Total Maximum Daily Loads of Fecal Bacteria for the Non-Tidal Georges Creek Basin in Garrett and Allegany Counties, Maryland

REVISED FINAL

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List of Abbreviations

ARCC	Average rates of correct classification
ARA	Antibiotic Resistance Analysis
BMP	Best Management Practice
BST	Bacteria Source Tracking
CAFO	Confined Animal Feeding Operations
cfs	Cubic Feet per Second
CFR	Code of Federal Regulations
CFU	Colony Forming Units
COMAR	Code of Maryland Regulations
CSO	Combined Sewer Overflow
CWA	Clean Water Act
CWP	Center for Watershed Protection
DNR	Department of Natural Resources
EPA	Environmental Protection Agency
GIS	Geographic Information System
LA	Load Allocation
MACS	Maryland Agricultural Cost Share Program
MDE	Maryland Department of the Environment
MDP	Maryland Department of Planning
ml	Milliliter(s)
MOS	Margin of Safety
MPN	Most Probable Number
MRLC	Multi-Resolution Land Cover
MPR	Maximum Practicable Reduction
MS4	Municipal Separate Storm Sewer System
MST	Microbial Source Tracking
NPDES	National Pollutant Discharge Elimination System
NRCS	National Resources Conservation Service
RCC	Rates of Correct Classification
SHA	State Highway Administration
SSO	Sanitary Sewer Overflows
STATSGO	State Soil Geographic
TARSA	Technical and Regulatory Services Administration
TMDL	Total Maximum Daily Load
USGS	United States Geological Survey
WSSC	Washington Suburban Sanitary Commission
WQIA	Water Quality Improvement Act
WLA	Wasteload Allocation
WQLS	Water Quality Limited Segment
WRAS	Watershed Restoration Action Strategy
WWTP	Wastewater Treatment Plan

EXECUTIVE SUMMARY

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in the non-tidal portion of Georges Creek (basin number 02-14-10-04). Section 303(d) of the federal Clean Water Act (CWA) and the EPA implementing regulations direct each state to identify and list waters, known as water quality limited segments (WQLSs), in which current required controls of a specified substance are inadequate to achieve water quality standards. For each WQLS, the state is required to either establish a Total Maximum Daily Load (TMDL) of the specified substance that the waterbody can receive without violating water quality standards, or demonstrate that water quality standards are being met.

The Maryland Department of the Environment (MDE) has identified the mainstem of Georges Creek, a designated Use IP waterbody (Water Contact Recreation, Protection of Aquatic Life and Public Water Supply), and all its tributaries, designated Use I waterbodies (Water Contact Recreation and Protection of Aquatic Life) [Code of Maryland Regulations (COMAR) 26.08.02.08R(b)] in the State's 303(d) List as impaired by sediments (1996), bacteria (fecal coliform) (2002), low pH (1998 & 2002) and impacts to biological communities (2002). This document proposes to establish a TMDL for fecal bacteria in Georges Creek and its tributaries that will allow for the attainment of the designated use primary contact recreation. The listings for sediments, low pH and impacts to biological communities will be addressed separately at a future date. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years was considered.

To establish baseline and allowable pollutant loads for this TMDL, a flow duration curve approach, using flow strata estimated from United States Geological Survey (USGS) daily flow monitoring data and bacteria monitoring data, was used. The sources of fecal bacteria are estimated at four representative stations in the Georges Creek watershed where samples were collected for one year. Multiple antibiotic resistance analysis (ARA) source tracking was used to determine the relative proportion of domestic (pets and human associated animals), human (human waste), livestock (agricultural related animals), and wildlife (mammals and waterfowl) source categories.

The allowable load is determined by estimating a baseline load from current monitoring data. The baseline load is estimated using a long-term geometric mean and weighting factors from the flow duration curve. The TMDL load for fecal bacteria entering Georges Creek is established after considering four different hydrological conditions: high flow and low flow annual conditions; and high flow and low flow seasonal conditions (the period between May 1st and September 30th where water contact recreation is more prevalent). This allowable load is reported in the units of Most Probable Number (MPN)/day and represents a long-term load estimated over a variety of hydrological conditions and not a literal daily limit.

Two scenarios were developed; the first assessing whether attainment of current water quality standards could be achieved with maximum practicable reductions (MPRs) applied, and the second requiring higher maximum reductions. Scenario solutions were based on an optimization

method where the objective was to minimize the overall risk to human health, assuming that the risk varies over the four bacteria source categories. In the four subwatersheds of Georges Creek, it was estimated that water quality standards could not be attained with the MPRs. Thus, a second scenario allowing greater reductions, which may not be feasible, was applied.

The fecal bacteria TMDL developed for the Georges Creek watershed is 479.7 billion MPN *E. coli*/day. The TMDL is distributed between load allocation (LA) for nonpoint sources and waste load allocations (WLA) for point sources, including National Pollutant Discharge Elimination System (NPDES) wastewater treatment plants (WWTPs) and NPDES combined sewer overflows (CSOs). The LA is 476.8 billion *E. coli* MPN/day. The WWTP WLA is 2.9 billion *E. coli* MPN/day and the CSO WLA is 0.0 billion *E. coli* MPN/day. The margin of safety (MOS) has been incorporated using a conservative assumption by estimating the loading capacity of the stream based on a more stringent water quality endpoint concentration. The *E. coli* water quality criterion concentration was reduced by 5%, from 126 MPN/100ml to 119.7 MPN/100ml.

Once the EPA has approved a TMDL, and it is known what measures must be taken to reduce pollution levels, implementation of best management practices (BMPs) is expected to take place. MDE intends for the required reduction to be implemented in an iterative process that first addresses those sources with the largest impacts to water quality and creating the greatest risks to human health, with consideration given to ease and cost of implementation. In addition, follow up monitoring plans will be established to track progress and to assess the implementation efforts. As previously stated, water quality standards cannot be attained in the Georges Creek subwatersheds, using the MPR scenario. This may occur in subwatersheds where wildlife is a significant component or in subwatersheds that require very high reductions of fecal bacteria loads to meet water quality standards. In these cases, it is expected that the first stage of TMDL implementation will be to implement the MPR scenario. MDE cannot provide EPA reasonable assurance at this time that the TMDL allocations can be met, given the magnitude of the LA allocation and known efficiencies for relevant urban Best Management Practices. However, progress will be made through the iterative implementation process described above and the situation will be reevaluated in the future.

1.0 INTRODUCTION

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in Georges Creek (basin number 02-14-10-04). Section 303(d)(1)(C) of the federal Clean Water Act (CWA) and the EPA implementing regulations direct each state to develop a TMDL for each impaired water quality limited segment (WQLS) on the Section 303(d) List, taking into account seasonal variations and a protective margin of safety (MOS) to account for uncertainty. A TMDL reflects the total pollutant loading of the impairing substance a water body can receive and still meet water quality standards.

TMDLs are established to achieve and maintain water quality standards. A water quality standard is the combination of a designated use for a particular body of water and the water quality criteria designed to protect that use. Designated uses include activities such as swimming, drinking water supply, and shellfish propagation and harvest. Water quality criteria consist of narrative statements and numeric values designed to protect the designated uses. Criteria may differ among waters with different designated uses.

The Maryland Department of the Environment (MDE) has identified the mainstem of Georges Creek, a designated Use I-P waterbody (Water Contact Recreation, Protection of Aquatic Life and Public Water Supply), and all its tributaries, designated Use I waterbodies (Water Contact Recreation and Protection of Aquatic Life) [Code of Maryland Regulations (COMAR) 26.08.02.08R(b)] in the State's 303(d) List as impaired by sediments (1996), bacteria (fecal coliform) (2002), low pH (1998 & 2002) and impacts to biological communities (2002). This document proposes to establish a TMDL for fecal bacteria in Georges Creek and its tributaries that will allow for the attainment of the designated use primary contact recreation. The listings for sediments, low pH and impacts to biological communities will be addressed separately at a future date. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years was considered.

Fecal bacteria are microscopic single-celled organisms (primarily fecal coliforms and fecal streptococci) found in the wastes of warm-blooded animals. Their presence in water is used to assess the sanitary quality of water for body-contact recreation, for consumption of molluscan bivalves (shellfish), and for drinking water. Excessive amounts of fecal bacteria in surface water used for recreation are known to indicate an increased risk of pathogen-induced illness to humans. Infections due to pathogen-contaminated recreation waters include gastrointestinal, respiratory, eye, ear, nose, throat, and skin diseases (EPA, 1986).

In 1986, EPA published "Ambient Water Quality Criteria for Bacteria" in which three indicator organisms were assessed to determine their correlation with swimming-associated illnesses. Fecal coliform, *E. coli* and enterococci were the indicators used in the analysis. Fecal coliform are a subgroup of total coliform bacteria and *E. coli* are a subgroup of fecal coliform. Although most *E. coli* are harmless and are found in great quantities in the intestines of people and warm-blooded animals, certain pathogenic strains may cause illness. Enterococci are a subgroup of bacteria in the fecal streptococcus group. Fecal coliform, *E. coli* and enterococci can all be classified as fecal bacteria. The results of the EPA study (EPA, 1986) demonstrated that fecal

coliform showed less correlation to swimming-associated gastroenteritis than either *E. coli* or enterococci.

The Georges Creek watershed was listed on the Maryland 303(d) List using fecal coliform as the indicator organism. Based on EPA's guidance (EPA, 1986), adopted by Maryland in 2004, the State has revised the bacteria water quality criteria and it is now based on water column limits for either *E. coli* or enterococci. Because multiple monitoring datasets are available within this watershed for various pathogen indicators, the general term fecal bacteria will be used to refer to the impairing substance throughout this document. The TMDL will be based on the pathogen indicator organisms specified in Maryland's current bacteria water quality criteria, either *E. coli* or enterococci. The indicator organism used in the Georges Creek TMDL analysis was *E. coli*.

2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

Location

The Georges Creek watershed encompasses 47,694 acres (75 square miles) in Allegany and Garrett Counties (See Figure 2.1.1). The headwaters of Georges Creek begin in Frostburg, Maryland. The mainstem of Georges Creek flows southwest until its confluence with the North Branch Potomac River below the town of Westernport, Maryland. Several tributaries feed the mainstem of Georges Creek including Elklick Run, Mill Run, Winebrenner Run and Koontz Run. The drainage area for the watershed lies between Dans Mountain and Big Savage Mountain. Towns within the watershed area include: Frostburg, Midlothian, Midland, Lonaconing, Barton, Luke, and Westernport. Dans Mountain State Park and portions of the Savage River State Forest also lie within the Georges Creek watershed.

Geology/Soils

The Georges Creek watershed lies in the Appalachian Plateaus Province, draining to the North Branch Potomac River. The bedrock of this region consists principally of gently folded shale, siltstone, and sandstone. Folding has produced elongated arches across the region, which exposes Devonian rocks at the surface. Most of the natural gas fields in Maryland are associated with these anticlinal folds in the Appalachian Plateau. In the intervening synclinal basins, coal-bearing strata of Pennsylvanian and Permian ages are preserved. The topography in the watershed is often steep and deeply carved by winding streams, with elevations ranging up to 3,360 feet at the peak of Backbone Mountain, which is the highest point in Maryland.

The Georges Creek watershed lies predominantly in the Dekalb soil series. A small portion of the watershed in the southeastern region lies in the Hazleton soil series. The Dekalb soil series consists of moderately deep, well-drained, loamy soils that developed in material weathered in place from sandstone and some conglomerate and shale bedrock. These nearly level to very steep soils are normally found in stony, mountainous regions. Dekalb soils have rapid permeability and internal drainage. The Hazleton soil series consists of deep, well-drained, loamy soils. These soils developed in materials weathered in place from sandstone and shale bedrock. These nearly level to moderately steep soils occur on the top and upper and middle side slopes of hills and mountains. Hazleton soils have moderately rapid permeability and rapid internal drainage (Allegany County, Maryland Soil Conservation Service, 1977). The spatial distributions for each soil series are shown in Figure 2.1.2.

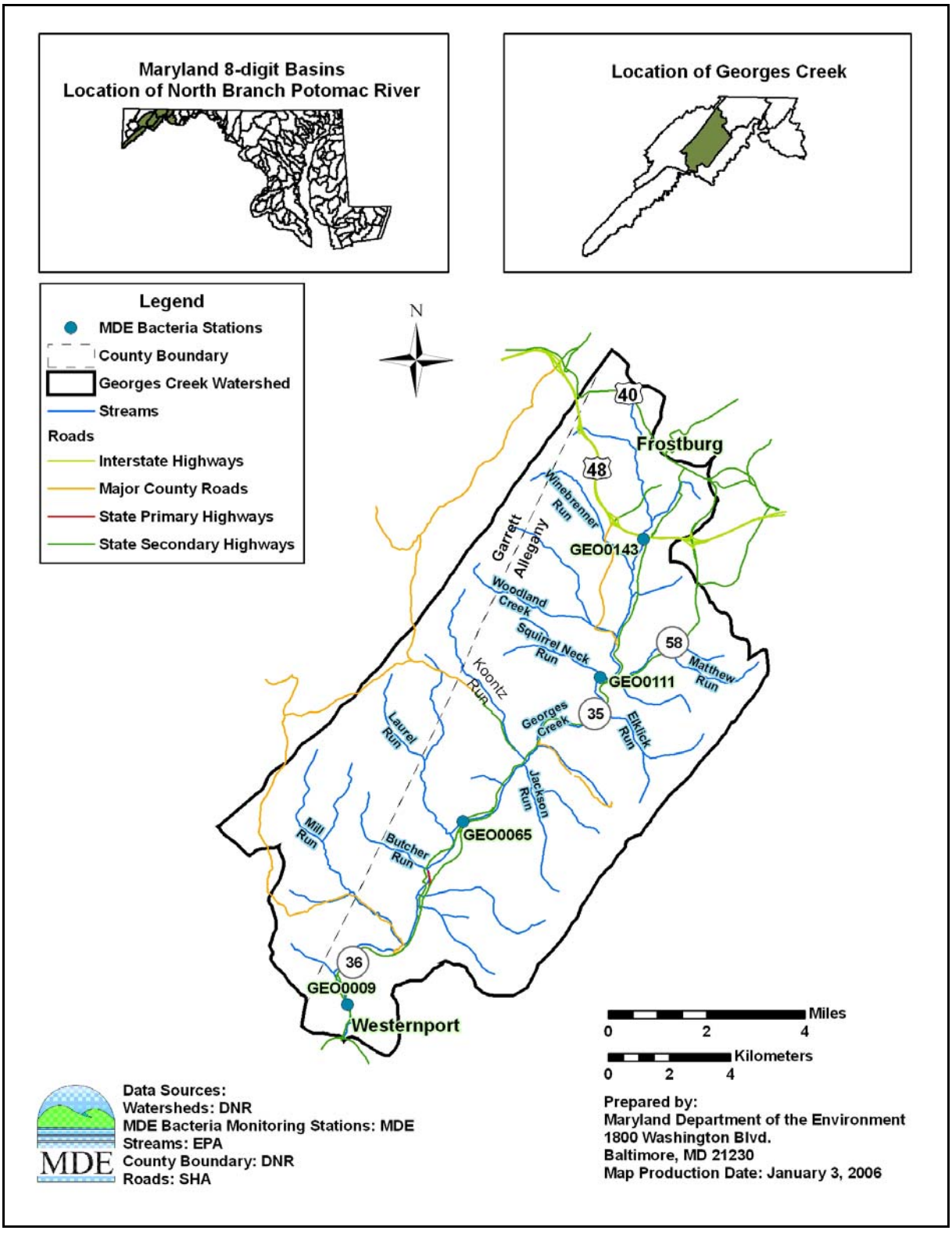

Figure 2.1.1: Location Map of the Georges Creek Watershed

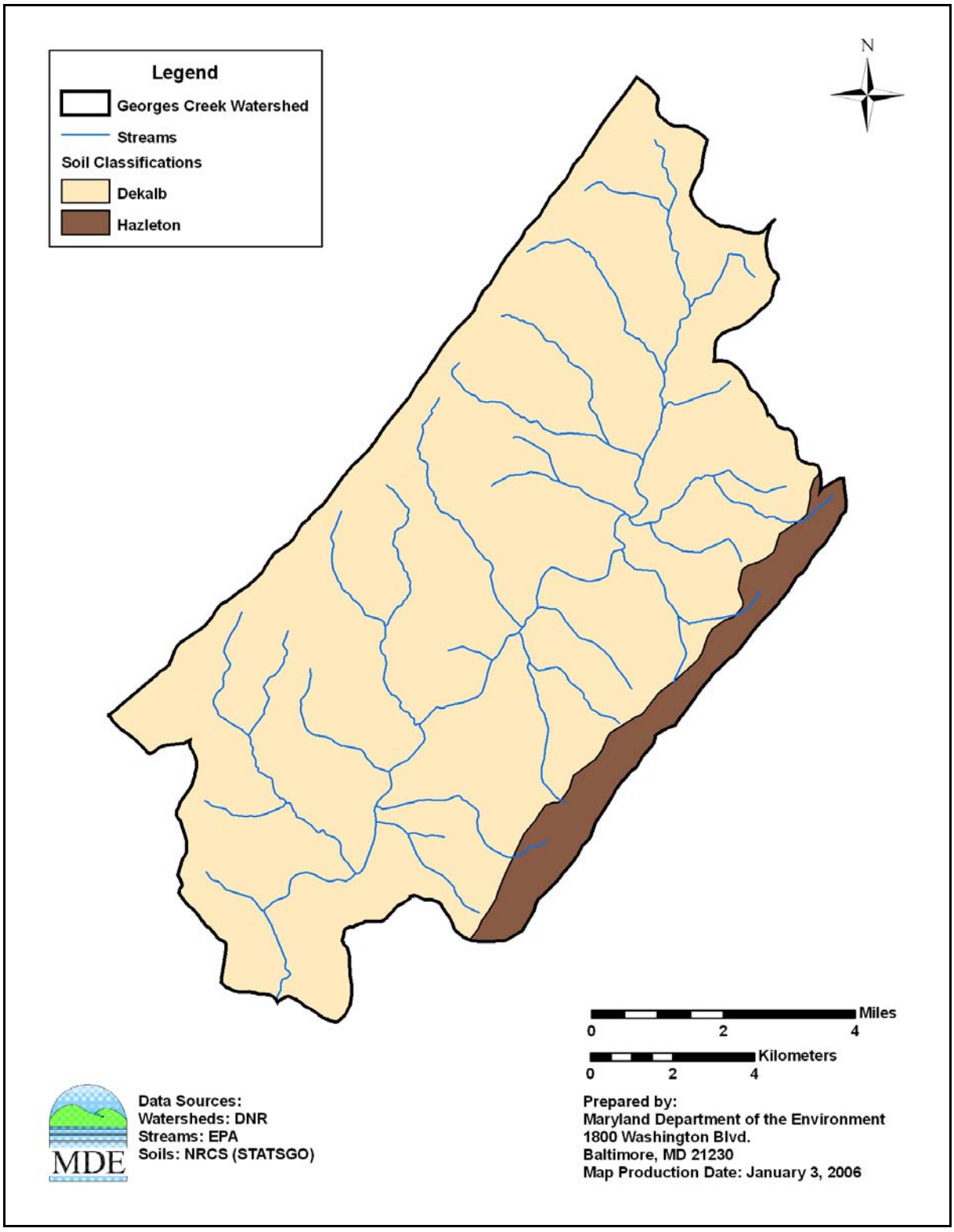

Figure 2.1.2: General Soil Series in the Georges Creek Watershed

Land Use

The 2002 Maryland Department of Planning (MDP) land use/land cover data shows that the Georges Creek watershed is characterized as primarily forested. There are 34,210 acres (53.5 square miles) of park and forest lands evenly dispersed throughout the watershed, such as the Savage River State Forest and Dans Mountain State Park. The watershed contains 3,911 acres (6.1 square miles) of residential land use and 3,528 acres (5.5 square miles) of commercial land use, which are located primarily in the city of Frostburg, town of Westernport and along the main branch of Georges Creek. Crops and pasture lands are dispersed through out the watershed. Total crops and pasture areas constitute 2,110 (4 square miles) and 3,923 acres (8 square miles), respectively. The land use percentage distribution for the Georges Creek watershed is shown in Table 2.1.1, and spatial distributions for each land use are shown in Figure 2.1.3.

Table 2.1.1: Land Use Percentage Distribution for Georges Creek Watershed

Land Type	Acreage	Percentage
Forest	34,210	72%
Residential	3,911	8%
Commercial	3,528	8%
Crops	2,110	4%
Pasture	3,923	8%
Water	12	0%
Totals	**47,694**	**100%**

Population

The total population in the Georges Creek watershed is estimated to be 13,603. Figure 2.1.4 displays the population density in the watershed. The human population and the number of households were estimated based on a weighted average from the Geographic Information System (GIS) 2000 Census Block and the 2002 MDP land use cover. Since the Georges Creek watershed is a sub-area of the Census Block, the GIS tool was used to extract the areas from the 2000 Census Block within the watershed. Based on the land use for residential density (low, medium, high) from the MDP land use cover, the number of dwellings per acre was calculated using Table 2.1.2 in the Georges Creek watershed.

Table 2.1.2: Number of Dwellings Per Acre

Land use Code	Dwellings Per Acre
11 Low Density Residential	1
12 Medium Density Residential	5
13 High Density Residential	8

Based on the number of households from the total population from the Census Block and the number of dwellings per acre from the MDP land use cover, population per subwatershed was calculated (Table 2.1.3).

