Comparison of models for bacterial regrowth in water distribution systems
by Naomi Ruth Wright Nichols

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in Environmental Engineering
Montana State University
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Abstract:
This thesis evaluates dynamic water quality modeling programs for predicting microbial behavior in drinking water systems. The specific computer programs evaluated were BAM, a biofilm system modeling program and EPANET, a hydraulic modeling program with some water quality modeling capabilities.

Experimental data from microbial regrowth research was used in conjunction with BAM to develop and calibrate a model descriptive of the processes occurring in a drinking water pipe. The key processes affecting BAM predictions of microbial regrowth were then identified. This information was utilized to configure EPANET to simulate microbial regrowth. The capabilities and limitations of the EPANET water quality model for simulating regrowth events in a distribution system were then evaluated by correlating the EPANET results to experimental data obtained from pilot scale pipe loop experiments.

The BAM program was successfully used to duplicate pilot scale experimental results for HPC bacterial populations and to determine values of the unknown kinetic parameters. The development of the BAM model yielded important information regarding biofilm systems in a water pipeline. Through the model calibration process it was discovered that although the BAM program requires numerous input terms, many of them do not have a significant influence on the simulation results.

Analysis of the modeling equations determined that detachment of cells from the biofilm into the bulk fluid is the most significant process resulting in bulk fluid bacterial population increases, and is a first order function of the film thickness. An important result, which relates to the accuracy of the EPANET model of regrowth, was the conclusion that rate of regrowth is a function of the substrate concentration since the biofilm growth and subsequent detachment depend on the available substrate.

Although EPANET was capable of simulating microbial populations, the model does not accurately simulate regrowth since it does not account for the substrate limitation to microbial growth. Further development of the EPANET model for the simulation of bacterial populations should include the following improvements: o The ability to simulate substrate and bacterial populations concurrently.

o Development of more complex equations for modeling reaction rates.

o Modifications to the mass transfer calculation methods.

COMPARISON OF MODELS FOR BACTERIAL REGROWTH

IN WATER DISTRIBUTION SYSTEMS

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Naomi Ruth Wright Nichols

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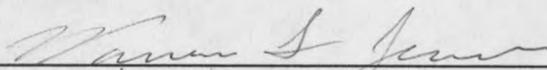
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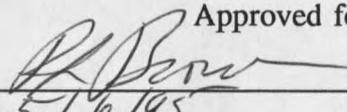Date   Chairperson, Graduate Committee

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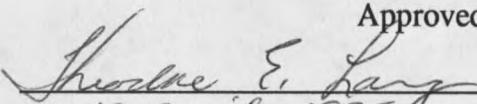
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ABSTRACT

This thesis evaluates dynamic water quality modeling programs for predicting microbial behavior in drinking water systems. The specific computer programs evaluated were BAM, a biofilm system modeling program and EPANET, a hydraulic modeling program with some water quality modeling capabilities.

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Although EPANET was capable of simulating microbial populations, the model does not accurately simulate regrowth since it does not account for the substrate limitation to microbial growth. Further development of the EPANET model for the simulation of bacterial populations should include the following improvements:

o The ability to simulate substrate and bacterial populations concurrently.
o Development of more complex equations for modeling reaction rates.
o Modifications to the mass transfer calculation methods.

CHAPTER 1

INTRODUCTION

The quality of drinking water supplied to the 253 million Americans currently served by public water systems has long been a concern of Federal and State regulatory agencies and water utilities. This interest has become focused on the changes in quality which occur within water distribution systems and has led to increased research efforts to characterize and understand the hydraulic, chemical and bacteriological behavior of these systems.

Federal control of drinking water quality is the responsibility of the United States Environmental Protection Agency (EPA). The EPA, through the Safe Drinking Water Act and its 1986 Amendments (SDWAA), regulates water quality by specifying maximum contaminant levels (MCLs) for contaminants in drinking water. Water utilities, entities that supply water to the public, are required by law to provide drinking water that does not contain contaminants at levels that exceed the MCLs specified by the SDWAA.

