Preliminary Report
Review of Pathogen Loading Data

Report prepared for
Whippany River Watershed Action Committee
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Table of Contents

1.0 Introduction - Overview of Fecal Coliform Loading in Developed Watersheds

Microbial pollution of the Whippany River is of particular interest as fecal coliform, which is typically found in the digestive system of warm-blooded animals, may be an indicator of the presence of pathogenic organisms. The coliform family of bacteria includes total coliforms, fecal coliforms and the group *Escherichia coli* (*E. coli*). Each of these bacteria can indicate the presence of fecal wastes in surface waters and are generally utilized as indicator organisms for the possible presence of other harmful bacteria, viruses and protozoa. Examples of bacterial pathogens frequently associated with storm water include *Shigella* spp., *Salmonella* spp. and *Pseudonomas auerognosa* while protozoan pathogens associated with storm water include *Giardia* and *Cryptosporidium.*

The sources of fecal coliform loading on a watershed scale are diffuse and difficult to track. The Whippany River watershed, encompassing 68.7 mi^2, consists of varying land use characteristics ranging from largely forested land in the headwater reaches to increasingly developed land near the eastern border of the watershed associated with the terminal reaches of the River. Associated with varying land use are a multitude of differential factors which influence fecal coliform loading. Fecal coliform sources, in the simplest sense, are derived from either human or animal fecal wastes. Difficulty arises in parsing out the contributing organism, pathway and fate of fecal coliform.

In the Whippany River watershed fecal coliform loading may be derived from human sources which are ultimately transferred to receiving waters via waste treatment systems. These systems are either individual lot septic systems, which are primarily confined to the less densely populated western portion of the watershed, or from wastewater treatment facilities associated with the more heavily developed areas of the watershed. Septic systems, when properly designed and installed in appropriate locations, can achieve virtually complete bacteria removal over a distance of 50 to 300 feet but may not necessarily remove enteric viruses (Schueler 2000). Fecal coliform are effectively removed from properly functioning septic systems due to filtering and straining through the soil profile. However, many septic systems fail in properly treating bacteria due to improper design, placement, constraining soils, or lack of maintenance. Regional rates of septic system failures have been reported to range from five to nearly 40%, with an average of about 10% (Schueler 2000). While an average of a 10% failure rate has been obtained through review of the scientific literature actual septic failure rates are extremely site specific and are dependent on numerous factors including soils, proximity of the system to waterways, distance to bedrock or other confining layers, maintenance and age. While many states have protocols in place to document septic failure rates for planning purposes, New Jersey has just began to systematically collect such data. As such, determining septic failure loading of fecal coliform bacteria throughout the Whippany River watershed is inherently difficult and will likely contain a degree of error without an extensive field reconnaissance survey. Secondary pathways of human sourced fecal coliform loading are derived from water treatment facilities and their associated pipe infrastructure. With the advent of modern wastewater treatment facilities the historical loading of fecal coliform has been drastically reduced but is far from eliminated. Many sewer systems are an episodic or chronic source of fecal coliform loading due to sanitary sewer overflows (SSOs), illicit connections to storm sewers or illegal dumping into the storm drain system. While combined sewer overflows (CSOs) may contribute a significant portion of the fecal coliform load in some watersheds they are not a factor in the Whippany River watershed. If the aforementioned issues are addressed then the actual loading of fecal coliform from water treatment facilities is generally below the standard water quality threshold of 200 cfu/100 ml (Field 1990). In New Jersey, site specific fecal coliform effluent data is routinely collected by wastewater treatment facilities as a condition of their NJPDES permit. As such, this information may be utilized to refine the contribution of fecal coliform from point source discharges throughout the Whippany River watershed.

The majority of fecal coliform loading found in urbanized portions of watersheds with properly functioning sewage treatment systems may be derived from non-human sources. Genetic studies conducted by Alderiso *et al.* (1996) and Trial *et al.* (1993) independently concluded that 95% of fecal coliform found in urban stormwater were of non-human sources (Schueler 2000). Non-human sources of fecal coliforms in urbanized portions of the Whippany River watershed may be derived from dogs, cats, raccoons, deer, rodents, waterfowl and any other warm blooded animal. Waterfowl have been speculated to be a major source of localized fecal coliform loading at suburban areas due to the prevalence of appropriate habitat and food sources in the way of stormwater detention basins and ample swaths of turf grass. In these settings, many waterfowl populations flourish, particularly Canada Geese (*Branta canadensis*). Hussong *et al* (1979) has calculated fecal coliform loading rates for wild and captive Canada Geese and subsequently applied these rates to field experiments which recorded Goose density and “bird hours” spent in several study ponds. Loading rates calculated from this data were compared to recoverable fecal coliforms from pond water at the surface and at the sediments resulting in a positive correlation (r = 0.79, n = 18) between waterfowl concentrations and surface water fecal coliform concentrations. While a positive correlation was noted, difficulty was reported in properly assessing fecal coliform recovery due to variation associated with un-controllable variables such as fecal die off, water temperature and non-point source (NPS) inputs (Hussong *et al* 1979). In addition, the settling velocity of fecal coliforms to the sediments is highly dependent on whether or not fecal coliform bacteria are adhered to larger sediment particles and the flushing rate of the basin.

Domesticated pets, primarily cats and dogs, may be a considerable source of fecal coliform loading in suburban and urbanized watershed areas, especially watersheds without stringent pet waste removal ordinances. For example, a single gram of dog feces can contain up to 23 million fecal coliform bacteria (van der Wel 1995). An additional source of wildlife derived fecal coliform is that from raccoons, which have adapted to living a portion of their lives within the stormwater infrastructure of suburban and urban watersheds. Such instances have been documented in the Whippany River watershed

(Van Orden 2004). Furthermore, Blankenship (1996) has reported that exceedance of *E. coli* standards in a Virginia costal area was due to the local raccoon population.

In addition to the sources of fecal coliform, habitat for fecal coliform proliferation is an important concern in addressing fecal coliform loading to surface waters. Popular opinion is that most fecal coliform simply die off in an aquatic environment. Research has shown that many of the bacteria do not die off, but instead sink to the bottom sediments of lakes and streams whereby they remain viable. Sediment conditions are typically favorable for thriving fecal coliform bacteria populations, especially if the sediments consist of a considerable about of organic matter. In addition, some studies have shown strong evidence that stormwater pipes may be a major bacterial source due to end-of-pipe sampling bacteria concentrations being up to an order of magnitude greater than any source area in the contributing watershed (Pitt and McClean 1986).

As evidenced above, the ubiquitous nature of fecal coliform bacteria on a watershed wide scale necessitates a multi-faceted approach to source identification and control. Watershed based modeling in concert with microbial source tracking (MST), in addition to field reconnaissance previously conducted by Dr. George Van Orden and many Whippany River Watershed Action Committee members, will allow for the proper identification of the relative contribution of multiple sources of fecal coliform to the River. This information will allow for the prioritization of best management practices which serve to mitigate fecal loading loadings.

2.0 Modeling the Pollutant Load to the Whippany River using AVGWLF

2.1 Introduction

The interconnectivity between streams and their watersheds is a central tenant in non-point source (NPS) pollution control. Watershed size and the land uses, soil types, topography and geology in concert with variable climatic conditions all influence the quantity of water, its temporal distribution and the nutrient, sediment and fecal coliform load associated with inflows to the river. A direct correlation exists between watershed disturbance and increased fecal coliform loading. The conversion of forests to agricultural, residential, commercial and industrial lands brings about an increase in fecal coliform loading due to increased domestic animal populations, human sewage disposal practices, nuisance waterfowl and sediment disturbance. Furthermore, increased watershed disturbance leads to increasing loading of phosphorus, nitrogen and sediments, which also affect water quality through accelerated eutrophication.

In order to discern between the sources of fecal coliform loading to the Whippany River it is necessary to model the source and transport of fecal coliform based on a variety of controlling mechanisms. For this analysis Princeton Hydro has chosen to utilize AVGWLF to model fecal coliform, phosphorus, nitrogen and sediment loading to the Whippany River. While the main focus of this study is on fecal coliform loading, as the River is listed on the State's 303(d) list for this parameter, it is crucial to model nutrient and sediment loading to this River as well in order to gain a full understanding of any additional impairment due to eutrophication.

The modeling of NPS pollution on a watershed wide scale is a tedious task due to large spatial and temporal variations which must be considered, in addition to the large amount of data that must be compiled, integrated, analyzed and interpreted (Evans 2008). Recently, Geographic Information Systems (GIS) have been utilized to integrate watershed simulation models in order to increase computational efficiency and accuracy of complex hydrologic and pollutant transport calculations. One such example has been the integration of the Generalized Watershed Loading Function (GWLF) model developed by Haith and Shoemaker (1987) with ArcView by Dr. Barry Evans. The resultant model package, AVGWLF, has been endorsed by the U.S. EPA as a "mid-level" model which contains algorithms for simulating most of the key mechanisms controlling hydrologic and nutrient fluxes within a watershed (USEPA 1999). AVGWLF was originally developed for Pennsylvania and is formatted to utilize GIS data files from this state. Nevertheless, this model has been successfully calibrated and utilized to accurately compute the hydrologic and nutrient budgets for lakes and streams by the New England Interstate Water Pollution Control Commission (NEIWPCC 2007). Furthermore, Princeton Hydro has successfully utilized the AVGWLF model in New Jersey to model the hydrologic and pollutant load to Manalapan Lake (Princeton Hydro 2009).

The GWLF model provides the ability to simulate runoff, sediment, nitrogen and phosphorus loads from a watershed given variable size-source areas. It also has algorithms for calculating septic loads and allows for the inclusion of point source nutrient loading. GWLF is a continuous simulation model that utilizes daily time steps for weather data and water balance calculations. Monthly calculations are made for nutrient and sediment loads based on the daily water balance accumulated monthly values. GWLF is considered to be a combined distributed / lumped parameter watershed model. For surface loading, it is distributed in the sense that it allows for the inclusion of multiple land use scenarios but each area is assumed to be homogenous in regard to various attributes considered by the model. In addition, the model does not spatially route watershed transport of sediments and nutrients but simply aggregates loads from each source area. For sub-surface loading, GWLF acts as a lumped parameter model using a water balance approach. No distinct areas are considered for sub-surface flow contributions. Daily water balances are computed for an unsaturated zone as well as a saturated sub-surface zone, where infiltration is computed as the differenced between precipitation and snowmelt minus surface runoff plus evapotranspiration (Evans 2008).

Hydrologic loading is simulated through the GWLF model utilizing the Soil Conservation Service – Curve Number (SCS-CN) approach with daily weather (temperature and precipitation) as inputs. Erosion and sediment yield are estimated utilizing monthly erosion calculations based on the Universal Soil Loss Equation (USLE) algorithm (with monthly rainfall-runoff coefficients) and a monthly composite of the KLSCP values for each source areas (LU/LC combination). A sediment delivery ratio based on watershed size and a transport capacity average daily runoff is then applied to the calculated erosion to determine sediment yield for each source area. Surface nutrient losses are determined by applying dissolved N and P coefficients to surface runoff and a sediment coefficient to the yield portion for each agricultural land use source area. Point sources, manured areas and septic systems are also integrated into nutrient loading calculations as the latter two sources may provide a significant nutrient and fecal coliforms source in more rural areas. Urban nutrient inputs are assumed to be solid-phase and are modeled utilizing an exponential accumulation and washoff function. Sub-surface losses are calculated using dissolved nitrogen and phosphorus coefficients for shallow groundwater contributions to stream nutrient loads while the sub-surface sub-model considers a single, lumped parameter contributing area. Evapotranspiration is determined using daily weather data and a cover factor dependent upon LU/LC. Finally, a water balance is performed utilizing supplied or computed precipitation, snowmelt, initial unsaturated zone storage, maximum available zone storage and evapotranspiration values (Evans, 2008).

With the development of AVGWLF came some significant enhancements to the GWLF model that is particularly pertinent to the development of a restoration plan for the Whippany River. Specifically, a significant revision to the original GWLF model is the inclusion of a pathogen loading routine which allows for the estimation of fecal coliform loading from point sources (waste water treatment facilities) and non-point sources including urban areas, septic systems, farm animals and wildlife. With respect to farm animals, fecal coliform loads are estimated based on the number of animals, their average weight and fecal coliform loading rates. Farm animals are subsequently broken down into "grazing" and "non-grazing" types. Each grazing section subsequently contains fields which may be manipulated to determine the percentage of time the animals spend grazing, in streams or in confined areas. Furthermore, fields may be manipulated to specify base nitrogen, phosphorus and fecal coliform loss rates to surface waters. In the case of wildlife loadings, estimates are assumed to be equivalent to those loads generated by a population density of 25 deer per acre of "natural area" within the watershed, with all forested land use considered as "natural areas" for modeling purposes. The value of 25 is a default value and can be altered by the modeler based on site specific conditions. It is assumed that 90% of fecal coliform loadings in natural areas die prior to reaching surface waters, although the die off rate can be manipulated in the AVGWLF input files.

Fecal coliform load estimation for urban areas are made based on the concept of "event mean concentrations" (EMC) which is essentially a concentration of a given pollutant expected to be present in runoff during a precipitation event. For fecal coliform, AVGWLF utilizes a default concentration of 9.60×10^3 coliform-forming units / 100ml (USEPA 2001). This concentration is subsequently multiplied by water volume over urban land use areas to compute a fecal coliform load and then adjusted for a 90% die off rate prior to the bacteria reaching surface waters. Again, both the EMC and die off rate may be altered by the modeler.

Septic fecal coliform loads are calculated using information on septic systems and typical per capita production rates as based on census data. This information is utilized in concert with a default fecal coliform production rate of 2.0×10^9 organisms per person per day to calculate total fecal coliform organisms per month. This preliminary load is reduced using an estimate of septic system failure rate under the assumption that only failing septic systems contribute fecal coliforms to surface waters. Failing systems are derived from the "other" category in the census data although failure rates can be manipulated by the modeler to more accurately reflect local conditions.

Fecal coliform loadings from wastewater treatment plants are derived by multiplying water discharge by a standard effluent concentration of 200 cfu/100 m. The effluent concentration may be altered by the modeler if site specific data is available.

Finally, it is assumed that 50% of all fecal coliforms will die shortly after transport to surface waters although this default value can be changed by the modeler as necessary.

Output data from AVGWLF includes monthly and annual water budgets in addition to sediment, nitrogen, phosphorus and fecal coliform loads. Nutrient reduction through present and future Best Management Practices (BMPs) can also be evaluated. The modeled pollutant loads can be adjusted for any established BMPs through the utilization of a "scenario editor" which creates a scenario file. This file can subsequently be imported into the Pollution Reduction Impact Comparison Tool (PRedICT) to evaluate the effect of urban and rural BMP implementation on further reducing the pollutant load.

As previously mentioned, AVGWLF was developed by Pennsylvania State University for ArcView GIS software (versions 3.2 and 3.3) and is utilized to create the necessary input data for the execution of the GWLF-E model. Within AVGWLF, ArcView compatible shape files and grids are manipulated for the derivation of numerous model input parameters. In order for the input parameters to be estimated properly, it is imperative that each of the required grid and shape files are created and formatted correctly. As such, Dr. Evans has written an AVGWLF Format Guide (Evans 2008) which provides the formatting requirements for each dataset. In order to run the AVGWLF model for the Whippany River it was necessary for Princeton Hydro to manipulate New Jersey and Federal GIS data so it was properly formatted for model execution. The following sections detail the data utilized to run the model.

2.2 Data Development Methodology

AVGWLF is a customized interface developed by Penn State University for ArcView GIS software (v. 3.x) that is used to create the necessary input data for executing the GWLF-E model. In order to execute the model the modeler is prompted to input various "non-spatial" parameters (e.g. climate data, length of growing season and manure spreading period) and spatial parameters which are used to automatically derive values for required model input parameters which are subsequently written to various input files utilized in model execution. In order to run AVGWLF there are required spatial files and "optional" files. The exclusion of optional spatial data files will prompt AVGWLF to utilize default values for the parameters associated with these files. In order to run AVGWLF in areas outside of Pennsylvania (where the model was developed) it is necessary to format spatial data according to the guidelines set forth in "A Guide To Creating Software-Compatible Data Sets" (Evans and Corradini 2008). This document provides specific guidelines to formatting all spatial data correctly for the proper execution of the GWLF-E model.

Data file creation for the Whippany River modeling project was conducted according to the instructions set forth in "A Guide To Creating Software Compatible Data Sets" (Evans and Corradini 2008). All manipulated and created data is compatible with ArcView 3.x software and all projections were set to meters. Princeton Hydro formatted the following data layers to execute the GWLF-E model:

Required Layers

Shape Files
- Basins (polygons)
- Streams (lines)
- Weather Stations (points)
- Soils (polygons)

Grid Files

- Land Use/Cover
- Surface Elevation – Digital Elevation Maps (DEM)

Weather Files

- Daily weather / precipitation data (Microsoft Excel® .csv files)

Optional Layers

Shape Files

- Point Sources (points)
- Septic Systems (polygons)

As previously mentioned, model input parameters associated with optional data layers are automatically assigned a default value by AVGWLF. Princeton Hydro changed default model parameters whenever site specific data was available. The following section details the data layers utilized to execute AVGWLF.

Basins

The basins file represents the watershed boundary of the Whippany River. Princeton Hydro utilized the NJDEP approved watershed boundary which was characterized by ten HUC 14s. Specifically, the basins layer for the Whippany River Restoration and Protection Plan consists of the following HUC14's:

- 02030103020010
- 02030103020020
- 02030103020030
- 02030103020040
- 02030103020050
- 02030103020060
- 02030103020070
- 02030103020080
- 02030103020090
- 02030103020100

Streams

The stream layer utilized in AVGWLF modeling was the United States Geological Survey – National Hydrography Dataset High Resolution stream layer (1:24,000 resolution). This layer was chosen as it is the recommended resolution per format guidelines and therefore is of sufficient scale for the accurate estimation of stream bank erosion and slope length factor. Furthermore, Princeton Hydro confirmed the selection of this layer with Dr. Barry Evans (via personal communication 4/20/09).

Weather Stations

This file is utilized in AVGWLF to identify the locations of weather stations which are associated with daily weather information utilized to create the “weather.dat” input file for GWLF-E. A minimum of two (2) weather stations are needed to run AVGWLF while a minimum of two (2) years of weather data is recommended for an accurate analysis. Princeton Hydro chose to model watershed conditions under a weather period of seven (7) years (2000-2007) utilizing daily climate data from two (2) weather stations. The weather stations chosen for this analysis were:

- Canoe Brook (ID: 281335)
- Cranford (ID: 282023)

These stations were chosen as they contained the most complete dataset over the modeling period (2000 – 2007) while being in closest spatial proximity to the Whippany River watershed.

Soils

The soils layer is utilized to hold information pertaining to various soils-related properties. Specifically, this layer contains four fields which represent the following soil characteristics:

- Water Holding Capacity
- Soil Erodibility (“K” factor)
- Dominant Soil Hydrologic Group
- Soil Organic Matter Content (Not actually utilized in current version of AVGWLF)

Princeton Hydro utilized the United States Department of Agriculture (USDA) Soil Survey Geographic (SSURGO) Database for all soils information.

Land Use / Land Cover (LU/LC)

The LU/LC layer is one of the most critical layers utilized within AVGWLF since it largely dictates pollutant loads derived by land surface conditions. Princeton Hydro utilized the 2005 C-CAP Land Cover data obtained from NOAA Coastal Services Center. This source was chosen since the LU/LC data was collected during the model period. Furthermore, this data set focused on land cover (i.e. vegetative type and cover) more so than land use, which allows for a more accurate modeling of hydrology and nutrient transport. Land cover ID fields were re-categorized by Princeton Hydro to reflect necessary naming structure based on the AVGWLF format guide.

Surface Elevation

The surface elevation data layer is utilized to calculate land slope-related data within AVGWLF, such as the slope length factor which is utilized in the USLE to predict watershed erosion. Princeton Hydro utilized the USGS 100m DEM for modeling purposes. While more refined elevation data was available (USGS 30m DEM and County 4m LIDAR data) such data would have caused large errors due to insufficient allowances for internal memory (Evans and Corradini 2008). Furthermore, highly refined elevation data is only recommended with highly refined stream layers (i.e. LIDAR stream layers). Pairing the 1:24,000k stream layer with 100m DEM layers allows for the accurate prediction of hydrologic and pollutant loading processes (Dr. Barry Evans via personal communication 4/20/09). Prior to the utilization of the 100 m DEM Princeton Hydro filled any sinks in order to negate computational errors.

Point Sources

The point source file is utilized to define the locations of point source discharges throughout the watershed. This point file is associated with a database which contains fields for a unique identifier, total nitrogen load per year (kg/yr), total phosphorus load per year (kg/yr) and a field which signifies if monthly flow and concentration data is available. The point source file may be edited within AVGWLF in order to adjust monthly discharge and total nitrogen and phosphorus loads.

Princeton Hydro developed the point source data file through data obtained by the NJPDES Surface Water Discharges GIS layer. This layer was utilized in concert with the watershed boundary to determine the location of point source discharges within the watershed. Following this determination, Princeton Hydro downloaded monthly discharge and nutrient load information from the NJDEP Record Access Program (OPRA) and created databases which linked the load information to the point source GIS layer. In total, thirteen (13) point source dischargers were identified within the watershed. Of these dischargers, five (5) were waste water treatment facilities and considered as significant contributors to the hydrologic or pollutant load of the Whippany River. Of the five (5) dischargers, four of the five were included in the original Whippany River TMDL (1999). The five point source dischargers that were included for modeling are listed in Table 2.1

Table 2.1: Whippany River – Point Source Dischargers

Name	NJPDES Number	Included in TMDL?
Greystone Park	NJ0026689	Yes
Hanover Sewer	NJ0024902	Yes
Butterworth	NJ0024911	Yes
Morristown Sewer	NJ0025496	Yes
Green at Florham Park	NJ0003476	No

Septic System Layer

The septic system layer is utilized to provide information pertaining to the number of people using on-lot waste disposal systems within a given area. This information is commonly obtained from United States Census data or may be obtained from local sources if such information is available. The septic system layer is comprised of four (4) fields in AVGWLF:

- TRACT - Unique identifier for polygon
- SEW_SEPT - # of people on septic systems
- SEW_PUB - # of people on public sewers
- SEW_OTHR - # of people on “direct discharges”

As previously mentioned, the aforementioned fields are commonly derived from census data. For the purpose of this study the latest census which included data pertaining to wastewater treatment was from the 1990 US census. This dataset was also utilized as the source of census data for the AVGWLF Pennsylvania dataset and utilized by the New England Interstate Water Pollution Control Commission (NEIWPCC) in the development of the AVGWLF New England datasets. The 1990 census lists wastewater treatment type by “Housing Unit.” A “housing unit” is defined by the United States Census Bureau as follows:

> “*Housing Units--A housing unit is a house, an apartment, a mobile home or trailer, a group of rooms or a single room occupied as separate living quarters or, if vacant, intended for occupancy as separate living quarters. Separate living quarters are those in which the occupants live and eat separately from any other persons in the building and which have direct access from outside the building or through a common hall.*

The occupants may be a single family, one person living alone, two or more families living together, or any other group of related or unrelated persons who share living arrangements. For vacant units, the criteria of separateness and direct access are applied to the intended occupants whenever possible. If that information cannot be obtained, the criteria are applied to the previous occupants.

