VIRGINIA WATER RESOURCES RESEARCH CENTER

BACTERIA TOTAL MAXIMUM DAILY LOAD ISSUES: REPORT OF THE BACTERIA TMDL SUBCOMMITTEE

OF THE

WATER QUALITY ACADEMIC ADVISORY COMMITTEE

SPECIAL REPORT

VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY
BLACKSBURG, VIRGINIA

2004

This special report is a publication of the Virginia Water Resources Research Center and was published with funds provided in part by the Virginia Department of Environmental Quality. The contents of this publication do not necessarily reflect the views or polices of the Virginia Department of Environmental Quality or the Virginia Water Resources Research Center. The mention of commercial products, trade names, or services does not constitute an endorsement or recommendation.

Additional copies are available while the supply lasts and may be obtained from the
Virginia Water Resources Research Center
23 Agnew Hall
Blacksburg, VA 24061
(540) 231-5624
FAX: (540) 231-6673
e-mail: water@vt.edu
homepage address: http://www.vwrrc.vt.edu

Single copies are free to Virginia residents.

Tamim Younos, Interim Director

BACTERIA TOTAL MAXIMUM DAILY LOAD ISSUES:
REPORT OF THE BACTERIA TMDL SUBCOMMITTEE OF THE WATER QUALITY ACADEMIC ADVISORY COMMITTEE

**Prepared for the
Virginia Department of Environmental Quality,
Division of Water Quality Programs**

Theo Dillaha (Chair)
Department of Biological Systems Engineering
Virginia Tech

Carl Hershner
Resource Management and Policy
Virginia Institute of Marine Science

Howard Kator
Biological Sciences
Virginia Institute of Marine Science

Saied Mostaghimi
Department of Biological Systems Engineering
Virginia Tech

Leonard A. Shabman
Virginia Water Resources Research Center
Virginia Tech

Eric P. Smith
Department of Statistics
Virginia Tech

Tamim Younos
Virginia Water Resources Research Center
Virginia Tech

Carl E. Zipper
Department of Crop and Soil Environmental Sciences
Virginia Tech

Virginia Water Resources Research Center
23 Agnew Hall
Virginia Tech
Blacksburg, VA 24061

October 2002

VWRRC Special Report No. SR 24-2004

TABLE OF CONTENTS

Bacteria Total Maximum Daily Load Issues: Report of the Bacteria TMDL Subcommittee of the Water Quality Academic Advisory Committee

Introduction

In the 1997 *Water Quality Monitoring, Information and Restoration Act (WQMIR)*, the Virginia General Assembly directed the Virginia Department of Environmental Quality (DEQ) to develop the EPA-required 303(d) and 305(b) reports in consultation with experts from the state's universities. Also, the WQMIR requires the DEQ to "develop and publish a procedure governing its process for defining and determining impaired waters and shall provide for public comment on the procedure" with the assumption that these 303(d) procedures will be developed after consultation with scientists from the state's universities. To meet the WQMIR academic consultation requirements, DEQ asked the Virginia Water Resources Research Center (VWRRC) to organize and coordinate a Water Quality Academic Advisory Committee (AAC) as an independent advisory body.

In 1997-1998, the AAC reviewed and evaluated the scientific merits of the DEQ's existing and evolving water quality assessment procedures for the 305(b) and 303(d) reports. The AAC's 1997-1998 findings submitted to DEQ are documented in VWRRC Special Report No. SR-8-1998. In 1999-2000, the AAC addressed topics of concern to the DEQ in three general areas: issues relating to biological monitoring protocols, modeling techniques and other methods relating stressor to benthic degradation and fecal contamination, and water quality goals and setting water quality standards. The report of the AAC to DEQ for years 1999 and 2000 is VWRRC Special Report No. SR18-2000. Electronic copies of the special reports are available from the VWRRC Website: www.vwrrc.vt.edu.

The Water Quality Academic Advisory Committee work effort for 2001-2002 is a logical extension of the previous work efforts. The fiscal year 2002 work plan was organized around a review of and report on water quality standards and the assessment of their attainment. See Appendix A for a list of the 2002 AAC members. This report summarizes the efforts of the AAC subcommittee's response to bacteria total maximum daily load (TMDL) issues.

Purpose

The responsibility of the AAC subcommittee on bacteria TMDLs in 2001-2002 was to address specific issues raised by DEQ related to the scientific merits of Hydrological Simulation Program--Fortran (HSPF) modeling, bacteria source tracking (BST), and TMDL development using the flow duration/BST approach (also referred to as the cheaper-better-faster or CBF approach).

Procedures

The AAC subcommittee on bacteria TMDLs held a workshop on February 22, 2002 in Charlottesville, Virginia with 18 experts on BST and TMDL development to discuss issues related to the development of bacteria TMDLs and the use of BST in TMDL development in Virginia. The workshop participants (Appendix B) discussed DEQ's questions concerning bacteria TMDL issues (Figure 1) and helped the AAC members develop responses to DEQ's questions.

I. – Questions about HSPF Modeling

1. What is the best way to use truncated and minimum concentration data during model calibration and validation?
2. What is the best way to represent fecal coliform (FC) concentrations during storm recessions?
3. What is the best way(s) to represent unknown source inputs that contribute significantly to the bacteria load during base flow conditions?
4. How reasonable is it to keep fecal production rates constant throughout the state for humans, livestock, and wildlife?
5. In general, how much flexibility do we need in fecal production rates to allow for reasonable calibrations and still maintain some statewide consistency?
6. In terms of addressing the impairment, what should be the time step of the geometric mean calculation, 720-hour geometric mean, 30-day geometric mean of daily average, 30-day geometric mean of daily median, *etc.*?
7. Recommendations for consistency in model (HSPF) application.

II. – Questions about Bacteria Source Tracking (BST)

1. What are the uses of BST in TMDL development?
2. What spatial distribution and number of samples are required for watershed characterization/source assessment using BST?
3. What is the utility of and conditions for effective BST use as a HSPF model calibration tool compared to traditional calibration/land use approaches with HSPF?
4. Should model calibration be to land use loading or measured BST?
5. What is the proper role of BST in TMDL development?
6. How can the usefulness of BST for TMDL development and implementation be enhanced?

III. – Questions about TMDL Development Using the Flow Duration/BST (or the CBF) Approach

1. Is the BST/flow duration approach a suitable (defensible and approvable) method for fecal coliform TMDL development?
2. Which is the preferred method for fecal coliform TMDL development? The flow duration/BST approach or the HSPF/land use approach?
3. How can the flow duration/BST approach be improved?

Figure 1. DEQ Questions for the AAC.

I. – Questions about HSPF Modeling

HSPF 1. – What is the best way to use truncated and minimum concentration data during model calibration and validation?

Procedures used by the DEQ's ambient water quality program for fecal coliform enumeration were designed to determine if waters exceed the state water quality standard of 1000 colony forming units per 100 milliliters water (1000 cfu/100mL) but were not designed for absolute enumeration of fecal coliform counts. Consequently, samples were diluted according to standard methods to enumerate counts in the range of 100 to 8,000 or 100 to 16,000 cfu/100mL. As a result, coliform counts less than 100 are recorded as 100, and counts greater than the upper limit are recorded as 8,000 or 16,000. This approach presents a problem during calibration of models used for development of fecal coliform TMDLs because predicted model peaks and sweep samples with higher dilutions often exceed the truncated ambient water quality values by one to three orders of magnitude. There is a similar problem with values below the lower detection limit, as the model predictions and sweep sample results are often less than the lower detection limit. Thus, it is impossible to determine if the models are accurately predicting fecal coliform concentration outside of the range of 100 to 8,000 or 16,000 cfu/100mL.

There is no good way to calibrate the models used for TMDL development using truncated values. To facilitate the Virginia TMDL program, the DEQ should immediately increase the dilution range used in its bacterial monitoring program. Initially, the range should be 1 to 1,000,000 cfu/100mL, but as the DEQ collects data at each ambient water quality monitoring station and defines the observed range for each station, the required dilution range can be decreased. Until adequate improved data are collected for TMDL development and implementation purposes, the AAC recommends that truncated data be used as follows.

