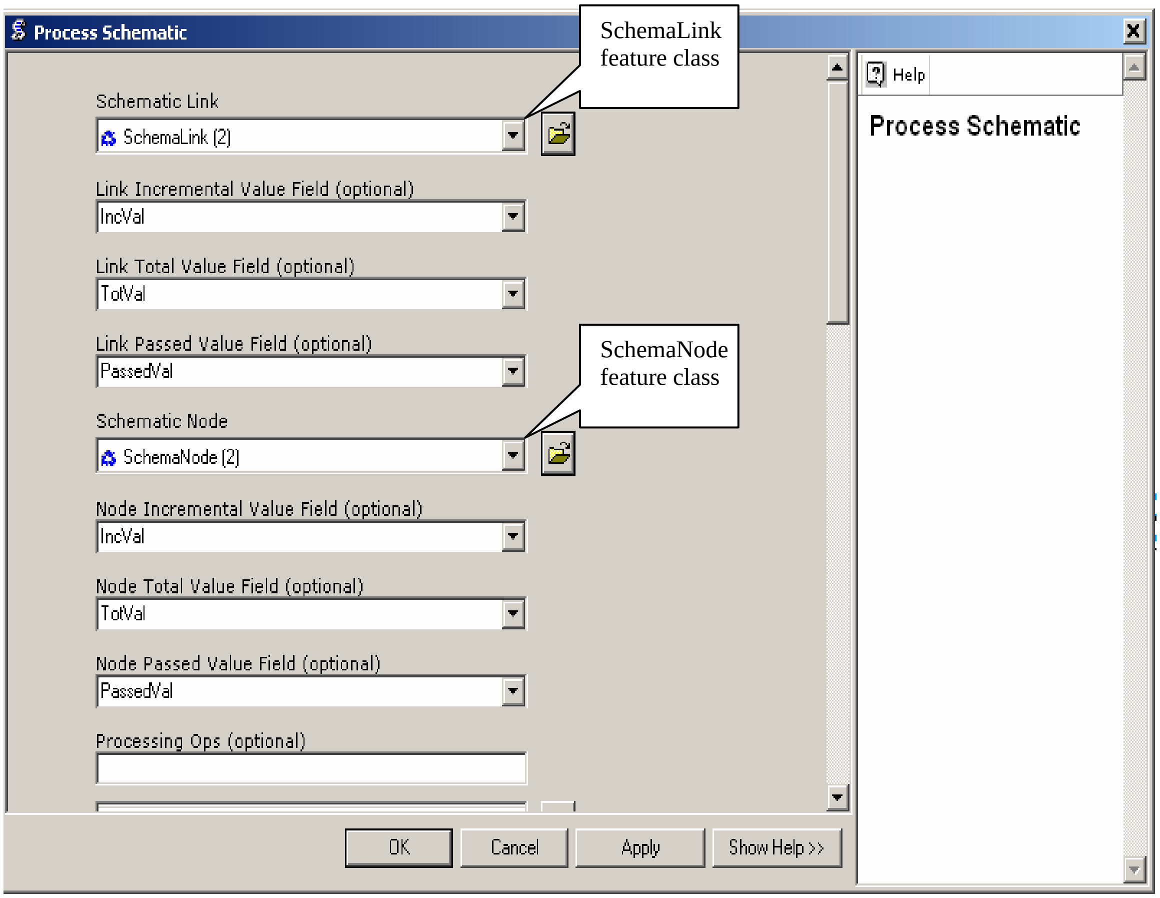
1. Add Velocity field to SchemaLink feature class.
2. Go to **Options… | Add Field**. (Name: “Velocity”, Type: “Double”).
3. Go to **Editor | Start Editing…**, and edit within the Personal Geodatabase that contains the Schematic Network.
4. Open the attribute table of the SchemaLink feature class, and manually input the velocities (calculated from above equation) for each of the links as previously explained.
5. Go to **Editor | Stop Editing**, and save edits.

Travel Time Calculations

1. Open the attribute table of the SchemaLink feature class.
2. Right-click on the field: “TravelTime_day”
3. Double-click on the flow length field, push the “ / ” button, and double-click on the velocity field in order to calculate: TravelTime_day = FlowLength/Velocity.

Appendix 6.3: Process Schematic

Once the Schematic Network was created, the input feature classes, corresponding fields, and DLLs were set in the Process Schematic as shown below. This set-up tells the script (Process Schematic) to implement decay (*clsdecay.dll*) on SchemaLink LinkTypes 1 and 2, which will decay bacteria as they travel from the watersheds to the streams and during their travel time along the streams), and to run a CFSTR model (*clsCFSTR.dll*) on SchemaNode SrcType 3 (Copano Bay waters segments).



Schematic Link: SchemaLink (2)

Link Incremental Value Field (optional): IncVal

Link Total Value Field (optional): TotVal

Link Passed Value Field (optional): PassedVal

Schematic Node: SchemaNode (2)

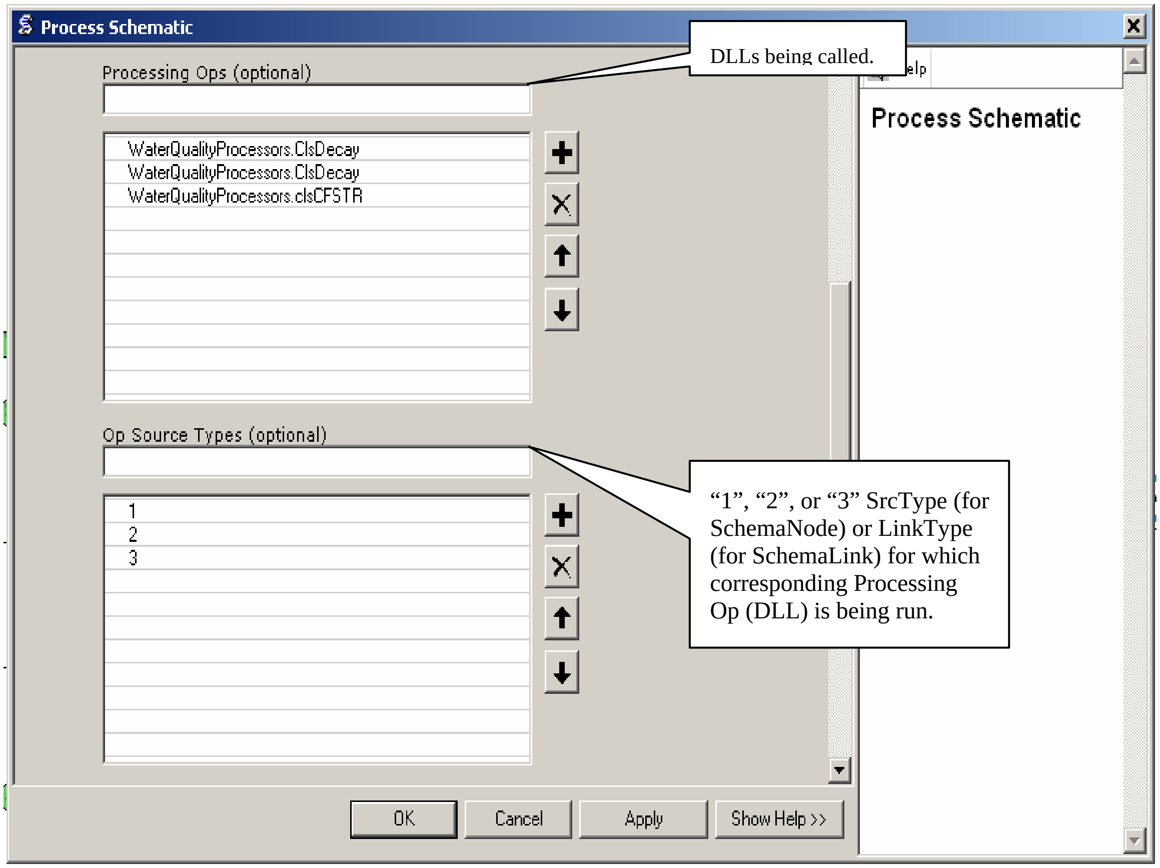
Node Incremental Value Field (optional): IncVal

Node Total Value Field (optional): TotVal

Node Passed Value Field (optional): PassedVal

Processing Ops (optional):

Note: Each row (shown below) corresponds to the same row of the following fields. For example, the Processing Op in the first row, WaterQualityProcessors.ClsDecay (*clsdecay.dll*), simulates decay of the bacteria loadings along LinkType 1 (Op Source Type) and passes the value (Op Behavior Type: Pass).

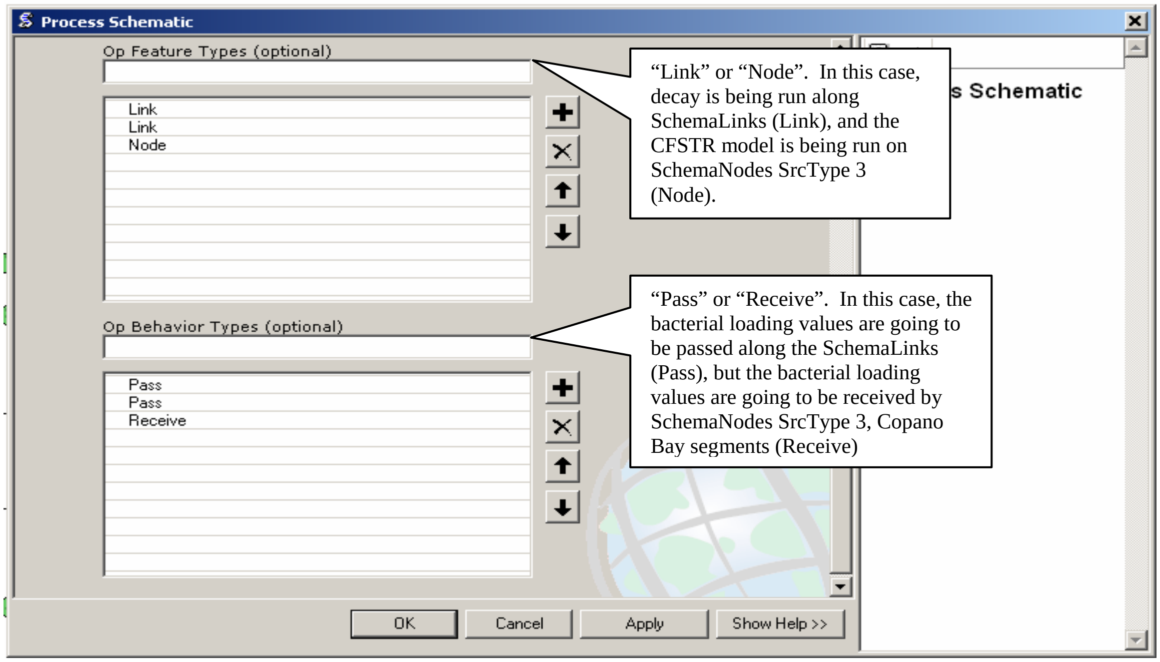


WaterQualityProcessors.ClsDecay
WaterQualityProcessors.ClsDecay
WaterQualityProcessors.clsCFSTR

1
2
3

DLLs being called.

"1", "2", or "3" SrcType (for SchemaNode) or LinkType (for SchemaLink) for which corresponding Processing Op (DLL) is being run.



Op Feature Types (optional)

Link
Link
Node

"Link" or "Node". In this case, decay is being run along SchemaLinks (Link), and the CFSTR model is being run on SchemaNodes SrcType 3 (Node).

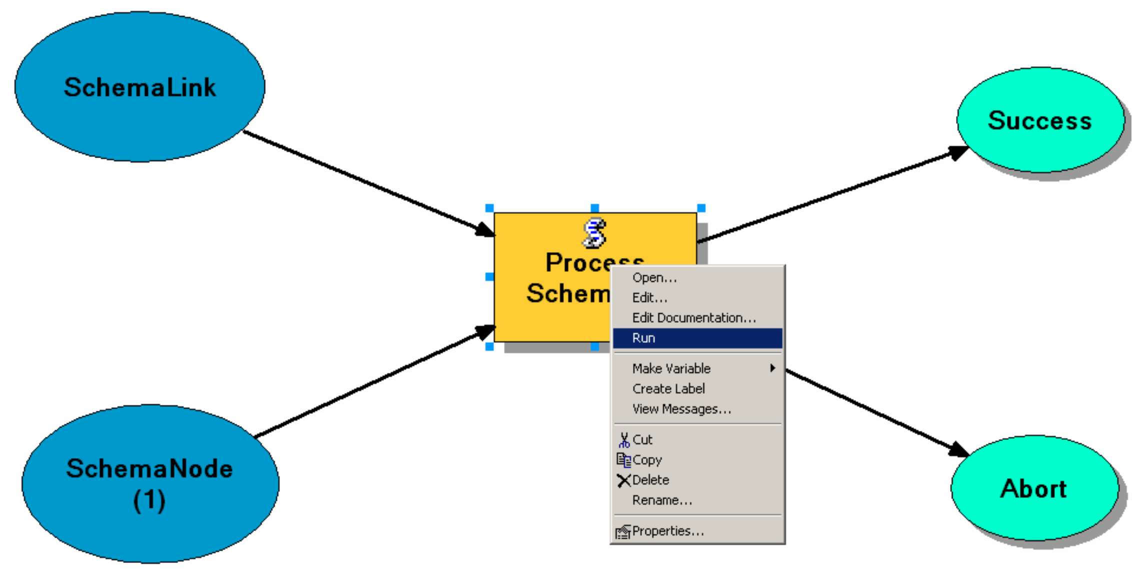
Op Behavior Types (optional)

Pass
Pass
Receive

"Pass" or "Receive". In this case, the bacterial loading values are going to be passed along the SchemaLinks (Pass), but the bacterial loading values are going to be received by SchemaNodes SrcType 3, Copano Bay segments (Receive)

Run Process Schematic

1. Right-click on "Process Schematic", and **Run**.
2. Results are found in the attribute tables of SchemaLink and SchemaNode (under the fields: PassedVal and TotVal).
    a. SchemaNode
        i. Src Type 2
            1. The populated values in the "PassedVal" and "TotVal" fields are bacterial loadings (cfu/year).
            2. These values can be converted to cfu/m^3 by dividing by the cumulative upstream runoff (m^3/year), and this concentration can be converted to cfu/100mL by dividing by 10,000.
        ii. Src Type 3
            1. The populated values in the "TotVal" field are bacterial concentrations in cfu/m^3.
            2. This value can be converted into bacterial loading (cfu/year) by multiplying by the cumulative upstream runoff (m^3/year) to that SchemaNode.


SchemaLink
SchemaNode (1)
Process Schem
Success
Abort
Open...
Edit...
Edit Documentation...
Run
Make Variable
Create Label
View Messages...
Cut
Copy
Delete
Rename...
Properties...

Appendix 7.1: Monte Carlo Simulation Model Worksheets

This appendix gives explanations of all the worksheets that are used in the Monte Carlo Simulation Model that was created by Ernest To. The **bold** headings indicate the name of the worksheet, and the descriptions below explain the important features. The key parameters and how the parameters are used in modeling fecal coliform concentrations are also discussed in the appropriate sections.

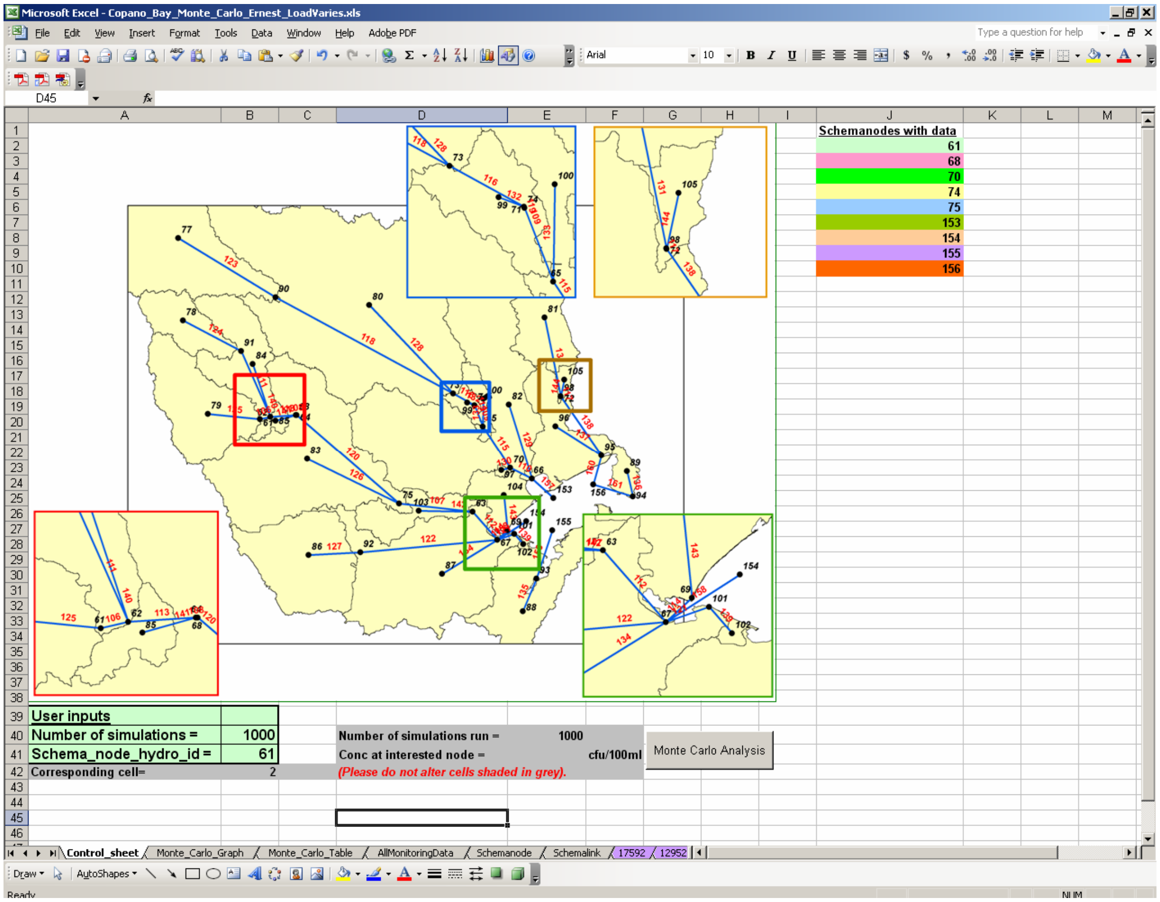
Control_Sheet

This worksheet (Figure 7A.1) shows the Copano Bay watershed along with all the SchemaNodes and SchemaLinks (number identifiers of the nodes and links in the Schematic Network.)

SchemaNodes with data are the SchemaNodes that have bacterial monitoring stations and monitoring data at the locations of the nodes, and thus, the bacterial monitoring data (from TCEQ 1999-2005) is what is plotted as “Existing” data when the model is run.

User inputs is where the user identifies the location (SchemaNode) where he/she wants to model the bacteria concentrations (CFU/100 mL) and can compare to the existing monitoring data (1999-2005) if the node is at a bacterial monitoring station. The number of simulations can be specified as well. Currently, SchemaNode 61 (Bacterial Monitoring Station 17592) is modeled with 1000 simulations.

To run the model, click on the “Monte Carlo Analysis” button.



