Total Maximum Daily Loads of Fecal Bacteria for the Little Youghiogheny River Basin in Garrett County, Maryland

FINAL

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Submitted to:

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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
cfs	Cubic Feet per Second
CFR	Code of Federal Regulations
CFU	Colony Forming Units
COMAR	Code of Maryland Regulations
CSO	Combined Sewer Overflow
CSS	Combined Sewer System
CWA	Clean Water Act
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
MGD	Millions of Gallons per Day
ml	Milliliter(s)
MOS	Margin of Safety
MPN	Most Probable Number
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
RESAC	Mid-Atlantic Regional Earth Science Applications Center
SSO	Sanitary Sewer Overflows
SW	Stormwater
STATSGO	State Soil Geographic Database
TMDL	Total Maximum Daily Load
USGS	United States Geological Survey
WQIA	Water Quality Improvement Act
WLA	Waste Load Allocation
WQLS	Water Quality Limited Segment
WWTP	Wastewater Treatment Plant

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 Little Youghiogheny River watershed (MD basin number 05-02-02-02). Section 303(d) of the federal Clean Water Act (CWA) and the EPA's 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, states are 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 Little Youghiogheny River and its tributaries in the State of Maryland's 303(d) List as impaired by nutrients (listed in 1996), sediments (1996), fecal bacteria (2002) and impacts to biological communities (2002 and 2006). Broadford Lake, located within the Little Youghiogheny River watershed, has been identified as impaired by nutrients (1998) and methylmercury (2002). The Little Youghiogheny River has been designated as Use III-P (Nontidal Cold Water and Public Water Supply). Broad Ford Run and all its tributaries above Broadford Dam have been designated as Use I-P (Water Contact Recreation, Protection of Aquatic Life, and Public Water Supply). All other waters of the watershed are designated as Use I (Water Contact Recreation and Protection of Aquatic Life). See Code of Maryland Regulations (COMAR) 26.08.02.08S. This document proposes to establish a TMDL for fecal bacteria in the Little Youghiogheny River watershed that will allow for attainment of the beneficial use designation of water contact recreation. The Little Youghiogheny River listings for nutrients and sediments have been addressed by TMDLs approved in 2001 and 2007, respectively. The Broadford Lake listings for nutrients and methylmercury have been addressed respectively by a TMDL, approved by EPA in 2000, and a Water Quality Analysis, approved in 2004. The listings for impacts to biological communities will be addressed separately at a future date. MDE monitored the Little Youghiogheny River watershed from 2003-2004 for fecal bacteria. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years were considered.

For this TMDL analysis, the Little Youghiogheny River watershed has been divided into six subwatersheds. For convenience, the subwatersheds will be referenced by the downstream bacteria monitoring station's name and location: LYO0051 (Little Youghiogheny River above Broad Ford Run), BFR0028 (Broad Ford Run above lake), BFR0001 (Broad Ford Run at mouth), ZBQ0005 (unnamed tributary), TRO0012 (Trout Run) and LYO0015 (Little Youghiogheny River in Oakland). The pollutant loads set forth in this document are for these six subwatersheds. To establish baseline and allowable pollutant loads for this TMDL, bacteria data from MDE were used in conjunction with flows estimated from regional regression equations (Versar 2004).

The sources of fecal bacteria are estimated at six representative stations in the Little Youghiogheny River 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 (agriculture-related animals), and wildlife (mammals and waterfowl) source categories.

The baseline load is estimated from current monitoring data using a long-term geometric mean and average flows from regional regression equations. The TMDL for fecal bacteria entering the Little Youghiogheny River watershed is established after considering two different loading conditions: an average annual condition and an average seasonal dry weather condition (the period between May 1st and September 30th when water contact recreation is more prevalent). The allowable load quantified by the TMDL is reported in units of Most Probable Number (MPN)/day and represents a long-term load estimated over average flow conditions.

Two scenarios were developed, with the first assessing if attainment of current water quality standards could be achieved by applying maximum practicable reductions (MPRs), and the second applying higher reductions than MPRs. 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 five of the six subwatersheds, it was estimated that water quality standards could not be attained with MPRs; therefore, higher maximum reductions were applied.

The baseline loads are summarized in the following table:

MD 8-Digit Little Youghiogheny River Watershed Fecal Bacteria Baseline Loads (Billion MPN *E. coli*/year)

Total Baseline Load (BL)	=	**Nonpoint Source BL**	+	**Stormwater BL**	+	**WWTP BL**
1,216,388	=	1,214,821	+	0	+	1,567

The MD 8-digit Little Youghiogheny River watershed TMDL, representing the sum of individual TMDLs for the six subwatersheds, is distributed between a load allocation (LA) for nonpoint sources and waste load allocations (WLA) for point sources. Point sources include any National Pollutant Discharge Elimination System (NPDES) wastewater treatment plants (WWTPs) and NPDES regulated stormwater (SW) discharges, including county and municipal separate storm sewer systems (MS4s). The margin of safety (MOS) has been incorporated using a conservative assumption by estimating the loading capacity of the stream based on a water quality endpoint concentration more stringent than the applicable MD water quality standard criterion. The *E. coli* water quality criterion concentration was reduced by 5%, from 126 MPN/100ml to 119.7 MPN/100ml.

The MD 8-digit Little Youghiogheny River watershed TMDL of fecal bacteria is presented in the following table:

MD 8-Digit Little Youghiogheny River Watershed Fecal Bacteria TMDL (Billion MPN *E. coli*/year)

TMDL	**=**	**LA**	**+**	**WLA**			**+**	**MOS**
				SW WLA	**+**	**WWTP WLA**		
83,539	=	81,972	+	0	+	1,567	+	Incorporated

The long-term annual average TMDL represents a reduction of approximately 93% from the baseline load of 1,216,388 billion MPN *E. coli*/year.

Pursuant to recent EPA guidance (US EPA 2006a), maximum daily load (MDL) expressions of the long-term annual average TMDLs are also provided, as shown in the following table:

MD 8-Digit Little Youghiogheny River Watershed Fecal Bacteria MDL Summary (Billion MPN *E. coli*/day)

MDL	**=**	**LA**	**+**	**WLA**			**+**	**MOS**
				SW WLA	**+**	**WWTP WLA**		
1,650	=	1,637	+	0	+	13	+	Incorporated

Once EPA has approved a TMDL, MDE intends for the required reductions 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 could be attained in one of the six subwatersheds using MPRs. However, in the five other subwatersheds water quality standards cannot be attained under the MPR scenario. MPRs may not be sufficient in subwatersheds where wildlife is a significant component or where very high reductions of fecal bacteria loads are required to meet water quality standards. In these cases, it is expected that the MPR scenario will be the first stage of TMDL implementation. 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 the Little Youghiogheny River watershed (MD basin number 05-02-02-02). Section 303(d)(1)(C) of the federal Clean Water Act (CWA) and the U.S. Environmental Protection Agency's (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 waterbody 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 Little Youghiogheny River and its tributaries in the State of Maryland's 303(d) List as impaired by nutrients (listed in 1996), sediments (1996), fecal bacteria (2002) and impacts to biological communities (2002 and 2006). Broadford Lake, located within the Little Youghiogheny River watershed, has been identified as impaired by nutrients (1998) and methylmercury (2002). The Little Youghiogheny River has been designated as Use III-P (Nontidal Cold Water and Public Water Supply). Broad Ford Run and all its tributaries above Broadford Dam have been designated as Use I-P (Water Contact Recreation, Protection of Aquatic Life, and Public Water Supply). All other waters of the watershed are designated as Use I (Water Contact Recreation and Protection of Aquatic Life). See Code of Maryland Regulations (COMAR) 26.08.02.08S. This document proposes to establish a TMDL for fecal bacteria in the Little Youghiogheny River watershed that will allow for attainment of the beneficial use designation of water contact recreation. The Little Youghiogheny River listings for nutrients and sediments have been addressed by TMDLs approved in 2001 and 2007 respectively. The Broadford Lake listings for nutrients and methylmercury have been addressed respectively by a TMDL, approved by EPA in 2000, and a Water Quality Analysis, approved in 2004. The listings for impacts to biological communities will be addressed separately at a future date. MDE monitored the Little Youghiogheny River watershed from 2003-2004 for fecal bacteria. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years were considered.

Fecal bacteria are microscopic single-celled organisms (primarily fecal coliform 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 (US 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 bacteria are a subgroup of total coliform bacteria and *E. coli* bacteria are a subgroup of fecal coliform bacteria. Most *E. coli* are harmless and are found in great quantities in the intestines of people and warm-blooded animals. However, 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 demonstrated that fecal coliform showed less correlation to swimming-associated gastroenteritis than did either *E. coli* or enterococci.

Based on EPA's guidance (US 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 MD's current bacteria water quality criteria, either *E. coli* or enterococci. The indicator organism used in the Little Youghiogheny River watershed TMDL analysis was *E. coli*.

2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

Location

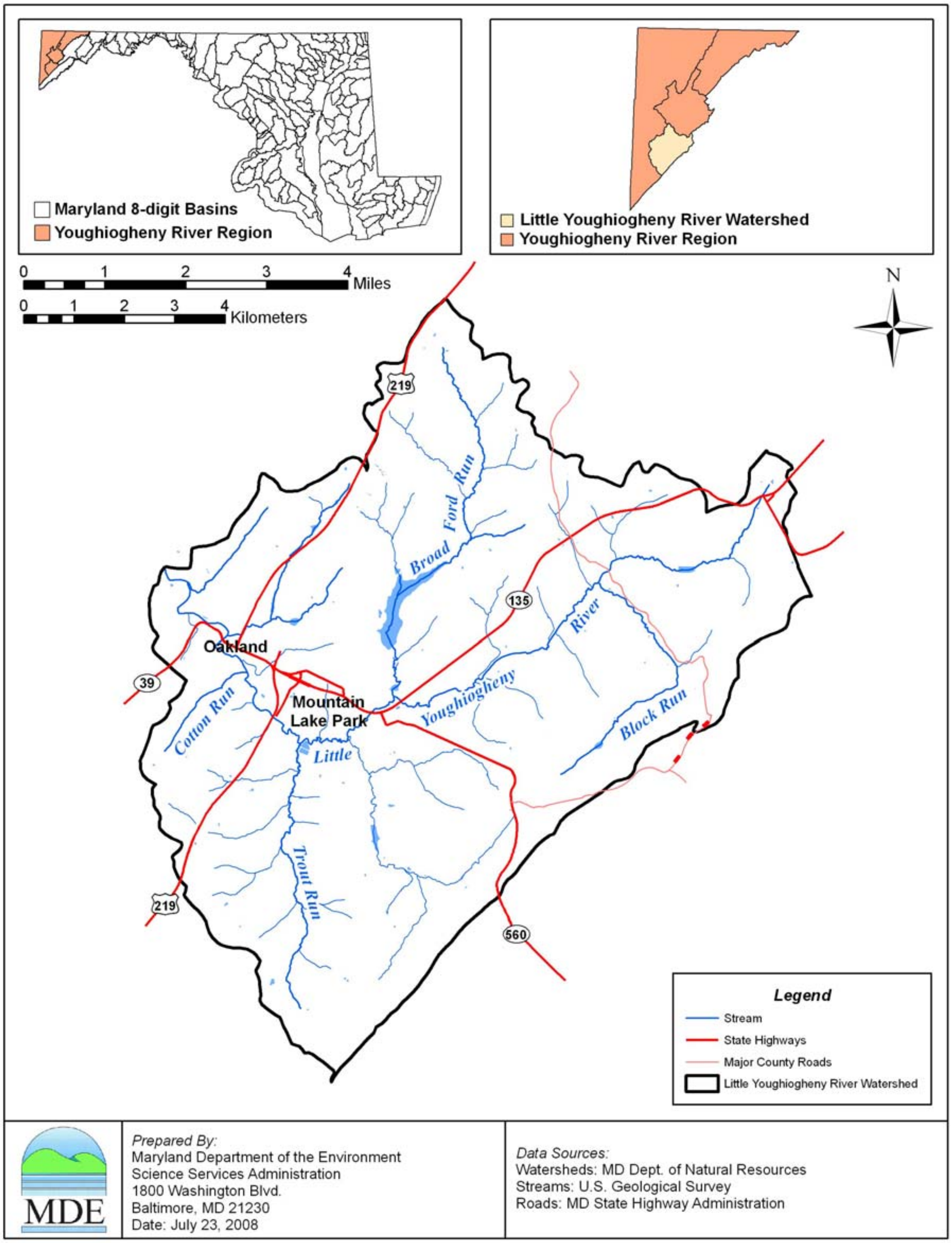
The Little Youghiogheny River is a tributary of the Youghiogheny River, located in Garrett County, Maryland (see Figure 2.1.1). The Youghiogheny River flows northward into Pennsylvania, joining the Monongahela and Allegheny Rivers to form the Ohio River. The mainstem of the Little Youghiogheny is about 11 miles long with a watershed covering about 26,000 acres. The watershed is bounded towards the southeast by Backbone Mountain. The headwaters of the Little Youghiogheny River begin north of Deer Park, MD and the river drains into the Youghiogheny River near Oakland, MD. Tributaries of the Little Youghiogheny River include Block Run, Broad Ford Run, Trout Run and Cotton Run.

Geology

The Little Youghiogheny River watershed lies in the Allegheny Plateau. The geological strata include shale and sandstone of the Devonian Chemung and Hampshire formations (MGS, 2006). Soils in the watershed are primarily Calvin-Gilpin association, gently sloping to steep, moderately deep, well-drained soils formed over acid, red to gray shale, and sandstone (USDA - SCS, 1974).

Hydrology

The hydrology of the Little Youghiogheny differs from typical Appalachian streams, due to relatively little elevation change along its river channel. The sluggish, meandering river is more depositional than erosional (MDE 1997). During a low-flow stream survey of the Little Youghiogheny River from the Trout Run Waster Water Treatment Plant (WWTP) to the confluence with the Youghiogheny River, velocities averaged 0.13 feet per second and depths averaged about 1 to 1.5 feet.



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Date: July 23, 2008

Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Roads: MD State Highway Administration

Figure 2.1.1: Location Map of the Little Youghiogheny River Watershed

Land Use

Based on the 2002 Maryland Department of Planning (MDP) land use/land cover data, the watershed can be characterized as primarily forest and agricultural. The land use percentage distribution is shown in Table 2.1.1, and spatial distributions for each land use are shown in Figure 2.1.2. Table 2.1.2 shows the land use percentage distribution for each subwatershed considered in the analysis. Note that the subwatersheds are identified by their MDE monitoring station, and are listed by flow from upstream to downstream.

Table 2.1.1: Land Use Percentage Distribution for the Little Youghiogheny River Watershed

Land Type	Acreage	Percentage
Forest	10,455	44.3
Agricultural	8,225	34.9
Urban	3,589	15.2
Pasture	1,133	4.8
Water	176	0.7
Total	**23,577**	**100**

Table 2.1.2: Land Use Percentage Distribution for the Little Youghiogheny River Subwatersheds

Station / Subwatershed	Land Use Area (%)				
	Agricultural	Forest	Pasture	Urban	Water
LYO0051 / L. Yough. above Broad Ford Run	18.6	63.2	4.8	13.2	0.1
BFR0028 / Broad Ford Run above lake	39.9	35.4	11.2	13.5	0
BFR0001 / Broad Ford Run at mouth	27.0	35.1	6.0	26.2	5.6
ZBQ0005 / Unnamed tributary	41.5	52.1	1.3	4.8	0.3
TRO0012 / Trout Run	63.3	29.9	3.0	3.8	0
LYO0015 / L. Yough. in Oakland	45.4	19.8	4.7	29.8	0.3

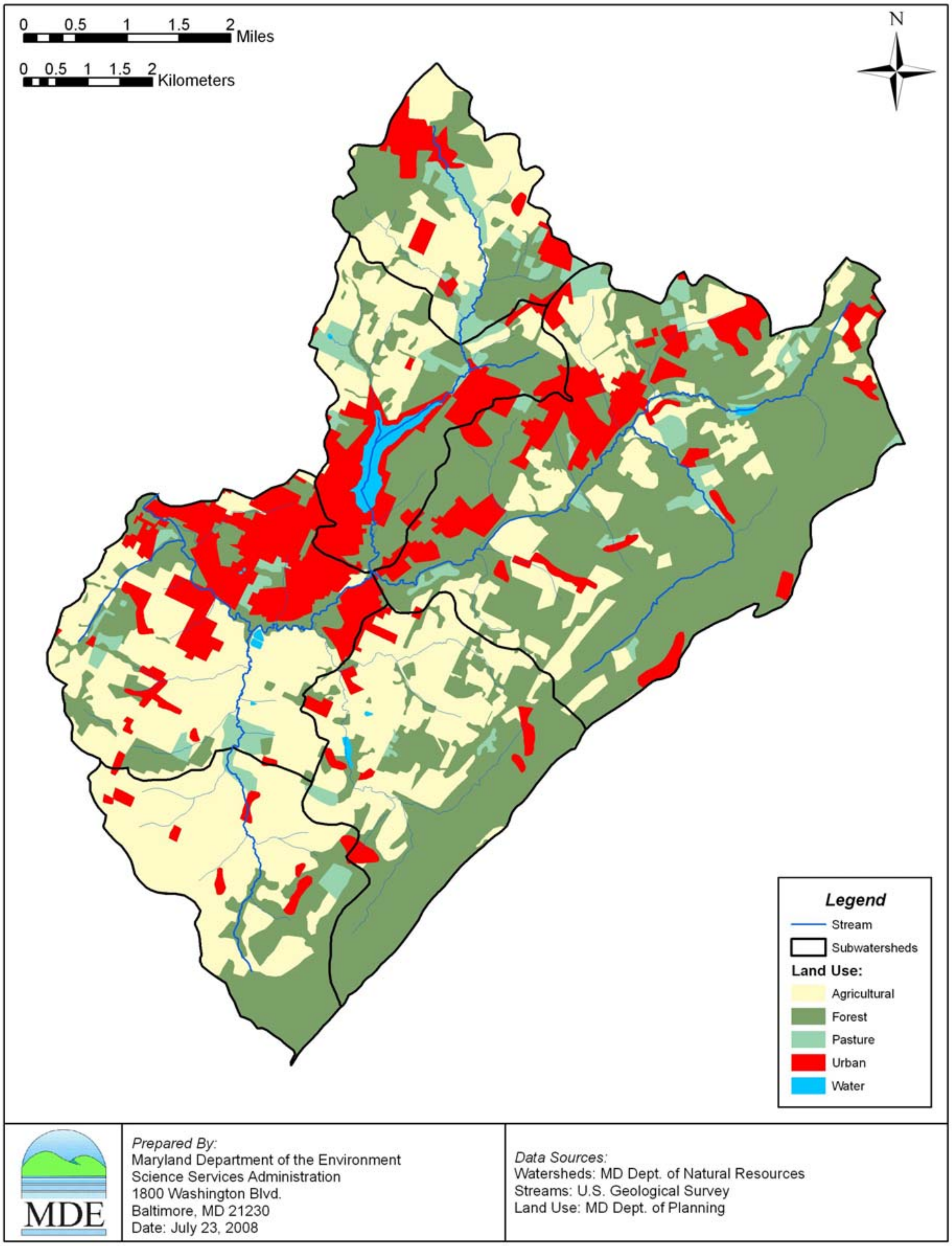


Figure 2.1.2: Land Use of the Little Youghiogheny River Watershed

Population

The total population in the Little Youghiogheny River watershed is estimated to be 6,245 people. Figure 2.1.3 depicts the population density in the region. The human population and the number of dwellings were estimated based on a weighted average from the 2000 Census GIS Block Groups and the 2002 MDP Land Use Land Cover. Since the boundaries of the watershed differ from the boundaries of the block groups, residential land use data were used to extract the necessary areas of the Census block groups. The MDP residential density designations shown in Table 2.1.3 were used for this estimation.