Both occupied and vacant housing units are included in the housing unit inventory, except that recreational vehicles, boats, vans, tents, railroad cars, and the like are included only if they are occupied as someone's usual place of residence. Vacant mobile homes are included provided they are intended for occupancy on the site where they stand. Vacant mobile homes on dealers' sales lots, at the factory, or in storage yards are excluded from the housing inventory."

Princeton Hydro first downloaded 1990 census data for Morris County, NJ from http://nhgis.org which served as the basis for the number of housing units using the three aforementioned wastewater treatment devices (sewer, septic, and other). While data from the 2000 census was available, this census did not include wastewater treatment data. Next, the number of housing units, county wide, was summed and compared to the sum of the number of housing units in Morris County, NJ from the 2000 census. In comparing this data the percent increase in county wide housing units (11.96%) was calculated. The number of housing units for each wastewater treatment device under the 1990 census was then proportionally increased by 11.96% to more accurately reflect population during the modeling period. Following this increase it was necessary to calculate the number of people in each housing unit to arrive at a total population served by each wastewater treatment category per census tract. To calculate the population Princeton Hydro calculated the mean household size for Morris County, NJ (2.73) and then multiplied this by each housing unit to arrive at a total population for each wastewater treatment device per census tract. The calculated population was then summed over the entire county and compared to the population estimate provided by the 2000 census. This comparison yielded a 1.24 Percent Error between the calculated population and that reported through the 2000 census. The updated wastewater population data was then joined with the 1990 census tract boundary shapefile and utilized in modeling. The following assumptions were made in this methodology:

- The percent increase in housing units is homogenous county wide, and
- Wastewater treatment proportions remained the same from 1990 through 2000

The aforementioned assumptions seem more than reasonable given the lack of updated septic survey data. The inclusion of 2000 census population estimates provided an additional degree of refinement to the 1990 census wastewater data.

2.3 Input Data

The GIS data layers detailed above were subsequently manipulated within AVGWLF to compute model input parameters which were utilized to execute the GWLF-E model. Specifically, four input files are created for execution of the GWLF-E model:

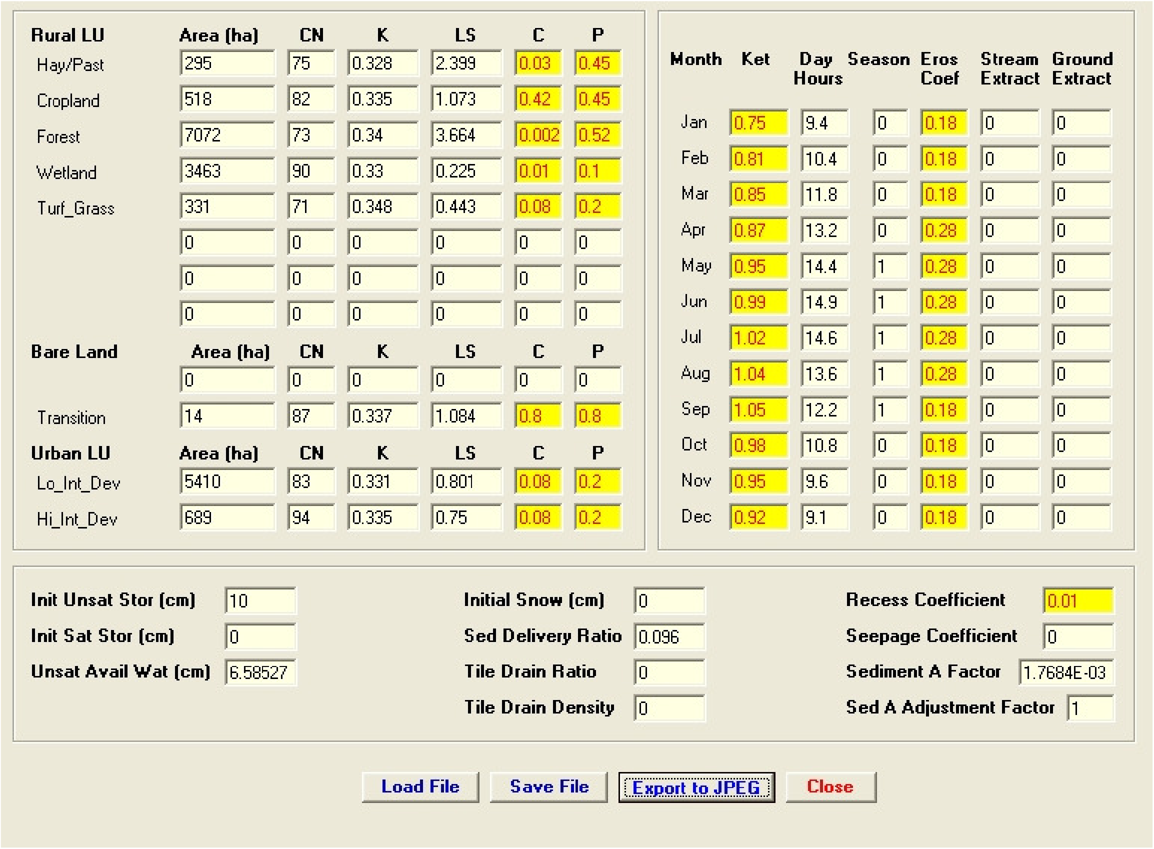
- Weather.dat
- Nutrient.dat
- Transport.dat
- Animal.dat

This section details the model input parameters which were utilized to model the fecal coliform, phosphorus, nitrogen and sediment loads to the Whippany River. Any changes to default parameters made by Princeton Hydro are specified herein. For brevity, this section will include the model input files for the watershed as an aggregate even though each HUC14 was modeled separately. Changes to default parameters were consistent for each sub-watershed with the exception of goose population data, which was area weighted.

Transport.dat File

The following Figure (2.1) provides the transport input file utilized to execute the GWLF-E model.

Figure 2.1: Whippany River AVGWLF – Transport Input File



Rural LU	Area (ha)	CN	K	LS	C	P
Hay/Past	295	75	0.328	2.399	0.03	0.45
Cropland	518	82	0.335	1.073	0.42	0.45
Forest	7072	73	0.34	3.664	0.002	0.52
Wetland	3463	90	0.33	0.225	0.01	0.1
Turf_Grass	331	71	0.348	0.443	0.08	0.2
	0	0	0	0	0	0
	0	0	0	0	0	0
	0	0	0	0	0	0
Bare Land	**Area (ha)**	**CN**	**K**	**LS**	**C**	**P**
	0	0	0	0	0	0
Transition	14	87	0.337	1.084	0.8	0.8
Urban LU	**Area (ha)**	**CN**	**K**	**LS**	**C**	**P**
Lo_Int_Dev	5410	83	0.331	0.801	0.08	0.2
Hi_Int_Dev	689	94	0.335	0.75	0.08	0.2

Month	Ket	Day Hours	Season	Eros Coef	Stream Extract	Ground Extract
Jan	0.75	9.4	0	0.18	0	0
Feb	0.81	10.4	0	0.18	0	0
Mar	0.85	11.8	0	0.18	0	0
Apr	0.87	13.2	0	0.28	0	0
May	0.95	14.4	1	0.28	0	0
Jun	0.99	14.9	1	0.28	0	0
Jul	1.02	14.6	1	0.28	0	0
Aug	1.04	13.6	1	0.28	0	0
Sep	1.05	12.2	1	0.18	0	0
Oct	0.98	10.8	0	0.18	0	0
Nov	0.95	9.6	0	0.18	0	0
Dec	0.92	9.1	0	0.18	0	0

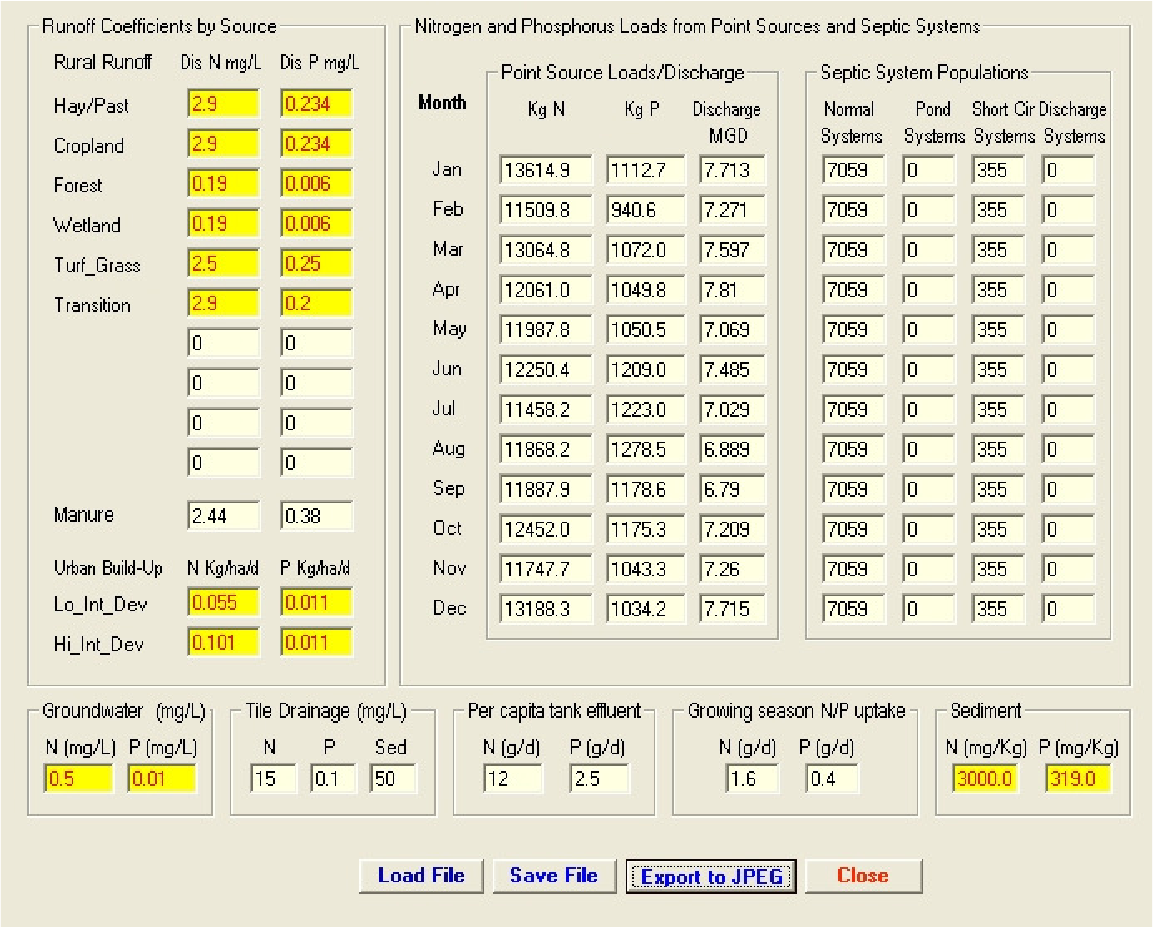
Init Unsat Stor (cm) 10
Init Sat Stor (cm) 0
Unsat Avail Wat (cm) 6.58527
Initial Snow (cm) 0
Sed Delivery Ratio 0.096
Tile Drain Ratio 0
Tile Drain Density 0
Recess Coefficient 0.01
Seepage Coefficient 0
Sediment A Factor 1.7684E-03
Sed A Adjustment Factor 1

Princeton Hydro changed the "recession coefficient" from a default value of 0.10 to 0.01 to more accurately reflect groundwater recession rates. A recession coefficient of 0.01 was iteratively chosen during hydrology calibration. The "Tile Drain Ratio" was also changed from a default value of 0.5 to 0.0 as there is no tile drainage within the Whippany River watershed.

Nutrient.dat File

The following Figure (2.2) provides the nutrient input file utilized to execute the GWLF-E model.

Figure 2.2: Whippany River AVGWLF – Nutrient Input File



Runoff Coefficients by Source

Rural Runoff	Dis N mg/L	Dis P mg/L
Hay/Past	2.9	0.234
Cropland	2.9	0.234
Forest	0.19	0.006
Wetland	0.19	0.006
Turf_Grass	2.5	0.25
Transition	2.9	0.2
	0	0
	0	0
	0	0
	0	0
Manure	2.44	0.38
Urban Build-Up	N Kg/ha/d	P Kg/ha/d
Lo_Int_Dev	0.055	0.011
Hi_Int_Dev	0.101	0.011

Nitrogen and Phosphorus Loads from Point Sources and Septic Systems

Month	Point Source Loads/Discharge			Septic System Populations			
	Kg N	Kg P	Discharge MGD	Normal Systems	Pond Systems	Short Cir Systems	Discharge Systems
Jan	13614.9	1112.7	7.713	7059	0	355	0
Feb	11509.8	940.6	7.271	7059	0	355	0
Mar	13064.8	1072.0	7.597	7059	0	355	0
Apr	12061.0	1049.8	7.81	7059	0	355	0
May	11987.8	1050.5	7.069	7059	0	355	0
Jun	12250.4	1209.0	7.485	7059	0	355	0
Jul	11458.2	1223.0	7.029	7059	0	355	0
Aug	11868.2	1278.5	6.889	7059	0	355	0
Sep	11887.9	1178.6	6.79	7059	0	355	0
Oct	12452.0	1175.3	7.209	7059	0	355	0
Nov	11747.7	1043.3	7.26	7059	0	355	0
Dec	13188.3	1034.2	7.715	7059	0	355	0

Groundwater (mg/L): N (mg/L) 0.5; P (mg/L) 0.01
Tile Drainage (mg/L): N 15; P 0.1; Sed 50
Per capita tank effluent: N (g/d) 12; P (g/d) 2.5
Growing season N/P uptake: N (g/d) 1.6; P (g/d) 0.4
Sediment: N (mg/Kg) 3000.0; P (mg/Kg) 319.0

Princeton Hydro changed numerous model input parameters within the nutrient input file to more accurately reflect watershed conditions for the Whippany River. Specifically, dissolved phosphorus concentrations for Hay/Past, Cropland and Turfgrass were changed from default concentrations of 0.0079, 0.0079 & 0.0 mg/L to 0.234, 0.234 and 0.25 mg/L respectively. The changes made to Hay/Past and Cropland were reflective of those revisions made by the NEIWPCC to the New England dataset. The Turf Grass concentration was based on Princeton Hydro's in-house database of total dissolved phosphorus concentrations derived from turf grass areas at Lake Hopatcong (Princeton Hydro 2009). Low Intensity Development nitrogen and phosphorus loading coefficients were also changed from default values of 0.012 and 0.002 kg/ha/d to 0.055 and 0.011

kg/ha/d; respectively. These changes were consistent with those made by the NEIWPCC to the New England dataset and more accurately reflect nutrient loading from suburban land use categories.

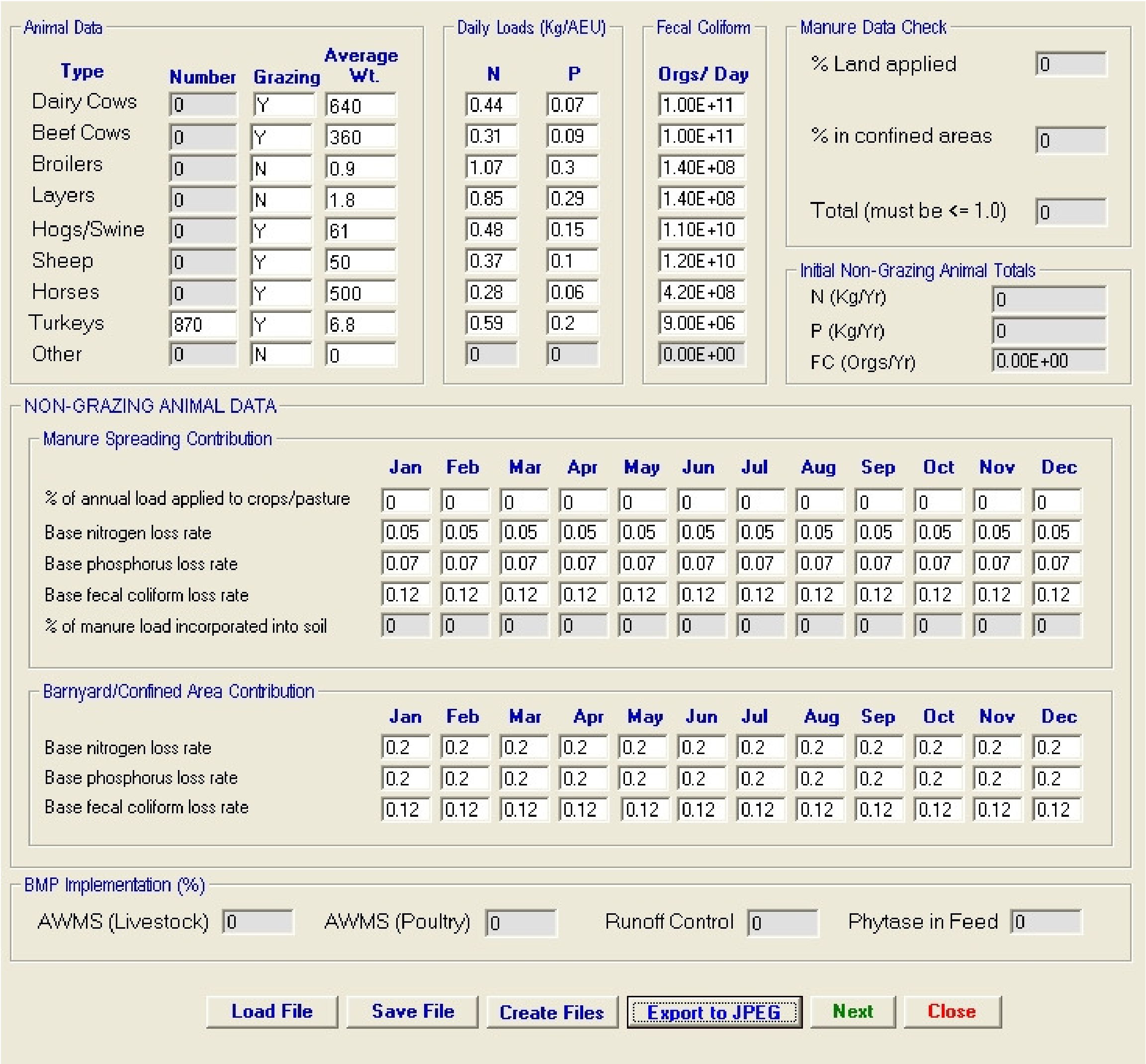
Point Source loads in the nutrient input file were derived from empirical discharge and nutrient concentration data as part of NJDPES monitoring requirements. Septic system population data was changed to reflect a malfunction rate of 5%. This malfunction rate was chosen by Princeton Hydro based on our experience with septic revisions throughout the State of New Jersey. As previously mentioned, septic failure is highly site specific and while it is impossible to know the true failure rate without an extensive field survey we feel that a 5% malfunction rate is a conservative estimate based on the scientific literature. The 5% malfunction rate was assigned to the “Short Circuiting Systems” category. This category represents malfunctioning systems that discharge waste to underlying water tables or groundwater without sufficient renovation.

The groundwater nitrogen concentration was changed from a default concentration of 1.0 mg/L to 0.50 mg/L. The input value of 0.50 mg/L was based on Princeton Hydro’s in house database of baseflow total nitrogen concentrations from several tributaries which drain to the Whippany River. Finally, the sediment phosphorus concentration was changed from a default value of 750 mg/Kg to 319 mg/Kg. 319 mg/Kg (n = 17) is the mean soil phosphorus concentration for New Jersey from the National Cooperative Soil Survey.

Animal.dat File

The following figures (2.3 – 2.4) provide the animal input file utilized to execute the GWLF-E model.