Schemanodes with data

61
68
70
74
75
153
154
155
156

User inputs

Number of simulations = 1000

Schema_node_hydro_id = 61

Corresponding cell= 2

Number of simulations run = 1000

Conc at interested node = cfu/100ml

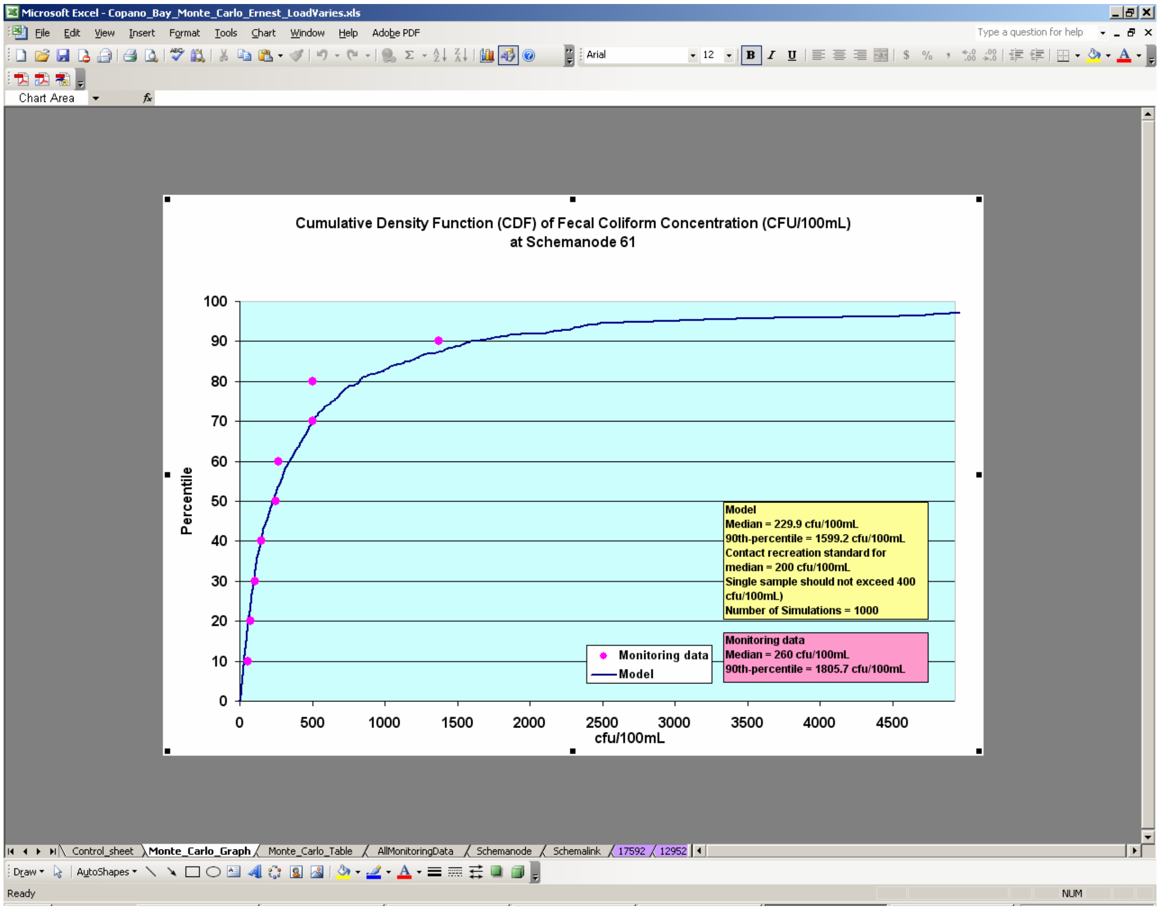
(Please do not alter cells shaded in grey).

Monte Carlo Analysis

Figure 7A.1 Control Sheet of Monte Carlo Simulation Model (User Interface)

Monte_Carlo_Graph (Figure 7A.2)

Once the model is run, this worksheet (shown in Figure 7A.2) will become the active sheet. It is the graph that compares the modeled bacteria concentrations to the existing monitoring data. The yellow box shows the median and 90th-percentile fecal coliform concentrations generated by the model (from the input parameters and bacterial loadings) and the current standards at this location (and in this case, it is contact recreation use standards for Aransas River.) The pink box shows the median and 90th-percentile fecal coliform concentrations from the existing monitoring data (1999-2005 from bacterial monitoring station 17592.)



Cumulative Density Function (CDF) of Fecal Coliform Concentration (CFU/100mL)
at Schemanode 61

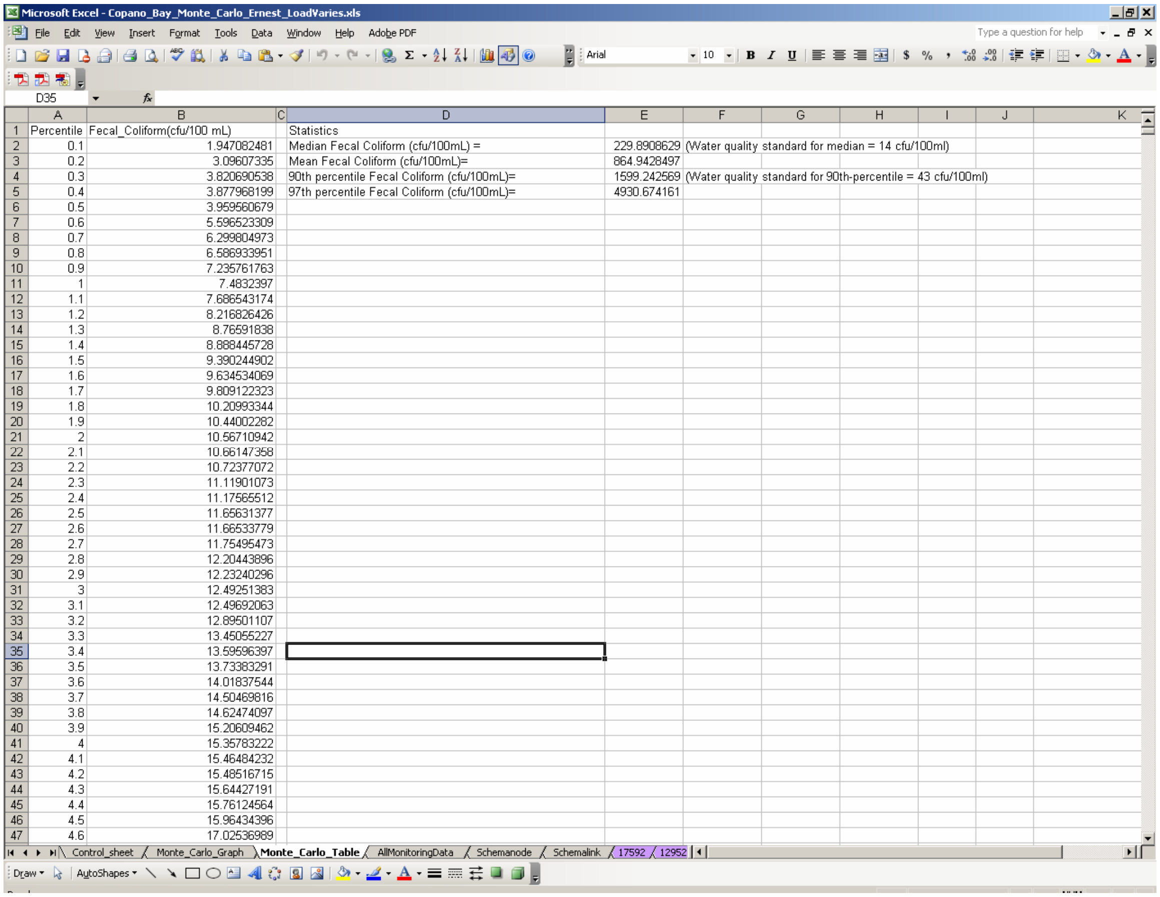
Model
Median = 229.9 cfu/100mL
90th-percentile = 1599.2 cfu/100mL
Contact recreation standard for median = 200 cfu/100mL
Single sample should not exceed 400 cfu/100mL)
Number of Simulations = 1000

Monitoring data
Median = 260 cfu/100mL
90th-percentile = 1805.7 cfu/100mL

Figure 7A.2 Existing versus Modeled Fecal Coliform Concentrations of Monte Carlo Simulation Model

Monte_Carlo_Table

This worksheet (shown in Figure 7A.3) shows all the simulations (in this case, 1000) that were run from the model and the fecal coliform concentrations calculated at the SchemaNode of interest for each simulation.

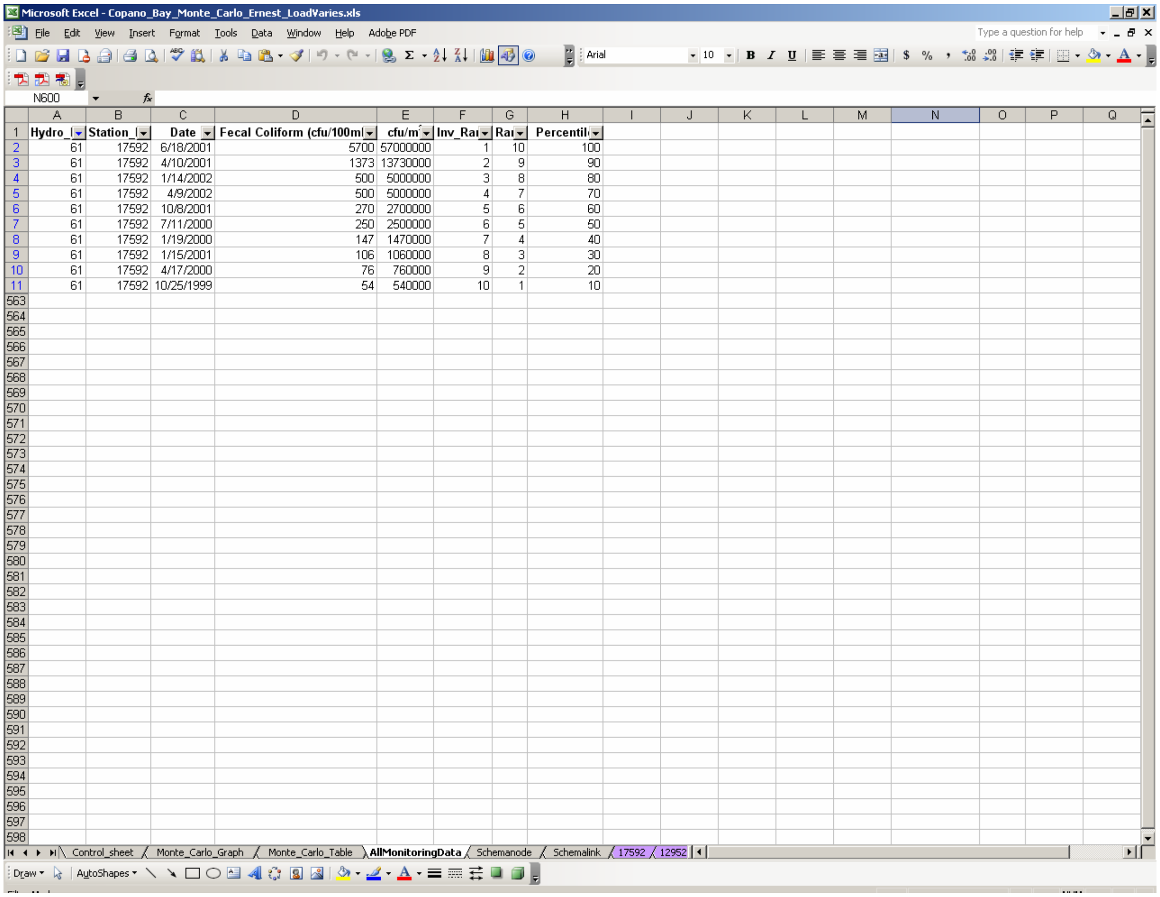


	A	B	C	D	E	F
1	Percentile	Fecal_Coliform(cfu/100 mL)		Statistics		
2	0.1	1.947082481		Median Fecal Coliform (cfu/100mL) =	229.8908629	(Water quality standard for median = 14 cfu/100ml)
3	0.2	3.09607335		Mean Fecal Coliform (cfu/100mL)=	864.9428497	
4	0.3	3.820690538		90th percentile Fecal Coliform (cfu/100mL)=	1599.242569	(Water quality standard for 90th-percentile = 43 cfu/100ml)
5	0.4	3.877968199		97th percentile Fecal Coliform (cfu/100mL)=	4930.674161	
6	0.5	3.959560679				
7	0.6	5.596523309				
8	0.7	6.299804973				
9	0.8	6.586933951				
10	0.9	7.235761763				
11	1	7.4832397				
12	1.1	7.686543174				
13	1.2	8.216826426				
14	1.3	8.76591838				
15	1.4	8.888445728				
16	1.5	9.390244902				
17	1.6	9.634534069				
18	1.7	9.809122323				
19	1.8	10.20993344				
20	1.9	10.44002282				
21	2	10.56710942				
22	2.1	10.66147358				
23	2.2	10.72377072				
24	2.3	11.11901073				
25	2.4	11.17565512				
26	2.5	11.65631377				
27	2.6	11.66533779				
28	2.7	11.75495473				
29	2.8	12.20443896				
30	2.9	12.23240296				
31	3	12.49251383				
32	3.1	12.49692063				
33	3.2	12.89501107				
34	3.3	13.45055227				
35	3.4	13.59596397				
36	3.5	13.73383291				
37	3.6	14.01837544				
38	3.7	14.50469816				
39	3.8	14.62474097				
40	3.9	15.20609462				
41	4	15.35783222				
42	4.1	15.46484232				
43	4.2	15.48516715				
44	4.3	15.64427191				
45	4.4	15.76124564				
46	4.5	15.96434396				
47	4.6	17.02536989				

Figure 7A.3 Modeled Fecal Coliform Concentrations in Table Format of Monte Carlo Simulation Model

AllMonitoringData

This worksheet (shown in Figure 7A.4) shows all the monitoring data that exists for the SchemaNode of interest from 1999-2005, so as you can see, for bacterial monitoring station 17592, only ten fecal coliform measurements were made in six years.



Hydro_I	Station_I	Date	Fecal Coliform (cfu/100ml	cfu/m	Inv_Ra	Ra	Percentil
61	17592	6/18/2001	5700	57000000	1	10	100
61	17592	4/10/2001	1373	13730000	2	9	90
61	17592	1/14/2002	500	5000000	3	8	80
61	17592	4/9/2002	500	5000000	4	7	70
61	17592	10/8/2001	270	2700000	5	6	60
61	17592	7/11/2000	250	2500000	6	5	50
61	17592	1/19/2000	147	1470000	7	4	40
61	17592	1/15/2001	106	1060000	8	3	30
61	17592	4/17/2000	76	760000	9	2	20
61	17592	10/25/1999	54	540000	10	1	10

Figure 7A.4 Existing Monitoring Data at SchemaNode of Interest

Schemanode

This is the SchemaNode feature class (all the nodes in the model network that can be seen in “Control_sheet”.) The full worksheet can be seen in Figure 7A.5, which is shown in three subsequent figures. These are descriptions of all the fields on this worksheet:

- “ObjectID” is the value randomly assigned to each SchemaNode feature.
- “HydroID” is the number identifier for each SchemaNode (the same HydroIDs are used in this Model as in the Schematic Processor Model and Schematic Network in Chapter 6.)
- “SrcType” is the type of SchemaNode. SrcType = 1 represents a watershed; SrcType = 2 represents a drainage point of a watershed; SrcType = 3 represents a Copano Bay segment.

- “IncVal” is the incremental loading that is added to the model at that SchemaNode location. (However, this field is inactive in this model.)

- “TotVal” is the incremental loading (“IncVal”) added to the upstream loading. (However, this field is inactive in this model.)

- “FLOW_m3_yr” is the flow associated with each Copano Bay segment, the flowrate of the water draining to each Copano Bay segment. (These values are the same that were calculated in Section 6.3.3.4.)

- “Volume” is the volume of each Copano Bay segment (calculated from bathymetry data and surface area.) (These values are the same that were calculated in Section 6.3.3.3.)

- “DecayCoef_day” is the decay coefficient associated with each SchemaNode, which is 2 days^{-1}.

- “PassedVal” is the calculated bacterial loading that is passed onto the downstream SchemaLink. (However, this field is inactive in this model.)

- “CumRunoff_m3_yr” is the cumulative runoff (from upstream watersheds) to each specified SchemaNode location. This field is used to calculate the concentration (CFU/100mL) at each location and will be described later.

- “Animal_cfu_year” is the calculated annual bacterial loading (CFU/year) excreted by livestock animals. Loading calculations are described in Section 5.2.

- “NonPoint_cfu_year” is the calculated annual non-point bacterial loading (CFU/year) associated with different land use types (excluding agriculture, pasture, etc.) Loading calculations are described in Section 5.1.

- “Birds_cfu_year” is the calculated annual bacterial loading (CFU/year) excreted by waterbirds. Loading calculations are described in Section 5.3.

- “WWTP” is the calculated annual bacterial loading (CFU/year) generated by WWTPs, and “WWTP_2” is to account for the loading if two WWTPs discharge to the same SchemaNode. Loading calculations are described in Section 5.4.

- “Human_Septic” is the calculated bacterial loading (CFU/year) that is produced from septic systems. Loading calculations are described in Section 5.5.

- “Total (CFU/year)” is the bacteria loading that is calculated for each node based on a lognormal distribution that is created from the median bacterial loading (Column S: “Load_param1”, which is the sum of Columns L thru Q - all the calculated bacteria loadings) and an associated multiplication factor (Column T: “Load_param2”), which is one of the parameters that is adjusted such that existing monitoring data can be matched. This multiplication factor is associated with the coefficient of variance. If you go to “multi_factor_vs_cov” worksheet, you can see the associated coefficient of variance with each multiplication factor. (Note: cov = standard deviation/mean.) Thus, the higher the multiplication factor, the wider the spread and range of the bacterial loadings. The Excel formula for this column is: Column R = Column S * EXP(Column T * NORMINV(ABS(RAND()),0,1))

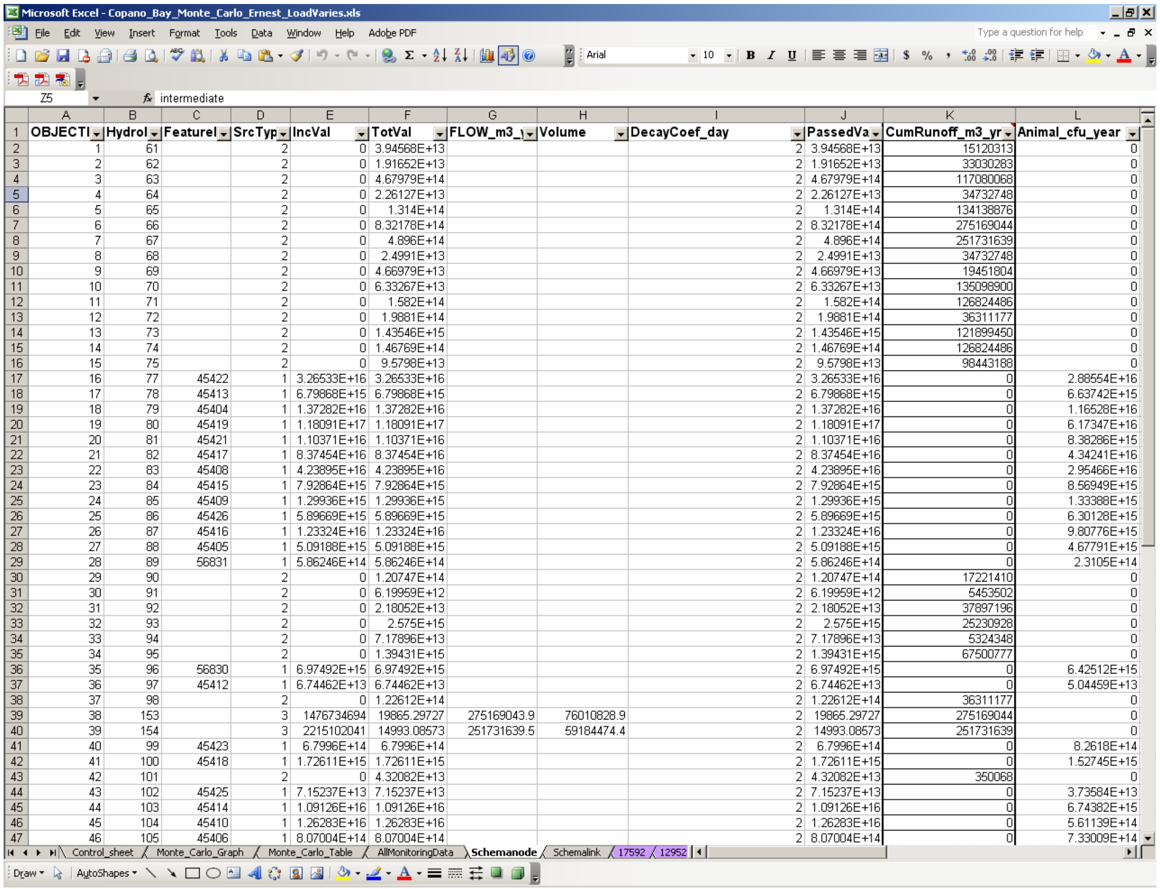
- “Load_param1” is the sum of all the bacterial loadings and would represent the median total bacterial loading to each SchemaNode. The Excel formula for this column is: Column S = Column L + Column M + Column N + Column O + Column P + Column Q.