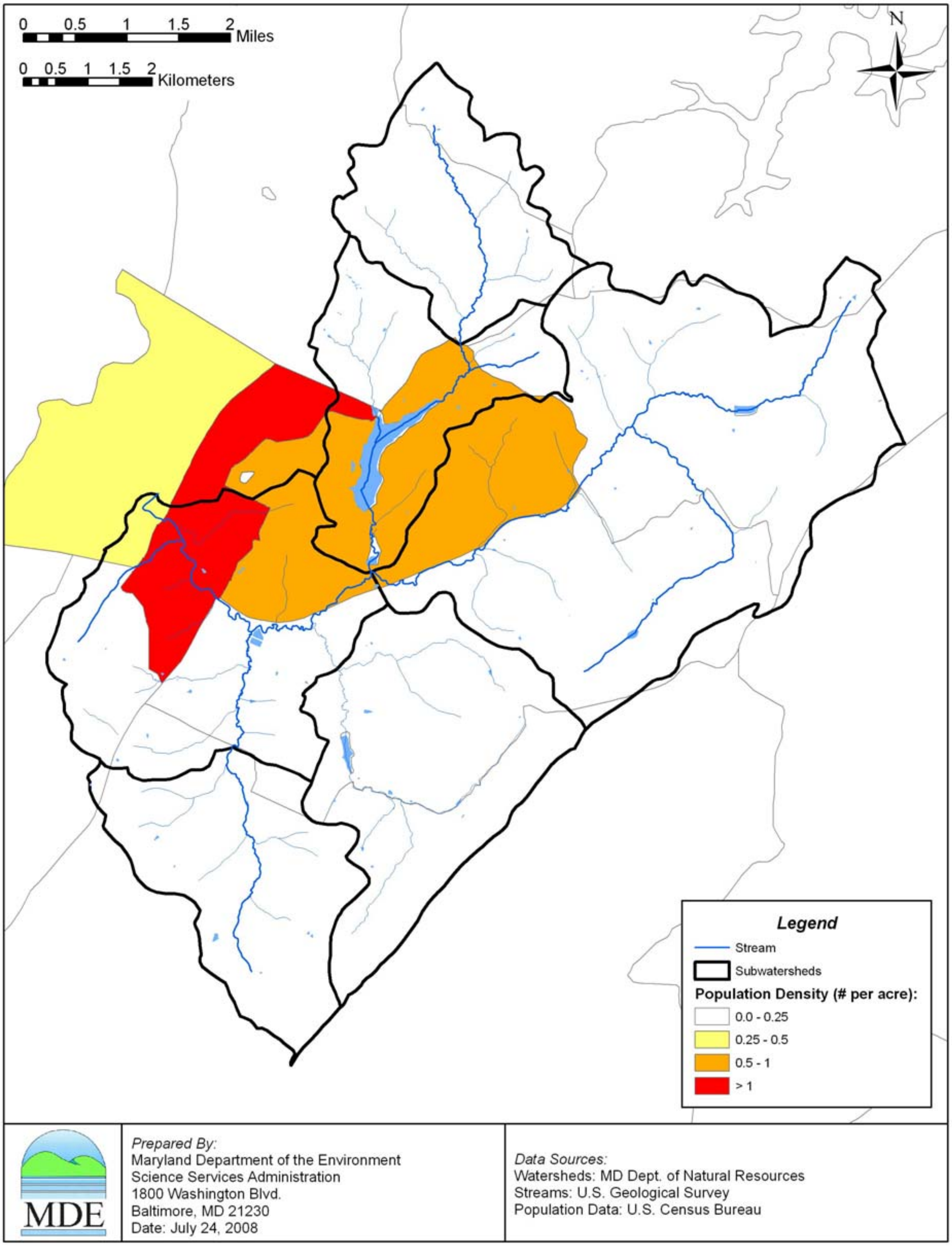
Table 2.1.3: Number of Dwellings Per Acre

Land Use Code	Dwellings Per Acre
Low Density Residential	1
Medium Density Residential	5
High Density Residential	8

Based on these densities and the population data from the census block groups, the population for each subwatershed was estimated and is presented in Table 2.1.4.

Table 2.1.4: Total Population per Subwatershed in the Little Youghiogheny River Watershed

Station / Subwatershed	Population
LYO0051 / L. Yough. above Broad Ford Run	1,203
BFR0028 / Broad Ford Run above Lake	325
BFR0001 / Broad Ford Run at mouth	878
ZBQ0005 / Unnamed tributary	256
TRO0012 / Trout Run	89
LYO0015 / L. Yough. in Oakland	3,494
Total	**6,245**



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Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Population Data: U.S. Census Bureau

Figure 2.1.3: Population Density in the Little Youghiogheny River Watershed

2.2 Water Quality Characterization

EPA's guidance document, "Ambient Water Quality Criteria for Bacteria" (1986), recommended that states use *E. coli* (for fresh water) or enterococci (for fresh or salt water) as pathogen indicators. 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).

As per EPA's guidance, Maryland has adopted the new indicator organisms, *E. coli* and enterococci, for the protection of public health in Use I, II, III and IV waters. These bacteria listings were originally assessed using fecal coliform bacteria. The analysis was based on a geometric mean of the monitoring data, where the result had to be less than or equal to 200 MPN/100ml. From EPA's analysis (US EPA 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.

<u>Bacteria Monitoring</u>

Table 2.2.1 lists the historical monitoring data for the Little Youghiogheny River watershed. MDE conducted monitoring sampling at six stations in the Little Youghiogheny River watershed from November 2003 through October 2004. The locations of these stations are shown in Tables 2.2.2 and 2.2.3 and in Figure 2.2.1. Observations recorded from the six MDE monitoring stations are provided in Appendix A.

Bacteria counts are highly variable, which is typical due to the nature of bacteria and their relationship to flow. The *E. coli* counts for the six stations ranged between 3 and 24,192 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the Little Youghiogheny River Watershed

Organization	Date	Design	Summary
DNR	01/1991 through 12/1995	Fecal Coliform*	1 station 1 sample per month
MDE	11/2003 through 10/2004	*E. coli*	6 stations 2 samples per month
MDE	11/2003 through 10/2004	BST (*Enterococcus)*	6 stations 1 sample per month

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

Table 2.2.2: Location of DNR CORE Station in the Little Youghiogheny River Watershed

Station	Tributary	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
LYO0004	Little Youghiogheny River	39.418	-79.419

Table 2.2.3: Locations of MDE Monitoring Stations in the Little Youghiogheny River Watershed

Tributary	Station	Observation Period	Total Observations	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
Little Youghiogheny River	LYO0051	2003 - 2004	24	39.398	-79.369
Broad Ford Run	BFR0028	2003 - 2004	24	39.431	-79.355
Broad Ford Run	BFR0001	2003 - 2004	24	39.400	-79.372
unnamed	ZBQ0005	2003 - 2004	24	39.385	-79.376
Trout Run	TRO0012	2003 - 2004	24	39.374	-79.394
Little Youghiogheny River	LYO0015	2003 - 2004	24	39.409	-79.410

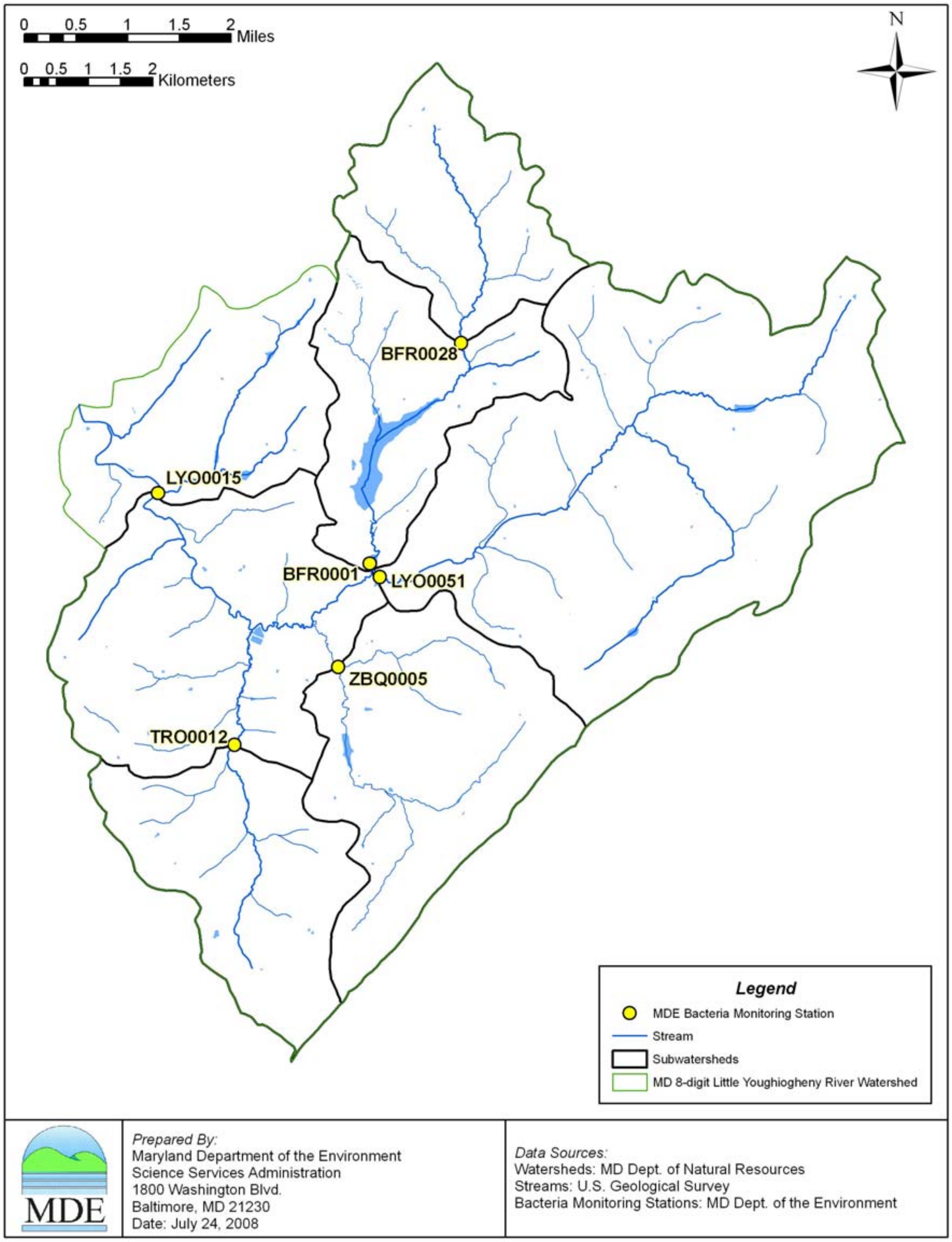


Figure 2.2.1: Monitoring Stations and Subwatersheds in the Little Youghiogheny River Watershed

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The Maryland water quality standard's Surface Water Use Designation for the Little Youghiogheny River is Use III-P (Nontidal Cold Water and Public Water Supply). Broad Ford Run and all its tributaries above Broadford Dam have been designated as Use I-P (Water Contact Recreation, Protection of Aquatic Life, and Public Water Supply). All other waters of the watershed are designated as Use I (Water Contact Recreation and Protection of Aquatic Life). (COMAR 26.08.02.08S) The Little Youghiogheny River watershed was listed on Maryland's 303(d) List as impaired by fecal bacteria in 2002, due to elevated fecal coliform concentrations detected at the DNR CORE monitoring station LYO0004.

Water Quality Criteria

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

Table 2.3.1: Bacteria Criteria Values
(Source: COMAR 26.08.02.03-3 Water Quality Criteria Specific to Designated Uses; Table 1)

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 2008 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 from the previous year where there are at least five representative sampling events. The data shall be from samples collected during steady-state, dry weather conditions and during the beach season (Memorial Day through Labor Day) to be representative of the critical condition (highest use). If the resulting steady-state geometric mean is greater than 35 cfu/100 ml enterococci in marine/estuarine waters, 33 cfu/100 ml enterococci in freshwater or 126 cfu/100 ml *E. coli* in freshwater, the waterbody will be included for further assessment. If fewer than five representative sampling events for an area being assessed are available, data from the previous two years will be evaluated.

Water Quality Assessment

Bacteria water quality impairment in the Little Youghiogheny River watershed was assessed by comparing both the annual and the seasonal (May 1st –September 30th) dry weather 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 without bias.

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 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.

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 Little Youghiogheny River watershed. However, option 2 could not be used to calculate the steady-state geometric means due to the absence of an appropriate USGS gauging station in or nearby the watershed or any other reliable source of long term flow information. Thus using option 3, the steady-state geometric mean concentration for both the annual and the dry weather seasonal periods at each monitoring station is calculated as follows:

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

where,

M_i = log mean concentration at station i
$C_{i,j}$ = concentration for sample j at station i
n_i = number of samples at station i

Finally, the geometric mean is back transformed from log space using the following equation:

$$C_{gm} = 10^{M_i} \qquad (2)$$

where,

C_{gm} = steady-state geometric mean concentration

Tables 2.3.3 and 2.3.4 present the maximum and minimum concentrations and the steady-state geometric mean for the Little Youghiogheny River subwatersheds for the annual and dry weather seasonal (May 1st –September 30th) periods.

Table 2.3.2: Little Youghiogheny River Watershed Annual Steady-State Geometric Means

Station / Tributary	**Number of Samples**	***E. coli* Minimum Concentration** (MPN/100ml)	***E. coli* Maximum Concentration** (MPN/100ml)	**Annual Steady State Geometric Mean** (MPN/100ml)
LYO0051 L. Yough. above Broad Ford Run	24	3	4,106	236
BFR0028 Broad Ford Run above lake	24	20	4,611	337
BFR0001 Broad Ford Run at mouth	24	20	3,609	217
ZBQ0005 Unnamed tributary	24	733	24,192	4,578
TRO0012 Trout Run	24	120	24,192	1,513
LYO0015 L. Yough. in Oakland	24	74	8,164	695

Table 2.3.3: Little Youghiogheny River Watershed Seasonal (May 1 - September 30) Dry Weather Period Steady-State Geometric Means

Station / Tributary	Number of Samples	*E. coli* Minimum Concentration (MPN/100ml)	*E. coli* Maximum Concentration (MPN/100ml)	Seasonal Steady State Geometric Mean (MPN/100ml)
LYO0051 L. Yough. above Broad Ford Run	9	275	1,187	464
BFR0028 Broad Ford Run above lake	9	187	1,723	788
BFR0001 Broad Ford Run at mouth	9	52	1,989	344
ZBQ0005 Unnamed tributary	9	1,259	24,192	6,906
TRO0012 Trout Run	9	1,274	9,804	4,624
LYO0015 L. Yough. in Oakland	9	211	1,043	703

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. During rain events, surface runoff transports water and fecal bacteria over the land surface and discharges to the stream system. This transport is dictated by rainfall, soil type, land use, and topography of the watershed. 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. 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 sources generally arise from failing septic systems and their associated drain fields or leaking infrastructure (i.e., sewer systems).

The Little Youghiogheny River watershed is serviced by both sewer systems and septic systems. Wastewater collected by the Trout Run WWTP is treated and discharged into the Little Youghiogheny River.

On-site disposal (septic) systems are located throughout the Little Youghiogheny River watershed. Table 2.4.1 presents the number of septic systems per subwatershed. Figure 2.4.1 displays the areas that are serviced by sewers and the locations of the septic systems.