- During model calibration, the frequency of simulated daily fecal coliform values should be equal to or slightly greater that the fraction of observed values that exceed the upper detection limit. Similarly, if there is a lower detection limit, the frequency of simulated values below the detection limit should be approximately equal to the frequency of measured values below the lower detection limit.

- Simulated concentrations should be at or above high-truncated concentrations and at or below minimum concentration values during visual calibration.

- Truncated data should not be assumed to be the maximum or minimum concentrations. They should be viewed as minimum concentrations for high concentration periods and maximum concentrations for low concentration periods during calibration.

- Supplemental sampling during TMDL development is desirable to identify expected site-specific peak values. Supplemental sampling should be conducted during periods with stormwater runoff. During calibration, the model should be calibrated so that predicted hourly fecal coliform concentrations are "in the range" of the sweep values during similar simulated flow conditions.

HSPF 2. – What is the best way to represent fecal coliform (FC) concentrations during storm recessions?

There are concerns that the HSPF model, as used in the development of fecal coliform TMDLs in Virginia, under represents fecal coliform concentrations during storm recessions because it does not simulate the expected release of fecal coliform bacteria from benthic sediment during flow events. Until recently, there was no way to determine if HSPF under represented recession concentrations because systematic monitoring had not been conducted during storm flow periods. During the U.S. Geological Survey's (USGS) Accotink Creek, Blacks Run, and Christians Creek TMDL studies, the USGS measured fecal coliform concentrations during the hydrograph rising and recession limbs of runoff events. According to the USGS, fecal coliform concentrations dropped slowly during the recession limbs of monitored hydrographs. The USGS reported that they increased predicted concentrations during the recession limb to better match observed concentrations by inflating simulated fecal coliform concentration in groundwater and interflow. Because the USGS data have not been released for external review (as of September 2002), it is not possible for the AAC to assess whether this simulated increase in fecal coliform concentration in groundwater and interflow is justified, but it may be a reasonable approach. The Virginia Tech TMDL Development Group performed a limited analysis of predicted fecal coliform concentrations during recession limbs. Fecal coliform concentrations obtained during the recession limbs of the simulated storms declined gradually as one would expect. In the absence of monitored recession limb concentrations, it appeared that HSPF did a reasonable job of simulating concentrations during the recession limb. Until data or research becomes available that provides evidence to the contrary, the ACC recommends that fecal coliform concentrations predicted by HSPF during recession limbs be assumed valid.

HSPF 3. – What is the best way(s) to represent unknown source inputs that contribute significantly to the bacteria load during base flow conditions?

All known TMDL developers to date have estimated direct deposition of fecal material in streams by livestock and wildlife as point source loads. This is reasonable. Typically, loads are varied monthly in response to changing populations and access to streams, and loading is constant for the month and does not vary during the 24-hour day. However, some evidence suggests that since many wild animals are nocturnal, direct deposits due to nocturnal wildlife should only be simulated as being deposited in streams at night. In contrast, waterfowl are generally active during the daytime, so their direct deposits should be simulated during the daylight hours. Livestock are more active during the daytime and are reported to avoid riparian zones during the night. Consequently, livestock deposits to streams should probably only be simulated during daylight hours. In other words, direct deposits to streams by wildlife and livestock should be varied daily according to the habits of the species considered. It is not known if varying loads throughout the 24-hour day will have a significant effect on model results (as compared to constant loads), but variable loads during the day are preferable because they more accurately reflect animal activity.

Release of fecal coliform bacteria from sediment during storms and base flow conditions is not typically simulated in TMDLs developed using HSPF. HSPF has the capability to simulate fecal coliform in both free (dissolved) and adsorbed phases if sediment transport is simulated, but experimental data do not exist to describe the equilibrium between free fecal coliform and fecal coliform adsorbed to sediment. In the Accotink Creek, Blacks Run, and Christians Creek TMDLs, release of fecal coliform from sediment during baseflow conditions was simulated by calibrating the fecal coliform concentration in groundwater (that is responsible for baseflow) to observed concentrations during baseflow. This approach is reasonable if sufficient fecal coliform data are available for calibration, but these data have only been available during the USGS study. If this approach is used, it is critical to understand that the calibrated baseflow concentrations represent the release of fecal coliform from sediment, and they do not represent fecal coliform in groundwater. Thus, if fecal coliform must be reduced during the TMDL, the reduction should be in "release from sediment" or the "sources that contribute to the sediment load," not to the groundwater load. Until research is conducted to better describe the equilibrium between free and sediment adsorbed fecal coliform and die-off rates for fecal coliform in sediment, the AAC recommends that fecal coliform continue to be modeled using the presently used free bacteria (dissolved) approach.

There are very limited data concerning fecal coliform concentrations in interflow and in the portion of groundwater that contributes to baseflow. Most groundwater data are from wells used for potable water, and these wells typically obtain water from deeper aquifers that are more protected from bacterial contamination. Thus, samples from wells probably underestimate the concentrations of fecal coliform in shallower groundwater that contributes to baseflow. Sampling of unprotected shallow wells and springs near streams probably provides a better estimate of fecal concentrations in groundwater contributing to baseflow. If springs are sampled to ascertain bacterial concentrations in shallow groundwater, it is preferable to sample protected springs where the concentrations will be representative of the groundwater quality rather than contamination of the groundwater after it surfaces. The AAC could find no information on bacterial concentrations in interflow, although it would be reasonable to assume that they are higher than those in groundwater. Until research is conducted to measure bacterial concentrations in interflow, the AAC recommends that interflow concentrations be 50% larger than the estimated groundwater concentrations.

HSPF 4. – How reasonable is it to keep fecal production rates constant throughout the state for humans, livestock, and wildlife?

The ACC's best professional judgment is that fecal matter production rates vary by a factor of one or two, and fecal coliform concentrations in excreted fecal material for a given species vary by two to four orders of magnitude (over time for a given individual and from individual to individual). Thus, there is a high degree of uncertainty in overall fecal coliform production rates.

To accurately predict actual fecal production rates in a watershed, one would need to collect a large number of samples from all species and for various ages of each species. This intensive sampling is not economically feasible for TMDL development purposes. Consequently, the AAC recommends that TMDLs be developed using standard fecal production rates published for humans and livestock unless statistically valid research is conducted to develop better values specifically for Virginia conditions. There is much less information in the literature on fecal production rates for wildlife, but some is available, and some has been collected through the early fecal coliform TMDLs developed in Virginia. The AAC recommends that existing literature values be used for wildlife production rates unless research is conducted to develop regional databases on fecal production rates and concentration data. Published production rates are probably best for humans, intermediate for livestock, and poorest for wildlife.

Because of the high degree of uncertainty in fecal coliform production rates, some TMDL developers have attempted to calibrate fecal coliform production rates and densities to improve predictions of in-stream fecal coliform concentrations. Site-specific densities can readily be obtained through source sampling to reduce uncertainty in these values. If calibration of fecal coliform rates is performed, the modeler is faced with the question of which sources to calibrate. Extensive in-stream sampling with BST analysis may possibly provide guidance for this level of discernment if one assumes that BST can accurately and quantitatively differentiate between different species. BST has not been proven to be this accurate. It is the opinion of the AAC that calibration of fecal coliform production rates and densities should be avoided.

HSPF 5. – In general, how much flexibility do we need in fecal production rates to allow for reasonable calibrations and still maintain some statewide consistency?

As discussed for the previous question, it is the best professional judgment of the AAC that standard values for fecal coliform production rates should be used across Virginia unless/until watershed or regional values become available through research. Since funding for this research is not likely given the state's current economic situation, the AAC recommends that the state develop a set of fecal coliform production rates and that these values be used for TMDL development without calibration. Published values probably have less uncertainty than BST analyses, which are used for calibration. Likewise, there is probably less uncertainty in published fecal coliform production rates than there is in truncated ambient water quality monitoring concentrations.

HSPF 6. – In terms of addressing the impairment, what should be the time step of the geometric mean calculation, 720-hour geometric mean, 30-day geometric mean of daily average, 30-day geometric mean of daily median, *etc.*?