- “Load_param2” is a multiplication factor that is used (along with “Load_param1”) to create a bacterial loading normal distribution. This multiplication factor is associated with the coefficient of variance, and the “multi_factor_vs_cov” worksheet shows the relationship.

The remaining fields are what are modified to calculate the modeled fecal coliform concentrations.

- “Total_value” is the upstream decayed bacterial loading plus the incremental bacterial loading added to the model at the specified node location.

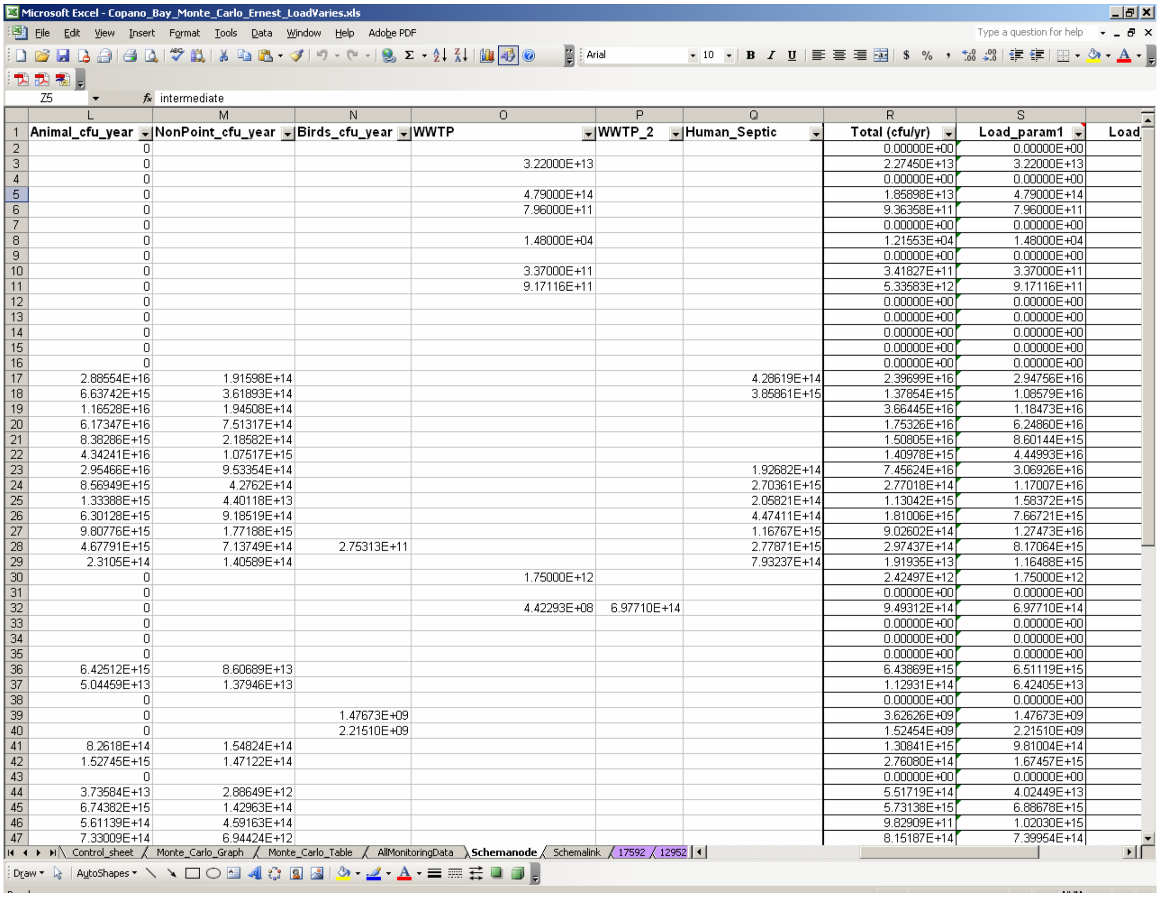
- “Conc/100mL”, for SrcType 2 nodes, = “Total_value” / (10,000 * “CumRunoff_m3_yr”)



Z5 intermediate

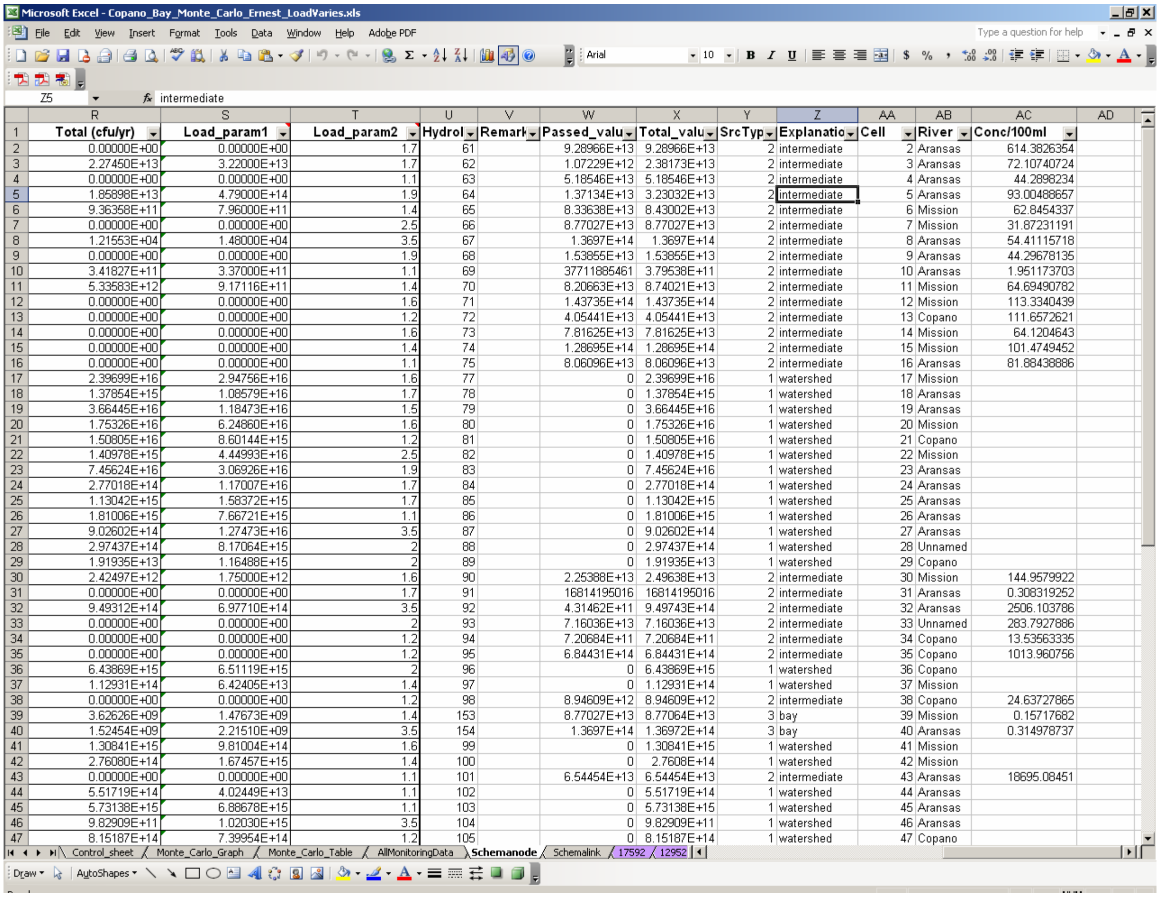
	A	B	C	D	E	F	G	H	I	J	K	L
1	OBJECTI	Hydrol	Featurel	SrcTyp	IncVal	TotVal	FLOW_m3_	Volume	DecayCoef_day	PassedVa	CumRunoff_m3_yr	Animal_cfu_year
2	1	61		2	0	3.94568E+13			2	3.94568E+13	15120313	0
3	2	62		2	0	1.91652E+13			2	1.91652E+13	33030283	0
4	3	63		2	0	4.67979E+14			2	4.67979E+14	117080068	0
5	4	64		2	0	2.26127E+13			2	2.26127E+13	34732748	0
6	5	65		2	0	1.314E+14			2	1.314E+14	134138876	0
7	6	66		2	0	8.32178E+14			2	8.32178E+14	275169044	0
8	7	67		2	0	4.896E+14			2	4.896E+14	251731639	0
9	8	68		2	0	2.4991E+13			2	2.4991E+13	34732748	0
10	9	69		2	0	4.66979E+13			2	4.66979E+13	19451804	0
11	10	70		2	0	6.33267E+13			2	6.33267E+13	135098900	0
12	11	71		2	0	1.582E+14			2	1.582E+14	126824486	0
13	12	72		2	0	1.9881E+14			2	1.9881E+14	36311177	0
14	13	73		2	0	1.43546E+15			2	1.43546E+15	121899450	0
15	14	74		2	0	1.46769E+14			2	1.46769E+14	126824486	0
16	15	75		2	0	9.5798E+13			2	9.5798E+13	98443188	0
17	16	77	45422	1	3.26533E+16	3.26533E+16			2	3.26533E+16	0	2.88554E+16
18	17	78	45413	1	6.79868E+15	6.79868E+15			2	6.79868E+15	0	6.63742E+15
19	18	79	45404	1	1.37282E+16	1.37282E+16			2	1.37282E+16	0	1.16528E+16
20	19	80	45419	1	1.18091E+17	1.18091E+17			2	1.18091E+17	0	6.17347E+16
21	20	81	45421	1	1.10371E+16	1.10371E+16			2	1.10371E+16	0	8.38286E+15
22	21	82	45417	1	8.37454E+16	8.37454E+16			2	8.37454E+16	0	4.34241E+16
23	22	83	45408	1	4.23895E+16	4.23895E+16			2	4.23895E+16	0	2.95466E+16
24	23	84	45415	1	7.92864E+15	7.92864E+15			2	7.92864E+15	0	8.56949E+15
25	24	85	45409	1	1.29936E+15	1.29936E+15			2	1.29936E+15	0	1.33388E+15
26	25	86	45426	1	5.89669E+15	5.89669E+15			2	5.89669E+15	0	6.30128E+15
27	26	87	45416	1	1.23324E+16	1.23324E+16			2	1.23324E+16	0	9.80776E+15
28	27	88	45405	1	5.09188E+15	5.09188E+15			2	5.09188E+15	0	4.67791E+15
29	28	89	56831	1	5.86246E+14	5.86246E+14			2	5.86246E+14	0	2.3105E+14
30	29	90		2	0	1.20747E+14			2	1.20747E+14	17221410	0
31	30	91		2	0	6.19959E+12			2	6.19959E+12	5453502	0
32	31	92		2	0	2.18052E+13			2	2.18052E+13	37897196	0
33	32	93		2	0	2.575E+15			2	2.575E+15	25230928	0
34	33	94		2	0	7.17896E+13			2	7.17896E+13	5324348	0
35	34	95		2	0	1.39431E+15			2	1.39431E+15	67500777	0
36	35	96	56830	1	6.97492E+15	6.97492E+15			2	6.97492E+15	0	6.42512E+15
37	36	97	45412	1	6.74462E+13	6.74462E+13			2	6.74462E+13	0	5.04459E+13
38	37	98		2	0	1.22612E+14			2	1.22612E+14	36311177	0
39	38	153		3	1476734694	19865.29727	275169043.9	76010828.9	2	19865.29727	275169044	0
40	39	154		3	2215102041	14993.08573	251731639.5	59184474.4	2	14993.08573	251731639	0
41	40	99	45423	1	6.7996E+14	6.7996E+14			2	6.7996E+14	0	8.2618E+14
42	41	100	45418	1	1.72611E+15	1.72611E+15			2	1.72611E+15	0	1.52745E+15
43	42	101		2	0	4.32082E+13			2	4.32082E+13	350068	0
44	43	102	45425	1	7.15237E+13	7.15237E+13			2	7.15237E+13	0	3.73584E+13
45	44	103	45414	1	1.09126E+16	1.09126E+16			2	1.09126E+16	0	6.74382E+15
46	45	104	45410	1	1.26283E+16	1.26283E+16			2	1.26283E+16	0	5.61139E+14
47	46	105	45406	1	8.07004E+14	8.07004E+14			2	8.07004E+14	0	7.33009E+14

Figure 7A.5 SchemaNode Fields for Monte Carlo Simulation Model



	L	M	N	O	P	Q	R	S	
1	Animal_cfu_year	NonPoint_cfu_year	Birds_cfu_year	WWTP	WWTP_2	Human_Septic	Total (cfu/yr)	Load_param1	Load
2	0						0.00000E+00	0.00000E+00	
3	0			3.22000E+13			2.27450E+13	3.22000E+13	
4	0						0.00000E+00	0.00000E+00	
5	0			4.79000E+14			1.85898E+13	4.79000E+14	
6	0			7.96000E+11			9.36358E+11	7.96000E+11	
7	0						0.00000E+00	0.00000E+00	
8	0			1.48000E+04			1.21553E+04	1.48000E+04	
9	0						0.00000E+00	0.00000E+00	
10	0			3.37000E+11			3.41827E+11	3.37000E+11	
11	0			9.17116E+11			5.33583E+12	9.17116E+11	
12	0						0.00000E+00	0.00000E+00	
13	0						0.00000E+00	0.00000E+00	
14	0						0.00000E+00	0.00000E+00	
15	0						0.00000E+00	0.00000E+00	
16	0						0.00000E+00	0.00000E+00	
17	2.88554E+16	1.91598E+14				4.28619E+14	2.39699E+16	2.94756E+16	
18	6.63742E+15	3.61893E+14				3.85861E+15	1.37854E+15	1.08579E+16	
19	1.16528E+16	1.94508E+14					3.66445E+16	1.18473E+16	
20	6.17347E+16	7.51317E+14					1.75326E+16	6.24860E+16	
21	8.38286E+15	2.18582E+14					1.50805E+16	8.60144E+15	
22	4.34241E+16	1.07517E+15					1.40978E+15	4.44993E+16	
23	2.95466E+16	9.53354E+14				1.92682E+14	7.45624E+16	3.06926E+16	
24	8.56949E+15	4.2762E+14				2.70361E+15	2.77018E+14	1.17007E+16	
25	1.33388E+15	4.40118E+13				2.05821E+14	1.13042E+15	1.58372E+15	
26	6.30128E+15	9.18519E+14				4.47411E+14	1.81006E+15	7.66721E+15	
27	9.80776E+15	1.77188E+15				1.16767E+15	9.02602E+14	1.27473E+16	
28	4.67791E+15	7.13749E+14	2.75313E+11			2.77871E+15	2.97437E+14	8.17064E+15	
29	2.3105E+14	1.40589E+14				7.93237E+14	1.91935E+13	1.16488E+15	
30	0			1.75000E+12			2.42497E+12	1.75000E+12	
31	0						0.00000E+00	0.00000E+00	
32	0			4.42293E+08	6.97710E+14		9.49312E+14	6.97710E+14	
33	0						0.00000E+00	0.00000E+00	
34	0						0.00000E+00	0.00000E+00	
35	0						0.00000E+00	0.00000E+00	
36	6.42512E+15	8.60689E+13					6.43869E+15	6.51119E+15	
37	5.04459E+13	1.37946E+13					1.12931E+14	6.42405E+13	
38	0						0.00000E+00	0.00000E+00	
39	0		1.47673E+09				3.62626E+09	1.47673E+09	
40	0		2.21510E+09				1.52454E+09	2.21510E+09	
41	8.2618E+14	1.54824E+14					1.30841E+15	9.81004E+14	
42	1.52745E+15	1.47122E+14					2.76080E+14	1.67457E+15	
43	0						0.00000E+00	0.00000E+00	
44	3.73584E+13	2.88649E+12					5.51719E+14	4.02449E+13	
45	6.74382E+15	1.42963E+14					5.73138E+15	6.88678E+15	
46	5.61139E+14	4.59163E+14					9.82909E+11	1.02030E+15	
47	7.33009E+14	6.94424E+12					8.15187E+14	7.39954E+14	

Figure 7A.5 (Continued)