Table 2.4.1: Septic Systems per Subwatershed

Station / Subwatershed	Septic Systems
LYO0051 / L. Yough. above Broad Ford Run	412
BFR0028 / Broad Ford Run above Lake	129
BFR0001 / Broad Ford Run at mouth	104
ZBQ0005 / Unnamed tributary	130
TRO0012 / Trout Run	83
LYO0015 / L. Yough. in Oakland	627
Total	**1,485**

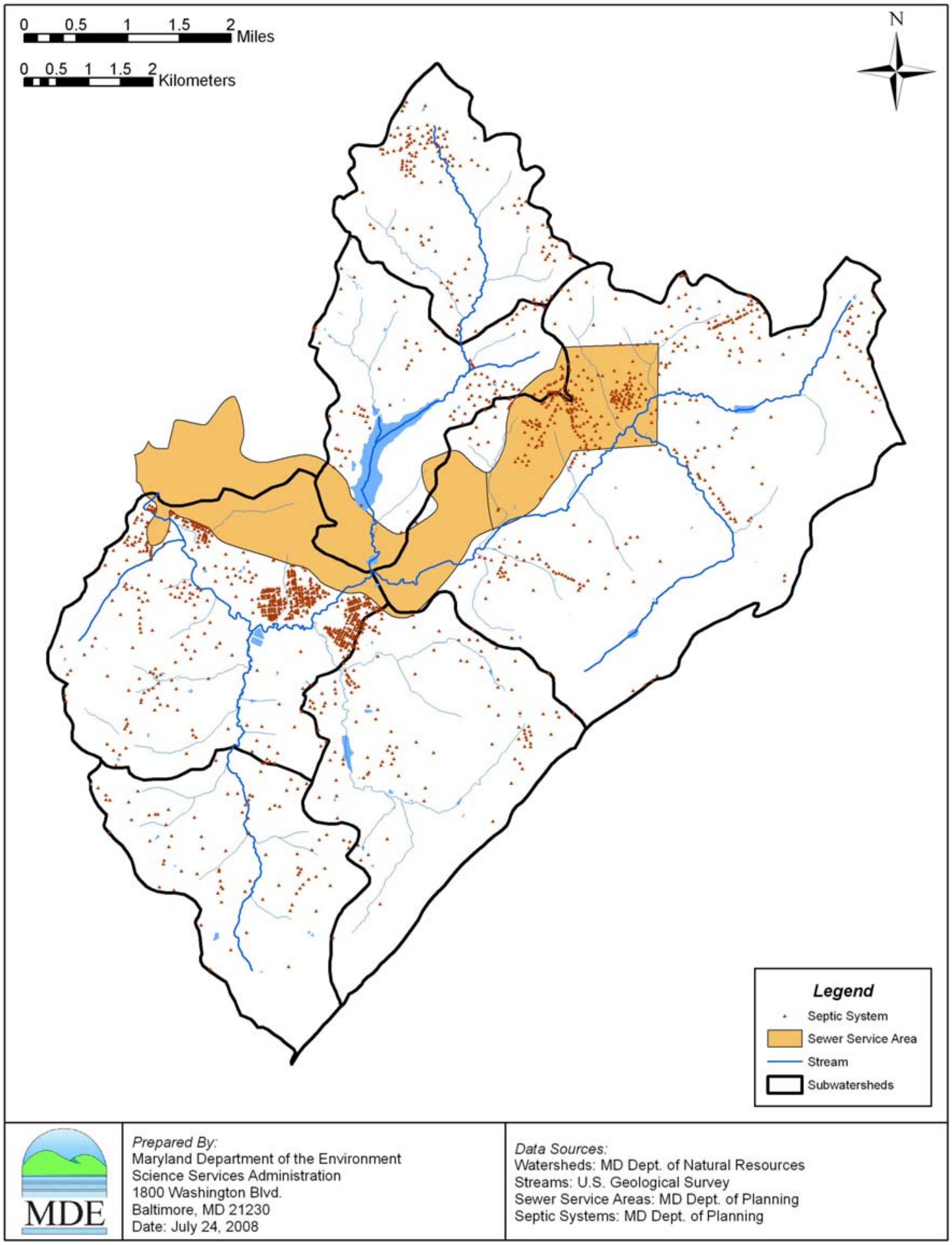


Figure 2.4.1: Sanitary Sewer Service Areas and Septic Locations in the Little Youghiogheny River Watershed

Point Source Assessment

There are two broad types of National Pollutant Discharge Elimination System (NPDES) permits considered in this analysis, individual and general. Both types of permits include industrial and municipal categories. Individual permits are issued for industrial and municipal WWTPs and Phase I municipal separate storm sewer systems (MS4s). MDE general permits have been established for surface water discharges from: Phase II and other MS4 entities; surface coal mines; mineral mines; quarries; borrow pits; ready-mix concrete; asphalt plants; seafood processors; hydrostatic testing of tanks and pipelines; marinas; concentrated animal feeding operations; and stormwater associated with industrial activities.

NPDES Regulated Stormwater

Bacteria sources associated with MS4s and other NPDES regulated stormwater discharges are considered point sources. Stormwater runoff is an important source of water pollution, including bacterial pollution. An MS4 is a conveyance or system of conveyances (roads with drainage systems, municipal streets, catch basins, curbs, gutters, ditches, man-made channels, storm drains) designed or used for collecting or conveying stormwater and delivering it to a waterbody. MS4 programs are designed to reduce the amount of pollution that enters a waterbody from storm sewer systems to the maximum extent practicable.

There are not any NPDES regulated MS4s within the Little Youghiogheny River watershed. Additionally, there are two industrial stormwater permits in the watershed. Potential fecal bacteria loads from these facilities are considered to be insignificant relative to the overall load contribution and therefore are not included in the TMDL analysis.

Sanitary Sewer Overflows

Sanitary Sewer Overflows (SSOs) occur when the capacity of a separate sanitary sewer is exceeded. There are several factors that may contribute to SSOs from a sewerage 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 must be reported to MDE's Water Management Administration in accordance with COMAR 26.08.10 to be addressed under the State's enforcement program.

There were a total of four SSOs reported to MDE between November 2003 and October 2004 in the Little Youghiogheny River watershed. Approximately 992,000 gallons of SSOs were discharged through various waterways (surface water, groundwater, sanitary sewers, etc.). Figure 2.4.2 shows the locations where SSOs occurred between November 2003 and October 2004.

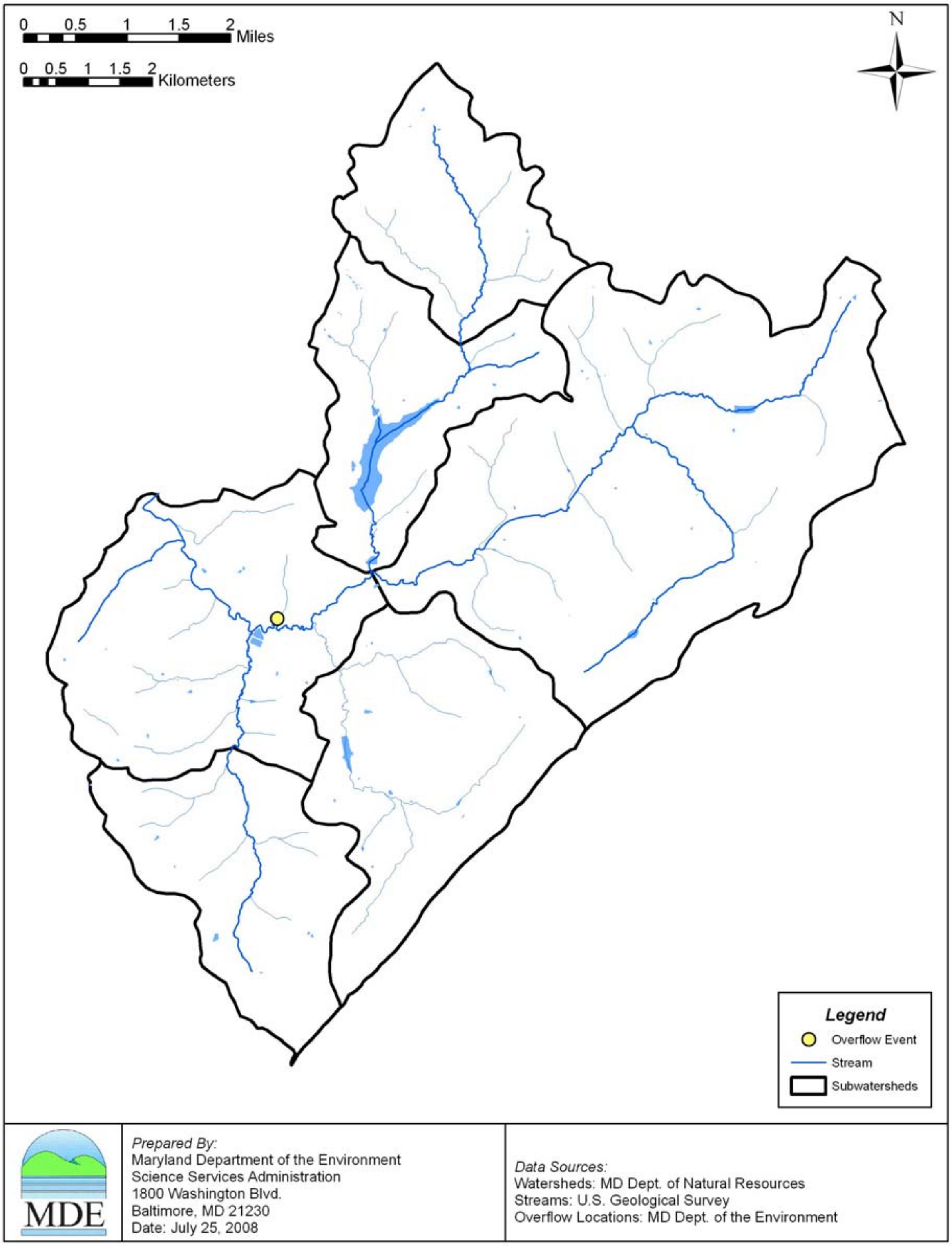
Municipal and Industrial Wastewater Treatment Plants (WWTPs)

Wastewater treatment plants are designed to treat wastewater before it is discharged to a stream or river. The goals of wastewater treatment are to protect the public health, protect aquatic life, and to prevent harmful substances from entering the environment.

Based on MDE's point source permitting information, there is one active municipal NPDES permitted point source facility with permits regulating the discharge of fecal bacteria in the Little Youghiogheny River watershed. This facility, Trout Run WWTP, treats approximately 0.8 MGD (million gallons per day). There are no industrial facilities in the Little Youghiogheny River watershed with NPDES permits regulating the discharge of fecal bacteria. Table 2.4.2 lists the municipal facility and Figure 2.4.3 shows its location in the watershed.

Table 2.4.2: NPDES Permitted Facilities Regulated for Fecal Bacteria Discharge in the Little Youghiogheny River Watershed

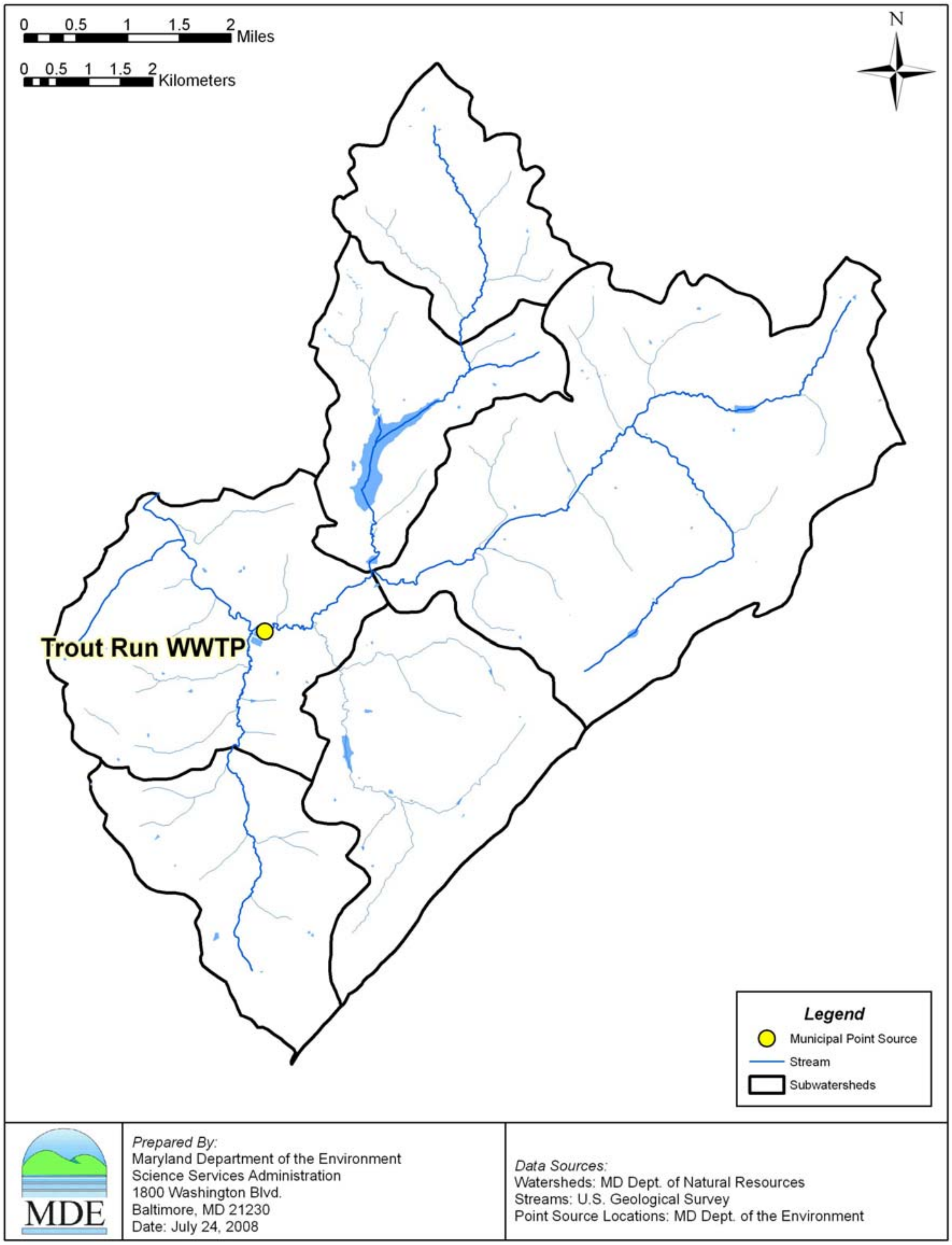
Facility	NPDES Permit No.	County	Average Flow (MGD)	Fecal Coliform Concentration Average Maximum (MPN/100ml)	Fecal Coliform Load (Billion MPN/day)
Trout Run WWTP	MD0051497	Garrett	0.795	118	3.55



Prepared By:
Maryland Department of the Environment
Science Services Administration
1800 Washington Blvd.
Baltimore, MD 21230
Date: July 25, 2008

Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Overflow Locations: MD Dept. of the Environment

Figure 2.4.2: Sanitary Sewer Overflows in the Little Youghiogheny River Watershed



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Date: July 24, 2008

Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Point Source Locations: MD Dept. of the Environment

Figure 2.4.3: Permitted Point Sources Discharging Fecal Bacteria in the Little Youghiogheny River Watershed

Bacteria Source Tracking

Bacteria source tracking (BST) was used to identify the relative contributions of different sources of bacteria to in-stream water samples. BST monitoring was conducted at six stations in the Little Youghiogheny River watershed, where samples were collected once per month 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 water samples. Details of the BST methodology and data can be found in Appendix C.

An accurate representation of the expected contribution of each source at each station is estimated by using a weighted mean of the identified sample results. The weighting factors are based on the $\log_{10}$ of the bacteria concentration. The procedure for calculating the 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 an initial weighted percentage (MS) of each source. The weighting is based on the $\log_{10}$ bacteria concentration for the water sample.
3. Adjust the weighted percentage based on the classification of known sources.

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

$$MS_l = \sum_{k=1}^{5} \frac{A_{l,k} * IMS_k}{P_k} \qquad (3)$$

where,

$$IMS_k = \frac{\sum_{j=1}^{n} \log_{10}(C_j) * S_{j,k}}{\sum_{j=1}^{n_i} \log_{10}(C_j)} \qquad (4)$$

and where,

MS_l = weighted mean proportion of isolates of source l
IMS_k = initial weighted mean proportion of isolates of source k
$A_{l,k}$ = number of known source l isolates initially predicted as source k
P_k = number of total known isolates initially predicted as source k
j = sample
k = source category (1=human, 2=domestic, 3=livestock, 4=wildlife, 5=unknown)
l = final source category (1=human, 2=domestic, 3=livestock, 4=wildlife)
C_j = concentration for sample j
$S_{j,k}$ = proportion of isolates for sample j, of source k
n = number of samples

The complete distributions of the annual and seasonal dry weather period source loads are listed in Tables 2.4.3 and 2.4.4. Details of the BST data and tables with the BST analysis results can be found in Appendix C.

Table 2.4.3: Distribution of Fecal Bacteria Source Loads in the Little Youghiogheny River Watershed for the Annual Period

Station	% Domestic Animals	% Human	% Livestock	% Wildlife
LYO0051	7.7	25.6	21.4	45.4
BFR0028	4.6	22.8	26.5	46.1
BFR0001	7.8	38.6	15.3	38.3
ZBQ0005	19.7	24.4	19.5	36.4
TRO0012	3.7	24.7	22.5	49.1
LYO0015	7.0	24.3	19.0	49.7

Table 2.4.4: Distribution of Fecal Bacteria Source Loads in the Little Youghiogheny River Watershed for the Seasonal (May 1st – September 30th) Dry Weather Period

Station	% Domestic Animals	% Human	% Livestock	% Wildlife
LYO0051	7.0	28.8	20.0	44.2
BFR0028	1.0	33.7	21.2	44.1
BFR0001	7.4	55.0	12.0	25.6
ZBQ0005	8.2	28.6	22.9	40.4
TRO0012	2.0	22.0	26.1	50.0
LYO0015	4.3	19.8	18.8	57.1

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 assure attainment of water quality standards in the Little Youghiogheny River 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 of the many complexities involved in estimating 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. This analysis methodology is based on available monitoring data and is 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 annual average TMDL loading caps and how maximum daily loads are estimated. 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 (WLAs) for point sources and load allocations (LAs) for non point 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, as well as 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, the Code of Federal Regulations (40 CFR 130.2(i)) states 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 an accurate estimation of source inputs is 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., enterococci), are expressed in either colony forming units (CFU) or most probable number (MPN) of colonies. The first method (US EPA 1985) is a direct estimate of the bacteria colonies (Method 1600). The second method is a statistical estimate of the number of colonies (ONPG MUG Standard Method 9223B, AOAC 991.15). Sample results indicate the extreme variability in the total bacteria counts (see Appendix A). The distribution of the sample results 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 also be problematic due to the many assumptions required and limited available data. Lack of specific numeric and spatial location data for several source categories, from failing septic systems to domestic animals, livestock, and wildlife populations, can create many potential uncertainties in traditional water quality modeling. For this reason, MDE applies an analytical method combined with the bacteria source tracking described above for the calculation of this TMDL.

