APEX Bacteria add-on

Eunmi Hong, Yongeun Park, Yakov Pachepsky

Environmental Microbial and Food Safety Laboratory

Beltsville Agricultural Research Center

USDA-ARS

September, 2017

Contents

Disclaimer

Although the code has been tested by its developers, no warranty, expressed or implied, is made as to the accuracy and functioning of the program modifications and related program material, nor shall the fact of distribution constitute any such warranty, and no responsibility is assumed by the developers in connection therewith.

Abstract

Water quality models can be essential tools for alleviating pathogen load to water sources, evaluating microbial contamination-related risks, guiding the microbial water quality monitoring, and assessing the effect of agricultural management on the microbial water quality. The Agricultural Policy/Environmental eXtender (APEX) is the watershed-scale water quality model that includes highly detailed representation of agricultural management practices. APEX currently does not have bacterial fate and transport simulation capabilities. The objective of this work was to develop the first APEX bacterial fate and transport add-on that could use the APEX conceptualization of watershed processes, current knowledge about the microbial fate dynamics, and recently introduced concepts of the in-stream microbial fate and transport. The add-on simulates fate and transport of manure-borne and animal waste-borne bacteria. Manure depositions from different days are treated separately. APEX simulates manure erosion and the add-on assumes that bacteria survive in and are exported with manure particulates. Manure weathering and rainfall-triggered bacteria regrowth are accounted for. The two-stage bacteria survival kinetics is simulated in manure and in streams. Bacteria enter stream water with eroded manure, with resuspended sediment at high flow events and with hyporheic transport during the low flow periods. The governing equations are presented, and input variables and output files are described. The modified APEX subroutines, new bacteria fate and transport routines, and examples of input and output files are placed at the website along with this report. Opportunities of expanding the add-on are outlined.

Introduction

Models appear to be essential tools for packaging and applying the accumulated knowledge to the selection of best management practices that would alleviate pathogen load and improve the microbial water quality (Oliver et al., 2016; Cho et al., 2016). Water quality models can be essential tools for alleviating pathogen load to water sources, evaluating microbial contamination-related risks, guiding the microbial water quality monitoring, and assessing the effect of agricultural management on the microbial water quality (De Brauwere et al., 2014, Sokolova et al., 2015; Whelan et al., 2014). Process-based models enable users to evaluate various management scenarios focused on pathogen contamination alleviation.

The Agricultural Policy/Environmental eXtender (APEX) is the watershed-scale water quality model that includes highly detailed representation of agricultural management practices, e.g. irrigation, tillage operation, conservation practices, chemical fertilizer and manure application, pesticide use, in various cropping systems as well as surface runoff and erosion losses of sediment and manure (Williams and Izaurralde, 2006). APEX currently does not have bacterial fate and transport simulation capabilities. Bacterial fate and transport submodel is expected to be a useful APEX component that can allow users to investigate the site- and management-specific potential for microbial contamination of water and soil and the efficiency of mitigation strategies.

The objective of this work was to develop the first APEX bacterial fate and transport add-on module that could use the APEX conceptualization of watershed processes, current knowledge about the microbial fate dynamics, and recently introduced concepts of the in-stream microbial fate and transport.

Governing equations

Manure application

The main sources of microorganisms on agricultural fields or pasture are animal manures or animal waste deposited at grazing lands. The term ‘manure” is used below for brevity to cover both manure fertilizer and waste at grazing lands as bacteria sources.

The add-on does not distinguish between above ground and below ground stores of manure and manure-borne bacteria as it is difficult to separate these two compartments between soil and manure in field experiments. It considers a single manure store. Thus, no separate above- and belowground survival kinetics is considered. This approach was proposed and tested in earlier models, i.e. in (Walker and Stedinger, 1999; Collins and Rutherford, 2004; Wilkinson et al., 2011). It is assumed that bacteria of interest predominantly survive in manure matrix and move with manure particles.

In APEX, a watershed is subdivided into several subareas. Subarea is a spatial unit that is assumed to be homogeneous in terms of all environmental and management parameters. The bacteria add-on performs simulations for each subarea separately.