One result of compliance with the drinking water quality regulations is an increase in water system operation and maintenance costs. In order to conform with the current regulations, and avoid violating any of the numerous MCLs, treatment techniques have become more complex. The regulations also require extensive monitoring of the treatment operations and sampling within the distribution system to ensure the

preservation of water quality. The necessary treatment, sampling, testing and analyses result in substantial expenses.

EPA estimates the cost to comply with the current SDWAA regulations to be $1.4 billion annually. Monitoring accounts for $253 million of this expense (JAWWA, Feb. 1994). Although the costs associated with complying with the SDWAA are considerable, the alternative can also be very expensive. In 1993, the largest civil fine ever collected under the SDWAA, $900,000, was paid by the Butte Water Company for supplying the city of Butte, MT with water that contained unacceptable levels of particulates (JAWWA, Feb. 1994). Particulates can harbor bacteria, viruses and/or parasites which cause a variety of severe health problems.

In addition to the fines levied by EPA for non-compliance, water utilities are often faced with lawsuits as a result of supplying low-quality drinking water. Over 1,400 legal claims, totalling approximately $25 million, have been filed against the city of Milwaukee, WI as a result of a 1993 cryptosporidiosis outbreak (JAWWA, May 1994).

The Milwaukee outbreak, which caused diarrhea in approximately 403,000 people, was caused by the protozoal parasite *Cryptosporidium*. The parasite entered the water distribution system as a result of decreased filtration efficiency and deteriorated raw water quality. Turbidity measurement at the time indicated inefficient filtration but none of the EPA regulations were violated (JAWWA, May, 1994).

The ongoing advance of technology has elevated the importance of the ability to predict drinking water quality. As the tools to measure contaminants in drinking water (indicators of water quality) become more sophisticated, detection limits become lower

and the list of regulated substances expands. The increasingly strict regulations on drinking water have led to increases in water system operational costs. In order to optimize treatment operations and thus minimize costs, water utility operators need the ability to predict the results of their treatment techniques beyond the treatment plant.

The cases in Butte and Milwaukee were both situations where a computer model of the distribution system water quality may have predicted the presence of pathogens at the point of consumption. However, there are currently no computer programs available that have the capabilities to simultaneously model all the physical, chemical and biological processes occurring within a drinking water distribution system.

There are numerous instances of waterborne disease outbreaks in municipal drinking water distribution systems every year. The cause of the outbreak can often be identified as a inadequate treatment or a distribution system deficiency, such as a water main break or a cross-connection to the sewer system. However, there are many cases where the cause is unknown.

Coliform bacteria are used as an indicator of the presence of disease-causing microorganisms in a water system. An indicator organism is one whose presence infers that contamination has occurred and suggests the nature and extent of the contaminant (Peavy, Rowe and Tchobanoglous, 1985).

As a measure to prevent disease outbreaks, EPA promulgated the Total Coliform Rule in June 1989, which states that coliform bacteria should not be detected in more than 5% of the samples of finished drinking water. However, coliform bacteria are

known to inhabit the biofilms present on pipe walls, and their presence within the biofilm environment complicates efforts to monitor bacterial quality (EPA, 1992).

A biofilm is defined as an accumulation of cells immobilized at a substratum (such as a pipe wall) and frequently embedded in an organic polymer matrix of microbial origin (Characklis and Marshall, 1989). Once microorganisms have entered a distribution system, they can attach to the pipe surfaces and grow within a biofilm. Biofilms can harbor a variety of microorganisms, including coliform bacteria and other opportunistic pathogens, organisms that cause disease in individuals with weak immune systems, but do not infect healthy people (EPA, 1992).

Biofilm growth, which has not been linked to disease outbreaks, can hide the presence of pathogenic bacteria that enter the water system through a loss of integrity of the treatment or distribution systems (EPA, 1992). As the biofilm accumulates, eventually portions of it will be sloughed off the pipe wall. The process of the microorganisms re-entering the bulk water is known as regrowth. When elevated levels of microorganisms in drinking water samples are observed, the occurrence of regrowth makes it difficult to determine the source of contamination.

In an effort to predict the complex behavior of biofilm systems, computer programs were developed in the 1980's to model many of the processes occurring in a biofilm system (Wanner, 1989). The Swiss Federal Institute for Water Resources and Water Pollution Control has made a significant contribution to the biofilm modeling field with the program BIOSIM, written by Reicher, Ruchti and Wanner.