4.2 Analytical Framework

As explained previously, this analysis uses annual average flows and critical conditions to estimate the Little Youghiogheny River watershed's TMDL. This analytical method, combined with water quality monitoring data and BST, provides a better description of water quality and meets TMDL requirements.

In brief, baseline loads are estimated first for each subwatershed by using bacteria monitoring data and average flows estimated from regional regression equations. These baseline loads are divided into four bacteria source categories, using the results of BST analysis. Next, the percent reduction required to meet the water quality criterion in each subwatershed is estimated from the observed bacteria concentrations after determining the critical condition and accounting for seasonality. Critical condition and seasonality are determined by assessing annual and dry weather seasonal loading conditions. Finally, TMDLs for each subwatershed are estimated by applying these percent reductions.

Figure 4.2.1 illustrates how the hydrological, water quality and BST data are linked together for the TMDL development.

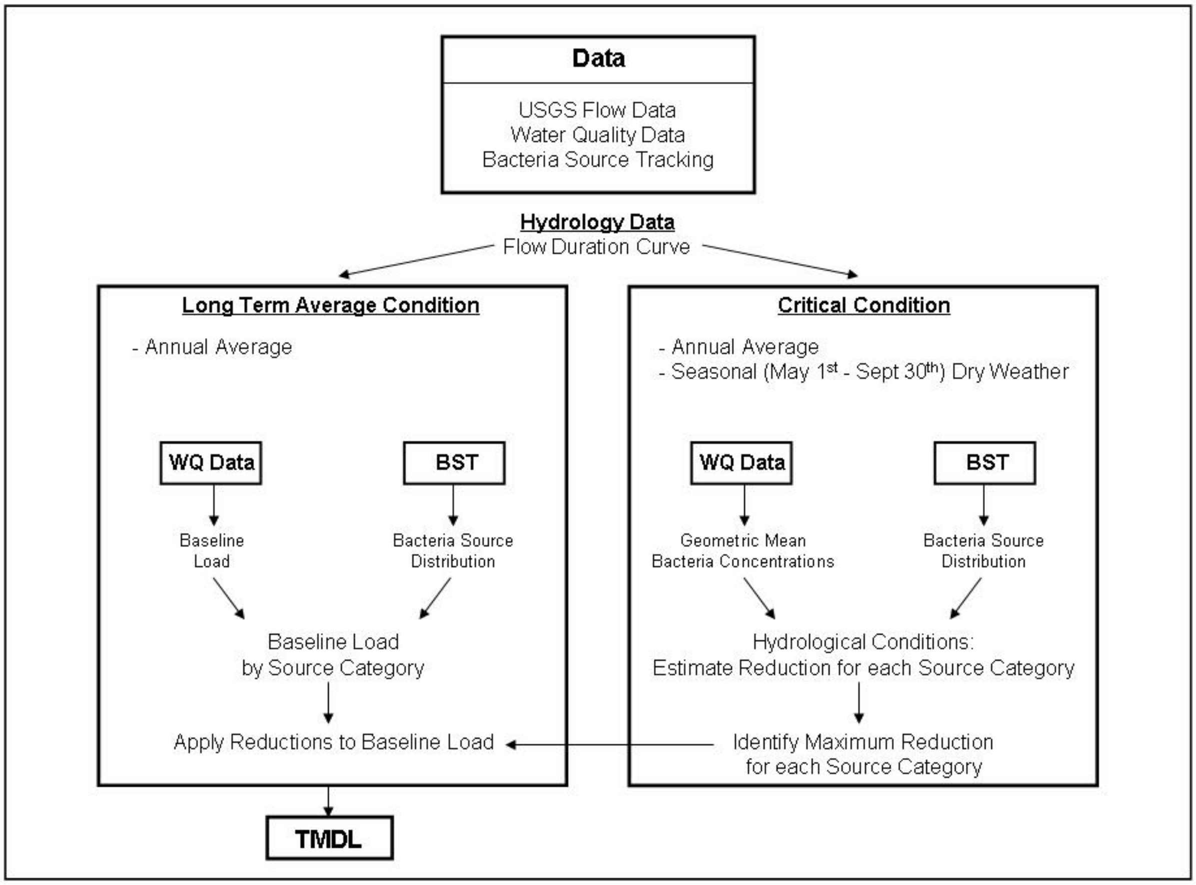

Figure 4.2.1: Diagram of the Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads are estimated for all subwatersheds of the Little Youghiogheny River watershed. Baseline loads estimated in this TMDL analysis are reported as long-term average annual loads. These loads are estimated using daily average flows and geometric mean concentrations and bias correction factors (calculated from bacteria monitoring data).

Due to the particular hydrological characteristics of the watershed and lack of available flow data, the daily average flows used in this analysis were based on regional equations developed by Versar. Flow regression equations specific to Maryland were developed by Versar using regression analysis in the manner used by Dillow (1998). Dillow developed a method to estimate peak flows for Maryland grouped by three physiographic provinces: Blue Ridge and Piedmont regions (Piedmont Group); the Appalachian Plateau (Mountain Group); and the Western and Eastern Coastal Plain (Coastal Plain Group). For details on how these flow regression equations were developed please refer to "Development of Regional Flow Duration

Curves (FDC) in Maryland" (Versar, 2004). Also, see Appendix B of this report for a discussion of the flow analysis used to develop the TMDL.

The Little Youghiogheny River watershed is located in the Appalachian Plateau physiographic province. The FDC regression equation for mountain gauges was used to estimate the mean flow in each of the six subwatersheds as follows:

$$\text{Mean Flow (cfs)} = 10^{(0.2019 + 0.9778 * \log_{10}(A))} \tag{5}$$

where,

A = drainage area (mi^2)

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 bias correction 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.

With calculated geometric means and arithmetic means for each subwatershed, the bias correction factors are estimated as follows:

$$F_1 = A/C \tag{6}$$

where,

F_1 = bias correction factor
A = long term annual arithmetic mean
C = long term annual geometric mean

The baseline loads are then estimated as follows:

$$L = Q * C * F_1 * F_2 \tag{7}$$

where,

L = daily average load (Billion MPN/day) at monitoring station
Q = daily average flow (cfs)
C = geometric mean (MPN/100ml)
F_1 = bias correction factor
F_2 = unit conversion factor (0.0245)

Estimating Subwatershed Loads

There are a total of six subwatersheds considered in this analysis, corresponding to the six monitoring stations. Subwatersheds with more than one monitoring station were subdivided into unique watershed segments, thus allowing individual load and reduction targets to be determined for each. In the Little Youghiogheny River watershed two stations have upstream monitoring stations, as listed in Table 4.3.1. In these two cases the subwatershed is differentiated by adding the extension “sub” to the name of the downstream monitoring station. For example, BFR0001sub signifies only the area and load between stations BFR0001 and BFR0028, while BFR0001 refers to the cumulative area draining to that station.

Table 4.3.1: Subdivided Watersheds in the Little Youghiogheny River Watershed

Subwatershed	Upstream Station(s)
BFR0001sub	BFR0028
LYO0015sub	LYO0051, BFR0001, ZBQ0005, TRO0012

Bacteria loads from these subwatersheds are joined by loads from their upstream subwatersheds to result in the concentration measured at the downstream monitoring station. However, for the purposes of this TMDL, the bacteria concentration measured at each monitoring station is assumed to be representative of that corresponding subwatershed and independent of flow from upstream subwatersheds. For example, the load transported from upstream station BFR0028 is not considered in the estimation of the load from subwatershed BFR0001sub. Instead the bacteria concentration measured at station BFR0001 is assigned to that subwatershed.

This assumption is used due to a special scenario seen in the subwatershed of LYO0015sub. For this subwatershed, bacteria loadings from upstream subwatersheds are significantly greater than the cumulative load measured at the downstream station. This occurrence indicates that the bacteria loads are not carried on as they are transported downstream. Attributing the measured concentration solely to the immediate subwatershed will result in a slightly conservative estimate of bacteria loads but will also allow a more consistent methodology throughout the watershed than applying unpredictable upstream loads.

Source estimates from the BST analysis are completed for each station and are based on the contribution from the upstream watershed. Given the uncertainty of in-stream bacteria processes and the complexity involved in back-calculating an accurate source transport factor, the sources for the subwatersheds defined in Table 4.3.1 were assigned from the analysis of their downstream stations.

Results of the baseline load calculations are presented in Table 4.3.2. A summary of the baseline loads is given in Table 4.3.3.

Table 4.3.2: Baseline Loads Calculations

Subwatershed	Area (mi^2)	Estimated Average Flow (cfs)	Annual *E. coli* Geometric Mean Concentration (MPN/100ml)	Baseline *E. coli* Load (Billion MPN/year)
LYO0051	13.0	19.6	236	88,582
BFR0028	3.5	5.4	337	37,518
BFR0001sub	4.0	6.1	217	28,870
ZBQ0005	5.6	8.6	4,578	596,195
TRO0012	4.2	6.5	1,513	324,091
LYO0015sub	6.5	10.0	695	141,131

Table 4.3.3: Baseline Loads Summary

MD 8-Digit Little Youghiogheny River Watershed Fecal Bacteria Baseline Loads (Billion MPN *E. coli*/year)						
Total Baseline Load	=	**Nonpoint Source BL**	+	**Stormwater BL**	+	**WWTP BL**
1,216,388	=	1,214,821	+	0	+	1,567

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 both the annual and dry weather seasonal conditions. Seasonality is assessed as the period when water contact recreation is expected, specifically dry weather days during May 1st through September 30th. The critical condition requirement is met by determining the maximum reduction per bacteria source that satisfies both conditions and meets the water quality standard, thereby minimizing the risk to water contact recreation. It is assumed that the reduction applied to a bacteria source category will be constant through both conditions.

As explained in Section 4.3 above, since long term flow data were not available in the Little Youghiogheny River watershed, average flows estimated from the regression equation were used. Seasonality in the Little Youghiogheny River watershed was addressed by the monitoring data only. The monitoring data for all stations located in the Little Youghiogheny River watershed cover a sufficient temporal span (at least one year) to estimate annual and seasonal condition loads.

The reductions of fecal bacteria required to meet water quality standards in each subwatershed of the Little Youghiogheny River watershed are shown in Table 4.4.1.

Table 4.4.1: Required Fecal Bacteria Reductions (by Condition) to Meet Water Quality Standards

Station	Condition	Domestic Animals %	Human %	Livestock %	Wildlife %
LYO0051	Annual	75.0	98.0	86.0	0.0
	Seasonal	98.0	98.0	98.0	44.2
	Maximum Source Reduction	**98.0**	**98.0**	**98.0**	**44.2**
BFR0028	Annual	98.0	98.0	98.0	25.2
	Seasonal	98.0	98.0	98.0	68.1
	Maximum Source Reduction	**98.0**	**98.0**	**98.0**	**68.1**
BFR0001sub	Annual	21.6	95.0	42.4	0.0
	Seasonal	53.4	95.0	75.0	0.0
	Maximum Source Reduction	**53.4**	**95.0**	**75.0**	**0.0**
ZBQ0005	Annual	98.0	98.0	98.0	96.3
	Seasonal	98.0	98.9	98.0	98.0
	Maximum Source Reduction	**98.0**	**98.9**	**98.0**	**98.0**
TRO0012	Annual	98.0	98.0	98.0	86.0
	Seasonal	98.0	98.0	98.0	96.8
	Maximum Source Reduction	**98.0**	**98.0**	**98.0**	**96.8**
LYO0015sub	Annual	98.0	95.4	98.0	68.6
	Seasonal	98.0	95.4	98.0	72.6
	Maximum Source Reduction	**98.0**	**95.4**	**98.0**	**72.6**

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.

Based on EPA guidance, the MOS can be achieved through two approaches (EPA 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. The second approach was used for this TMDL 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 Scenario Descriptions

Source Distribution

The final bacteria source distribution and corresponding baseline loads are derived from the source proportions listed in Table 2.4.3. The source distribution and baseline loads used in the TMDL scenarios are presented in Table 4.6.1. As stated in Section 4.3, the source distributions for subwatershed BFR0001sub and LYO0015sub were based on the sources identified at stations BFR0001 and LYO0015 respectively.

Table 4.6.1: Bacteria Source Distributions and Corresponding Baseline Loads Used in the Annual Average TMDL Analysis

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Load (Billion *E. coli* MPN/year)
	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	
LYO0051	7.7	6,778	25.6	22,638	21.4	18,982	45.4	40,184	88,582
BFR0028	4.6	1,724	22.8	8,558	26.5	9,951	46.1	17,286	37,518
BFR0001sub	7.8	2,245	38.6	11,150	15.3	4,424	38.3	11,050	28,870
ZBQ0005	19.7	117,681	24.4	145,258	19.5	116,232	36.4	217,025	596,195
TRO0012	3.7	12,016	24.7	80,128	22.5	72,791	49.1	159,157	324,091
LYO0015sub	7.0	9,902	24.3	34,279	19.0	26,797	49.7	70,154	141,131

First Scenario: Fecal Bacteria Practicable Reduction Targets

The maximum practicable reduction (MPR) for each of the four source categories is listed in Table 4.6.2. These values are based on review of the available literature and best professional judgment. It is assumed that human sources would potentially have the highest risk of causing 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. For this reason, in the subwatershed of LYO0015 the human source reduction had to be limited in order to maintain the permitted loads of the WWTP. The domestic animal category includes sources from pets (e.g., dogs) and the MPR is based on the estimated success of education and outreach programs.

Table 4.6.2: Maximum Practicable Reduction Targets

Max Practicable Reduction per Source	Human	Domestic	Livestock	Wildlife
	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 wastes offer a public health risk that is orders of magnitude less than that associated with human waste.[4]

[1] Health Effects Criteria for Fresh Recreational Waters. EPA-600/1-84-004. U.S. Environmental Protection Agency, Washington, DC. EPA. 1984.

[2] Preliminary Data Summary of Urban Storm Water Best Management Practices. EPA-821-R-99-012. U.S. Environmental Protection Agency, Washington, DC. EPA. 1999.

[3] Agricultural BMP Descriptions as Defined for The Chesapeake Bay Program Watershed Model. Nutrient Subcommittee Agricultural Nutrient Reduction Workshop. EPA. 2004.

[4] Environmental Indicators and Shellfish Safety. 1994. Edited by Cameron, R., Mackeney and Merle D. Pierson, Chapman & Hall.

As previously stated, these maximum practicable reduction targets are based on the available literature and best professional judgment. There is much uncertainty with estimated reductions from best management practices (BMP). The BMP efficiency for bacteria reduction ranged from –6% to +99% based on a total of 10 observations (US EPA 1999). The MPR to agricultural lands was based on sediment reductions identified by EPA (US 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 animals and livestock next (3), and wildlife the lowest (1) (See Table 4.6.2). The model was defined as follows:

$$\text{Risk Score} = \text{Min} \sum_{i=1}^{4} P_j * W_j \qquad (8)$$

where,

$$P_j = \frac{(1 - R_i) * Pb_j}{1 - TR} \qquad (9)$$

and,

$$TR = \frac{C - C_{cr}}{C} \tag{10}$$

Therefore the risk score can be represented as:

$$Risk\ Score = Min \sum_{i=1}^{4} \left[\frac{(1 - R_j) * Pb_j}{(1 - \frac{C - Ccr}{C})} * W_j \right] \tag{11}$$

where,

i = loading condition
j = bacteria source category =human, domestic animal, livestock and wildlife
P_j = % of each source category (human, domestic animals, livestock and wildlife) in final allocation
W_j = weight of risk per source category = 5, 3 or 1
R_j = percent reduction applied by source category (human, domestic animals, livestock and wildlife) for the specified loading condition (variable)
Pb_j = original (baseline) percent distribution by source category (variable)
TR = total reduction (constant within each loading condition) = Target reduction
C = in-stream concentration
Ccr = water quality criterion

The model is subject to the following constraints:

$C = Ccr$
$0 \leq R_{human} \leq 95\%$
$0 \leq R_{pets} \leq 75\%$
$0 \leq R_{livestock} \leq 75\%$
$R_{wildlife} = 0$
$P_j \geq 1\%$

In all but one of the subwatersheds, the constraints of this scenario could not be satisfied, indicating there was not a practicable solution. A summary of the first scenario analysis results is presented in Table 4.6.3.

Table 4.6.3: Practicable Reduction Scenario Results

Subwatershed	Applied Reductions				Total Reduction %	Target Reduction %*
	Domestic %	Human %	Livestock %	Wildlife %		
LYO0051	75.0	95.0	75.0	0.0	46.1	73.6
BFR0028	75.0	95.0	75.0	0.0	45.0	84.2
BFR0001sub	53.4	95.0	75.0	0.0	52.3	52.3
ZBQ0005	75.0	95.0	75.0	0.0	52.6	98.2
TRO0012	75.0	95.0	75.0	0.0	43.1	97.4
LYO0015sub	75.0	95.0	75.0	0.0	42.6	84.7

* needed to meet water quality standards

Second Scenario: Fecal Bacteria Reductions Higher than MPRs

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

To further develop the TMDL, a second scenario was analyzed in which the constraints on the MPRs were relaxed. In these subwatersheds, the maximum allowable reduction was increased up to 98% for all sources, including wildlife. A similar optimization procedure as before was used to minimize risk. Again, the objective is to minimize the sum of the risk for all conditions while meeting the scenario reduction constraints. The model was defined in the same manner as considered in the practicable reduction scenario but subject to the following constraints:

$$
\begin{aligned}
C &= Ccr \\
0 \leq R_{human} &\leq 98\% \\
0 \leq R_{pets} &\leq 98\% \\
0 \leq R_{livestock} &\leq 98\% \\
0 \leq R_{wildlife} &\leq 98\% \\
P_j &\geq 1\%
\end{aligned}
$$

The human source reduction for the subwatershed LYO0015sub was further constrained to no greater than 95.4% in order to maintain the permitted load of the WWTP.

A summary of the results of this second scenario analysis is presented in Table 4.6.4. For subwatershed ZBQ0005 a maximum reduction constraint of 98% for all bacterial sources was insufficient in order to meet the target reduction, therefore the constraint for this subwatershed was further relaxed to a maximum reduction of up to 100%.