Figure 2.3: Whippany River AVGWLF – Animal Input File (1 of 2)



Animal Data				Daily Loads (Kg/AEU)		Fecal Coliform
Type	Number	Grazing	Average Wt.	N	P	Orgs/ Day
Dairy Cows	0	Y	640	0.44	0.07	1.00E+11
Beef Cows	0	Y	360	0.31	0.09	1.00E+11
Broilers	0	N	0.9	1.07	0.3	1.40E+08
Layers	0	N	1.8	0.85	0.29	1.40E+08
Hogs/Swine	0	Y	61	0.48	0.15	1.10E+10
Sheep	0	Y	50	0.37	0.1	1.20E+10
Horses	0	Y	500	0.28	0.06	4.20E+08
Turkeys	870	Y	6.8	0.59	0.2	9.00E+06
Other	0	N	0	0	0	0.00E+00

Manure Data Check

% Land applied 0
% in confined areas 0
Total (must be <= 1.0) 0

Initial Non-Grazing Animal Totals

N (Kg/Yr) 0
P (Kg/Yr) 0
FC (Orgs/Yr) 0.00E+00

NON-GRAZING ANIMAL DATA

Manure Spreading Contribution

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
% of annual load applied to crops/pasture	0	0	0	0	0	0	0	0	0	0	0	0
Base nitrogen loss rate	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
Base phosphorus loss rate	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
Base fecal coliform loss rate	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12
% of manure load incorporated into soil	0	0	0	0	0	0	0	0	0	0	0	0

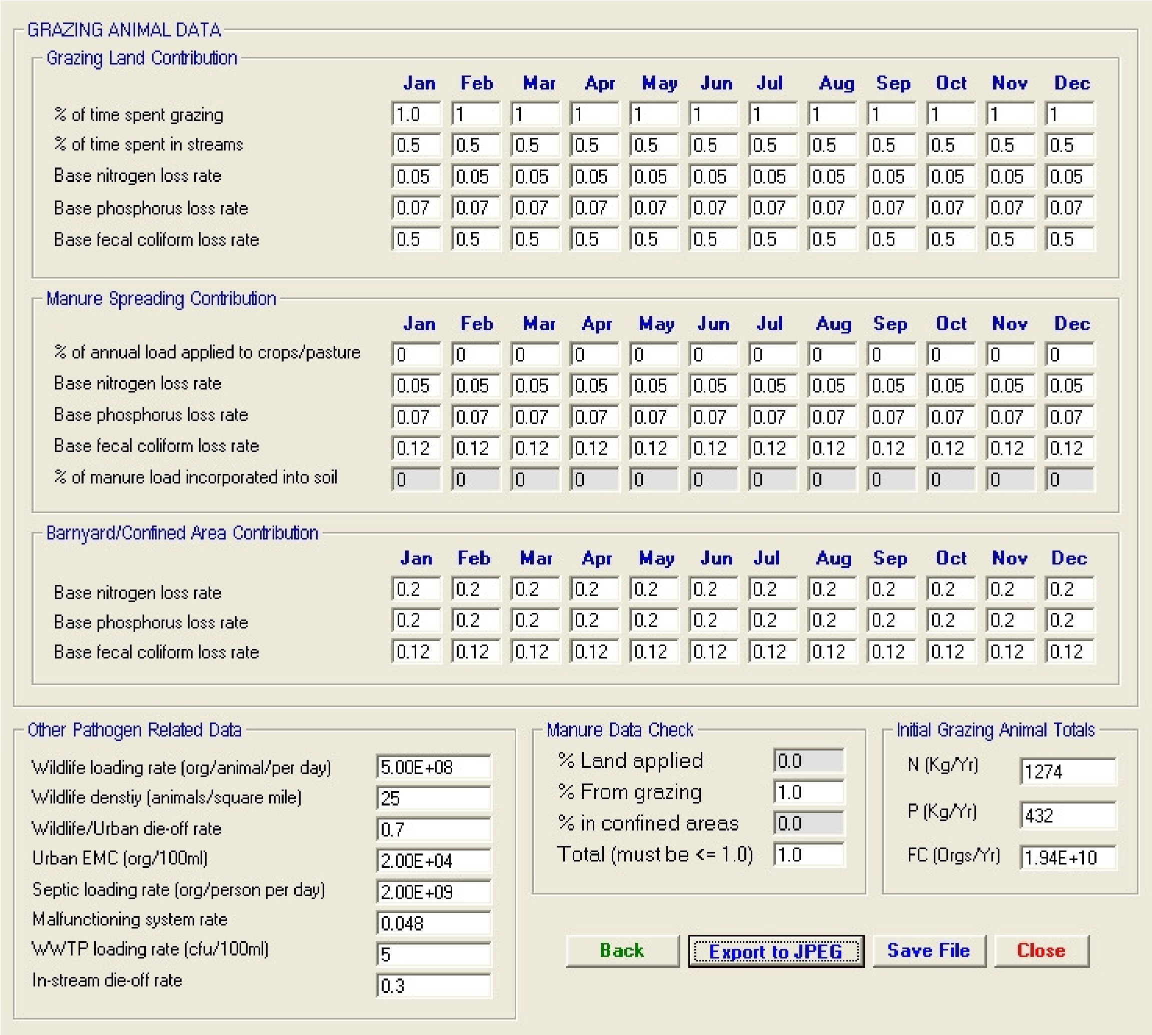
Barnyard/Confined Area Contribution

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Base nitrogen loss rate	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
Base phosphorus loss rate	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
Base fecal coliform loss rate	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12

BMP Implementation (%)

AWMS (Livestock) 0
AWMS (Poultry) 0
Runoff Control 0
Phytase in Feed 0

Figure 2.4: Whippany River AVGWLF – Animal Input File (2 of 2)



GRAZING ANIMAL DATA

Grazing Land Contribution

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
% of time spent grazing	1.0	1	1	1	1	1	1	1	1	1	1	1
% of time spent in streams	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Base nitrogen loss rate	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
Base phosphorus loss rate	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
Base fecal coliform loss rate	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5

Manure Spreading Contribution

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
% of annual load applied to crops/pasture	0	0	0	0	0	0	0	0	0	0	0	0
Base nitrogen loss rate	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
Base phosphorus loss rate	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
Base fecal coliform loss rate	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12
% of manure load incorporated into soil	0	0	0	0	0	0	0	0	0	0	0	0

Barnyard/Confined Area Contribution

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Base nitrogen loss rate	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
Base phosphorus loss rate	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
Base fecal coliform loss rate	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12

Other Pathogen Related Data

Wildlife loading rate (org/animal/per day)	5.00E+08
Wildlife denstiy (animals/square mile)	25
Wildlife/Urban die-off rate	0.7
Urban EMC (org/100ml)	2.00E+04
Septic loading rate (org/person per day)	2.00E+09
Malfunctioning system rate	0.048
WWTP loading rate (cfu/100ml)	5
In-stream die-off rate	0.3

Manure Data Check

% Land applied	0.0
% From grazing	1.0
% in confined areas	0.0
Total (must be <= 1.0)	1.0

Initial Grazing Animal Totals

N (Kg/Yr)	1274
P (Kg/Yr)	432
FC (Orgs/Yr)	1.94E+10

Princeton Hydro modeled the nutrient and fecal coliform load of Canada geese through the manipulation of the Animal.dat input file. Specifically, Princeton Hydro entered the Canada goose data (population, weight, nitrogen, phosphorus and fecal coliform loading rates) into the "Turkey" field of the animal data file. While this field is labeled "Turkey," this is simply a default naming scheme. As such, the alteration of animal input parameters allow for the simulation of nutrient and fecal coliform loading from any animal. Therefore, the naming scheme used in the tables within this section of the report has no bearing on nutrient or fecal coliform loading rates or transport to surface waters.

Estimated Canada goose population data for the state of New Jersey was obtained from the Atlantic Flyway Breeding Survey through the USGS Migratory Bird Data Center.

The Atlantic Flyway Breeding Waterfowl Survey was designed primarily to estimate breeding population size of mallards, black ducks, wood ducks and Canada geese. The survey uses criteria derived in the mid-continent to determine the number of indicated pairs and total indicated birds from count data. Estimates of bird counts are not corrected for time-of-day and feeding-site effects, two variables which may be significant in migratory waterfowl populations. As such, while these statistics are useful in evaluating population trends or changes in populations there is a degree of error in utilizing this data for absolute measures of abundance. Given this degree of error, Princeton Hydro integrated the standard error associated with the bird count estimates and also reviewed this data in conjunction with bird count data provided by The Whippany River Watershed Action Committee. Following the input of Canada goose population data Princeton Hydro adjusted the fecal coliform loading rate to 9.00 x 10^6 organisms/day as consistent with the loading rate reported by Hussong *et al.* (1978). Nitrogen and phosphorus loading rates were maintained at default values. In addition, the weight was maintained at the default 6.8 lbs.

Following the input of population and loading rates for Canada geese it was necessary to properly simulate fecal deposition and transport to the Whippany River. The Animal.dat input file for AVGWLF was originally formatted for the simulation of farm animal loadings. As such, these loadings are divided into “grazing animal loads” and “non-grazing animal loads.” For both grazing and non-grazing animals, the calculation of loads delivered to surface water is primarily dependent upon how the initial loads generated by the animals are distributed among the various “source” areas (or pathways) such as confined areas, manure-spreading areas and grazing (pasture) areas (Evans, 2008). For the purpose of simulating nutrient and fecal coliform loadings associated with Canada goose waste deposition Princeton Hydro assigned a category of “grazing.” Algorithmically, waste associated with Canada geese is produced on a monthly basis and deposited onto pasture land. In addition, grazing animals can contribute waste via “direct deposit” to streams where unimpeded access is available.

Waste losses as a result of animal grazing include runoff from grazing land (crop and pasture) as well as “direct deposits” to streams where unimpeded access is available. The “% of annual loads applied to crops and pasture” under the non-grazing animal section were all set to zero since the Canada geese were modeled as grazing animals. In section 2 (Figure 2.4) Princeton Hydro set the “% of time spent grazing” monthly fields to 1, meaning that all waste deposition was derived from grazing activity. Furthermore, “% of time spent in streams” was set to 0.5 (50%). It should be noted that percent of time spent grazing and percent of time spent in streams are not additive functions. The loss rate associated with fecal coliform was changed to 0.5, meaning 50% of land deposited fecal coliform is available for transport to surface waters. Loss rates for nitrogen and phosphorus were unchanged.

Since all waste deposition was associated with grazing, the “% of annual load applied to crops/pasture” was set to zero for each month. The “Manure Data Check” box, confirmed that all waste deposition was derived from grazing activities as indicated by the "1" in the "% from grazing" field.

Following the specification of Canada goose related input parameters it was necessary to address pathogen related loading data to more accurately describe fecal coliform loading to the Whippany River. In the "Other Pathogen Related Data" section Princeton Hydro adjusted the Wildlife/Urban and Stream die-off rates from default values of 0.9 and 0.5 to 0.7 and 0.3 respectively. The default "Urban EMC" was changed from a default concentration of 9.60×10^3 to 2.00×10^4, as indicated in Schueler (2000). Finally, the WWTP loading rate was changed from a default concentration of 200 cfu / 100 ml to 5 cfu / 100 ml as based on the mean effluent discharge concentration from all five point sources within the Whippany River watershed.

2.4 Model Calibration and Verification

Model calibration for the Whippany River study relied on iteratively adjusting model input parameters until a best fit was obtained between modeled and observed data. For the purposes of calibration Princeton Hydro focused primarily on hydrology as this variable is the primary determinant in accurately assessing pollutant loading to the River. Furthermore, a substantial amount of data was available for the modeling period (2000-2007) through the USGS gaging station (USGS 01381500 - Whippany River at Morristown, NJ) which facilitated calibration. Accurately calibrating phosphorus, nitrogen and sediment loading would require consistent water quality monitoring of these parameters, over a wide range of flow regimes. Furthermore, the sampling stations associated with nutrient grab samples would need to be located at, or in very close proximity to, discharge stations. Since this data was not available Princeton Hydro was not able to statistically calibrate phosphorus, nitrogen or sediment loads. Nevertheless, careful selection of model input parameters which govern the fate and transport of these pollutants should allow for a certain degree of accuracy in predicting phosphorus, nitrogen and sediment loading to the River. Fecal coliform load calibration was conducted by matching modeled fecal coliform loads, on an aggregate watershed basis, to the monitoring data collected by Princeton Hydro at site 8 during the 2009 sample year. Site 8 was the most downstream sample site of the project area and correlated with the modeled watershed endpoint.

In order to calibrate model hydrology, Princeton Hydro compared mean monthly discharge values, normalized for watershed area, obtained from the USGS gaging site to those modeled utilizing AVGWLF. In order to statistically evaluate correlation Princeton Hydro utilized two statistical measures, the Nash-Sutcliffe coefficient (eq. 1) and the Pearson product-moment correlation (eq. 2). The Nash-Sutcliffe coefficient is calculated according to equation 1:

$$NS = \frac{\sum (y - x)^2}{\sum (x - \bar{x})^2} \qquad \text{(Equation 1)}$$

where $\bar{x}$ is the mean of the observed (x) data, and y is the model-simulated value. The Nash-Sutcliffe coefficient is an indicator of the "goodness of fit" between observed and modeled data and is a metric recommended by the American Society of Civil Engineers (ASCE 1993) for use in hydrological studies. In regards to this coefficient, values may range from - ∞ to 1. A Nash-Sutcliffe coefficient of 1 is indicative of a perfect fit between observed and modeled data while values equal to and less than zero indicate that the model is predicting no better than using the mean of the historical observed data. For monthly comparisons of hydrology, a Nash-Sutcliffe coefficient of 0.74 was obtained.

The Pearson coefficient (*r*) is calculated according to equation 2:

$$r_{xy} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{(n-1)s_x s_y} \qquad \text{(Equation 2)}$$

where $\bar{x}$ and $\bar{y}$ are the sample means of *X* and *Y*, s_x and s_y are the sample standard deviations of *X* and *Y*.

The *r* value is a measure of the degree of linear association between two variables, in this case, the association between observed and modeled hydrology. The *r* can range from -1 to 1, with 1 indicating a perfect fit between observed and modeled data. For monthly comparisons of hydrology a *r* value of 0.93 was obtained. Furthermore, a coefficient of determination (r^2) value of 0.86 was calculated, indicating an excellent correlation between observed and predicted normalized monthly discharge.

Princeton Hydro obtained excellent correlation between observed and modeled hydrology through changing the "recession coefficient" to 0.01 and the "tile drain ratio" to zero. The results of calibrated hydrology are hereby presented graphically in Figures 2.5 – 2.6.

Figure 2.5: Whippany River AVGWLF – Hydrology Comparison

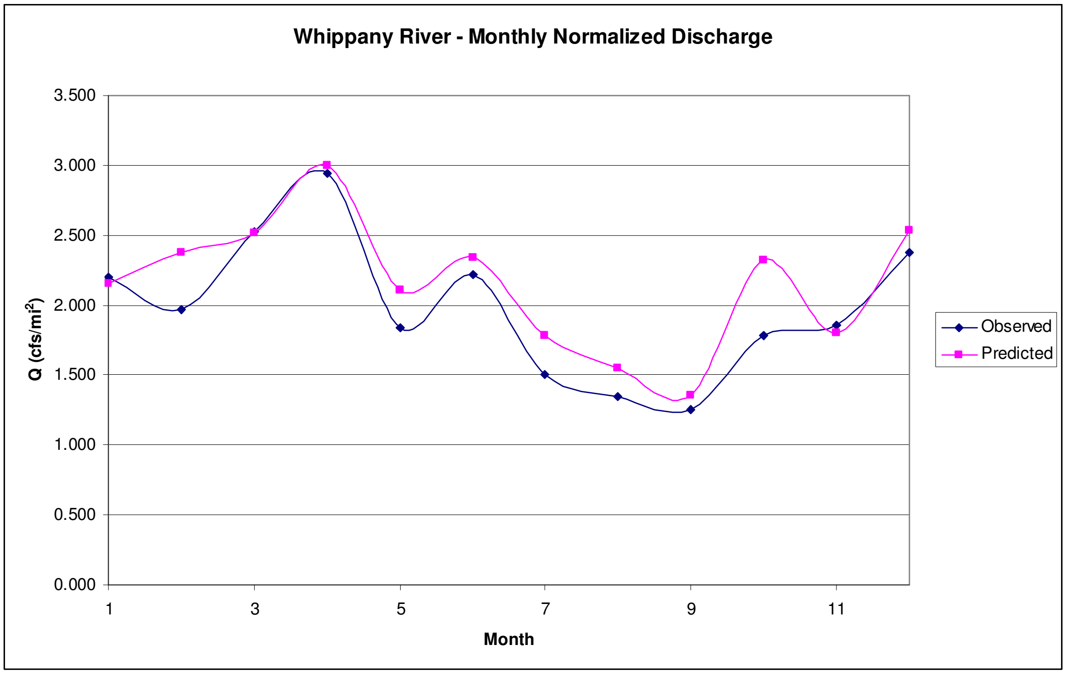
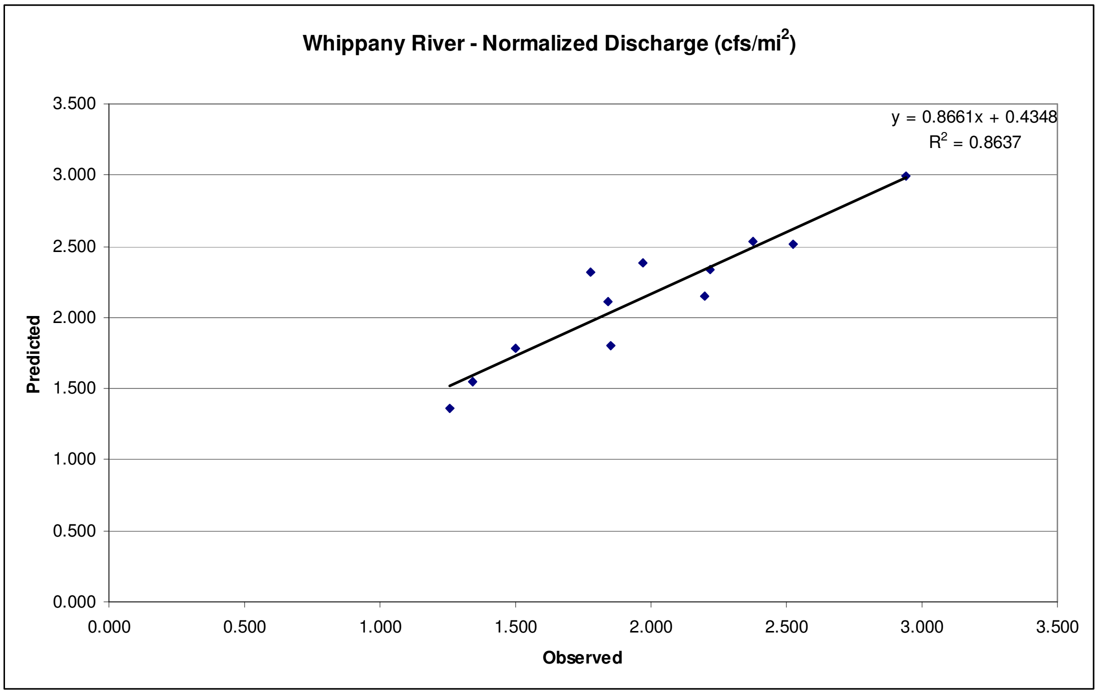


Figure 2.6: Whippany River AVGWLF – Linear Correlation



2.5 Model Results

Modeling efforts for the Whippany River were conducted utilizing two different spatial scales. Modeling was conducted on a HUC14, sub-watershed basis and as an aggregate watershed. Slight differences in hydrology and pollutant loads resulted between these two methods due to algorithms within AVGWLF pertaining to certain spatially based parameters and lumping of land cover categories.

Hydrology

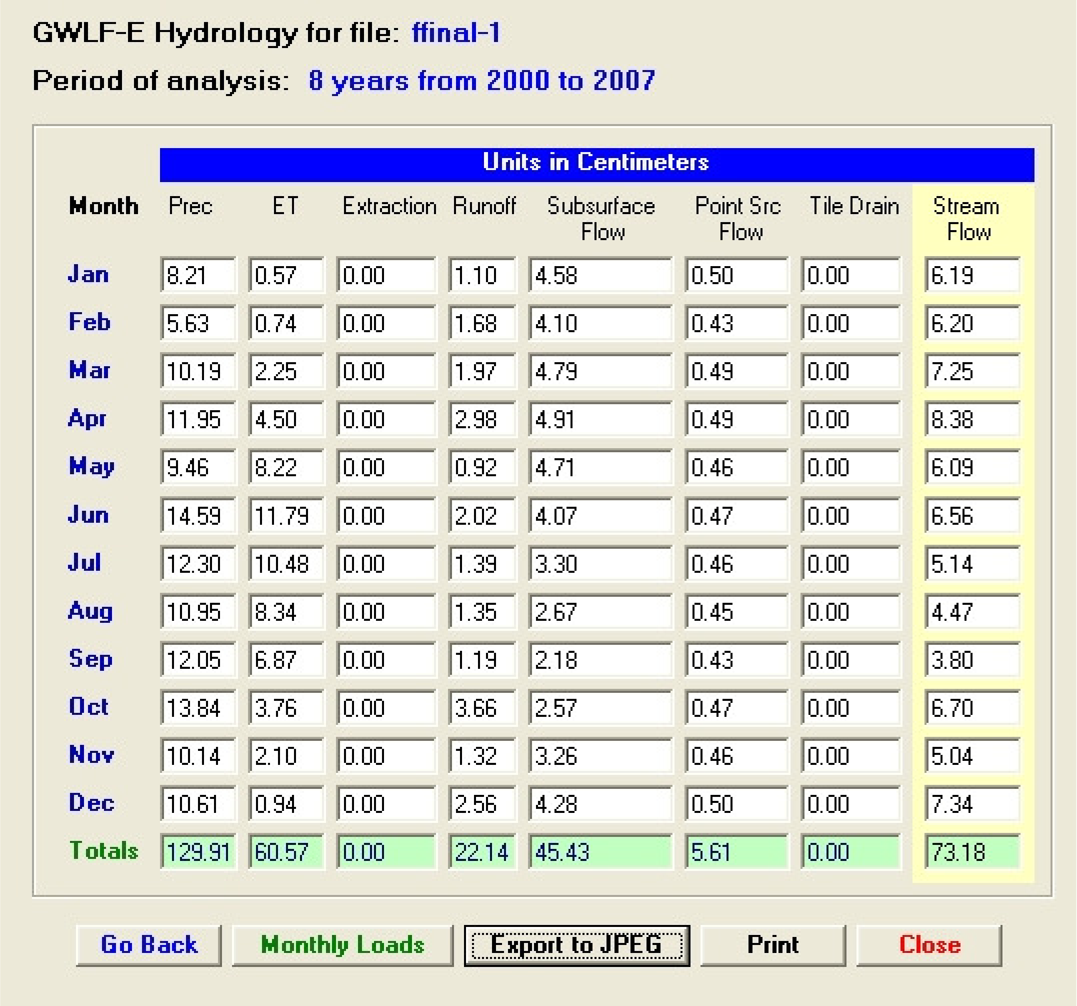
Monthly streamflow for the Whippany River, modeled as an aggregate watershed, is presented in Table 2.2.