The AAC panel of experts discussed this question at length because the different techniques may yield significantly different values. It is the unequivocal judgment of the AAC that the use of the "mean" of the hourly (or smaller time steps) values to determine the representative value for the day is statistically invalid and provides the worst possible representation of the daily value. The representative daily value can best be evaluated by the geometric mean of the hourly (or smaller time step) values or the median of all the values for the day. For consistency and statistical validity, the AAC recommends that the daily value also be a geometric mean and that it should be calculated using the geometric mean of the 24 hourly (or smaller time steps) values. For example, the daily value of 24 hourly values would equal:

$$\sqrt[24]{x_1 * x_2 * x_3 * \ldots * x_{24}}$$

Alternately, the geometric mean can be calculated using all the hourly values in a month. For example, for a month with 30 days, the geometric mean of the hourly values over the 30-day period would equal:

$$\sqrt[720]{x_1 * x_2 * x_3 * \ldots * x_{720}}$$

where 720 = 30 days $*$ 24 hours per day. This approach is statistically consistent.

HSPF 7. – Recommendations for consistency in model (HSPF) application.

Guidance should be specific on where and how to represent failed septic systems and straight pipes. Better guidance should be provided on direct deposition contributions from various types of livestock and wildlife. Septic systems, straight pipes, and direct deposition should be input within each sub-watershed, not uniformly at the watershed outlet. Calibration should focus on the parameters for which there are the greatest uncertainty, not for parameters where reasonable estimates exist or that can be measured (such as fecal coliform densities in excreted manure). The Virginia Department of Conservation and Recreation (DCR) and DEQ should develop a database of recommended parameter values for fecal production rates, time that various animals spend in streams, when direct deposit fecal material is deposited in streams for each species, septic system failure rates, and other similar model inputs. For consistency, all contractors should use these values unless better site-specific data are available.

II. – Questions about Bacteria Source Tracking (BST)

Bacterial source tracking or BST is a controversial topic with respect to its role in the development of bacteria TMDLs. BST employs a variety of techniques to attempt to identify the sources of fecal bacteria in streams. Techniques that have been used include: antibiotic resistance analysis (ARA), identification of source-specific bacteriophages, fatty acid profiles, carbon source, ratio of fecal coliforms to enterococci, ribotyping, Pulse Field Gel Electrophoresis, and Random Amplified Polymorphic DNA. Two techniques have been used in TMDL development in Virginia: antibiotic resistance analysis in most TMDLs and ribotyping in three USGS TMDLs. The primary issues associated with BST involve the uncertainty associated with their classifications between species and how waters should be sampled to collect representative samples for BST analysis used for TMDLs. Unfortunately, it is difficult to answer these questions as BST is a new science and still under development, and the accuracy of the different methods has not been researched adequately. For example, as of September 2002, the AAC is aware of no attempts to test the accuracy of BST procedures using standard/blind samples with known concentrations of mixed bacteria species or with spikes of known species in mixed samples. Until the various BST methods are evaluated using standard quality control procedures, it will not be possible to define the accuracy of the various procedures in quantifying the distribution of species within a mixed sample.

It is our understanding that a national test with blind BST samples will be conducted in October 2002 and that many BST labs in Virginia (MapTech, Hagedorn, Wiggins, and others) will participate in this test. When the results of this experiment are compiled and released, we will have a much better understanding of the accuracy and precision of the various BST procedures, and we will be better able to respond to the DEQ questions.

There is also considerable uncertainty in the various statistical procedures used to classify isolates. Different labs use different procedures, and results vary greatly depending on the classification scheme. In general, the BST classification approach involves collecting fecal samples from known sources. These samples are analyzed, and a library of information is developed. Then, when a new sample from an unknown source is collected, the source from which it comes is predicted using the information in the library. Two methods for analyzing the data in the library and for predicting the source are logistic regression and discriminant analysis. There are of course many other methods that might be applied (*e.g.*, regression trees, neural networks). The results of the analysis are estimated probabilities that the sample comes from different sources and then classified into one of the sources. There are a number of problems with the analysis and collection of data that need to be addressed before the method is put into general practice.

1. Handling of unknown sources: Unknown sources are simply ones that are not in the library. The unknown source might be ducks or other animals for which source data have not been collected. A method is needed that allows for an "unknown group" as part of the analysis and classification.

2. Development of methods for improved classification: A current study indicated that as the number of potential sources increased, the correct classification of the sources decreased (B. Wiggins, presentation at the AAC meeting in Charlottesville, February, 2002). This is a disturbing result as it indicates a decrease in resolution as the number of groups increases. We believe that there is a significant scientific problem with the BST methodology if classification accuracy decreases with the number of groups used. Results should be similar or better as the number of groups increases.

3. Laboratory analysis issues: There are several issues related to the number of isolates that are used, how many tests are applied, how the resulting data are recorded, and the processing of these data. For example, Dr. Hagedorn of Virginia Tech conducted a preliminary study of the effects on classification owing to the number of isolates analyzed. As indicated in Table 1, classification percentages vary depending on the number of isolates analyzed. The variation range within a site where 24 to 48 isolates were analyzed is reasonable, with a maximum range of 13%. However, when the number of isolates analyzed is decreased to 5 (rows in italics), there are noticeable changes in the classification percentages. The within site variation range goes up to 53% when considering 5 to 48 analyzed isolates. This suggests that classifications involving 5 or fewer isolates are not statistically valid.

Even when "sufficient" isolates are used, there is still a great deal of uncertainty as to how BST results can best be used. For example, in Table 2, the results of three BST samples are presented for a monitoring station on Linville Creek in Virginia. These samples used 24 isolates, and classification required 75% confidence for an isolate to be assigned to one of the four broad classification categories. If the results are accurate, they indicate that wildlife is the most significant source of fecal bacteria at this station during the summer with extreme low flow conditions. In fact, if these results are accurate and indicative of fecal bacterial levels in Linville Creek, they indicate that for two sampling dates, we are 75% confident that wildlife alone will exceed the existing instantaneous Virginia fecal coliform standard of 1000 cfu/100mL by a factor of 2.4 to 4.6 (assuming that fecal coliform and enterococci have similar die-off rates). Contributions from humans, livestock, and urban sources (presumably pets) combined appear minor (4 to 25%) if the unknown classification is not considered. The unknown classification however ranges from 4 to 50%, with a mean of 24%. If the percentage of bacteria associated with the unknown isolates is considered, then the unknowns alone violate the existing 200 cfu/100mL 30-day geometric mean standard.

Table 1. Effect of number of isolates analyzed on BST classification (personal communication, Charles Hagedorn, Virginia Tech, 2002). Shows classification results using different numbers of isolates that were based on an *Escherichia coli* library for Naked Creek, June 2001 samples.

Site	Fecal Coliform Conc., cfu/100mL	No. of Isolates	Poultry (%)	Cow (%)	Deer (%)	Geese (%)	Horse (%)	Human (%)	Sheep (%)	Unknown Wildlife (%)
1	2,860	48	0.0	50.4	10.0	5.6	5.6	4.4	0.0	24.0
1	2,860	36	0.0	47.5	12.4	4.8	7.5	10.5	0.0	17.3
1	2,860	24	0.0	43.9	7.0	9.5	12.1	7.7	0.0	19.8
1	*2,860*	*5*	*0.0*	*40.0*	*0.0*	*0.0*	*0.0*	*40.0*	*0.0*	*20.0*
2	4,080	48	10.9	54.4	17.4	0.0	7.4	0.0	0.0	10.0
2	4,080	36	15.0	46.1	14.0	0.0	9.5	0.0	0.0	15.4
2	4,080	24	9.5	41.0	12.5	0.0	11.9	0.0	0.0	25.1
2	*4,080*	*5*	*0.0*	*80.0*	*20.0*	*0.0*	*0.0*	*0.0*	*0.0*	*0.0*
3	2,030	48	4.8	42.9	5.0	9.8	7.1	5.7	0.0	24.8
3	2,030	36	2.0	52.9	3.0	5.5	6.0	8.8	0.0	21.8
3	2,030	24	5.0	48.7	4.4	11.6	8.5	8.3	0.0	13.5
3	*2,030*	*5*	*0.0*	*0.0*	*40.0*	*20.0*	*0.0*	*20.0*	*0.0*	*0.0*
4	470	48	0.0	47.8	16.7	4.4	6.7	7.8	0.0	16.7
4	470	36	0.0	45.4	15.0	5.8	9.0	6.2	0.0	18.6
4	470	24	0.0	43.5	17.6	8.7	8.9	8.5	0.0	12.8
4	*470*	*5*	*0.0*	*20.0*	*40.0*	*40.0*	*0.0*	*0.0*	*0.0*	*0.0*

Table 2. BST classification using the ARA method for three samples in Linville Creek with 24 isolates and 75% confidence in classifications.