Table 2.1.3: Total Population Per Subwatershed in Georges Creek Watershed

Subwatershed	Population	Dwellings
GEO0009	2,000	2,085
GEO0065	2,560	2,780
GEO0111	1,901	2,368
GEO0143	7,142	3,885
Total	13,603	11,118

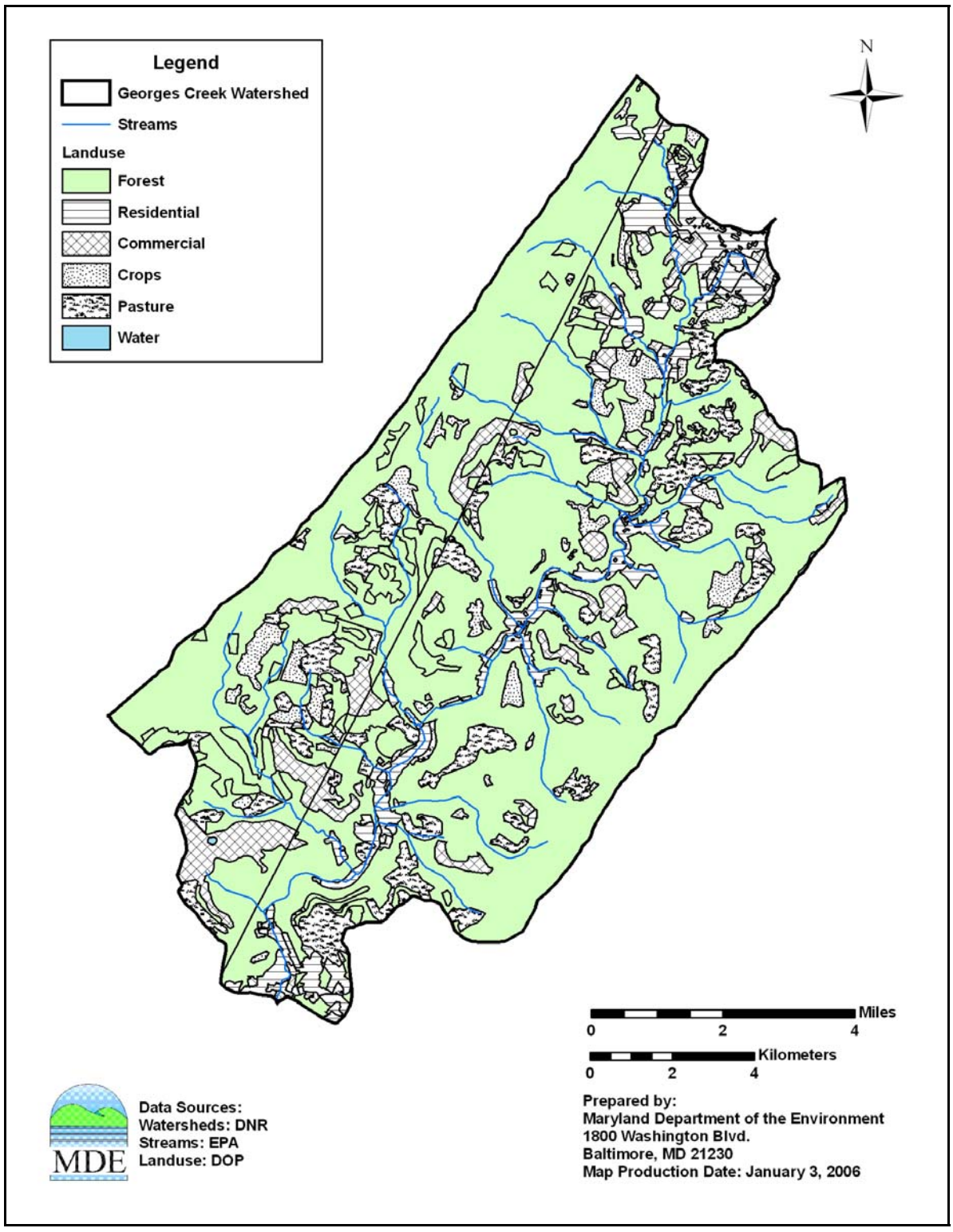

Figure 2.1.3: Land Use of the Georges Creek Watershed

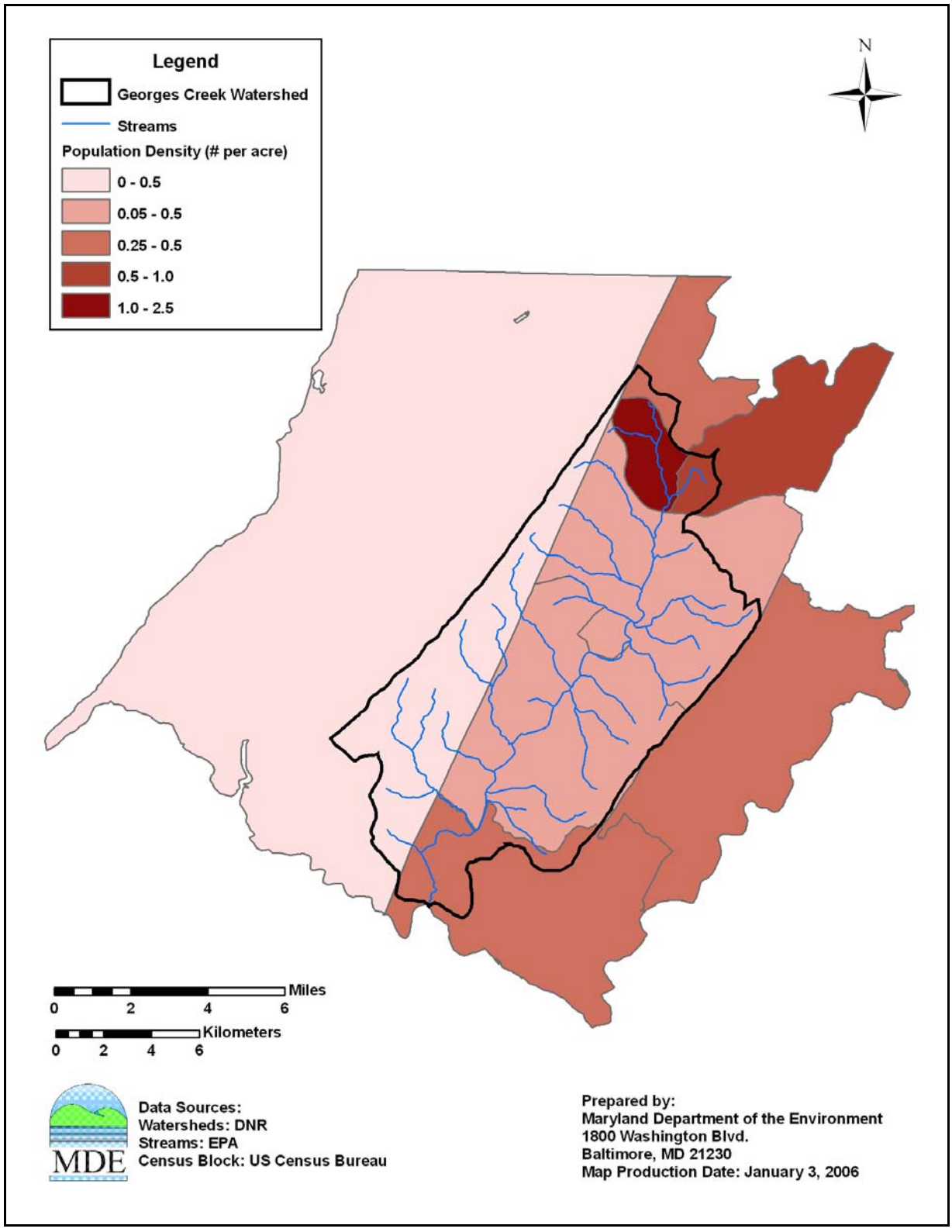

Figure 2.1.4: Population Density in Georges Creek Watershed

2.2 Water Quality Characterization

From EPA's guidance document "Ambient Water Quality Criteria for Bacteria" (1986), fecal bacteria, *E. coli*, and enterococci were assessed as indicator organisms for predicting human health impacts. A statistical analysis found that the highest correlation to gastrointestinal illness was linked to elevated levels of *E. coli* and enterococci in fresh water (enterococci in salt water), leading EPA to propose that states use *E. coli* or enterococci as pathogen indicators.

Pursuant to EPA's guidance, Maryland has adopted the new indicator organisms, *E. coli* and enterococci, for the protection of public health in Use I, II, and IV waters. These bacteria listings were originally assessed using fecal coliform bacteria. The assessment was based on a geometric mean of the monitoring data, where the result could not exceed a geometric mean of 200 MPN/100ml. From EPA's analysis (USEPA, 1986), this fecal coliform geometric mean target equates to an approximate risk of 8 illnesses per 1,000 swimmers at fresh water beaches and 19 illnesses per 1,000 swimmers at marine beaches (enterococci only), which is consistent with MDE's revised Use I bacteria criteria. Therefore the original 303(d) List fecal coliform listings can be addressed using the refined bacteria indicator organisms to ensure that risk levels are acceptable.

Bacteria Monitoring

Table 2.2.1 lists the historical monitoring data for the Georges Creek watershed. Monitoring Station GEO0009 (CORE) was used by the Maryland Department of Natural Resources (DNR) to identify the bacterial impairment. MDE conducted bacteria monitoring at four stations from October 2002 through October 2003. In addition to the bacteria monitoring stations, there is one United States Geological Survey (USGS) gauging station located in the Georges Creek watershed that was used in deriving the stream flow in Georges Creek. The locations of these stations are shown in Table 2.2.2 – Table 2.2.4 and Figure 2.2.1. Observations recorded during 2002-2003 from the four MDE monitoring stations are shown in Appendix A.

Bacteria counts are highly variable in Georges Creek. This is typical for all streams due to the nature of bacteria and its relationship to flow. Results of bacteria counts for the four monitoring stations are shown in Appendix A. Data were collected from September 2002 through November 2003. Bacteria counts ranged between 10 and 155,307 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the Georges Creek Watershed

Sponsor	Location	Date	Design	Summary
DNR - Core Monitoring	MD	1/18/95 to 12/14/99	Fecal Coliform*	GEO0009: Georges Creek north of Town of Westernport
MDE	MD	10/02 to 10/03	*E. coli*	4 station Enumeration 2x per month
MDE	MD	10/02 to 10/03	BST (Enterococci)*	Bacteria Source Tracking (BST) - Antibiotic Resistance Analysis (ARA) 4 stations 1 sample per month

*Only *E. coli* was used for this analysis.

Table 2.2.2: Locations of DNR (CORE) Monitoring Station in the Georges Creek Watershed

Monitoring Station	Observation Period	Total Observations	LATITUDE Decimal Degrees	LONGITUDE Decimal Degrees
GEO0009	1/18/95 - 12/14/99	60	39.4940	-79.0448

Table 2.2.3: Locations of MDE Monitoring Stations in the Georges Creek Watershed

Monitoring Station	Observation Period	Total Observations	LATITUDE Decimal Degrees	LONGITUDE Decimal Degrees
GEO0009	2002-2003	25	39.4940	-79.0448
GEO0065	2002-2003	25	39.5487	-79.0024
GEO0111	2002-2003	25	39.5920	-78.9514
GEO0143	2002-2003	25	39.6330	-78.9361

Table 2.2.4: Locations of USGS Gauging Stations in Georges Creek Watershed

Monitoring Station	Observation Period	Total Observations	LATITUDE Decimal Degrees	LONGITUDE Decimal Degrees
1599000	1988-2004	6164	39.4940	-79.0448

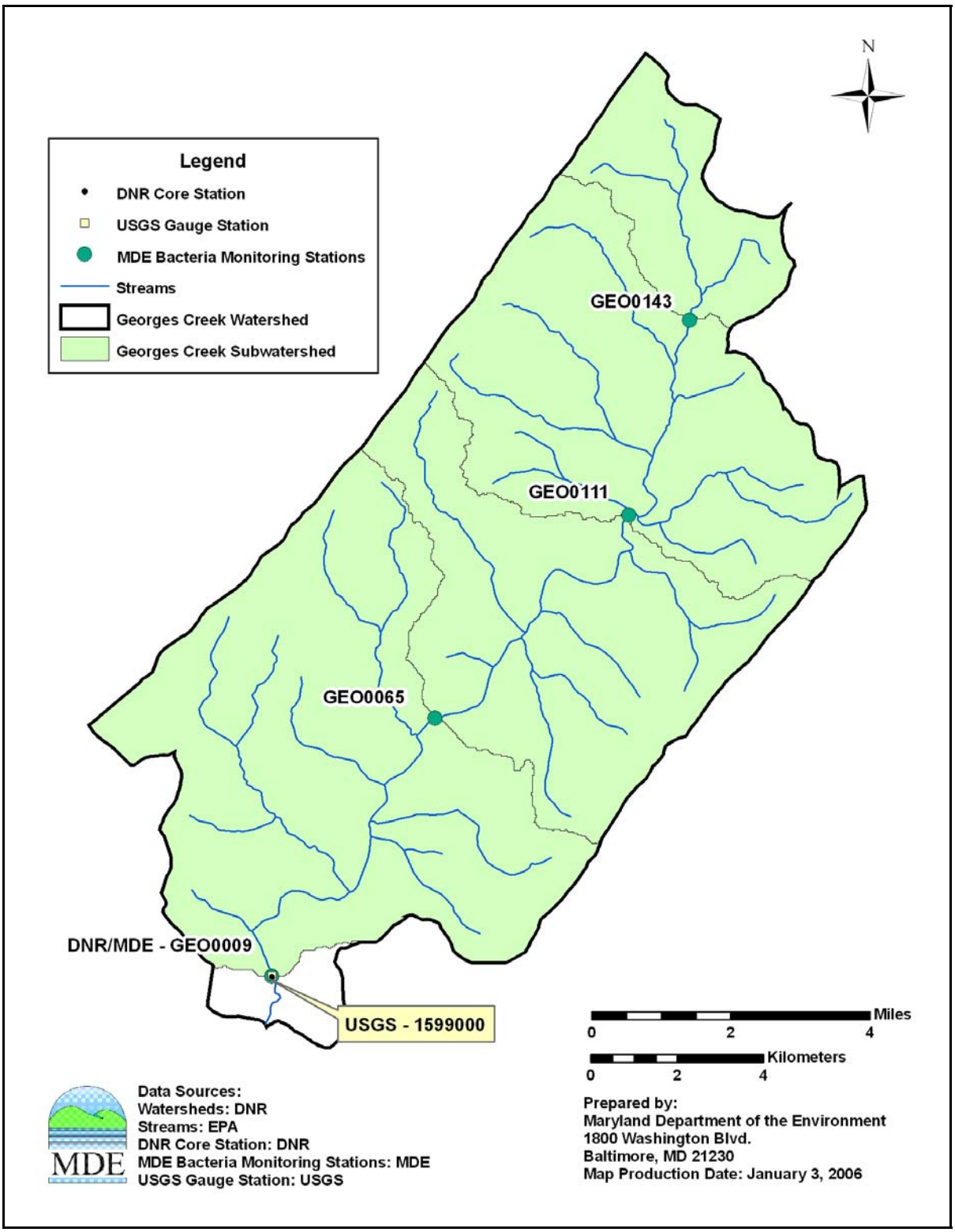

Figure 2.2.1: Monitoring Stations in the Georges Creek Watershed

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The Maryland water quality standards Surface Water Use Designations for the Georges Creek watershed are Use I-P (Water Contact Recreation, Protection of Aquatic Life and Public Water Supply) for the mainstem of Georges Creek, and Use I (Water Contact Recreation and Protection of Aquatic Life) for all its tributaries [Code of Maryland Regulations (COMAR) 26.08.02.08R(b)]. Georges Creek has been included on the final 2004 Integrated 303(d) List as impaired by sediments (1996), bacteria (fecal coliform) (2002), low pH (1998 & 2002) and impacts to biological communities (2002).

Water Quality Criteria

The State water quality standard for bacteria (*E. coli*) used in this study is as follows (COMAR Section 26.08.02.03-3):

Table 2.3.1: Bacteria Criteria Values from Table 1 COMAR 26.08.02.03-3 Water Quality Criteria Specific to Designated Uses.

Indicator	**Steady State Geometric Mean Indicator Density**
Freshwater	
E. coli	126 MPN/100ml

Interpretation of Bacteria Data for General Recreational Use

The relevant portion (for freshwater) of the listing methodology pursuant to the 2006 integrated 303(d) List for all Use Waters - Water Contact Recreation and Protection of Aquatic Life is as follows:

Recreational Waters

A steady-state geometric mean will be calculated with available data where there are at least five representative sampling events. The data shall be from samples collected during steady-state conditions and during the beach season (Memorial Day through Labor Day) to be representative of the critical condition. If the resulting steady state geometric mean is greater than 126 cfu/100 ml *E. coli* in freshwater, the waterbody will be listed as impaired. If fewer than five representative sampling events for an area being assessed are available, data from the previous two years will be evaluated in the same way. The single sample maximum criterion applies only to beaches and is to be used for closure and advisory decisions based on short term exceedances of the geometric mean portion of the standard.

Water Quality Assessment

Water quality impairment in Georges Creek was assessed by comparing both the annual and the seasonal (May 1st – September 30th) steady state geometric means of *E. coli* concentrations with the water quality criterion. The steady state condition is defined as unbiased sampling targeting average flow conditions and/or equally sampling or providing for unbiased sampling of high and low flows. The 1986 EPA criteria document assumed steady state flow in determining the risk at various bacterial concentrations, and therefore the chosen criterion value also reflects steady state conditions (EPA, 1986). The steady state geometric mean condition can be estimated either by monitoring design or more practically by statistical analysis as follows:

1. A stratified monitoring design is used where the number of samples collected is proportional to the duration of high flows, mid flows and low flows within the watershed. This sample design allows a geometric mean to be calculated directly from the monitoring data.

2. Routine monitoring typically results in samples from varying hydrologic conditions (*i.e.*, high flows, mid flows and low flows) where the numbers of samples are not proportional to the duration of those conditions. Averaging these results without consideration of the sampling conditions results in a biased estimate of the steady state geometric mean. The potential bias of the steady state geometric means can be reduced by weighting the samples results collected during high flow, mid flow and low flow regimes by the proportion of time each flow regime is expected to occur. This ensures that the high flow and low flow conditions are proportionally balanced on an annual and seasonal basis.

3. If (1) the monitoring design was not stratified based on flow regime or (2) flow information is not available to weight the samples accordingly, then a geometric mean of sequential monitoring data can be used as an estimate of the steady state geometric mean condition for the specified period.

A routine monitoring design was used to collect bacteria data in the Georges Creek watershed. To estimate the steady state geometric means, the monitoring data were first reviewed by plotting the sample results versus their corresponding daily flow duration percentile. Graphs illustrating these results can be found in Appendix B.

To calculate the steady state geometric means with routine monitoring data, a conceptual model was developed by dividing the daily flow frequency for the stream segment into strata that are representative of hydrologic conditions. A conceptual continuum of flows is illustrated in Figure 2.3.1.

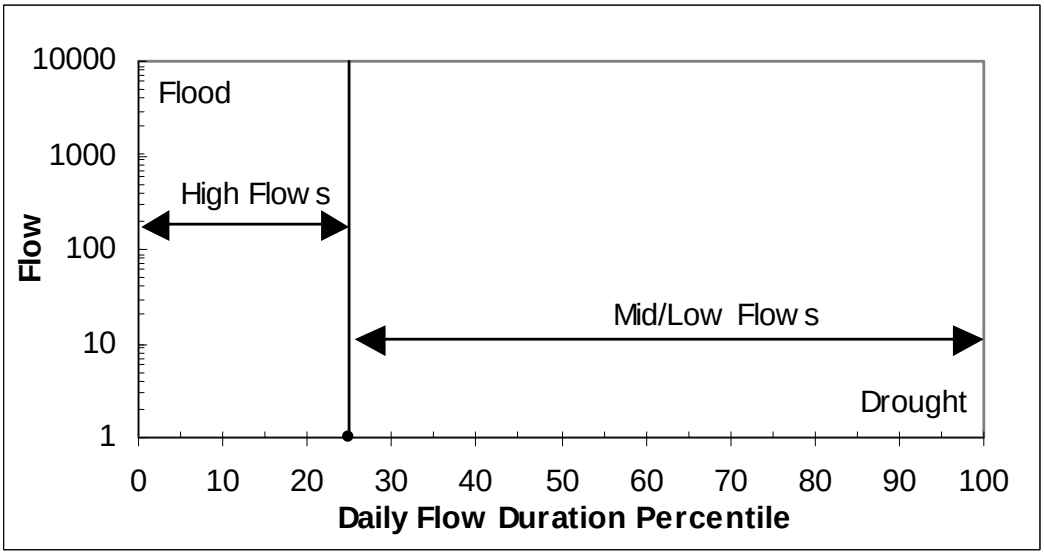

Figure 2.3.1: Conceptual Diagram of Flow Duration Zones

During high flows a significant portion of the total stream flow is from surface flow contributions. Low flow conditions represent periods with minimal rainfall and surface runoff. There is typically a transitional period (mid flows) between the high and low flow durations that is representative of varying contributions of surface flow inputs that result from differing rainfall volumes and antecedent soil moisture conditions. The division of the entire flow regime into strata enables the estimation of a less biased geometric mean from routine monitoring data that more closely approaches steady state. Based on a flow analysis of several watersheds throughout Maryland, it was determined that flows within the 25th to 30th daily flow duration percentiles were representative of average daily flows. It is assumed for this analysis that flows above the 25th percentile represent high flows and flows below the 25th percentile represent mid/low flows. A detailed method of how the flow strata were defined is presented in Appendix B.

Factors for estimating a steady state geometric mean are based on the frequency of each flow stratum. The weighting factor accounts for the proportion of time that each flow stratum represents. The weighting factors for an average hydrological year used in the Georges Creek TMDL analysis are presented in the following table (Table 2.3.2).

Table 2.3.2: Weighting factors for Average Hydrology Year Used for Estimation of Geometric Means in the Georges Creek Watershed (Average Hydrology Year)

Flow Duration Zone	Duration Interval	Weighting Factor
High Flows	0 – 25%	0.25
Mid/Low Flows	25 – 100%	0.75

Bacteria enumeration results for samples within a specified flow stratum will receive their corresponding weighting factor. The steady state geometric mean is calculated as follows:

$$M = \sum_{i=1}^{2} M_i * W_i \qquad (1)$$

where

$$M_i = \frac{\sum_{j=1}^{n_i} \log_{10}(C_{i,j})}{n_i} \qquad (2)$$

M = log weighted mean
Mi = log mean concentration for stratum i
Wi = Proportion of stratum i
Ci,j = Concentration for sample j in stratum i
n_i = number of samples in stratum i

Finally the steady state geometric mean concentration is estimated using the following equation:

$$C_{gm} = 10^{M} \qquad (3)$$

Cgm = Steady state geometric mean concentration

Tables 2.3.3 and 2.3.4 present the maximum and minimum concentrations by stratum, geometric means by stratum and the overall steady state geometric mean for the Georges Creek subwatersheds for the annual and the seasonal (May 1st –September 30th) periods.

Table 2.3.3: Georges Creek Annual Steady State Geometric Mean by Stratum per Subwatersheds

Station	Flow Stratum	# Samples	*E. coli* Minimum (MPN/100ml)	*E. coli* Maximum (MPN/100ml)	Annual Steady State Geometric Mean (MPN/100ml)	Annual Overall Geometric Mean (MPN/100ml)
GEO0009	High	9	576	24,192	5053	650
	Low	16	10	3,076	328	
GEO0065	High	9	52	676	193	232
	Low	16	10	5,172	247	
GEO0111	High	9	10	529	158	98
	Low	16	10	1,515	83	
GEO0143	High	9	122	155,307	4943	748
	Low	16	20	24,192	399	

Table 2.3.4: Georges Creek Seasonal (May 1st-September 30th) Period Steady State Geometric Mean by Stratum per Subwatersheds

Station	Flow Stratum	# Samples	*E. coli* Minimum (MPN/100ml)	*E. coli* Maximum (MPN/100ml)	Annual Steady State Geometric Mean (MPN/100ml)	Annual Overall Geometric Mean (MPN/100ml)
GEO0009	High	4	576	12,033	4,192	1,328
	Low	6	240	3,076	905	
GEO0065	High	4	243	676	342	778
	Low	6	464	5,172	1,024	
GEO0111	High	4	246	350	309	244
	Low	6	96	583	225	
GEO0143	High	4	2,382	155,307	22,450	3,141
	Low	6	228	24,192	1,630	

2.4 Source Assessment

Nonpoint Source Assessment

Nonpoint sources of fecal bacteria do not have one discharge point but occur over the entire length of a stream or waterbody. Many types of nonpoint sources introduce fecal bacteria to the land surface, including the manure spreading process, direct deposition from livestock during the grazing season, and excretions from pets and wildlife. As runoff occurs during rain events, surface runoff transports water and fecal bacteria over the land surface and discharges to the stream system. The deposition of non-human fecal bacteria directly to the stream occurs when livestock or wildlife have direct access to the waterbody. Nonpoint source contributions from human activities generally arise from failing septic systems and their associated drain fields or leaking infrastructure (*i.e.*, sewer systems). In summary, the transport of fecal bacteria from the land surface to the stream system is dictated by the rainfall, soil type, land use, and topography of the watershed.