Table 2.2: Whippany River Hydrology

Month	Volume	Discharge	Normalized Discharge
	(m^3)	(cfs)	(cfs/mi^2)
January	1.12 x 10^7	147.7	2.149
February	1.12 x 10^7	163.5	2.380
March	1.31 x 10^7	172.7	2.514
April	1.51 x 10^7	205.7	2.994
May	1.10 x 10^7	145.0	2.111
June	1.18 x 10^7	160.7	2.340
July	9.28 x 10^6	122.3	1.781
August	8.07 x 10^6	106.4	1.549
September	6.85 x 10^6	93.3	1.358
October	1.21 x 10^7	159.5	2.322
November	9.09 x 10^6	123.8	1.802
December	1.32 x 10^7	174.0	2.533

As mentioned above, calibration of modeled streamflow to observed streamflow at the Whippany River USGS gage allowed for excellent correlation between observed versus predicted values, as evaluated utilizing the Nash-Sutcliffe and Pearson Product Correlation Coefficient. While accurately modeling streamflow is important it is especially useful to break down the component parts of the hydrologic cycle. In this sense, we are able to separate sub-surface flow to stream systems from surface runoff. Since the large majority of NPS pollution is derived from surface runoff it is critical that this component is parsed out from the hydrograph from a management and restoration perspective. The following Figures (2.7 – 2.8) (depicts the different components of the hydrologic cycle of the Whippany River, when modeled as an aggregate watershed.

Figure 2.7: Whippany River Hydrology



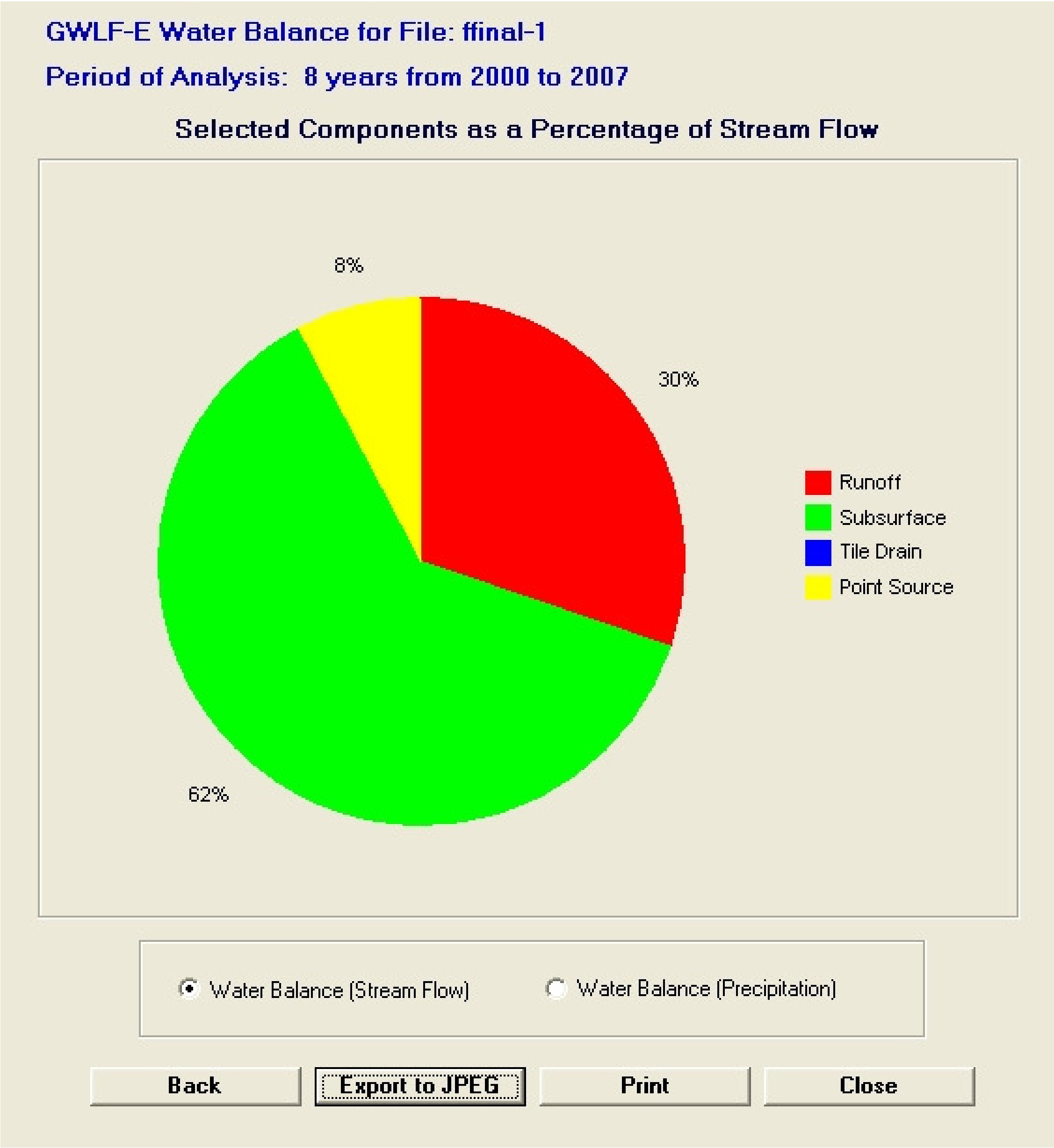
GWLF-E Hydrology for file: ffinal-1

Period of analysis: 8 years from 2000 to 2007

Units in Centimeters

Month	Prec	ET	Extraction	Runoff	Subsurface Flow	Point Src Flow	Tile Drain	Stream Flow
Jan	8.21	0.57	0.00	1.10	4.58	0.50	0.00	6.19
Feb	5.63	0.74	0.00	1.68	4.10	0.43	0.00	6.20
Mar	10.19	2.25	0.00	1.97	4.79	0.49	0.00	7.25
Apr	11.95	4.50	0.00	2.98	4.91	0.49	0.00	8.38
May	9.46	8.22	0.00	0.92	4.71	0.46	0.00	6.09
Jun	14.59	11.79	0.00	2.02	4.07	0.47	0.00	6.56
Jul	12.30	10.48	0.00	1.39	3.30	0.46	0.00	5.14
Aug	10.95	8.34	0.00	1.35	2.67	0.45	0.00	4.47
Sep	12.05	6.87	0.00	1.19	2.18	0.43	0.00	3.80
Oct	13.84	3.76	0.00	3.66	2.57	0.47	0.00	6.70
Nov	10.14	2.10	0.00	1.32	3.26	0.46	0.00	5.04
Dec	10.61	0.94	0.00	2.56	4.28	0.50	0.00	7.34
Totals	129.91	60.57	0.00	22.14	45.43	5.61	0.00	73.18

Figure 2.8: Whippany River Hydrology



GWLF-E Water Balance for File: ffinal-1

Period of Analysis: 8 years from 2000 to 2007

● Water Balance (Stream Flow)

○ Water Balance (Precipitation)

As evidenced above, the Whippany River watershed received an average of 129.9 cm (51.1 in) of precipitation over the modeled period. During this period, 62% of streamflow was derived from sub-surface sources while 30% was derived from surface runoff. 8% of streamflow was derived from point sources associated with wastewater treatment plant discharge.

The following sections provide a breakdown of the hydrologic cycle for each of the ten HUC14 sub-watersheds which comprised the project area. It should be noted, that while hydrology was calculated on an aggregate and sub-watershed basis for the project area, that the differences in total volume were minimal between the two spatial scales (% difference = 0.52%).

Table 2.3: Sub-watershed Streamflow (1 of 2)

Monthly Streamflow Volume (m^3)					
Month	HUC14*				
	010	020	030	040	050
Jan	9.80 x 10^5	9.95 x 10^5	1.27 x 10^6	1.10 x 10^6	1.45 x 10^6
Feb	9.06 x 10^5	9.24 x 10^5	1.20 x 10^6	1.05 x 10^6	1.38 x 10^6
Mar	1.05 x 10^6	1.08 x 10^6	1.39 x 10^6	1.22 x 10^6	1.59 x 10^6
Apr	1.22 x 10^6	1.25 x 10^6	1.60 x 10^6	1.40 x 10^6	1.78 x 10^6
May	1.01 x 10^6	1.04 x 10^6	1.27 x 10^6	1.08 x 10^6	1.36 x 10^6
Jun	9.63 x 10^5	9.89 x 10^5	1.27 x 10^6	1.12 x 10^6	1.47 x 10^6
Jul	7.93 x 10^5	8.07 x 10^5	1.03 x 10^6	9.20 x 10^5	1.24 x 10^6
Aug	6.96 x 10^5	6.95 x 10^5	9.10 x 10^5	8.27 x 10^5	1.14 x 10^6
Sep	5.82 x 10^5	5.66 x 10^5	7.74 x 10^5	7.14 x 10^5	1.04 x 10^6
Oct	8.88 x 10^5	8.75 x 10^5	1.25 x 10^6	1.14 x 10^6	1.60 x 10^6
Nov	8.10 x 10^5	8.04 x 10^5	1.06 x 10^6	9.28 x 10^5	1.28 x 10^6
Dec	1.07 x 10^6	1.08 x 10^6	1.43 x 10^6	1.26 x 10^6	1.68 x 10^6

* - Last three digits of HUC 14's are presented, All within 02030103020 HUC11 watershed.

Table 2.4: Sub-watershed Streamflow (2 of 2)

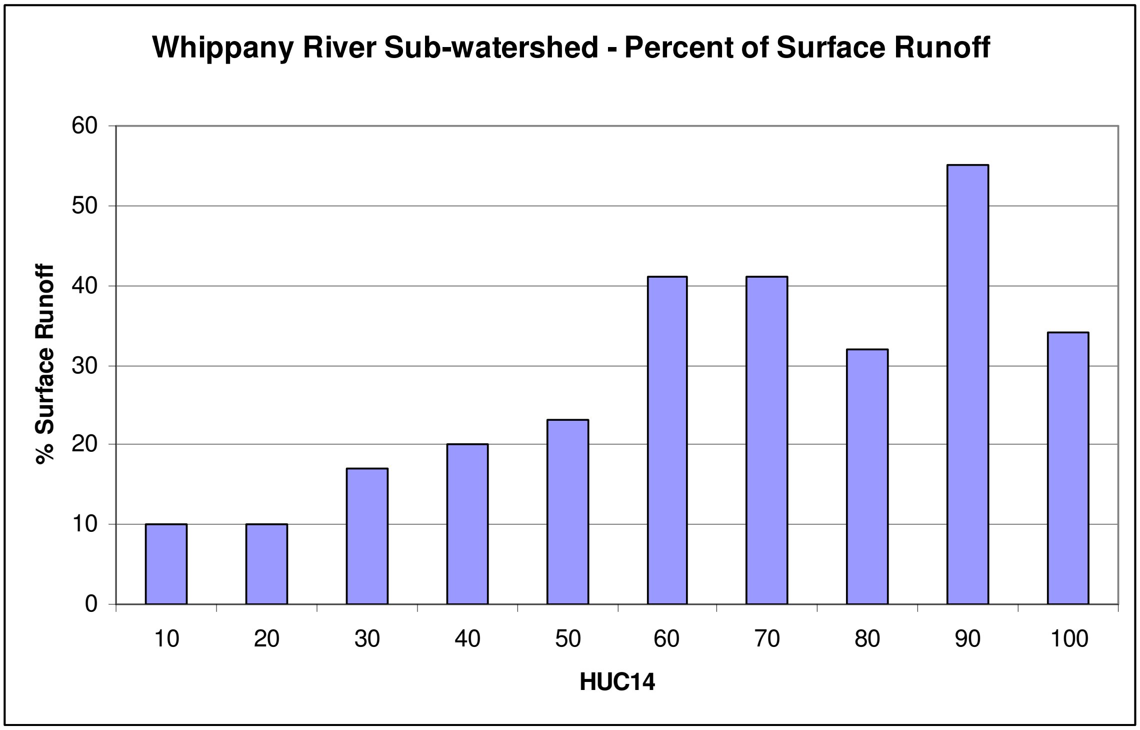
Monthly Streamflow Volume (m^3)					
Month	HUC14*				
	060	070	080	090	100
Jan	7.42×10^5	1.43×10^6	1.55×10^6	6.88×10^5	1.02×10^6
Feb	7.71×10^5	1.52×10^6	1.55×10^6	7.78×10^5	1.04×10^6
Mar	9.02×10^5	1.80×10^6	1.80×10^6	9.57×10^5	1.23×10^6
Apr	1.05×10^6	2.11×10^6	2.08×10^6	1.14×10^6	1.38×10^6
May	7.12×10^5	1.45×10^6	1.47×10^6	7.23×10^5	9.93×10^5
Jun	8.10×10^5	1.63×10^6	1.62×10^6	8.60×10^5	1.11×10^6
Jul	6.19×10^5	1.25×10^6	1.27×10^6	6.51×10^5	8.95×10^5
Aug	5.32×10^5	1.04×10^6	1.13×10^6	5.48×10^5	7.83×10^5
Sep	4.60×10^5	8.63×10^5	9.84×10^5	4.71×10^5	6.83×10^5
Oct	8.76×10^5	1.65×10^6	1.78×10^6	8.93×10^5	1.14×10^6
Nov	6.05×10^5	1.12×10^6	1.31×10^6	4.99×10^5	8.28×10^5
Dec	9.21×10^5	1.77×10^6	1.88×10^6	8.80×10^5	1.21×10^6

* - Last three digits of HUC 14's are presented, All within 02030103020 HUC11 watershed.

Table 2.5: Whippany River – Sub-watershed Hydrology Percent Transport

Sub-watershed Hydrology – Percent Transport			
HUC14	Subsurface	Runoff	Point Source
	(%)	(%)	(%)
010	90	10	0
020	90	10	0
030	81	17	2
040	59	20	21
050	53	23	24
060	59	41	0
070	58	41	1
080	68	32	0
090	45	55	0
100	43	34	23

Figure 2.9: Whippany River – Sub-watershed Hydrology Percent Transport



Surface runoff was highest in the 090 HUC14 followed by 060 and 070 which are associated with the more densely developed downstream reaches of the project area. Increased surface water transport from these areas is a result of increased impervious coverage associated with urban and suburban development.

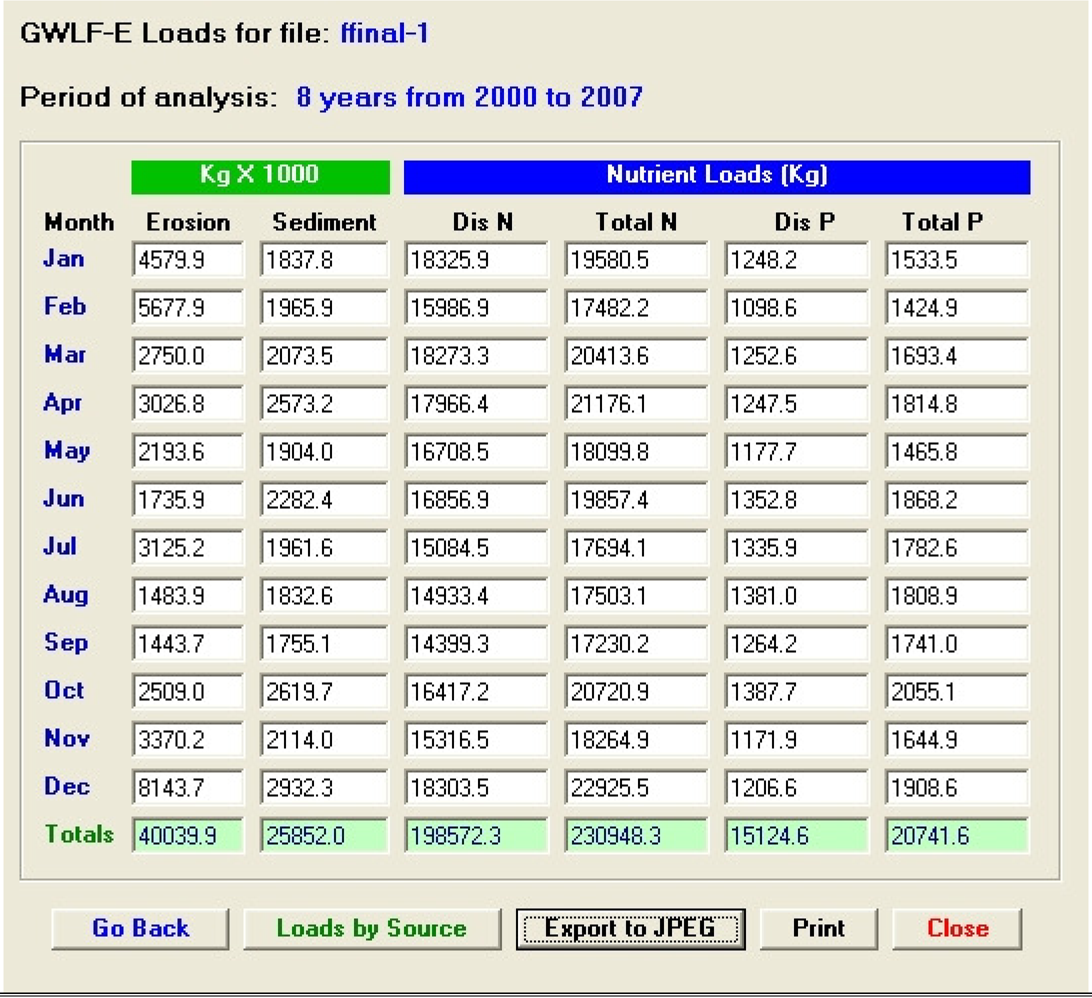
Nutrient Loading

While fecal coliform is the focus of this project, both in terms of modeling and BMP implementation, the influx of sediments, phosphorus and nitrogen to the River are critical in assessing impacts of eutrophication. The following sections detail the phosphorus, nitrogen and sediment inputs to the River on an aggregate and HUC-14 basis. Such information may be viewed in concert with fecal coliform loadings to prioritize and optimize BMP implementation therefore leading to improved water quality conditions throughout the River and all waters downstream.

Aggregate Analysis Including Point Sources

Nutrient loading to the Whippany River, on an aggregate basis, is presented by month in Figure 2.10 and broken down by source in Figure 2.11.

Figure 2.10: Monthly Nutrient & Sediment Loading

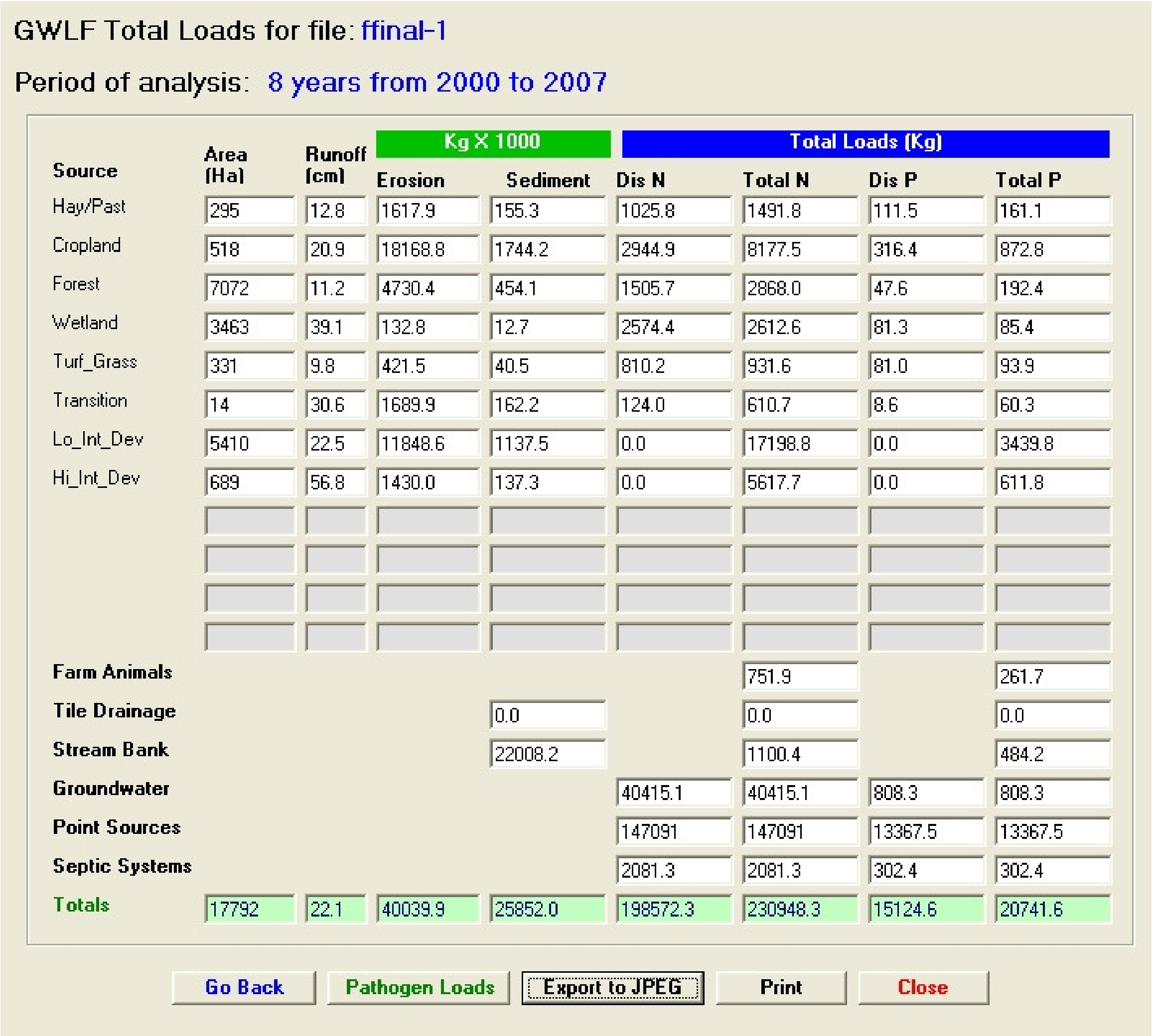


GWLF-E Loads for file: ffinal-1

Period of analysis: 8 years from 2000 to 2007

	Kg X 1000		Nutrient Loads (Kg)			
Month	Erosion	Sediment	Dis N	Total N	Dis P	Total P
Jan	4579.9	1837.8	18325.9	19580.5	1248.2	1533.5
Feb	5677.9	1965.9	15986.9	17482.2	1098.6	1424.9
Mar	2750.0	2073.5	18273.3	20413.6	1252.6	1693.4
Apr	3026.8	2573.2	17966.4	21176.1	1247.5	1814.8
May	2193.6	1904.0	16708.5	18099.8	1177.7	1465.8
Jun	1735.9	2282.4	16856.9	19857.4	1352.8	1868.2
Jul	3125.2	1961.6	15084.5	17694.1	1335.9	1782.6
Aug	1483.9	1832.6	14933.4	17503.1	1381.0	1808.9
Sep	1443.7	1755.1	14399.3	17230.2	1264.2	1741.0
Oct	2509.0	2619.7	16417.2	20720.9	1387.7	2055.1
Nov	3370.2	2114.0	15316.5	18264.9	1171.9	1644.9
Dec	8143.7	2932.3	18303.5	22925.5	1206.6	1908.6
Totals	40039.9	25852.0	198572.3	230948.3	15124.6	20741.6

Figure 2.11: Nutrient and Sediment Load Sources



GWLF Total Loads for file: ffinal-1

Period of analysis: 8 years from 2000 to 2007

			Kg X 1000		Total Loads (Kg)			
Source	**Area (Ha)**	**Runoff (cm)**	**Erosion**	**Sediment**	**Dis N**	**Total N**	**Dis P**	**Total P**
Hay/Past	295	12.8	1617.9	155.3	1025.8	1491.8	111.5	161.1
Cropland	518	20.9	18168.8	1744.2	2944.9	8177.5	316.4	872.8
Forest	7072	11.2	4730.4	454.1	1505.7	2868.0	47.6	192.4
Wetland	3463	39.1	132.8	12.7	2574.4	2612.6	81.3	85.4
Turf_Grass	331	9.8	421.5	40.5	810.2	931.6	81.0	93.9
Transition	14	30.6	1689.9	162.2	124.0	610.7	8.6	60.3
Lo_Int_Dev	5410	22.5	11848.6	1137.5	0.0	17198.8	0.0	3439.8
Hi_Int_Dev	689	56.8	1430.0	137.3	0.0	5617.7	0.0	611.8
Farm Animals						751.9		261.7
Tile Drainage				0.0		0.0		0.0
Stream Bank				22008.2		1100.4		484.2
Groundwater					40415.1	40415.1	808.3	808.3
Point Sources					147091	147091	13367.5	13367.5
Septic Systems					2081.3	2081.3	302.4	302.4
Totals	17792	22.1	40039.9	25852.0	198572.3	230948.3	15124.6	20741.6

The annual load of Sediment, total nitrogen and total phosphorus to the Whippany River is 2.59 x 10^7, 2.31 x 10^5 and 2.07 x 10^4 respectively. The following figures (2.12 – 2.14) depict the percent contribution of each loading source for sediment, nitrogen and phosphorus, respectively.