The BIOSIM model was modified by the Center for Biofilm Engineering at Montana State University to create a more user-friendly program and to allow the simulation of the effects of a biocide. The modified program is BAM, the acronym for Biofilm Accumulation Model (Goldstein, 1992).

BAM simulates the evolution of a mixed culture biofilm system within a series of "units". The BAM program is capable of modeling the development and maintenance of a biofilm within a single drinking water pipe, but does not have the ability to model a network of pipes, such as a drinking water distribution system.

Water distribution system modeling was initiated in the 1950s and 1960s with the development of computerized hydraulic models. Hydraulic models are capable of simulating the physical properties of water systems over extended time periods, with varying demand and operational conditions.

In recent years, the development of hydraulic modeling programs has expanded to include source tracing and water age. Source tracing identifies, at every point in the distribution system, the percentages of the total flow from each water supply source. The water age feature determines the total travel time from each source to every point in the system.

KYPIPE and CYBERNET, based on the KYPIPE algorithm, are two programs which contain these capabilities. Another model, PICCOLO, has been developed in France. EPANET, a program developed at the EPA Risk Reduction Engineering Laboratory by Lewis Rossman in the Drinking Water Research Division combines hydraulic modeling and dynamic water quality modeling. EPANET has source tracing

and water age features, as well as the ability to track the concentration of a substance throughout a network over time.

Although EPANET was not developed to simulate microbial growth, its modeling equations account for reactions in the bulk fluid and at the pipe wall. Therefore, the potential exists for using EPANET to model a biofilm system.

The application of EPANET's dynamic water quality module for simulating bacterial regrowth was investigated as presented herein. The BAM program was utilized to simulate the formation of a biofilm on the wall of a drinking water pipeline, and then coupled with EPANET in an effort to model regrowth of bacteria within a drinking water distribution system. The modeling results were compared to actual water quality data to assess the feasibility of combining dynamic and biofilm system modeling.

The water quality data was obtained from pilot scale experiments that use a pipe loop system to create typical water distribution system conditions. The pipe loop system consists of a length of mild steel pipe which is fed treated drinking water. The water recirculates through the pipe loop to simulate relevant distribution system conditions. Bacterial growth is monitored by measuring the bacterial populations in the influent water, effluent water and at the pipe wall. The concentration of cells in the biofilm at the pipe wall are measured from samples taken from removable circular sections of the pipe (coupons).

The pipe loop experimental data was used to estimate initial conditions for the BAM input file and to develop data sets to correlate with BAM and EPANET results.

CHAPTER 2

PROBLEM STATEMENT

The ability to predict water quality is useful for providing public health protection and for maximizing water system operation economy. However, current methods for predicting water quality are limited by the capabilities of the available computer models. The goal of this thesis is to evaluate dynamic water quality models for predicting microbial behavior in drinking water systems. This goal will be accomplished by completing the following objectives.

Objective I

Using experimental data from microbial regrowth research and a biofilm modeling computer program (BAM), develop and calibrate a model descriptive of the biofilm processes occurring in a drinking water pipe.

Objective II

Identify the key processes affecting BAM predictions of microbial regrowth.

Objective III

Evaluate the accuracy of EPANET modeling results. Assess the capabilities and limitations of the EPANET water quality model for simulating regrowth events in the distribution system.