Sewer Systems

Sanitary sewer overflows (SSOs) occur when the capacity of a sanitary sewer is exceeded. There are several factors that may contribute to SSOs from a sewer system, including pipe capacity, operations and maintenance effectiveness, sewer design, age of system, pipe materials, geology and building codes. SSOs are prohibited by the facilities' permits and therefore must be reported to MDE's Water Management Administration pursuant to COMAR 26.08.10 to be addressed under the State's enforcement program.

The Georges Creek wastewater treatment plant (WWTP), located north of Westernport, Maryland is the only municipal treatment plant in the Georges Creek watershed. This WWTP serves most sewered areas within the watershed. The town of Westernport conveys its wastewater to the Upper North Branch Commission WWTP and the Town of Frostburg delivers its sewage to the City of Cumberland through the Allegany County Sanitary Commission and the LaVale Sanitary Commission conveyance systems. The sewer collection systems within the Georges Creek watershed are combined sewer systems (CSSs), receiving stormwater as well as wastewater. The CSSs service only 11% (5,168 acres) of the watershed, primarily along the main stem of the Georges Creek and the city of Frostburg and town of Westernport. Figure 2.4.1 displays the sewer service area in the Georges Creek watershed.

There were a total of eight SSO events reported between October 2002 and October 2003. Approximately 28,330,000 gallons of SSO discharge were released through various waterways (surface water, groundwater, sanitary sewers, etc.) in the Georges Creek main stem and tributaries (MDE, Water Management Administration). Figure 2.4.2 depicts the location where SSOs occurred during 2002 and 2003 in the Georges Creek watershed.

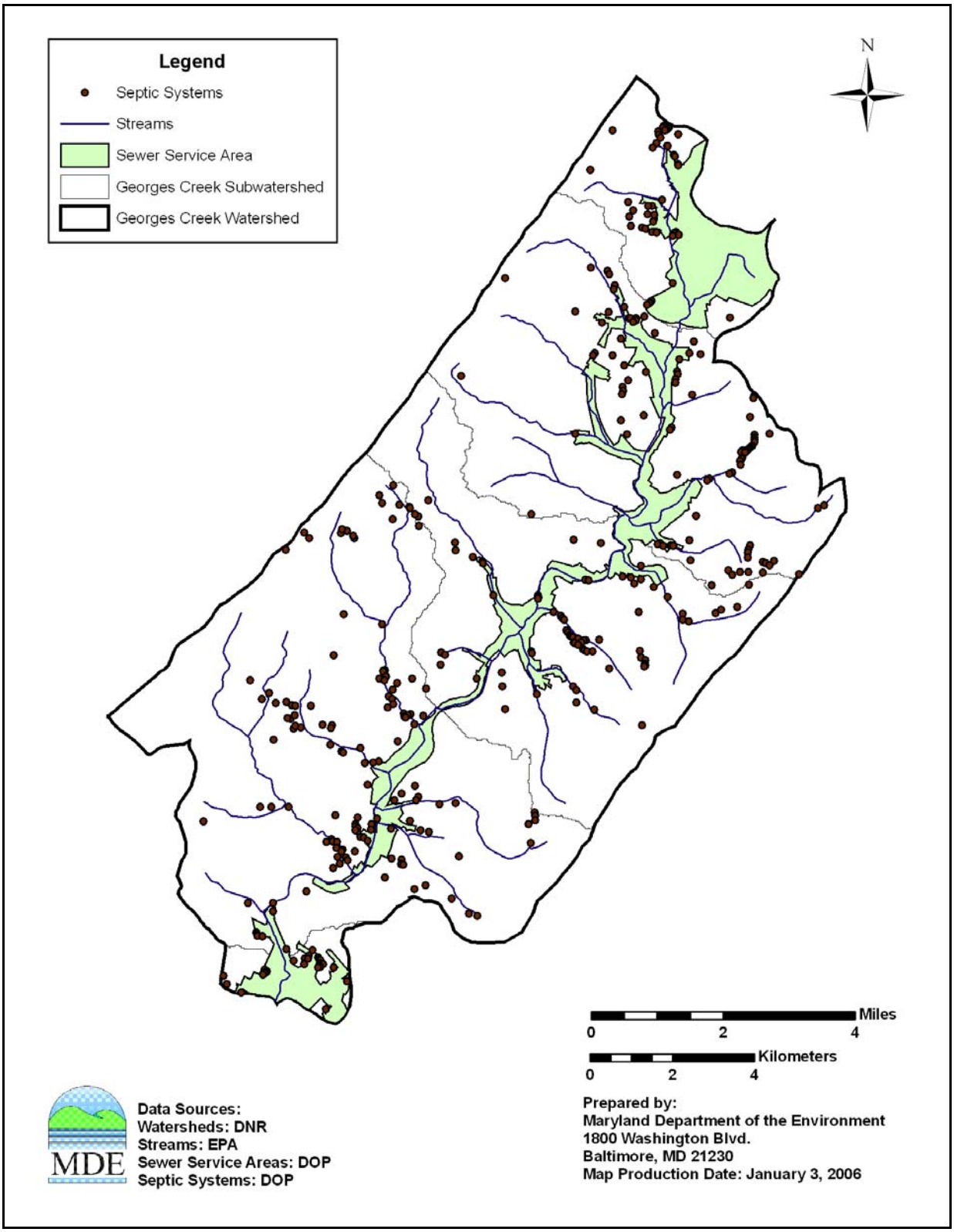

Figure 2.4.1: Sanitary Sewer Service Area and Septics in the Georges Creek Watershed

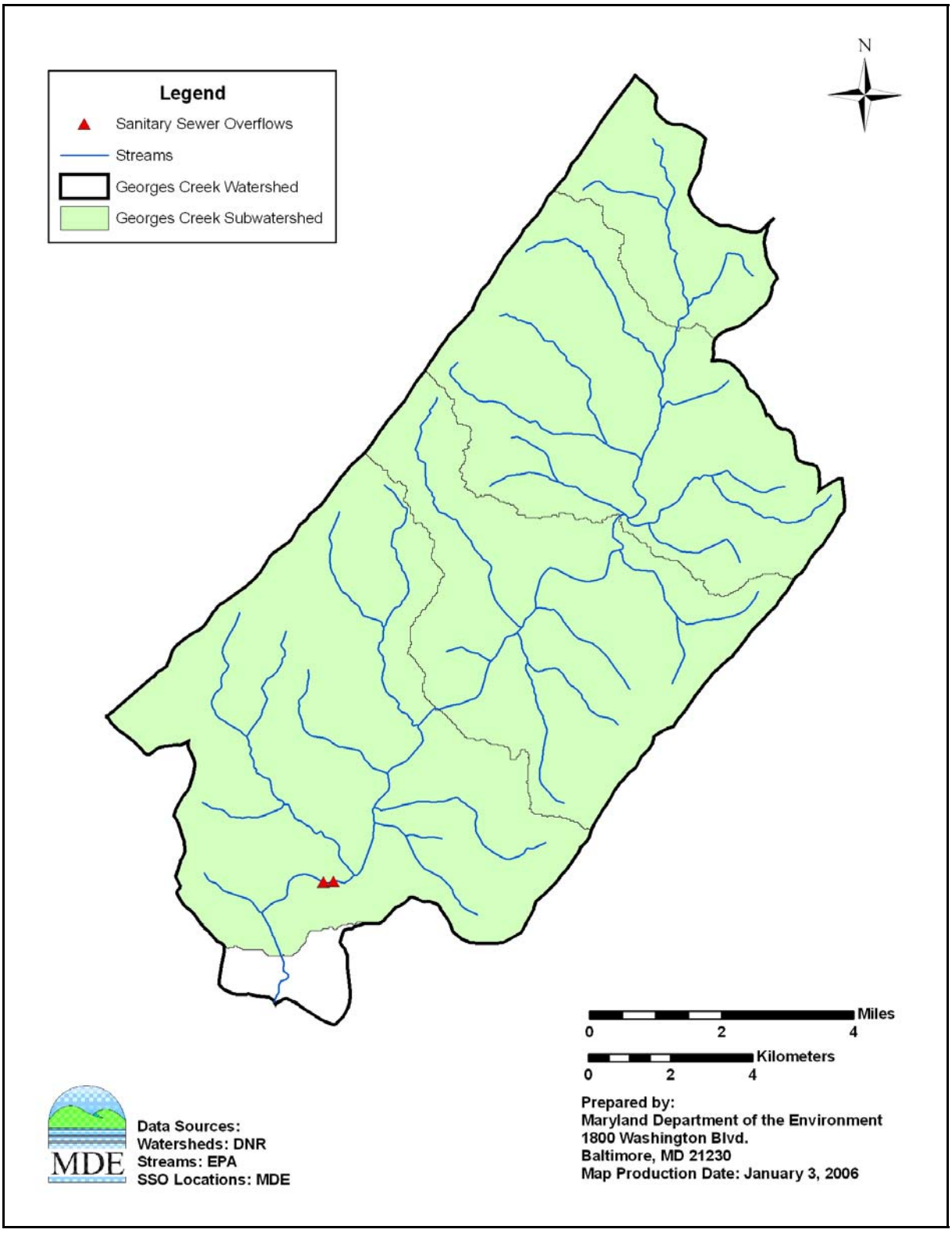

Figure 2.4.2: Location of Sanitary Sewer Overflows in the Georges Creek Watershed

Septic Systems

Several septic systems are located throughout the watershed in areas where no sewer service exists (See Figure 2.4.1). Table 2.4.1 displays the number of septic systems and households per subwatershed.

Table 2.4.1: Septic Systems and Households per Subwatershed in Georges Creek Watershed

Subwatershed Station	Septics Systems (units)	Households per Subwatershed
GEO0009	130	2085
GEO0065	78	2780
GEO0111	96	2368
GEO0143	46	3885

Point Source Assessment

Stormwater

The Georges Creek watershed is located within Allegany and Garrett Counties. These jurisdictions have no NPDES Municipal Separate Storm Sewer (MS4) permits to regulate stormwater discharges.

Municipal and Industrial WWTPs

There is only one municipal treatment plant in the Georges Creek watershed, the Georges Creek WWTP, located north of Westernport, Maryland (Table 2.4.2 and Figure 2.4.3). The Georges Creek WWTP sewer collection system services most of the sewered areas in the watershed except for the Town of Westernport, which conveys its wastewater to the Upper North Branch Commission WWTP, and the Town of Frostburg, which delivers its sewage to the City of Cumberland through the Allegany County Sanitary Commission and the LaVale Sanitary Commission conveyance systems. The Georges Creek WWTP sewer collection system is a CSS, receiving stormwater as well as wastewater. The Georges Creek WWTP (permit MD0060071) discharges into the Georges Creek main stem a mile north of the Town of Westernport. Human source of bacteria can be obtained at this location.

Table 2.4.2: NPDES Permit Holders discharging directly in the Georges Creek Watershed (02-14-10-04)

Permittee	NPDES Permit No.	County	Average Annual Flow (MGD)	Average Annual Concentrations (MPN/100ml)	Load Per Day (Billion MPN/day)
Georges Creek WWTP	MD0060071	Allegany	0.70	739.97	19.64

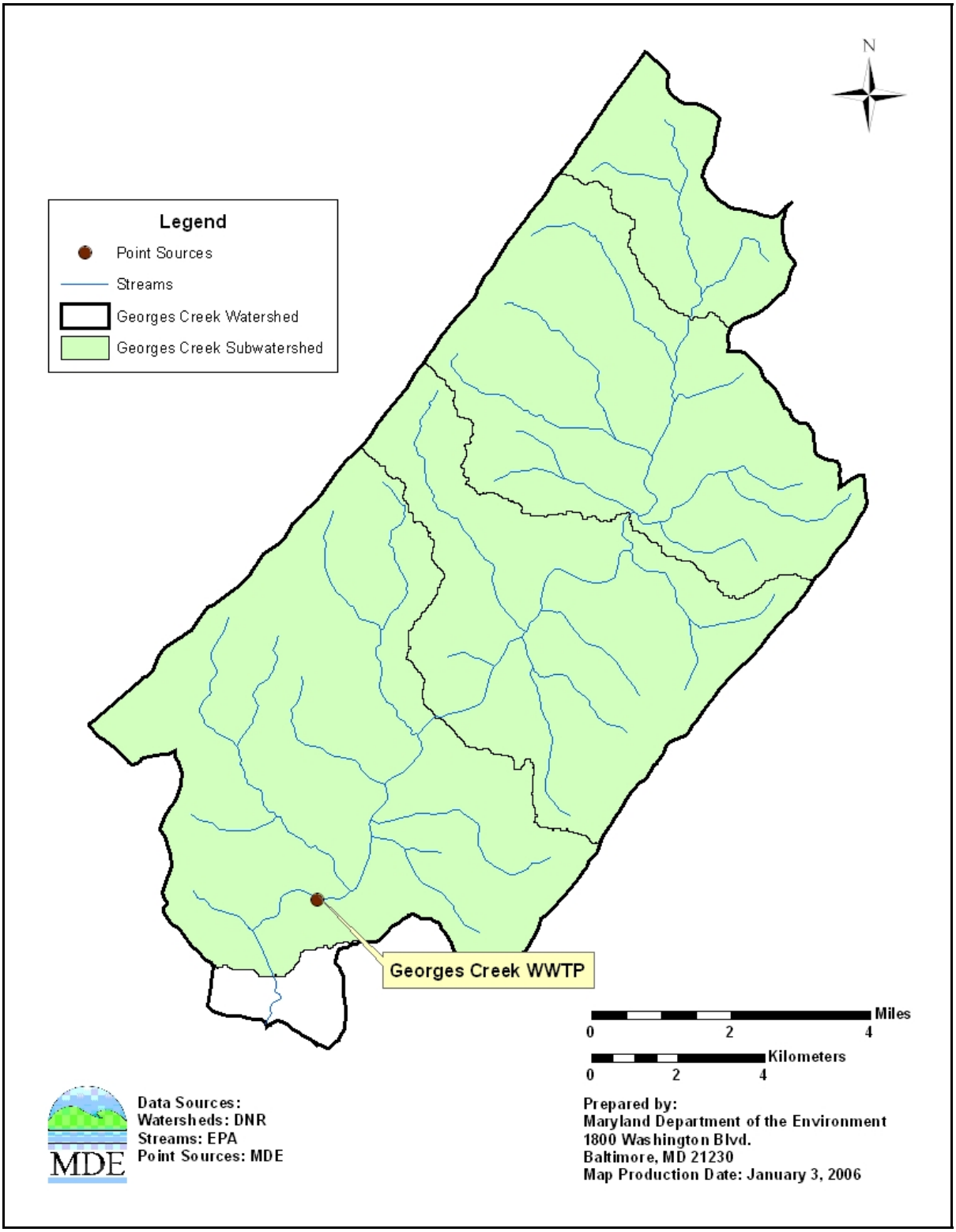

Figure 2.4.3: Permitted Point Sources in the Georges Creek Watershed

Combined Sewer Overflows

Combined sewer overflows (CSOs) are designed to release sewage combined with stormwater when the capacity of a CSS is exceeded, in order to prevent backups within the collection system. Like SSOs, there are several factors that may contribute to CSOs from a sewerage system, including pipe capacity, operations and maintenance effectiveness, sewer design, age of system, pipe materials, geology and building codes. CSOs are designed to discharge, unlike SSOs, which are accidental releases, and are subject to NPDES permit requirements. Long Term Control Plans (LTCPs) were developed for CSSs in Georges Creek pursuant to consent decrees between the Maryland Department of the Environment and three jurisdictions, the Town of Westernport, the City of Frostburg and Allegany County, operating these CSSs to control or eliminate all CSOs. The consent decrees were ordered by the Circuit Court of Allegany County on December 14, 2001 for the City of Frostburg and Allegany County, and on September 6, 2002 for the Town of Westernport. LTCPs for these jurisdictions must be implemented by October 1, 2023. For more detailed information on the consent decrees and LTCPs, please refer to Consent Decree Case Numbers 01-C-00-18342-L and 01-C-00-01848-L and the LTCPs documents in the References section of this report.

In the Georges Creek watershed there are three NPDES permitted CSSs operated by the City of Frostburg, the Town of Westernport and Allegany County, which monitor CSO discharges to the main branch and tributaries of Georges Creek. Table 2.4.3 and Figure 2.4.4 display the location of the CSOs discharging into Georges Creek and its tributaries. Although the two Westernport Permit System CSOs are within the Georges Creek watershed, both are located downstream of the area covered by this TMDL analysis.

Table 2.4.3: Locations of Combined Sewer Overflows in Georges Creek Watershed

CSS Permit System	NPDES #	Outfall	Location	Latitude	Longitude
Town of Westernport Combined Sewer System	MD0067384	001	Waverly Street	39.4898	-79.0426
		002	Washington Street	39.4844	-79.0460
Allegany County Combined Sewer System	MD0067407	001	Wrights Crossing	39.6386	-78.9326
		002	Braddock Estates	39.6381	-78.9333
		003	Grahamtown	39.6393	-78.9321
City of Frostburg Combined Sewer System	MD0067423	001	Paul Street	39.6520	-78.9242
		002	Grant Street	39.6506	-78.9239
		003	Grant & Green Street 01	39.6497	-78.9231
		004	Grant & Green Street 02	39.6489	-78.9228
		005	McColloh Street	39.6408	-78.9147

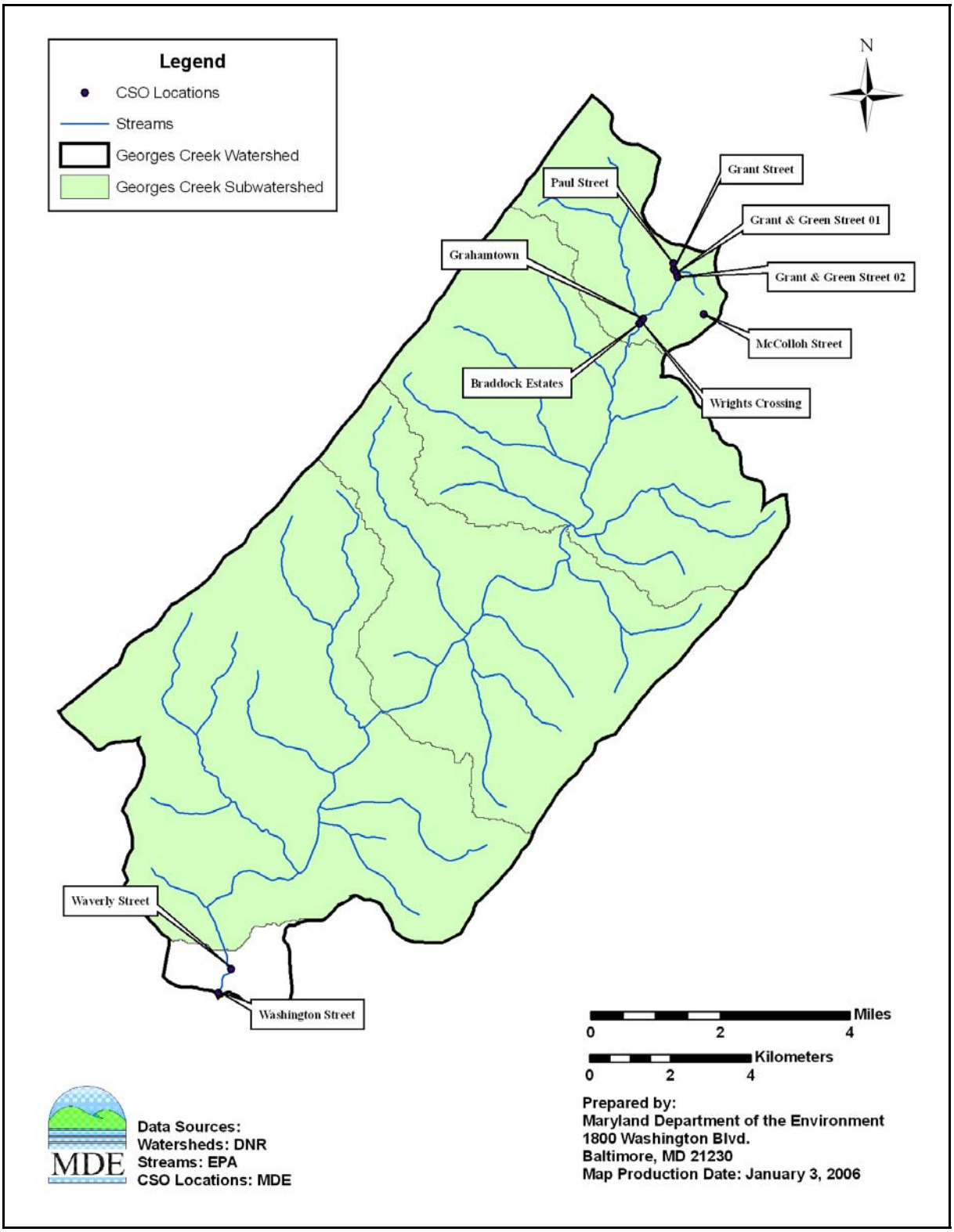

Figure 2.4.4: Combined Sewer Overflow Locations in the Georges Creek Watershed

There were a total of 369 CSO events reported between October 2002 and October 2003. Approximately 65,437,801 gallons of discharge were released from CSO in the Georges Creek mainstem and tributaries (MDE, Water Management Administration).

Bacteria Source Tracking

Bacteria source tracking (BST) was used to identify the relative contribution of bacteria from different sources in in-stream water samples. BST monitoring was conducted at four stations throughout the Georges Creek watershed with 12 samples (one per month) collected for a one-year duration. Sources are defined as domestic (pets and human associated animals), human (human waste), livestock (agricultural animals), and wildlife (mammals and waterfowl). To identify sources, samples are collected within the watershed from known fecal sources, and the patterns of antibiotic resistance of these known sources are compared to isolates of unknown bacteria from ambient samples. Details of the BST methodology and data can be found in Appendix C.