Date	Fecal Coliform cfu/100 mL	Enterococci cfu/100 mL	ARA – Enterococci, cfu/100mL				
			Wildlife	Human	Livestock	Urban	Unknown
5/15/2002	900	400	46%	2%	2%	0%	50%
6/12/2002	6000	460	77%	0%	4%	15%	4%
7/25/2002	4100	830	58%	6%	2%	17%	17%

In spite of the current uncertainty in BST methods, the AAC believes that BST holds great promise for identification and enumeration of bacteria species in water. To achieve this promise, the AAC recommends that in the short term, the state reduce the use of BST in TMDL development and sponsor research to reduce uncertainties associated with BST accuracy. We are concerned that the current use of BST is wasteful of limited resources available for TMDL development (approximately $500/ BST sample) because we do not have any idea of how accurate the various BST procedures are. We believe that a few well-designed research projects (such as the national blind sample experiment) could answer these questions within a short period of time. In addition, the AAC recommends that an environmental statistician be contracted by DEQ to conduct an extensive evaluation of statistical issues associated with the analysis and collection of BST data. The statistician could develop a recommended set of statistical procedures for BST classification and monitoring in Virginia. With these issues in mind, we will try to address the following DEQ questions concerning the proper use of BST in TMDLs.

BST 1. – What are the uses of Bacteria Source Tracking (BST) in TMDL development?

As discussed above, BST can be used for many purposes in TMDL development. As the uncertainty associated with BST is better defined and decreases, BST will become much more useful. Given the current uncertainties associated with BST, we believe that its best current uses are to:

- provide qualitative information on the species contributing fecal bacteria to impaired waters.
- provide semi-quantitative information on the sources of fecal bacteria present in a stream at a specific point.
- assure the public that all sources of fecal bacteria are being considered during TMDL development.

Given the current uncertainties associated with BST, the AAC recommends that until additional research is conducted and uncertainties are reduced, BST should not be used to:

- quantify the distribution of fecal coliform sources in streams,
- identify pathway or transport mechanisms,
- specify reductions in specific sources required to meet water quality standards,
- calibrate models.

BST 2. – What spatial distribution and number of samples are required for watershed characterization/source assessment using BST?

It is impossible to answer this question at the current time with any degree of confidence because of the uncertainty associated with BST classification accuracy. Guidelines have been developed for designing monitoring systems that answer questions related to watershed characterization and source assessment for other pollutants. To develop such monitoring systems requires knowledge of the accuracy of analytical methods, the variability typically associated with each pollutant, and correlations between the pollutant and other factors such as flow. Because of the newness of BST, these relationships have not been defined. Our best professional judgment is as follows:

- The number and distribution of required BST samples is very site-specific and depends on the objective of the sampling for a particular study.
- Sampling must be adequate to characterize distribution of sources during the conditions causing violations of the water quality standards. BST enumeration should focus on samples that are in violation of water quality standards. For example, if violations occur predominately during the summer during low flow conditions, then BST samples should

be collected during this period. If violations occur during higher flow conditions, the BST should also be conducted during high flow conditions.

- The number of samples collected must be adequate for statistical inference.
- If BST results are used to estimate loadings from different species over a long period of time, it is important to flow-weight the distribution of different BST samples.
- The BST results for fecal coliform enumerations that do not result in violations of the standard should be given less weight or discarded when assessing source contributions.

BST 3. – What is the utility of and conditions for effective BST use as a HSPF model calibration tool compared to traditional calibration/land use approaches with HSPF?

There is a high degree of uncertainty associated with the fecal bacteria concentrations predicted by HSPF. The more extensive fecal coliform concentration data sets collected by the USGS as part of the Accotink Creek, Blacks Run, and Christians Creek TMDLs may be useful in defining this uncertainty when they become available to the public. As HSPF is currently used, it is not feasible to calibrate HSPF sources to in-stream concentrations because HSPF lumps all sources during simulation. If BST was affordable and if the uncertainty associated with BST were better defined, BST could be used to confirm/calibrate concentrations in streams from different sources as predicted by the model at the time that BST samples are collected. This approach assumes that HSPF was run so that it simulated the loadings, transport, and die-off of each fecal bacteria source separately. HSPF can do this, but to our knowledge, individual fecal bacteria sources have never been simulated this way. If this approach is used, HSPF simulations of individual fecal bacteria species could be calibrated to BST derived in-stream concentrations for each fecal bacteria species. The concentrations produced by the individual species would then need to be summed to calculate the overall in-stream fecal bacteria concentrations used to determine compliance with water quality standards.

Some TMDL developers in Virginia, such as Virginia Tech and MapTech, Inc., have used HSPF to estimate in-stream fecal bacteria loadings for individual fecal bacteria sources. These sources include pervious land segment nonpoint sources (*e.g*., runoff from pastureland), impervious land segment nonpoint sources (*e.g*., runoff from streets and roads), direct nonpoint sources by livestock, direct nonpoint sources by wildlife, permitted point sources, unpermitted point sources (*e.g.*, direct pipes and failing septic systems), and combined sewer overflows. The contributions from the individual sources are estimated by turning off all sources but one and then running the model with a single source. For example, if the model is run for three years, the model will predict the concentration versus time for the single source simulated and the cumulative loading for the source over the simulated three-year time. If accurate BST data for the same source were available, they could be used to calibrate this source. Unfortunately, because of the high cost of BST analysis, it is unlikely that sufficient BST derived data points would be available for calibration of loads. BST might be useful to check predicted concentrations on days with BST derived concentrations.

Another problem with using BST to calibrate HSPF is that BST is generally only conducted during the 12 months immediately prior to TMDL development because of the short time frames associated with TMDL contracts. HSPF is rarely used to simulate streamflow conditions during this period because flow and meteorological data required by HSPF are often not available until six to eight months after collection. Thus BST data are generally not available for the period that HSPF is simulating.

Serious discrepancies between fecal bacteria concentrations predicted by BST and HSPF should be investigated. In the event of serious discrepancies, best professional judgment and common sense should be used to make final decisions because of known uncertainties with both BST and HSPF.

BST 4. – Should model calibration be to land use loading or measured BST?

The answer to this question depends on the confidence given to the accuracy of BST. Based upon the discussion above and the results from the Virginia TMDLs employing intensive BST (Accotink Creek, Blacks Run, and Christians Creek), the AAC believes that calibration based solely on BST is unwarranted at the present time. However, the difficulties encountered in the Accotink Creek, Blacks Run, and Christians Creek TMDLs are likely the result of the limited number of isolates used. At its current state of development, the AAC believes that BST is best used as a check of land use loading based assessments.

BST 5. – What is the proper role of BST in TMDL development?

At its current state of development, BST can best be used to:

- Supplement land use loading based analysis.
- Help communicate contributing source information to the public.
- Identify minor and major sources and indicate the relative importance of each.

BST 6. – How can the usefulness of BST for TMDL development and implementation be enhanced?

Research must be conducted to:

- Identify the best statistical methods for species classification and accounting for unknown species (species not in the reference library).
- Quantify BST accuracy and predictive ability by testing various BST labs with blind samples containing known concentrations of various fecal bacteria species.
- All BST data (raw and processed) collected in state sponsored studies should be saved by the state in a central database so that they can be reclassified when better classification techniques become available. The reclassified data can then be used in future BST research and water quality protection programs.

III. – Questions about TMDL Development Using the Flow Duration/BST (or the CBF) Approach

The proposed Virginia flow duration/BST approach for TMDL development, also referred to as the cheaper-better-faster (CBF) approach, is based on a Kansas load-duration approach, which is described below. The Kansas example uses a TMDL development approach for atrazine, but the same approach can be used for fecal coliform.