Table 4.6.4: Reduction Results Based on Optimization Model Allowing Up to 98% Reduction

Subwatershed	Applied Reductions				Total Reduction %	Target Reduction %*
	Domestic %	Human %	Livestock %	Wildlife %		
LYO0051	98.0	98.0	98.0	44.2	73.6	73.6
BFR0028	98.0	98.0	98.0	68.1	84.2	84.2
BFR0001sub	53.4	95.0	75.0	0.0	52.3	52.3
ZBQ0005	98.0	98.9	98.0	98.0	98.2	98.2
TRO0012	98.0	98.0	98.0	96.8	97.4	97.4
LYO0015sub	98.0	95.4	98.0	72.6	84.7	84.7

* needed to meet water quality standards

4.7 TMDL Loading Caps

The TMDL loading cap is an estimate of the assimilative capacity of the monitored watershed. The TMDL loading caps are provided in billion MPN *E. coli*/day. These loading caps are for the six subwatersheds located upstream of their respective monitoring stations (LYO0051, BFR0028, BFR0001, ZBQ0005, TRO0012 and LYO0015).

Annual Average TMDL

As explained in the sections above, the annual average 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. This annual average baseline load is estimated using the geometric mean concentration and the average flow.

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. This reduction, estimated as explained in Section 4.4, represents the maximum reduction per source that satisfies the two loading conditions in each subwatershed, and that is required to meet water quality standards.

$$\text{TMDL Loading Cap} = L_b * (1 - R) \qquad (12)$$

where,

L_b = current or baseline load estimated from monitoring data
R = reduction required from baseline to meet water quality criterion.

The annual average bacteria TMDL loading caps for the subwatersheds are shown in Tables 4.7.1 and 4.7.2.

Table 4.7.1: Annual Average TMDL Loading Caps

Subwatershed	*E. coli* Baseline Load (Billion MPN/year)	Long-Term Average *E. coli* TMDL Load (Billion MPN/year)	% Reduction
LYO0051	88,582	23,401	73.6
BFR0028	37,518	5,919	84.2
BFR0001sub	28,870	13,761	52.3
ZBQ0005	596,195	10,567	98.2
TRO0012	324,091	8,357	97.4
LYO0015sub	141,131	21,534	84.7
Total	**1,216,388**	**83,539**	**93.1**

Table 4.7.2: Annual Average TMDL Loading Caps by Source Category

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Load (Billion *E. coli* MPN/year)
	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	%	Load (Billion *E. coli* MPN/year)	
LYO0051	0.6	136	1.9	453	1.6	380	95.9	22,433	23,401
BFR0028	0.6	34	2.9	171	3.4	199	93.2	5,514	5,919
BFR0001sub	7.6	1,047	4.1	557	8.0	1,106	80.3	11,050	13,761
ZBQ0005	22.3	2,354	14.6	1,548	22.0	2,325	41.1	4,340	10,567
TRO0012	2.9	240	19.2	1,603	17.4	1,456	60.5	5,059	8,357
LYO0015sub	0.9	198	7.3	1,567	2.5	536	89.3	19,233	21,534

Maximum Daily Loads

Recent EPA guidance (US EPA 2006a) recommends that maximum daily load (MDL) expressions of long-term annual average TMDLs should also be provided as part of the TMDL analysis and report. Selection of an appropriate method for translating a TMDL based on a longer time period into one using a daily time period requires decisions regarding 1) the level of resolution, and 2) the level of protection. The level of resolution pertains to the amount of detail used in specifying the maximum daily load. The level of protection represents how often the maximum daily load (MDL) is expected to be exceeded. Draft EPA/TetraTech guidance on daily loads (Limno-Tech 2007) provides three categories of options for both level of resolution and level of protection, and discusses these categories in detail.

For the Little Youghiogheny River watershed MDLs, a “representative daily load” option was selected as the level of resolution, and a value “that will be exceeded with a pre-defined probability” was selected as the level of protection. In these options, the MDLs have an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the MDLs were estimated following EPA’s “*Technical Support Document for Water Quality-Based Toxics Control*” (1991 TSD) (EPA 1991b); and “*Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages*” (EPA 2006b).

There are three steps to the overall process of estimating these MDLs. First, all the data available from each monitoring station are examined and the percentile rank of the highest observed concentration (at each station) is computed. The highest computed percentile rank is the upper bound percentile to be used in estimating the MDLs.

Secondly, the long-term annual average TMDL (see Table 4.7.1) concentrations are estimated. This is conducted for each station using a statistical methodology (the “Statistical Theory of Rollback,” or “STR,” described more fully in Appendix D).

Third, based on the estimated long-term average (LTA) TMDL concentrations, the MDL at each station is estimated using the upper boundary percentile computed in the first step above. Finally, MDLs are computed from these MDL concentrations and their corresponding flows.

Results of the fecal bacteria MDL analysis for the Little Youghiogheny River subwatersheds are shown in Table 4.7.3.

Table 4.7.3: Little Youghiogheny River Watershed Maximum Daily Loads Summary

Subwatershed	Maximum Daily Load (Billion *E. coli* MPN/day)
LYO0051	520
BFR0028	122
BFR0001sub	264
ZBQ0005	166
TRO0012	237
LYO0015sub	342

See Appendix D for a more detailed explanation of the procedure for obtaining these daily loads.

4.8 TMDL Allocations

The Little Youghiogheny River watershed fecal bacteria TMDL is composed of the following components:

TMDL = LA + WLA + MOS (13)

where,

LA = Little Youghiogheny River Watershed Load Allocation
WLA = Little Youghiogheny River Watershed Waste Load Allocation
MOS = Margin of Safety

The TMDL allocations for the Little Youghiogheny River watershed include a load allocation (LA) for certain nonpoint sources, and waste load allocations (WLA) for point sources including WWTPs and NPDES-regulated stormwater discharges. An explanation of the distribution of nonpoint source loads and point source loads to the LA and to the WLA is provided in the subsections that follow.

The margin of safety (MOS) is explicit and is incorporated in the analysis using a conservative assumption; it is not specified as a separate term. The assumption is that a 5% reduction of the criterion concentration established by MD to meet the applicable water quality standard will result in more conservative allowable loads of fecal bacteria, and thus provide the MOS. The final loads are based on average hydrological conditions, with reductions estimated based on critical loading conditions. The load reduction scenario results in load allocations that will achieve water quality standards. The State reserves the right to revise these allocations provided such revisions are consistent with the achievement of water quality standards.

Bacteria Source Categories and Allocation Distributions

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 the LA (those nonpoint sources or portions thereof not transported and discharged by stormwater systems) and the WLA (point sources including WWTPs, and NPDES regulated stormwater discharges). Only the final LA or WLA is reported in this TMDL.

Table 4.8.1: Potential Source Contributions for TMDL Allocation Categories in the Little Youghiogheny River Watershed

Source Category	TMDL Allocation Categories		
	LA	WLA	
		WWTP	Stormwater
Human	X	X	
Domestic	X		
Livestock	X		
Wildlife	X		

LA

All four bacteria source categories could potentially contribute to nonpoint source loads. For human sources, if the watershed has no MS4s or other NPDES-regulated Phase I or Phase II stormwater discharges, as is the case in the Little Youghiogheny River watershed, the nonpoint source contribution is estimated by subtracting any WWTP and/or CSO loads from the TMDL human load, and is then assigned to the LA. Livestock loads are all assigned to the LA. The domestic animals (pets) and wildlife loads are assigned to the LA in watersheds with no MS4s or other NPDES-regulated stormwater systems.

WLA

NPDES Regulated Stormwater

EPA's guidance document, "Establishing Total Maximum Daily Load (TMDL) Waste Load Allocations (WLAs) for Storm Water Sources and NPDES Permit Requirements Based on Those WLAs" (November 2002), advises that all individual and general NPDES Phase I and Phase II stormwater permits are point sources subject to WLA assignment in the TMDL. There are no MS4 permits or other NPDES-regulated Phase I or Phase II stormwater discharges in the Little Youghiogheny River watershed.

Municipal and Industrial WWTPs

As explained in the source assessment section above, there is one NPDES permitted point source facility with a permit regulating the discharge of fecal bacteria in the Little Youghiogheny River watershed. This facility discharges into the subwatershed of LYO0015. The WLA for the WWTP is estimated using the design flow of the plant stated in the facility's NPDES permit and the *E. coli* criterion of 126 MPN/100ml. Bacteria loads assigned to the WWTP are allocated as the WWTP-WLA and are presented in Table 4.8.2.

Table 4.8.2: Waste Load Allocation for Municipal and Industrial WWTPs

Facility	**NPDES Permit No.**	**County**	**Permit Flow (MGD)**	**Permit *E. coli* Concentration (MPN/100ml)**	**Permit *E.* coli TMDL (Billion MPN/year)**	**Permit *E.* coli MDL (Billion MPN/day)**
Trout Run WWTP	MD0051497	Garrett	0.9	126	1,567	13.35

4.9 Summary

The long-term annual average TMDL and TMDL allocations are presented in Table 4.9.1. Table 4.9.2 presents the maximum daily loads for the subwatersheds.

Table 4.9.1: Little Youghiogheny River Watershed Annual Average TMDL

Subwatershed	**Total Allocation**	**LA**	**SW-WLA**	**WWTP-WLA**
	(Billion MPN *E. coli* /year)			
LYO0051	23,401	23,401	0	0
BFR0028	5,919	5,919	0	0
BFR0001sub	13,761	13,761	0	0
ZBQ0005	10,567	10,567	0	0
TRO0012	8,357	8,357	0	0
LYO0015sub	21,534	19,967	0	1,567
Total[1]	**83,539**	**81,972**	**0**	**1,567**

[1] The MOS is incorporated.

Table 4.9.2: Little Youghiogheny River Watershed Maximum Daily Loads

Subwatershed	Total Allocation	LA	SW-WLA	WWTP-WLA
	(Billion MPN *E. coli* /day)			
LYO0051	520	520	0	0
BFR0028	122	122	0	0
BFR0001sub	264	264	0	0
ZBQ0005	166	166	0	0
TRO0012	237	237	0	0
LYO0015sub	342	329	0	13
Total[1]	**1,650**	**1,637**	**0**	**13**

[1] The MOS is incorporated.

The long-term annual average fecal bacteria TMDL summary for the Little Youghiogheny River watershed is presented in Table 4.9.3.

Table 4.9.3: Little Youghiogheny River Watershed Annual Average TMDL Summary

(Billion MPN *E. coli*/year)								
TMDL	=	**LA**	+	**WLA**			+	**MOS**
				SW WLA	+	**WWTP WLA**		
83,539	=	81,972	+	N/A	+	1,567	+	Incorporated

The maximum daily loads of fecal bacteria for the Little Youghiogheny River watershed are summarized in Table 4.9.4.

Table 4.9.4: Little Youghiogheny River Watershed MDL Summary

(Billion MPN *E. coli*/day)								
				WLA				
MDL	**=**	**LA**	**+**	**SW WLA**	**+**	**WWTP WLA**	**+**	**MOS**
1,650	=	1,637	+	N/A	+	13	+	Incorporated

In certain watersheds, the goal of meeting water quality standards may require very high reductions that are not achievable with current technologies and management practices. In this situation, where there is no feasible TMDL scenario, MPRs are increased to provide estimates of the reductions required to meet water quality standards. In all but one of the Little Youghiogheny River subwatersheds, water quality standards cannot be achieved with the maximum practicable reduction rates specified in Table 4.6.3. The TMDLs shown in Tables 4.9.1 and 4.9.2 represent reductions from current bacteria loadings that are beyond practical reductions. In cases where such high reductions are required to meet standards, it is expected that the first stage of implementation will be to carry out 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 waste load allocations can and will be implemented. In the Little Youghiogheny River watershed, the TMDL analysis indicates that, for five of the six subwatersheds, the reductions of fecal bacteria loads are beyond the MPR targets. These MPR targets were defined based on a literature review of BMPs effectiveness and assuming a zero reduction for wildlife sources. Little Youghiogheny River and its tributaries may not be able to attain water quality standards. The fecal bacteria load reductions required to meet water quality criteria in five of the six Little Youghiogheny River subwatersheds are not feasible by implementing effluent limitations and cost-effective, reasonable BMPs to nonpoint sources. Therefore, MDE proposes a staged approach to implementation beginning with the MPR scenario, with regularly scheduled follow-up monitoring to assess the effectiveness of the implementation plan.

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.

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 meet water quality standards. However, while neither Maryland nor EPA is proposing the elimination of wildlife to allow for the attainment of water quality standards, managing the overpopulation of wildlife remains 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 – Bacteria Data

Table A-1: Measured Bacteria Concentrations

Station	Date	*E. coli* Concentration (MPN/100ml)
LYO0051	11/5/2003	354
	11/19/2003	754
	12/3/2003	74
	1/7/2004	97
	1/12/2004	341
	1/22/2004	119
	2/4/2004	259
	2/19/2004	246
	3/3/2004	249
	3/17/2004	51
	4/7/2004	3
	4/21/2004	62
	5/12/2004	199
	5/26/2004	934
	6/9/2004	1187
	6/23/2004	820
	7/8/2004	442
	7/21/2004	275
	8/11/2004	393
	8/25/2004	426
	9/9/2004	4106
	9/22/2004	272
	10/6/2004	41
	10/20/2004	439

Station	Date	*E. coli* Concentration (MPN/100ml)
BFR0028	11/5/2003	122
	11/19/2003	1500
	12/3/2003	121
	1/7/2004	20
	1/12/2004	228
	1/22/2004	146
	2/4/2004	441
	2/19/2004	74
	3/3/2004	472
	3/17/2004	31
	4/7/2004	52
	4/21/2004	327
	5/12/2004	1607
	5/26/2004	2909
	6/9/2004	669
	6/23/2004	857
	7/8/2004	556
	7/21/2004	1723
	8/11/2004	1301
	8/25/2004	187
	9/9/2004	4611
	9/22/2004	187
	10/6/2004	161
	10/20/2004	435

Station	Date	*E. coli* Concentration (MPN/100ml)
BFR0001	11/5/2003	201
	11/19/2003	985
	12/3/2003	31
	1/7/2004	109
	1/12/2004	171
	1/22/2004	529
	2/4/2004	1198
	2/19/2004	199
	3/3/2004	20
	3/17/2004	110
	4/7/2004	41
	4/21/2004	31
	5/12/2004	1081
	5/26/2004	441
	6/9/2004	1989
	6/23/2004	529
	7/8/2004	437
	7/21/2004	203
	8/11/2004	52
	8/25/2004	216
	9/9/2004	3609
	9/22/2004	135
	10/6/2004	41
	10/20/2004	299

Station	Date	*E. coli* Concentration (MPN/100ml)
ZBQ0005	11/5/2003	733
	11/19/2003	9208
	12/3/2003	1607
	1/7/2004	816
	1/12/2004	1793
	1/22/2004	5475
	2/4/2004	2489
	2/19/2004	24192
	3/3/2004	1332
	3/17/2004	884
	4/7/2004	12996.5
	4/21/2004	8664
	5/12/2004	2143
	5/26/2004	9804
	6/9/2004	4611
	6/23/2004	1259
	7/8/2004	12996
	7/21/2004	24192
	8/11/2004	2481
	8/25/2004	15530
	9/9/2004	6131
	9/22/2004	24192
	10/6/2004	6131
	10/20/2004	7701

Station	Date	*E. coli* Concentration (MPN/100ml)
TRO0012	11/5/2003	573
	11/19/2003	24191.7
	12/3/2003	148
	1/7/2004	121
	1/12/2004	120
	1/22/2004	341
	2/4/2004	24192
	2/19/2004	228
	3/3/2004	278
	3/17/2004	158
	4/7/2004	345
	4/21/2004	683
	5/12/2004	4352
	5/26/2004	24192
	6/9/2004	4884
	6/23/2004	1274
	7/8/2004	4106
	7/21/2004	9804
	8/11/2004	4106
	8/25/2004	1935
	9/9/2004	19862
	9/22/2004	4611
	10/6/2004	1291
	10/20/2004	1439

Station	Date	*E. coli* Concentration (MPN/100ml)
LYO0015	11/5/2003	583
	11/19/2003	8164
	12/3/2003	74
	1/7/2004	218
	1/12/2004	108
	1/22/2004	211
	2/4/2004	3448
	2/19/2004	3255
	3/3/2004	448
	3/17/2004	691
	4/7/2004	324
	4/21/2004	213
	5/12/2004	907
	5/26/2004	5794
	6/9/2004	650
	6/23/2004	1043
	7/8/2004	211
	7/21/2004	316
	8/11/2004	464
	8/25/2004	620
	9/9/2004	7270
	9/22/2004	613
	10/6/2004	1643
	10/20/2004	763