	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD
1	Total (cfu/yr)	Load_param1	Load_param2	HydroI	Remark	Passed_valu	Total_valu	SrcTyp	Explanatio	Cell	River	Conc/100ml	
2	0.00000E+00	0.00000E+00	1.7	61		9.28966E+13	9.28966E+13	2	intermediate	2	Aransas	614.3826354	
3	2.27450E+13	3.22000E+13	1.7	62		1.07229E+12	2.38173E+13	2	intermediate	3	Aransas	72.10740724	
4	0.00000E+00	0.00000E+00	1.1	63		5.18546E+13	5.18546E+13	2	intermediate	4	Aransas	44.2898234	
5	1.85898E+13	4.79000E+14	1.9	64		1.37134E+13	3.23032E+13	2	intermediate	5	Aransas	93.00488657	
6	9.36358E+11	7.96000E+11	1.4	65		8.33638E+13	8.43002E+13	2	intermediate	6	Mission	62.8454337	
7	0.00000E+00	0.00000E+00	2.5	66		8.77027E+13	8.77027E+13	2	intermediate	7	Mission	31.87231191	
8	1.21553E+04	1.48000E+04	3.5	67		1.3697E+14	1.3697E+14	2	intermediate	8	Aransas	54.41115718	
9	0.00000E+00	0.00000E+00	1.9	68		1.53855E+13	1.53855E+13	2	intermediate	9	Aransas	44.29678135	
10	3.41827E+11	3.37000E+11	1.1	69		37711885461	3.79538E+11	2	intermediate	10	Aransas	1.951173703	
11	5.33583E+12	9.17116E+11	1.4	70		8.20663E+13	8.74021E+13	2	intermediate	11	Mission	64.69490782	
12	0.00000E+00	0.00000E+00	1.6	71		1.43735E+14	1.43735E+14	2	intermediate	12	Mission	113.3340439	
13	0.00000E+00	0.00000E+00	1.2	72		4.05441E+13	4.05441E+13	2	intermediate	13	Copano	111.6572621	
14	0.00000E+00	0.00000E+00	1.6	73		7.81625E+13	7.81625E+13	2	intermediate	14	Mission	64.1204643	
15	0.00000E+00	0.00000E+00	1.4	74		1.28695E+14	1.28695E+14	2	intermediate	15	Mission	101.4749452	
16	0.00000E+00	0.00000E+00	1.1	75		8.06096E+13	8.06096E+13	2	intermediate	16	Aransas	81.88438886	
17	2.39699E+16	2.94756E+16	1.6	77		0	2.39699E+16	1	watershed	17	Mission		
18	1.37854E+15	1.08579E+16	1.7	78		0	1.37854E+15	1	watershed	18	Aransas		
19	3.66445E+16	1.18473E+16	1.5	79		0	3.66445E+16	1	watershed	19	Aransas		
20	1.75326E+16	6.24860E+16	1.6	80		0	1.75326E+16	1	watershed	20	Mission		
21	1.50805E+16	8.60144E+15	1.2	81		0	1.50805E+16	1	watershed	21	Copano		
22	1.40978E+15	4.44993E+16	2.5	82		0	1.40978E+15	1	watershed	22	Mission		
23	7.45624E+16	3.06926E+16	1.9	83		0	7.45624E+16	1	watershed	23	Aransas		
24	2.77018E+14	1.17007E+16	1.7	84		0	2.77018E+14	1	watershed	24	Aransas		
25	1.13042E+15	1.58372E+15	1.7	85		0	1.13042E+15	1	watershed	25	Aransas		
26	1.81006E+15	7.66721E+15	1.1	86		0	1.81006E+15	1	watershed	26	Aransas		
27	9.02602E+14	1.27473E+16	3.5	87		0	9.02602E+14	1	watershed	27	Aransas		
28	2.97437E+14	8.17064E+15	2	88		0	2.97437E+14	1	watershed	28	Unnamed		
29	1.91935E+13	1.16488E+15	2	89		0	1.91935E+13	1	watershed	29	Copano		
30	2.42497E+12	1.75000E+12	1.6	90		2.25388E+13	2.49638E+13	2	intermediate	30	Mission	144.9579922	
31	0.00000E+00	0.00000E+00	1.7	91		16814195016	16814195016	2	intermediate	31	Aransas	0.308319252	
32	9.49312E+14	6.97710E+14	3.5	92		4.31462E+11	9.49743E+14	2	intermediate	32	Aransas	2506.103786	
33	0.00000E+00	0.00000E+00	2	93		7.16036E+13	7.16036E+13	2	intermediate	33	Unnamed	283.7927886	
34	0.00000E+00	0.00000E+00	1.2	94		7.20684E+11	7.20684E+11	2	intermediate	34	Copano	13.53563335	
35	0.00000E+00	0.00000E+00	1.2	95		6.84431E+14	6.84431E+14	2	intermediate	35	Copano	1013.960756	
36	6.43869E+15	6.51119E+15	2	96		0	6.43869E+15	1	watershed	36	Copano		
37	1.12931E+14	6.42405E+13	1.4	97		0	1.12931E+14	1	watershed	37	Mission		
38	0.00000E+00	0.00000E+00	1.2	98		8.94609E+12	8.94609E+12	2	intermediate	38	Copano	24.63727865	
39	3.62626E+09	1.47673E+09	1.4	153		8.77027E+13	8.77064E+13	3	bay	39	Mission	0.15717682	
40	1.52454E+09	2.21510E+09	3.5	154		1.3697E+14	1.36972E+14	3	bay	40	Aransas	0.314978737	
41	1.30841E+15	9.81004E+14	1.6	99		0	1.30841E+15	1	watershed	41	Mission		
42	2.76080E+14	1.67457E+15	1.4	100		0	2.7608E+14	1	watershed	42	Mission		
43	0.00000E+00	0.00000E+00	1.1	101		6.54454E+13	6.54454E+13	2	intermediate	43	Aransas	18695.08451	
44	5.51719E+14	4.02449E+13	1.1	102		0	5.51719E+14	1	watershed	44	Aransas		
45	5.73138E+15	6.88678E+15	1.1	103		0	5.73138E+15	1	watershed	45	Aransas		
46	9.82909E+11	1.02030E+15	3.5	104		0	9.82909E+11	1	watershed	46	Aransas		
47	8.15187E+14	7.39954E+14	1.2	105		0	8.15187E+14	1	watershed	47	Copano		

Figure 7A.5 (Continued)

Schemalink (Figure 7A.6)

This is the SchemaLink feature class (all the links in the model network that can be seen in “Control_sheet”.) These are descriptions of all the fields on this worksheet:

- “FromNodeID” is the HydroID of the upstream SchemaNode to the SchemaLink.
- “ToNodeID” is the HydroID of the downstream SchemaNode to the SchemaLink.
- “LinkType” is the type of SchemaLink it is. LinkType = 1 represents the transport of bacteria in a watershed (applies following equation: downstream loading = upstream loading * exp (-kt)); LinkType = 2 represents transport of bacteria along a river, which applies the same first-order decay equation as LinkType = 1. LinkType = 3 represents the transport of bacteria in a bay segment (applies the following equation: upstream loading/(cumulative runoff + k*Volume).)

- “kd_name” is just an identifier to the decay coefficient associated with each SchemaLink.

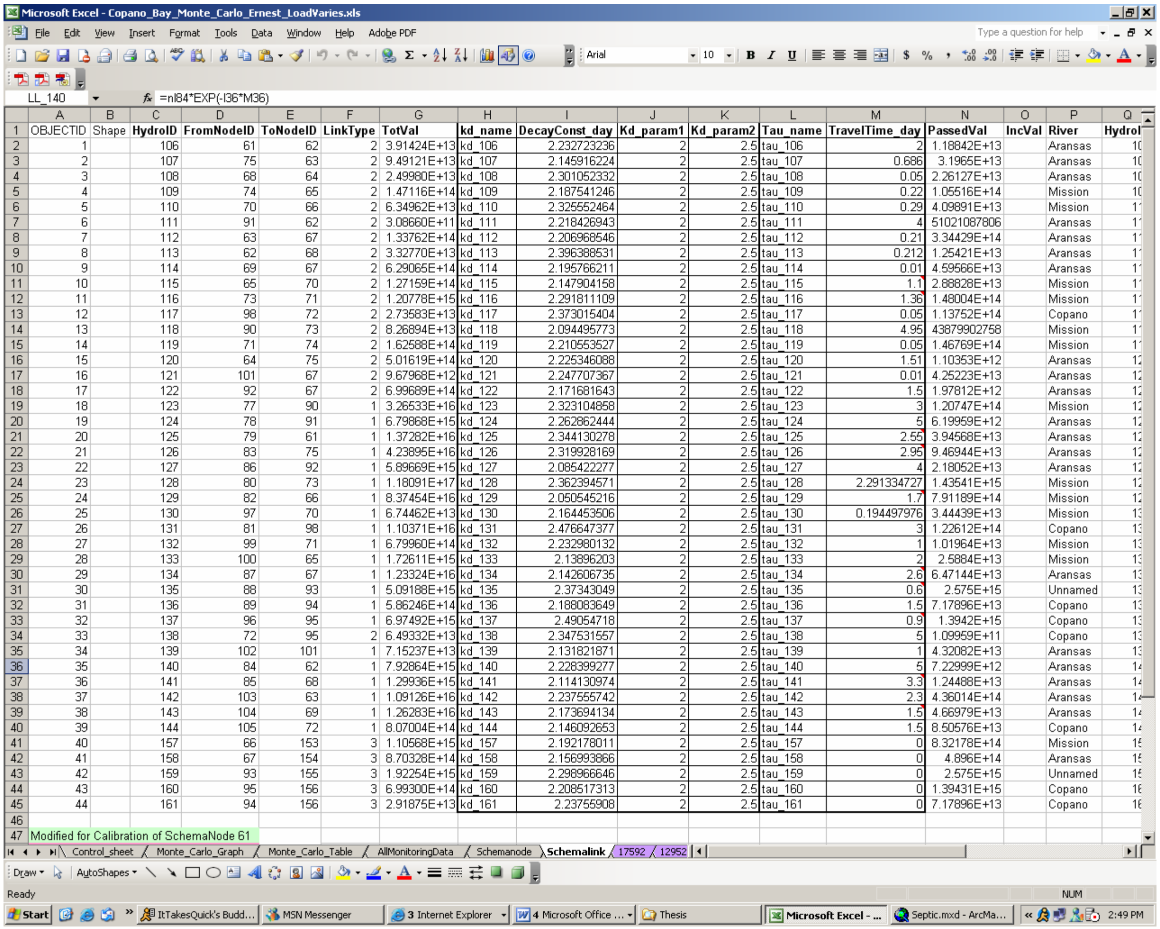
- “DecayConst_day” is the decay coefficient that is calculated for each SchemaLink (and simulation) from a beta distribution (alpha = 2 and beta = 2) and from the upper and lower boundaries of 2 (“Kd_param1”, Column J) and 2.5 days^{-1} (“Kd_param2”, Column K). The Excel formula for this column is: BETAINV(ABS(RAND()),2,2, Column J, Column K)

- “Kd_param1” is the lower boundary of the beta distribution associated with the decay distribution, which is 2 days^{-1} for this model.

- “Kd_param2” is the upper boundary of the beta distribution associated with the decay distribution, which is 2.5 days^{-1} for this model.

- “Tau_name” is an identifier to the travel time that is associated with each SchemaLink.

- **“TravelTime_day”** is the travel time (residence time) associated with each SchemaLink. This parameter is adjusted to try to match up with the median fecal coliform concentrations. (The adjacent upstream SchemaLink – to the SchemaNode of interest - is usually the most influential and sensitive to the model.) The initial residence times (calculated in Section 6.3.3.2) were used before calibration, and then the appropriate residence times were adjusted.



Microsoft Excel - Copano_Bay_Monte_Carlo_Ernest_LoadVaries.xls

LL_140 =nI84*EXP(-I36*M36)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	OBJECTID	Shape	HydroID	FromNodeID	ToNodeID	LinkType	TotVal	kd_name	DecayConst_day	Kd_param1	Kd_param2	Tau_name	TravelTime_day	PassedVal	IncVal	River
2	1		106	61	62	2	3.91424E+13	kd_106	2.232723236	2	2.5	tau_106	2	1.18842E+13		Aransas
3	2		107	75	63	2	9.49121E+13	kd_107	2.145916224	2	2.5	tau_107	0.686	3.1965E+13		Aransas
4	3		108	68	64	2	2.49980E+13	kd_108	2.301052332	2	2.5	tau_108	0.05	2.26127E+13		Aransas
5	4		109	74	65	2	1.47116E+14	kd_109	2.187541246	2	2.5	tau_109	0.22	1.05516E+14		Mission
6	5		110	70	66	2	6.34962E+13	kd_110	2.325552464	2	2.5	tau_110	0.29	4.09891E+13		Mission
7	6		111	91	62	2	3.08660E+11	kd_111	2.218426943	2	2.5	tau_111	4	51021087806		Aransas
8	7		112	63	67	2	1.33762E+14	kd_112	2.206968546	2	2.5	tau_112	0.21	3.34429E+14		Aransas
9	8		113	62	68	2	3.32770E+13	kd_113	2.396388531	2	2.5	tau_113	0.212	1.25421E+13		Aransas
10	9		114	69	67	2	6.29065E+14	kd_114	2.195766211	2	2.5	tau_114	0.01	4.59566E+13		Aransas
11	10		115	65	70	2	1.27159E+14	kd_115	2.147904158	2	2.5	tau_115	1.1	2.88828E+13		Mission
12	11		116	73	71	2	1.20778E+15	kd_116	2.291811109	2	2.5	tau_116	1.36	1.48004E+14		Mission
13	12		117	98	72	2	2.73583E+13	kd_117	2.373015404	2	2.5	tau_117	0.05	1.13752E+14		Copano
14	13		118	90	73	2	8.26894E+13	kd_118	2.094495773	2	2.5	tau_118	4.95	43879902758		Mission
15	14		119	71	74	2	1.62588E+14	kd_119	2.210553527	2	2.5	tau_119	0.05	1.46769E+14		Mission
16	15		120	64	75	2	5.01619E+14	kd_120	2.225346088	2	2.5	tau_120	1.51	1.10353E+12		Aransas
17	16		121	101	67	2	9.67968E+12	kd_121	2.247707367	2	2.5	tau_121	0.01	4.25223E+13		Aransas
18	17		122	92	67	2	6.99689E+14	kd_122	2.171681643	2	2.5	tau_122	1.5	1.97812E+12		Aransas
19	18		123	77	90	1	3.26533E+16	kd_123	2.323104858	2	2.5	tau_123	3	1.20747E+14		Mission
20	19		124	78	91	1	6.79868E+15	kd_124	2.262862444	2	2.5	tau_124	5	6.19959E+12		Aransas
21	20		125	79	61	1	1.37282E+16	kd_125	2.344130278	2	2.5	tau_125	2.55	3.94568E+13		Aransas
22	21		126	83	75	1	4.23895E+16	kd_126	2.319928169	2	2.5	tau_126	2.95	9.46944E+13		Aransas
23	22		127	86	92	1	5.89669E+15	kd_127	2.085422277	2	2.5	tau_127	4	2.18052E+13		Aransas
24	23		128	80	73	1	1.18091E+17	kd_128	2.362394571	2	2.5	tau_128	2.291334727	1.43541E+15		Mission
25	24		129	82	66	1	8.37454E+16	kd_129	2.050545216	2	2.5	tau_129	1.7	7.91189E+14		Mission
26	25		130	97	70	1	6.74462E+13	kd_130	2.164453506	2	2.5	tau_130	0.194497976	3.44439E+13		Mission
27	26		131	81	98	1	1.10371E+16	kd_131	2.476647377	2	2.5	tau_131	3	1.22612E+14		Copano
28	27		132	99	71	1	6.79960E+14	kd_132	2.232980132	2	2.5	tau_132	1	1.01964E+13		Mission
29	28		133	100	65	1	1.72611E+15	kd_133	2.13896203	2	2.5	tau_133	2	2.5884E+13		Mission
30	29		134	87	67	1	1.23324E+16	kd_134	2.142606735	2	2.5	tau_134	2.6	6.47144E+13		Aransas
31	30		135	88	93	1	5.09188E+15	kd_135	2.37343049	2	2.5	tau_135	0.6	2.575E+15		Unnamed
32	31		136	89	94	1	5.86246E+14	kd_136	2.188083649	2	2.5	tau_136	1.5	7.17896E+13		Copano
33	32		137	96	95	1	6.97492E+15	kd_137	2.49054718	2	2.5	tau_137	0.9	1.3942E+15		Copano
34	33		138	72	95	2	6.49332E+13	kd_138	2.347531557	2	2.5	tau_138	5	1.09959E+11		Copano
35	34		139	102	101	1	7.15237E+13	kd_139	2.131821871	2	2.5	tau_139	1	4.32082E+13		Aransas
36	35		140	84	62	1	7.92864E+15	kd_140	2.228399277	2	2.5	tau_140	5	7.22999E+12		Aransas
37	36		141	85	68	1	1.29936E+15	kd_141	2.114130974	2	2.5	tau_141	3.3	1.24488E+13		Aransas
38	37		142	103	63	1	1.09126E+16	kd_142	2.237555742	2	2.5	tau_142	2.3	4.36014E+14		Aransas
39	38		143	104	69	1	1.26283E+16	kd_143	2.173694134	2	2.5	tau_143	1.5	4.66979E+13		Aransas
40	39		144	105	72	1	8.07004E+14	kd_144	2.146092653	2	2.5	tau_144	1.5	8.50576E+13		Copano
41	40		157	66	153	3	1.10568E+15	kd_157	2.192178011	2	2.5	tau_157	0	8.32178E+14		Mission
42	41		158	67	154	3	8.70328E+14	kd_158	2.156993866	2	2.5	tau_158	0	4.896E+14		Aransas
43	42		159	93	155	3	1.92254E+15	kd_159	2.298966646	2	2.5	tau_159	0	2.575E+15		Unnamed
44	43		160	95	156	3	6.99300E+14	kd_160	2.208517313	2	2.5	tau_160	0	1.39431E+15		Copano
45	44		161	94	156	3	2.91875E+13	kd_161	2.23755908	2	2.5	tau_161	0	7.17896E+13		Copano
46																
47	Modified for Calibration of SchemaNode 61															

Figure 7A.6 SchemaLink Fields for Monte Carlo Simulation Model

Appendix 7.2: Load Reduction Scenario #1 Results

This appendix gives the load reduction results of all the water segments (Aransas and Mission River Tidals, Aransas and Mission River Above Tidals, and Copano Bay) for Load Reduction Scenario #1. Load Reduction Scenario #1 is the load reduction necessary to meet fecal coliform water quality standards for all water segments at each location in the model that was analyzed. The locations where the model was analyzed were the upstream and downstream portions of the Above Tidals and Tidals, the locations of the bacterial monitoring stations, and the Copano Bay water segments. However, each portion of the model that was analyzed (that did not meet fecal coliform water quality standards) was not always verified by existing monitoring data, so the results are inconclusive based on lack of monitoring data. Thus, these load reductions are only presented to show possible problem areas.

Aransas River Above Tidal

The Aransas River Above Tidal (shown in Figure 7A.7) must meet contact recreation use standards for fecal coliform, but the primary bacterial indicator is *E. coli* for this segment. However, the results presented are based on fecal coliform water quality standards because a fecal coliform model was created. For fecal coliform, the geometric mean of the samples must be less than 200 CFU/100mL, and single samples must be less than 400 CFU/100mL, but TCEQ allows 25% of the samples to exceed 400 CFU/100mL. The upstream portion of the Aransas River Above Tidal (SchemaNode 62), which is indicated in Figure 7A.7 with an orange circle, was observed in the calibrated Monte Carlo Simulation Model first, and this node is directly upstream of Station 12952.

Without any load reductions in the upstream watersheds, two runs of 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted to investigate background variation of the model. The percentile at which 400 CFU/100mL was reached in the model was recorded to ensure that the percentile is greater than 75%. However, the geometric mean of 1000 samples could not be calculated using the GEOMEAN() function in Microsoft Excel, so a separate run of 100 simulations was performed to obtain the geometric mean modeled at SchemaNode 62. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.1.

As shown in Table 7A.1 (0% load reduction), the model suggests that the upstream portion of the Aransas River Above Tidal is in compliance with fecal coliform water quality standards. In Run #1, the percent of samples exceeding 400 CFU/100mL is 20.6%, which is less than 25%; however, to increase the safety factor, the effect of load reductions at the upstream WWTP was tested[19]. The location of the WWTP is shown in Figure 7A.7. The median bacterial loading from this WWTP (City of Beeville Moore Street WWTP) was calculated based on two annual fecal coliform measurements and the average flow rate (of the monthly flow rates from 1998-2005) reported on the discharge monitoring reports (DMR); see Section 5.4. The number of runs of simulations and the modeled results at SchemaNode 62 with various load reductions at the WWTP are also shown in Table 7A.1.