The daily increase of the total number of manure-borne bacteria after manure application or animal waste deposition is computed as

$$N_d = M_a \cdot N_i \tag{1}$$

$$N_m^+ = N_m + N_d \tag{2}$$

where N_d is the total number of bacteria cells in deposited daily manure, BNU ha^{-1}, BNU is the unit of bacteria cell numbers, i.e. CFU or MPN, M_a is the application rate of manure (MT of manure) ha^{-1}, here and below MT denotes the metric ton, N_i is the concentration of bacteria cells in manure, BNU (MT of manure)$^{-1}$, N_m^+ is the daily increase in the total number of bacteria cells due to deposition, BNU ha^{-1}, and N_m is the total number of the bacteria cells in manure in the beginning of the day, BNU ha^{-1}.

The specific feature of APEX is the explicit simulation of manure erosion during rainfall or irrigation. Manure erosion may occur upon runoff events. The bacteria add-on simulates the bacteria removal with the eroded manure. Manure is subject to weathering and bioturbation between rainfall events. If manure is plowed in, the initial number of bacteria cells in manure is obtained by distributing bacteria from the incorporated manure across the plow layer and then by considering only bacteria in the top one-centimeter depth of soil. The fate and transport of manure-borne bacteria is simulated on daily basis as shown in equation (3):

$$\Delta N_m = \text{Deposition – inactivation – export in runoff + regrowth}$$

$$= N_d - (10^{-k_s} \cdot N_m^+) - (\tfrac{M_e}{M_t} \cdot N_m^+) + (10^{k_r} \cdot N_m^+) \tag{3}$$

where ΔN_m is the daily change of the total number of bacteria cells in the manure store, BNU ha^{-1}, k_s is the rate of bacteria inactivation in manure which is the function of the thermal time and manure properties, d^{-1}, M_e is the amount of eroded manure, MT ha^{-1}, M_t is the total manure amount in manure store, MT ha^{-1}, and k_r is a constant value added to the logarithm of concentration to simulate the regrowth of bacteria caused by rainfall.

The manure erosion is estimated in APEX as:

$$M_e = k_e \cdot (Q \cdot q_p)^{0.5} \cdot PE \cdot SL \cdot M_t^{p_1} \cdot e^{-p_2 \cdot AGPM} \tag{4}$$

where k_e is the erosion rate coefficient, Q is the daily runoff, mm, q_p is the peak runoff rate, mm h^{-1}, PE is the erosion control practice factor, SL is the slope length and steepness factor, $AGPM$ is the standing live and dead plant material, MT ha^{-1}, and $p_1$and p_2 are parameters reflecting the sensitivity of M_e to the total amount of manure and aboveground biomass.

Bacteria survival in manure depends on the type of manure, temperature, time after application, and incorporation (Park et al., 2016). Bacteria survival in manure or animal waste is simulated with a two-stage log-linear equation. The rate constants are dependent on temperature that controls bacteria survival (Franz et al., 2008; Martinez et al., 2013). The daily change in the decimal logarithm of total number of bacteria cells is simulated as:

$$\mathrm{Log}\, N = -k_{s,m} \tag{5}$$

$$k_{s,m} = \begin{cases} k_{s,1,m}(\tau), & t \leq t_{s,m,1} \\ k_{s,2,m}(\tau), & t > t_{s,m,1} \end{cases} \tag{6}$$

where $k_{s,m}$ is the rate coefficient which is the function of temperature τ at time t, $t_{s,m,1}$ is the duration of the first stage, d, τ is the average daily temperature, °C, and $k_{s,1,m}(\tau)$ and $k_{s,2.m}(\tau)$ are survival rates at the first and second survival stage respectively.