An accurate representation of the expected contribution from each source is estimated by using a stratified weighted mean of the identified sample results over the specified period. The weighting factors are based on the log10 of the bacteria concentration and the percent of time that represents the high stream flow or low stream flow (see Appendix B). The procedure for calculating the stratified weighted mean of the sources per monitoring station is as follows:

1. Calculate the percentage of isolates per source per each sample date (S).
2. Calculate the weighted percentage (MS) of each source per flow strata (high/low) (see Section 4). The weighting is based on the log10 bacteria concentration for the water sample.
3. The final weighted mean source percentage, for each source category, is based on the proportion of time in each flow duration zone (see Appendix C).

The weighted mean for each source category is calculated using the following equations:

$$M_k = \sum_{i=1}^{2} MS_{i,k} * W_i \qquad (4)$$

where

$$MS_{i,k} = \frac{\sum_{j=1}^{n_i} \log_{10}(C_{i,j}) * S_{i,j,k}}{n_i} \qquad (5)$$

M_k = weighted mean proportion of isolates of source k
$MS_{i,k}$ = Weighted mean proportion of isolates for source k in stratum i
W_i = Proportion covered by stratum i
i = stratum
j = sample
k = Source category (1 = human, 2 = domestic, 3 = livestock, 4 = wildlife, 5 = unknown)
Ci,j = Concentration for sample j in stratum i
Si,j,k = Proportion of isolates for sample j, of source k in stratum i
ni = number of samples in stratum i

The complete distributions of the annual and seasonal periods source loads are listed in Table 2.4.4 and 2.4.5. Details of the BST data can be found in Appendix C.

Table 2.4.4: Distribution of Fecal Bacteria Source Loads in the Georges Creek Watershed for the Average Annual Period

STATION	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
GEO0009	High Flow	13	19	2	8	58
	Low Flow	15	32	5	15	33
	Weighted	14	29	5	13	39
GEO0065	High Flow	16	25	2	12	45
	Low Flow	13	39	3	13	32
	Weighted	14	36	3	13	35
GEO0111	High Flow	5	23	0	29	44
	Low Flow	11	23	4	21	41
	Weighted	9	23	3	23	42
GEO0143	High Flow	9	33	2	11	45
	Low Flow	9	34	3	8	46
	Weighted	9	34	3	9	45

Table 2.4.5: Distribution of Fecal Bacteria Source Loads in the Georges Creek Watershed for the Seasonal Period (May 1st – September 30th)

STATION	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
GEO0009	High Flow	21	21	0	4	54
	Low Flow	18	23	4	21	34
	Weighted	18	23	3	17	39
GEO0065	High Flow	9	22	0	9	60
	Low Flow	8	60	0	7	25
	Weighted	9	50	0	7	34
GEO0111	High Flow	4	16	0	23	57
	Low Flow	9	26	3	21	41
	Weighted	8	24	2	21	45
GEO0143	High Flow	12	25	3	10	50
	Low Flow	11	38	2	7	42
	Weighted	12	33	3	8	44

3.0 TARGETED WATER QUALITY GOAL

The overall objective of the fecal bacteria TMDL set forth in this document is to establish the loading caps needed to ensure attainment of water quality standards in the Georges Creek watershed. These standards are described fully in Section 2.3, "Water Quality Impairment".

4.0 TOTAL MAXIMUM DAILY LOADS AND SOURCE ALLOCATION

4.1 Overview

This section provides an overview of the non-tidal fecal bacteria TMDL development, with a discussion on the many complexities involved with the estimation of bacteria concentrations, loads and sources. The second section presents the analysis framework and how the hydrological, water quality and BST data are linked together in the TMDL process. The third section describes the analysis for estimating a representative geometric mean fecal bacteria concentration and baseline loads. The analysis methodology is based on available monitoring data and specific to a free flowing stream system. The fourth section addresses the critical condition and seasonality. The fifth section presents the margin of safety. The sixth section discusses TMDL loading caps. The seventh section presents TMDL scenario descriptions. The eighth section presents the load allocations. Finally, in section nine, the TMDL equation is summarized.

To be most effective, the TMDL provides a basis for allocating loads among the known pollutant sources in the watershed so that appropriate control measures can be implemented and water quality standards achieved. By definition, the TMDL is the sum of the individual waste load allocations (WLA) for point sources, load allocations (LA) for nonpoint sources and natural background sources. A margin of safety (MOS) is also included and accounts for the uncertainty in the analytical procedures used for water quality modeling, and the limits in scientific and technical understanding of water quality in natural systems. Although this formulation suggests that the TMDL be expressed as a load, federal regulations (40 CFR 130.2(i)) provide that the TMDL can be expressed in terms of "mass per time, toxicity or other appropriate measure."

For many reasons, bacteria are difficult to simulate in water quality models. They reproduce and die off in a non-linear fashion as a function of many environmental factors, including temperature, pH, turbidity (UV light penetration), and settling. They occur in concentrations that vary widely (*i.e.*, over orders of magnitude) and accurate estimation of source inputs are difficult to develop. Finally, limited data are available to characterize the effectiveness of any program or practice at reducing bacteria loads (Schueler, 1999).

Bacteria concentrations, determined through laboratory analysis of in-stream water samples for bacteria indicators (*e.g.*, *E. coli*), are expressed in either colony forming units (CFU) or most probable number (MPN) of colonies. The first method (Method 1600) is a direct estimate of the bacteria colonies (EPA, 1985), and the second (Method 9223B) is a statistical estimate of the number of colonies (APHA, 1998). Enumeration results demonstrate the extreme variability in the total bacteria counts. The distribution of the enumeration results from water samples tends to be lognormal, with a strong positive skew of the data. Estimating loads of constituents that vary by orders of magnitude can introduce much uncertainty and result in large confidence intervals around the final results.

Estimating bacteria sources can be problematic due to the many assumptions required and the limited available data. For example, when considering septic systems, information is required on

spatial location of failing septic systems, consideration of transport to in-stream assessment location and estimation of the load from the septic system (degree of failure). Secondary sources, such as illicit discharges, also add to the uncertainty in a bacteria water quality model.

Estimating domestic animal sources requires information regarding the pet population in a watershed, how often the owners clean up after them, and the spatial location of the pet waste relative to the stream (near-field for upland transport). Livestock sources are limited by spatial resolution of Agricultural Census information (available at the county level), site-specific issues relating to animals' confinement, and confidentiality of data related to the development of Nutrient Management Plans. The most uncertain source category is wildlife. In an urban environment, this can result from the increased deer populations near streams to rat populations in storm sewers. In rural areas, estimation of wildlife populations and habitat locations in a watershed is required.

MDE appreciates the inherent uncertainty in developing traditional water quality models for the calculation of bacteria TMDLs. Traditional water quality modeling is very expensive and time consuming and, as identified, contains many potential uncertainties. MDE believes it should be reserved for specific constituents and complex situations. In this TMDL, MDE applies an analytical method which, when combined with BST analysis, appears to provide reasonable results (Cleland, 2003). Using this approach, MDE can address more impaired streams in the same time period than using the traditional water quality modeling methods.

4.2 Analysis Framework

This TMDL analysis uses flow duration curves to identify flow intervals that are used as indicator hydrological conditions (*i.e.* annual average, critical conditions). As explained previously, this analytical method combined with water quality monitoring data and BST provides a better description of water quality and meets TMDL requirements.

Figure 4.2.1 illustrates how the hydrological (flow duration curve), water quality and BST data are linked together for the TMDL development.

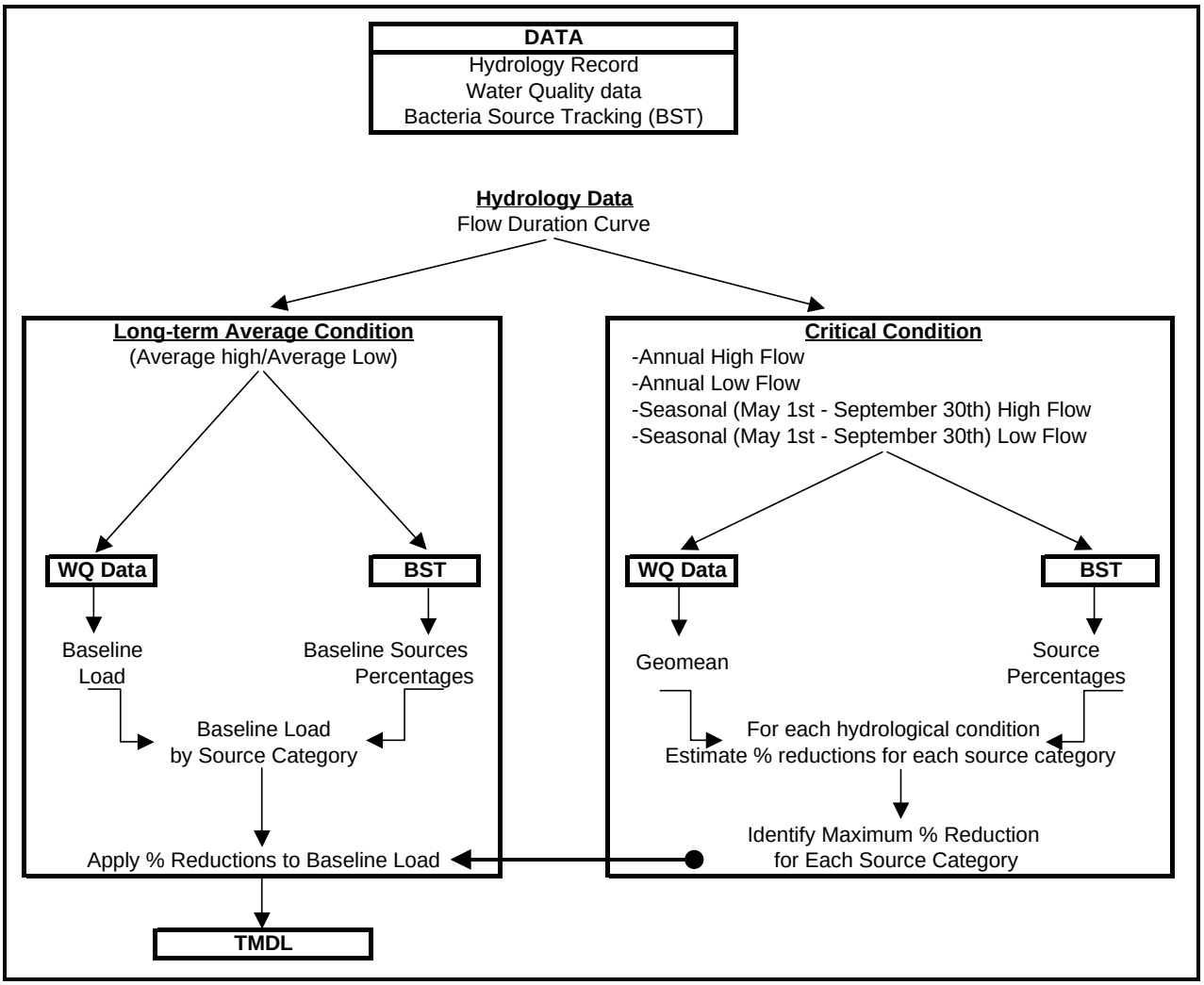

Figure 4.2.1: Diagram of Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads estimated in this TMDL analysis are reported in long-term average loads. The geometric mean concentration is calculated from the log transformation of the raw data. Statistical theory tells us that when back transformed values are used to calculate average daily loads or total annual loads, the loads will be biased low (Richards, 1998). To avoid this bias, a factor should be added to the log-concentration before it is back transformed. There are several methods of determining this bias correction factor ranging from parametric estimates resulting from the theory of the log-normal distribution to non-parametric estimates using a smearing factor. [Ferguson, 1986; Cohn *et al*., 1989; Duan, 1983]. There is much literature on the applicability and results from these various methods with a summary provided in Richards (1998). Each has advantages and conditions of applicability. A non-parametric estimate of the bias correction factor (Duan, 1983) was used in this TMDL analysis.

The bias correction factor is estimated as follows:

$F_1 = A_i / C_i$

F_1 = Bias correction factor
A_i = Long term annual arithmetic mean for stratum i
C_i = Long term annual geometric mean for stratum i

Daily average flows are estimated for each flow stratum using the watershed area ratio approach, since nearby long-term flow monitoring data are available.

The loads for each stratum are estimated as follows:

$$L_i = Q_i * C_i * F_1 * F_2 \quad (6)$$

where

Li = Daily average load (MPN/day) at each station for stratum i
Qi = Daily average flow (cfs) for stratum i
Ci = long term annual geometric mean for stratum i
F1= Bias correction factor
F2= Unit conversion factor from cfs*MPN/100ml to MPN/day (2.4466x107)

For each subwatershed, the total baseline load is estimated as follows:

$$L_t = \sum_{i=1}^{2} L_i * W_i \quad (7)$$

Lt = Daily average load at station (MPN/day)
Wi= Proportion or weighting factor of stratum i

In the Georges Creek watershed, a weighting factor of 0.25 for high flow and 0.75 for low flow were used to estimate the average annual baseline load expressed as billion MPN *E. coli*/day. Results are as follows:

Table 4.3.1: Baseline Load Calculations

Station		GEO0143	GEO0111sub	GEO0065sub	GEO0009sub
Area (mi^2)		6.2	19.9	18.2	28.4
High Flow	Daily Average Flow (cfs)	21.9	70.6	64.6	100.6
	E. coli Concentration (MPN/100ml)	4942.9	157.5	397.9	12207.5
	Smearing Factor	6.3	1.6	1.3	1.5
Low Flow	Daily Average Flow (cfs)	3.2	10.2	9.4	14.6
	E. coli Concentration (MPN/100ml)	398.9	83.1	297.3	1508.7
	Smearing Factor	5.8	2.6	3	2.2
Baseline Load (Billion MPN/day)		4298.7	151.9	352.7	12519.5

The Georges Creek watershed was delineated into four subwatershed segments based on the location of each monitoring station. Baseline loads were estimated for each station. For subwatersheds with upstream monitoring stations, the total baseline load from upstream stations was multiplied by a transport factor derived from first order decay. The decay factor for *E. coli* used in the analysis was obtained from the study "Pathogen Decay in Urban Waters" by Easton *et al.* (2001), and was estimated by linear regression of counts of microorganisms versus time (die-off plots). The estimated transported loads were then subtracted from the downstream cumulative load to estimate the adjacent subwatershed baseline load. For stations GEO0009, GEO0065 and GEO0111 there is an upstream monitoring station (Figure 4.3.1). These subwatersheds were defined with the extension sub to the station name (*e.g.*, GEO0009sub).

In the Georges Creek analysis, the baseline load at the upstream station GEO0143 is significantly greater than the cumulative baseline load at the downstream station GEO0111. Bacteria loads are significantly greater upstream due to the existence of several CSOs, which greatly elevate bacteria levels during storm events. As these bacteria loads are transported downstream, they come into contact with high concentrations of metals and acidity due to the presences of acid

mine drainage, in which bacteria cannot survive and quickly die off. For this reason, transported loads from Station GEO0143 to station GEO 0111 will not be considered and the entire load as measured at station GEO0111 will be assigned to the subwatershed GEO0111sub. There are no CSOs and no major sources of bacteria in subwatershed GEO0111sub; therefore the downstream loads (loads measured at station GEO0111) are significantly less.

The CSOs and acid mine drainage scenario as explained above do not occur in the remaining subwatersheds of the Georges Creek, and the cumulative baseline loads at stations GEO0065 and GEO0009 are greater than the upstream load. Therefore, the transported load will be factored in when calculating the baseline load for these two subwatersheds.

The general equation for the flow mass balance is:

$$\sum Q_{us} + Q_{sub} = Q_{ds} \qquad (8)$$

where

Q_{us} = Upstream flow
Q_{sub} = Subwatershed flow
Q_{ds} = Downstream flow

and the general equations for bacteria loading mass balance:

$$\sum (e^{kt} * Q_{us} * C_{us}) + Q_{sub} * C_{sub} = Q_{ds} * C_{ds} \qquad (9)$$

where

C_{us} = Upstream bacteria concentration
k = Bacteria (*E. coli)* decay coefficient (1/day) = 0.762 day^{-1}
t = travel time from upstream watershed to outlet
C_{sub} = Subwatershed bacteria concentration
C_{ds} = Downstream bacteria concentration

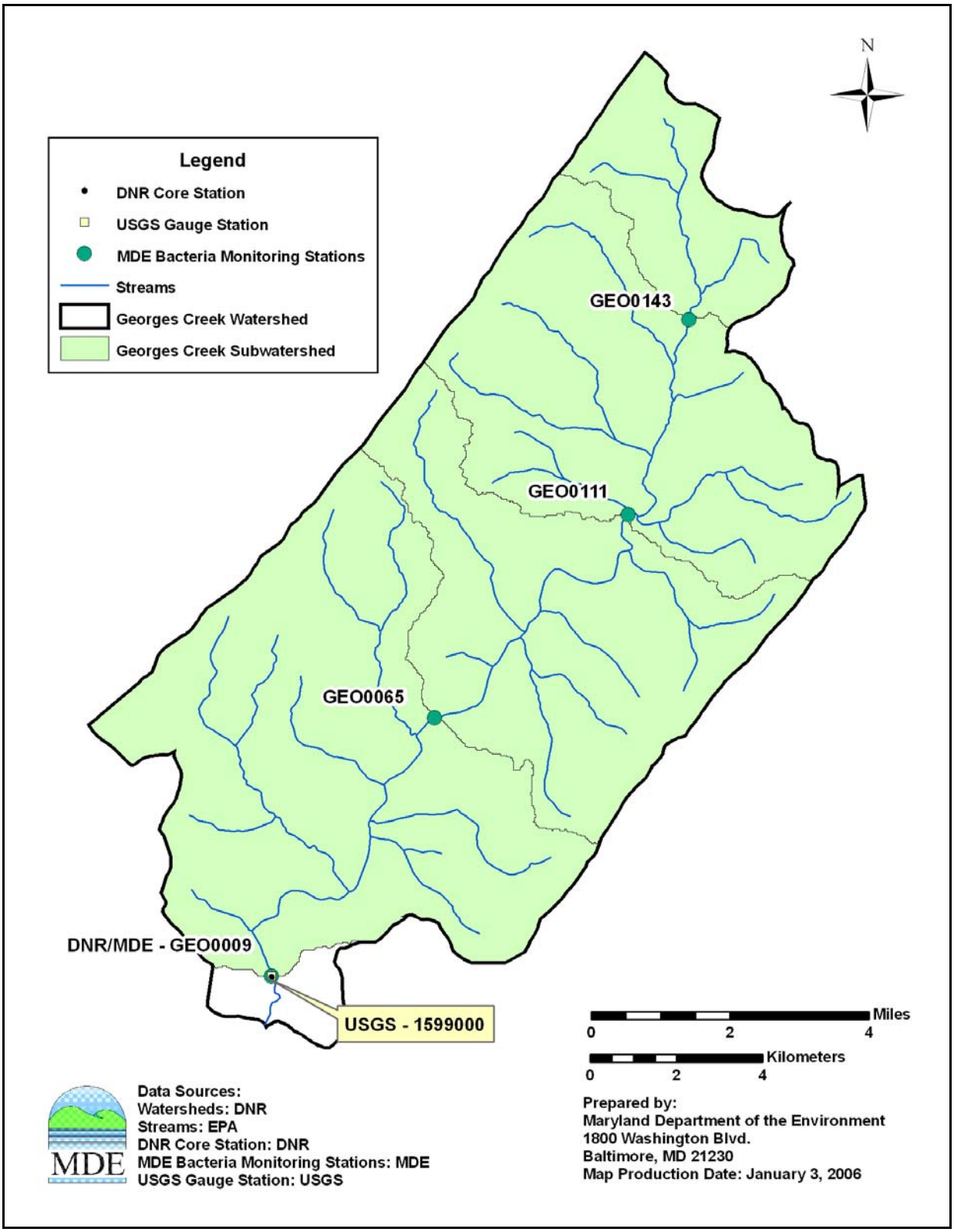

Figure 4.3.1: Monitoring Stations and Subwatersheds in the Georges Creek Watershed

The concentrations in the subwatersheds were estimated by considering the ratio of high flow concentration to low flow concentrations in the upstream watersheds. If the total load and average flow were used to estimate the geometric mean concentration, this estimated concentration would be biased if there was a correlation with flow and concentration. For example, in two strata, the steady state geometric mean is estimated as follows:

$$L = (Q_{high} * W_{high} * C_{high}) + (Q_{low} * W_{low} * C_{low}) \quad (10)$$

L = Average Load
Q_i = Average flow for stratum i
W_i= Proportion of stratum i
C_i = Concentration for stratum i
n_i = number of samples in stratum i

The load in equation (10) is based on two concentrations and therefore when using the mass balance approach and the total load, this results in two unknowns, C_{high} and C_{low}, with one equation. Thus a relationship between C_{high} and C_{low}, must be estimated to solve for the concentration in both strata. This relationship is estimated using the average of the ratios estimated from the monitoring data in the upstream watersheds. Using this relationship, the following two equations result:

$$C_{low} = \frac{L}{Q_{high} * R * W_{high} + Q_{low} * W_{low}} \quad (11)$$

where

$$R = \frac{C_{high}}{C_{low}} \quad (12)$$

and the final geometric mean concentration is estimated as follows:

$$GM = 10^{W_{high} \log_{10}(C_{high}) + W_{low} \log_{10}(C_{low})} \quad (13)$$

Source estimates from the bacteria source tracking analysis are completed for each station and are based on the contribution from the upstream watershed, if applicable. Given the uncertainty of in-stream bacteria processes and the complexity involved in back-calculating an accurate source transport factor, the sources for GEO0009sub, GEO0065sub and GEO0111sub were assigned from the analysis for GEO0009, GEO0065 and GEO0111, respectively.

4.4 Critical Condition and Seasonality

Federal regulations (40 CFR 130.7(c)(1)) require TMDLs to take into account critical conditions for stream flow, loading, and water quality parameters. The intent of this requirement is to ensure that the water quality of the waterbody is protected during times when it is most vulnerable.

For this TMDL the critical condition is determined by assessing annual and seasonal hydrological conditions for high flow and low flow periods. Seasonality is captured by assessing the time period when water contact recreation is expected (May 1st - September 30th). The average hydrological condition over a 15-year period is approximately 25% high flow and 75% low flow as defined in Appendix B. Using the definition of a high flow condition occurring when the daily flow duration interval is less than 25% and a low flow condition occurring when the daily flow duration interval is greater than 25%, critical hydrological condition can be estimated by the percent of high or low flows during a specific period and hydrological condition.

As stated above, Maryland's proposed fecal bacteria TMDL for Georges Creek has been determined by assessing various hydrological conditions to account for seasonal and annual averaging periods. The following four conditions as shown in Table 4.4.1 were used to account for the critical condition: annual high flow, annual low flow, seasonal high flow and seasonal low flow.