Figure 2.12: Sediment Load Sources

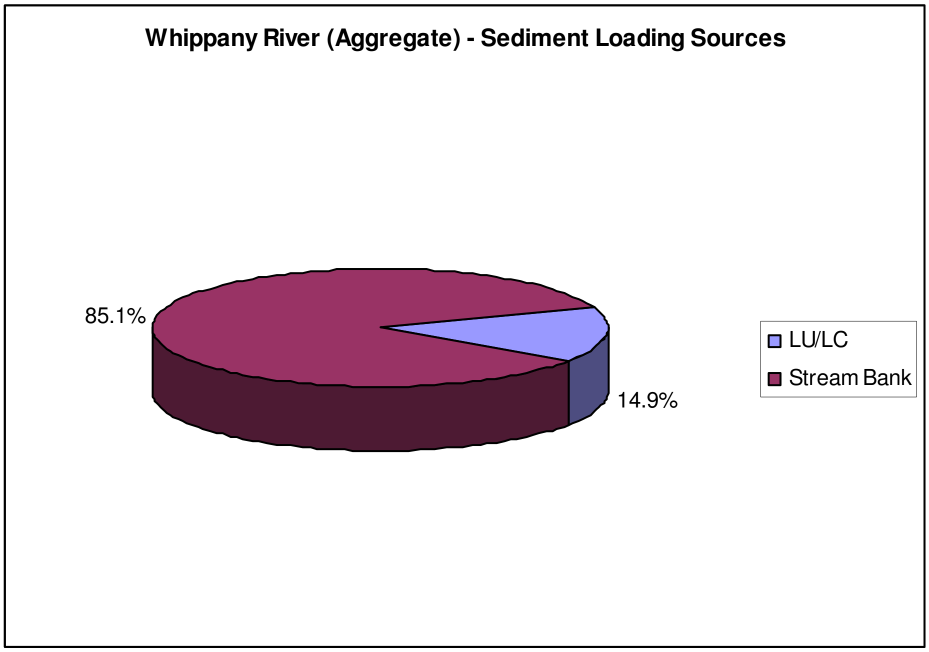


Figure 2.13: Nitrogen Load Sources

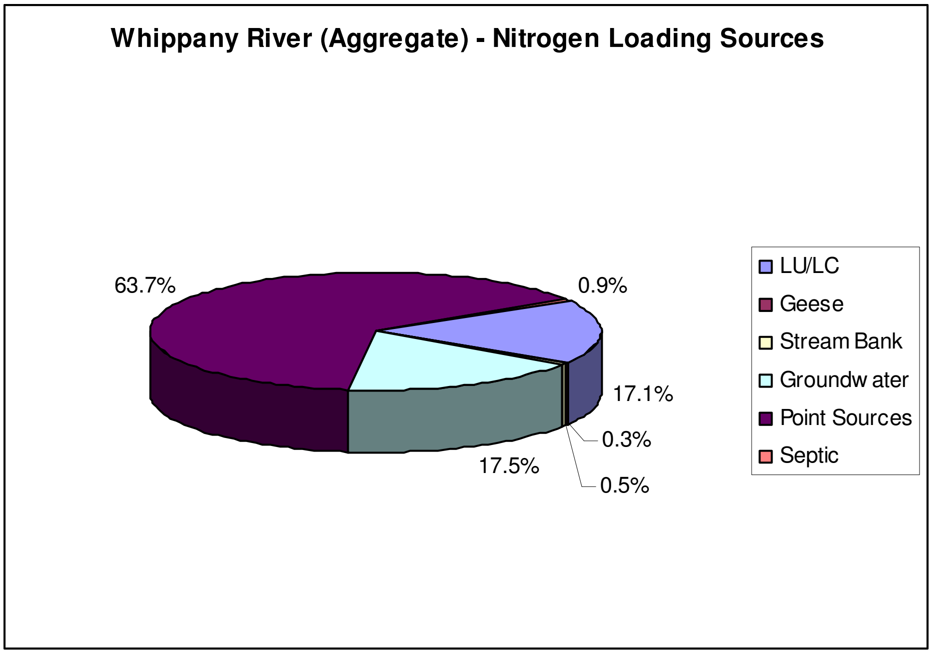
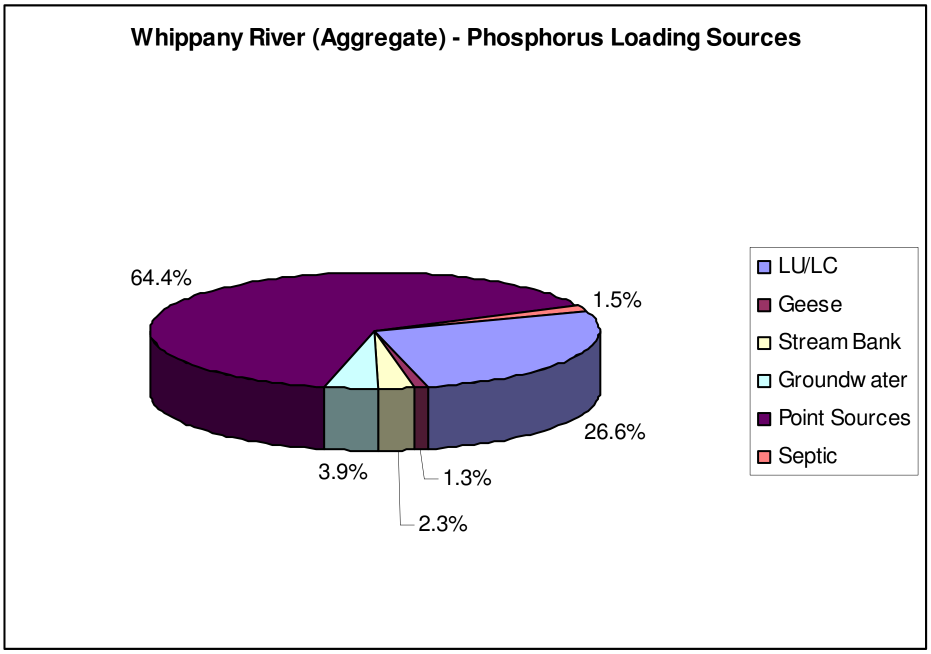


Figure 2.14: Whippany River - Phosphorus Load Sources



Sediment loading to the Whippany River, on an aggregate basis, is derived primarily from stream bank and bed sources, which comprise 85.1% of the annual sediment load to the river. Overland erosion accounts for approximately 14.9% of the load. Elevated sediment loading from stream bank and bed sources is likely due to altered hydrologic regimes derived from increased impervious areas associated with development. Specifically, increased impervious area in a watershed has the effect of increasing surface water runoff while concomitantly decreasing groundwater infiltration. These hydrological changes result in storm events characterized by an increased volume of discharge over a shorter period of time, commonly referred to as “flashy” storm events. Increased hydrologic loading, over a shorter period of time, is associated with increased kinetic energy which scours stream banks and beds thereby transporting elevated sediment loads.

Nitrogen loading to the Whippany River is derived primarily by point sources, which comprise approximately 63.7% of the total nitrogen load to the River on an annual basis. The second greatest loading contributor is groundwater while the third is from watershed based sources. All other loading sources (Stream bank, Geese and Septic) are negligible on a watershed wide scale but may be relatively large source areas on finer spatial scales.

Phosphorus loads to the River are also derived primarily by point sources, which contribute approximately 64.4% of the annual P load to the River. The second greatest source, comprising approximately 26.6% of the annual P load, is from watershed based sources. The remaining sources (Geese, stream bank, groundwater and septic) contribute negligible loads on a watershed wide scale, but like nitrogen, may be significant source areas on a localized basis.

Sub-watershed Analysis Including Point Sources

Table 2.6 presents the sub-watershed load of TP, TN and Sediment loading.

Table 2.6: Whippany River – Sub-watershed Loading

Sub-watershed	TP	TN	Sediment
	(kg/yr)	(kg/yr)	(kg*1000/yr)
010	474	7829	946
020	735	10795	1774
030	1311	17789	3306
040	3833	29251	1841
050	2903	62829	1340
060	612	6306	683
070	1631	17427	2028
080	1144	12240	1560
090	419	4918	668
100	8481	72536	885
Sum	21544	241920	15031

Table 2.7 provides pollutant loads, normalized for sub-watershed area. As such, this table may be utilized to objectively compare nutrient loads per unit area thereby allowing for direct prioritization of those sub-watersheds which may be contributing excessive pollutant loads.

Table 2.7: Whippany River – Sub-watershed Loading

Sub-watershed	Area	TP	TN	Sediment
	(ha)	(kg/yr)	(kg/yr)	(kg*1000/yr)
010	1548	.31	5.06	.61
020	1617	.45	6.68	1.10
030	1999	.66	8.90	1.65
040	1442	2.66	20.29	1.28
050	1736	1.67	36.19	.77
060	1311	.47	4.81	.52
070	2683	.61	6.50	.76
080	2466	.46	4.96	.63
090	1560	.27	3.15	.43
100	1452	5.84	49.96	.61

As listed above, sub-watershed 100 accounts for the greatest per unit area contribution of TP and TN to the River followed by sub-watersheds 050 and 040. The 030 sub-watershed contributes the greatest sediment load on a per unit area basis. When reviewing this data it is critical to remember that point sources were included in this analysis in order to refine loading estimates to the River. While point source loading is important in assessing loading and the overall nutrient and sediment budget to the Whippany River, such sources are costly to mitigate and are generally not targeted for BMP implementation, although this does not have to be the case. Nevertheless, it is useful to parse out this loading source to examine the non-point source loadings to the Whippany River. In doing so, BMPs can be designed to focus on those sub-watersheds and source areas which are contributing a disproportionably high NPS load to the River.

Sub-watershed Analysis Minus Point Sources

Table 2.8 lists sub-watershed monthly TP, TN and sediment loads. The presented values do not include point source loads.

Table 2.8: Whippany River – Sub-watershed Loading Minus Point Source

Sub-watershed	TP	TN	Sediment
	(kg/yr)	(kg/yr)	(kg*1000/yr)
010	474.37	7828.58	945.58
020	735.32	10795.34	1774.24
030	1229.20	14648.47	3306.44
040	685.48	8241.62	1841.40
050	917.38	9790.75	1339.89
060	612.12	6306.19	682.94
070	1274.58	13148.58	2027.86
080	1144.35	12239.61	1560.05
090	418.82	4917.56	667.95
100	685.33	6911.48	885.16
Sum	8176.95	94828.16	15031.49

As previously mentioned, not all HUC14s are identically sized. Therefore, Table 2.9 normalizes the NPS pollutant loads per sub-watershed area in order to prioritize those sub-watersheds which are contributing a disproportionate NPS load per unit area.

Table 2.9: Whippany River – Sub-watershed Loading Minus Point Source

Sub-shed	Area	TP	TN	Sediment
	(ha)	(kg/ha)	(kg/ha)	(kg*1000/ha)
10	1548	0.31	5.06	0.61
20	1617	0.45	6.68	1.10
30	1999	0.61	7.33	1.65
40	1442	0.48	5.72	1.28
50	1736	0.53	5.64	0.77
60	1311	0.47	4.81	0.52
70	2683	0.48	4.90	0.76
80	2466	0.46	4.96	0.63
90	1560	0.27	3.15	0.43
100	1452	0.47	4.76	0.61

The greatest TP, TN and sediment load per unit area is derived from the 030 sub-watershed. In order to effectively manage the NPS load of pollutants to the river it is necessary to analyze the contributing sources of phosphorus, nitrogen and sediments. The following figures (2.15 – 2.17) present the percent source contribution of pollutants over the entire watershed, when modeled on a sub-watershed basis.

Figure 2.15: Whippany River - NPS TP Load

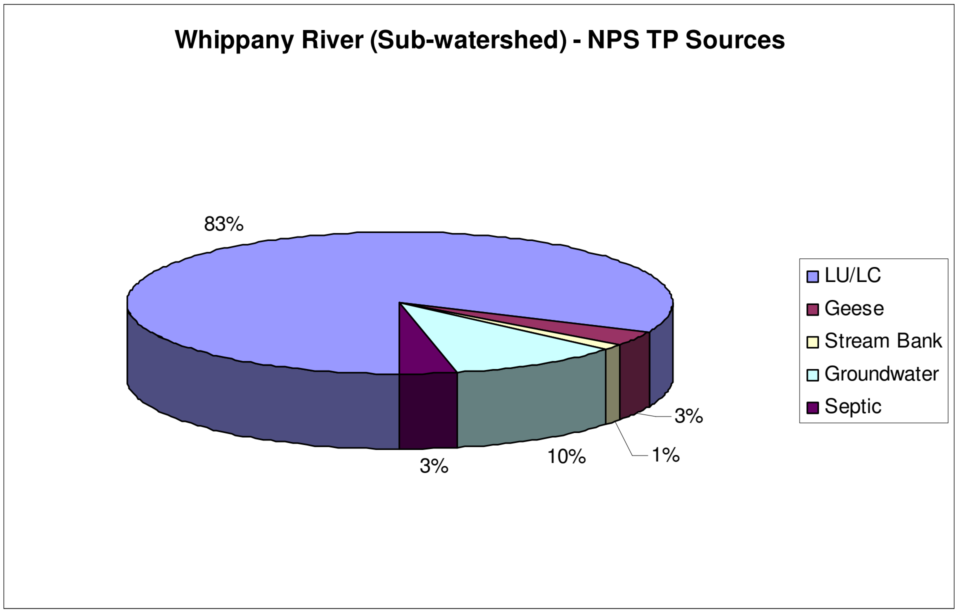


Figure 2.16: Whippany River - NPS TN Load

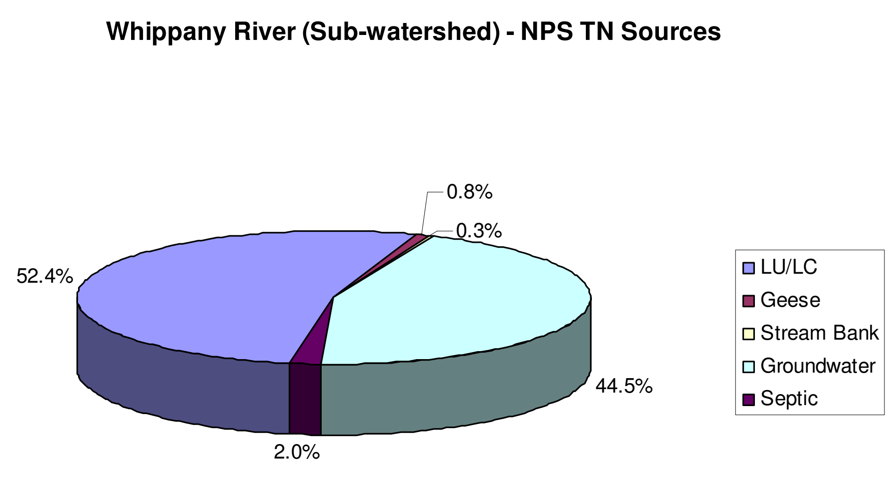
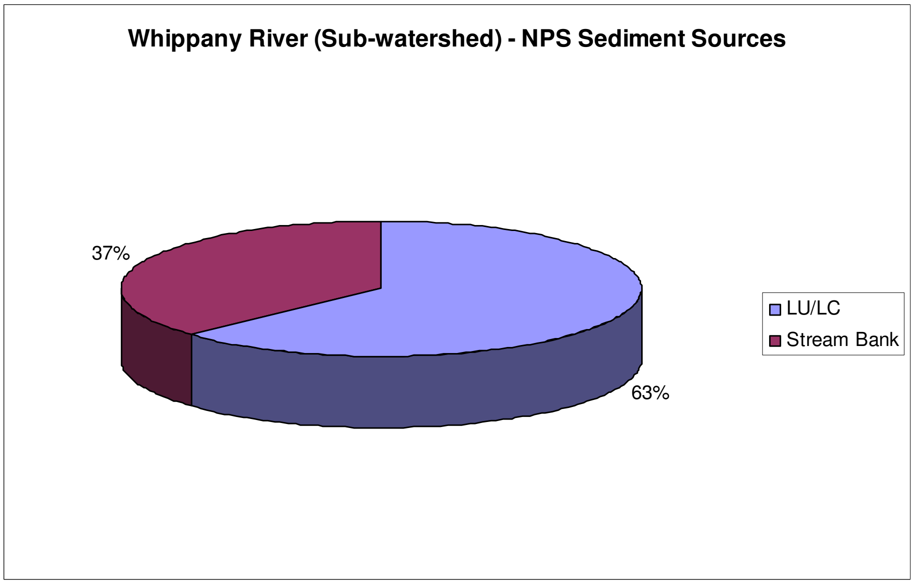


Figure 2.17: Whippany River - NPS Sediment Load



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As previously mentioned, the 030 sub-watershed contributes the greatest NPS pollutant load, per unit area. The following figures (2.18-2.20) present the percent source contributors of TP, TN and sediments to the River.