The bacteria population may grow, remain stable or die off during the first survival stage, and decrease during the second stage of survival. On the second stage, the values of $k_{s,2}(\tau)$ can be described with the Q_{10} model (Martinez et al., 2013).

$$k_{s,2,m}(\tau) = k_{s,2,m}(20) Q_{10,m}^{\frac{\tau-20}{10}} \tag{7}$$

where $k_{s,2,m}(20)$ is the survival rate at 20 ºC, $Q_{10,m}$ reflects the sensitivity of $k_{s,2,m}$ to temperature that is equal to the change in survival rate occurring as temperature changes by 10 °C. Increase in temperature causes increase in the value of $k_{s,2,m}$ and faster inactivation. The database on parameters in equations (6) and (7) for *E. coli* and fecal coliforms has been published by Park et al. (2016).

The bacteria add-on assumes growth of bacteria in manure on a rainy day. According to Martinez et al. (2013), periods with sudden increases in bacteria concentration correspond to rainfall. The effect of several sequential rainy days to bacteria growth is not known and therefore only the first rainy day is assumed to promote the growth with the rate k_r (see Eq. 3).

Bacteria export in runoff depends on the amount of eroded manure. The fraction of bacteria exported with eroded manure is assumed proportional to the fraction of manure that is exported. The APEX manure erosion equation is modified to account for manure weathering:

$$k_e = p_3 \cdot 10^{-k_w \cdot t_a} \tag{8}$$

where p_3 is manure erosion equation coefficient, k_w is the manure weathering rate coefficient, d^{-1}, and t_a, d, is the manure weathering time, i.e. time between manure application and rainfall.

The bacteria add-on stores and manure amounts and corresponding bacteria numbers separately for each application day. Fate and transport of bacteria from each manure application are simulated separately. Manure erosion and bacteria export for each application day is simulated proportionally to the fraction of the remaining manure from this day application in the total amount of manure available to date.

In-stream processes

In-stream microbial fate and transport processes are simulated at the reach scale and include 1) passive release of bacteria with resuspended streambed sediment during high flow events, 2) the transport of bacteria from streambed sediment during low flow periods, 3) the deposition with settling sediment, and 4) the die-off and survival.

Transport of bacteria from streambed sediments to the water column as the consequence of sediment resuspension during high flow events is simulated based on the linear dependence of the total number of released organisms $N_{B,res}$, BNU, on the mass of resuspended sediment $M_{S,res}$, MT (Kim et al., 2010).

$$N_{B,res} = M_{S,res} \cdot C_B \tag{9}$$

where C_B, BNU (T sediment)$^{-1}$, is the bacteria concentration in streambed sediments.

The active microbial transport from the streambed sediment to water column is conceptualized as a groundwater flux-independent phenomenon (Park et al., 2017; Pachepsky et. al., 2017). Total number of bacteria cells released into the overlying water in a day is proportional to the bottom area of the stream reach and the concentration of bacteria in the streambed $\mathrm{C_B}$:

$$\mathrm{N_A} = \gamma \cdot \mathrm{A_{bottom}} \cdot \mathrm{C_B} \tag{10}$$

where N_A is the total number of bacteria cells released from bottom sediment by active transport, BNU, d^{-1}, $\mathrm{A_{bottom}}$ is the bottom area of the stream reach, m^2, and γ is the bacteria release rate factor, MT m^{-2} d^{-1}.

The net numbers of bacteria deposited with sediment settling is calculated using the following equations:

$$\mathrm{N_{B,dep}} = \mathrm{N_{B,W}} \cdot \frac{\mathrm{K_p} \cdot \mathrm{M_{S,dep}}}{\mathrm{Q_c} + \mathrm{K_p} \cdot \mathrm{M_{S,W}}} \tag{11}$$

$$\log_{10} \mathrm{K_p} = -\,1.6 \; + 1.98 \cdot \log \mathrm{CLAY} \tag{12}$$

where $\mathrm{N_{B,dep}}$ is the total number of bacteria cells deposited, CFU, $\mathrm{N_{B,W}}$ is the total number of bacteria cells in water, BNU, $\mathrm{K_p}$ is the partitioning coefficient of bacteria between the sediments and water, m^3 MT^{-1}, $\mathrm{M_{S,dep}}$ is the mass of deposited sediments, MT, $\mathrm{M_{S,W}}$ is the mass of sediments in water, MT, and $\mathrm{Q_c}$ is the volume of water in the stream reach, m^3, CLAY is the percentage of clay in sediment (Pachepsky et al., 2006).