CHAPTER 3

THEORY

Biofilm Models

A biofilm is a thin layer of microorganisms attached to a solid surface. Biofilms can develop on almost any surface exposed to an aqueous environment (Reichert, Ruchti and Wanner, 1989). A biofilm system, represented in Figure 1 (adapted from *Biofilms)*, consists of different compartments, generally a solid substratum, the biofilm, bulk water and possibly gas. Analysis and prediction of biofilm behavior is complicated by the heterogeneous nature of the biofilm and the variety of physical, chemical and biological processes that occur within the biofilm system (Characklis and Marshall, 1989).
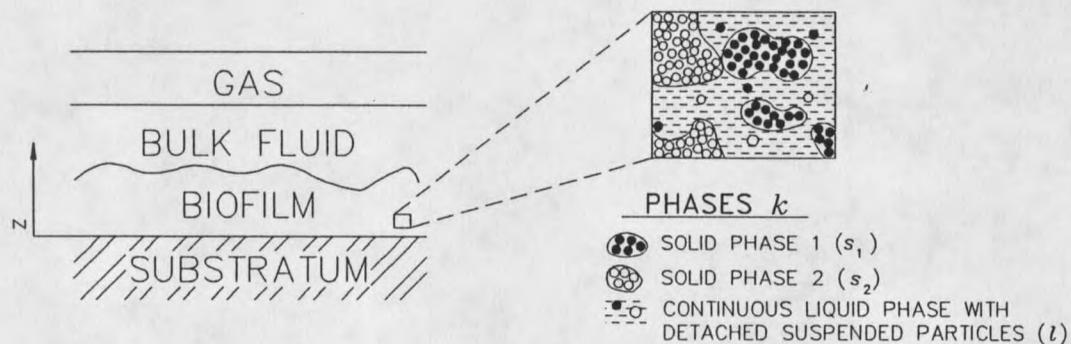
FIGURE 1
BIOFILM SYSTEM

The following conceptual and mathematical descriptions of a biofilm system are based on Chapter 11 of *Biofilms*, contributed by Gujer and Wanner (Characklis and Marshall, 1989). Numerous variables are contained in the equations presented in the following text, which are defined as they are introduced. A summary table of these terms is provided by the Nomenclature section.

The biofilm compartment consists of a continuous liquid phase, which contains different dissolved and suspended particles, and solid phases of attached particulate materials such as microorganisms and extracellular material, as depicted in Figure 1. Each phase *k* occupies a fraction of the total biofilm volume. The sum of the volume fractions for the liquid phase and the solid phases must equal 1, expressed by Equation 1:

$$\sum_k \varepsilon_k = \varepsilon_l + \sum_s \varepsilon_s = 1 \tag{1}$$

where ϵ = local volume fraction of the total biofilm volume

Description of Processes

The many processes which affect the formation and subsequent behavior of a biofilm can be classified into three general categories: transport processes, transformation processes and interfacial transfer processes. These processes are summarized below:

Transport processes. Biofilm transport processes include molecular diffusion, turbulent or eddy diffusion and advection.

Transformation processes. These processes are characterized by a molecular rearrangement and may be chemical, biochemical or microbial in nature (Characklis and Marshall, 1989). For the biofilm systems present in a water distribution pipeline, these processes include growth, decay and inactivation of microorganisms.

Interfacial transfer processes. Attachment and detachment are included in this category, as well as the physical processes of adsorption, absorption and desorption which occur within the biofilm matrix.

In order to develop a model of biofilm behavior, these processes must be described in mathematical terms, through a series of equations. The primary equation is the biofilm mass balance equation, which is written as:

$$\frac{\partial \varepsilon_k * C_{ki}}{\partial t} = \frac{-\partial J_{ki}}{\partial z} + r_{ki} \qquad (2)$$

where C_{ki} = mass of component i contained within a unit volume of phase k (M/L^3)

J_{ki} = flux of component i within phase k per unit total cross-sectional area of biofilm (transport process rate) (M/L^2T)

r_{ki} = rate of production of component i within phase k per unit total volume of biofilm (transformation process rate) (M/L^3T)

In addition to the mass balance on the biofilm, boundary or continuity conditions must be defined for the interfaces between the compartments of the biofilm system. The continuity condition is expressed by the following equation for the interface between two compartments:

$$u_I*(\varepsilon_{k1}*C_{ki1}-\varepsilon_{k2}*C_{ki2})=J_{ki1}-J_{ki2}+r_{ki}''$$ (3)

where u_I =   velocity of the interface relative to the fixed coordinate z (L/T)

r_{ki}'' =   amount of component i produced per unit total cross-sectional area of the interface (interfacial transfer process rate) (M/L^{2}T)

The indices 1 and 2 refer to the sides of the interface, side 2 has higher z coordinates.

BAM Program

Based on the fundamental equations presented above and assumptions concerning the various processes, the computer model BIOSIM was developed which allows simulation of the dynamics of biofilm systems (Reichert, Ruchti and Wanner, 1989). The assumptions made and the resulting simplified equations used by the BIOSIM model are included as Appendix A. In general, the BIOSIM model simulates the processes of molecular diffusion, advection, attachment, detachment and any transformation processes defined by the user.