Table 4.4.1: Hydrological Conditions Used to Account for Critical Condition and Seasonality

Hydrological Condition		Averaging Period	Water Quality Data Used	Fraction High Flow	Fraction Low Flow	Condition Period
Annual	High flow	365 days	All	0.56	0.44	Jan 1997 - Jan 1998
	Low flow	365 days	All	0.06	0.94	May 1995 - May 1996
Seasonal	High flow	May 1st – Sept 30th	May 1st – Sept 30th	0.46	0.54	May 2003 - Sep 2003
	Low flow	May 1st – Sept 30th	May 1st – Sept 30th	0.00	1.00	May 2002 - Sep 2002

The critical condition is determined by the maximum reduction per source that satisfy all four conditions, and is required to meet the water quality standard while minimizing the risk to water contact recreation. It is assumed that the reduction that can be implemented to a bacteria source category will be constant through all conditions (*e.g.*, pet waste can be reduced by 75%).

The monitoring data for all stations located in the Georges Creek watershed cover a sufficient temporal span (at least one year) to estimate annual and seasonal conditions. The required reductions to meet water quality standards at each station for each hydrological condition are presented in Table 4.4.2.

Table 4.4.2: Required Reductions to Meet Water Quality Standards

Station	Hydrological Condition		Domestic %	Human %	Livestock %	Wildlife %
GEO0143	Annual	Wet	98%	98%	98%	68%
		Dry	63%	98%	48%	0%
	Seasonal	Wet	98%	98%	98%	97%
		Dry	98%	98%	98%	52%
	Maximum Source Reduction		**98%**	**98%**	**98%**	**97%**
GEO0111sub	Annual	Wet	0%	0%	0%	0%
		Dry	0%	0%	0%	0%
	Seasonal	Wet	97%	98%	81%	2%
		Dry	33%	98%	30%	0%
	Maximum Source Reduction		**97%**	**98%**	**81%**	**2%**
GEO0065sub	Annual	Wet	67%	98%	0%	0%
		Dry	28%	98%	0%	0%
	Seasonal	Wet	98%	98%	0%	40%
		Dry	98%	98%	0%	16%
	Maximum Source Reduction		**98%**	**98%**	**0%**	**40%**
GEO0009sub	Annual	Wet	98%	98%	98%	96%
		Dry	98%	98%	98%	76%
	Seasonal	Wet	98%	98%	98%	98%
		Dry	98%	98%	98%	95%
	Maximum Source Reduction		**98%**	**98%**	**98%**	**98%**

4.5 Margin of Safety

A margin of safety (MOS) is required as part of this TMDL in recognition of the many uncertainties in the understanding and simulation of bacteriological water quality in natural systems and in statistical estimates of indicators. As mentioned in Section 4.1, it is difficult to estimate stream loadings for fecal bacteria due to the variation in loadings across sample locations and time. Load estimation methods should be both precise and accurate to obtain the true estimate of the mean load. Refined precision in the load estimation is due to using a stratified approach along the flow duration intervals thus reducing the variation in the estimates. Moreover, Richards (1998) reports that averaging methods are generally biased, and the bias increases as the size of the averaging window increases. Finally, accuracy in the load estimation is based on minimal bias in the final result when compared to the true value.

Based on EPA guidance, the MOS can be achieved through two approaches (EPA, April 1991). One approach is to reserve a portion of the loading capacity as a separate term in the TMDL (*i.e.*, TMDL = LA + WLA + MOS). The second approach is to incorporate the MOS as conservative assumptions used in the TMDL analysis. For this TMDL, the second approach was used by estimating the loading capacity of the stream based on a reduced (more stringent) water quality criterion concentration. The *E. coli* water quality criterion concentration was reduced by 5%, from 126 *E. coli* MPN/100ml to 119.7 *E. coli* MPN/100ml.

4.6 TMDL Loading Caps

The TMDL loading cap is an estimate of the assimilative capacity of the monitored watershed and is provided in MPN/day. The loading caps presented in this section are for the watersheds located upstream of monitoring stations GEO0143, GEO0111, GEO0065 and GEO0009.

The TMDL is based on a long-term average hydrological condition. Estimation of the TMDL requires knowledge of how the bacteria concentrations vary with flow rate or the flow duration interval. This concentration versus flow relationship is accounted for by using the strata defined on the flow duration curve.

The TMDL loading caps are estimated by first determining the baseline or current condition loads for each subwatershed and the associated geometric mean from the available monitoring data. The baseline load is estimated using the geometric mean concentration and average daily flow for each flow stratum. The loads from these two strata are then weighted to represent average conditions (see Table 4.3.1), based on the proportion of each stratum, to estimate the total long-term loading rate.

Next, the percent reduction required to meet the water quality criterion is estimated from the observed bacteria concentrations accounting for the critical conditions (See Section 4.4). A reduction in concentration is proportional to a reduction in load, thus the TMDL is equal to the current baseline load multiplied by one minus the required reduction.

$$TMDL = L_b * (1 - R) \quad (12)$$

where

Lb = Current or baseline load estimated from monitoring data
R = Reduction required from baseline to meet water quality criterion

The bacteria TMDL for the subwatersheds ar shown in Table 4.6.1.

Table 4.6.1: Georges Creek Watershed TMDL Summary

Station	Baseline Load (Billion *E. coli* MPN/day)	TMDL Load (Billion *E. coli* MPN/day)	% Target Reduction
GEO0143	4298.7	95.7	97.8%
GEO0111sub	151.9	62.0	59.2%
GEO0065sub	352.7	63.8	81.9%
GEO0009sub	12519.5	258.1	97.9%
Total	17322.8	479.7	-

4.7 Scenario Descriptions

Source Distribution

The final source distribution is derived from the source proportions listed in Table 2.4.2. For the purposes of the TMDL analysis and allocations, the percentage of sources identified as "unknown" were removed and the known sources were then scaled up proportionally so that they totaled 100%. The source distribution used in this scenario is presented in Table 4.7.1.

Table 4.7.1: Baseline Source Distributions

Station	Domestic		Human		Livestock		Wildlife	
	%	Load (Billion *E.coli* MPN/day)	%	Load (Billion *E coli* MPN/day)	%	Load (Billion *E.coli* MPN/day)	%	Load (Billion *E.coli* MPN/day)
GEO0143	16.4%	704.5	62.4%	2680.8	5.0%	213.3	16.3%	700.2
GEO0111sub	15.7%	23.9	40.1%	60.9	5.0%	7.6	39.2%	59.6
GEO0065sub	21.2%	74.7	54.4%	191.9	4.6%	16.4	19.8%	69.7
GEO0009sub	23.6%	2955.4	47.2%	5905.2	7.5%	939.9	21.7%	2719.0

Practicable Reduction Targets

The maximum practicable reduction (MPR) for each of the four source categories is listed in Table 4.7.2. These values are based on best professional judgment and a review of the available literature. It is assumed that human sources would potentially confer the highest risk of gastrointestinal illness and therefore should have the highest reduction. If a domestic WWTP is located in the upstream watershed, this is considered in the MPR so as to not violate the permitted loads. The domestic animal category includes sources from pets (*e.g.*, dogs) and the MPR is based on an estimated success of education and outreach programs.

Table 4.7.2: Maximum Practicable Reduction Targets

	Human	Domestic	Livestock	Wildlife
Max Practical Reduction per Source	95%*	75%	75%	0%
Rationale	(a) Direct source inputs (b) Human pathogens more prevalent in humans than animals. (c) Enteric viral diseases spread from human to human[1]	Target goal reflects uncertainty in effectiveness of urban BMPs[2] and is also based on best professional judgment	Target goal based on sediment reductions from BMPs[3] and best professional judgment	No programmatic approaches for wildlife reduction to meet water quality standards Waters contaminated by wild animal waste offer a public health risk that is orders of magnitude less than that associated with human waste.[4]

*Since much of the human sources in this watershed are due to infrastructure failure, correction of exfiltration required by consent decrees may result in greater reductions than in other watersheds.

[1]USEPA. 1984. Health Effects Criteria for Fresh Recreational Waters. EPA-600/1-84-004. U.S. Environmental Protection Agency, Washington, DC.
[2]USEPA. 1999. Preliminary Data Summary of Urban Storm Water Best Management Practices. EPA-821-R-99-012. U.S. Environmental Protection Agency, Washington, DC.
[3]USEPA. 2004. Agricultural BMP Descriptions as Defined for The Chesapeake Bay Program Watershed Model. Nutrient Subcommittee Agricultural Nutrient Reduction Workshop.
[4]Environmental Indicators and Shellfish Safety. 1994. Edited by Cameron, R., Mackeney and Merle D. Pierson, Chapman & Hall.

As previously stated, these practicable reduction targets are based on the available literature and best professional judgment. There is much uncertainty with estimated reductions from best management practices (BMPs). The BMP efficiency for bacteria reduction ranged from –6% to +99% based on a total of 10 observations (EPA, 1999). The MPR to agricultural lands was based on sediment reductions identified by the EPA (EPA, 2004).

The practicable reduction scenario was developed based on an optimization analysis whereby a subjective estimate of risk was minimized, and constraints were set on maximum reduction and allowable background conditions. Risk was defined on a scale of one to five, where it was assumed that human sources had the highest risk (5), domestic animal and livestock next (3) and wildlife the lowest (1) (see Table 4.7.2). The objective is to minimize the sum of the risk for all conditions while meeting the maximum practicable reduction constraints. The model was defined as follows:

$$\text{Min} \sum_{i=1}^{4} (Ph*5 + Pd*3 + Pl*3 + Pw*1) \qquad i = \text{hydrological condition}$$

Subject to

C = Ccr
0 <= Rh <= 95%
0 <= Rl <= 75%
0 <= Rd <= 75%
Rw = 0
Ph, Pl, Pd, Pw >= 1%

Where

Ph = % human source in final allocation
Pd = % domestic animal source in final allocation
Pl = % livestock source in final allocation
Pw = % wildlife source in final allocation
C = In-stream concentration
Ccr = Water quality criterion
Rh = Reduction applied to human sources
Rl = Reduction applied to livestock sources
Rd = Reduction applied to domestic animal sources
Rw = Reduction applied to wildlife sources

In all four subwatersheds, the constraints of this scenario could not be satisfied indicating there was not a practicable solution. A summary of the analysis is presented in Table 4.7.3.

Table 4.7.3: Practicable Reduction Results

Station	Applied Reductions				Achievable
	Domestic %	Human %	Livestock %	Wildlife %	
GEO0143	75.0%	95.0%	75.0%	0.0%	No
GEO0111sub	75.0%	95.0%	75.0%	0.0%	No
GEO0065sub	75.0%	95.0%	75.0%	0.0%	No
GEO0009sub	75.0%	95.0%	75.0%	0.0%	No

The TMDL must specify load allocations that will meet the water quality standards. In the practicable reduction targets scenario all four subwatersheds could not meet water quality standards based on MPRs.

To further develop the TMDL, the constraints on the MPRs were relaxed in all four subwatersheds where the water quality attainment was not achievable with the MPRs. In this subwatershed, the maximum allowable reduction was increased to 98% for all sources, including wildlife. A similar optimization procedure was used to minimize risk. Again, the objective is to minimize the sum of the risk for all conditions while meeting the maximum practicable reduction constraints. The model was defined as follows:

Min $\sum_{i=1}^{7}$ (Ph*5 + Pd*3 + Pl*3 + Pw*1) i = hydrological condition

Subject to

C = Ccr
0 <= Rh <= 98%
0 <= Rl <= 98%
0 <= Rd <= 98%
0 <= Rw <= 98%
Ph, Pl, Pd, Pw >= 1%

Where

Ph = % human source in final allocation
Pd = % domestic animal source in final allocation
Pl = % livestock source in final allocation
Pw = % wildlife source in final allocation
C = In-stream concentration
Ccr = Water quality criterion
Rh = Reduction applied to human sources
Rl = Reduction applied to livestock sources
Rd = Reduction applied to domestic animal sources
Rw = Reduction applied to wildlife sources

The required reductions and TMDL allocations by source category for each subwatershed are presented in Table 4.7.4 and Table 4.7.5, respectively.

Table 4.7.4: TMDL Reduction Results: Optimization Model Up to 98% Reduction

Station	Domestic %	Human %	Livestock %	Wildlife %	Target Reduction
GEO0143	98.0%	98.0%	98.0%	96.6%	97.8%
GEO0111sub	96.5%	98.0%	80.9%	1.8%	59.2%
GEO0065sub	98.0%	98.0%	0.0%	39.6%	81.9%
GEO0009sub	98.0%	98.0%	98.0%	97.7%	97.9%

Table 4.7.5: TMDL Reduction Results: Reduced Loads by Source

Station	Domestic (Billion *E. coli* MPN /day)	Human (Billion *E coli* MPN /day)	Livestock (Billion *E. coli* MPN /day)	Wildlife (Billion *E. coli* MPN /day)	Total (Billion *E. coli* MPN /day)
GEO0143	14.1	53.6	4.3	23.7	95.7
GEO0111sub	0.8	1.2	1.4	58.6	62.0
GEO0065sub	1.5	3.8	16.4	42.1	63.8
GEO0009sub	59.1	118.1	18.8	62.1	258.1

4.8 TMDL Allocation

The TMDL allocation includes waste load allocations (WLA) for point sources, for stormwater (where MS4 permits are required), and the load allocation (LA) for nonpoint sources. The margin of safety is explicit and is expressed as a 5% reduction of the *E. coli* water quality criterion concentration, from 126 MPN/100ml to 119.7 MPN/100ml. TMDL allocations in the Georges Creek watershed are based on critical conditions. The final loads represent loads based on average hydrological conditions. The load reduction scenario results in a load allocation that will achieve water quality standards. The State reserves the right to revise these allocations provided such allocations are consistent with the achievement of water quality standards.

The bacteria sources are grouped into four categories that are also consistent with divisions for various management strategies. The categories are human, domestic animal, livestock and wildlife. TMDL allocation rules are presented in Table 4.8.1. This table identifies how the TMDL will be allocated among WWTPs, MS4 permits, CSO permits and the LA.

Table 4.8.1: Potential Source Contributions for Georges Creek TMDL Allocations

Allocation Category	LA	WLA		
		WWTP	MS4	CSOs
Human	X	X		
Domestic	X			
Livestock	X			
Wildlife	X			

For the human sources, the nonpoint source contribution (LA) in subwatersheds with WWTPs is estimated by subtracting the WWTP load from the final human load. All three jurisdiction with CSOs permitted to discharge in the Georges Creek have developed their Long Term Control Plans (LTCP) and CSOs are expected to be eliminated by the dates stated in the LTCPs. Therefore, the final human load is assigned to either LA and/or WWTP.

Domestic pet allocation is assigned to the MS4 WLA if there are MS4 permit(s) covering the watershed. No MS4 permits exist for the Georges Creek watershed therefore, pet allocation is assigned to LA.

Wildlife and Livestock are also assigned to the LA. Note that only the final LA or WLA is reported in this TMDL.

Municipal and Industrial WWTPs

There is one point source facility permitted to discharge bacteria directly into Georges Creek (See Table 4.8.2). The WWTP flow used in the TMDL allocation is based on the flow specified in the NPDES permit. Since Maryland has now adopted new indicator bacteria organisms, it is expected that the revised permit will now specify geometric mean concentrations for *E. coli* instead of fecal coliform.

Table 4.8.2: Municipal Waste Water Treatment Plants Load Allocation

Permittee	NPDES Permit No.	County	Permit Flow (MGD)	Permit Concentrations (*E. coli* MPN/100ml)	Permit Load (Billion *E. coli* MPN/day)	% of TMDL
Georges Creek WWTP	MD0060071	Allegany	0.60	126	2.86	1.11

4.9 Summary

The TMDLs for the Georges Creek subwatersheds are presented in Table 4.9.1.

Table 4.9.1: Georges Creek Watershed TMDL

Station	TMDL Load (Billion *E. coli* MPN/day)	LA Load (Billion *E. coli* MPN/day)	WLA-PS Load (Billion *E. coli* MPN/day)	WLA-CSO Load (Billion *E. coli* MPN/day)
GEO0143	95.7	95.7	0.0	0
GEO0111sub	62.0	62.0	0.0	0
GEO0065sub	63.8	63.8	0.0	0
GEO0009sub	258.1	255.2	2.9	0
Total	**479.7**	**476.8**	**2.9**	**0**

In the four subwatersheds, based on the practicable reduction rates specified, water quality standards cannot be achieved. This may occur in watersheds where wildlife is a significant component or watersheds that require very high reductions to meet water quality standards. However, if there is no feasible TMDL scenario, then MPRs are increased to provide estimates of the reductions required to meet water quality standards. For these watersheds, it is noted that the reductions may be beyond practical limits. In this case, it is expected that the first stage of implementation will be to implement the MPR scenario.

5.0 ASSURANCE OF IMPLEMENTATION

Section 303(d) of the Clean Water Act and current EPA regulations require reasonable assurance that the TMDL load and wasteload allocations can and will be implemented. In the Georges Creek watershed, the TMDL analysis indicates that reduction of fecal bacteria loads from all sources including wildlife are beyond the MPR targets. The Georges Creek may not be able to attain water quality standards. The extent of the fecal bacteria load reductions required to meet water quality criteria in the four subwatersheds of the Georges Creek and in downstream waters are not feasible by effluent limitations and also by implementing cost-effective and reasonable best management practices to nonpoint sources. Therefore, MDE cannot assure that the TMDL load and wasteload allocations can be implemented.

The most significant planned implementation measures in the Georges Creek watershed measures involve the upgrade or separation of combined sewer systems in the City of Frostburg, Allegany County, and the Town of Westernport. Each of these jurisdictions is obligated under a judicial consent decree and judgment to adopt and implement a long term control plan ("LTCP") to eliminate dry weather overflows and minimize wet weather overflows. See Consent Decrees and Judgments, Consolidated Case Number 01-C-00-18342L (December 14, 2001), and Consolidated Case Number: 01-C-00-18487-L (September 6, 2002). The three jurisdictions have submitted and MDE has approved LTCPs that will separate their sanitary and stormwater sewers and/or eliminate all CSO outfalls. The judicial decrees and judgment require the jurisdictions to implement these LTCPs by 2023. Deadlines for LTCP implementation will be incorporated into NPDES permits and, if shorter than the court ordered deadline, permits will reflect what can be feasibly accomplished with consideration to the complexity of the engineering, the availability of resources, and the need for inter-jurisdictional coordination.

Additional reductions will be achieved through the implementation of BMPs; however, the literature reports considerable uncertainty concerning the effectiveness of BMPs in treating bacteria. As an example, pet waste education programs have varying results based on stakeholder involvement. Additionally, the extent of wildlife reduction associated with various BMPs methods (*e.g.*, structural, non-structural, etc.) is uncertain. Therefore, MDE intends for the required reductions to be implemented in an iterative process that first addresses those sources with the largest impact on water quality and human health risk, with consideration given to ease of implementation and cost. The iterative implementation of BMPs in the watershed has several benefits: tracking of water quality improvements following BMP implementation through follow-up stream monitoring; providing a mechanism for developing public support through periodic updates on BMP implementation; and helping to ensure that the most cost-effective practices are implemented first.

Potential funding sources for implementation include the Maryland's Agricultural Cost Share Program (MACS) which provides grants to farmers to help protect natural resources and the Environmental Quality and Incentives Program which focuses on implementing conservation practices and BMPs on land involved with livestock and production. Though not directly linked, it is assumed that the nutrient management plans from the Water Quality Improvement Act of 1998 (WQIA) will have some reduction of bacteria from manure application practices.

In 2000, the Maryland DNR initiated the Watershed Restoration Action Strategy (WRAS) Program as one of several new approaches to implementing water quality and habitat restoration and protection. The WRAS Program encourages local governments to focus on priority watersheds for restoration and protection. Since the program's inception, local governments have received grants and technical assistance from DNR for 20 WRAS projects in which local people identify local watershed priorities for restoration, protection and implementation. WRAS information provides a potential targeting tool to direct future efforts in implementation

DNR and Allegany County formed a partnership to develop a WRAS for the Georges Creek watershed. As part of the WRAS development process, a Stream Corridor Assessment (SCA) survey of Georges Creek was conducted from August 2001 to May 2002. Approximately 108 miles of streams were surveyed to identify environmental problems in the watershed (*e.g.*, exposed pipes). However, additional information is required to determine if there is a bacteria input from an exposed or failing pipe. A WRAS plan has been developed based on this SCA and other information to correct these environmental problems (DNR, 2002).

Additionally, MDE's "Managing Maryland for Results" states the following related to separate sewer system overflows and combined sewer system overflows (MDE, 2005):

> **Objective 4.5:** Reduce the quantity in gallons of sewage overflows [total for Combined Sewer System Overflows (CSO) and Separate Sewer System Overflows (SSO)] equivalent to a 50% reduction of 2001 amounts (50, 821,102 gallons) by the year 2010 through implementation of EPA's minimum control strategies, long-termcontrol plans (LTCPs), and collection system improvements in capacity, inflow and infiltration reduction, operation and maintenance.
>
> **Strategy 4.5.1:** MDE adopted new regulations effective March 28, 2005 to detail procedures that must be followed regarding reporting overflows or treatment plant bypasses and also to require public notification of certain sewage overflows.
>
> **Strategy 4.5.2:** MDE will inspect and take enforcement actions against those CSO jurisdictions that have not developed long-term control plans by dates set within current consent or judicial orders.
>
> **Strategy 4.5.3:** MDE will take enforcement actions to require that jurisdictions experiencing significant or repeated SSOs take appropriate steps to eliminate overflows, and will fulfill the commitment in the EPA 106 grant for NPDES enforcement regarding the initiation of formal enforcement actions against 20% of jurisdictions in Maryland with CSOs and significant SSO problems annually. Under Section 106 of the Clean Water Act, EPA is authorized to issue grants to states for the purpose of assisting in establishing and carrying out pollution control programs.

Implementation and Wildlife Sources

It is expected that in some waters for which TMDLs will be developed, the bacteria source analysis indicates that after controls are in place for all anthropogenic sources, the waterbody

will not meet water quality standards. Neither Maryland, nor EPA is proposing the elimination of wildlife to allow for the attainment of water quality standards although managing the overpopulation of wildlife is an option for state and local stakeholders.

After developing and implementing to the maximum extent possible a reduction goal based on the anthropogenic sources identified in the TMDL, Maryland anticipates that implementation to reduce the controllable nonpoint sources may also reduce some wildlife inputs to the waters.