The $\mathrm{Q_{10}}$ model is utilized for bacteria die-off and survival in water which is mathematically similar to equation of survival in manures (Blaustein et al., 2013). Water temperature is calculated from average daily water temperature (Stefan and Preud’homme, 1993).

$$\log(\mathrm{N_w}) = -\mathrm{k_{s,w}} \tag{13}$$

$$\mathrm{k_{s,w}}(\tau_\mathrm{w}) = \mathrm{k_{s,w}}(20)\mathrm{Q}_{10,\mathrm{w}}^{\frac{\tau_\mathrm{w}-20}{10}} \tag{14}$$

$$\tau_\mathrm{w} = 5.0 + 0.75 * \bar{\tau}_\mathrm{av} \tag{15}$$

where $\mathrm{k_{s,w}}$ is the rate coefficient which is the function of temperature, τ_w is the average daily water temperature, °C, $\mathrm{k_{s,w}}(20)$ is the survival rate at 20°C, parameter $\mathrm{Q_{10,w}}$ reflects the sensitivity of $\mathrm{k_{s,2,w}}$ to temperature, and $\bar{\tau}_\mathrm{av}$ is the average air temperature on the day, °C.

The sine function or the stepwise function can be used to simulate bacteria concentrations in streambed sediment $\mathrm{C_B}$. The sine function is calculated using the following equation:

$$\log \mathrm{C_B} = \mathrm{c_1} \cdot \sin(\mathrm{c_2} \cdot \frac{\mathrm{Days}-\mathrm{c_3}}{366} \cdot \pi) + \mathrm{c_4} \tag{16}$$

Here c_1 the amplitude, c_2 is the angular frequency, c_3 is the phase, days, and $c_4$is the bias. Kim et al. (2010) reported the following parameter values for a Pennsylvania stream: c_1 = 1.543, c_2 = 2.194, c_3= 187 days, and c_4= 3.870.

The stepwise function is calculated using the following equation:

$$\log C_B = \begin{cases} \log C_{B,mean} - H \log \Delta C_B\,, & j < j_{start} \\ \log C_{B,mean} + H \log \Delta C_B\,, & j_{start} \le j \le j_{end} \\ \log C_{B,mean} - H \log \Delta C_B\,, & j > j_{end} \end{cases} \tag{17}$$

where j is the day of year, log$C_{B,mean}$ is the mean of logarithms of bacteria concentrations in cold and warm periods over the year, $\log \Delta C_B$ is the half of the annual magnitude of the logarithm of bacteria concentration in sediment, H=1 and H =-1 for northern and southern hemisphere, respectively, and $\mathrm{j_{start}}$ and $\mathrm{j_{end}}$ are days of year when the first and second seasonal switches of concentrations in sediment occur. On the day $\mathrm{j_{start}}$, logC_B switches from winter to summer values and from summer to winter value if H =1 and H =-1, respectively.

APEX code additions and modifications

Modification of subroutines in original APEX model

Table 1 shows the list of modified subroutines in original APEX model. MAIN.90, BSIM.f90, BSUB.f90, EYSED.f90, NFERT.f90, ROUTE.f90 and RTADD.f90 in original APEX model were revised. Only these subroutines are placed at the web site along with this report.