Figure 2.18: Whippany River – HUC 030 NPS TP Load

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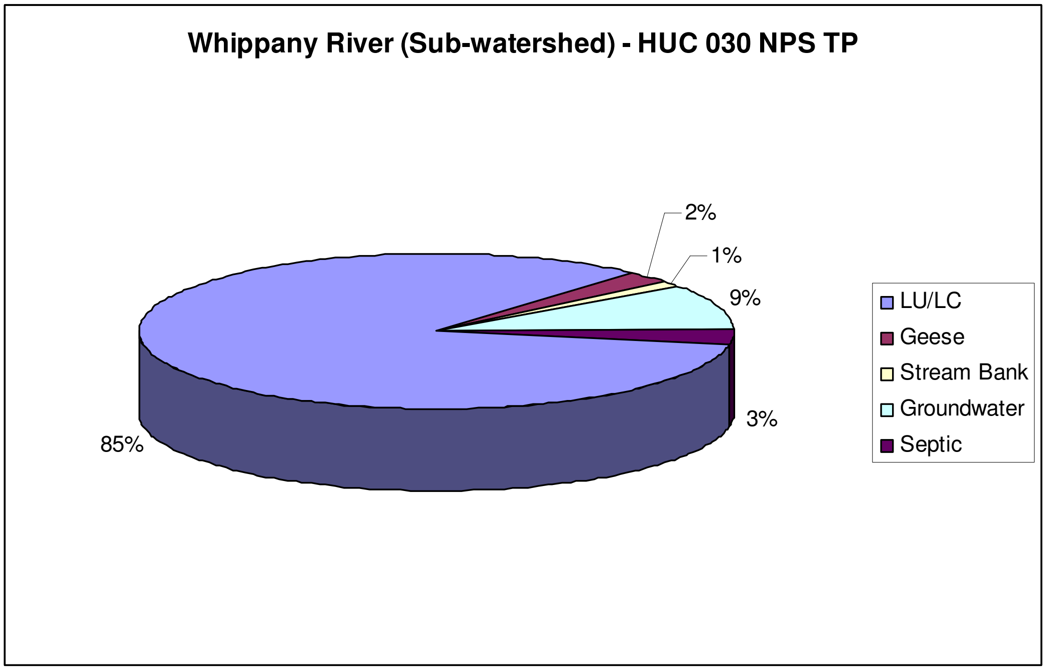


Figure 2.19: Whippany River – HUC 030 NPS TN Load

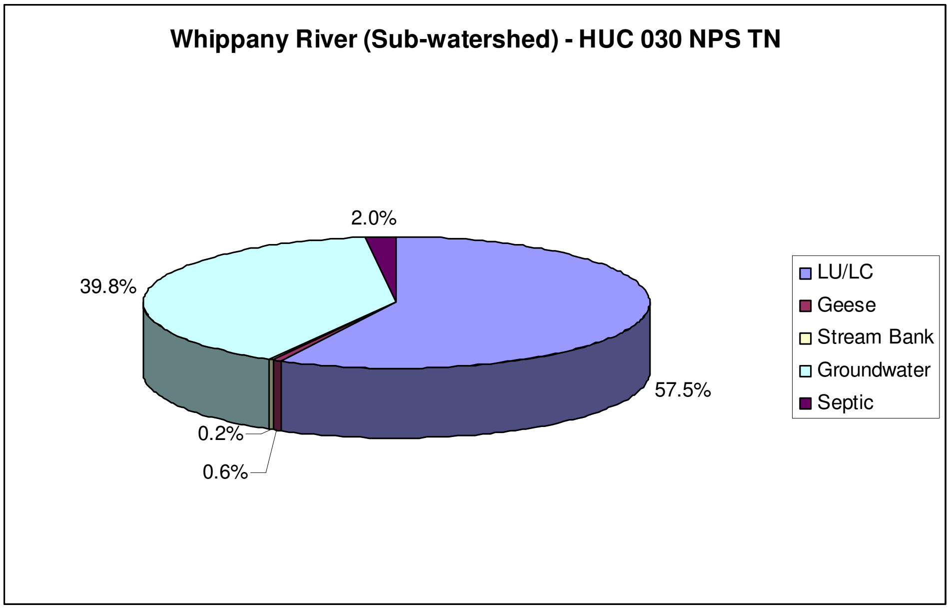
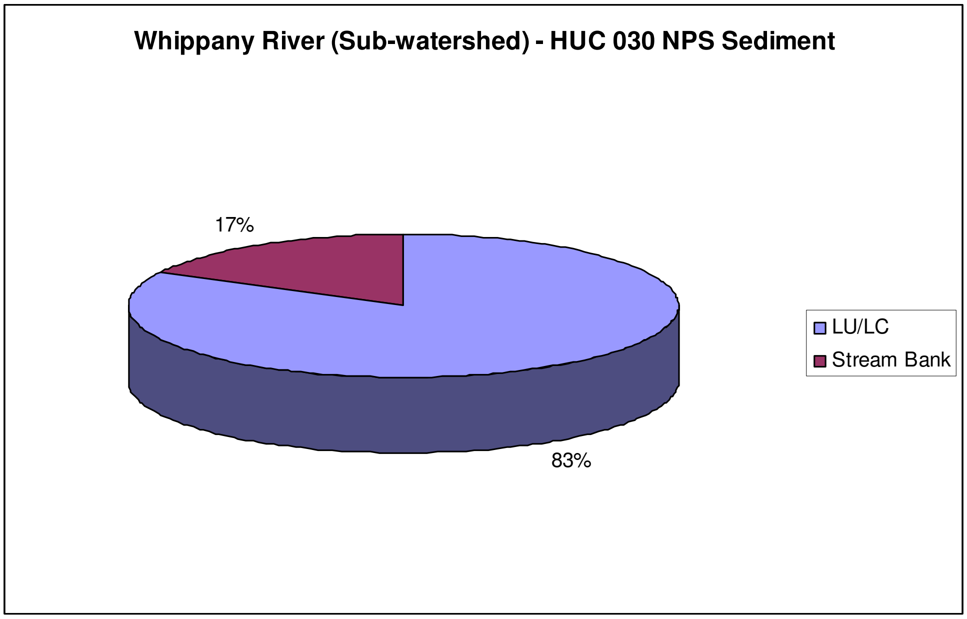


Figure 2.20: Whippany River – HUC 030 NPS Sediment Load



Variations in Aggregate versus Sub-watershed Loadings

As previously mentioned, all modeling was conducted on a watershed aggregate and sub-watershed basis. Due to certain spatially derived parameters, the sum of nutrient loads on a sub-watershed basis does not exactly equal those when modeling the watershed as an aggregate. Specifically, the percent difference of aggregate versus sub-watershed phosphorus, nitrogen and sediment loads is 3.8%, 4.6% and 52.9%; respectively. The markedly higher percent difference in sediment loading is due to erosion and transport algorithms within AVGWLF which depend on certain spatial and hydrologic factors. Specifically, stream bank erosion tends to account for a much greater percentage of total sediment yields on an aggregate watershed basis. Stream bank erosion accounted for 85% of the total annual sediment yield on an aggregate basis versus 37% on a sub-watershed basis. The discrepancy between stream bank erosion on an aggregate versus sub-watershed scale is explained when viewing the underlying equation which dictates this loading contribution. Specifically, the stream bank erosion routine is premised on the "Lateral Erosion Rate" (eq. 3):

$$\mathrm{LER} = a * q^{0.6} \qquad \text{(Equation 3)}$$

where "LER" equals an estimated lateral erosion rate in meters/month, "a" equals an empirically derived constant related to the mass of soil eroded from the stream bank depending on various watershed conditions, and "q" equals monthly stream flow in m^3/second.

When modeling the watershed as an aggregate, AVGWLF is modeling the transport of water, nutrients, bacteria and sediments to the most downstream point of the aggregate basin. As such, this point has a significantly greater volume of water moving through it than any of the smaller sub-watersheds. Elevated streamflow results in a greater LER thereby increasing the portion of sediment derived from stream bank erosion on an aggregate scale.

Sediment yield within AVGWLF may also be derived from watershed based sources. In calculating sediment yield from overland erosion AVGWLF estimates erosion as based on the USLE equation which is subsequently modified with a "Sediment Delivery Ratio" (SDR) to compute the mass of eroded sediments which are actually delivered to surface waters. The SDR is presented in equation 4:

$$\mathrm{SDR} = 0.451(b^{-0.296}) \qquad \text{(Equation 4)}$$

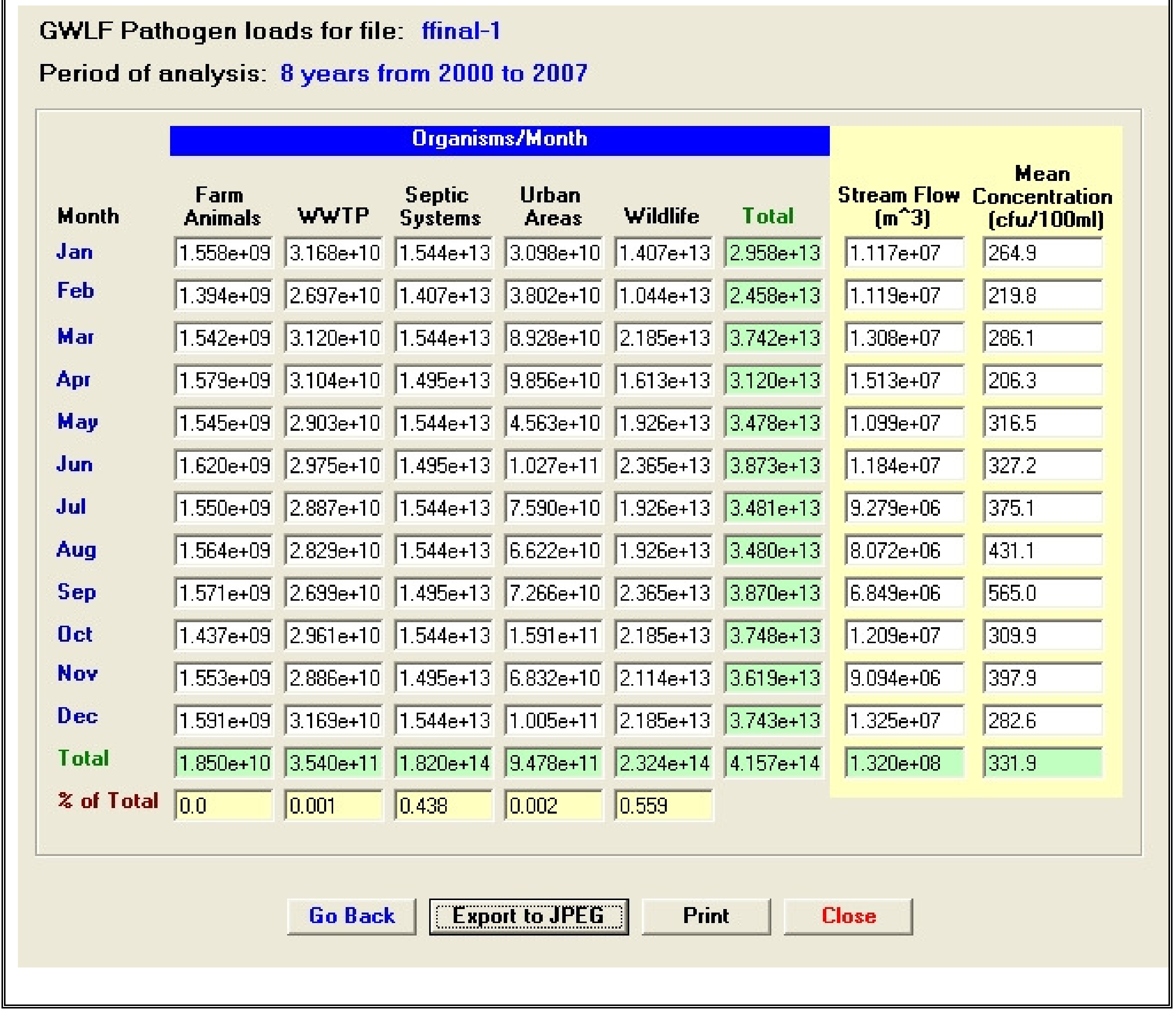
Where "SDR" equals the sediment delivery ratio and "b" equals the size of the watershed, in square kilometers. In reviewing equation 4, it is clear that conducting sediment modeling on a sub-watershed basis will provide greater watershed based sediment yield than when conducting modeling on an aggregate basis due to smaller watershed size and therefore, greater transport of eroded sediments to surface waters.

In viewing the sediment output yields from AVGWLF it is necessary to be cognizant of the spatial scale associated with the model output. Neither the aggregate or sub-watershed modeling scales are wrong, but their results need to be interpreted in the proper context.

Fecal Coliform Loading

The following figure (2.21) illustrates the fecal coliform load to the River when the watershed was modeled as an aggregate.

Figure 2.21: Whippany River (Aggregate) – Fecal Coliform Load



GWLF Pathogen loads for file: ffinal-1

Period of analysis: 8 years from 2000 to 2007

	Organisms/Month							
Month	Farm Animals	WWTP	Septic Systems	Urban Areas	Wildlife	Total	Stream Flow (m^3)	Mean Concentration (cfu/100ml)
Jan	1.558e+09	3.168e+10	1.544e+13	3.098e+10	1.407e+13	2.958e+13	1.117e+07	264.9
Feb	1.394e+09	2.697e+10	1.407e+13	3.802e+10	1.044e+13	2.458e+13	1.119e+07	219.8
Mar	1.542e+09	3.120e+10	1.544e+13	8.928e+10	2.185e+13	3.742e+13	1.308e+07	286.1
Apr	1.579e+09	3.104e+10	1.495e+13	9.856e+10	1.613e+13	3.120e+13	1.513e+07	206.3
May	1.545e+09	2.903e+10	1.544e+13	4.563e+10	1.926e+13	3.478e+13	1.099e+07	316.5
Jun	1.620e+09	2.975e+10	1.495e+13	1.027e+11	2.365e+13	3.873e+13	1.184e+07	327.2
Jul	1.550e+09	2.887e+10	1.544e+13	7.590e+10	1.926e+13	3.481e+13	9.279e+06	375.1
Aug	1.564e+09	2.829e+10	1.544e+13	6.622e+10	1.926e+13	3.480e+13	8.072e+06	431.1
Sep	1.571e+09	2.699e+10	1.495e+13	7.266e+10	2.365e+13	3.870e+13	6.849e+06	565.0
Oct	1.437e+09	2.961e+10	1.544e+13	1.591e+11	2.185e+13	3.748e+13	1.209e+07	309.9
Nov	1.553e+09	2.886e+10	1.495e+13	6.832e+10	2.114e+13	3.619e+13	9.094e+06	397.9
Dec	1.591e+09	3.169e+10	1.544e+13	1.005e+11	2.185e+13	3.743e+13	1.325e+07	282.6
Total	1.850e+10	3.540e+11	1.820e+14	9.478e+11	2.324e+14	4.157e+14	1.320e+08	331.9
% of Total	0.0	0.001	0.438	0.002	0.559			

On an aggregate basis, approximately 4.157 x 10^{14} fecal coliform organisms are transported to the Whippany River on an annual basis. This load translates to a mean annual fecal coliform concentration of approximately 331.9 cfu/100 ml. The greatest contributing source is wildlife, which contributes 56% of the total annual fecal coliform load. It should be noted that Canada geese were modeled separately from wildlife and are listed as "Farm Animals" for modeling purposes. Canada geese were the smallest contributor of fecal coliform on an annual basis, contributing 0.005% of the total annual fecal coliform load. Septic systems were the second largest contributing source, comprising 44% of the total annual fecal coliform load.

The following table lists the fecal coliform load, modeled on a sub-watershed basis, to the Whippany River.

Table 2.10: Whippany River (Sub-watershed) – Fecal Coliform

Sub-watershed	Area	Fecal Load (organisms)	
	(ha)	Absolute	Normalized
010	1548	6.35×10^{13}	4.10×10^{10}
020	1617	3.43×10^{13}	2.12×10^{10}
030	1999	5.74×10^{13}	2.87×10^{10}
040	1442	6.35×10^{13}	4.40×10^{10}
050	1736	5.65×10^{13}	3.25×10^{10}
060	1311	4.86×10^{13}	3.71×10^{10}
070	2683	5.74×10^{13}	2.14×10^{10}
080	2466	6.62×10^{13}	2.68×10^{10}
090	1560	6.11×10^{13}	3.92×10^{10}
100	1452	6.24×10^{13}	4.30×10^{10}
Sum	17814	5.71×10^{14}	

Total annual fecal coliform loading to the Whippany River, when modeled as a sub-watershed, is 5.71×10^{14} organisms. This load represents a 31.4% difference from the aggregate watershed load. Table 2.11 lists each sub-watershed and the percent contribution of fecal coliform from each of the five modeled source areas.

Table 2.11: Whippany River (Sub-watershed) – Fecal Coliform Percent Source Areas

HUC	Geese	WWTP	Septic	Urban	Wildlife
010	0.003	0.000	82.047	1.099	16.850
020	0.005	0.000	65.598	2.085	32.362
030	0.004	0.016	43.206	1.547	55.226
040	0.002	0.149	38.583	1.398	59.843
050	0.003	0.257	22.832	1.715	75.221
060	0.003	0.000	5.741	1.868	92.387
070	0.005	0.010	13.606	1.688	84.843
080	0.004	0.000	15.257	1.464	83.233
090	0.003	0.000	5.008	1.589	93.453
100	0.002	0.160	5.032	1.521	93.269

As evidenced above, the highest fecal coliform loading sources in the headwaters (HUC 010 and 020) are septic while those in all other HUC’s are derived primarily by wildlife sources. Urban sources of fecal coliform loading were routinely low with percentages ranging from a minimum of 1.099% at HUC 010 to 2.085 at HUC 020. Fecal coliform derived from wastewater treatment plants was a minor contributor to the overall load with percentages ranging from 0.010 % to 0.257 %. These low percentages are consistent with NJPDES effluent fecal coliform concentrations which were, on average, 5 cfu / 100 ml for all dischargers. Geese, when modeled as a separate loading source, were also a very minor contributor of fecal coliform on a sub-watershed scale with percentages ranging from 0.002 % to 0.005%.

3.0 Field Data Collection

3.1 Methodology

Pathogen field sampling (E coli and fecal coliform) conducted by Princeton Hydro and WRWAC personnel involved the collection of water samples under both base flow and storm flow conditions. Pathogen sampling was conducted in conformance with the NJDEP approved project Quality Assurance Protection Plan (QAPP). The details of the sampling methodologies and quality assurance and quality protection practices and procedures are provided in the QAPP which is attached as an appendix to this report. The QAPP was structured in accordance with the practices and procedures of *Standard Methods for the Analysis of Water and Wastewater, 20th Edition* (American Public Health Association 1998), NJDEP Field Sampling Procedures Manual (2005. Section 6.8.2.2.1 Stream/Flowing Water) and/or other applicable US EPA guidance document, such as Volunteer Stream Monitoring: A Methods Manual (EPA 11/97).

Sampling was conducted at the eight sampling stations established in concert by Princeton Hydro and WRWAC. At each of the eight sampling stations both discrete water samples and *in-situ* water data were collected. The eight sampled stations were consistent in location with sampling stations previously monitored as part of past sampling programs conducted by WRWAC.

The location of each of the sampled stations was recorded in the field utilizing a hand-held GPS. In addition, a permanent marker, in the form of a driven painted stake and/or PK nail, was used to in the field to visually confirm the location of each sampling station. The combination of the field marker and GPS coordinates ensured all those participating in the sample collection effort consistently sampled each stream at the same location on each date. This also enabled all involved in the review of the data generated through this effort to confirm the location at which the data were collected.

Table 3.1 – Station Locations

Station ID	Approximate Location
1	Randolph – Brownsede Rd
2	Morris – Washington Valley Road
3	Morris – Lake Valley Road
4	Morristown – Speedwell Lake
5	Hanover – Mount Pleasant Avenue
6	East Hanover – Ridgedale Avenue
7	Parsippany – South Beverwyck Road
8	Parsippany – Edwards Road

Princeton Hydro (Field Monitoring Certification #10006) trained the WRWAC volunteers in the collection of discrete water quality samples (under storm conditions) and the measurement of the *in-situ* parameters of dissolved oxygen, pH, temperature and specific conductivity utilizing WRWAC purchased field equipment. Specifics on sampling techniques, the documentation of existing conditions, preservation of discrete water samples and the proper completion of COC sheets were covered during a one-day training class conducted on 26 October 2008. This class also included some field demonstrations on proper sampling protocol. After the classroom presentation, Princeton Hydro accompanied the WRWAC to the sampling stations where any and all on-site questions and issues were addressed at that time.

Discrete and *in-situ* water quality monitoring was conducted over the course of a calendar year in keeping with the NJDEP approved project schedule and QAPP. Princeton Hydro personnel collected all of the base flow water samples. Base flow sampling was defined as conditions during which a minimum of 72 hours have elapsed since the previous storm event that had resulted in 0.1 inches or less of precipitation. WRWAC personnel, with assistance from Princeton Hydro, collected water samples during four storm events. Storm sampling was defined as conditions during which a minimum of 0.1 inches of rain fell and a minimum of 72 hours have elapsed since the previous storm event that had resulted in 0.1 inches or greater of precipitation. *In-situ* data (pH, temperature, specific conductivity and dissolved oxygen) were recorded during the majority of these events using properly calibrated field equipment. The base flow monitoring effort also entailed conducting five (5) sampling events during a single 30-day period (7 August – 3 September 2009). To prevent any cross-contamination of the samples, all discrete grab samples were collected directly into the appropriate laboratory supplied container. WRWAC and Princeton Hydro personnel transported the samples (storm and base flow) to Integrated Analytical Laboratories (Randolph, NJ) within the proper holding times and in accordance with required the chain of custody protocols

3.2 Results

The resulting pathogen data developed through the above detailed field sampling effort (Appendix I) were compared to New Jersey Water Quality Standards (N.J.A.C. 7:9B) and applicable EPA Reference Criteria. The following provides a summary of the resulting data:

In-situ **Parameters**

pH

A measure of the acidity or alkalinity of the water, pH is based on a scale of 0 to 14. A pH of 0.0 is the most acidic, a pH of 14.0 is the most alkaline, and a pH of 7.0 is neutral. pH can have a profound effect on the chemical and biological components of an aquatic ecosystem, therefore, it is an extremely important ecological parameter.

The pH measured at all the stations during the sampling program tended to be well within the surface water standard pH range (6.5 to 8.5), with the majority of the recorded data within the range of 7.0 to 7.7. Higher values tended to be measured under conditions characterized by high algal and plant photosynthesis activity. In general, Station 7 tended to have the highest pH values; however the pH values of all the streams were fairly similar and consistent throughout the program.

Specific Conductivity

Specific Conductivity is a proxy measurement of dissolved substances (i.e. nutrients, minerals, salts) in water. The higher the conductivity, the more dissolved substances present in the water. Specific Conductivity is an indirect way of measuring the dissolved solids present in the stream, as well as measuring the electrical conductivity of water, adjusted for temperature, based on the dissolved substances present.

Specific conductivity values were fairly consistent both on a temporal and spatial scale. As with pH the values measured at Station 7 were consistently elevated relative to the other stream stations. However this highest specific conductivity value measured on any of the sampling dates was recorded at Station 6.

Dissolved Oxygen

The amount of dissolved oxygen (DO) in a stream is one of the best indicators of an ecosystem's health. Oxygen diffuses directly from the atmosphere and is produced by the photosynthetic activities of macrophyte (aquatic plants) and algae. DO is utilized by the respiratory activities of aquatic organisms. Most aquatic ecosystems require at least 5-6 mg/l of DO to support a diverse community of aquatic species. The presence of little or no DO can indicate unhealthy water; possibly due to excessive organic enrichment, septic influence or stagnancy.

DO concentrations at the majority of the sampled stations were typically greater than the NJDEP surface water standard of 5.0 mg/L. The exception was Station 6, which consistently had depressed DO concentrations. Additionally, Station 8 periodically had reduced DO concentrations (<50% saturation). Watershed-wide, as can be expected, somewhat lower DO concentrations were measured at almost of the stream stations during the summer sampling events as compared to the spring or fall sampling events. This is a direct function of water temperature and flow. At warmer water temperatures DO saturation is reached at a lower DO concentration; that is the warmer the water the solubility of DO. As stream flow and related turbulence decreases this also results in less dissolved oxygen in the water simply as a function of reduced mixing and atmospheric diffusion.

Temperature

Water temperature is a critical parameter measured in lotic systems. The temperature of water exhibits an inverse relationship with the solubility of gases, such as dissolved oxygen. As such, colder water may retain more DO than warmer waters. Conditions may arise in streams whereby water temperatures increase due to deforestation of riparian areas, decreased groundwater inputs and thermal pollution from impervious surfaces. Such thermal pollution results in a reduction in DO retention capacity and may directly impact species diversity.