The BAM model, a modified version of the BIOSIM program, was used in this research to simulate the formation and performance of a biofilm on the wall of a drinking

water pipeline. The simulated processes included the growth and decay of microorganisms within a biofilm and the bulk fluid, the consumption of substrate (food) for microbial growth, the detachment of the microorganisms from the wall into the bulk fluid, the advection of microbial cells as a result of net growth and the diffusion of substrate into the biofilm. Figure 2 is a representation of the processes modeled by the BAM program.
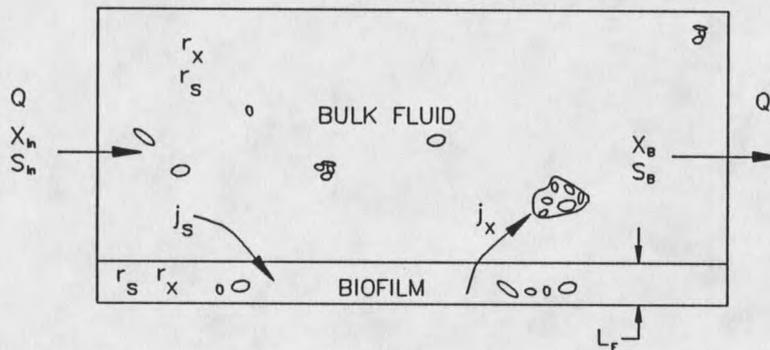
Q = FLOW RATE
S = SUBSTRATE (AOC)
X = PARTICULATES (CELLS)
L_F = BIOFILM THICKNESS
r_i = PROCESS RATE
j_i = MASS FLUX

PROCESSES SIMULATED

r_x { GROWTH OF CELLS IN BULK FLUID & BIOFILM
DECAY OF CELLS IN BULK FLUID & BIOFILM

j_x { DETACHMENT OF CELLS FROM BIOFILM
ADVECTIVE FLUX OF BIOFILM CELLS

r_s SUBSTRATE CONSUMPTION

j_s SUBSTRATE DIFFUSION

FIGURE 2
BAM REPRESENTATION OF PROCESSES

BAM models the transport, transformation and interfacial transfer of i components which are either particulate (X) or dissolved (S) species. For the distribution system application, the particulate species are microorganisms (heterotrophic plate count and coliform bacteria) and the dissolved species is the substrate, assimilable organic carbon (AOC). The equations used by BAM for representing the various processes are presented in the BIOSIM users manual and described below:

Transformation Processes. The growth of microorganisms within the biofilm and the bulk fluid was assumed to follow Monod kinetics, written as:

$$\mu = \mu_m * \left(\frac{C_S}{K_S + C_S} \right) \tag{4}$$

where μ = specific growth rate (1/T)

μ_m = maximum specific growth rate (1/T)

C_S = substrate (AOC) concentration (M/L^3)

K_S = half-saturation constant (M/L^3)

Assuming that microbial decay is a first order process, the net transformation rate of the particulate species (microorganisms) was defined as:

$$r_X = \mu * C_X - b * C_X \tag{5}$$

where b = decay rate coefficient (1/T)

C_X = concentration of particulates (bacteria) (M/L^3)

The transformation rate of the dissolved species (substrate) was defined as:

$$r_S = \frac{-\mu * C_X}{Y_{X/S}} \qquad (6)$$

where $Y_{X/S}$ = Yield coefficient (grams of microorganisms produced per gram of

substrate) (M/M)

These transformation process rate (r_i) equations apply to both the bulk fluid and

the biofilm. The rate equations are differentiated by subscripts for the bulk fluid (B) and

the biofilm (F) which apply to the process rate and to the component concentrations.