Step 1: The first step in the Kansas load duration approach is to develop a flow duration curve for the gage site of interest. This is done by generating a flow frequency table and plotting the points as indicated in Figure 2.

% Exceed	Flow
99	694.2
95	803.3
90	920.2
85	1213.3
80	1629.7
75	2081.3
70	2692.9
65	3130.3
60	3583.3
55	4177.9
50	5092.2
45	6074.7
40	7068.8
35	8398.1
30	9801.8
25	11617.5
20	13838.5
15	17136.8
10	22281.1

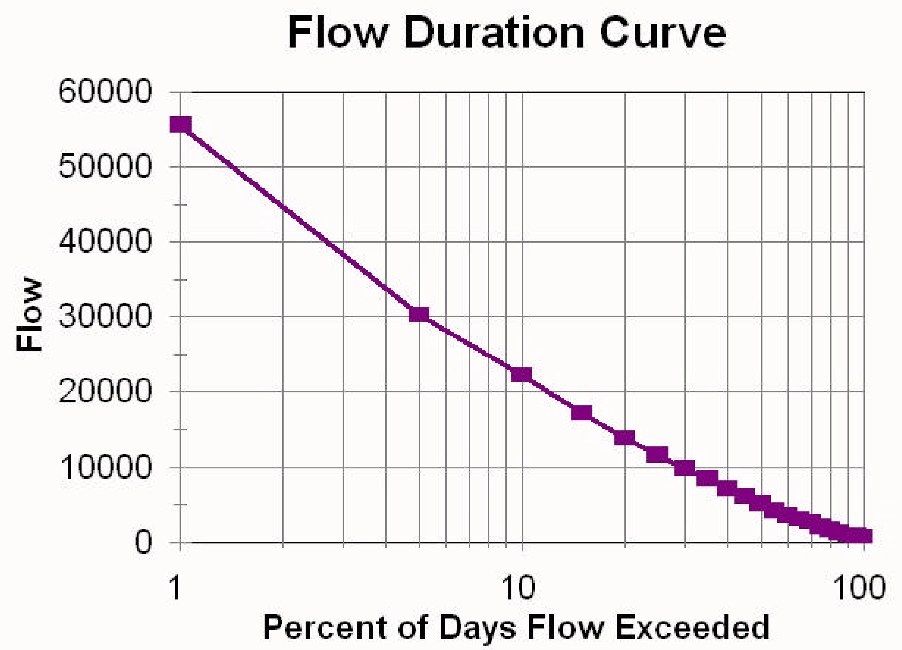

Figure 2. Flow duration curve for impaired stream or a reference watershed if flow data are not available for the impaired stream.

Step 2: The flow curve is translated into a load duration (TMDL) curve. To accomplish this, the flow value is multiplied by the applicable water quality standard and a unit's conversion factor and then plotted as shown in Figure 3.

Prob.	Flow	Atrazine (lbs/day)
99	694.2	11.50
95	803.3	13.31
90	920.2	15.25
85	1213.3	20.10
80	1629.7	27.00
75	2081.3	34.49
70	2692.9	44.62
65	3130.3	51.87
60	3583.3	59.38
55	4177.9	69.23
50	5092.2	84.38
45	6074.7	100.66
40	7068.8	117.13
35	8398.1	139.16
30	9801.8	162.42
25	11617.5	192.50
20	13838.5	229.30
15	17136.8	283.96
10	22281.1	369.20
5	30245.9	501.17
1	55562.3	920.67

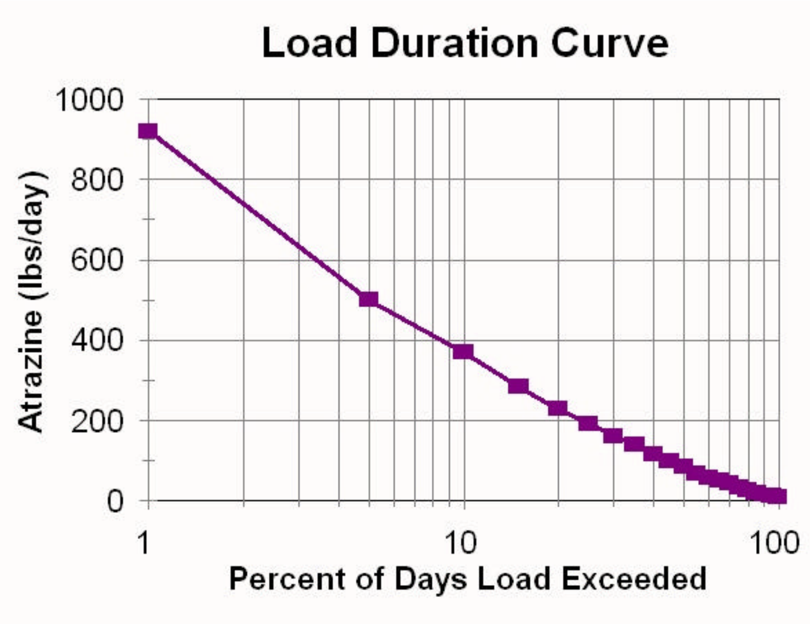

Figure 3. Load duration curve for impaired stream or a reference watershed if flow data are not available for the impaired stream.

Step 3: Water quality data from the impaired watershed are converted to a load by multiplying the observed concentrations by the average daily flow (on the day the samples were taken). Then, the loads are plotted on the TMDL graph as shown in Figure 4 (the six triangle points).

Prob.	Flow	Atrazine (lbs/day)	Atrazine Load
99	694.2	11.50	4.33
95	803.3	13.31	
90	920.2	15.25	
85	1213.3	20.10	12.92
80	1629.7	27.00	
75	2081.3	34.49	
70	2692.9	44.62	122.91
65	3130.3	51.87	
60	3583.3	59.38	95.87
55	4177.9	69.23	
50	5092.2	84.38	
45	6074.7	100.66	
40	7068.8	117.13	
35	8398.1	139.16	
30	9801.8	162.42	
25	11617.5	192.50	
20	13838.5	229.30	
15	17136.8	283.96	154.43
10	22281.1	369.20	804.32
5	30245.9	501.17	
1	55562.3	920.67	

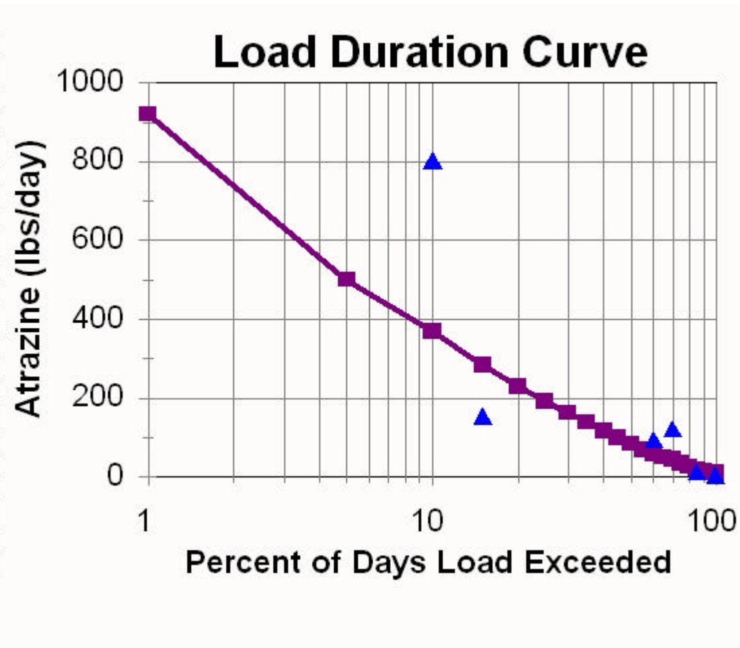

Figure 4. TMDL curve for impaired stream.