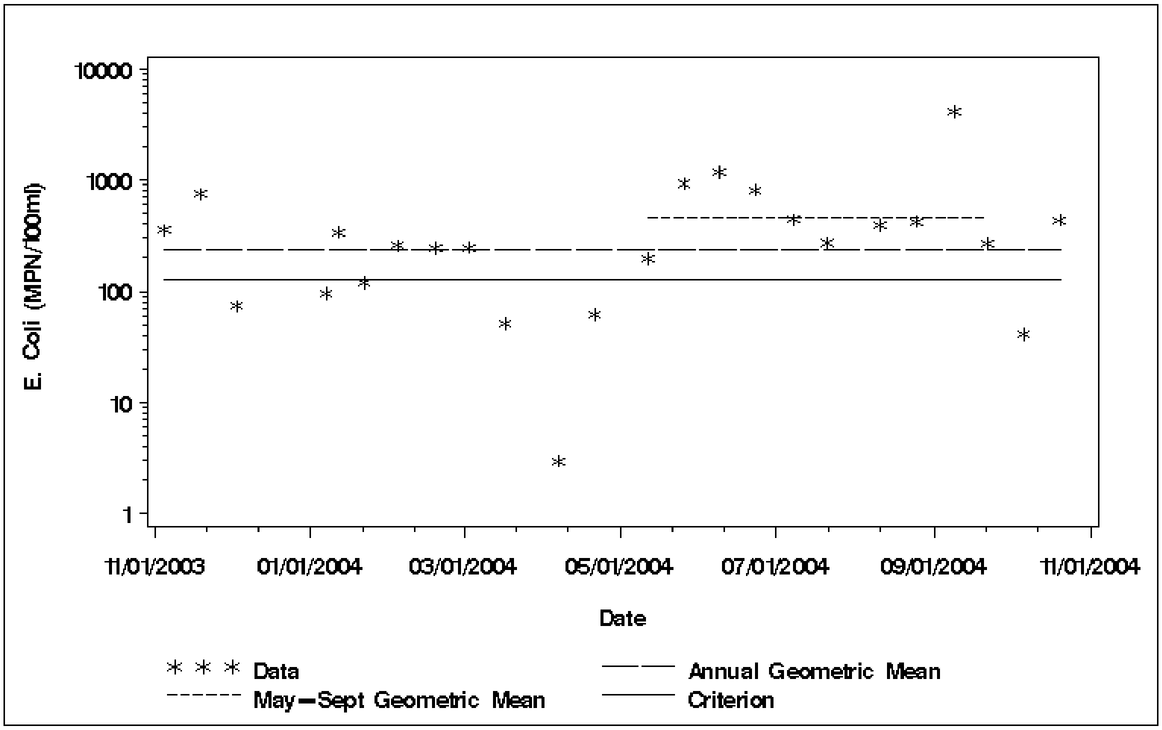

Figure A-1: *E. coli* Concentration vs. Time for MDE Monitoring Station LYO0051

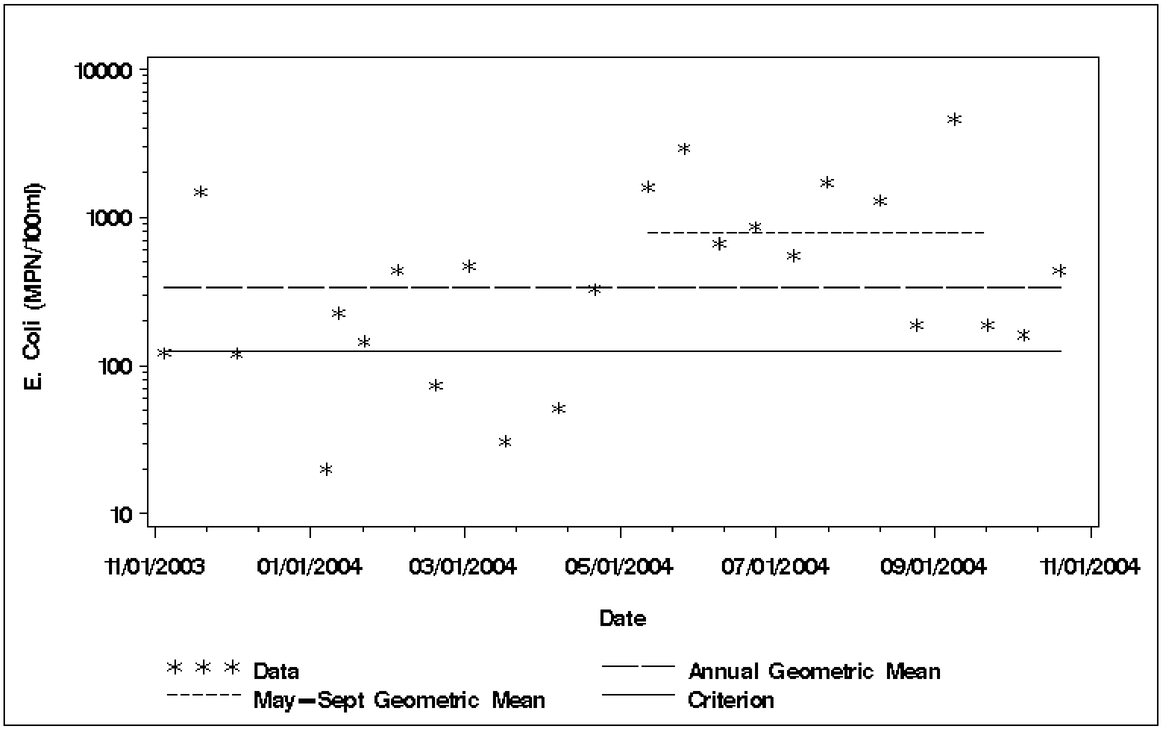

Figure A-2: *E. coli* Concentration vs. Time for MDE Monitoring Station BFR0028

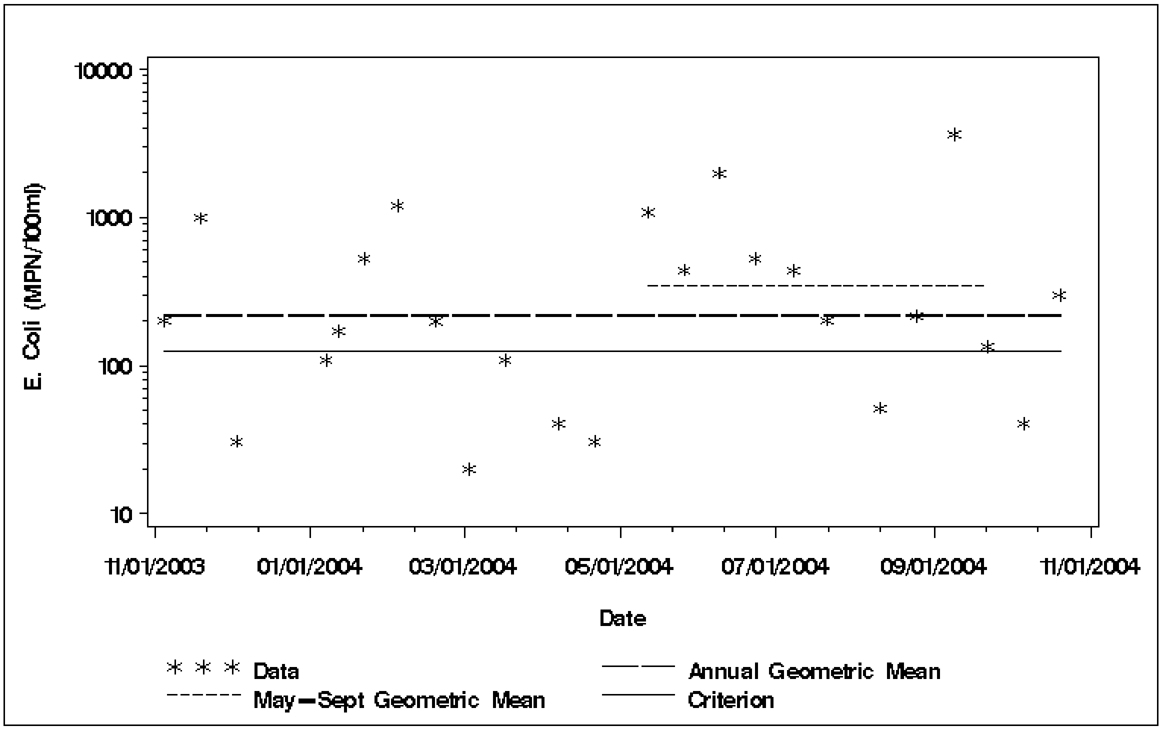

Figure A-3: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station BFR0001**

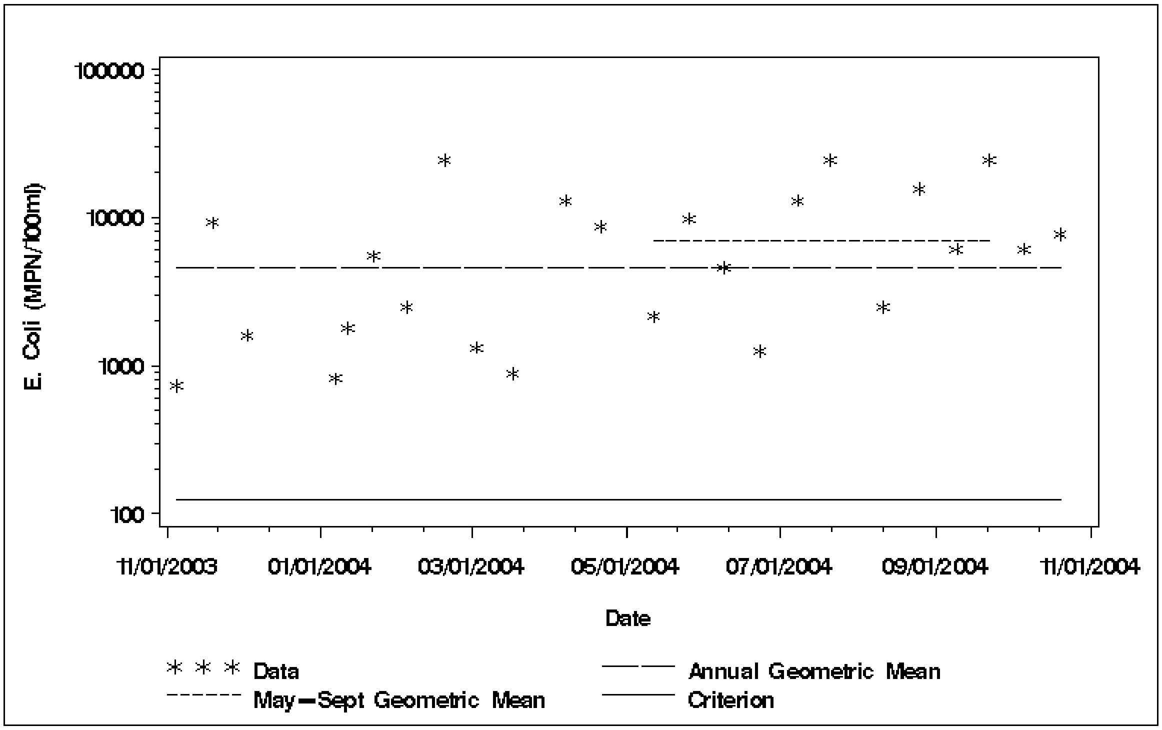

Figure A-4: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station ZBQ0005**

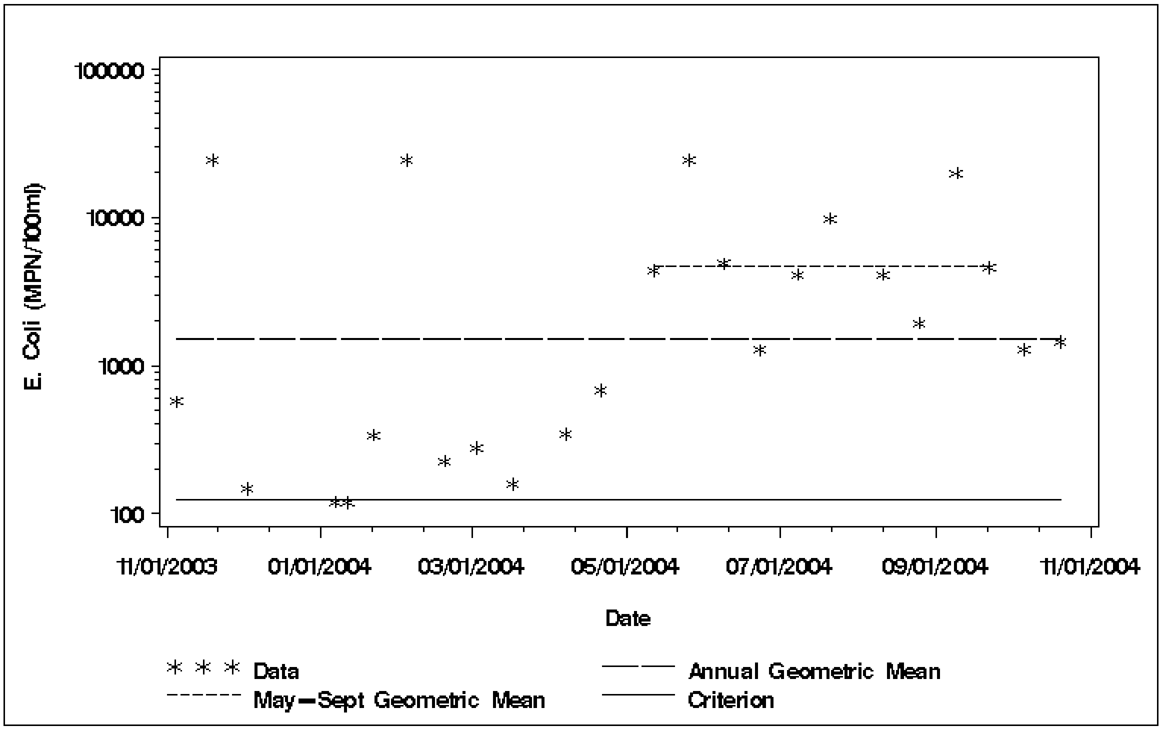

Figure A-5: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station TRO0012**

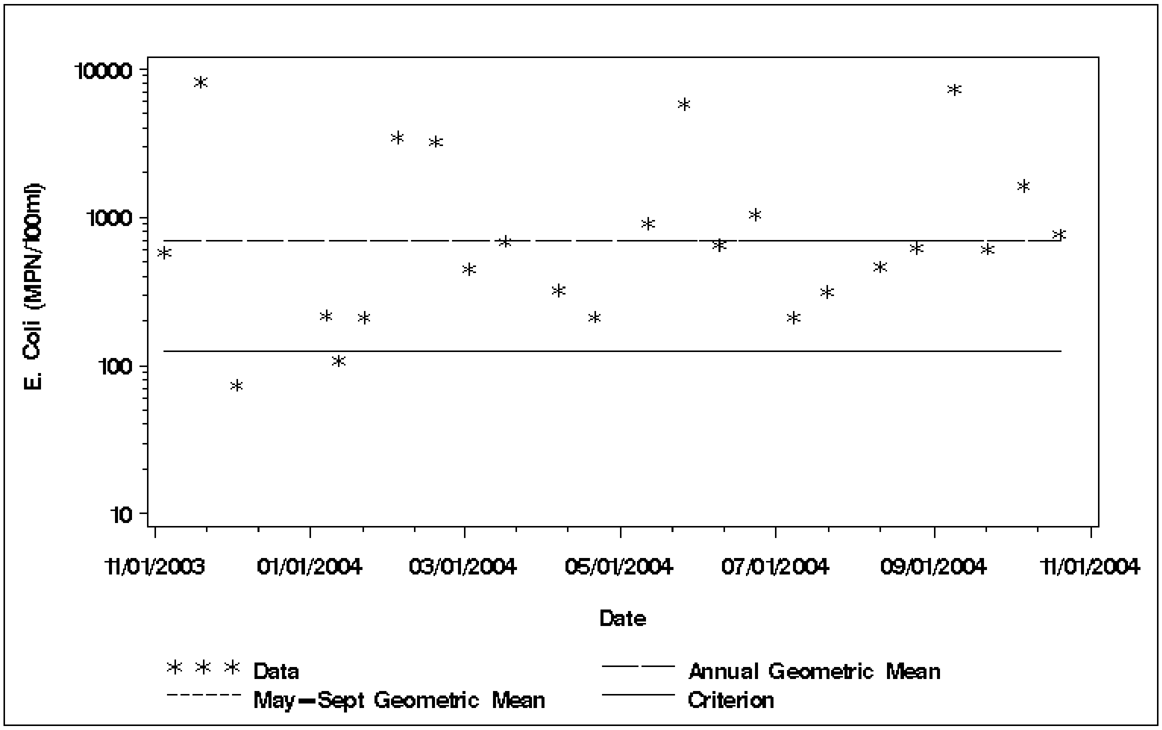

Figure A-6: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station LYO0015**

Appendix B - Flow Analysis

The Little Youghiogheny River watershed has no active USGS flow gauges. The flow analysis for the development of this TMDL was originally directed towards the development of flow duration curves. As explained in Section 4.2 of the main document, flow duration curves are needed for the conceptual model to divide the daily flow frequency into strata that are representative of hydrologic conditions. For this purpose, nearby flow gauges were analyzed to determine their possible use in the Little Youghiogheny River watershed flow analysis.

The one nearby USGS gauge, 03075500 (Youghiogheny River near Oakland, MD), was determined to have significantly differing watershed characteristics as compared to the Little Youghiogheny River watershed, making it unsuitable for use in this analysis. For this reason, the conceptual model used in previous MDE non-tidal bacteria TMDLs that was developed to better represent differing hydrologic conditions could not be used. The TMDL analysis for the Little Youghiogheny River watershed is based on average flow conditions.

Typical methods for estimating flows at an ungauged location include using regional regression equations or a drainage area ratio approach with a gauged basin. The drainage area ratio approach was discarded because an appropriate flow gauge could not be established.

Previous regression studies for predicting flows in Maryland are by Dillow (1995), Rule (1999), Moglen et. al. (2002) and Versar (2004). All of these studies identify that the most statistically significant watershed characteristic for predicting flow is the watershed area. Results from Versar (2004) indicated that for the mountain region, the flow regression equations give a reasonably accurate description of mean flows with a R^2 value of 0.9094 and a standard deviation of 0.1697.

Average flows were estimated in the six subwatersheds of the Little Youghiogheny River watershed as follows, using the flow regression equations from Versar's 2004 study, "Development of Regional Flow Duration Curves in Maryland".

$$\textit{Mean Flow (cfs)} = 10^{(0.2019 + 0.9778 * \log_{10}(A))}$$

where,

A = drainage area (mi^2)

Table B-1: Mean Flow Regression Equation Results

Subwatershed	Area (acres)	Area (mi^2)	Estimated Average Flow (cfs)
LYO0051	8,345	13.0	19.6
BFR0028	2,224	3.5	5.4
BFR0001sub	2,541	4.0	6.1
ZBQ0005	3,572	5.6	8.6
TRO0012	2,714	4.2	6.5
LYO0015sub	4,180	6.5	10.0

REFERENCES FOR APPENDIX B

Dillow, J.J.A., (1996). Technique for Estimating Magnitude and Frequency of Peak Flow in Maryland: U.S. Geological Survey Water –Resources Investigations Report 97-4279.

Moglen, G.E., Thomas, W.O. and Miller, A.C. (2002). Evaluation of Alternative Statistical Method for Estimating Frequency of Peak Flows in Maryland: Maryland Department of Transportation State Highway Administration Final Report SP907CRB.

Rule, T. C. 1999.

Versar (2004). Development of Regional Flow Duration Curves in Maryland. Prepared for Maryland Department of the Environment.