As displayed in Appendix A, the lowest water temperatures were recorded in the early summer while the highest temperatures were recorded in the mid to late summer. The forested stream corridors and groundwater based flow from the upper reaches of the watershed allowed the streams to warm slower than impounded reaches of the river (i.e. ponds and lakes). As a result, the temperatures of the streams in the upper reaches of the watershed (Stations 1-4) were generally cooler than that of the lower reaches (Stations 5-8).

Discrete Water Sample Results

Fecal coliform bacteria and E. coli (a species of bacteria in the fecal coliform group) are both relatively easily measured indicator organisms that are used to evaluate fecal contamination in surface waters. The measurement of these parameters provide a means of evaluating the public safety of using a surface water in a given capacity, typically as a source of potable water, but more often for direct contact recreation given that these organisms are often used as a proxy indicator for pathogenic organisms. As noted above, both indicator bacteria were measured under storm and base flow conditions.

Fecal Coliform

The presence of fecal coliform in aquatic environments may indicate that the water has been contaminated with the fecal material of humans or other animals. Fecal coliform bacteria can enter these systems through direct discharge of waste from mammals and birds, from agricultural and storm water runoff and from sewage. Failing home septic systems can allow coliform in the effluent to flow into the water table, aquifers, drainage ditches and adjacent surface waters. Older sewage connections that are connected to storm drain pipes (illicit connections) can also allow sanitary sewage into surface waters.

Pets, especially dogs, can contribute to fecal contamination of surface waters. Runoff from roads, parking lots, and yards can carry animal wastes to streams through storm infrastructure. Birds can be a significant source of fecal coliform bacteria. Swans, geese, gulls and other waterfowl can all elevate bacterial counts; especially in wetlands, lakes, ponds and rivers.

Agricultural practices such as allowing livestock to graze near water bodies, spreading manure as fertilizer on fields during wet periods, using sewage sludge biosolids and allowing livestock watering in streams can all contribute to fecal coliform contamination.

Until 2008, the New Jersey Water Quality Standards (NJAC 7:9B) were based on fecal coliform levels. The allowable concentration for direct contact recreation (swimming) for fecal coliform was at 200 cfu/100 ml. However, the standard has since been updated and is now based on *E. Coli* concentrations as opposed to fecal coliform concentrations. However, fecal coliform data continue to be useful and meaningful in the analysis of pathogen impairments. Additionally, given the extensive historic fecal coliform database compiled by WRWAC. Furthermore, the TMDL developed for the Whippany River was specifically created to address fecal coliform loading in this waterbody.

Using a maximum allowable fecal coliform concentration of 200 cfu/100 ml, it is clear that the overwhelming majority of the stream samples collected during the course of this study yielded fecal coliform concentrations greater than this threshold. Specifically, the measured fecal coliform concentrations ranged from a minimum of 85 cfu/100 ml to a maximum of 1,900 cfu/100 ml during base flow conditions. Station 1 had the highest concentration of fecal coliform during four of the eight base flow monitoring events. Station 6 and Station 8 had the highest concentration during two base flow monitoring events each.

Storm flow concentrations measured during the 16 October 2009 event ranged from a minimum of 620 cfu/100 ml at Station1 to a maximum of 5,100 cfu/ 100 ml at Station 3.

Escherichia coli

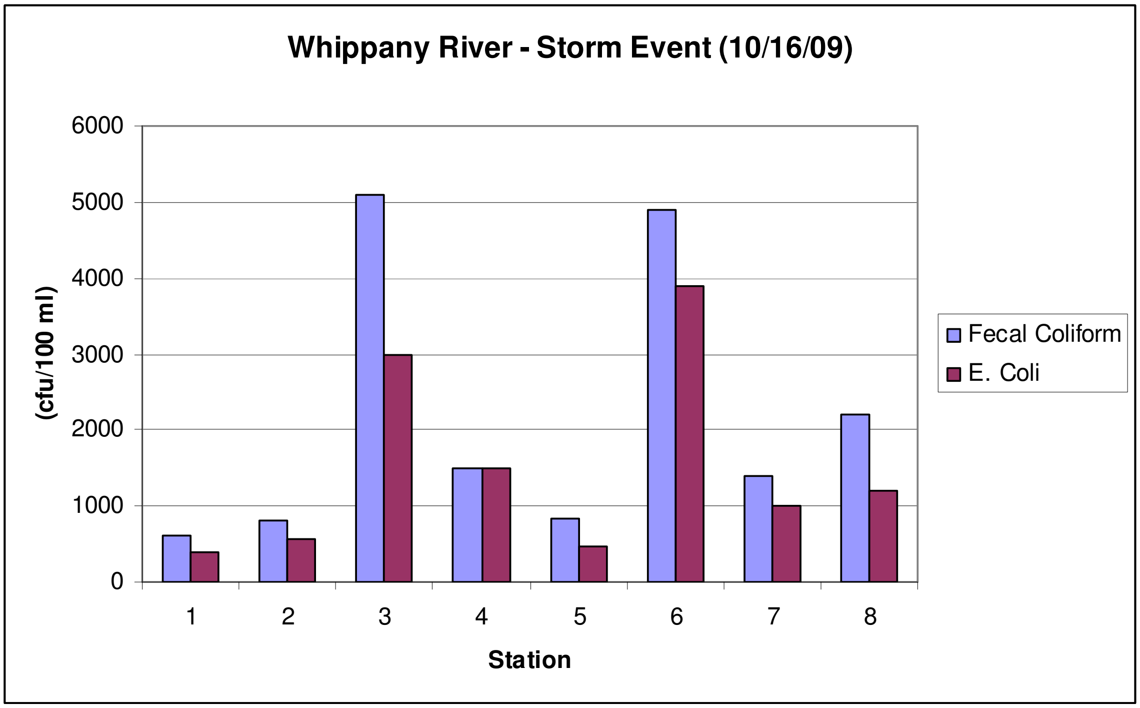
Escherichia coli (E. coli) is commonly found in the lower intestine of warm blooded organisms. This makes them a more valuable indicator species than the more ubiquitous fecal coliform, especially when attempting to link pathogen impairments to human sources. Additionally because *E. coli* can only survive in the environment for a short amount of time once discharged with feces for the intestinal tract, their detection in water samples further heightens the probability of a recent fecal contamination event.

However, it must be emphasized that although linked to warm blooded organisms, the presence of *E. coli* is not automatically indicative of human waste. As well as birds and other mammals, *E. coli* bacteria have also been found in some fish and turtles, and sand and soil can also harbor *E. coli* bacteria.

As per the 2008 New Jersey Water Quality Standards, allowable limit for direct contact recreation is an E. coli average concentration of 126 cfu/100 ml; with a single concentration not to exceed 235 cfu/100 ml. Utilizing this not to exceed single standard concentration of 235 cfu/100 ml, it is clear that the overwhelming majority of stream samples collected during the course of this project yielded E. coli. Concentrations that exceeded this standard. Single E. coli. Concentrations ranged from a minimum of 52 cfu/100 ml to a maximum of 1,840 cfu/100 ml. *E. coli* results tended to mirror the fecal coliform results. Station 1 had the highest concentration of *E. coli.* During four of the eight monitoring events and Station 6 and Station 8 each had the highest concentration during the two remaining monitoring events.

Stormwater *E. coli* concentrations measured during the 16 October 2009 storm event ranged from a minimum of 400 cfu/100 ml at Station 1 to a maximum of 3900 cfu/100 ml at Station 6. Fecal and *E. coli* concentrations measured during the 16 October 2009 storm event are presented in Figure 3.1.

Figure 3.1: Storm Event – 10/16/09



4.0 Microbial Source Tracking Utilizing Antibiotic Resistance Analysis

4.1 Introduction

In order to properly address the fecal coliform TMDL for the Whippany River it is necessary to not only model the sources and absolute loads of fecal coliform but to also validate the sources so proper best management practices can be utilized.

In order to validate the source areas modeled using GWLF Princeton Hydro, in conjunction with Monmouth University, employed microbial source tracking (MST) analysis using the Antibiotic Resistance Analysis (ARA). The following sections provide a brief introduction into fecal coliform source tracking, methodology and results. The introductory text, methodology and data analysis for the MST portion of this project were conducted by *Witty, et al.* (2010).

Microbial Source Tracking (MST) is a general term which refers to several techniques with promise for determining the sources of fecal pollution in aquatic ecosystems. MST uses characteristics of microorganisms that are associated with particular hosts and assumes that humans and animals have host-specific or host-adapted strains of Escherichia coli or other indicator bacteria (Edge and Schaefer, 2006; Stoeckel, 2005; USEPA, 2005a-b). Three approaches to MST are well characterized: genetic profiling, phage typing and antibiotic resistance analysis (ARA).

Phage typing is based on identifying the F^+ coliphages which infect *E. coli*. There are four types of these bacteriophages: two human associated strains, one animal associated strain, and one strain associated with both humans and animals. The disadvantage of phage typing is that it only discriminates between human and nonhuman sources; it does not distinguish among different animal host species (e.g., cows, ducks, cats, raccoons) (USEPA, 2005a).

The concept exploited by genetic MST is that strains of *E. coli* in the guts of, for example, geese will have identifiable genetic differences to the *E. coli* strains from humans or various other forms of wildlife. Molecular genetic techniques can be used to detect these differences in bacterial DNA. These include pulsed-field gel electrophoresis (PFGE), ribotyping and repetitive element sequence-based polymerase chain reaction (rep-PCR). For all these methods bacterial DNA samples are obtained from environmental samples then analyzed to produce a genetic profile for that particular strain of bacteria. Results are compared to profiles in a library of bacterial strains from known host species (USEPA, 2005a).

Antibiotic Resistance Analysis (ARA) is a phenotype library-based MST method developed for microbial source tracking. It uses the assumption that bacteria from the guts of humans and other animals have different antibiotic resistance profiles. We assume the antibiotic resistance profiles differ because humans and other animals are exposed to different antibiotics treatments and will develop varying resistance to those antibiotics (Atherholt, 2005: USEPA, 2005a). ARA can target *E. coli*, fecal streptococci or *Enterococcus* sp.

Previous experience, including the creation of an extensive library of antibiotic resistance (AR) profiles for bacteria isolated from humans and various other animals, forms the basis of our ARA research. Specific, known fecal samples from organisms designated as important based on previous estimates of pollution in particular watersheds have been harvested and used to build our ARA library.

None of the methods for MST described above, including the ARA, is completely satisfactory. Genetic approaches generally give the most reliable results but, as with most molecular methods, are often prohibitively expensive. Antibiotic resistance and genetic profiling methods are both library-dependent, requiring a reference library or database of hundreds or even thousands of different bacteria strains collected from host species in the region under investigation. With both these approaches, it is fairly common to either find no match or to find too many matches (i.e., pattern overlap). Because of this, matches are not always completely clear and must be cross-referenced with other types of information or data.

Therefore MST/ARA is not an exact science and provides a survey of many samples rather than intensive analysis of one strain. When combined with statistical analysis it provides a coherent picture of the whole watershed. Because it creates a broad picture this method greatly expands our ability to better identify sources of fecal related contamination and water quality impairments. This makes MST/ARA particularly useful in prescribing remedial actions that specifically address these sources when developing watershed based pollutant load reduction plans.

The foundation of this MST work is a library of AR profiles from *E. coli* strains that were isolated from humans and various other animals. Monmouth University developed this AR profile library during research activity conducted in Monmouth and Ocean Counties from 2000-2003. The *E. coli* library was developed from isolates of twenty host species from coastal watersheds in the region. The hosts included in this database were selected because of their potential contribution to bacterial loadings in Monmouth and Ocean County watersheds.

4.2 MST Methodology

Feces for 3 – 12 individuals of each species were collected and processed according to our established ARA procedures. This resulted in the creation of a searchable library (database) with AR profiles for over 5000 fecal *E. coli* isolates from the various host organisms targeted for study.

The resulting library was grouped into five categories (Table 4.1): humans, pets, farm animals, avifauna (birds), and non-avifauna (wild mammals). The AR profiles were categorized in this manner because: (1) the number of replicate fecal samples for some types of animals was limited; and (2) environmental factors can cause pattern overlap which results when AR profiles of multiple host species are similar. In addition, categorizing AR profiles into these groupings was essential for making accurate determinations of the relative contribution of each source group to water quality problems at specific sampling sites.

Table 4.1: ARA Library Categories

Category	**Species Included**
Humans	Humans only
Pets	Domestic and stray cats, domestic dogs
Farm Animals	Horses, pigs, cattle, chickens
Avifauna	Canada geese, gulls, mallard ducks, black ducks, brant, canvasback ducks
Non-avifauna	Raccoons, muskrats, skunks, opossum, deer, rats, mice

Single colonies of *E. coli* isolated from fecal samples were grown in the presence of twelve antibiotics (see below). The antibiotics were selected primarily because of their widespread applications in animals and humans, as well as their diverse mode of action and molecular target (Kaspar 1990). All were purchased from Sigma-Aldrich, St. Louis, MO and antibiotic plates used for ARA were less than 3 weeks old.

Fresh fecal samples or anal swabs from domestic animals, livestock, wild animals, and avifauna were collected into sterile Whirl-Pak bags. In order to develop resistance patterns for humans in the watershed, grab samples of sewage treatment plant influent were collected in sterile 500 ml Nalgene bottles. Samples were kept in a cooler with ice and delivered to the lab for processing and ARA testing within 6 hours after collection. In the laboratory, fecal and influent samples were processed according to established guidelines for culturing fecal *E. coli* in wastewater samples (APHA, 1998) as follows:

Approximately 100-500 mg of the fecal or influent sample were suspended in 10-50 ml of multiple antibiotic resistance (MAR) saline (8.5 g NaCl, 0.3 g KH_2PO_4, and 0.6 g Na_2HPO_4 per liter at pH 7.3) and vortexed until the sample was thoroughly mixed. The salinity of MAR saline (8 ppt) approximates the salinity of brackish estuarine waters. After allowing particulate material to settle to the bottom of the culture tube, approximately 3-25 ml (depending on the fecal sample) of the mixture was filtered though a 0.45 μm pore-size GN-6 filter (Gelman Laboratory, Ann Arbor, MI). Using sterile forceps, the filter was transferred to a 15 × 60 mm culture plate containing mTEC agar. Plates were incubated at 35°C ± 0.5ºC for 2 hours, then sealed in a Whirl-Pak® bag and placed on a rack in a 44.5°C ± 0.2ºC water bath for 22-24 hours.

Following isolation, clones of *E. coli* isolated from fecal samples for each target species were subjected to ARA testing according to our established guidelines and procedures adapted from Parveen *et al.* (1997) and Wiggins *et al.* (1999) which are outlined below.

Lactose-fermenting (blue) colonies from mTEC agar plates were picked with sterile micropipette tips and used to inoculate individual wells of a 96-well plate containing 200 µl aliquots of Trypticase Soy (T-Soy) broth. Whenever possible, 48 independent isolates were used. Multiwell plates were incubated in an environmental chamber at 35°C overnight. T-Soy agar antibiotic plates (105 × 15 mm) were prepared by adding the desired amount of antibiotic to T-Soy agar cooled to 50°C:

Table 4.2: ARA Library Categories

Antibiotic	**Dose (µg/ml)**
ampicillin	40
amoxicillin	15
chlortetracycline	25
kanamycin	25
nalidixic acid	25
neomycin	50
oxytetracycline	25
penicillin G	75
streptomycin sulfate	15
sulfathiazole	750
tetracycline	25
vancomycin	10

Using a 48-prong stainless steel replica plater, *E. coli* isolates were replica plated from multiwall plates onto two control plates, one of T-Soy agar and one of T-Soy agar containing 100 µg/ml of 4-methylumbelliferyl-β-D-glucuronide (MUG; Sigma), and each of the 12 T-Soy agar antibiotic plates.

Controls for antibiotic activity were used. All plates were streaked with cells from a fresh overnight culture of *E. coli* (American Type Culture Collection 9637 or JM109 *E. coli*) as a negative control (sensitive to all antibiotics except penicillin G and vancomycin) and *Pseudomonas aeruginosa* (85W1703; Ward's, Rochester, NY) as a positive control (resistant to all antibiotics except sulfathiazole, neomycin, and tetracycline). Plates were incubated in an environmental chamber at 35°C overnight.

MUG fluorescence was used to assay β-D-glucuronidase activity, which is typical of the *Enterobacteriaceae*. MUG activity and detergent resistance, i.e. growth of blue colonies on modified mTEC agar, was considered diagnostic for *E. coli*. MUG-positive *E. coli* isolates on T-Soy agar/MUG plates were verified by fluorescence under long-wave UV light. MUG-negative isolates were not scored. To further verify the presence of gram-negative bacteria, fecal isolates were periodically subjected to Gram-staining with *E. coli* and *P. aeruginosa* as controls.

Upon completion of sample processing, isolates were scored as antibiotic resistant if colony diameter and growth on an antibiotic plate was indistinguishable from growth on T-Soy, and T-Soy + MUG plates. Any colonies showing more than 15% reduction in size were scored as sensitive.

Scores were tallied on standardized ARA scoring sheets that were developed for our studies. Once scored, ARA patterns were identified. ARA indices (number of antibiotics to which isolates were resistant ÷ total number of antibiotics tested) from individual organisms of a given species were recorded in Excel files and catalogued in a searchable database for use in comparing patterns obtained from water and sediment samples collected in local watersheds to our library of AR profiles.

AR patterns for each animal in the database were compared to the entire database to determine the average rate for correct classification (ARCC). The ARCC was calculated to determine the percentage of correctly and incorrectly classified isolates. This measure allows us to examine the feasibility of using the database to accurately identify the source of an unknown sample. Generally, ARCCs below 25% represent random classification and thus are inaccurate for identifying sources of fecal isolates.

As shown in Table 4.3, ARCCs for the four major categories of organisms studied were above the 25% level of random classification generally accepted for ARA analysis. In particular, the ARCC for humans was high (93.1%) suggesting that ARA analysis is a more specific tool for identifying human sources of fecal pollution than for determining specific animals sources of fecal pollution. ARCCs for other categories of animal species showed slightly lower values, which is not surprising given the number of pattern overlaps between species. Nonetheless, ARCCs for pets, farm animals, and wild animals were higher than 25%; therefore, the current ARA database does have sufficient specificity for categorizing unknown sources of fecal pollution as originating from humans, pets, farm animals, or wild animals.

Table 4.3: Average Rate of Correct Classification (ARCC) of Fecal *E. coli* Isolates by ARA

Source	Number of Isolates	ARCC (%)
Humans	475	93.1%
Pets	722	64.6%
Farm Animals	1215	81.1%
Wild Animals		
-Avifauna	1331	74.4%
-Non-avifauna	536	78.9%

Water Sample Processing

Surface water and sediment samples collected for ARA analysis were delivered to the Monmouth University lab by Princeton Hydro and processed according to USEPA Method 1603: *E. coli* in Water by Membrane Filtration Using Modified Membrane-Thermotolerant *E. coli* Agar (Modified mTEC) (USEPA, 2002) and then subjected to ARA testing according to the procedures adapted from Parveen *et al*. (1997) and Wiggins *et al*. (1999) outlined above.

Upon completion of the sample processing, *E. coli* isolates from these samples were also scored as antibiotic resistant or sensitive and scores were tallied using the standardized ARA scoring sheets developed for our MST studies. Once scored, AR profiles from the water and sediment samples were identified. AR indices (number of antibiotics to which isolates were resistant ÷ total number of antibiotics tested) for these samples were recorded in Excel files and catalogued in a searchable database for use in comparing profiles obtained from water and sediment samples collected in the watershed to the AR profiles in the fecal source library.

4.3 MST Data Analysis

Because up to 48 *E. coli* isolates were isolated from each water sample, large numbers of comparisons are needed to compare each to the 562 database types in the fecal source library (i.e. a calculation of 26,976 correlation coefficients). After consultation with software program designers to determine a suitable method for processing the large amount of statistical information generated for each sample, SYSTAT 11 software was selected (SYSTAT Software Inc.) to handle these data. SYSTAT 11 provides robust statistical analysis capabilities that provide meaningful results to large and complex data sets. Once analyzed, these data were used to develop profiles of the various sources of fecal contamination in the Whippany River watershed.

4.4 MST Results

The following tables (4.4 – 4.11) present the results of ARA analysis for the eight (8) stations sampled throughout the 2009 growing season.