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Appendix A – Table of Bacteria Concentration Raw Data per Sampling Date with Corresponding Daily Flow Frequency

Station	Date	Daily flow frequency	*E. coli* MPN/100ml
GEO0009	10/08/2002	96.1233	34.1
GEO0009	11/07/2002	29.8783	1223.0
GEO0009	11/20/2002	28.6618	9.7
GEO0009	12/02/2002	59.6594	41.9
GEO0009	12/17/2002	40.3893	789.0
GEO0009	01/07/2003	16.8694	24192.0
GEO0009	01/21/2003	42.9035	472.0
GEO0009	02/03/2003	56.1882	228.0
GEO0009	03/18/2003	1.1517	6867.0
GEO0009	04/01/2003	19.7405	1178.0
GEO0009	04/15/2003	9.8135	7270.0
GEO0009	04/21/2003	19.8865	4884.0
GEO0009	04/28/2003	32.0032	231.0
GEO0009	05/05/2003	35.0527	1616.0
GEO0009	05/19/2003	8.5320	6867.0
GEO0009	06/02/2003	6.4720	12033.0
GEO0009	06/16/2003	9.2620	6488.0
GEO0009	07/07/2003	36.5450	2143.0
GEO0009	07/21/2003	52.5710	435.0
GEO0009	08/04/2003	41.5410	3076.0
GEO0009	08/18/2003	68.5158	495.0
GEO0009	09/08/2003	63.9578	240.0
GEO0009	09/22/2003	5.2230	576.0
GEO0009	10/07/2003	26.6342	240.0
GEO0009	10/21/2003	40.3893	410.0
GEO0065	10/08/2002	96.1233	70.8
GEO0065	11/07/2002	29.8783	1134.0
GEO0065	11/20/2002	28.6618	7.4

Station	Date	Daily flow frequency	*E. coli* MPN/100ml
GEO0065	12/02/2002	59.6594	40.2
GEO0065	12/17/2002	40.3893	41.0
GEO0065	01/07/2003	16.8694	134.0
GEO0065	01/21/2003	42.9035	110.0
GEO0065	02/03/2003	56.1882	246.0
GEO0065	03/18/2003	1.1517	226.0
GEO0065	04/01/2003	19.7405	52.0
GEO0065	04/15/2003	9.8135	201.0
GEO0065	04/21/2003	19.8865	86.0
GEO0065	04/28/2003	32.0032	107.0
GEO0065	05/05/2003	35.0527	5172.0
GEO0065	05/19/2003	8.5320	676.0
GEO0065	06/02/2003	6.4720	243.0
GEO0065	06/16/2003	9.2620	243.0
GEO0065	07/07/2003	36.5450	857.0
GEO0065	07/21/2003	52.5710	464.0
GEO0065	08/04/2003	41.5410	1785.0
GEO0065	08/18/2003	68.5158	594.0
GEO0065	09/08/2003	63.9578	529.0
GEO0065	09/22/2003	5.2230	341.0
GEO0065	10/07/2003	26.6342	97.0
GEO0065	10/21/2003	40.3893	591.0
GEO0111	10/08/2002	96.1233	34.5
GEO0111	11/07/2002	29.8783	1515.0
GEO0111	11/20/2002	28.6618	8.5
GEO0111	12/02/2002	59.6594	48.9
GEO0111	12/17/2002	40.3893	52.0
GEO0111	01/07/2003	16.8694	288.0
GEO0111	01/21/2003	42.9035	20.0
GEO0111	02/03/2003	56.1882	52.0

Station	Date	Daily flow frequency	*E. coli* MPN/100ml
GEO0111	03/18/2003	1.1517	529.0
GEO0111	04/01/2003	19.7405	10.0
GEO0111	04/15/2003	9.8135	216.0
GEO0111	04/21/2003	19.8865	20.0
GEO0111	04/28/2003	32.0032	41.0
GEO0111	05/05/2003	35.0527	583.0
GEO0111	05/19/2003	8.5320	345.0
GEO0111	06/02/2003	6.4720	305.0
GEO0111	06/16/2003	9.2620	246.0
GEO0111	07/07/2003	36.5450	96.0
GEO0111	07/21/2003	52.5710	98.0
GEO0111	08/04/2003	41.5410	419.0
GEO0111	08/18/2003	68.5158	203.0
GEO0111	09/08/2003	63.9578	281.0
GEO0111	09/22/2003	5.2230	350.0
GEO0111	10/07/2003	26.6342	20.0
GEO0111	10/21/2003	40.3893	41.0
GEO0143	10/08/2002	96.1233	133.3
GEO0143	11/07/2002	29.8783	1391.0
GEO0143	11/20/2002	28.6618	151.5
GEO0143	12/02/2002	59.6594	55.6
GEO0143	12/17/2002	40.3893	1333.0
GEO0143	01/07/2003	16.8694	488.0
GEO0143	01/21/2003	42.9035	20.0
GEO0143	02/03/2003	56.1882	52.0
GEO0143	03/18/2003	1.1517	24192.0
GEO0143	04/01/2003	19.7405	122.0
GEO0143	04/15/2003	9.8135	24192.0
GEO0143	04/21/2003	19.8865	199.0
GEO0143	04/28/2003	32.0032	97.0

Station	Date	Daily flow frequency	*E. coli* MPN/100ml
GEO0143	05/05/2003	35.0527	24192.0
GEO0143	05/19/2003	8.5320	155307.0
GEO0143	06/02/2003	6.4720	61310.0
GEO0143	06/16/2003	9.2620	11198.5
GEO0143	07/07/2003	36.5450	2282.0
GEO0143	07/21/2003	52.5710	228.0
GEO0143	08/04/2003	41.5410	5172.0
GEO0143	08/18/2003	68.5158	907.0
GEO0143	09/08/2003	63.9578	318.0
GEO0143	09/22/2003	5.2230	2382.0
GEO0143	10/07/2003	26.6342	862.0
GEO0143	10/21/2003	40.3893	121.0

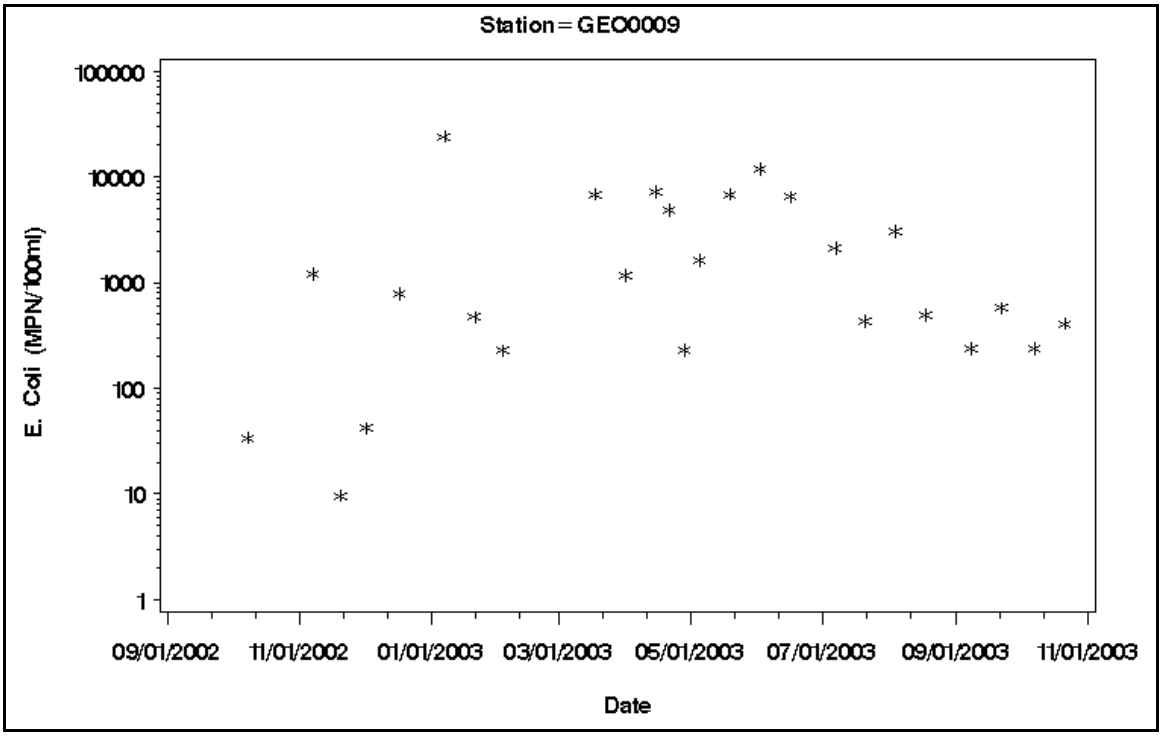

Figure A-1: *E. coli* Concentration vs. Time for Georges Creek Monitoring Station GEO0009

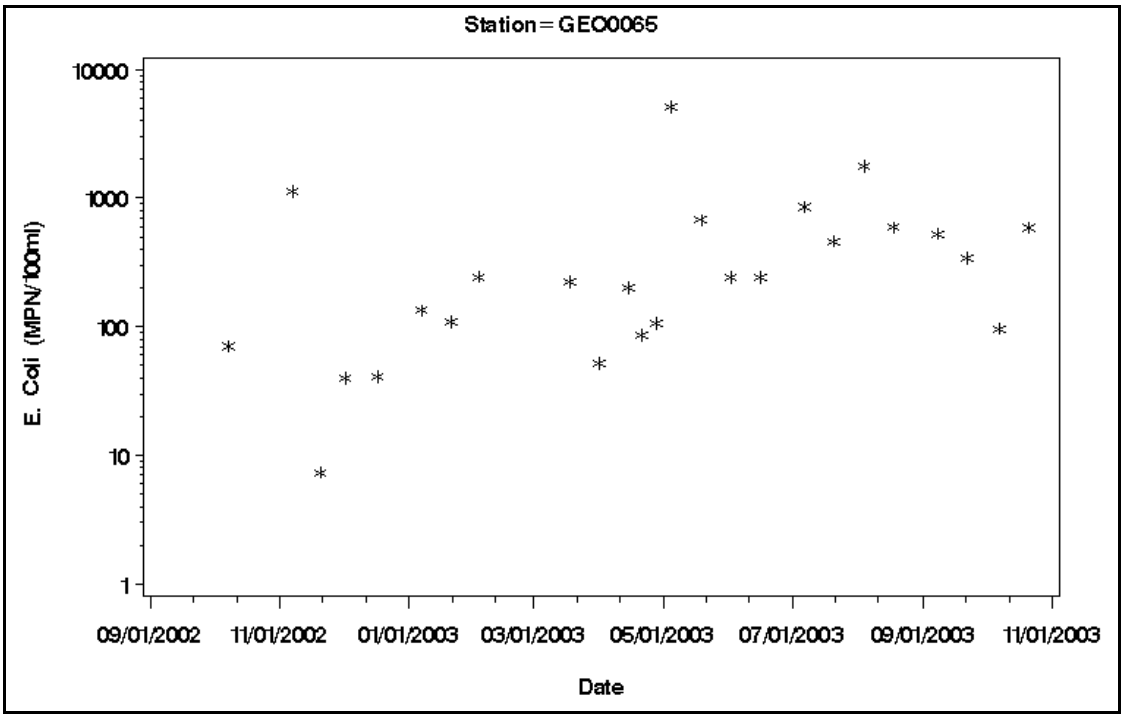

Figure A-2: *E. coli* Concentration vs. Time for Georges Creek Monitoring Station GEO0065

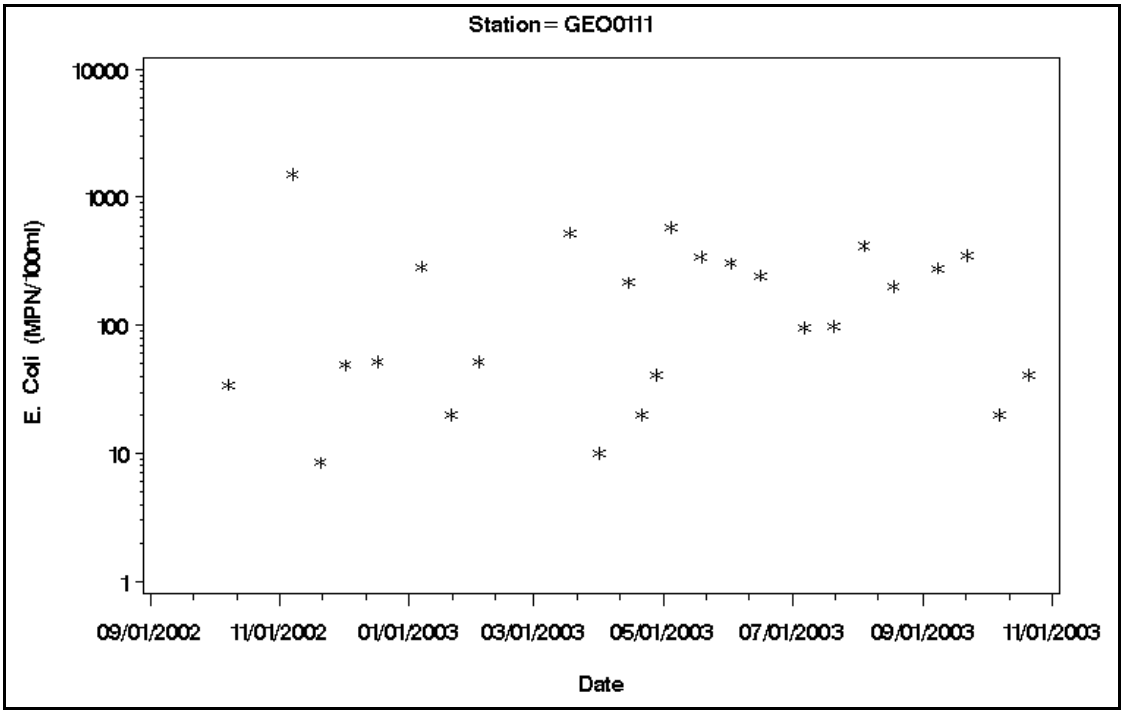

Figure A-3: *E. coli* Concentration vs. Time for Georges Creek Monitoring Station GEO0111

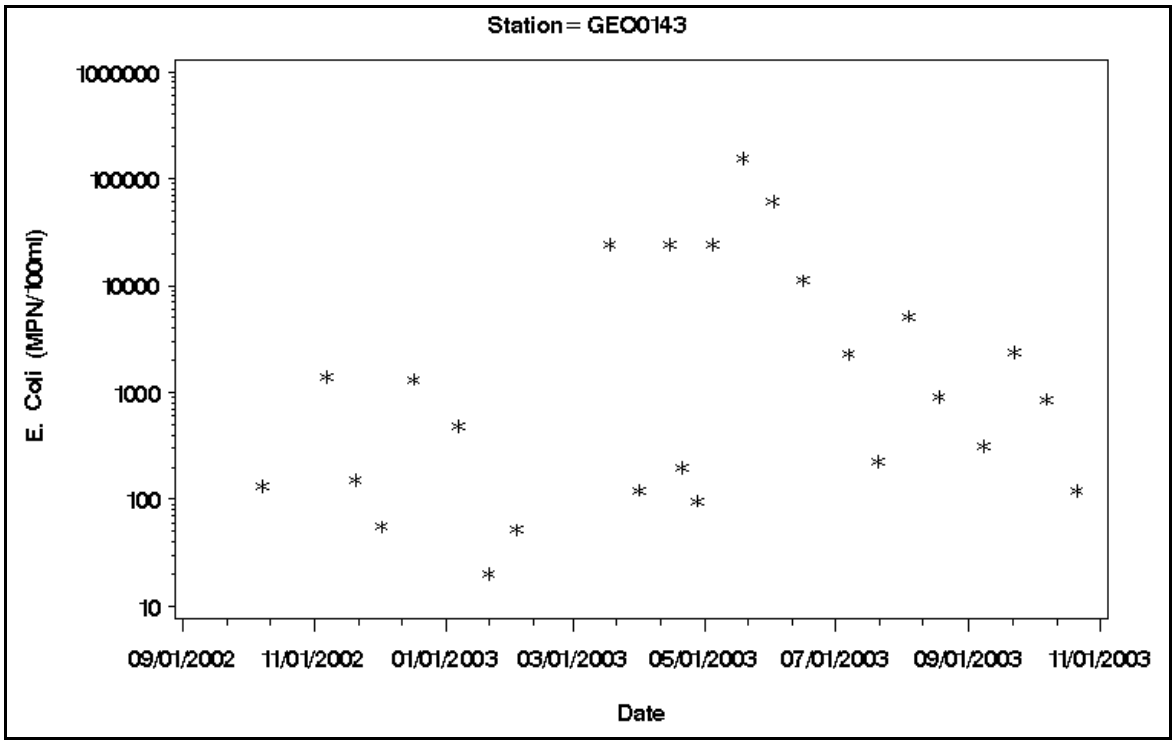

Figure A-4: *E. coli* Concentration vs. Time for Georges Creek Monitoring Station GEO0143

Appendix B - Flow Duration Curve Analysis to Define Strata

The Georges Creek watershed was assessed to determine hydrologically significant strata. The purpose of these strata is to apply weights to monitoring data and thus (1) reduce bias associated with the monitoring design and (2) approximate a critical condition for TMDL development. The strata group hydrologically similar water quality samples and provide a better estimate of the mean concentration at the monitoring station.

The flow duration curve for a watershed is a plot of all possible daily flows, ranked from highest to lowest, versus their probability of exceedence. In general, the higher flows will tend to be dominated by excess runoff from rain events and the lower flows will result from drought type conditions. The mid range flows are a combination of high base flow with limited runoff and lower base flow with excess runoff. The range of these mid level flows will vary with soil antecedent conditions. The purpose of the following analysis is to identify hydrologically significant groups, based on the previously described flow regimes, within the flow duration curve.

Flow Analysis

The Georges Creek Watershed has one active (01599000) USGS flow gauge. The gauge and dates of information used are as follows:

Table B-1: USGS Gauges in the Georges Creek Watershed

USGS Gage #	Dates used	Description
01599000	October 1, 1988 to August 17, 2005	Georges Creek in Town of Westernport

A flow duration curve for this gauge is presented in Figure B-1.

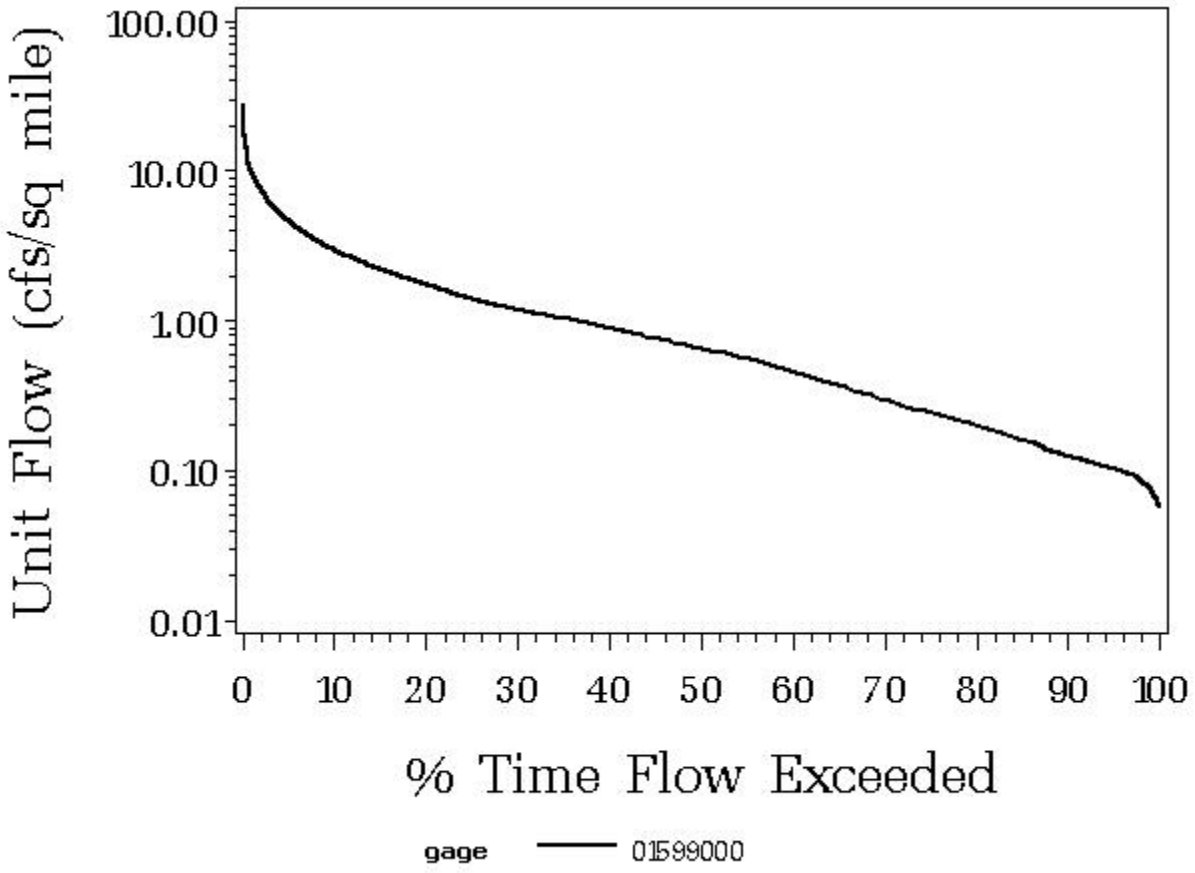

Figure B-1: Georges Creek Flow Duration Curves

Based on the long-term flow data for the Georges Creek watershed and other watersheds in the region (i. e. Wills Creek), the long term average daily unit flows ranges between 1.2 to 1.6 cfs/sq. mile, which corresponds to a range of 20th to 28th flow frequency based on the flow duration curves of these watersheds. Using the definition of a high flow condition occurring when flows are higher than the long-term average flow and a low flow condition occurring when flows are lower than the long-term average flow, the 25th percentile threshold was selected to define the limits between high flow and low flows. Therefore, a high flow condition will be defined as occurring when the daily flow duration percentile is less than 25% and a low flow condition will be define as occurring when the daily flow duration percentile is greater than 25%. Definitions of high and low range flows are presented in Table B-2.

Table B-2: Definition of Flow Regimes

High flow	Represents conditions where stream flow tends to be dominated by surface runoff.
Low flow	Represents conditions where stream flow tends to be more dominated by groundwater flow.

Flow-Data Analysis

The final analysis to define the daily flow duration intervals (flow regions, strata) includes the bacteria monitoring data. Bacteria (enterococci or *E. coli*) monitoring data are "placed" within the regions (stratum) based on the daily flow duration percentile of the date of sampling. Figures B-2 to B-5 show the Georges Creek *E. coli* monitoring data with corresponding flow frequency for the annual average and the seasonal conditions.

Maryland's water quality standards for bacteria state that a steady-state geometric mean will be calculated with available data where there are at least five representative sampling events. The data shall be from samples collected during steady-state conditions and during the beach season (Memorial Day through Labor Day) to be representative of the critical condition. If fewer than five representative sampling events are available, the previous two years will be evaluated. In Georges Creek, there are sufficient samples in the high flow strata to estimate the geometric means. For the low flow strata less than five samples exist; therefore, the mid and low flow strata will be combined to calculate the geometric mean.

Weighting factors for estimating a weighted geometric mean are based on the frequency of each flow stratum during the averaging period. The weighting factors for the averaging periods and hydrological conditions are presented in Table B-3. Averaging periods are defined in this report as:

(1) Annual Average Hydrological Condition
(2) Annual High Flow Condition
(3) Annual Low Flow Condition
(4) Seasonal (May 1st – September 30th) High Flow Condition
(5) Seasonal (May 1st – September 30th) Low Flow Condition

Weighted geometric means for the average annual and the seasonal conditions are plotted with the monitoring data on Figures B-2 to B-5.