Appendix C – BST Report

Maryland Department of the Environment

Identifying Sources of Fecal Pollution in Shellfish and Nontidal Waters in Maryland Watersheds

November 2005 – June 2007

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Department of Biological Sciences and Environmental Health Science
Salisbury University, Salisbury, MD

Final Report
June 30, 2007

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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: Deep Creek, Dividing Creek, Little Youghiogheny River, Patapsco River, Prettyboy Reservoir, and the Youghiogheny River. Also included in the study were the following tidal shellfish harvesting areas: the Chester River, Corsica River, Herring and Turnville Creeks, Laws and Upper Thorofare, Manokin River, and the Pocomoke River watersheds. 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 Pocomoke 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 eight (8) *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. *Enterococci* 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, cow, goat, horse, dog, bear, beaver, deer, duck, fox, goose, heron, opossum, rabbit, raccoon, and squirrel). 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 the nontidal Little Youghiogheny River and the Youghiogheny River Watersheds using patterns from scat obtained from both watersheds, and the water isolate patterns of each were compared to the combined library. A combined known-source library was also used for the nontidal Patapsco River and Pretty Boy Reservoir Watersheds, with water isolate patterns of each compared to this combined library. For the tidal watersheds, no combined known-source libraries were used for any shellfish harvesting area; a known-source isolate library collected from each area was used for the particular watershed.

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). The first step in the tree-building process splits the library into two nodes by considering every binary split associated with every variable. The split is chosen that maximizes a specified index of homogeneity for isolate sources within each of the nodes. In subsequent steps, the same process is applied to each resulting node until a *stopping* criterion is satisfied. Nodes where an additional split would lead to only an insignificant increase in the *homogeneity index* relative to 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 isolate with an unknown source), based that is most populous among the library isolates in the node. Each water sample isolate (*i.e*., an 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]

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

[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.

Little Youghiogheny River Watershed ARA Results

Known-Source Library. A 597 known-source isolate library was constructed from sources in the Little Youghiogheny River Watershed (Table C-2a) and combined with 525 known-source isolate library for the Youghiogheny River (Table C-2b), for a total of 1,122 know-source isolates in the LYO-YOU library (Table C-2c). The number of unique antibiotic resistance patterns was calculated for each library, and the known sources in the combined library were grouped into four categories: human, livestock (cow, horse), pet (dog), and wildlife (deer, duck, goose) (Table C-2a, Table C-2b, Table C-2c). 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: Category, total number, and number of unique patterns in the Little Youghiogheny River known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
Human	human	139	100
Livestock	cow, horse	155	46
Pet	dog	64	48
Wildlife	deer, duck, goose	239	85
Total		597	279

Table C-2b: Category, total number, and number of unique patterns in the Youghiogheny River known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
human	human	158	113
livestock	cow, horse	127	32
pet	dog	73	47
wildlife	deer, duck, goose	167	59
Total		525	251

Table C-2c: Category and total number in the combined Little Youghiogheny and Youghiogheny Rivers known-source library.

Category	Potential Sources	Total Isolates
human	human	297
livestock	cow, horse	282
Pet	Dog	137
wildlife	deer, duck, goose	406
Total		1,122

For Little Youghiogheny River Watershed, a cutoff probability of 0.60 (60%) using the combined LYO-YOU library was shown to yield an overall rate of correct classification of 84% (Table C-3). The resulting rates of correction classification (RCCs) for the four categories of sources in the Little Youghiogheny River portion of the library are shown in Table C-4.

Table C-3: Number of isolates not classified, percent unknown, and percent correct for eight (8) threshold probabilities for LYO known-source isolates using the combined LYO – YOU known-source library.

Threshold	0	0.25	0.375	0.5	**0.6**	0.7	0.8	0.9
% correct	70.9%	70.9%	70.9%	71.2%	**84.3%**	89.9%	95.3%	96.9%
% unknown	0.0%	0.0%	0.5%	5.4%	**35.0%**	48.6%	64.0%	73.4%
# not classified	0	0	3	32	**209**	290	382	438

Figure C-1: Little Youghiogheny River Classification Model: Percent Correct versus Percent Unknown using the Little Youghiogheny River library.

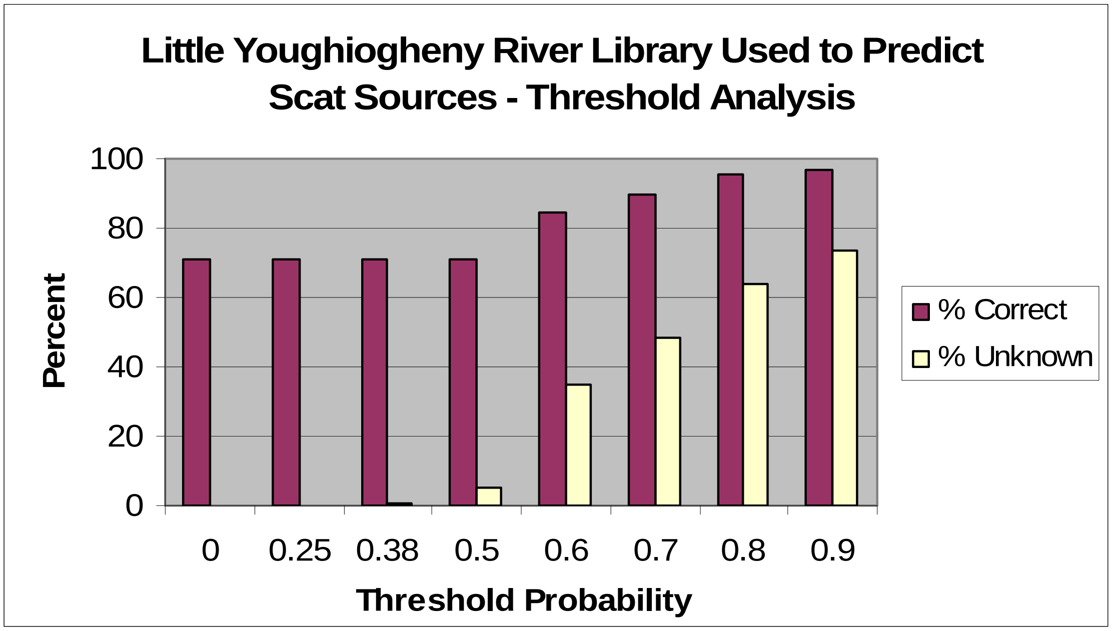


Table C-4: Actual species categories versus predicted categories, at 60% probability cutoff, with rates of correct classification (RCC) for each category.

	Predicted						
Actual	Human	Livestock	Pet	Wildlife	Unknown	Total	RCC*
human	93	7	8	3	28	139	83.8%
livestock	2	91	3	2	57	155	92.9%
pet	0	1	58	0	5	64	98.3%
wildlife	12	18	5	85	119	239	70.8%
Total	107	117	74	90	209	597	

*RCC = Actual number of predicted species category / Total number predicted. Example: 163 pet correctly predicted / 175 total number predicted for pet = 163/175 = 93%.

Little Youghiogheny River Water Samples. Monthly monitoring from six (6) monitoring stations on Little Youghiogheny River 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 less than 24. A total of 1,517 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table C-5, indicate that 61% of the water isolates were able to be classified to a probable host source when using a 0.60 (60%) probability threshold.

Table C-5: Probable host source distribution of water isolates, by species category, number of isolates, and percent isolates and based on the LYO-YOU combination library model classified at a cutoff probability of 60%.

Source	Count	Percent	Percent Without Unknowns
human	337	22.2%	36.2%
livestock	177	11.7%	19.0%
pet	140	9.2%	15.0%
wildlife	278	18.3%	29.8%
unknown	585	38.6%	
Total	1517	100.0%	100.0%
% classified	**61.4%**		

*Percentages may not add up to 100% due to rounding.

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

Table C-6: *Enterococcus* isolates obtained from water collected during the spring, summer, fall, and winter seasons at the Little Youghiogheny River's six (6) monitoring stations.

Station	Spring	Summer	Fall	Winter	Total
LYO0015	66	72	72	72	282
TRO0012	63	71	72	65	271
ZBQ0005	61	70	68	71	270
BFR0001	72	41	44	54	211
BFR0028	58	72	65	49	244
LYO0051	52	72	58	57	239
Total	372	398	379	368	1517

Tables C-7 and C-8 on the following pages show the number and percent of the probable sources for each monitoring station by month.

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

			Predicted	Source			
Station	Station	Station	Station	Station	Station	Station	Station
LYO0015	11/19/03	2	3	5	2	12	24
TRO0012	11/19/03	2	4	1	2	15	24
ZBQ0005	11/19/03	8	0	9	0	5	22
BFR0001	11/19/03	4	2	6	7	4	23
BFR0028	11/19/03	3	2	2	6	6	19
LYO0051	11/19/03	4	2	2	5	8	21
LYO0015	12/03/03	7	2	3	8	4	24
TRO0012	12/03/03	7	5	0	9	3	24
ZBQ0005	12/03/03	1	1	19	0	1	22
BFR0001	12/03/03	4	5	2	1	8	20
BFR0028	12/03/03	0	12	1	5	4	22
LYO0051	12/03/03	4	2	0	2	5	13
LYO0015	01/07/04	11	1	1	4	7	24
TRO0012	01/07/04	6	1	2	1	7	17
ZBQ0005	01/07/04	5	1	6	2	9	23
BFR0001	01/07/04	8	1	1	1	9	20
BFR0028	01/07/04	7	6	2	3	2	20
LYO0051	01/07/04	3	0	0	2	4	9
LYO0015	02/04/04	10	2	3	3	6	24
TRO0012	02/04/04	8	1	1	3	11	24
ZBQ0005	02/04/04	0	2	16	0	6	24
BFR0001	02/04/04	13	1	1	3	6	24
BFR0028	02/04/04	1	2	0	1	1	5
LYO0051	02/04/04	4	14	0	1	5	24
LYO0015	03/03/04	9	2	0	3	10	24
TRO0012	03/03/04	11	1	1	4	7	24
ZBQ0005	03/03/04	6	4	0	5	9	24
BFR0001	03/03/04	0	3	1	2	4	10
BFR0028	03/03/04	1	6	3	3	11	24
LYO0051	03/03/04	7	0	8	2	7	24
LYO0015	04/07/04	2	3	0	1	12	18
TRO0012	04/07/04	3	0	0	1	11	15
ZBQ0005	04/07/04	3	4	5	0	1	13
BFR0001	04/07/04	7	0	0	2	15	24
BFR0028	04/07/04	0	3	2	0	5	10
LYO0051	04/07/04	0	1	0	0	4	5

Table C-7: BST Analysis: Number of Isolates per Station per Date (continued).

			Predicted	Source			
Station	Station	Station	Station	Station	Station	Station	Station
TRO0012	05/12/04	9	2	0	3	10	24
ZBQ0005	05/12/04	9	4	1	0	10	24
BFR0001	05/12/04	18	0	1	0	5	24
BFR0028	05/12/04	6	1	0	9	8	24
LYO0051	05/12/04	14	1	3	2	3	23
LYO0015	06/09/04	1	0	0	6	17	24
TRO0012	06/09/04	1	3	0	7	13	24
ZBQ0005	06/09/04	5	2	0	3	14	24
BFR0001	06/09/04	15	0	0	1	8	24
BFR0028	06/09/04	16	1	0	4	3	24
LYO0051	06/09/04	3	0	3	0	18	24
LYO0015	07/08/04	4	3	3	4	10	24
TRO0012	07/08/04	1	9	1	6	6	23
ZBQ0005	07/08/04	4	5	4	3	6	22
BFR0001	07/08/04	7	0	3	0	0	10
BFR0028	07/08/04	8	10	0	1	5	24
LYO0051	07/08/04	4	2	1	9	8	24
LYO0015	08/11/04	7	1	0	3	13	24
TRO0012	08/11/04	5	3	0	6	10	24
ZBQ0005	08/11/04	5	1	3	5	10	24
BFR0001	08/11/04	0	2	0	1	4	7
BFR0028	08/11/04	1	1	0	3	19	24
LYO0051	08/11/04	3	5	0	3	13	24
LYO0015	09/09/04	2	2	4	11	5	24
TRO0012	09/09/04	2	2	1	10	9	24
ZBQ0005	09/09/04	2	2	0	8	12	24
BFR0001	09/09/04	4	0	2	12	6	24
BFR0028	09/09/04	1	0	1	6	16	24
LYO0051	09/09/04	1	0	3	9	11	24
LYO0015	10/06/04	2	4	0	11	7	24
TRO0012	10/06/04	2	3	2	7	10	24
ZBQ0005	10/06/04	2	3	0	12	7	24
BFR0001	10/06/04	0	0	0	0	1	1
BFR0028	10/06/04	0	3	0	4	17	24
LYO0051	10/06/04	1	2	0	3	18	24
Total		337	177	140	278	585	1517

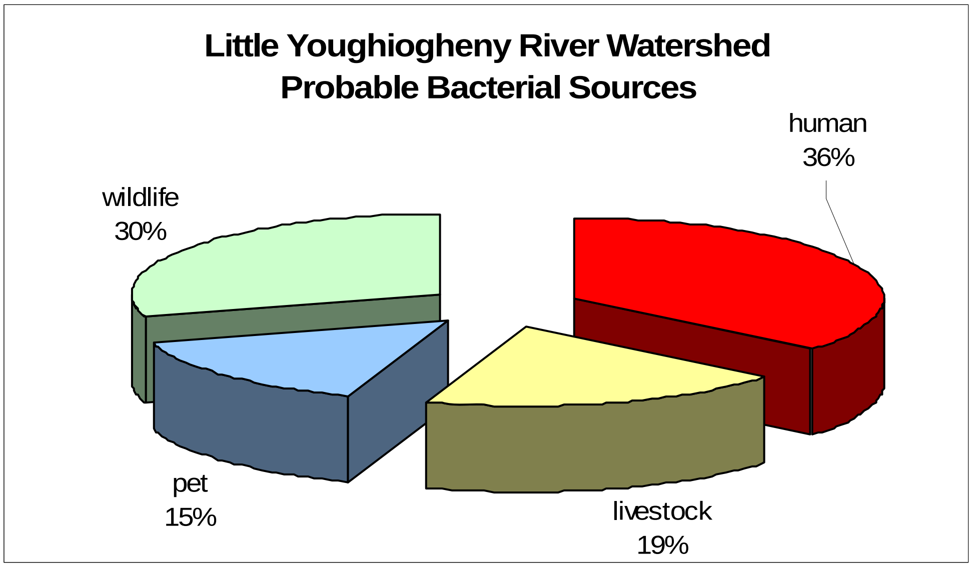
Table C-8: BST Analysis: Percent of Isolates per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
LYO0015	11/19/03	8.3%	12.5%	20.8%	8.3%	50.0%	100.0%
TRO0012	11/19/03	8.3%	16.7%	4.2%	8.3%	62.5%	100.0%
ZBQ0005	11/19/03	36.4%	0.0%	40.9%	0.0%	22.7%	100.0%
BFR0001	11/19/03	17.4%	8.7%	26.1%	30.4%	17.4%	100.0%
BFR0028	11/19/03	15.8%	10.5%	10.5%	31.6%	31.6%	100.0%
LYO0051	11/19/03	19.0%	9.5%	9.5%	23.8%	38.1%	100.0%
LYO0015	12/03/03	29.2%	8.3%	12.5%	33.3%	16.7%	100.0%
TRO0012	12/03/03	29.2%	20.8%	0.0%	37.5%	12.5%	100.0%
ZBQ0005	12/03/03	4.5%	4.5%	86.4%	0.0%	4.5%	100.0%
BFR0001	12/03/03	20.0%	25.0%	10.0%	5.0%	40.0%	100.0%
BFR0028	12/03/03	0.0%	54.5%	4.5%	22.7%	18.2%	100.0%
LYO0051	12/03/03	30.8%	15.4%	0.0%	15.4%	38.5%	100.0%
LYO0015	01/07/04	45.8%	4.2%	4.2%	16.7%	29.2%	100.0%
TRO0012	01/07/04	35.3%	5.9%	11.8%	5.9%	41.2%	100.0%
ZBQ0005	01/07/04	21.7%	4.3%	26.1%	8.7%	39.1%	100.0%
BFR0001	01/07/04	40.0%	5.0%	5.0%	5.0%	45.0%	100.0%
BFR0028	01/07/04	35.0%	30.0%	10.0%	15.0%	10.0%	100.0%
LYO0051	01/07/04	33.3%	0.0%	0.0%	22.2%	44.4%	100.0%
LYO0015	02/04/04	41.7%	8.3%	12.5%	12.5%	25.0%	100.0%
TRO0012	02/04/04	33.3%	4.2%	4.2%	12.5%	45.8%	100.0%
ZBQ0005	02/04/04	0.0%	8.3%	66.7%	0.0%	25.0%	100.0%
BFR0001	02/04/04	54.2%	4.2%	4.2%	12.5%	25.0%	100.0%
BFR0028	02/04/04	20.0%	40.0%	0.0%	20.0%	20.0%	100.0%
LYO0051	02/04/04	16.7%	58.3%	0.0%	4.2%	20.8%	100.0%
LYO0015	03/03/04	37.5%	8.3%	0.0%	12.5%	41.7%	100.0%
TRO0012	03/03/04	45.8%	4.2%	4.2%	16.7%	29.2%	100.0%
ZBQ0005	03/03/04	25.0%	16.7%	0.0%	20.8%	37.5%	100.0%
BFR0001	03/03/04	0.0%	30.0%	10.0%	20.0%	40.0%	100.0%
BFR0028	03/03/04	4.2%	25.0%	12.5%	12.5%	45.8%	100.0%
LYO0051	03/03/04	29.2%	0.0%	33.3%	8.3%	29.2%	100.0%
LYO0015	04/07/04	11.1%	16.7%	0.0%	5.6%	66.7%	100.0%
TRO0012	04/07/04	20.0%	0.0%	0.0%	6.7%	73.3%	100.0%
ZBQ0005	04/07/04	23.1%	30.8%	38.5%	0.0%	7.7%	100.0%
BFR0001	04/07/04	29.2%	0.0%	0.0%	8.3%	62.5%	100.0%
BFR0028	04/07/04	0.0%	30.0%	20.0%	0.0%	50.0%	100.0%
LYO0051	04/07/04	0.0%	20.0%	0.0%	0.0%	80.0%	100.0%
LYO0015	05/12/04	4.2%	4.2%	4.2%	50.0%	37.5%	100.0%
TRO0012	05/12/04	37.5%	8.3%	0.0%	12.5%	41.7%	100.0%
ZBQ0005	05/12/04	37.5%	16.7%	4.2%	0.0%	41.7%	100.0%
BFR0001	05/12/04	75.0%	0.0%	4.2%	0.0%	20.8%	100.0%
BFR0028	05/12/04	25.0%	4.2%	0.0%	37.5%	33.3%	100.0%

Table C-8: BST Analysis: Percent of Isolates per Station per Date (continued).