Table 1. List of modified submodule in original APEX model

Names of original → modified subroutines	**Description**
MAIN.f90 → MAIN_rev.f90	Main program of APEX that initializes variables and computes values for the simulation period. Bacteria add-o variables are initialized.
BSIM.f90 → BSIM_rev.f90	Subroutine that daily simulation for the entire watershed. Added the bacteria add-on use.
BSUB.f90 → BSUB_rev.f90	Subroutine for driving daily subarea simulation. Added call of the ‘Microbe.f90’ submodule
EYSED.f90 → EYSED_rev.f90	Subroutine for predicting daily soil loss caused by water erosion. Manure erosion for each deposition separately
NFERT.f90 → NFERT_rev.f90	Subroutine that applies fertilizer at specified dates and rates or automatically. Added info for the manure application.
RTSED.f90 → RTSED_rev.f90	Subroutine that routes sediment through a reach using a daily time step. Call of the ‘RtMicrobe.f90’ module is added
ROUTE.f90 → ROUTE_rev.f90	Subroutine controls routing operations. Routing bacteria is included.
RTADD.f90 → RTADD_rev.f90	Subroutine that adds subarea outputs to routed outputs to determine total output from a reach. Printout results for bacteria

Added subroutines

Table 2 shows the list of added subroutines into original APEX model. Subroutines for allocating, deallocating and initializing variables and new equations of bacteria fate and transport in the soil and at the reach scale were added into the APEX model. These subroutines are place to the website along with this report.

Table 2. List of added submodule into the original APEX model

Name of submodule	**Description**
ALLOCATE_PARMS_Microbe.f90	Subroutine that allocates arrays associated with the new bacteria submodule
ADEALLOCATE_Microbe.f90	Subroutine that deallocates arrays associated with the new bacteria submodule
AINLZ_Microbe.f90	Subroutine that initializes variables associated with the bacteria add-on
Microbe.f90	Subroutine that performs the daily simulation for fate and transport of bacteria in manure. This module includes bacteria survival and release to runoff.
Microbe_array.f90	Subroutine that deals with daily manure or animal waste application and daily bacteria addition to fields.
modparm_microbe.f90	Subroutine that defines variables used in the new subroutines Microbe.f90 and RtMicrobe.f90.
RtMicrobe.f90	Subroutine that predicts in-stream bacteria fate and transport processes at the reach scale.

Running the code

The bacteria module is coded in FORTRAN for consistency with the parent APEX model and coupled with the APEX model as a subroutine. The model has been compiled using Intel® Visual Fortran Composer XE for Windows.

The input files such as ‘Control.txt’ and ‘Control_name.dat’ must be in same folder where the executable file is. The output files will be created at the same folder. The bacteria subroutine runs with the daily time step along with other APEX components for each subarea. Bacteria fate and transport variables are computed based on other state variables such as the daily amount of applied or deposited manure, daily temperature, stream reach length, depth, and profile, runoff depth, water yield, amount of manure eroded from a subarea, and amount of the suspended and deposited sediment during the run time.

Input and output variables and files

Definitions of parameters and variables are presented Table 3 and 4. Except the text information, data values are introduced either as an integer number or a real number.

Input data

Table 3 shows the input parameters of the bacterial add-on in the control.txt file.

Table 3. Input parameters of the bacterial add-on

Name	**Meaning**	**Unit**	**Symbol in equations**
Gamma_parm	Rate of bacteria release from bottom sediment	T $m^{-2}d^{-1}$	γ
Hemisphere	1 (northern hemisphere) -1 (southern hemisphere)	-	

Jstart	Day of the year when first seasonal switch occurs	d	j_{start}
Jend	Day of the year when second seasonal switch occurs	d	j_{end}
Manure_first_phase_rate	Bacteria survival rate in manure during the first survival stage	d^{-1}	$k_{s,1,m}$
Manure_second_phase_rate	Bacteria survival rate in manure at 20 ^{o}C during the second survival stage	d^{-1}	$k_{s,2,m}\ (20)$
Max_length	Maximum number of manure applications data on which are accounted for	d	
MECOEFF1	Manure erosion equation coefficient	-	k_w
MECOEFF2	Manure weathering rate	d^{-1}	p_3
Microbe_mean_sediment	Average bacteria concentration in sediment over cold and warm periods	BNU (T of sediment)$^{-1}$	$C_{B,mean}$
Microbe_per_unit_mass_of_manure	Initial bacteria concentration in animal waste or manure	BNU (T of manure)$^{-1}$	N_i
Q10_manure	Temperature sensitivity parameter during the second survival stage in manure	-	$Q_{10,m}$
Q10_water	Temperature sensitivity parameter in water	-	$Q_{10,w}$