For example, the equation for the transformation of microorganisms (X) within the

biofilm (F) is written as:

$$(r_X)_F = \left(\frac{\mu_m * (C_S)_F}{K_S + (C_S)_F} - b \right) * (C_X)_F \qquad (7)$$

where $(C_S)_F$ = concentration of substrate in the biofilm

$(C_X)_F$ = concentration of cells in the biofilm = $\varrho_X * \epsilon_S = \varrho_F$ (M/L^3)

ϱ_X = density of cells (M/L^3)

ϱ_F = biofilm mass density (M/L^3)

Interfacial Transfer Processes. The interfacial transfer rate was modeled as a net

detachment rate, the sum of detachment and attachment, since the magnitude of the

individual processes cannot be identified. The modeled detachment rate r''_{de} is the

product of a detachment velocity, u_{de}, and the concentration of microorganisms in the

film, $(C_X)_F$.

The BAM program can model detachment velocity in a variety of ways: as a

function of biofilm thickness (L_F), biofilm thickness squared, growth rate, or

concentration of microorganisms. The detachment can also be equal to a constant. A negative value for the detachment velocity would be used to represent attachment. As presented in Chapter 5 of this thesis, each of these methods was investigated to determine the most accurate representation of detachment from the pipe wall.

Transport Processes. The transport processes modeled by BAM are the advective flux of microbial cells and the diffusion of substrate into the biofilm. The advective flux, j_X, is described by the following equation:

$$j_X = u_F * (C_X)_F \qquad (8)$$

where u_F =   velocity by which particulate mass is displaced relative to the solid surface (substratum) (L/T)

The diffusion of substrate is calculated using Fick's first law to determine the mass flux of the substrate, j_S:

$$j_S = -f * D * \frac{\partial (C_S)_B}{\partial z} \qquad (9)$$

where D =   diffusivity in pure water (L^2/T)

   f =   ratio of the diffusivities in the biofilm and in pure water

Biofilm. The development of the biofilm is described by:

$$\frac{d(L_F)}{dt} = u_L = u_F(z = L_F) - u_{de} \qquad (10)$$

where L_F =   biofilm thickness (L)

u_L = velocity by which biofilm surface is displaced relative to the substratum (L/T)

u_F = velocity particulate mass is displaced relative to the solid surface (L/T)

u_{de} = net detachment velocity (L/T)

Bulk Fluid. The dynamics of both the dissolved and the suspended particulate components (i) in the bulk fluid are described by the mass balance equation:

$$\frac{d(V_B*(C_i)_B)}{dt}=Q*\left((C_i)_{B_o}-(C_i)_B\right)+A_F*j_i+V_B*(r_i)_B \qquad (11)$$

where $(C_i)_B$ = concentration of component i in the bulk fluid (M/L^3)

$(C_i)_{Bo}$ = concentration of component i in the influent (M/L^3)

V_B = bulk fluid volume (L^3)

Q = volumetric inflow rate (L^3/T)

A_F = area in the unit covered by biofilm (L^2)

j_i = mass flux between biofilm and bulk fluid per unit area of film (M/L^{2}T)

$(r_i)_B$ = net transformation rate in the bulk fluid (M/L^{3}T)

Water Quality Models

The existing dynamic water quality models that simulate the movement and transformation of substances in water under time-varying conditions use simplified

mathematical relationships to represent the physical, biological and chemical processes occurring in a distribution system. The concentration of substances is assumed to follow the first order decay function; that is, the rate of consumption of a substance is proportional to its concentration.

This relationship has been generally accepted as a model of chlorine decay. However, the application of this function to modeling the regrowth of microorganisms within a drinking water system is highly questionable.

EPANET Program

EPANET, developed by the Environmental Protection Agency's Drinking Water Research Division of the Risk Reduction Engineering Laboratory, can perform extended period simulations of hydraulic and water quality behavior within drinking water distribution systems. The water quality module has been successfully used to simulate chlorine decay, fluoride tracer analysis, and source tracing.

The following summary of the EPANET algorithm has been condensed from the EPANET Users Manual.