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[19] The WWTP load reductions were based on the overestimated bacterial loadings from WWTPs (explained in Section 5.4.2).

Table 7A.1 Modeled Results at SchemaNode 62 with Various WWTP Load Reductions

Run #	Load Reduction (%)	Geometric Mean (CFU/100mL)	Percent > 400 CFU/100mL
1	0	95.3	20.6
2	0	104.3	18.5
1	10	76.1	20.8
2	10	106.4	17.9
1	20	91.9	17.8
2	20	90.1	15.9
1	30	113.1	16.5
2	30	100.3	15.2
Simulations		100	1000

As shown in Table 7A.1, reducing the bacterial loadings from the upstream WWTP by 30% allows approximately 15% of the samples to exceed the 400 CFU/100mL standard. Modifying the disinfection process could reduce the fecal coliform load from the WWTP.

With a 30% reduction in bacterial load, the geometric mean should have been less than the geometric mean with a 20% reduction in load. However, this was not observed, and, in fact, Table 7A.1 shows that the geometric mean varies greatly throughout the runs. This variation can be explained by the inherent variation of the Monte Carlo analysis; this is a plausible explanation because the WWTP loadings are significantly less than loadings from non-point sources and therefore should not have a major impact on the overall fecal coliform concentration. However, to be conservative, the 30% load reduction from the WWTP was applied for the remainder of the load reduction calculations. Recall that the WWTP loadings were largely overestimated in these calculations (Section 5.4.2).

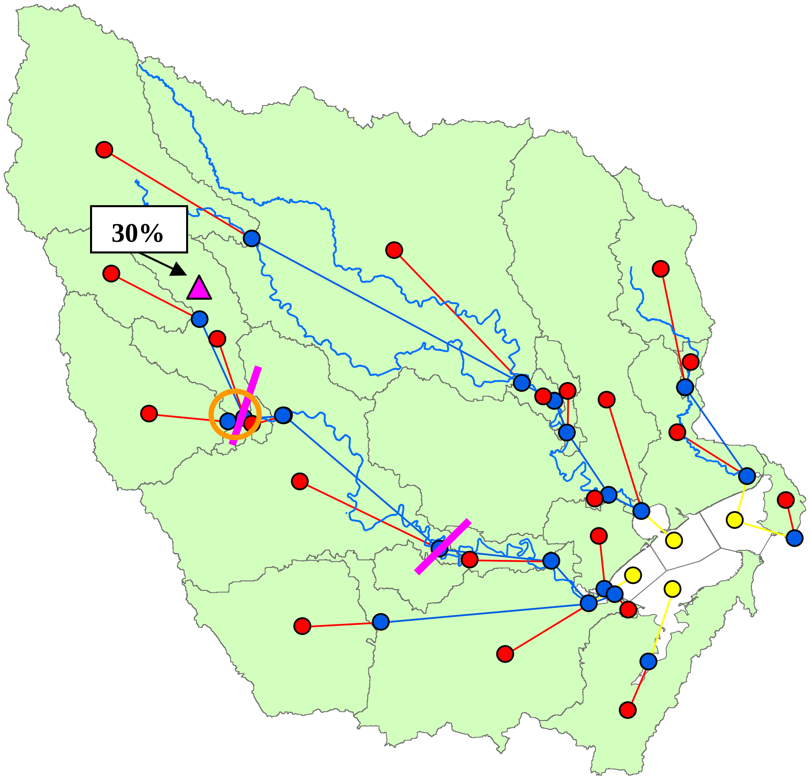

Figure 7A.7 Load Reductions for SchemaNode 62: Aransas River Above Tidal

The next downstream SchemaNode (indicated in Figure 7A.8 by an orange circle) along the Aransas River Above Tidal that is compared to standards in the model is SchemaNode 68, which is also the location of Station 12952.

With only the 30% load reduction applied at the upstream WWTP, two runs each of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.2.

Table 7A.2 Modeled Results at SchemaNode 68 with No Additional Load Reductions

Run #	**Load Reduction (%)**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	60.2	8.7
2	0	71.7	9.1
Simulations		100	1000

The upstream portion of the Aransas River Above Tidal is well in compliance with fecal coliform water quality standards based on modeled results (shown in Table 7A.2.)

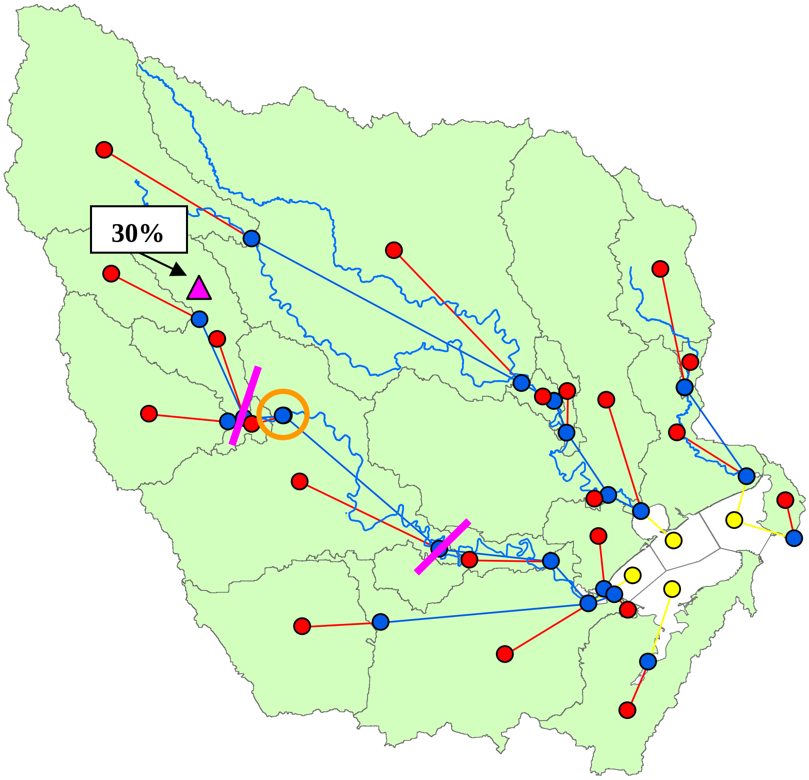

Figure 7A.8 Load Reductions for SchemaNode 68: Aransas River Above Tidal

The next downstream SchemaNode (indicated in Figure 7A.9 by an orange circle) along the Aransas River Above Tidal that is compared to standards in the model is SchemaNode 75, which is also the location of Station 12948.

With only the 30% load reduction applied at the upstream WWTP, two runs each of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.3.

As shown in Table 7A.3 (0% load reduction), the model suggests that the downstream portion of the Aransas River Above Tidal is in compliance with fecal coliform water quality standards. However, in Run #2, the percent of samples exceeding 400 CFU/100mL is 18.2%, which is less than 25%; however, to increase the safety factor, the effect of load reductions at the upstream WWTP was tested. The location of the WWTP is shown in Figure 7A.9. The median bacterial loading from this WWTP (Chase Field WWTP) was calculated based on literature values because no fecal coliform measurements were reported on the DMR; see Section 5.4. The number of runs of simulations and the modeled results at SchemaNode 75 with various load reductions at the WWTP are also shown in Table 7A.3.

Table 7A.3 Modeled Results at SchemaNode 75 with Various Additional WWTP Load Reductions

Run #	Load Reduction (%)	Geometric Mean (CFU/100mL)	Percent > 400 CFU/100mL
1	0	81.3	17.2
2	0	97.1	18.2
1	10	93.2	17.8
2	10	122.7	15.1
1	30	97.1	15
2	30	114.0	16.5
1	45	81.3	16.2
2	45	92.3	14.1
Simulations		100	1000

Reducing the bacterial loadings from the upstream WWTP by 30-45% allows approximately 15% of the samples to exceed the 400 CFU/100mL standard (shown in Table 7A.3.) The variation in the runs could just be the inherent variation of the Monte Carlo analysis; this is a plausible explanation because the WWTP loadings are significantly less than loadings from non-point sources and therefore should not have a major impact on the overall fecal coliform concentration. However, to be conservative, the 45% load reduction from the WWTP was applied for the remainder of the load reduction calculations.

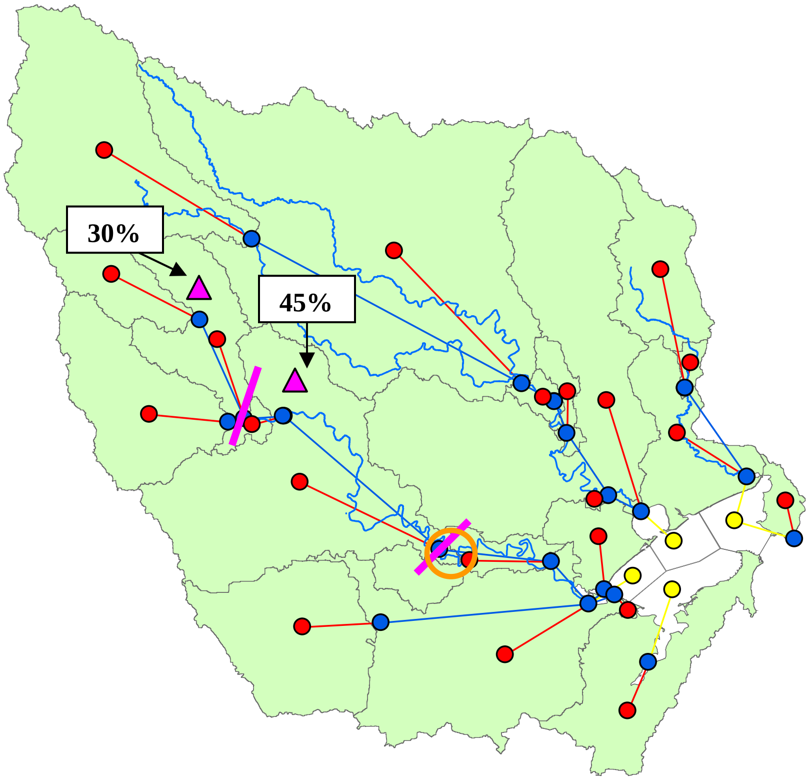

Figure 7A.9 Load Reductions for SchemaNode 75: Aransas River Above Tidal

Aransas River Tidal

The Aransas River Tidal (shown in Figure 7A.10) must meet contact recreation use standards for fecal coliform, but the primary bacterial indicator is enterococci for this segment. However, the results presented are based on fecal coliform water quality standards because a fecal coliform model was created. For fecal coliform, the geometric mean of the samples must be less than 200 CFU/100mL, and single samples must be less than 400 CFU/100mL, but TCEQ allows 25% of the samples to exceed 400 CFU/100mL. The upstream portion of the Aransas River Tidal (SchemaNode 75) was analyzed as the downstream node to Aransas River Above Tidal, so will not be analyzed again in this section.

The next downstream SchemaNode (indicated in Figure 7A.10 by an orange circle) along the Aransas River Tidal that is compared to standards in the model is SchemaNode 63.

With only the 30% and 45% load reductions applied at the upstream WWTPs, two runs each of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL is shown in Table 7A.4.

Table 7A.4 Modeled Results at SchemaNode 63 with No Additional Load Reductions

Run #	**Load Reduction (%)**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	74.2	4.4
2	0	56.6	4.9
Simulations		100	1000

The middle portion of the Aransas River Tidal is well in compliance with fecal coliform water quality standards based on modeled results (shown in Table 7A.4.) Thus, no additional load reductions are necessary for this portion of the model.

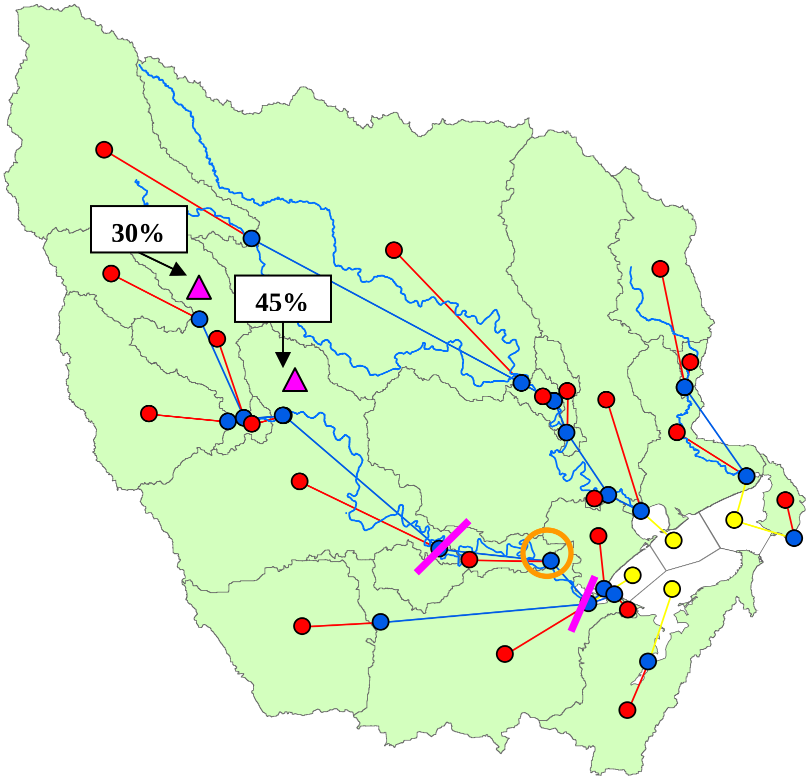

Figure 7A.10 Load Reductions for SchemaNode 63: Aransas River Tidal

The next downstream SchemaNode (indicated in Figure 7A.11 by an orange circle) along the Aransas River Tidal that is compared to standards in the model is SchemaNode 67.

With only the 30% and 45% load reductions applied at the upstream WWTPs, two runs each of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. The geometric mean and percent of samples exceeding 400 CFU/100mL is shown in Table 7A.5.

The downstream portion of the Aransas River Tidal exceeds fecal coliform water quality standards for both criteria (geometric mean > 200 CFU/100mL and more than 25% of samples > 400 CFU/100mL) based on modeled results when no additional load reductions are applied (as seen in Table 7A.5.)

Load reductions from the upstream WWTPs, whose locations are shown in Figure 7A.11, were considered. The median bacterial loadings from these WWTPs, which are a Water Reclamation Facility, the City of Taft Baird WWTP, the City of Sinton Main WWTP, and the City of Odem WWTP, were calculated based on literature values or DMRs[20]. If the bacterial loadings at all four WWTPs were reduced by 75%, both contact recreation use standards for fecal coliform are exceeded (shown in Table 7A.5).

Thus, livestock bacterial loadings, which may be more easily controlled than other non-point sources and septic system loadings, were also reduced in an attempt to meet water quality standards. The livestock bacterial loadings were reduced at the two watersheds (Figure 7A.11) that are directly upstream of the Aransas River Tidal.

Table 7A.5 gives the number of runs of simulations and the modeled results at SchemaNode 67 with various load reductions at the WWTPs and of non-point and livestock sources.

Table 7A.5 Modeled Results at SchemaNode 67 with Various Additional WWTP/Livestock/Non-point Load Reductions

Run #	**Load Reduction (%)**	**Bacteria Source**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	N/A	**454.8**	**44.5**
1	75	WWTPs	**269.9**	**42.2**
1	50	WWTPs	**423.2**	**38.0**
2	50	Livestock	**323.8**	**39.5**
1	75	WWTPs	119.2	**26.2**
2	75	Livestock/Non-point	137.7	24.5
1	95	WWTPs	167.9	22.2
2	75	Livestock/Non-point	119.3	24.5
1	95	WWTPs	97.8	22.1
2	80	Livestock/Non-point	138.6	20.8
1	95	WWTPs	131.1	18.9
2	85	Livestock/Non-point	119.6	18.2
Simulations			100	1000

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[20] The WWTP load reductions were based on the overestimated bacterial loadings from WWTPs (explained in Section 5.4.2).

Reducing the bacterial loadings from the upstream WWTPs by 95% and the livestock and non-point bacterial loadings by 85% in the adjacent upstream watersheds allows approximately 18% of the samples to exceed the 400 CFU/100mL standard and results in a geometric mean less than 200 CFU/100mL (shown in Table 7A.5.) The reductions necessary to meet fecal coliform contact recreation use standards downstream of the Aransas River Tidal based on modeled results are shown in Figure 7A.11. Reduction of livestock and non-point bacterial loadings would require implementations of best management practices (BMPs), and reduction of WWTP bacterial loadings would require proper disinfection before discharging into surface waters.

Significant reductions are needed to meet contact recreation use standards on the downstream portion of the Aransas River Tidal. Because there is no monitoring data available for this location, the load reductions are based on the calibration of the model at the existing monitoring stations and from modeled results.

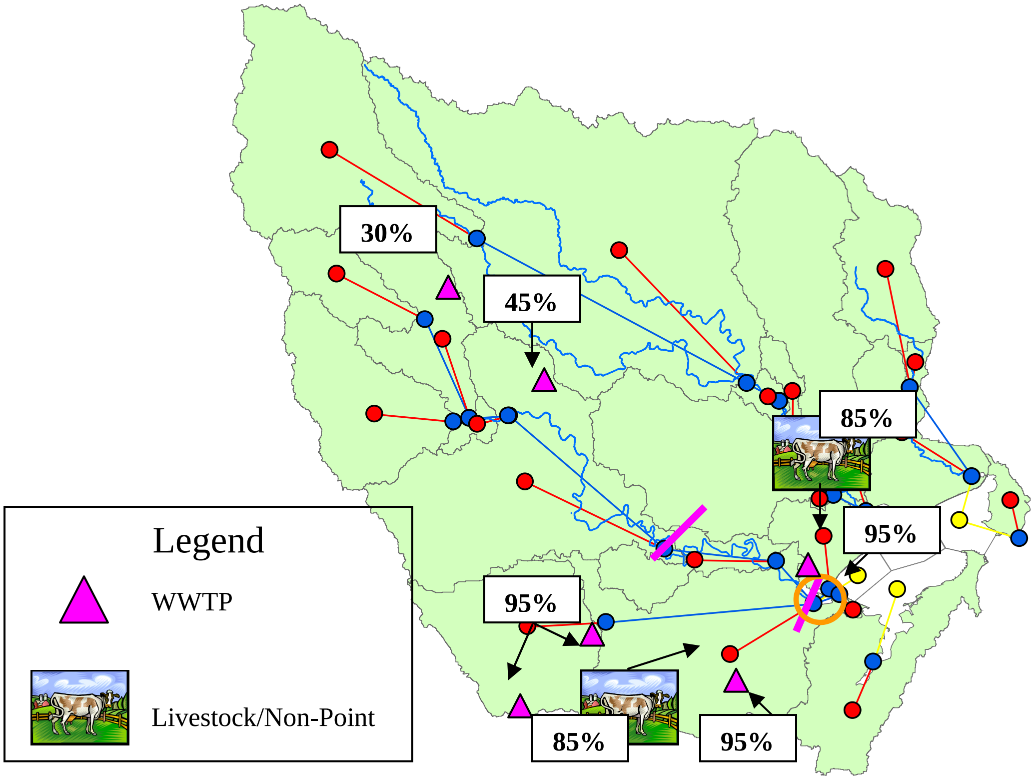

Figure 7A.11 Load Reductions for SchemaNode 67: Aransas River Tidal

Mission River Above Tidal

The Mission River Above Tidal (shown in Figure 7A.12) must meet contact recreation use standards for fecal coliform, but the primary bacterial indicator is *E. coli* for this segment. However, the results presented are based on fecal coliform water quality standards because a fecal coliform model was created. For fecal coliform, the geometric mean of the samples must be less than 200 CFU/100mL, and single samples must be less than 400 CFU/100mL, but TCEQ allows 25% of the samples to exceed 400 CFU/100mL. The upstream portion of the Mission River Above Tidal (SchemaNode 73), which is indicated in Figure 7A.12 with an orange circle, was analyzed in the calibrated Monte Carlo Simulation Model first, and this node is upstream of Station 12944.