Step 4: Regression analysis is then used to generate a best-fit line through the measured daily load points, or the analysis can be calculated on the observed values themselves (Figure 5). When the measured daily load line is below the load duration line (which is based on the standard), the water quality standard is not exceeded, and no reductions are required. If the measured daily load line is above the load duration line, as illustrated in Figure 5, then the water quality standard is exceeded. The required TMDL load reduction would be the greatest difference between the two lines for the flow conditions for which the water quality standard is applicable. Because Kansas does not require TMDLs to meet the standard for probabilities of less than 10 percent, the required reduction for the TMDL (maximum required reduction between the two arrows) would be 515-385 = 130 lbs/day. If the best-fit curve is not used and the TMDL is based on the measured existing values, then the required reduction would be: 804 – 385 = 419 lbs/day.

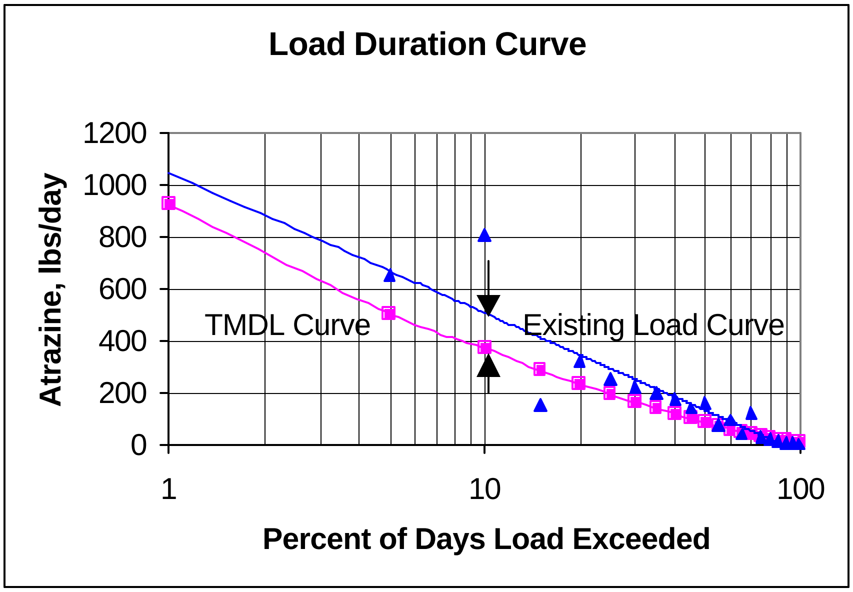

Figure 5. TMDL and existing load duration curves.

Step 5: There is no direct way to apportion required loading reductions between sources with the Kansas approach, but Kansas has developed a method to roughly apportion loads between point and nonpoint sources as shown in Figure 6. Loads that plot above the curve in the flow regime defined as being exceeded 85-99% of the time are assumed indicative of point sources. Loads plotting above the curve in the range of 10-70% exceedance are assumed to reflect nonpoint sources. A combination of the two source categories is assumed to occur in the transition zone of 70-85% exceedance. Loads plotting above the curve at exceedances less than 10% or more than 99% reflect extreme hydrologic conditions of flood or drought respectively, and Kansas does not require TMDLs for these conditions.

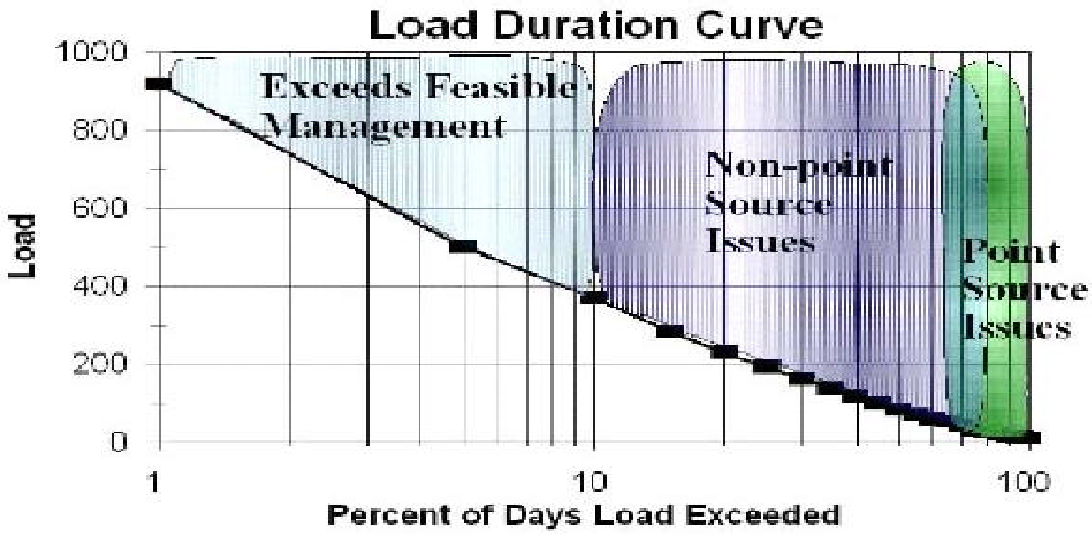

Figure 6. Load duration curve for impaired stream with assumed predominate sources as a function of load frequency.

Virginia Flow Duration/BST (or the Cheaper-Better-Faster) Approach

As we understand the proposed Virginia flow duration/BST (CBF) approach for fecal bacteria TMDLs, it is identical to the Kansas approach except that Virginia will not attempt to develop a regression curve. Both methods require that pollutant concentration and flow rate be measured simultaneously, and the Virginia method also requires BST analysis of the collected sample. The critical loading reduction will be based on the maximum difference between the allowable loading curve and the most extreme fecal bacteria load measured, in terms of the required percentage reduction.

As indicated in Table 3 (prepared by the DEQ), the critical condition identified (bolded row, largest required percentage) requires a 95% reduction in loading for the critical condition. Once this critical condition is defined, the TMDL would be developed for this condition. In this example, the TMDL would be based on an allowable load of 70 x 10^9 cfu/day. The critical actual load on this day is 1,400 x 10^9 cfu/day. The next step in the proposed Virginia approach is to allocate the required loading reductions based on 12 to 18 monthly BST samples collected concurrently with fecal bacteria samples and flow measurements prior to the development of the TMDL. With the proposed approach, the percentage in each classification in the 12 to 18 samples would be averaged to arrive at mean percentages for each classification, and the unknowns would be included in the wildlife classification. For the Four Mile Run example, this process resulted in three source categories: wildlife (69%), humans (18%), and canine (13%) (Table 4). The total load allocation is then distributed to the source categories in proportion to their BST percentage classification, and then each source is reduced by the required critical condition percentage reduction (95%) to arrive at the final load reductions for each source category. The calculated loads would constitute the TMDL.

With this method, detailed inventories of sources and land use are not required and no knowledge of past, current, and future watershed conditions are necessary for TMDL development. All that is required is 12 to 18 water quality samples for fecal bacteria enumeration and BST analysis plus flow measurements at the time of sample collection.

Table 3. Example TMDL using the proposed Virginia CBF approach.

Sample CBF TMDL for Four Mile Run (Virginia DEQ)					
Frequency % exceedance	**Flow** cfs	**Allowable Load** cfu x 10^9/day	**Actual Load** cfu x 10^9/day	**Reduction needed** %	cfu x 10^9/day
1	188	1840			
5	61	597			
10	29	284			
15	18	176	3200	94%	3024
20	13	127	32	0%	0
25	11	108	29	0%	0
30	9.1	89	22	0%	0
35	8	78			
40	**7.2**	**70**	**1400**	**95%**	**1330**
45	6.5	64	15	0%	0
50	5.9	58	820	93%	762
55	5.4	53	13	0%	0
60	5	49	200	76%	151
65	4.6	45			
70	4.2	41	30	0%	0
75	3.8	37			
80	3.4	33	43	23%	10
85	3	29			
90	2.3	23			
95	1.6	16			
99	1	10			

Table 4. CBF TMDL source load allocation and required reductions by source.

BST Analysis Results (means of BST samples)	
Source	**Percentage**
Human	18%
Canine	13%
Wildlife	69%
Raccoon[1]	19%
Deer[1]	6%
Waterfowl[1]	31%
Other[1]	13%
[1] *reclassified as wildlife*	

Source	**Source Percentage**	**Actual Load** [cfu/day]	**CBF TMDL Load Allocation** [cfu/day]	**CBF Reduction Needed**
All sources		1.40E+12	7.00E+10	95%
Wildlife	69	9.66E+11	4.83E+10	95%
Human	18	2.52E+11	1.26E+10	95%
Canine	13	1.82E+11	9.10E+09	95%

Advantages of the Virginia flow duration/BST approach (also known as the cheaper-better-faster or CBF approach) as identified by DEQ.