Regcoeff1	Amplitude (sine function)	-	c_1
Regcoeff2	Angular frequency (sine function)	-	c_2
Regcoeff3	Phase (sine function)	-	c_3
Regcoeff4	Bias (sine function)	-	c_4
Sediment_function	1 (sine function) 2 (stepwise function)		
Threshold_thermal_time_manure	Threshold value that separates the first and the second bacteria survival stages	d	$t_{s,m,1}$
Water_survival_rate	Survival rate at 20 °C in water	d^{-1}	$k_{s,w}\ (20)$

*BNU is the bacteria number unit, i.e. BNU ore MPN

Table 4 shows variables of the bacterial add-on.

Table 4. Variables of the bacterial add-on

Name	**Meaning**	**Unit**	**Symbol in equations**
Iiday	Manure application day	d	
Kpsed	Linear partitioning coefficient of bacteria between the suspended sediment and water	$m^3\ T^{-1}$	K_p
Manure_amount_present	Mass of manure present for each application for given subarea per unit area	$T\ (ha)^{-1}$	M_t
Manure_application_day	Manure application day	day	

Manure_sumb	Total mass of manure present for given subarea per unit area	T ha^{-1}	
Mapd	Manure application rate	T ha^{-1}	M_a
Microbe_active	Amount of bacteria released from streambed sediment by active transport	BNU	N_A
S_DEG	Amount of sediment resuspended in the reach	T	$M_{S,res}$
S_DEP	Amount of sediment deposited in the reach segment	T	$M_{S,dep}$
Microbe_deposition	Total number of bacteria deposited	BNU	$N_{B,dep}$
Microbe_from_manure_in_runoff	Total number of bacteria released from manure to runoff and entering a reach per unit area at subareas from all previous applications	BNU ha^{-1}	
Microbe_from_topsoil_in_runoff	Total number of bacteria released from manure to runoff and entering a reach per unit area at a subarea from all previous applications	BNU ha^{-1}	
Microbe_in_runoff	Total number of bacteria released to runoff and entering a reach per unit area at a subarea for each application	BNU ha^{-1}	
Microbe_in_topsoil_present	The total number of bacteria cells left in manure after release to runoff at subareas at each application.	BNU ha^{-1}	

Microbe_in_topsoil_present_min	Threshold total number of bacteria in manure	BNU ha^{-1}	
Microbe_resuspension	Total number of bacteria cells in resuspended sediment in a reach	BNU	$N_{B,res}$
Microbe_sediment	Bacteria concentration in the bottom sediment	BNU m^{-2}	C_B
Mmwsa	Entire watershed area	ha	
MTRT	Reach travel time	day	
MVARH (9)	Total number of bacteria cells entering a reach (inflow)	BNU	
MVARH (10)	Total number of bacteria cells leaving a reach (outflow)	BNU	
MVARH (20)	Concentration of bacteria cells in inflow to a reach	BNU m^{-3}	
MVARH (21)	Concentration of bacteria cells in outflow from a reach	BNU m^{-3}	
MVARH (30)	Total number of bacteria cells released from bottom sediment by active transport	BNU	
MVARH (31)	Total number of bacteria cells released from bottom sediment by active transport	BNU m^{-3}	
MVARH (32)	Total number of bacteria cells in resuspended sediment during high flow event	BNU	
MVARH (33)	Total number of bacteria cells in resuspended sediment during high flow event	BNU m^{-3}	
MVARW(21)	Amount of manure applied	MT	