Without any load reductions in the upstream watersheds, one run of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. The geometric mean and percent of samples exceeding 400 CFU/100mL is shown in Table 7A.6.

The upstream portion of the Mission River Above Tidal exceeds fecal coliform water quality standards for both criteria (geometric mean > 200 CFU/100mL and more than 25% of samples > 400 CFU/100mL) based on modeled results when no additional load reductions are applied (shown in Table 7A.6.)

Load reductions from the WWTP upstream of SchemaNode 73, shown in Figure 7A.12, were considered first. The bacterial loadings from this WWTP (Pettus Municipal Utility District WWTP) were calculated based on literature values since no fecal coliform concentration measurements were reported on the DMRs[21]. If the bacterial loadings at the WWTP are reduced by 100%, both contact recreation use standards for fecal coliform are exceeded. It is highly probable that the difference between no load reduction and 100% load reduction at the WWTP may be due to the natural variation of the Monte Carlo Simulation Model because the WWTP bacterial loadings are several orders of magnitude less than other non-point bacterial loadings, and these loadings have a substantial amount of time to decay before reaching SchemaNode 73 in the model.

Thus, livestock bacterial loadings, which are more easily controlled than other non-point sources and septic system loadings, were reduced along with WWTP loadings in an attempt to meet fecal coliform water quality standards. The livestock bacterial loadings were reduced at the two watersheds upstream of the Mission River Above Tidal (shown in Figure 7A.12.)

The number of runs of simulations and the modeled results at SchemaNode 73 with various WWTP and livestock load reductions are shown in Table 7A.6.

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[21] The WWTP load reductions were based on the overestimated bacterial loadings from WWTPs (explained in Section 5.4.2).

Table 7A.6 Modeled Results at SchemaNode 73 with Various Additional WWTP/Livestock Load Reductions

Run #	Load Reduction (%)	Bacteria Source	Geometric Mean (CFU/100mL)	Percent > 400 CFU/100mL
1	0	N/A	**308.0**	**39.3**
1	100	WWTP	**363.0**	**42.7**
1	50	WWTP	**225.5**	**26.4**
	50	Livestock (Node 80)		
1	50	WWTP	121.9	24
	50	Livestock		
1	50	WWTP	124.9	25
	60	Livestock		
1	50	WWTP	116.9	17.8
2	70	Livestock	99	19.1
1	50	WWTP	78.5	12.3
2	75	Livestock	64.5	15.1
Simulations			100	1000

Reducing the bacterial loadings from the upstream WWTPs by 50% and livestock bacterial loadings by 75% in the upstream watersheds allows approximately 14% of the samples to exceed 400 CFU/100mL and results in a geometric mean less than 200 CFU/100mL. The reductions necessary to meet fecal coliform contact recreation use standards at the upstream location of the Mission River Above Tidal based on modeled results are shown in Figure 7A.12. Reduction of livestock bacterial loadings would require implementations of agricultural best management practices (BMPs), and reduction of WWTP bacterial loadings would require proper disinfection before discharging into surface waters.

Significant reductions are needed to meet contact recreation use standards at the upstream portion of the Mission River Above Tidal. However, there is no monitoring data available for this location, so these reductions are based on the calibration of the model at the existing monitoring stations and from modeled results. Without any reductions at these upstream watersheds, the bacterial monitoring station 12944 meets fecal coliform contact recreation use standards in the model, which agrees with monitoring data[22].

However, the 50% load reduction from the WWTP and 75% load reduction from livestock were applied for the remainder of the load reduction calculations and scenarios (shown in Figure 7A.12). These load reductions will only significantly impact SchemaNode 73 and will not significantly affect the results of the remainder of the model due to the bacterial decay rates.

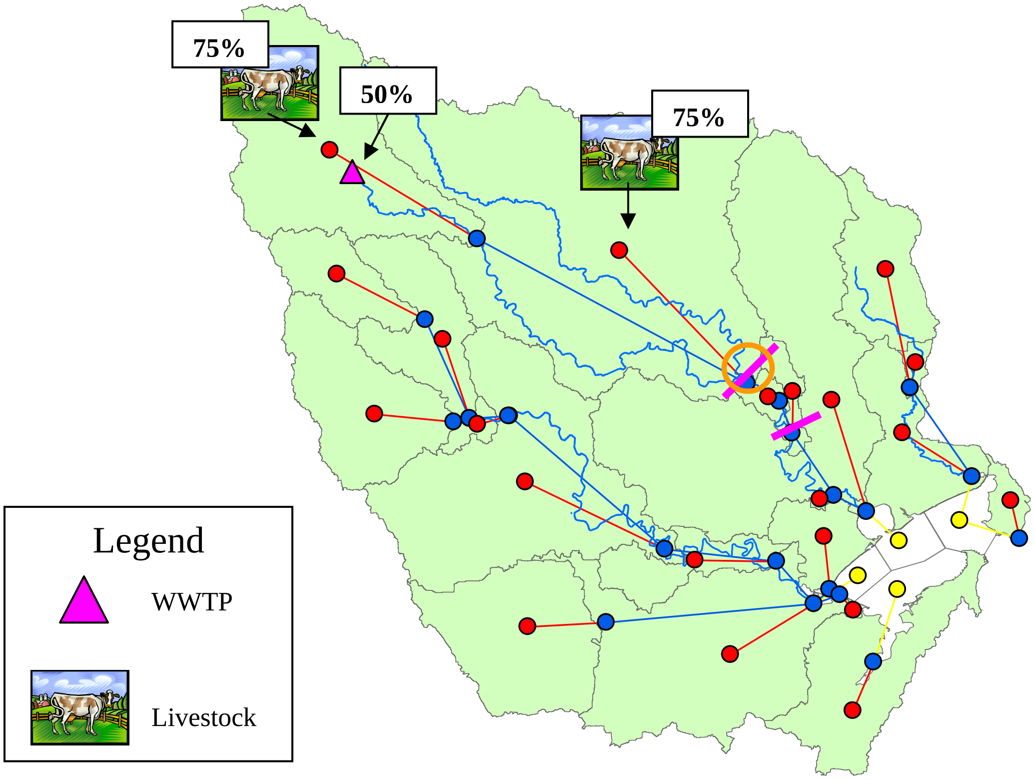

Figure 7A.12 Load Reductions for SchemaNode 73: Mission River Above Tidal

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[22] The model was calibrated at all bacterial monitoring stations.

The next downstream SchemaNode (indicated in Figure 7A.13 by an orange circle) along the Mission River Above Tidal that is compared to standards in the model is SchemaNode 74, which is also the location of Station 12944.

With only the 50% WWTP and 75% livestock load reductions applied at the upstream watersheds, two runs each of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.7. Even without the 50% WWTP and 75% livestock loading reductions for SchemaNode 73, the modeled geometric mean and percent of samples greater than 400 CFU/100mL are in compliance with fecal coliform water quality standards.

Table 7A.7 Modeled Results at SchemaNode 74 with No Additional Load Reductions

Run #	**Load Reduction (%)**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	92.8	15.2
2	0	62.8	15.5
Simulations		100	1000

The middle portion of the Mission River Above Tidal is in compliance with fecal coliform water quality standards based on modeled results (shown in Table 7A.7.) Thus, no additional load reductions are necessary for this portion of the model.

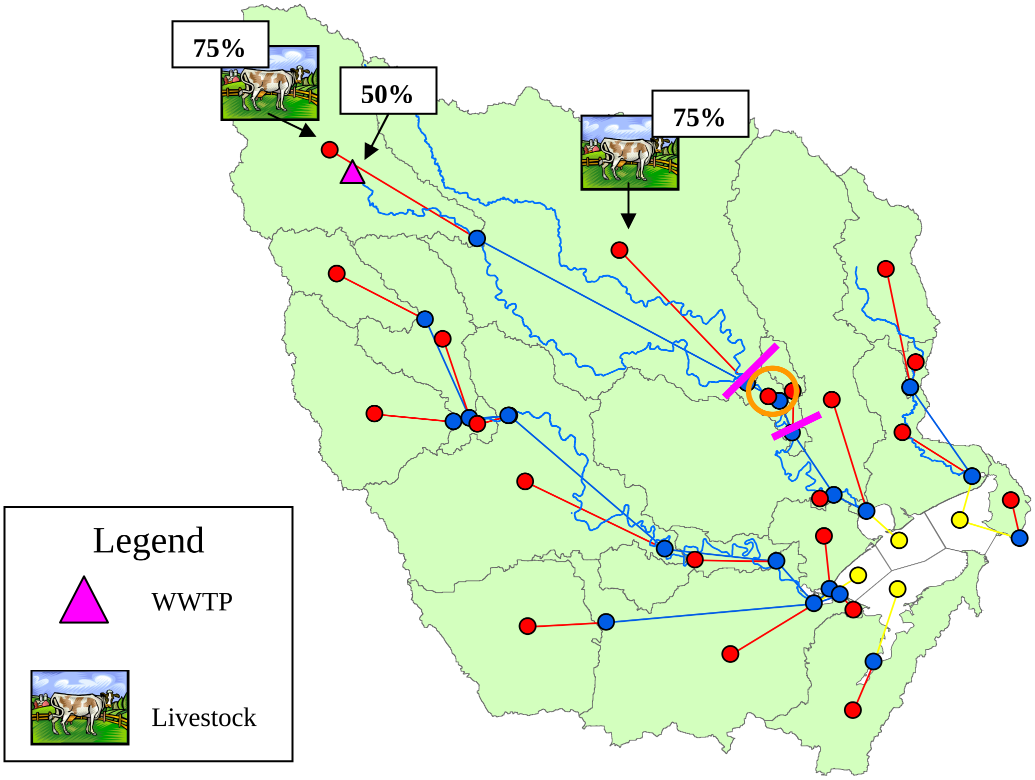

Figure 7A.13 Load Reductions for SchemaNode 74: Mission River Above Tidal

The next downstream SchemaNode (indicated in Figure 7A.14 by an orange circle) along the Mission River Above Tidal that is compared to standards in the model is SchemaNode 65.

With only the 50% WWTP and 75% livestock load reductions applied at the upstream watersheds, one run of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. The geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.8. Note: even without the 50% WWTP and 75% livestock loading reductions for SchemaNode 73, the modeled geometric mean and percent of samples greater than 400 CFU/100mL comply with fecal coliform water quality standards.

Table 7A.8 Modeled Results at SchemaNode 65 with No Additional Load Reductions

Run #	**Load Reduction (%)**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	89.6	10.5
Simulations		100	1000

The downstream portion of the Mission River Above Tidal is in compliance with fecal coliform water quality standards based on modeled results (shown in Table 7A.8.) Thus, no additional load reductions are necessary for this portion of the model.

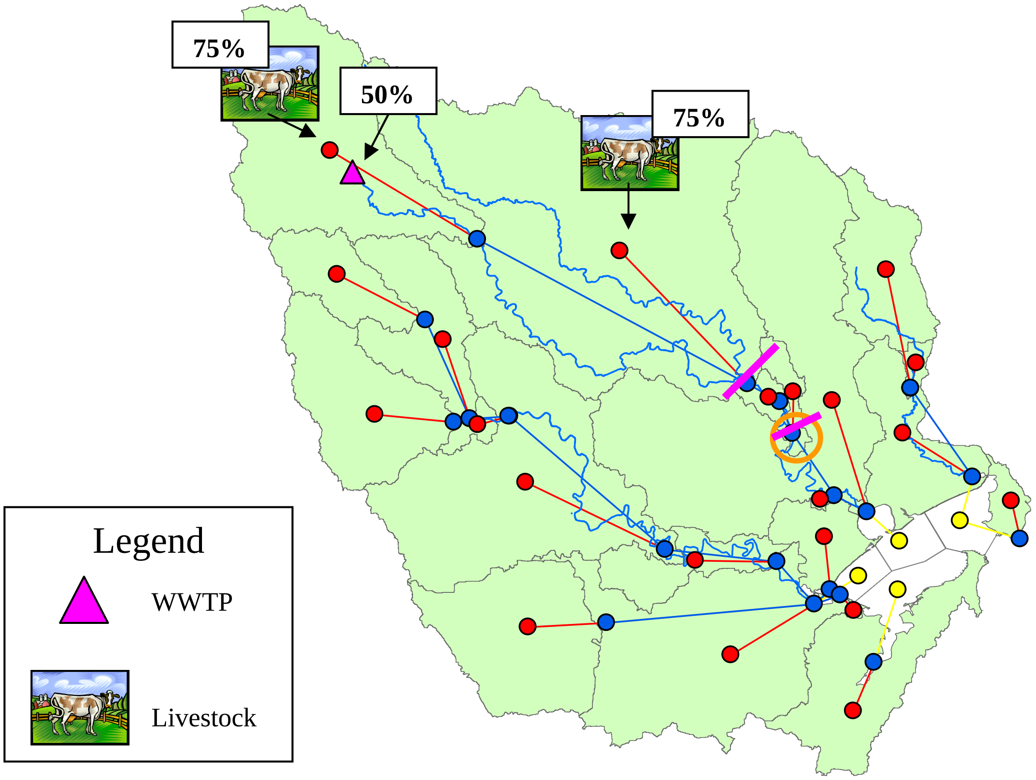

Figure 7A.14 Load Reductions for SchemaNode 65: Mission River Above Tidal

Mission River Tidal

The Mission River Tidal (shown in Figure 7A.15) must meet contact recreation use standards for fecal coliform, but the primary bacterial indicator is enterococci for this segment. However, the results presented are based on fecal coliform water quality standards because a fecal coliform model was created. For fecal coliform, the geometric mean of the samples must be less than 200 CFU/100mL, and single samples must be less than 400 CFU/100mL, but TCEQ allows 25% of the samples to exceed 400 CFU/100mL. The upstream portion of the Mission River Tidal (SchemaNode 65) was analyzed as the downstream node to Mission River Above Tidal, so it will not be analyzed again in this section.

The next downstream SchemaNode (indicated in Figure 7A.15 by an orange circle) along the Mission River Tidal that is compared to standards in the model is SchemaNode 70.

With only the 50% WWTP and 75% livestock load reductions applied at the upstream watersheds, one run of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. The geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.9.

Table 7A.9 Modeled Results at SchemaNode 70 with No Additional Load Reductions

Run #	**Load Reduction (%)**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	59.8	2.8
Simulations		100	1000

The middle portion of the Mission River Tidal is in compliance with fecal coliform water quality standards based on modeled results (shown in Table 7A.9). Thus, no additional load reductions are necessary for this portion of the model.

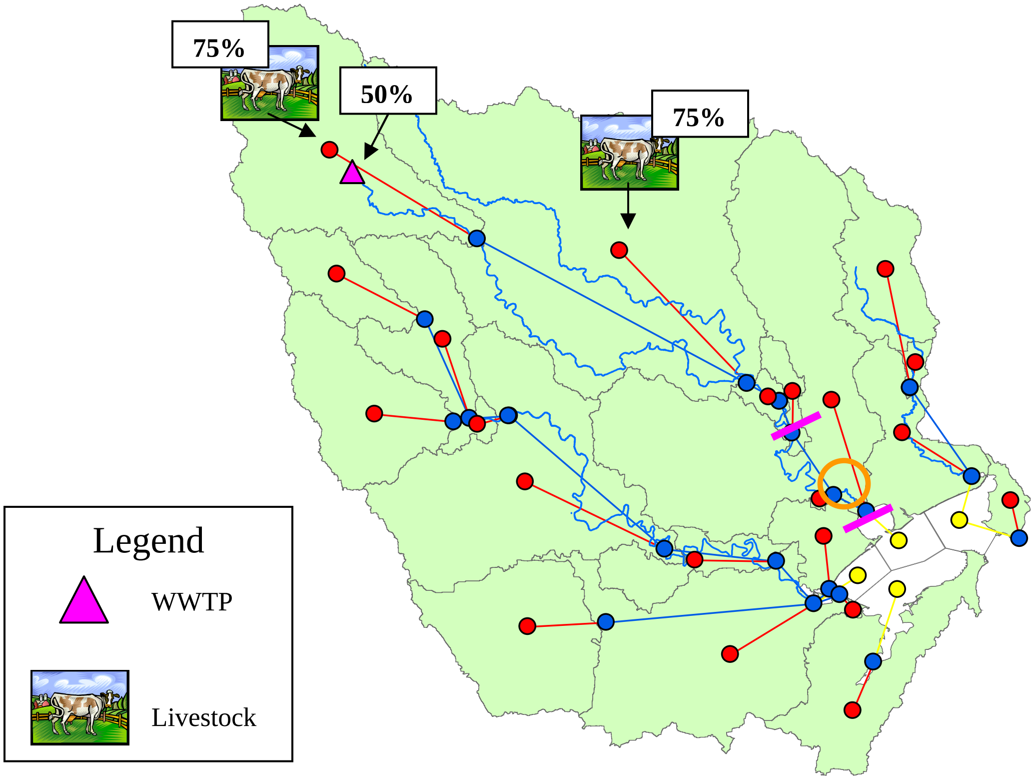

Figure 7A.15 Load Reductions for SchemaNode 70: Mission River Tidal

The next downstream SchemaNode (indicated in Figure 7A.16 by an orange circle) along the Mission River Tidal that is compared to standards in the model is SchemaNode 66.

With only the 50% WWTP and 75% livestock load reductions applied at the upstream watersheds, two runs of 100 and 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 and 100 simulation runs, the geometric mean and percent of samples exceeding 400 CFU/100mL are shown in Table 7A.10.

The downstream portion of the Mission River Tidal exceeds fecal coliform water quality standards for both criteria (geometric mean > 200 CFU/100mL and more than

25% of samples > 400 CFU/100mL) based on modeled results when no additional load reductions are applied (shown in Table 7A.10).

There are no WWTPs or septic systems in the upstream watershed that discharges directly to the downstream portion of the Mission River Tidal. Thus, livestock and non-point bacterial loadings were reduced in an attempt to meet water quality standards. The bacterial loadings were reduced at the watershed that is directly upstream of the Mission River Tidal; this watershed is shown in Figure 7A.16.

The number of runs of simulations and the modeled results at SchemaNode 66 with various load reductions of livestock and non-point bacterial loadings are also shown in Table 7A.10.

Table 7A.10 Modeled Results at SchemaNode 66 with Various Additional Livestock/Non-point Load Reductions

Run #	**Load Reduction (%)**	**Bacteria Source**	**Geometric Mean (CFU/100mL)**	**Percent > 400 CFU/100mL**
1	0	N/A	**433.5**	**50.2**
2	0	N/A	**553.9**	**48.5**
1	50	Livestock	**271.5**	**36.1**
	0	Non-point		
1	70	Livestock	181.5	**31.8**
	0	Non-point		
1	85	Livestock	77.1	22.8
2	0	Non-point	133.9	**25.1**
1	85	Livestock	94.3	22.4
2	50	Non-point	118.4	22.7
1	90	Livestock	118.7	18.9
2	0	Non-point	76.4	18.8
Simulations			100	1000

Reducing the livestock bacterial loadings by 90% in the adjacent upstream watershed allows approximately 19% of the samples to exceed the 400 CFU/100mL standard and results in a geometric mean less than 200 CFU/100mL (shown in Table 7A.10). The reductions necessary to meet fecal coliform contact recreation use standards downstream of the Mission River Tidal based on modeled results are shown in Figure 7A.16. The reduction of non-point bacterial loadings supplemented with livestock load reductions did not affect the quality of the river. The geometric mean increased when 50% reduction of non-point bacterial loadings was applied to the model (Table 7A.10). It is highly probable that the difference between non-point load reduction and no non-point reduction may be due to the natural variation of the Monte Carlo Simulation Model because the non-point bacterial loadings are several orders of magnitude less than livestock bacterial loadings.