1. Reduced data needs: The only data requirements are stream flow data for the TMDL target area; ambient water quality data during the 303(d) listing period; and concurrent fecal coliform enumeration, BST analysis, and stream flow measurements for pollutant source identification and quantification. Of the data requirements, only the BST information will have to be contracted and developed.
2. Many fecal coliform bacteria TMDLs can be done "in house" with only a slight increase in staffing. This approach will allow much of the $5 million needed for contractual services to be used for TMDL implementation.
3. Using the simpler model will enable Virginia to develop "cheaper and faster" bacteria TMDLs required by the consent decree schedule for years 2004 and 2006. The actual flow frequency/BST spreadsheet analysis can be completed in a couple of days compared to months for the more complex contracted modeling.
4. The TMDL will be based on actual in-stream measurements of flow and bacteria.
5. BST has gained widespread acceptance by the public, facilitating implementation.
6. Developed TMDLs will not need to consider high and low flow conditions with a less than 1% probably of occurrence.

The only disadvantage of the CBF approach identified by DEQ is that the method cannot account for the effects of the spatial distribution of sources.

The DEQ has not indicated how TMDLs would be implemented using the information from the flow duration/BST approach other than to indicate that the method will provide greater flexibility during implementation. Presumably, the required percentage reductions will be applied to all sources in a staged approach with sources that are presumed to be more critical reduced first through an adaptive implementation approach.

Both the DEQ and DCR have compared the results of the flow duration/BST approach with the results of TMDLs that were developed using the HSPF land based source assessment. The comparisons are not directly applicable because they were developed for slightly different water quality goals. The HSPF TMDLs were developed for a 30-day geometric mean standard of 200 cfu/100mL, while the CBF BST TMDLs were developed for an instantaneous daily standard of 1000 cfu/100ml. The reductions in fecal coliform loadings required for each type of TMDL are presented in Table 5. As indicated in Table 5, the CBF approach generally requires much greater loading reductions (approximately an order of magnitude) than the HSPF approach.

Table 5. Comparison of required reductions in fecal coliform loadings.

Blackwater River Segment	HSPF TMDL Reduction cfu/day	CBF TMDL Reduction cfu/day	Ratio of CBF/HSPF Reduction
South Fork	4.82E+11	4.84E+12	10.04
North Fork	7.28E+11	8.55E+12	11.74
Upper	1.07E+12	1.92E+13	17.94
Middle	2.02E+12	1.15E+13	5.69

With the above information as background, the AAC will try to address the DEQ's questions related to the proposed BST/flow duration or CBF approach.

CBF 1. – Is the BST/flow duration approach a suitable (defensible and approvable) method for fecal coliform TMDL development?

The BST/flow duration approach has been used to develop EPA approved TMDLs in Kansas for several pollutants. It would seem very appropriate for use with atrazine and similar pollutants, which only have a single source. However, Kansas is experiencing problems with the flow duration approach as they begin to implement TMDLs because the process does not collect any information on the sources of pollutants within the watersheds. Thus it is difficult to target pollution control resources to areas that are disproportionately responsible for the problem. It is therefore difficult for them to prioritize implementation activities and target their implementation resources to areas having the greatest impacts on water quality.

Since the general flow duration approach has resulted in approvable TMDLs in Kansas, we must assume that at least the loading portion of the proposed Virginia BST/flow duration approach would be approvable. The only difference with the Kansas approach is that DEQ has proposed to use BST with TMDLs to break the required source reductions down to the species level or general categories such as humans, livestock, pets, and wildlife. There are two possible problems with this approach. The major problem is the uncertainty associated with the BST approach, which was discussed previously. This uncertainty is apparent in the DEQ analysis of BST samples collected as part of the Blackwater River TMDLs, which is shown in Table 6.

Table 6. BST estimated fecal coliform sources for the Blackwater River TMDLs (based on 14 BST samples in each subwatershed).

Blackwater River Watersheds	Human		Livestock		Wildlife	
	%	Std Dev	%	Std Dev	%	Std Dev
South Fork	24.0	16.8	48.5	24.3	27.7	15.6
North Fork	22.3	25.8	42.3	26.4	35.4	23.4
Upper	24.0	21.4	48.6	25.2	27.4	15.9
Middle	29.8	27.2	48.0	25.8	22.2	18.2

As shown in Table 6, there is a very high degree of uncertainty in the BST results as indicated by the high standard deviations for sources in each watershed. On average, the standard deviations are 91, 55, and 66% of the mean values for the human, livestock and wildlife categories, respectively. It thus does not seem appropriate to use the mean classification percentage for a source with the critical load period. With the large standard deviations reported, this method could result in large overestimations or underestimations of loads attributed to that source. If one has confidence in the accuracy of BST, it might make more sense to use the BST classification percentages obtained on the critical loading condition sampling day rather than the mean BST classification percentage during all flow conditions.

Another critical issue with this approach is the adequacy of basing the TMDL on only 12 to 18 water quality samples and flows. There is no guarantee one will collect samples during the critical flow conditions. In the DEQ example, the Four Mile Run TMDL is based on 11 samples collected during periods with flows ranging from 3.4 to 18 cubic feet per second (cfs). Table 3 indicates that flows are lower than 3.4 cfs 20% of the time and that they exceed 18 cfs approximately 15% of the time. This means, that for this example TMDL, critical flow conditions were likely not captured.

Another problem identified by the DEQ is that the CBF procedure gives no indication of where the sources might be in the watershed. Thus when the implementation plan is developed, one must still generate most of the data that would have been generated in developing a land use – source loading based TMDL.

CBF 2. – Which is the preferred method for fecal coliform TMDL development? The flow duration/BST approach or the HSPF/land use approach?

If the goal of the Virginia TMDL program is to meet the requirements of the consent decree and generate approvable TMDLs at the least possible cost in the shortest period of time, then the flow duration/BST (CBF) procedure is probably preferred over the more detailed land used based approaches. However if the goal of the Virginia TMDL program is water quality improvement, then the more detailed land use/source modeling approaches are preferred. This conclusion is based on the following assumptions.

1. The detailed land use/source modeling approaches are not necessarily more accurate than the CBF approach. However, we do know that to do the land use/source modeling properly, one must learn a great deal about the impaired watershed including spatial and temporal changes in potential sources of the pollutant and pollutant transport mechanisms in the watershed. These analyses require development teams with expertise in hydrology, water quality, point and nonpoint source pollution control, agriculture, *etc*. In developing the TMDL, the team documents this information and assembles databases that will be useful for later TMDL implementation. In contrast, the CBF approach is not as labor intensive, but it does not provide source information that will be needed in developing implementation plans.

2. The CBF method may not be cheaper or faster than the more detailed land use/source modeling approaches in the long run. TMDLs developed to date using the more detailed approach have taken less time from start to completion than the suggested 12 to 18 months required for data collection for the CBF approach. In addition, there is not much difference in cost. The first detailed land use/source modeling approach TMDLs cost approximately $30,000 to $40,000 per TMDL, but prices have been dropping rapidly and are now in the range of $13,000 to $15,000 per TMDL with limited BST analysis. With estimated in-house DEQ costs per TMDL for the CBF approach of $6,000 to $9,000 for BST analysis alone and then additional costs for required public meetings, data collection, and spreadsheet analysis, the cost savings are about $4,000 to $7,000 per TMDL.

3. The above cost savings are not real because as soon as implementation begins, as required by Virginia law, it will be necessary to collect and analyze all of the land use

and source data that would have been collected during the detailed land use/source modeling approach. Thus dollars saved during the development of the TMDL will have to be spent during the development of the implementation plan. If the land use and source data are not collected, it will be difficult to allocate implementation funds in the most cost effective manner.