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
LYO0051	05/12/04	60.9%	4.3%	13.0%	8.7%	13.0%	100.0%
LYO0015	06/09/04	4.2%	0.0%	0.0%	25.0%	70.8%	100.0%
TRO0012	06/09/04	4.2%	12.5%	0.0%	29.2%	54.2%	100.0%
ZBQ0005	06/09/04	20.8%	8.3%	0.0%	12.5%	58.3%	100.0%
BFR0001	06/09/04	62.5%	0.0%	0.0%	4.2%	33.3%	100.0%
BFR0028	06/09/04	66.7%	4.2%	0.0%	16.7%	12.5%	100.0%
LYO0051	06/09/04	12.5%	0.0%	12.5%	0.0%	75.0%	100.0%
LYO0015	07/08/04	16.7%	12.5%	12.5%	16.7%	41.7%	100.0%
TRO0012	07/08/04	4.3%	39.1%	4.3%	26.1%	26.1%	100.0%
ZBQ0005	07/08/04	18.2%	22.7%	18.2%	13.6%	27.3%	100.0%
BFR0001	07/08/04	70.0%	0.0%	30.0%	0.0%	0.0%	100.0%
BFR0028	07/08/04	33.3%	41.7%	0.0%	4.2%	20.8%	100.0%
LYO0051	07/08/04	16.7%	8.3%	4.2%	37.5%	33.3%	100.0%
LYO0015	08/11/04	29.2%	4.2%	0.0%	12.5%	54.2%	100.0%
TRO0012	08/11/04	20.8%	12.5%	0.0%	25.0%	41.7%	100.0%
ZBQ0005	08/11/04	20.8%	4.2%	12.5%	20.8%	41.7%	100.0%
BFR0001	08/11/04	0.0%	28.6%	0.0%	14.3%	57.1%	100.0%
BFR0028	08/11/04	4.2%	4.2%	0.0%	12.5%	79.2%	100.0%
LYO0051	08/11/04	12.5%	20.8%	0.0%	12.5%	54.2%	100.0%
LYO0015	09/09/04	8.3%	8.3%	16.7%	45.8%	20.8%	100.0%
TRO0012	09/09/04	8.3%	8.3%	4.2%	41.7%	37.5%	100.0%
ZBQ0005	09/09/04	8.3%	8.3%	0.0%	33.3%	50.0%	100.0%
BFR0001	09/09/04	16.7%	0.0%	8.3%	50.0%	25.0%	100.0%
BFR0028	09/09/04	4.2%	0.0%	4.2%	25.0%	66.7%	100.0%
LYO0051	09/09/04	4.2%	0.0%	12.5%	37.5%	45.8%	100.0%
LYO0015	10/06/04	8.3%	16.7%	0.0%	45.8%	29.2%	100.0%
TRO0012	10/06/04	8.3%	12.5%	8.3%	29.2%	41.7%	100.0%
ZBQ0005	10/06/04	8.3%	12.5%	0.0%	50.0%	29.2%	100.0%
BFR0001	10/06/04	0.0%	0.0%	0.0%	0.0%	100.0%	100.0%
BFR0028	10/06/04	0.0%	12.5%	0.0%	16.7%	70.8%	100.0%
LYO0051	10/06/04	4.2%	8.3%	0.0%	12.5%	75.0%	100.0%
Total		22.2%	11.7%	9.2%	18.3%	38.6%	100.0%

Figure C-2. Little Youghiogheny River Watershed relative contributions by probable sources of *Enterococcus* contamination using the LYO-YOU combined library.



Little Youghiogheny River Summary

The use of ARA was successful for identification of probable bacterial sources in the Little Youghiogheny River Watershed. When water isolates were compared to the combined LYO-YOU library and potential sources predicted, 61% of the isolates were classified as to category by statistical analysis. The highest RCC, using the combined library, was 98% (for pet), with 93% (for livestock) the second highest. The RCCs for human sources and wildlife were 84% and 71%, respectively.

The largest category of potential sources in the watershed as a whole was human (36% of classified water isolates), followed by wildlife (30%), livestock (19%), and pet (15%) (Fig. C-2).

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Adjustment of BST Results

As explained in the BST Summary for the Little Youghiogheny River watershed, the percent of correct classification (RCC) for bacteria sources can introduce a potential misclassification of the more probable sources in the watershed. This is seen in Table C-4, which shows results of the analysis of samples from known sources. For example, out of 597, 155 isolates were known to be of livestock source but only 91 were classified by the analysis as being of livestock source. Of those 155, 2 were classified as human, 3 as pet, 2 as wildlife and 57 as unknown. Similarly, of the other three categories, 7 isolates known to be human, 1 isolate known to be pet, and 18 known wildlife isolates were classified as livestock, resulting in a total of 117 of all 597 isolates classified as livestock of which only 91 were known to be of livestock source.

The results provided by the BST methodology can be adjusted based on the known source percent of correct classification results provided in Table C-4.

Example:

The current BST methodology provides the following annual source percentages for station LYO0051:

Source Category	Original Percentage
Pets	8.32 %
Human	20.29 %
Livestock	10.98 %
Wildlife	17.18 %
Unknown	43.22 %

To get the correct human source percentage we redistributed the above percentages based on the % of correct classification as follows.

From Table C-4:

Source Category	Isolates known to be from Human Source	Total Isolates Predicted for Each category	Percentage
Pets	8	74	10.8 %
Human	93	107	86.9 %
Livestock	7	117	6.0 %
Wildlife	3	90	3.3 %
Unknown	28	209	13.4 %
Total	139	597	

Applying those percentages to the original estimated source distribution presented above will result in the adjusted percentage for human sources:

= (10.8 x 8.32) + (86.9 x 20.29) + (6.0 x 10.98) + (3.3 x 17.18) + (13.4 x 43.22) = 25.55 %

Thus the correct human source percentage, the value used in the TMDL analysis, is 25.55% and not 20.29%. Corrected percentages are also calculated as above for domestic animal (pet), livestock and wildlife sources. The classification of unknown is eliminated in the process as all known isolates are of known source. For station LYO0051 the corrected annual source percentages are as follows:

Source Category	**Adjusted Percentage**
Pets	7.7 %
Human	25.6 %
Livestock	21.4 %
Wildlife	45.4 %

Appendix D – Estimating Maximum Daily Loads

This appendix documents the technical approach used to define maximum daily loads of fecal bacteria consistent with the annual average TMDL which, when met, are protective of water quality standards in the Little Youghiogheny River watershed. The approach builds upon the TMDL analysis that was conducted to ensure that compliance with the annual average target will result in compliance with the applicable water quality standards. The annual average loading target was converted into allowable *daily* values by using the loadings developed from the TMDL analysis. The approach is consistent with available EPA guidance on generating daily loads for TMDLs.

The available guidance for developing daily loads does not specify a single allowable approach; it contains a range of options. Selection of a specific method for translating a time-series of allowable loads into expression of a TMDL requires decisions regarding both the level of resolution (e.g., single daily load for all conditions vs. loads that vary with environmental conditions) and level of probability associated with the TMDL.

Level of Resolution

The level of resolution pertains to the amount of detail used in specifying the maximum daily load. The draft EPA guidance on daily loads provides three categories of options for level of resolution.

1. **Representative daily load:** In this option, a single daily load (or multiple representative daily loads) is specified that covers all time periods and environmental conditions.
2. **Flow-variable daily load:** This option allows the maximum daily load to vary based upon the observed flow condition.
3. **Temporally-variable daily load:** This option allows the maximum daily load to vary based upon seasons or times of varying source or water body behavior.

Probability Level

Essentially all TMDLs have some probability of being exceeded, with the specific probability being either explicitly specified or implicitly assumed. This level of probability reflects, directly or indirectly, two separate phenomena:

1. Water quality criteria consist of components describing acceptable magnitude, duration, and frequency. The frequency component addresses how often conditions can allowably surpass the combined magnitude and duration components.
2. Pollutant loads, especially from wet weather sources, typically exhibit a large degree of variability over time. It is rarely practical to specify a “never to be exceeded value” for a daily load, as essentially any loading value has some finite probability of being exceeded.

The draft daily load guidance states that the probability component of the maximum daily load should be “based on a representative statistical measure” that is dependent upon the specific TMDL and best professional judgment of the developers. This statistical measure represents how often the maximum daily load is expected/allowed to be exceeded. The primary options for selecting this level of protection would be:

1. **The maximum daily load reflects some central tendency:** In this option, the maximum daily load is based upon the mean or median value of the range of loads expected to occur. The variability in the actual loads is not addressed.
2. **The maximum daily load reflects a level of protection implicitly provided by the selection of some "critical" period**: In this option, the maximum daily load is based upon the allowable load that is predicted to occur during some critical period examined during the analysis. The developer does not explicitly specify the probability of occurrence.
3. **The maximum daily load is a value that will be exceeded with a pre-defined probability:** In this option, a "reasonable" upper bound percentile is selected for the maximum daily load based upon a characterization of the variability of daily loads. For example, selection of the 95th percentile value would result in a maximum daily load that would be exceeded 5% of the time.

Selected Approach for Defining Maximum Daily Loads for Nonpoint Sources and MS4

To calculate the Little Youghiogheny River watershed MDL for non-point sources and MS4s, a "representative daily load" option was selected as the level of resolution, and a value "that will be exceeded with a pre-defined probability" was selected as the level of protection. In these options, the maximum daily load is one single daily load, with an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the maximum daily loads were estimated following EPA's "Technical Support Document for Water Quality-Based Toxics Control" (1991 TSD) (EPA 1991); and "Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages" (EPA 2006).

The 1991 TSD illustrates a way to identify a target maximum daily concentration from a long-term average concentration (LTA) based on a coefficient of variation (CV) and the assumption of a log-normal distribution of the data. The equations for determining both the upper boundary percentile and corresponding maximum daily load described in the TSD are as follows:

$$MDLC = LTA * e^{[Z\sigma - 0.5\sigma^2]} \qquad \text{(D1)}$$

and,

$$\text{MDL} = \text{MDLC*Q*F} \qquad \text{(D2)}$$

where,

MDLC = maximum daily load concentration (MPN/100ml)
LTAC = long-term average TMDL concentration (MPN/100ml)
MDL = Maximum Daily Load (MPN/day)
Z = z-score associated with upper bound percentile (unitless)

σ^2 = $\ln(CV^2 + 1)$
CV = coefficient of variation
Q = flow (cfs)
F = conversion factor

The first step is to use the bacteria monitoring data to estimate the upper bound percentile as the percentile of the highest observed bacteria concentration in each of the six monitoring stations of the Little Youghiogheny River watershed. Using the maximum value of *E. coli* observed in each monitoring station, and solving for the z-score using the above formula, the value of "z" and its corresponding percentile is found as shown below. The percentile associated with the particular value of z can be found in tables in statistics books or using the function NORMSINV(%) in EXCEL©.

$$Z = [\log_{10}(MOC) - \log(AM) + 0.5\sigma^2]/\sigma \qquad \text{(D3)}$$

where,

Z = z-score associated with upper bound percentile
MOC = maximum observed bacteria concentration (MPN/100ml)
AM = arithmetic mean observed bacteria concentrations (MPN/100ml)
σ^2 = $\ln(CV^2 + 1)$
CV = coefficient of variation (arithmetic)

Note that these equations use arithmetic parameters, not geometric parameters as used in the calculations of the long-term annual average TMDL. Therefore, bias correction factors are not necessary to estimate the loads as will be explained below.

The highest percentile of all the stations will define the upper bound percentile to be used in estimating the maximum daily limits. In the case of the Little Youghiogheny River watershed, a value measured at the LYO0051 station resulted in the highest percentile of the six stations. This value translates to the 97.8th percentile, which is the upper boundary percentile to be used in the computation of the maximum daily limits (MDLs) throughout this analysis. Results of the analysis to estimate the recurrence or upper boundary percentile are shown in Table D-1.

Table D-1: Percentiles of Maximum Observed Bacteria Concentrations

Subwatershed	Maximum Observed *E. coli* Concentration (MPN/100ml)	Percentile (%)
LYO0051	4,106	97.8
BFR0028	4,611	96.8
BFR0001	3,609	97.7
ZBQ0005	24,192	92.9
TRO0012	24,192	93.8
LYO0015	8,164	97.3

The 97.8th percentile value results in a maximum daily load that would not be exceeded 97.8% of the time, as, in a similar manner, a TMDL that represents the long term average condition would be expected to be exceeded half the time even after all required controls were implemented.

The MDLs are estimated based on a statistical methodology referred to as "Statistical Theory of Rollback (STR)". This method predicts concentrations of a pollutant after its sources have been controlled (post-control concentrations), in this case after annual average TMDL implementation. Using STR, the daily TMDLs are calculated as presented below.

First, the long-term average TMDL concentrations (C_{LTA}) are estimated by applying the required percent reduction to the baseline (monitoring data) concentrations (C_b) as follows:

From Section 4.3, equation (8):

$$L_b = Q * C_b * F_1$$

And from equation (13):

$$Annual\ Average\ TMDL = L_b * (1 - R)$$

Therefore,

$$L_b*(1-R) = Q*C*F_1*(1-R) \qquad \text{(D4)}$$

As explained before, a reduction in concentration is proportional to a reduction in load, thus the bacteria concentrations expected after reductions are applied are equal to the baseline concentrations multiplied by one minus the required reduction:

$$C_{LTA} = C_b * (1-R) \qquad \text{(D5)}$$

The TMDL concentrations estimated as explained above are shown in Table D-2.

Table D-2: Long-term Annual Average (LTA) TMDL Bacteria Concentrations

Subwatershed	LTA Geometric Mean *E. coli* Concentration (MPN/100ml)	LTA Arithmetic Mean* *E. coli* Concentration (MPN/100ml)
LYO0051	62	170
BFR0028	53	145
BFR0001	103	277
ZBQ0005	81	154
TRO0012	39	198
LYO0015	106	241

*Only arithmetic parameters are used in the daily loads analysis.

The next step is to calculate the 97.8th percentile (the MDL concentrations) of these expected concentrations (LTA concentrations) using the coefficient of variation of the baseline concentrations. Based on a general rule for coefficient of variations, the coefficient of variation of the distribution of pollutant concentrations does not change after these concentrations have been reduced or controlled by a fixed proportion (Ott 1995). Therefore, the coefficient of variation estimated using the monitoring data concentrations does not change, and it can be used to estimate the 97.8th percentile of the long-term average TMDL concentrations (LTAC) using equation (D1). These values are shown in Table D-3.

Table D-3: Maximum Daily Load (MDL) Concentrations

Subwatershed	Coefficient of Variation	MDL *E. coli* Concentration (MPN/100ml)
LYO0051	2.54	1,085
BFR0028	2.54	923
BFR0001	2.49	1,757
ZBQ0005	1.61	795
TRO0012	4.98	1,479
LYO0015	2.04	1,401

With the 97.8th percentiles of LTA TMDL bacteria concentrations estimated as explained above, the maximum daily load for MS4 and non-point sources for each subwatershed can be now estimated as:

$$\text{Daily TMDL (MPN/day)} = Q*(97.8^{th}C_{LTA})*F_1 \qquad \text{(D6)}$$

Selected Approach for Defining Maximum Daily Loads for Other Point Sources

The TMDL also considers contributions from other point sources (i.e., municipal and industrial WWTP) in watersheds that have NPDES permits with fecal bacteria limits. The TMDL analysis that defined the average annual TMDL held each of these sources constant at their existing NPDES permit limit (daily or monthly) for the entire year. The approach used to determine maximum daily loads was dependent upon whether a maximum daily load was specified within the permit. If a maximum daily load was specified within the permit, then the maximum design flow is multiplied by the maximum daily limit to obtain a maximum daily load. If a maximum daily limit was not specified in the permit, then the maximum daily loads are calculated from guidance in the TSD for Water Quality-based Toxics Control (EPA 1991). The long-term average annual TMDL was converted to maximum daily limits using Table 5-2 of the TSD assuming a coefficient of variation of 0.6 and a 99th percentile probability. This results in a dimensionless multiplication factor of 3.11. The average annual bacteria loads for WWTPs are reported in billion MPN/year. In the Little Youghiogheny River watershed, to estimate the maximum daily loads for WWTPs, the annual average loads are multiplied by the multiplication factor as follows:

$$\text{WWTP-WLA MDL}_{\text{(billion MPN/day)}} = [\text{WWTP-WLA}_{\text{(billion MPN/year)}}]*(3.11/365) \qquad \text{(D7)}$$

The Maximum Daily Loads for the Little Youghiogheny River subwatersheds are presented in Table D-4 below.

Table D-4: Maximum Daily Loads Summary

Subwatershed	Maximum Daily Load (Billion *E. coli* MPN/day)
LYO0051	520
BFR0028	122
BFR0001sub	264
ZBQ0005	166
TRO0012	237
LYO0015sub	342

Maximum Daily Loads Allocations

Using the MDLs estimated as explained above, loads are allocated following the same methodology as the annual average TMDL (See section 4.8). The maximum daily load allocations for the Little Youghiogheny River watershed are presented in Table D-5.

Table D-5: Little Youghiogheny River Watershed Maximum Daily Loads

Subwatershed	Total Allocation	LA	SW-WLA	WWTP-WLA
	(Billion MPN *E. coli* /day)			
LYO0051	520	520	0	0
BFR0028	122	122	0	0
BFR0001sub	264	264	0	0
ZBQ0005	166	166	0	0
TRO0012	237	237	0	0
LYO0015sub	342	329	0	13
Total[1]	**1,650**	**1,637**	**0**	**13**

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