Significant reductions are needed to meet fecal coliform contact recreation use standards on the downstream portion of the Mission River Tidal. However, no monitoring data are available for this location, so these reductions are based on the calibration of the model at the existing monitoring stations and from modeled results.

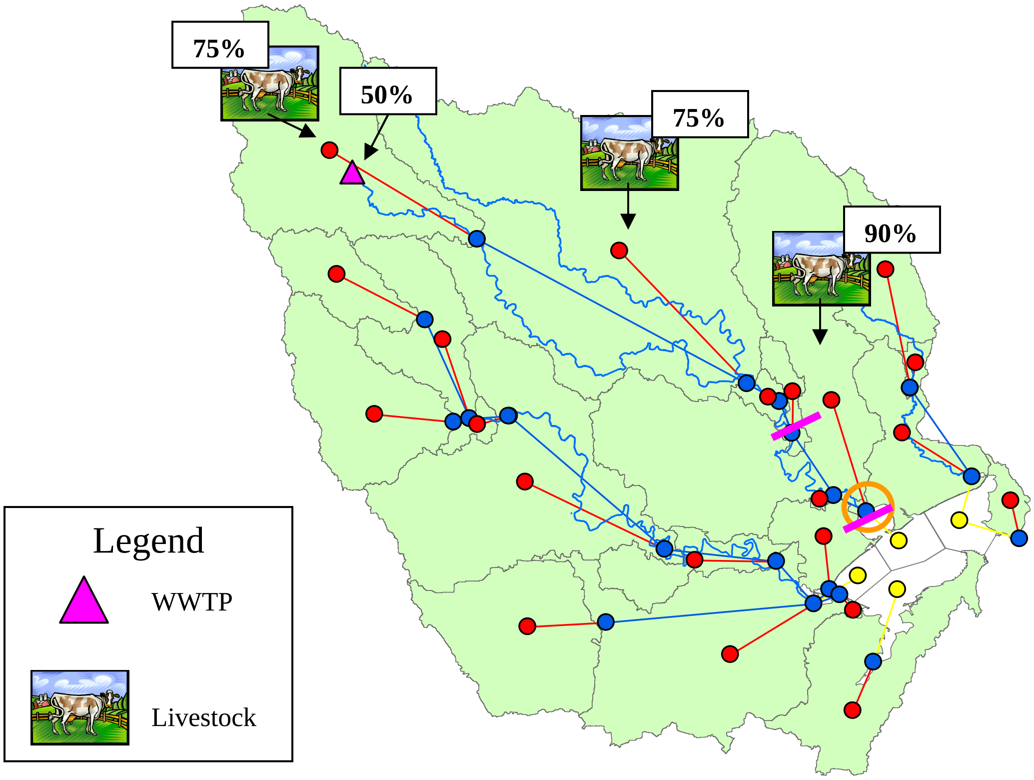

Figure 7A.16 Load Reductions for SchemaNode 66: Mission River Tidal

Copano Bay

Copano Bay must meet oyster harvesting use standards for fecal coliform. The median of the samples (within a two-year period) must be less than 14 CFU/100mL, and the 90th-percentile of the samples must be less than 43 CFU/100mL (i.e., 10% of the samples are allowed to exceed 43 CFU/100mL.)

Aransas River drains into Copano Bay Segment 2 (shown in Figure 7A.17), represented by SchemaNode 154. Without any additional load reductions in the upstream watersheds than those applied in Figure 7A.11, two runs of 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 simulation runs, the median and 90th-percentile CFU/100mL are shown in Table 7A.11.

Table 7A.11 Modeled Results at SchemaNode 154 with No Additional Load Reductions (Aransas Tidal Load Reductions Included)

Run #	Load Reduction (%)	Median (CFU/100mL)	90th-percentile > 43 CFU/100mL
1	0	0.43	7.21
2	0	0.43	8.08
Simulations		100	1000

The Copano Bay Segment 2 is in compliance with fecal coliform water quality standards based on modeled results if the Aransas River Tidal load reductions are applied (shown in Table 7A.11.) Thus, no additional load reductions are necessary for this portion of the model if load reductions for the downstream Aransas River Tidal are applied.

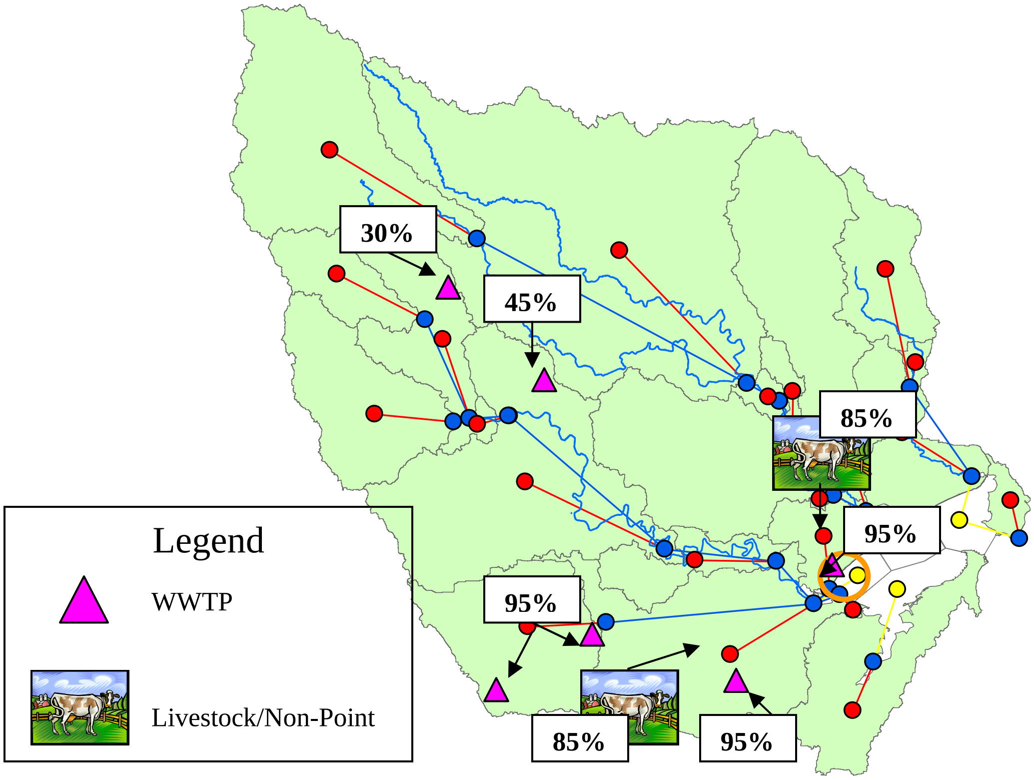

Figure 7A.17 Load Reductions for SchemaNode 154: Copano Bay (Including Aransas Tidal Reductions)

However, the load reductions required for the downstream portion of the Aransas River Tidal were determined from the modeled results, and there are no monitoring data at this location to verify the results of the model. A possible reason the reductions of the loads are significantly high is because the Model models all the bacteria from the adjacent watersheds draining to the Aransas River Tidal before discharging into the Bay. However, some of this loading could be discharging directly into the Bay.

Mission River drains into Copano Bay Segment 3 (shown in Figure 7A.18), represented by SchemaNode 153. Without any additional load reductions in the upstream watersheds than those in Figure 7A.18, two runs of 1000 simulations of the calibrated Monte Carlo Simulation Model were conducted. For the two separate 1000 simulation runs, the median and 90th-percentile CFU/100mL are shown in Table 7A.12.

Table 7A.12 Modeled Results at SchemaNode 153 with No Additional Load Reductions (Mission Tidal Load Reductions Included)

Run #	Load Reduction (%)	Median (CFU/100mL)	90th-percentile > 43 CFU/100mL
1	0	0.36	4.95
2	0	0.35	5.11
Simulations		100	1000

Copano Bay Segment 3 is in compliance with fecal coliform water quality standards based on modeled results if the Mission River Tidal load reductions are applied (shown in Table 7A.12). Thus, no additional load reductions are necessary for this portion of the model if load reductions for the downstream Mission River Tidal are applied.

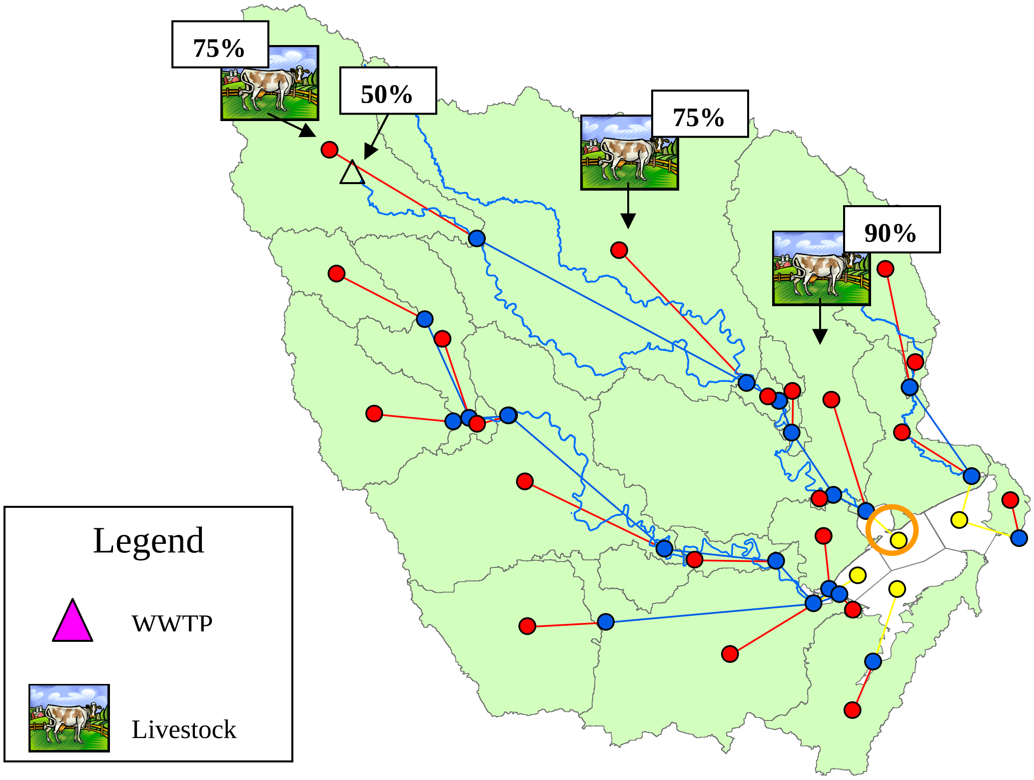

Figure 7A.18 Load Reductions for SchemaNode 153: Copano Bay (Including Mission River Tidal Reductions)

However, the load reductions required for the downstream portion of the Mission River Tidal were determined from the modeled results, and there are no monitoring data at this location to verify the results of the model.

Summary

Considering only fecal coliform water quality standards, the load reductions required to satisfy the standards for all portions of the model that were analyzed (i.e., the upstream and downstream portion of the Above Tidals and Tidals, the locations of the bacterial monitoring stations, and the four segments in Copano Bay) are shown in Figure 7A.19. This load reduction scenario is referred to as Load Reduction Scenario #1.

However, bacterial monitoring data cannot verify all the locations in the model where fecal coliform water quality standards are exceeded. Thus, these load reductions are inconclusive and are only presented to show possible problem areas.

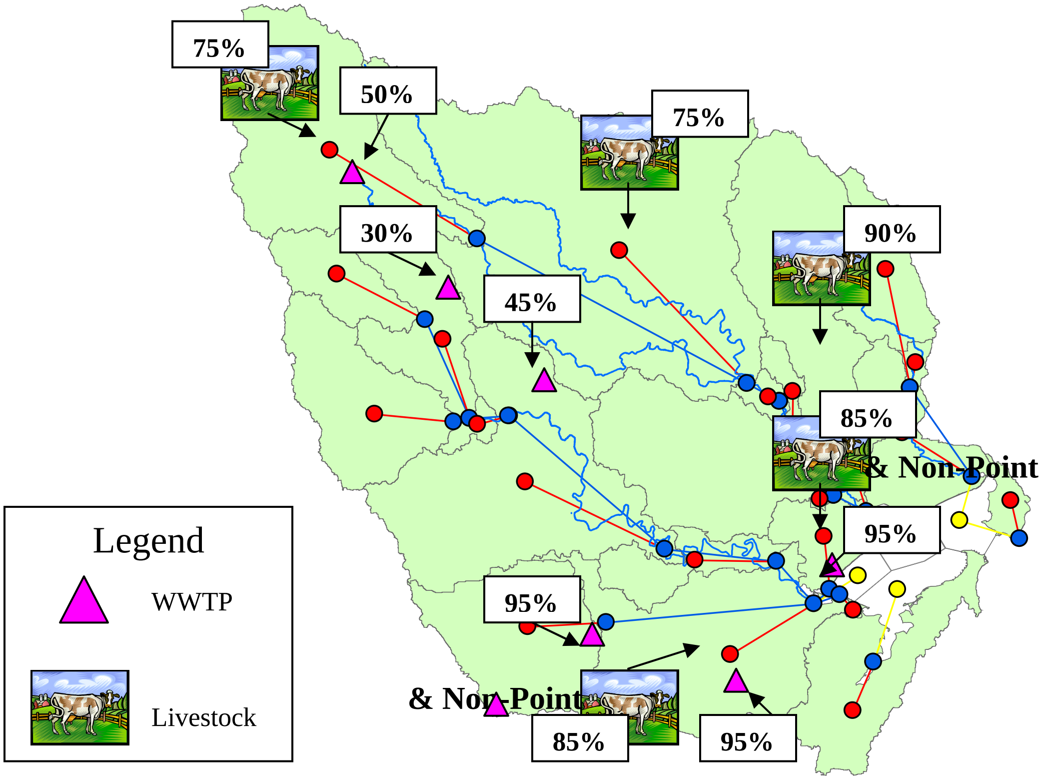

Figure 7A.19 Load Reductions to Satisfy Fecal Coliform Standards for Modeled Conditions

Appendix 8.2: Load Allocations for Scenario #1

This appendix gives the load allocations of all the water segments (Aransas and Mission River Tidals, Aransas and Mission River Above Tidals, and Copano Bay) for Load Reduction Scenario #1. Load Reduction Scenario #1 contains the load reduction necessary to meet fecal coliform water quality standards for all water segments at each location in the model that was analyzed. The locations where the model was analyzed were the upstream and downstream portions of the Above Tidals and Tidals, the locations of the bacterial monitoring stations, and the Copano Bay water segments. However, each portion of the model that was analyzed (that did not meet fecal coliform water quality standards) was not verified by existing monitoring data, so the results are inconclusive based on lack of monitoring data. Thus, these load reductions are only presented to show possible problem areas.

Aransas River Above Tidal

The recommended load reductions (for Load Reduction Scenario #1) were from upstream WWTPs. The WWTPs and the Aransas River Above Tidal, and the SchemaNodes and SchemaLinks of interest are shown in Figure 8A.1.

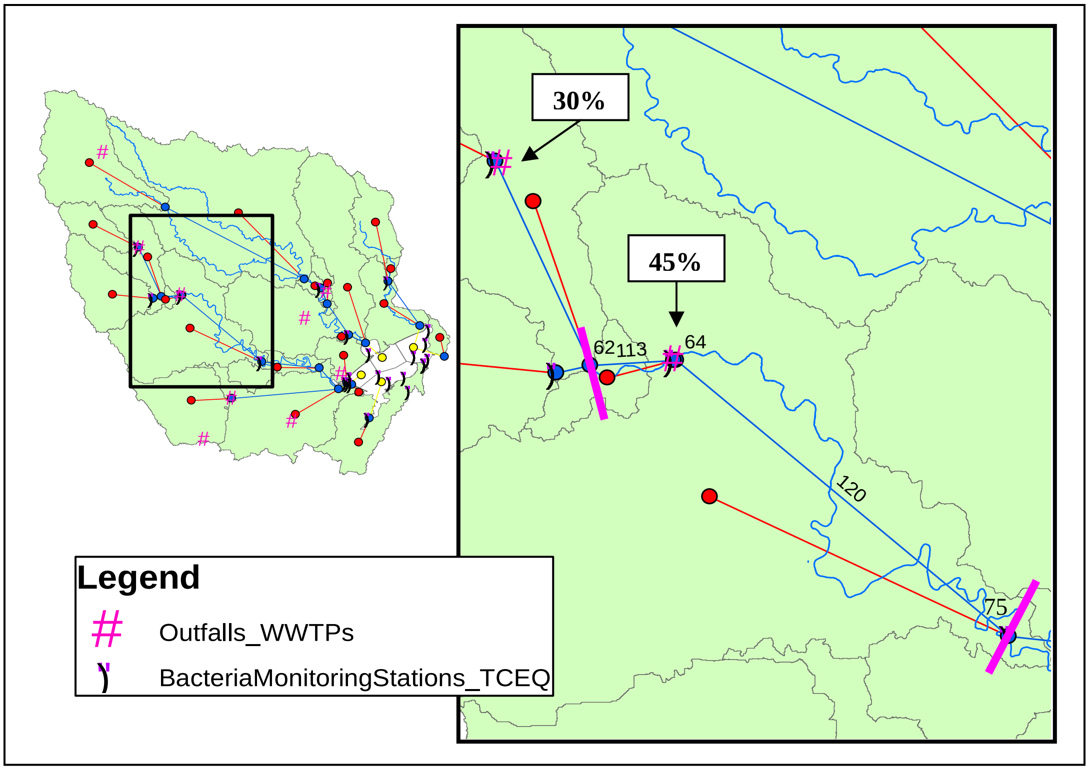

Figure 8A.1 Load Reduction Scenario #1: Aransas River Above Tidal

Since the current loadings were found at the upstream and downstream portions of the water segments, the corresponding load reductions were found for the upstream and downstream portions. The load reduction at the WWTP source for the upstream portion of the Aransas River Above Tidal (SchemaNode 62) is shown in Table 8A.1; only the 30% load reduction WWTP would affect the water quality at the upstream portion. Since the WWTP discharges to the upstream node of the Aransas River Above Tidal, the residence time is zero days. However, the WWTP bacterial loading was largely overestimated (explained in Section 5.4.2); thus, the load reduction from WWTP would be even less than what is indicated.

Table 8A.1 Load Reduction Scenario #1 at Upstream Node of Aransas River Above Tidal

SchemaNode	Current WWTP Loading (CFU/year)	Load Reduction at Source (CFU/year)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/year)
62	3.22E+13	9.66E+12	0	9.66E+12
Total Load Reduction (CFU/year)				9.66E+12
Current Loading (CFU/year), Table 8.1				3.35E+13
Allowable Load (CFU/year)				2.38E+13

The load reduction at the WWTP sources for the downstream portion of the Aransas River Above Tidal (SchemaNode 75) is shown in Table 8A.2; the 30% and 45% load reductions from WWTPs would affect the water quality at the downstream portion. The 30% WWTP loading (applied at SchemaNode 62) would decay along SchemaLinks 113 and 120 (total residence time = 1.772 days), and the 45% WWTP loading (applied at SchemaNode 64) would decay along SchemaLink 120 (residence time of 1.51 days.)