MVARW(30)	Total number of bacteria cells in manure applied	BNU	
Mwsa	Area of subareas	ha	
Number_of_manure_applications_to_date	Number of days after manure application	days	
PRMT62_new	Modified PARM62, manure erosion equation coefficient value	-	PE
Sedin	Mass of the bottom sediment in a reach	T	$M_{S,W}$
Streamflow(1)	Daily volume of inflow to a reach	m^3	
Streamflow(2)	Daily volume of outflow from a reach	m^3	
Streamflowvarh(1)	Flow rate of the reach inflow	m^3 s^{-1}	
Streamflowvarh(2)	Flow rate of the reach outflow	m^3 s^{-1}	
Streamflowvarw	Inflow to a reach from subareas	mm	
Thermal_time_manure	Cumulative thermal time in manure	day	
Today_thermal_time_manure	Thermal time in manure	day	
Total_microbe_in_topsoil	The total number of bacteria left in all previous manure depositions after release to runoff at a subarea.	BNU/ha	ΔN_m
Water_metric	Total volume of water in a reach	m^3	
Wtemp	Water temperature	^{o}C	T_w
YMNU_each	Mass of manure eroded at subareas	T ha^{-1}	
YMNU_ratio	Fraction of manure eroded	-	

Output data

The bacteria add-on creates 3 output files: Microbe.RCH, Microbe.SAD, and Microbe.DWS. This output files contain simulation date and results of simulation. These results include simulated bacteria concentrations in runoff (CFU ml^{-1}).

(1) Microbe.RCH

Name	**Meaning**
RCID	Reach ID
Year, Day, Tday	Year, Month, day
Rain (mm)	Precipitation
Area (ha)	Area of subarea or reach outlet
WYin ($m^{3/}s$)	Inflow into a reach
WYout (m^3/s)	Outflow from a reach
Min (BNU/m^3)	Total number of bacteria cells entering a reach
Mout (BNU/m^3)	Total number of bacteria cells leaving a reach

(2) Microbe.SAD

Name	**Meaning**
#	Subarea number
ID	Subarea ID
Y, M, D	Year, Month, day
CPNM	Crop name
M (BNU /ha)	Total number of bacteria cells at the unit area
M (BNU)	Total number of bacteria cells
Area (ha)	Area of subarea

(3) Microbe.DWS (Daily watershed outlet file)

Name	**Meaning**
Y, M, D	Year, Month, day
Rain (mm)	Precipitation
Area (ha)	Entire watershed area
Flow (mm), Flow(m^3/s)	Flow and flowrate at the watershed outlet
M (BNU /ha), M (BNU /100 ml)	Total number of bacteria and average concentration in stream water
YMNU (MT/ha)	Total manure erosion
RSDM (MT/ha)	Amount of manure present

Outlook

The APEX capability to simulate fate and transport of manure-borne bacteria can be expanded to simulate sources of bacteria other than one consequent applications of one type of manure.

1) Stream reach-based sources

- Bacteria from retention ponds with release to streams
- Wildlife input
- Inputs from recreation sites
- Septic tanks and sewage lagoons

2) Subarea based sources

- Different types of manure
- Different manure application techniques
- Seasonality in manure microbial composition

The effect of the above-listed sources can be simulated in near future since the literature information is available to provide simple models for their simulations. These models will be added as needed when projects containing such sources will be developed.

Another expansion of microbial capabilities of APEX will require additional research. This is the expansion toward description of interactions of microbial communities with algae, the effect of nutrients on microbes of interest, and the microbial community structure as the factor of survival for specific microorganisms of interest. The above topics are currently active areas of study.

Yet another set of microbial processes to include in APEX are in-stream processes occurring in bottom sediment and periphyton. As the knowledge on fate of microorganisms of interest in these media will be accumulated, models can be included in APEX.

Overall the structure of APEX allows relatively painless expansion of the model to address microbial water quality issues.

References

Blaustein, R. A., Pachepsky, Y., Hill, R. L., Shelton, D. R., & Whelan, G. (2013). Escherichia coli survival in waters: temperature dependence. Water research, 47(2), 569-578.

Cho, K. H., Pachepsky, Y. A., Oliver, D. M., Muirhead, R. W., Park, Y., Quilliam, R. S., & Shelton, D. R. (2016). Modeling fate and transport of fecally-derived microorganisms at the watershed scale: State of the science and future opportunities. Water Research, 100, 38-56.