Table 4.4: Station 1

Whippany: Station One								
Relative Abundance								
Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.3947	0.5	0.5	0.548	0.513	0.545	0.543	0.547
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0	0.029	0	0	0
Avifauna	0.447	0.1	0.12	0.09	0.124	0.091	0.095	0.098
Non-Avifauna	0.158	0.4	0.3	0.362	0.333	0.364	0.362	0.355
Unclassified	0	0	0	0	0	0	0	0

Table 4.5: Station 2

Whippany: Station Two								
Relative Abundance								
Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.1224	0.6	0.6	0.529	0.508	0.541	0.527	0.518
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0	0	0	0	0
Avifauna	0.796	0.1	0.19	0.1	0.139	0.09	0.106	0.136
Non-Avifauna	0.082	0.4	0.3	0.371	0.353	0.369	0.367	0.332
Unclassified	0	0	0	0	0	0	0	0.014

Table 4.6: Station 3

Whippany: Station Three

Relative Abundance

Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.2273	0.1	0.53	0.535	0.523	0.447	0.47	0.533
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0	0	0	0	0.025
Avifauna	0.618	0.5	0.14	0.097	0.115	0.216	0.22	0.128
Non-Avifauna	0.155	0.4	0.3	0.367	0.363	0.306	0.297	0.312
Unclassified	0	0	0.03	0	0	0.031	0.014	0.002

Table 4.7: Station 4

Whippany: Station Four

Relative Abundance

Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.3896	0.5	0.63	0.541	0.545	0.395	0.574	0.538
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0.01	0	0	0	0	0
Avifauna	0.351	0.1	0.16	0.175	0.091	0.282	0.101	0.134
Non-Avifauna	0.26	0.4	0.19	0.311	0.364	0.323	0.311	0.328
Unclassified	0	0	0.01	0	0	0	0.014	0

Table 4.8: Station 5

Whippany: Station Five

Relative Abundance

Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.2017	0.6	0.6	0.209	0.533	0.348	0.234	0.532
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0	0	0	0	0
Avifauna	0.655	0.1	0.23	0.07	0.102	0.362	0.234	0.124
Non-Avifauna	0.134	0.3	0.2	0.023	0.364	0.188	0.085	0.343
Unclassified	0.008	0	0	0.698	0	0.101	0.447	0

Table 4.9: Station 6

Whippany: Station Six								
Relative Abundance								
Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.4271	0.5	0.5	0.535	0.535	0.322	0.597	0.534
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0.003	0	0	0	0
Avifauna	0.312	0.1	0.19	0.102	0.104	0.483	0.117	0.117
Non-Avifauna	0.261	0.4	0.3	0.358	0.361	0.187	0.233	0.349
Unclassified	0	0	0	0.003	0	0.009	0.083	0

Table 4.10: Station 7

Whippany: Station Seven								
Relative Abundance								
Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.5733	0.5	0.5	0.542	0.545	0	0.313	0.461
Pet	0	0	0	0	0	0	0	0
Farm Animal	0	0	0	0	0	0	0	0.025
Avifauna	0.134	0.1	0.17	0.09	0.099	0	0.461	0.141
Non-Avifauna	0.293	0.4	0.3	0.365	0.357	0	0.227	0.274
Unclassified	0	0	0	0.002	0	1	0	0.1

Table 4.11: Station 8

Whippany: Station Eight								
Relative Abundance								
Event	1	2	3	4	5	6	7	8
Species	7/18/2009	8/10/2009	8/22/2009	8/29/2009	9/4/2009	9/6/2009	9/19/2009	10/20/2009
Human	0.0706	0.5	0.6	0.545	0.532	0.361	0.179	0.46
Pet	0	0.4	0	0	0	0	0	0
Farm Animal	0	0	0	0.003	0	0	0	0
Avifauna	0.882	0.1	0.12	0.086	0.101	0.398	0.679	0.107
Non-Avifauna	0.047	0	0.2	0.366	0.363	0.241	0.143	0.273
Unclassified	0	0	0	0	0.004	0	0	0.16

4.5 Discussion

The most important components to fecal pollution in the Whippany River watershed are Human and Non-avifauna. Avifauna were low contributors, except in July and early September. Pet and Farm Animals were very minor contributors.

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Human pollution increased slightly over the summer and Non-Avifauna correspondingly decreased. The detection of human sources of fecal pollution is cause for concern. High levels of enteric pathogens such as *E. coli* are potential public health hazards (Erkenbrecher 1981; LaLiberte and Grimes 1982). While most isolates of *E. coli* are benign, there is a relationship between *E. coli* levels and other important pathogens that come from the same source. Therefore, even when benign *E. coli* are detected we must suspect the presence of a number of other pathogenic strains. This is a feature of fecal pollution that is consistently confirmed in traditional and advanced studies (Savichtcheva *et al.,* 2007). Harmful microbes often associated with fecal pollution from human sources can include pathogenic strains of *E. coli* and *Salmonella* which may cause gastroenteritis with varying degrees of severity.

Non-avian wild animal species such as raccoons, opossum, muskrats, and deer are common in this watershed. While fecal contributions from wild animals are generally considered less of a concern in terms of human health, wildlife feces has been identified as a potential source of *E. coli* (Somarelli *et al.* 2007), *Campylobacter,* and *Salmonella* pollution (Lillehaug *et al.* 2005). Many species of wildlife are also carriers of other bacterial and protozoan diseases. However, because humans do not live in close association with wild animals in the watershed and are not responsible for their veterinary care, we are much less aware of their pathologies. Therefore, wildlife must be categorized as a source of unknown or poorly quantified threats; nevertheless, a source that should be dealt with through implementation of appropriate BMPs. As shown through the AVGWLF modeling efforts, wildlife source of bacteria loading are particularly important within the Whippany River watershed (See Section 2, Table 2.11).

Avifauna pollution had a strong peak in July for all stations except 7 and Stations 4-8 had a second peak in early September, suggesting that flocks moved during those times. A concern for this watershed is pathogen contributions attributable to large flocks of waterfowl such as Canada geese, as well as various species of ducks. Given the number of corporate campuses, parks, small lakes/ponds, detention/retention basins, golf courses and ball fields occurring within the Whippany River watershed one can easily understand how avifauna loading becomes an issue of concern. The severity of the problem increases where large flocks of geese and ducks roost near waterbodies used for human activities, such as contact recreation. For example, Canada geese can transfer harmful bacteria in their feces including pathogenic *E. coli* (Hussong *et al.* 1979) and *Salmonella* (Feare *et al.* 1999). Geese also carry host adapted *Cryptosporidium* (Zhou *et al*. 2004), a human gut parasite. Waterfowl are also an important reservoir for avian influenza virus (Hanson *et al.* 2005). Pigeons are a reservoir for pathogenic strains of *E. coli* and many other diseases (Haag-Wackernagel and Moch, 2004; Haag-Wackernagel 2005) and may exchange them with cattle (Pedersen *et al*. 2006). Pigeons and mallard ducks are a reservoir for *Campylobacter* (Kobayashi *et al*. 2002).

While avifuana were not a significant contributor of pollution on a watershed scale they are likely a localized, discrete source of pollution at preferential habitats (i.e. stormwater retention basins, ponds and lakes associated with ample lawn areas). There is ample evidence in the form of actual observations as well as a long history of WRWAC water quality monitoring events documenting such impacts. As such, while the ARA data may not necessarily suggest an avifuauna problem of significant magnitude, this pathogen source cannot be overlooked or disregarded.

5.0 Fecal Coliform Source Area Comparison – AVGWLF and ARA Analysis

In order to properly assess the absolute load and source areas of fecal coliform loading to the River Princeton Hydro employed a multi-faceted approach consisting of field monitoring, ARA analysis and computer based watershed modeling (AVGWLF). While each of these methods has certain limitations, their strengths may be collectively utilized to provide relatively accurate insight into the sources of fecal coliform loading throughout the watershed. While historical concentration data has provided the scientific documentation that the River suffers from elevated fecal coliform concentrations there has been no strong evidence towards the source of elevated loadings. Historically, reports which have documented fecal coliform loading to the River have utilized a simplistic ratio of fecal coliform to fecal streptococci (FC/FS) to indicate possible source areas. While this method has been frequently utilized due to its low cost the accuracy of this metric is low. Limitations of the FC/FS method are as follows (Oram 2010):

- Bacterial concentrations can be greatly variable if the pH is outside of a 4-9 range,
- The faster die-off rate of fecal streptococci will alter the ratio as time from contamination increases,
- Pollution from several sources may alter the ratio,
- Ratios should not be used when FS counts are less than 100/100 mL.

An important component of source identification lies in the correlation of source areas through the utilization of data obtained from modeling and ARA analysis. Before such a comparison is made it should be noted that each of these methods have their limitations. As stated above, ARA analysis techniques are highly dependent on the accuracy and spatial representativeness of the library which is utilized to back reference samples. The AVGWLF model inherently lacks the ability to produce highly accurate results on a small temporal or spatial scale due to the complexity of watershed scale loading. Furthermore, modeling fecal coliform is inherently complex as it is a living organism and no single model can predict the complex factors of fate and transport coupled with biological factors such as reproduction and mortality.

With the knowledge of the aforementioned limitations one can objectively utilize both ARA methods and the AVGWLF model results to derive a reasonably accurate prediction of fecal coliform sources throughout the Whippany River watershed.

In order to parse out source areas Princeton Hydro compared the output of AVGWLF and ARA results at sampling Station 8. This station represents the most downstream point in the watershed and correlates with the aggregate watershed analysis conducted utilizing AVGWLF. Percent loadings derived from ARA analysis at Station 8 is presented in Figure 5.1 while mean source area loadings are presented in Table 5.1.

Figure 5.1: Station 8 – ARA Sources

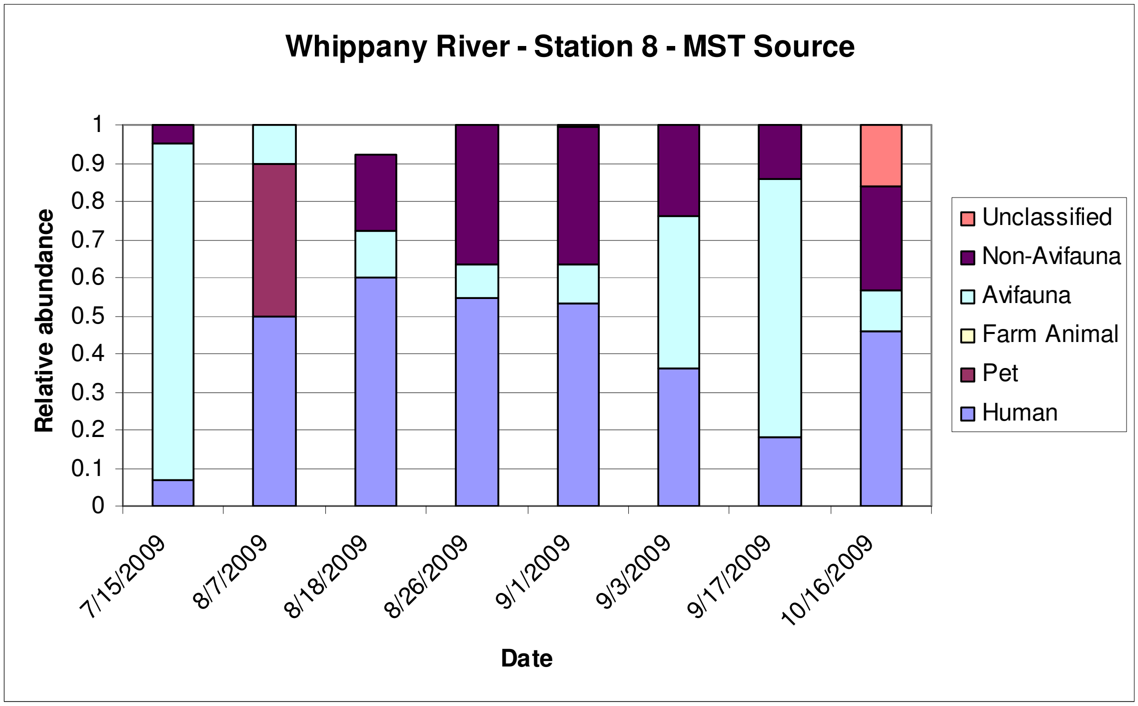

Table 5.1: Station 8 – ARA Sources

Station 8 – Mean ARA Sources						
Human	Pet	Farm Animal	Avifauna	Non-avifauna	Unclassified	Wildlife*
40.6%	5.0%	0%	30.9%	20.4%	2.1%	51.3%

*Sum of Avifauna and Non-avifauna

Of the 8 sampling events conducted from July through October 2009, seven were under baseflow conditions with the October 16th event representing stormflow conditions. Wildlife were the predominate sources of fecal loading to Station 8, representing 51.3% of the load. Of the wildlife loads, Avifauna were a greater source area than non-avifauna; representing 30.9% of the load. It should be mentioned that wildlife loads were skewed by the July 18th event which was characterized by an avifauna relative abundance of 0.882. Humans represented the second greatest source of fecal loading to the river, representing 40.6% of the cumulative load.

AVGWLF source output, when modeled as an aggregate over a seven year period, are presented in Table 5.2.

Table 5.2: AVGWLF Aggregate FC Sources

AVGWLF Aggregate Model – FC Sources

Farm Animals*	WWTP	Septic	Urban Areas	Wildlife
0%	0.1%	43.8%	0.2%	55.9%

* “Farm Animals” is a default category name in AVGWLF. For modeling purposes, “Farm animals” represent Canada geese (*Branta canadensis*).

Results generated from AVGWLF modeling indicate that wildlife are the greatest source of fecal coliform loading to the River, accounting for 55.9% of the entire load. Geese, which were modeled separately, and listed as “Farm Animals” under AVGWLF’s default naming structure, represented a negligible portion of the source load on a watershed wide scale. Human sources of fecal coliform are primarily represented by Septic, Wastewater Treatment Plants and Urban Areas. Fecal coliform derived from Septic sources represented 43.8% of the total load and is therefore the greatest manageable source of fecal coliform in the watershed.

6.0 Fecal Coliform Load Comparisons – AVGWLF Load versus Field Data

6.1 Introduction

In addition to analyzing the relative contributions of fecal coliform from various source areas to the River it is necessary to evaluate the modeled fecal coliform concentrations to measured concentrations. In doing so we may assess the applicability of the model in evaluating absolute load reductions from various best management practices. For this analysis Princeton Hydro reviewed the field collected data throughout the watershed under base and storm flow conditions versus that which was modeled utilizing AVGWLF. Specifically, field collected data from Station 8 was utilized as a basis of comparison to that of the AVGWLF aggregate model as both of these methods utilized the same sampling/modeling location and therefore allowed for spatial accuracy.

In order to objectively compare modeled and field data it is necessary to point out the strengths, weaknesses and sources of uncertainty in the data and model results.

First, nine field monitoring events were conducted; only one of which was under storm flow conditions. In addition, these events were conducted from 25 June 2009 through 16 October 2009. As such, there is inherent bias in evaluating the field data due to a skewed distribution of field data towards certain hydrological conditions (i.e. baseflow) and seasonality (i.e. summer). Specifically, 88.9% of the monitoring events were conducted under base flow conditions and therefore over represent base flow fecal coliform concentrations. Furthermore, sampling consisted of discrete "grab" samples and therefore only represents the concentration of fecal coliform in the water column during the discrete time of sampling (i.e. seconds). Finally, fecal coliform sampling was conducted only in the summer and may serve to over-estimate annual loadings due to environmental conditions which favor the reproduction and proliferation of fecal coliform.

In contrast, AVGWLF modeled fecal coliform loading from 2000 – 2007. The output from this period is a monthly mean concentration of fecal coliform averaged over the seven year period. As such, AVGWLF represents a long term mean but does not have the ability to provide the same level of spatial and temporal refinement which is achieved by field based sampling. Some of this uncertainty may be minimized through additional analysis of historical fecal coliform sampling conducted during the Whippany River Sanitary Survey (Van Orden 2004) but special care has to be taken to compare samples at similar spatial scales. Specifically, comparisons must be made at sampling stations which correlate with modeled sub-watershed endpoints.

6.2 Results and Conclusions

In order to provide some basis of comparison with modeled and field concentrations Princeton Hydro analyzed the mean fecal coliform concentrations from June through September from field data and the output results from AVGWLF. Mean fecal coliform concentrations measured at Station 8 during this time period (n = 7) was 618.5 cfu / 100 ml while the mean concentration outputted from AVGWLF was 424.6 cfu / 100 ml. While this analysis indicates that AVGWLF under-represents fecal coliform care must be taken in viewing these results in the context that only seven field samples were collected over a four month time period; all of which were collected under base flow conditions. Further correlation analysis of field versus modeled concentrations may be obtained through additional sampling over a greater range of hydrologic and seasonal regimes and may therefore offer a larger degree of power in statistical analysis.

Overall the AVGWLF, field data and ARA should be evaluated and used as follows. The AVGWLF data is best used as a means of quantifying the magnitude of pathogen loading and related problems. The data generated through the modeled approach are not biased by seasonal, sample collection problems, or sample size (i.e., number of samples). As such, these data are best suited for the overall evaluation and quantification of pathogen and pollutant loading problems. Similarly, these data are suitable for use in the prioritization of watershed management and related corrective measures and the subsequent quantification of the anticipated improvements. The field data, while limited by temporal and sample size related factors, does provide a very good means of assessing both site-specific and time-specific pathogen problems. These data can also be directly compared to the WRWAC historic database and of course the NJDEP surface water quality standards (NJAC 7:9B). Finally, although the ARA data has the most limited utility it was valuable in confirming some of the findings of the AVGWLF data as well as highlighting differences in fecal loading in the upper versus lower sections of the Whippany River watershed. As such, as was intended, the three data sources, while very different in scope and utility, provide a more complete overview of pathogen related water quality issues in the watershed, especially with respect the identification and prioritization of sources.

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Appendix A
Water Quality Data

Whippany River - 6/25/09 - Baseflow							
	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	14.28	0.369	9.09	7.42	88.5	85	52
2	16.74	0.292	8.60	7.51	88.0	500	96
3	16.88	0.375	7.81	7.32	80.4	360	132
4	18.09	0.440	8.30	7.13	87.6	240	104
5	21.04	0.533	7.70	7.33	86.7	300	116
6	21.85	0.422	2.20	7.03	30.1	156	136
7	21.94	0.686	8.27	7.59	94.1	340	196
8	21.04	0.497	4.71	7.00	52.6	680	560

Whippany River - 7/15/09 - Baseflow							
	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	13.68	0.400	9.90	6.85	96.8	300	250
2	15.21	0.324	8.87	7.32	89.7	320	192
3	16.23	0.405	8.63	7.61	86.8	380	300
4	17.80	0.519	9.10	7.54	96.2	180	140
5	19.59	0.613	8.95	7.66	98.2	340	232
6	20.15	0.820	6.23	7.45	69.8	650	450
7	21.01	0.709	8.20	7.75	93.3	450	224
8	20.73	0.689	8.28	7.67	93.6	248	200

Whippany River - 8/7/09 - Baseflow							
	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	15.06	0.394	9.35	7.42	93.7	450	360
2	17.06	0.317	8.07	7.36	84.7	640	520
3	18.06	0.387	7.23	7.63	77.4	600	520
4	18.23	0.492	7.75	7.51	84.8	480	400
5	20.62	0.582	8.51	7.59	95.6	1120	880
6	20.38	0.353	1.56	7.16	16.8	350	300
7	20.97	0.598	8.37	7.72	95	1040	760
8	20.67	0.456	4.8	7.62	50.6	1800	1450
8 dup	20.67	0.455	4.82	7.62	50.7	N/A	N/A

Whippany River - 8/18/09 - Baseflow							
	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	17.27	0.394	8.38	7.59	87.3	970	610
2	20.1	0.326	7.3	7.35	80.6	420	410
3	21.13	0.395	6.46	7.69	71.8	570	450
4	22.66	0.549	6.58	7.53	75.8	110	100
5	23.68	0.7	7.76	7.6	91.4	370	190
6	22.56	0.648	1.8	6.83	20.1	470	290
7	20.83	0.669	8.4	7.67	94	700	600
8	24.26	0.7	6.49	7.74	77.5	220	190
1 dup	17.27	0.394	8.4	7.6	87.3	N/A	N/A

Whippany River - 8/26/09 - Baseflow

	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	%DO	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	16.85	0.391	9.40	7.68	96.0	1380	1380
2	18.82	0.320	7.70	7.27	83.0	440	300
3	20.01	0.383	7.62	7.77	82.5	1000	440
4	20.97	0.512	7.44	7.60	83.2	210	100
5	22.34	0.590	8.32	7.67	95.4	800	100
6	22.09	0.347	1.68	6.96	18.8	580	240
7	21.02	0.626	8.58	7.71	96.5	880	340
8	22.26	0.492	5.05	7.45	57.9	860	260
7 DUP	21.02	0.625	8.57	7.70	96.5	N/A	N/A

Whippany River - 9/1/09 - Baseflow

	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	%DO	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	13.36	0.391	9.82	7.73	93.8	500	540
2	15.05	0.335	8.48	7.72	84.2	160	220
3	15.96	0.400	7.65	7.70	76.2	560	240
4	17.36	0.529	7.32	7.72	75.1	100	140
5	18.21	0.622	8.98	7.69	95.2	260	200
6	16.60	0.560	2.68	7.34	27.3	1280	880
7	16.50	0.662	9.57	7.89	97.9	260	240
8	18.31	0.645	7.66	7.73	81.3	420	200
4 DUP	17.35	0.529	7.3	7.72	76.2	N/A	N/A

Whippany River - 9/3/09 - Baseflow

	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(℃)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	13.43	0.394	10.17	7.67	96.3	1900	1840
2	14.62	0.338	9.02	7.63	88.7	307	280
3	15.36	0.408	8.23	7.78	80.5	700	330
4	16.91	0.564	7.69	7.69	78.5	210	67
5	18.21	0.671	9.20	7.73	97.1	330	190
6	16.31	0.602	3.10	7.48	33.0	533	540
7	16.19	0.696	9.72	7.99	100.1	240	90
8	18.31	0.716	8.08	7.53	85.7	260	130
1 DUP	13.43	0.394	10.17	7.67	96.3	N/A	N/A

Whippany River - 9/17/09 - Baseflow							
	IN-SITU (GRAB)					DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	FC	EC
	(°C)	(mS/cm)	(mg/L)	(units)	(%)	(cfu / 100 ml)	(cfu / 100 ml)
1	13.00	0.396	10.05	7.62	95.0	933	533
2	15.02	0.346	8.46	7.74	83.3	230	230
3	15.43	0.411	8.23	7.16	82.0	340	270
4	16.39	0.578	7.34	7.68	74.2	165	76
5	17.18	0.692	9.23	7.78	95.0	320	120
6	15.84	0.794	3.75	7.54	38.3	720	280
7	15.00	0.678	9.89	8.08	98.1	230	108
8	16.94	0.736	7.98	7.66	82.4	460	132
3 DUP	15.43	0.410	8.23	7.15	82.0	N/A	N/A

Whippany River - 10/16/2009 - Storm								
	IN-SITU (GRAB)						DISCRETE (GRAB)	
ID	TEMP	SP COND	DO	PH	DO%	TURBIDITY	FC	EC
	(°C)	(mS/cm)	(mg/L)	(units)	(%)	(ntu)	(cfu / 100 ml)	(cfu / 100 ml)
1	6.19	0.325	10.70	7.69	85.0	7	620	400
2	7.12	0.287	10.02	8.19	82.0	3.2	800	560
3	7.10	0.295	9.45	8.12	77.0	5.2	5100	3000
4	7.48	0.393	10.12	7.96	83.0	3.9	1500	1500
5	9.46	0.895	10.22	7.86	88.0	14.2	840	460
6	7.58	0.348	6.58	8.56	54.0	88.2	4900	3900
7	8.42	0.441	10.66	8.05	90.0	9.1	1400	1000
8	8.34	0.491	9.17	8.01	77.0	13.1	2200	1200