Table B-3: Weighting Factors for Estimation of Geometric Mean

Hydrological Condition		Averaging Period	Water Quality Data Used	Fraction High Flow	Fraction Low Flow
Annual	Long Term Average	365 days	All	0.25	0.75
Annual	High flow	365 days	All	0.56	0.44
	Low flow	365 days	All	0.06	0.94
Seasonal	High flow	May 1st – Sept 30th	May 1st – Sept 30th	0.46	0.54
	Low flow	May 1st – Sept 30th	May 1st – Sept 30th	0.00	1.00

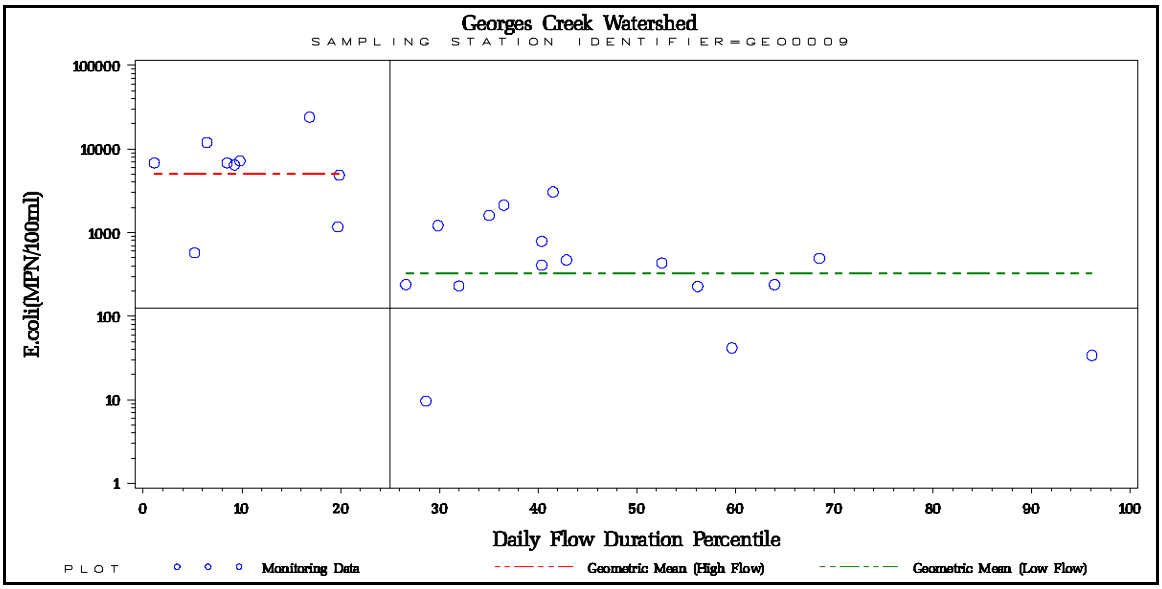

Figure B-2: *E. coli* Concentration vs. Flow Duration for Georges Creek Monitoring Station GEO0009 (Average Annual Condition)

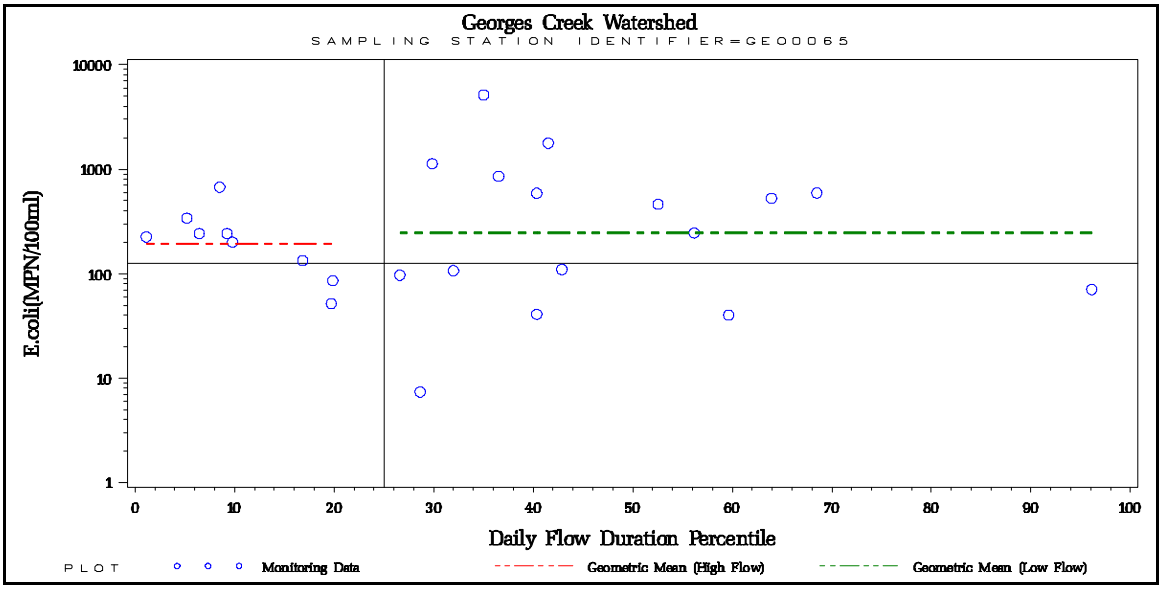

Figure B-3: *E. coli* Concentration vs. Flow Duration for Georges Creek Monitoring Station GEO0065 (Average Annual Condition)

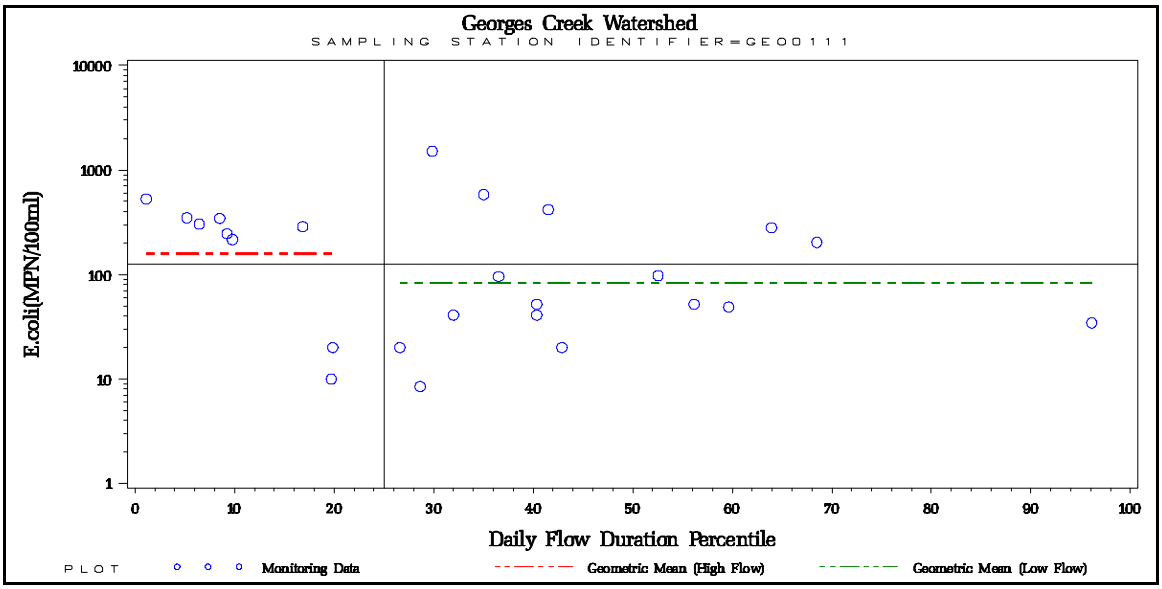

Figure B-4: *E. coli* Concentration vs. Flow Duration for Georges Creek Monitoring Station GEO0111 (Average Annual Condition)

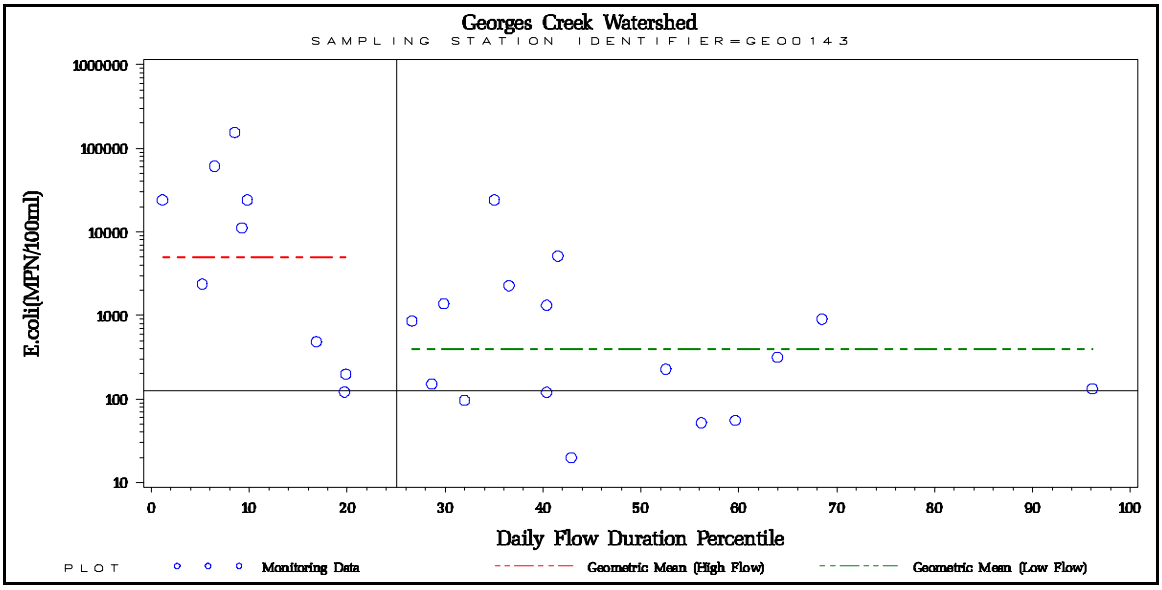

Figure B-5: *E. coli* Concentration vs. Flow Duration for Georges Creek Monitoring Station GEO0143 (Average Annual Condition)

Appendix C – Georges Creek Bacterial Source Tracking

Probable Sources of Enterococci Contamination

November 2003 – October 2005

Identifying Sources of Fecal Pollution in the Georges Creek Watershed, Maryland

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January 31, 2006

INTRODUCTION

Microbial Source Tracking. Microbial Source Tracking (MST) is a relatively recent scientific and technological innovation designed to distinguish the origins of enteric microorganisms found in environmental waters. Several different methods and a variety of different indicator organisms (both bacteria and viruses) have successfully been used for MST, as described in recent reviews (Scott *et al.*, 2002; Simpson *et al.*, 2002). When the indicator organism is bacteria, the term Bacterial Source Tracking (BST) is often used. Some common bacterial indicators for BST analysis include: *E. coli*, *Enterococcus* spp., *Bacteroides-Prevotella,* and *Bifidobacterium* spp.

Techniques for MST can be grouped into one of the following three categories: molecular (genotypic) methods, biochemical (phenotypic) methods, or chemical methods. Ribotyping, Pulsed-Field Gel Electrophoresis (PFGE), and Randomly-Amplified Polymorphic DNA (RAPD) are examples of molecular techniques. Biochemical methods include Antibiotic Resistance Analysis (ARA), F-specific coliphage typing, and Carbon Source Utilization (CSU) analysis. Chemical techniques detect chemical compounds associated with human activities, but do not provide any information regarding nonhuman sources. Examples of this type of technology include detection of optical brighteners from laundry detergents or caffeine (Simpson *et al*., 2002).

Many of the molecular and biochemical methods of MST are "library-based," requiring the collection of a database of fingerprints or patterns obtained from indicator organisms isolated from known sources. Statistical analysis determines fingerprints/patterns of known sources species or categories of species (*i.e.*, human, livestock, pets, wildlife). Indicator isolates collected from water samples are analyzed using the same MST method to obtain their fingerprints or patterns, which are then statistically compared to those in the library. Based upon this comparison, the final results are expressed in terms of the "statistical probability" that the water isolates came from a given source (Simpson *et al*. 2002).

In this BST project, we studied the following Maryland nontidal watersheds: Gwynns Falls, Jones Falls, Herring Run, Georges Creek, and Wills Creek. Also included in the study was the Patuxent River Watershed shellfish harvesting area. The methodology used was the ARA with *Enterococcus* spp. as the indicator organism. Previous BST publications have demonstrated the predictive value of using this particular technique and indicator organism (Hagedorn, 1999; Wiggins, 1999). A pilot study using PFGE, a genotypic BST method, was used on a subset of known-source isolates collected from the Patuxent River Watershed.

Antibiotic Resistance Analysis. A variety of different host species can potentially contribute to the fecal contamination found in natural waters. Many years ago, scientists speculated on the possibility of using resistance to antibiotics as a way of determining the sources of this fecal contamination (Bell *et al.*, 1983; Krumperman, 1983). In ARA, the premise is that bacteria isolated from different hosts can be discriminated based upon differences in the selective pressure of microbial populations found in the gastrointestinal tract of those hosts (humans, livestock, pets, wildlife) (Wiggins, 1996). Microorganisms isolated from the fecal material of wildlife would be expected to have a much lower level of resistance to antibiotics than isolates

collected from the fecal material of humans, livestock and pets. In addition, depending upon the specific antibiotics used in the analysis, isolates from humans, livestock and pets could be differentiated from each other.

In ARA, isolates from known sources are tested for resistance or sensitivity against a panel of antibiotics and antibiotic concentrations. This information is then used to construct a library of antibiotic resistance patterns from known-source bacterial isolates. Microbial isolates collected from water samples are then tested and their resistance results are recorded. Based upon a comparison of resistance patterns of water and library isolates, a statistical analysis can predict the likely host source of the water isolates. (Hagedorn 1999; Wiggins 1999).

LABORATORY METHODS

Isolation of *Enterococcus* from Known-Source Samples. Fecal samples, identified to source, were delivered to the Salisbury University (SU) BST lab by Maryland Department of the Environment (MDE) personnel. Fecal material suspended in phosphate buffered saline was plated onto selective m-Enterococcus agar. After incubation at 37^{o} C, up to 10 *Enterococcus* isolates were randomly selected from each fecal sample for ARA testing.

Isolation of Enterococcus from Water Samples. Water samples were collected by MDE staff and shipped overnight to MapTech Inc, Blacksburg, Va. Bacterial isolates were collected by membrane filtration. Up to 24 randomly selected *Enterococcus* isolates were collected from each water sample and all isolates were then shipped to the SU BST lab.

Antibiotic Resistance Analysis. Each bacterial isolate from both water and scat were grown in Enterococcosel® broth (Becton Dickinson, Sparks, MD) prior to ARA testing. *Enterococcus* are capable of hydrolyzing esculin, turning this broth black. Only esculin-positive isolates were tested for antibiotic resistance.

Bacterial isolates were plated onto tryptic soy agar plates, each containing a different concentration of a given antibiotic. Plates were incubated overnight at 37^{o} C and isolates then scored for growth (resistance) or no growth (sensitivity). Data consisting of a “1” for resistance or “0” for sensitivity for each isolate at each concentration of each antibiotic was then entered into a spread-sheet for statistical analysis.

The following table includes the antibiotics and concentrations used for isolates in analyses for all the study watersheds.

Table C-1: Antibiotics and concentrations used for ARA

Antibiotic	Concentration (µg/ml)
Amoxicillin	0.625
Cephalothin	10, 15, 30, 50
Chloramphenicol	10
Chlortetracycline	60, 80, 100
Erythromycin	10
Gentamycin	5, 10, 15
Neomycin	40, 60, 80
Oxytetracycline	20, 40, 60, 80, 100
Salinomycin	10
Streptomycin	40, 60, 80, 100
Tetracycline	10, 30, 50, 100
Vancomycin	2.5

KNOWN-SOURCE LIBRARY

Construction and Use. Fecal samples (scat) from known sources in each watershed were collected during the study period by MDE personnel and delivered to the BST Laboratory at SU. *Enterococcus* isolates were obtained from known sources (e.g., human, dog, cow, beaver, coyote, deer, fox, rabbit, and goose). For each watershed, a library of patterns of *Enterococcus* isolate responses to the panel of antibiotics was analyzed using the statistical software CART® (Salford Systems, San Diego, CA). *Enterococcus* isolate response patterns were also obtained from bacteria in water samples collected at the monitoring stations in each basin. Using statistical techniques, these patterns were then compared to those in the appropriate library to identify the probable source of each water isolate. A combined library of known sources was used for Georges Creek and Wills Creek Watersheds using patterns from scat obtained from both watersheds, and the water isolate patterns of each were compared to the combined library.

STATISTICAL ANALYSIS

We applied a tree classification method, [1]CART®, to build a model that classifies isolates into source categories based on ARA data. CART® builds a classification tree by recursively splitting the library of isolates into two nodes. Each split is determined by the antibiotic variables (antibiotic resistance measured for a collection of antibiotics at varying concentrations).

[1] The Elements of Statistical Learning: Data Mining, Inference, and Prediction. Hastie T, Tibshirani R, and Friedman J. Springer 2001.

The *stopping* criterion are referred to as *terminal* nodes.[2] The collection of *terminal* nodes defines the classification model. Each *terminal* node is associated with one source, the source that is most populous among the library isolates in the node. Each water sample isolate (*i.e.*, an isolate with an unknown source), based on its antibiotic resistance pattern, is identified with one specific *terminal* node and is assigned the source of the majority of library isolates in that *terminal* node[3].

ARA RESULTS

Georges Creek Watershed

Known-Source Library. An 827 known-source isolate library was constructed that included 436 isolates from sources in the Georges Creek Watershed combined with the 391 isolates from the adjacent Wills Creek Watershed. The known sources in the combined library were grouped into four categories: domestic (pets, specifically dogs), human, livestock (cow), and wildlife (deer, coyote, beaver, fox, rabbit) (Tables C-2a and C-2b). The library was analyzed for its ability to take a subset of the library isolates and correctly predict the identity of their host sources when they were treated as unknowns. Average rates of correct classification (ARCC) for the library were found by repeating this analysis using several probability cutoff points, as described above. The number-not-classified for each probability was determined. From these results, the percent unknown and percent correct classification (RCCs) was calculated (Table C-3).

Table C-2a: Georges Creek. Category, total number, and number of unique patterns in the Georges Creek portion of the combined Georges-Wills known source library

Category	Potential Sources	Total Isolates	Unique Patterns
Pet	dog	55	33
Human	human	135	93
Livestock	cow	54	8
Wildlife	deer, fox, rabbit	192	45
Total		**436**	**179**

[2] An ideal split, i.e., a split that achieves the theoretical maximum for homogeneity, would produce two nodes each containing library isolates from only one source.

[3] The CART® tree-classification method we employed includes various features to ensure the development of an optimal classification model. For brevity in exposition, we have chosen not to present details of those features, but suggest the following sources: Breiman L, et al. *Classification and Regression Trees*. Pacific Grove: Wadsworth, 1984; and Steinberg D and Colla P. *CART—Classification and Regression Trees.* San Diego, CA: Salford Systems, 1997.

Table C-2b: Combined GE-WI: Combined Georges-Wills Library. Category, total number, and number of unique patterns in Georges and Wills known-source libraries

Category	Potential Sources	Total Isolates	Unique Patterns (GE + WI)
Pet	dog	114	58
Human	human	219	147
Livestock	cow	123	40
Wildlife	beaver coyote, deer, fox, rabbit	371	90
Total		**827**	**335**

Table C-3: Georges Creek. Number of isolates not classified, percent unknown, and percent correct for six (6) cutoff probabilities for Georges Creek known source isolates using the combined Georges-Wills known-source library

Cutoff Probability	Number Not Classified	Percent Unknown	Percent Correct
.25	0	0%	75%
.375	0	0%	75%
.50	96	22%	79%
.60	105	24%	79.5%
.70	166	38%	81%
.80	228	53%	90.5%
.90	293	57%	94%

For Georges Creek Watershed, a cutoff probability of 0.70 (70%) was shown to yield an ARCC of 81%. An increase to a 0.80 (80%) cutoff increased the rate of correct classification significantly (Figure C-1). Therefore, using a cutoff probability of 0.80 (80%), the 228 isolates that were not useful in the prediction of probable sources were removed; leaving 599 isolates remaining in the combined library. This library was then used in the statistical prediction of probable sources of bacteria in water samples collected from the Georges Creek Watershed. The rates of correction classification for the four categories of sources in the Georges Creek portion of the library, using an (0.80) 80% probability cutoff, are shown in Table C-4 below.

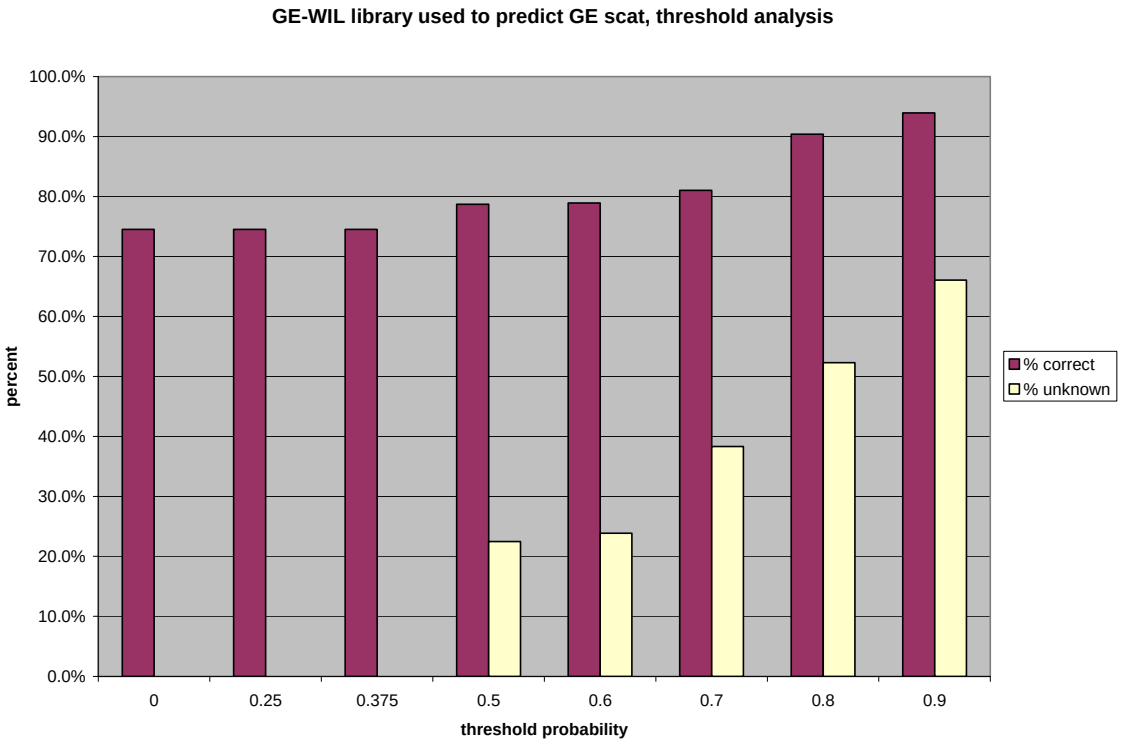

Figure C-1: Georges Creek Classification Model: Percent Correct versus Percent Unknown

Table C-4: Georges Creek. Actual species categories versus predicted categories, at 80% probability cutoff, with rates of correct classification (RCC) for each category

	Predicted →					
Actual ↓	HUMAN	LIVESTOCK	PET	WILDLIFE	TOTAL	RCC[1]
HUMAN	**87**	0	4	2	93	94%
LIVESTOCK	0	**2**	0	0	2	100%
PET	1	0	**40**	0	41	98%
WILDLIFE	4	0	9	**59**	72	82%
Total	92	2	53	6	**208**	

[1]RCC = Actual number of predicted species category / Total number predicted. Example: One hundred sixty-three (163) domestic correctly predicted /175 total number predicted for domestic = 163/175 = 93%.