The EPANET program represents water pipes as links and the endpoints of the pipes as nodes. The hydraulic model used by EPANET for extended period simulations solves the following set of equations for each link, with nodes a and b, and for each node n:

$$h_a - h_b = f(Q_{ab}) \qquad (12)$$

$$\sum_a Q_{an} - \sum_b Q_{nb} - Q_n = 0 \qquad (13)$$

For each storage node s, which represents a tank or reservoir, the following equations are used:

$$\frac{\partial y_s}{\partial t} = \frac{Q_s}{A_s} \qquad (14)$$

$$Q_s = \sum_a Q_{as} - \sum_b Q_{sb} \qquad (15)$$

$$h_s = E_s + y_s \qquad (16)$$

where h_a =   hydraulic grade line elevation at node a (elevation head plus pressure head) (L)

      Q_{ab} =   flow in pipe connecting nodes a and b (L^3/T)

      Q_s =   flow in or out of storage node s (L^3/T)

      $f(Q_{ab})$ =   functional relation between head loss and flow in a link, can be the Hazen-Williams, Darcy-Weisbach or Chezy-Manning formula (L)

                 = $(4.72 * L_{ab} * Q_{ab}^{1.85}) / (C^{1.85} * d^{4.87})$ for Hazen-Williams formula, when L_{ab} and d are expressed in feet and Q is expressed as ft^3/s

      L_{ab} =   pipe length (L)

      C   =   Hazen-Williams roughness coefficient

      d   =   pipe diameter (L)

Q_n = flow consumed or supplied at node n (L³/T)

y_s = height of water stored at node s (L)

A_s = cross-sectional area of storage node s (infinite for reservoirs) (L²)

E_s = elevation of node s (L)

From the specified storage node elevation and initial water height, equation 16 is used as a boundary condition for iteratively solving equations 12 and 13 for all flows Q_{ab} and heads h_a at time zero. The initial network hydraulic solution is utilized with equation 16 to calculate the storage node flow Q_s and the new storage water height for the next time step is determined from Equation 14. The solution process is repeated for each subsequent time step.

The results of the hydraulic simulation are used by the water quality simulator to track the fate of a dissolved substance flowing through the network over time. The flows generated by the hydraulic solution are utilized to solve the following conservation of mass equation for the substance within each link:

$$\frac{\partial(C_i)_B}{\partial t} = v * \frac{\partial(C_i)_B}{\partial L} + r_i \qquad (17)$$

where v = velocity = Q / cross-sectional area (A) (L/T)

A = $\pi d^2/4$ (L²)

r_i = rate of reaction of component i within link (M/L³T)

Equation 17 is solved with a specified initial substance concentration and the following boundary condition from conservation of mass at the beginning of a link (designated node o), with P links joining at node o:

$$(C_i)_{B_O} = \frac{\sum_P Q_P * (C_i)_{B_P}}{\sum_P Q_P + Q_E} + (C_i)_{B_E} \tag{18}$$

where $(C_i)_{BE}=$ substance mass introduced by any external source at node o (M)

    Q_E $=$ flow rate of external source (M/L^3)

The numerical method used by EPANET for solving these equations is known as the Discrete Volume Element Method (DVEM). For each hydraulic time period (of a duration specified by the user), a shorter water quality time step is calculated and each pipe is divided into a series of completely mixed volume segments. Within each water quality time period, the substance contained in every pipe segment is transferred to the next downstream segment. When the next segment is a node, conservation of mass is used to compute the resulting concentration leaving that node. The resulting concentrations at each node are then released into the head end segment of pipes with flow leaving the node. Following the transport phase, the mass within each pipe segment is reacted. This sequence is repeated for the subsequent water quality time steps until the next hydraulic time step, when new pressures and flow rates are calculated, and the entire process is repeated.

Equation 17 calculates the change in substance concentration as the result of hydraulic transport and reaction in the bulk fluid. The equation used for modeling the growth of a substance is given below:

$$r_i = +k_B*(C_i)_B + \left(\frac{k_f}{R_H}\right)*((C_i)_B - c_w) \tag{19}$$

where k_B =   first-order bulk reaction rate constant (1/T)

k_f =   mass transfer coefficient between bulk fluid and pipe wall (L/T)

R_H =   hydraulic radius of pipe = d/4 (L)

c_w =   substance concentration at the wall (M/L^3)

EPANET determines the concentration at the wall from the following mass balance equation:

$$k_f*((C_i)_B - c_w) = k_w * c_w \tag{20}$$

where k_w = wall reaction rate constant (L/T)

Equation 20 equates the mass transfer to a first order reaction rate at the pipe wall. For modeling the microbial population, the wall reaction rate corresponds to the mass flux at the biofilm surface, j_X at $z=L_F$, modeled in the BAM program. This relationship will be further analyzed in Chapter 4.