4. The CBF method has not been rigorously evaluated. We know there are significant uncertainties associated with BST analysis, but there are also uncertainties associated with the minimum number of samples and flow conditions that must be monitored to define the "critical load condition." DEQ has suggested that 12 to 18 samples be collected. However, there needs to be an absolute minimum number of samples collected and requirements for the flow conditions that will be sampled. For example, DEQ should establish monitoring requirements that specify sampling during low frequency flow conditions (*e.g.*, the lowest and highest 5 to 10% of flows for example) because these are likely to be the most important (as based on the AAC subcommittee's past experience). If these flows are not monitored, then there should be a requirement to extend the monitoring period before TMDL development. Likewise, if experience indicates that critical conditions are seasonal, then monitoring should be concentrated during the season when critical conditions occur.

CBF 3. – How can the flow duration/BST (CBF) approach be improved?

1. Sponsor an independent study to compare the results obtained using the flow duration/BST approach with those of alternative approaches for TMDL development and implementation.
2. Determine the uncertainty associated with BST analysis and investigate what effect this uncertainty has on the TMDLs developed.
3. If the CBF approach is used, the TMDL developers should collect detailed land use and fecal source data to identify priority areas within the watershed and principal pollutant transport mechanisms. If the final TMDL rule is approved and implemented, implementation plans will be required, and this information will be essential.
4. The CBF monitoring must be conducted during low probability of occurrence flow events. DEQ should specify the required flow probabilities (probably 3-10%).

General Suggestion

While it may be difficult to justify the flow duration/BST approach, it is not necessary to use the land use loading/modeling analysis. Another option for the DEQ to consider uses a representative/pilot watershed approach for watersheds in which there are similar impairments and for which other TMDLs in similar situations all call for similar reductions. In other words, the DEQ could develop fecal coliform (or other impairments) TMDLs for some watersheds and then extrapolate these results to similar watersheds in the region. Adaptive implementation could then be used in stages within the impaired watershed for the same priority sources identified during the pilot TMDLs.

Appendix A: Members of the 2001-2002 Academic Advisory Committee

Dr. Leonard A. Shabman (Chair)
Director, VWRRC
Virginia Tech
10 Sandy Hall (0444)
Blacksburg, VA 24061
540-231-6844
Fax: 540-231-6673
E-mail: shabman@vt.edu

Dr. E. Fred Benfield
Department of Biology
Virginia Tech
2125 Derring Hall (0406)
Blacksburg, VA 24061
540-231-5802
Fax: 540-231-9307
E-mail: benfield@vt.edu

Dr. Theo Dillaha
Department of Biological Systems Engineering
Virginia Tech
200 Seitz Hall (0303)
Blacksburg, VA 24061
540-231-6813
Fax: 540-231-3199
E-mail: dillaha@vt.edu

Dr. Carl Hershner
Chair, Resource Management and Policy
Virginia Institute of Marine Science
P.O. Box 1346
Gloucester Point, VA 23062-1346
804-642-7387
Fax: 804-642-7182
E-mail: carl@vims.edu

Dr. Howard I. Kator
Biological Sciences
Virginia Institute of Marine Science
P.O. Box 1346
Gloucester Point, VA 23062-1346
804-684-7341
Fax: 804-642-7399
E-mail: kator@vims.edu

Dr. Saied Mostaghimi
H. E. and Elizabeth F. Alphin Professor
Department of Biological Systems Engineering
Virginia Tech
200 Seitz Hall (0303)
Blacksburg, VA 24061
540-231-7605
Fax: 540-231-3199
E-Mail: smostagh@vt.edu

Dr. Eric P. Smith
Department of Statistics
Virginia Tech
406-A Hutcheson Hall (0439)
Blacksburg, VA 24061
540-231-7929
Fax: 540-231-3863
E-mail: epsmith@vt.edu

Dr. Leonard A. Smock
Chair, Department of Biology
Virginia Commonwealth University
P.O. Box 84201
Richmond, VA 23284-2012
804-828-1562
Fax: 804-828-0503
E-mail: lsmock@saturn.vcu.edu

Dr. Tamim Younos
Associate Director and Research Scientist,
VWRRC
Virginia Tech
10 Sandy Hall (0444)
Blacksburg, VA 24061
540-231-8039
Fax: 540-231-6673
E-mail: tyounos@vt.edu

Dr. Carl E. Zipper
Department of Crop and Soil Environmental
Sciences
Virginia Tech
330 Smyth Hall (0404)
Blacksburg, VA 24061
540-231-9782
Fax: 540-231-3075
E-mail: czip@vt.edu

Appendix B: AAC Bacteria TMDL Issues Workshop Participants

Kevin Brannan, Biological Systems Engineering, Virginia Tech, Blacksburg, VA 24061, 540-231-2145, Fax: 540-231-3199, E-mail: kbrannan@vt.edu

Theo Dillaha, Biological Systems Engineering, Virginia Tech, Blacksburg, VA 24061, 540-231-6813, Fax: 540 231-3199, E-mail: dillaha@vt.edu, (AAC member)

Charles Hagedorn, Professor of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061, 540-231-4895, Fax: 540-231-3431, Email: chagedor@vt.edu

Eric Hallerman, Fisheries and Wildlife Science, Virginia Tech, Blacksburg, VA. 24061, 540-231-3257, E-mail: ehallerm@vt.edu

Ken Hyer, Hydrologist, USGS, 1730 East Parham Road, Richmond, VA 23228, 804-261-2636, E-mail: kenhyer@usgs.gov

Howard I. Kator, Biological Sciences, Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, VA 23062-1346, 804-684-7341, Fax: 804-642-7399, E-mail: kator@vims.edu (AAC member)

Bill Keeling, Department of Conservation and Recreation, 203 Governor Street, Suite 213, Richmond, VA 23219-2094, 804-371-7485, E-mail: wgkeeling@dcr.state.va.us

Dave Lazarus, Virginia Department of Environmental Quality, Office of Water Quality Programs, P. O. Box 10009, Richmond, VA 23240-0009, 804-698-4299, Fax: 804-698-4136, E-mail: dslazarus@deq.state.va.us

Charles Martin, Virginia Department of Environmental Quality, Office of Water Quality Programs, P. O. Box 10009, Richmond, VA 23240-0009, 804-698-4462, Fax: 804-698-4266, E-mail: chmartin@deq.state.va.us

Phil McClellan, MapTech, Inc., Virginia Tech Corporate Research Center, 1715 Pratt Drive, Suite 3200, Blacksburg, VA 24060, 540-961-7864, Fax: 540-961-6392, E-mail: pmcclellan@maptech-inc.com

Saied Mostaghimi, Biological Systems Engineering, Virginia Tech, Blacksburg, VA 24061, 540-231-6813, Fax: 540-231-3199, E-mail: smostagh@vt.edu, (AAC member)

Douglas Moyer, Hydrologist, USGS, 1730 East Parham Road, Richmond, VA 23228, 804-261-2634, Fax: 804-261-2659, E-mail: dlmoyer@usgs.gov)

Jutta Schneider, Virginia Department of Environmental Quality, Office of Water Quality Programs, P. O. Box 10009, Richmond, VA 23240-0009, 804-698-4000, Fax: 804-698-4136, E-mail: jschneide@deq.state.va.us

Eric Smith, Department of Statistics, Virginia Tech, 410 Hutcheson Hall, Blacksburg, VA 24061, 540-231-7929, Fax: 540-231-3863, E-mail: epsmith@vt.edu (AAC member)

Carolyn Thomas, Environmental Sciences and Biology Department, Ferrum College, Garber 225, P. O. Box 1000, Ferrum, VA 24088, 540-365-4368, Fax: 540-365-4375, E-mail: cthomas@ferrum.edu

Bruce Wiggins, Biology Department, James Madison University, MSC 7801, Harrisonburg, VA 22807, 540-568-6196, Fax: 540-568-3333, E-mail: wigginba@jmu.edu

Gene Yagow, Biological Systems Engineering, Virginia Tech, Blacksburg, VA. 24061, 540-231-2145, Fax: 540 231-3199, E-mail: eyagow@vt.edu (workshop secretary)

Tamim Younos, Associate Director and Senior Researcher, Virginia Water Resources Research Center, Virginia Tech, Blacksburg, VA 24061, 540-231-8039, E-mail: tyounos@vt.edu (AAC member)