Table 8A.2 Load Reduction Scenario #1 at Downstream Node of Aransas River Above Tidal

SchemaNode	Current WWTP Loading (CFU/year)	Load Reduction at Source (CFU/year)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/year)
62	3.22E+13	9.66E+12	1.772	2.79E+11
64	4.79E+14	2.16E+14	1.510	1.05E+13
Total Load Reduction (CFU/year)				1.08E+13
Current Loading (CFU/year), Table 8.1				9.45E+13
Allowable Load (CFU/year)				8.37E+13

Aransas River Tidal

The recommended load reductions (for Load Reduction Scenario #1) were from upstream WWTPs, livestock, and other non-point bacterial sources. The percent of reductions and the corresponding sources (determined in Section 7.3.3), and the SchemaNodes and SchemaLinks of interest are shown in Figure 8A.2. Note that the load reductions for Aransas River Above Tidal were still applied to the model (shown in Figure 8A.1). However, these load reductions were significantly less (since farther upstream) than the load reductions shown in Figure 8A.2.

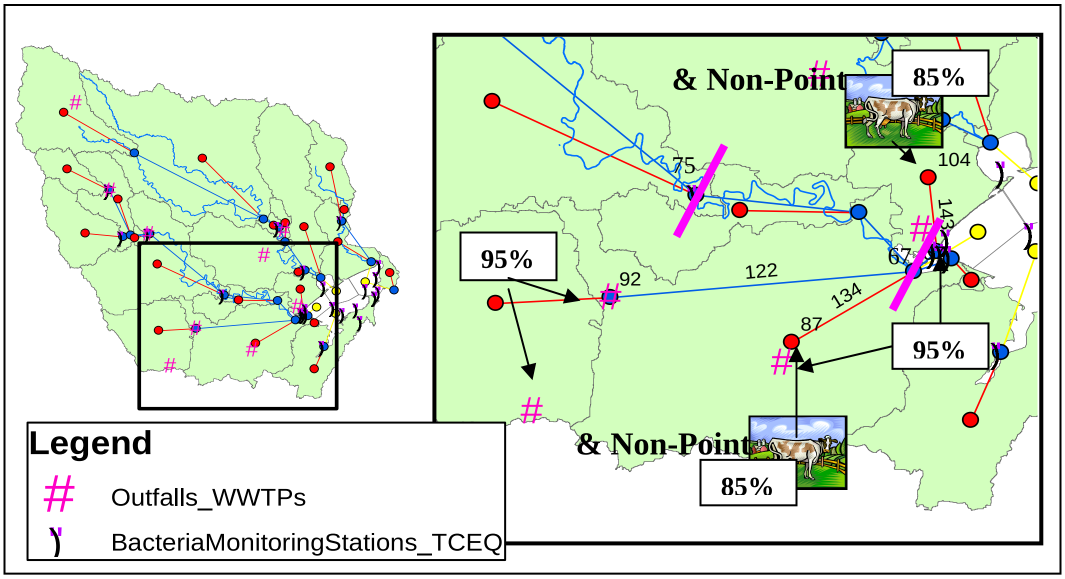

Figure 8A.2 Load Reduction Scenario #1: Aransas River Tidal

The load reductions and allowable loads for the upstream portion of the Aransas River Tidal were the same as the load reductions and allowable loads for the downstream portion of the Aransas River Above Tidal because it is the same SchemaNode (HydroID 75) in the Schematic Network. (See Table 8A.2 for the load reductions and allowable loads for the upstream portion of the Aransas River Tidal.) The load reductions at the bacterial sources for the downstream portion of the Aransas River Tidal (SchemaNode 67) are shown in Table 8A.3. Note: "WWTP, us" means the WWTPs that were accounted for upstream of the Aransas River Tidal, and notice that these upstream WWTPs contribute significantly less bacterial loading to the Aransas River Tidal than livestock/non-point sources.

Table 8A.3 Load Reduction Scenario #1 at Downstream Node of Aransas River Tidal

Schema-Node	**Source**	**Current Loading (CFU/yr)**	**Load Reduction at Source (CFU/yr)**	**Total Residence Time to Segment (days)**	**Equivalent Load at Segment (CFU/yr)**
62	WWTP, us	3.22E+13	9.66E+12	2.67	4.65E+10
64	WWTP, us	4.79E+14	2.16E+14	2.41	1.75E+12
67	WWTP	1.48E+04	1.41E+04	0.00	1.41E+04
69	WWTP	3.37E+11	3.20E+11	0.01	3.14E+11
87	Livestock/ Non-point	1.16E+16	9.84E+15	1.44	5.54E+14
92	WWTP	6.98E+14	6.63E+14	1.50	3.30E+13
104	Livestock/ Non-point	1.02E+15	8.67E+14	1.51	4.23E+13
Total Load Reduction (CFU/year)					6.32E+14
Current Loading (CFU/year), Table 8.3					8.69E+14
Allowable Load (CFU/year)					2.38E+14

Mission River Above Tidal

The recommended load reductions were from upstream WWTPs and livestock bacterial sources. The percent of reductions from the corresponding sources (determined in Section 7.3.3), and the SchemaNodes and SchemaLinks of interest are shown in Figure 8A.3.

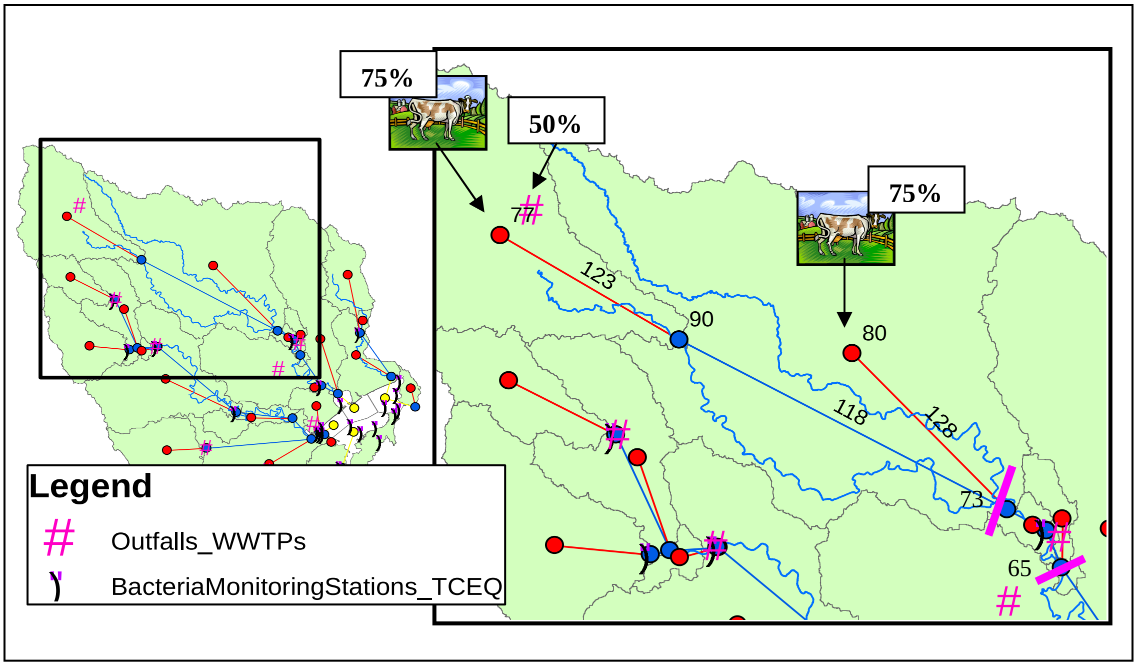

Figure 8A.3 Load Reduction Scenario #1: Mission River Above Tidal

The load reductions at the bacterial sources for the upstream portion of the Mission River Above Tidal (SchemaNode 73) are shown in Table 8A.4.

Table 8A.4 Load Reduction Scenario #1 at Upstream Node of Mission River Above Tidal

Schema-Node	Source	Current Loading (CFU/yr)	Load Reduction at Source (CFU/yr)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/yr)
77	Livestock	2.89E+16	2.16E+16	7.95	2.69E+09
80	Livestock	6.17E+16	4.63E+16	2.40	3.78E+14
90	WWTP	1.75E+12	8.75E+11	4.95	4.39E+07
Total Load Reduction (CFU/year)					3.78E+14
Current Loading (CFU/year), Table 8.5					5.10E+14
Allowable Load (CFU/year)					1.32E+14

The load reduction at the WWTP and livestock sources for the downstream portion of the Mission River Above Tidal (SchemaNode 65) is shown in Table 8A.5; the 50% and 75% load reductions from the WWTP and livestock would affect the water quality at all the downstream portions (just would impact less the farther downstream.)

Table 8A.5 Load Reduction Scenario #1 at Downstream Node of Mission River Above Tidal

Schema-Node	**Source**	**Current Loading (CFU/yr)**	**Load Reduction at Source (CFU/yr)**	**Total Residence Time to Segment (days)**	**Equivalent Load at Segment (CFU/yr)**
77	Livestock	2.89E+16	2.16E+16	9.64	9.16E+07
80	Livestock	6.17E+16	4.63E+16	4.09	1.29E+13
90	WWTP	1.75E+12	8.75E+11	6.64	1.49E+06
Total Load Reduction (CFU/year)					1.29E+13
Current Loading (CFU/year), Table 8.5					1.26E+14
Allowable Load (CFU/year)					1.13E+14

Mission River Tidal

The recommended load reductions (for Load Reduction Scenario #1) were from upstream WWTP/livestock bacterial sources (shown in Figure 8A.3) and livestock bacterial sources that are shown in Figure 8A.4. The percent of reductions and the corresponding sources (determined in Section 7.3.3), and the SchemaNodes and SchemaLinks of interest are shown in Figure 8A.4.

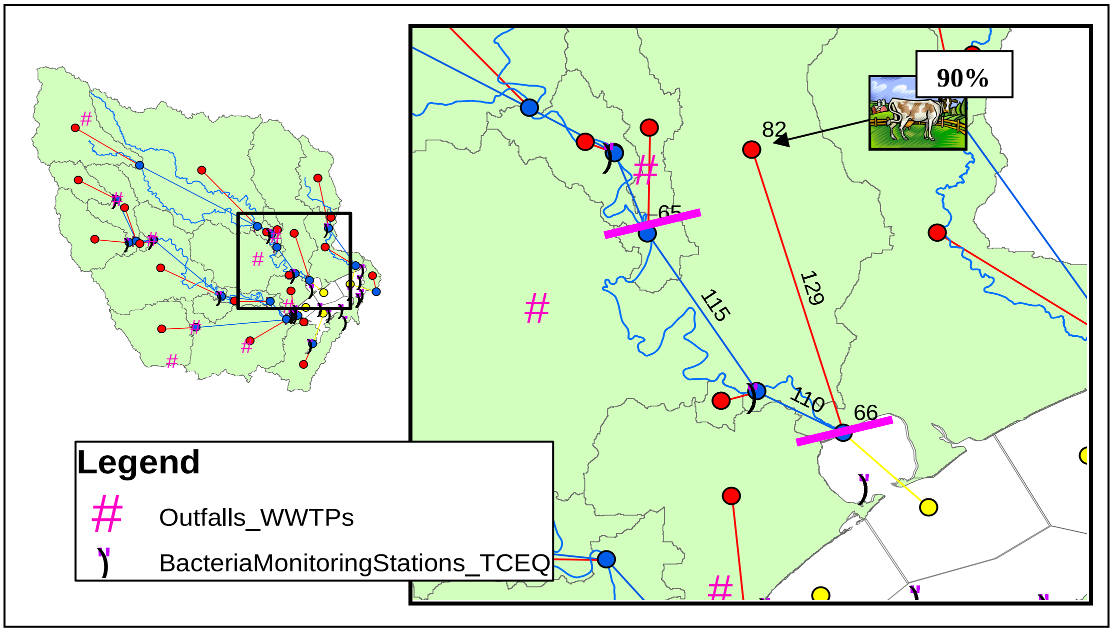

Figure 8A.4 Load Reduction Scenario #1: Mission River Tidal

The load reductions and allowable loads for the upstream portion of the Mission River Tidal were the same as the load reductions and allowable loads for the downstream portion of the Mission River Above Tidal because it is the same SchemaNode (HydroID 65) in the Schematic Network; see Table 8A.5 for the load reductions and allowable loads for the upstream portion of the Mission River Tidal. The load reductions at the bacterial sources for the downstream portion of the Mission River Tidal (SchemaNode 66) are shown in Table 8A.6.

Table 8A.6 Load Reduction Scenario #1 at Downstream Node of Mission River Tidal

Schema-Node	Source	Current Loading (CFU/yr)	Load Reduction at Source (CFU/yr)	Total Residence Time to Segment (days)	Equivalent Load at Segment (CFU/yr)
77	Livestock, us	2.89E+16	2.16E+16	10.94	6.81E+06
80	Livestock, us	6.17E+16	4.63E+16	5.39	9.57E+11
82	Livestock	4.34E+16	3.91E+16	1.86	9.48E+14
90	WWTP, us	1.75E+12	8.75E+11	7.89	1.23E+05
Total Load Reduction (CFU/year)					9.49E+14
Current Loading (CFU/year), Table 8.7					1.12E+15
Allowable Load (CFU/year)					1.66E+14

Copano Bay

The recommended load reductions (for Load Reduction Scenario #1) were from upstream WWTP/livestock/non-point bacterial sources (shown in Figure 7A.19.) No load reductions were necessary for Copano Bay segments 1 and 4.

The load reductions that were accounted for at the Aransas River outlet (Copano Bay Segment 2) are shown in Figure 7A.19. The Aransas River Tidal drains directly into Copano Bay Segment 2, and the only additional loadings to this portion of the Bay were avian. Since the avian loading cannot be reduced, the total load reduction applied at Segment 2 was the same load reduction that was found for the downstream portion of the Aransas River Tidal, which is given in Table 8A.3. The load reduction that occurs at the Copano Bay Aransas River outlet (Copano Bay Segment 2) based on the upstream load reductions that were made is shown in Table 8A.7. Note that this load reduction was significantly more than what would be necessary to meet the oyster water use fecal coliform standards in Copano Bay.

Table 8A.7 Load Reduction Scenario #1 at Copano Bay Aransas River Outlet, Segment 2

SchemaNode	Source	Equivalent Load at Tidal (CFU/yr)	Concentration in Bay (CFU/m^3)	Load in Bay (CFU/yr)
62	WWTP, us	4.65E+10	1.07E+00	2.69E+08
64	WWTP, us	1.75E+12	4.03E+01	1.02E+10
67	WWTP	1.41E+04	3.24E-07	8.14E+01
69	WWTP	3.14E+11	7.22E+00	1.82E+09
87	Livestock/ Non-point	5.54E+14	1.28E+04	3.21E+12
92	WWTP	3.30E+13	7.60E+02	1.91E+11
104	Livestock/ Non-point	4.23E+13	9.74E+02	2.45E+11
Cumulative Runoff. Q (m^3/yr), Section 6.3.3.4				2.52E+08
Volume of Copano Bay Segment, V (m^3), Section 6.3.3.3				5.92E+07
Decay Coefficient of Segment, k ($years^{-1}$), Section 6.3.3.1				7.30E+02
Total Load Reduction (CFU/year)				3.66E+12
Current Loading (CFU/year), Table 8.9				5.04E+12
Allowable Load (CFU/year)				1.38E+12

"Equivalent Load at Tidal (CFU/yr)" is the reduced loading at the downstream portion of the Aransas River Tidal, which is also given in Table 8A.3. "Concentration in Bay (CFU/m^3)" is the concentration of the bay based on each of the load reductions and is calculated using Equation 6.2, which is found in Section 6.3.2.2. The parameters for Copano Bay Segment 2 that were used to calculate this concentration are also listed in Table 8A.7. The load in the Bay was then calculated by using the following equation: "Concentration in Bay (CFU/m^3)" * "Cumulative Runoff, Q (m^3/yr)" to find the load equivalent in the Bay of the load reduction at each of the sources.

The load reductions that were accounted for at the Mission River outlet (Copano Bay Segment 3) are also shown in Figure 7A.19. The Mission River Tidal drains directly into Copano Bay Segment 3, and the only additional loadings to this portion of the Bay were avian. Since the avian loading cannot be reduced, the total load reduction applied at Segment 3 was the same load reduction that was found for the downstream portion of the Mission River Tidal, which is given in Table 8A.6. The load reduction that occurs at the

Copano Bay Mission River outlet (Copano Bay Segment 3) based on the upstream load reductions that were made is shown in Table 8A.8. Note that this load reduction was significantly more than what would be necessary to meet the oyster water use fecal coliform standards in Copano Bay.

Table 8A.8 Load Reduction Scenario #1 at Copano Bay Mission River Outlet, Segment 3

SchemaNode	Source	Equivalent Load at Tidal (CFU/yr)	Concentration in Bay (CFU/m^3)	Load in Bay (CFU/yr)
77	Livestock, us	6.81E+06	1.22E-04	3.36E+04
80	Livestock, us	9.57E+11	1.72E+01	4.72E+09
82	Livestock	9.48E+14	1.70E+04	4.68E+12
90	WWTP, us	1.23E+05	2.20E-06	6.05E+02
Cumulative Runoff. Q (m^3/yr), Section 6.3.3.4				2.75E+08
Volume of Copano Bay Segment, V (m^3), Section 6.3.3.3				7.60E+07
Decay Coefficient of Segment, k (years^{-1}), Section 6.3.3.1				7.30E+02
Total Load Reduction (CFU/year)				4.68E+12
Current Loading (CFU/year), Table 8.9				5.50E+12
Allowable Load (CFU/year)				8.18E+11

The total load reduction and allowable to Copano Bay was found by summing all the load reductions and current loadings from all four Copano Bay Segments. The load reductions, current loadings, and allowable loads necessary to meet fecal coliform standards for Load Reduction Scenario #1 are shown in Table 8A.9.

Table 8A.9 Load Reduction Scenario #1 at Copano Bay

Portion of Bay	Current Load (CFU/yr)	Load Reductions (CFU/yr)	Allowable Load (CFU/yr)
Aransas Outlet (Segment 2)	5.04E+12	3.66E+12	1.38E+12
Mission Outlet (Segment 3)	5.50E+12	4.68E+12	8.18E+11
Copano Creek Outlet (Segment 4)	1.46E+12	0.00E+00	1.46E+12
Watershed JunctionID Outlet (Segment 1)	5.06E+10	0.00E+00	5.06E+10
Total Load	1.20E+13	8.34E+12	3.70E+12

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Vita

Carrie Jo Gibson was born on April 15, 1981 in Bellevue, WA to her mother and father, Deborah Lynn Mohorovich and Terrence Lynn Gibson. She graduated from Lake Washington High School in June 2000, located in Kirkland, WA, with a 4.0 GPA while competing in varsity Track and Cross Country and taking honors and Advanced Placement (AP) courses. She then attended Gonzaga University in Spokane, WA with her twin sister, Kim, where she received her Bachelor's of Science degree in Civil Engineering May 9, 2004, maintaining a 3.91 GPA while competing in varsity Track and Cross Country.

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