Based on Equation 20, the reaction rate equation can be rearranged to eliminate the c_w term:

$$(r_i)_B = k_B*(C_i)_B + \frac{k_w*k_f}{R_H*(k_w+k_f)}*(C_i)_B = (K_1+K_2)*(C_i)_B \tag{21}$$

where K_1 and K_2 represent overall first order rate constants for the bulk fluid and the pipe wall reactions, respectively.

The elimination of the wall concentration simplifies the comparison of the EPANET and BAM modeling equations, as presented in Chapter 4.

CHAPTER 4

METHODS

Experimental Data

The basic approach to modeling water quality in drinking water distribution systems was to use experimental results to develop a Biofilm Accumulation Model (BAM) of biofilm growth and detachment. The BAM model parameters were used to predict rate constants for EPANET. EPANET was then used to model the regrowth of microorganisms in a distribution system network. Finally, the accuracy of the EPANET model was assessed to determine the feasibility of using the EPANET water quality module for regrowth phenomena.

The American Water Works Association Research Foundation (AWWARF) provided the Center for Biofilm Engineering at Montana State University with funds to conduct a project investigating regrowth in water distribution systems, *Factors Limiting Microbial Growth in the Distribution System.* As a major part of this project, experiments to study the development of biofilms and the related regrowth of microorganisms within water pipelines were initiated in 1992 and completed in 1995.

The pilot scale experimental setup includes annular reactors and pipe loops, designed to model the hydraulic conditions of a water distribution system pipeline. The two systems operate as continuous flow stirred tank reactors (CFSTR), in which no

concentration gradients exist within the bulk fluid volume, and are useful for observing and evaluating biofilm processes (Characklis, 1989).

The annular reactors and pipes, which are both mild steel, include removable mild steel circular sections known as coupons. The coupons are used to determine the concentration of microorganisms within the biofilm and thereby monitor biofilm development.

Compared to pipe loops, rotating annular reactors are more desirable to use as a monitor of biofilm processes, mainly due to their size. However, the degree of accuracy of annular reactors for modeling water distribution pipeline conditions has not been established. The results of the AWWARF project will determine if the annular reactor results duplicate the pipe loop results and can therefore be used as a more convenient monitoring device.

Since the pipe loops have been shown to be reasonable physical models of pipeline distribution conditions, the data obtained from the pipe loop experiments was used to develop the BAM model (Camper, 1991). Therefore, the following discussion of the experiments will refer to the pipe loops, although the annular reactors were operated under the same conditions.

The experiments completed at the time of this writing are briefly described below:

Description of Experiments

Experiment 1. Five pipe loops were configured in series to simulate 2, 4, 8 and 16 hour residence times in order to determine the most favorable residence time for

growth of microorganisms. All subsequent experiments were performed with parallel loops and at a 2 hour residence time since this was found to be the optimum time.

Experiment 2. Assimilable organic carbon (AOC) and temperature were varied in the 5 different loops to determine the effect of varying AOC and temperature on biofilm accumulation/microorganism growth.

Experiment 3. Chlorine and temperature were varied to determine the effect on the biofilm and the microorganisms. Experiment 3 was performed in the summer.

Experiment 4. Duplicate of experiment 3, performed in the winter.

A schematic of the two hour residence time pipe loop is included as Figure 3. The pipe loops were set up at the Bozeman Water Treatment Plant and fed water from the treatment plant clearwell. The loop influent water was dechlorinated through a GAC column and the AOC reduced by passage through filters containing biologically active carbon. Analysis of the influent water has shown that assimilable organic carbon was present in concentrations which average between .02 to .2 mg/L. Average heterotrophic plate count (HPC) bacterial concentrations showed annual variations of 4,000-30,000 CFU/mL and coliform bacteria were not detected.

The water was supplied to the 4" diameter loops at a rate of 3.7 m³/d (39 gpm) in order to maintain a 2 hour residence time. The recycle rate was set to achieve a flow through the pipe of 213 m³/d, corresponding to a velocity of 1 ft/s. For the pipe loops with substrate addition, assimilable organic carbon was added to the influent water at a