Collins, R., and Rutherford, K., 2004. Modelling bacterial water quality in streams draining pastoral land. *Water Res.* 38(3): 700-–712.

De Brauwere, A., Ouattara, N. K., & Servais, P. (2014). Modeling fecal indicator bacteria concentrations in natural surface waters: A review. Critical Reviews in Environmental Science and Technology, 44(21), 2380-2453.

Franz, Eelco, Alexander V. Semenov, Aad J. Termorshuizen, O. J. De Vos, Jan G. Bokhorst, and Ariena HC Van Bruggen. "Manure-amended soil characteristics affecting the survival of E. coli O157: H7 in 36 Dutch soils." Environmental Microbiology 10, no. 2 (2008): 313-327.

Kim, J. W., Pachepsky, Y. A., Shelton, D. R., & Coppock, C. (2010). Effect of streambed bacteria release on E. coli concentrations: Monitoring and modeling with the modified SWAT. Ecological Modelling, 221(12), 1592-1604.

Martinez, G., Pachepsky, Y. A., Shelton, D. R., Whelan, G., Zepp, R., Molina, M., & Panhorst, K. (2013). Using the Q 10 model to simulate E. coli survival in cowpats on grazing lands. Environment international, 54, 1-10.

Oliver, D. M., Porter, K. D. H., Pachepsky, Y. A., Muirhead, R. W., Reaney, S. M., Coffey, R., Quilliam, R. S. (2016). Predicting microbial water quality with models: Over-arching questions for managing risk in agricultural catchments. Science of the Total Environment, 544, 39-47.

Pachepsky, Y. A., Sadeghi, A. M., Bradford, S. A., Shelton, D. R., Guber, A. K., & Dao, T. (2006). Transport and fate of manure-borne pathogens: Modeling perspective. agricultural water management, 86(1), 81-92.

Pachepsky, Y., Stocker, M., Saldaña, M. O., & Shelton, D. (2017). Enrichment of stream water with fecal indicator organisms during baseflow periods. Environmental monitoring and assessment, 189(2), 51.

Park, Y., Pachepsky, Y., Hong, E. M., Shelton, D., & Coppock, C. (2017). Release from Streambed to Water Column during Baseflow Periods: A Modeling Study. Journal of Environmental Quality, 46(1), 219-226.

Park, Y., Pachepsky, Y., Shelton, D., Jeong, J., & Whelan, G. (2016). Survival of manure-borne Escherichia coli and fecal coliforms in soil: Temperature dependence as affected by site-specific factors. Journal of Environmental Quality, 45(3), 949-957.

Sokolova, E., Petterson, S. R., Dienus, O., Nyström, F., Lindgren, P. E., & Pettersson, T. J. (2015). Microbial risk assessment of drinking water based on hydrodynamic modelling of pathogen concentrations in source water. Science of the Total Environment, 526, 177-186.

Stefan, H. G., & Preud'homme, E. B. (1993). Stream temperature estimation from air temperature. JAWRA Journal of the American Water Resources Association, 29(1), 27-45.

Walker Jr., F.R. Jr., and Stedinger, J.R., 1999. Fate and transport model of *Cryptosporidium*. *J. Environ. Eng*. 125: 325-333.

Whelan, G., Kim, K., Pelton, M. A., Soller, J. A., Castleton, K. J., Molina, M., Pachepsky, Y., Zepp, R. (2014). An integrated environmental modeling framework for performing quantitative microbial risk assessments. Environmental Modelling and Software, 55, 77-91.

Wilkinson, R.J.,McKergow, R.J., Davies-Colley, R.J., Ballantine,D.J., and Young, R.G., 2011. Modelling storm-event E. coli pulses from the Motueka and Sherry Rivers in the South Island, New Zealand. *N. Z. J. Mar. Freshw. Res.* 45 (3): 369-393

Williams, J. R., & Izaurralde, R. C. (2006). The APEX model. Watershed models, 437-482.