Georges Creek Water Samples. Monthly monitoring from six (6) stations on Georges Creek was the source of water samples. The maximum number of *Enterococcus* isolates per water sample was 24, although the number of isolates that actually grew was sometimes fewer than 24. A total of 909 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table C-5, indicates that 57% of the water isolates were classified after excluding unknowns when using an 0.80 (80%) probability cutoff.

Table C-5: Probable host sources of water isolates by species category, number of isolates, and percent isolates classified at a cutoff probability of 80%

Category	Number.	% Isolates Classified 80% Prob.	% Isolates Classified (excluding unknowns)
DOMESTIC	95	10%	18%
HUMAN	264	29%	51%
LIVESTOCK	27	3%	5%
WILDLIFE	132	15%	25%
UNKNOWN	391	43%	
Missing Data	0		0
Total	909		
% Classified	**57%**		

The seasonal distribution of water isolates from samples collected at each sampling station is shown below in Table C-6.

Table C-6: Georges Creek. Enterococcus isolates obtained from water collected during the fall, winter, spring, and summer seasons for each of the six (6) monitoring stations

Station	Spring	Summer	Fall	Winter	Total
Barton	0	15	21	0	**36**
Frostburg	92	58	72	43	**265**
Gage	82	49	29	33	**193**
Lonaconing	81	48	19	35	**183**
Midland	83	64	40	23	**210**
Outlet	0	0	22	0	**22**
Total	**338**	**234**	**203**	**134**	**909**

Tables C-7 through C-11 on the following pages show the results of BST analysis from the estimation of number of isolates per station per date to the final estimation of the overall percentage of bacteria sources by subwatershed.

Table C-7: BST Analysis - Number of Isolates per Station per Date

Station	Date	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0009	**11/20/2002**	3	2	0	1	9
GEO0009	**12/02/2002**	0	2	2	0	1
GEO0009	**01/07/2003**	4	7	0	1	12
GEO0009	**02/03/2003**	2	5	0	1	1
GEO0009	**04/01/2003**	1	1	1	1	7
GEO0009	**04/15/2003**	1	3	0	4	16
GEO0009	**05/05/2003**	10	7	0	0	6
GEO0009	**06/02/2003**	5	5	0	1	13
GEO0009	**07/07/2003**	3	7	3	1	9
GEO0009	**08/04/2003**	2	5	0	6	6
GEO0009	**09/08/2003**	0	0	0	4	3
GEO0009	**10/07/2003**	0	5	0	0	4
GEO0065	**11/20/2002**	0	0	0	1	2
GEO0065	**12/02/2002**	4	0	0	0	3
GEO0065	**01/07/2003**	2	4	2	6	6
GEO0065	**02/03/2003**	3	4	2	1	5
GEO0065	**04/01/2003**	2	2	0	0	6
GEO0065	**04/15/2003**	6	9	0	2	7
GEO0065	**05/05/2003**	2	14	0	1	7
GEO0065	**06/02/2003**	2	5	0	2	14
GEO0065	**07/07/2003**	2	14	0	3	5
GEO0065	**08/04/2003**	2	15	0	1	6
GEO0065	**10/07/2003**	0	0	1	5	3
GEO0111	**11/20/2002**	0	3	0	3	3

Station	Date	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0111	**12/02/2002**	2	0	1	1	5
GEO0111	**01/07/2003**	0	10	0	7	6
GEO0111	**04/01/2003**	0	5	0	3	4
GEO0111	**04/15/2003**	3	2	0	10	9
GEO0111	**05/05/2003**	2	12	0	2	7
GEO0111	**06/02/2003**	1	0	0	2	21
GEO0111	**07/07/2003**	0	0	0	14	9
GEO0111	**08/04/2003**	5	5	0	3	11
GEO0111	**09/08/2003**	1	4	2	2	8
GEO0111	**09/22/2003**	1	7	0	8	6
GEO0143	**11/20/2002**	1	7	0	2	14
GEO0143	**12/02/2002**	2	4	0	4	5
GEO0143	**01/07/2003**	0	7	0	6	11
GEO0143	**02/03/2003**	1	4	4	3	7
GEO0143	**04/01/2003**	2	16	0	4	2
GEO0143	**04/15/2003**	2	8	0	0	14
GEO0143	**05/05/2003**	5	13	0	1	5
GEO0143	**06/02/2003**	3	6	0	1	10
GEO0143	**07/07/2003**	2	12	0	1	9
GEO0143	**08/04/2003**	1	6	2	1	13
GEO0143	**09/08/2003**	1	1	0	2	7
GEO0143	**09/22/2003**	2	4	2	4	12
GEO0143	**10/07/2003**	0	3	0	0	6

Table C-8: Percentage of Sources per Station per Date

Station	Date	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0009	**11/20/2002**	20.0000	13.3333	0.0000	6.6667	60.0000
GEO0009	**12/02/2002**	0.0000	40.0000	40.0000	0.0000	20.0000
GEO0009	**01/07/2003**	16.6667	29.1667	0.0000	4.1667	50.0000
GEO0009	**02/03/2003**	22.2222	55.5556	0.0000	11.1111	11.1111
GEO0009	**04/01/2003**	9.0909	9.0909	9.0909	9.0909	63.6364
GEO0009	**04/15/2003**	4.1667	12.5000	0.0000	16.6667	66.6667
GEO0009	**05/05/2003**	43.4783	30.4348	0.0000	0.0000	26.0870
GEO0009	**06/02/2003**	20.8333	20.8333	0.0000	4.1667	54.1667
GEO0009	**07/07/2003**	13.0435	30.4348	13.0435	4.3478	39.1304
GEO0009	**08/04/2003**	10.5263	26.3158	0.0000	31.5789	31.5789
GEO0009	**09/08/2003**	0.0000	0.0000	0.0000	57.1429	42.8571
GEO0009	**10/07/2003**	0.0000	55.5556	0.0000	0.0000	44.4444
GEO0065	**11/20/2002**	0.0000	0.0000	0.0000	33.3333	66.6667
GEO0065	**12/02/2002**	57.1429	0.0000	0.0000	0.0000	42.8571
GEO0065	**01/07/2003**	10.0000	20.0000	10.0000	30.0000	30.0000
GEO0065	**02/03/2003**	20.0000	26.6667	13.3333	6.6667	33.3333
GEO0065	**04/01/2003**	20.0000	20.0000	0.0000	0.0000	60.0000
GEO0065	**04/15/2003**	25.0000	37.5000	0.0000	8.3333	29.1667
GEO0065	**05/05/2003**	8.3333	58.3333	0.0000	4.1667	29.1667
GEO0065	**06/02/2003**	8.6957	21.7391	0.0000	8.6957	60.8696
GEO0065	**07/07/2003**	8.3333	58.3333	0.0000	12.5000	20.8333
GEO0065	**08/04/2003**	8.3333	62.5000	0.0000	4.1667	25.0000
GEO0065	**10/07/2003**	0.0000	0.0000	11.1111	55.5556	33.3333
GEO0111	**11/20/2002**	0.0000	33.3333	0.0000	33.3333	33.3333
GEO0111	**12/02/2002**	22.2222	0.0000	11.1111	11.1111	55.5556
GEO0111	**01/07/2003**	0.0000	43.4783	0.0000	30.4348	26.0870
GEO0111	**04/01/2003**	0.0000	41.6667	0.0000	25.0000	33.3333
GEO0111	**04/15/2003**	12.5000	8.3333	0.0000	41.6667	37.5000

Station	Date	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0111	**05/05/2003**	8.6957	52.1739	0.0000	8.6957	30.4348
GEO0111	**06/02/2003**	4.1667	0.0000	0.0000	8.3333	87.5000
GEO0111	**07/07/2003**	0.0000	0.0000	0.0000	60.8696	39.1304
GEO0111	**08/04/2003**	20.8333	20.8333	0.0000	12.5000	45.8333
GEO0111	**09/08/2003**	5.8824	23.5294	11.7647	11.7647	47.0588
GEO0111	**09/22/2003**	4.5455	31.8182	0.0000	36.3636	27.2727
GEO0143	**11/20/2002**	4.1667	29.1667	0.0000	8.3333	58.3333
GEO0143	**12/02/2002**	13.3333	26.6667	0.0000	26.6667	33.3333
GEO0143	**01/07/2003**	0.0000	29.1667	0.0000	25.0000	45.8333
GEO0143	**02/03/2003**	5.2632	21.0526	21.0526	15.7895	36.8421
GEO0143	**04/01/2003**	8.3333	66.6667	0.0000	16.6667	8.3333
GEO0143	**04/15/2003**	8.3333	33.3333	0.0000	0.0000	58.3333
GEO0143	**05/05/2003**	20.8333	54.1667	0.0000	4.1667	20.8333
GEO0143	**06/02/2003**	15.0000	30.0000	0.0000	5.0000	50.0000
GEO0143	**07/07/2003**	8.3333	50.0000	0.0000	4.1667	37.5000
GEO0143	**08/04/2003**	4.3478	26.0870	8.6957	4.3478	56.5217
GEO0143	**09/08/2003**	9.0909	9.0909	0.0000	18.1818	63.6364
GEO0143	**09/22/2003**	8.3333	16.6667	8.3333	16.6667	50.0000
GEO0143	**10/07/2003**	0.0000	33.3333	0.0000	0.0000	66.6667

Table C-9: *E. coli* Concentration and Percentage of Sources by Stratum (Annual Period)

Station	Date	flow regime (1=high/ 2=low)	*E. coli* Concentration MPN/100ml	log mean conc	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0009	**10/08/2002**	2	34.1	1.53275	.	.	.	.	.
GEO0009	**11/07/2002**	2	1223.0	3.08743	.	.	.	.	.
GEO0009	**11/20/2002**	2	9.7	0.98677	20.0000	13.3333	0.0000	6.6667	60.0000
GEO0009	**12/02/2002**	2	41.9	1.62221	0.0000	40.0000	40.0000	0.0000	20.0000
GEO0009	**12/17/2002**	2	789.0	2.89708	.	.	.	.	.
GEO0009	**01/07/2003**	1	24192.0	4.38367	16.6667	29.1667	0.0000	4.1667	50.0000
GEO0009	**01/21/2003**	2	472.0	2.67394	.	.	.	.	.
GEO0009	**02/03/2003**	2	228.0	2.35793	22.2222	55.5556	0.0000	11.1111	11.1111
GEO0009	**03/18/2003**	1	6867.0	3.83677	.	.	.	.	.
GEO0009	**04/01/2003**	1	1178.0	3.07115	9.0909	9.0909	9.0909	9.0909	63.6364
GEO0009	**04/15/2003**	1	7270.0	3.86153	4.1667	12.5000	0.0000	16.6667	66.6667
GEO0009	**04/21/2003**	1	4884.0	3.68878	.	.	.	.	.
GEO0009	**04/28/2003**	2	231.0	2.36361	.	.	.	.	.
GEO0009	**05/05/2003**	2	1616.0	3.20844	43.4783	30.4348	0.0000	0.0000	26.0870
GEO0009	**05/19/2003**	1	6867.0	3.83677	.	.	.	.	.
GEO0009	**06/02/2003**	1	12033.0	4.08037	20.8333	20.8333	0.0000	4.1667	54.1667
GEO0009	**06/16/2003**	1	6488.0	3.81211	.	.	.	.	.
GEO0009	**07/07/2003**	2	2143.0	3.33102	13.0435	30.4348	13.0435	4.3478	39.1304
GEO0009	**07/21/2003**	2	435.0	2.63849	.	.	.	.	.
GEO0009	**08/04/2003**	2	3076.0	3.48799	10.5263	26.3158	0.0000	31.5789	31.5789
GEO0009	**08/18/2003**	2	495.0	2.69461	.	.	.	.	.
GEO0009	**09/08/2003**	2	240.0	2.38021	0.0000	0.0000	0.0000	57.1429	42.8571
GEO0009	**09/22/2003**	1	576.0	2.76042	.	.	.	.	.
GEO0009	**10/07/2003**	2	240.0	2.38021	0.0000	55.5556	0.0000	0.0000	44.4444
GEO0009	**10/21/2003**	2	410.0	2.61278	.	.	.	.	.
GEO0065	**10/08/2002**	2	70.8	1.85003	.	.	.	.	.
GEO0065	**11/07/2002**	2	1134.0	3.05461	.	.	.	.	.

Station	Date	flow regime (1=high/ 2=low)	*E. coli* Concentration MPN/100ml	log mean conc	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0065	**11/20/2002**	2	7.4	0.86923	0.0000	0.0000	0.0000	33.3333	66.6667
GEO0065	**12/02/2002**	2	40.2	1.60423	57.1429	0.0000	0.0000	0.0000	42.8571
GEO0065	**12/17/2002**	2	41.0	1.61278	.	.	.	.	.
GEO0065	**01/07/2003**	1	134.0	2.12710	10.0000	20.0000	10.0000	30.0000	30.0000
GEO0065	**01/21/2003**	2	110.0	2.04139	.	.	.	.	.
GEO0065	**02/03/2003**	2	246.0	2.39094	20.0000	26.6667	13.3333	6.6667	33.3333
GEO0065	**03/18/2003**	1	226.0	2.35411	.	.	.	.	.
GEO0065	**04/01/2003**	1	52.0	1.71600	20.0000	20.0000	0.0000	0.0000	60.0000
GEO0065	**04/15/2003**	1	201.0	2.30320	25.0000	37.5000	0.0000	8.3333	29.1667
GEO0065	**04/21/2003**	1	86.0	1.93450	.	.	.	.	.
GEO0065	**04/28/2003**	2	107.0	2.02938	.	.	.	.	.
GEO0065	**05/05/2003**	2	5172.0	3.71366	8.3333	58.3333	0.0000	4.1667	29.1667
GEO0065	**05/19/2003**	1	676.0	2.82995	.	.	.	.	.
GEO0065	**06/02/2003**	1	243.0	2.38561	8.6957	21.7391	0.0000	8.6957	60.8696
GEO0065	**06/16/2003**	1	243.0	2.38561	.	.	.	.	.
GEO0065	**07/07/2003**	2	857.0	2.93298	8.3333	58.3333	0.0000	12.5000	20.8333
GEO0065	**07/21/2003**	2	464.0	2.66652	.	.	.	.	.
GEO0065	**08/04/2003**	2	1785.0	3.25164	8.3333	62.5000	0.0000	4.1667	25.0000
GEO0065	**08/18/2003**	2	594.0	2.77379	.	.	.	.	.
GEO0065	**09/08/2003**	2	529.0	2.72346	.	.	.	.	.
GEO0065	**09/22/2003**	1	341.0	2.53275	.	.	.	.	.
GEO0065	**10/07/2003**	2	97.0	1.98677	0.0000	0.0000	11.1111	55.5556	33.3333
GEO0065	**10/21/2003**	2	591.0	2.77159	.	.	.	.	.
GEO0111	**10/08/2002**	2	34.5	1.53782	.	.	.	.	.
GEO0111	**11/07/2002**	2	1515.0	3.18041	.	.	.	.	.
GEO0111	**11/20/2002**	2	8.5	0.92942	0.0000	33.3333	0.0000	33.3333	33.3333
GEO0111	**12/02/2002**	2	48.9	1.68931	22.2222	0.0000	11.1111	11.1111	55.5556
GEO0111	**12/17/2002**	2	52.0	1.71600	.	.	.	.	.
GEO0111	**01/07/2003**	1	288.0	2.45939	0.0000	43.4783	0.0000	30.4348	26.0870

Station	Date	flow regime (1=high/ 2=low)	*E. coli* Concentration MPN/100ml	log mean conc	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0111	**01/21/2003**	2	20.0	1.30103	.	.	.	.	.
GEO0111	**02/03/2003**	2	52.0	1.71600	.	.	.	.	.
GEO0111	**03/18/2003**	1	529.0	2.72346	.	.	.	.	.
GEO0111	**04/01/2003**	1	10.0	1.00000	0.0000	41.6667	0.0000	25.0000	33.3333
GEO0111	**04/15/2003**	1	216.0	2.33445	12.5000	8.3333	0.0000	41.6667	37.5000
GEO0111	**04/21/2003**	1	20.0	1.30103	.	.	.	.	.
GEO0111	**04/28/2003**	2	41.0	1.61278	.	.	.	.	.
GEO0111	**05/05/2003**	2	583.0	2.76567	8.6957	52.1739	0.0000	8.6957	30.4348
GEO0111	**05/19/2003**	1	345.0	2.53782	.	.	.	.	.
GEO0111	**06/02/2003**	1	305.0	2.48430	4.1667	0.0000	0.0000	8.3333	87.5000
GEO0111	**06/16/2003**	1	246.0	2.39094	.	.	.	.	.
GEO0111	**07/07/2003**	2	96.0	1.98227	0.0000	0.0000	0.0000	60.8696	39.1304
GEO0111	**07/21/2003**	2	98.0	1.99123	.	.	.	.	.
GEO0111	**08/04/2003**	2	419.0	2.62221	20.8333	20.8333	0.0000	12.5000	45.8333
GEO0111	**08/18/2003**	2	203.0	2.30750	.	.	.	.	.
GEO0111	**09/08/2003**	2	281.0	2.44871	5.8824	23.5294	11.7647	11.7647	47.0588
GEO0111	**09/22/2003**	1	350.0	2.54407	4.5455	31.8182	0.0000	36.3636	27.2727
GEO0111	**10/07/2003**	2	20.0	1.30103	.	.	.	.	.
GEO0111	**10/21/2003**	2	41.0	1.61278	.	.	.	.	.
GEO0143	**10/08/2002**	2	133.3	2.12483	.	.	.	.	.
GEO0143	**11/07/2002**	2	1391.0	3.14333	.	.	.	.	.
GEO0143	**11/20/2002**	2	151.5	2.18041	4.1667	29.1667	0.0000	8.3333	58.3333
GEO0143	**12/02/2002**	2	55.6	1.74507	13.3333	26.6667	0.0000	26.6667	33.3333
GEO0143	**12/17/2002**	2	1333.0	3.12483	.	.	.	.	.
GEO0143	**01/07/2003**	1	488.0	2.68842	0.0000	29.1667	0.0000	25.0000	45.8333
GEO0143	**01/21/2003**	2	20.0	1.30103	.	.	.	.	.
GEO0143	**02/03/2003**	2	52.0	1.71600	5.2632	21.0526	21.0526	15.7895	36.8421
GEO0143	**03/18/2003**	1	24192.0	4.38367	.	.	.	.	.
GEO0143	**04/01/2003**	1	122.0	2.08636	8.3333	66.6667	0.0000	16.6667	8.3333

Station	Date	flow regime (1=high/ 2=low)	*E. coli* Concentration MPN/100ml	log mean conc	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0143	**04/15/2003**	1	24192.0	4.38367	8.3333	33.3333	0.0000	0.0000	58.3333
GEO0143	**04/21/2003**	1	199.0	2.29885	.	.	.	.	.
GEO0143	**04/28/2003**	2	97.0	1.98677	.	.	.	.	.
GEO0143	**05/05/2003**	2	24192.0	4.38367	20.8333	54.1667	0.0000	4.1667	20.8333
GEO0143	**05/19/2003**	1	155307.0	5.19119	.	.	.	.	.
GEO0143	**06/02/2003**	1	61310.0	4.78753	15.0000	30.0000	0.0000	5.0000	50.0000
GEO0143	**06/16/2003**	1	11198.5	4.04916	.	.	.	.	.
GEO0143	**07/07/2003**	2	2282.0	3.35832	8.3333	50.0000	0.0000	4.1667	37.5000
GEO0143	**07/21/2003**	2	228.0	2.35793	.	.	.	.	.
GEO0143	**08/04/2003**	2	5172.0	3.71366	4.3478	26.0870	8.6957	4.3478	56.5217
GEO0143	**08/18/2003**	2	907.0	2.95761	.	.	.	.	.
GEO0143	**09/08/2003**	2	318.0	2.50243	9.0909	9.0909	0.0000	18.1818	63.6364
GEO0143	**09/22/2003**	1	2382.0	3.37694	8.3333	16.6667	8.3333	16.6667	50.0000
GEO0143	**10/07/2003**	2	862.0	2.93551	0.0000	33.3333	0.0000	0.0000	66.6667
GEO0143	**10/21/2003**	2	121.0	2.08279	.	.	.	.	.

Table C-10: Percentage of Sources per Station by Stratum (Annual Period)

Station	flow regime (1=high/2=low)	% domestic animals	% human	% livestock	% wildlife	% unknown
GEO0009	1	13.1248	18.7737	1.81334	8.2839	58.0043
GEO0009	2	14.7709	31.9969	5.48407	14.8531	32.8951
GEO0065	1	15.6958	25.2104	2.49312	12.1603	44.4403
GEO0065	2	13.2526	39.0882	3.22126	13.1929	31.2449
GEO0111	1	4.7214	23.0081	0.00000	28.6757	43.5949
GEO0111	2	10.5023	23.1172	3.82537	20.5865	41.9687
GEO0143	1	8.8825	32.5311	1.62451	10.5180	46.4439
GEO0143	2	8.8570	34.1290	3.03612	8.2406	45.7373

Table C-11: Overall Percentage of Sources per Station (Annual Period)

Station	% domestic animals	% human	% livestock	% wildlife	% unknown	total
GEO0009	14.3593	28.6911	4.56639	13.2108	39.1724	100
GEO0065	13.8634	35.6188	3.03923	12.9348	34.5438	100
GEO0111	9.0571	23.0899	2.86903	22.6088	42.3752	100
GEO0143	8.8634	33.7295	2.68321	8.8100	45.9139	100

Georges Creek Summary

The use of ARA was successful for identification of bacterial sources in the Georges Creek Watershed as evidenced by the high RCCs (82% – 100%) for source categories in the library. The lower RCC of 82% (for wildlife) is acceptable, especially given that no remedial action will be taken for wildlife sources. When water isolates were compared to the library and potential sources predicted, 57% of the isolates were classified by statistical analysis. The largest category of potential sources in the watershed as a whole was human (51% of classified water isolates), followed by pet and wildlife (18% and 25% of classified isolates, respectively). The potential contribution by livestock was low and made up only 5% of classified isolates.

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