Sediment-Associated Bacteria Release and Settling in SWAT bacteria routing

Model and SWAT add-on manual

Jung Woo Kim, Yakov Pachepsky, Daniel R. Shelton

Environmental Microbial and Food Safety Laboratory

Beltsville Agricultural Research Center

USDA-ARS

August, 2009

Abstract

Streambed sediment has been attracting attention as a reservoir for bacteria, including pathogenic strains. Soil and Water Assessment Tool (SWAT2005) includes bacteria transport subroutine in which bacteria die-off is the only in-stream process. The purpose of this technical bulletin was to describe SWAT bacteria routing module by including sediment-associated bacteria release and settling in streams. Streambed bacteria release and settling were computed based on the sediment resuspension and deposition modules in SWAT. The model and the necessary modifications of the SWAT 2005 code are presented.

Disclaimer

Contents

Abbreviations

cfu – colony forming units

List of symbols

$bact_{ch}$	the amount of bacteria in the stream water in the reach segment (# cfu)
$bact_{ch,i}$	the amount of bacteria in the stream water in the reach segment at the beginning of the time period (# cfu)
$bact_{deg}$	the amount of bacteria released from streambed in the reach segment (# cfu)
$bact_{dep}$	the amount of bacteria attached on the deposited sediments in stream water in the reach segment (# cfu)
$bact_{free}$	the amount of free-floating bacteria in the stream water in the reach segment (# cfu)
$bact_{sus}$	the amount of bacteria attached on the suspended sediments in the stream water in the reach segment (# cfu)
bsc_1 - bsc_4	the regression coefficients in streambed bacteria concentration equation
$clay$	the percentage of clay in suspended sediment in stream water in the reach segment
$conc_{bact,ch}$	the concentration of bacteria in the stream water in the reach segment (# cfu/100 mL)
$conc_{bact,sed}$	the concentration of bacteria in the upper layer of streambed in the reach segment (# cfu/ton sediment)
$conc_{sed,ch,i}$	the initial sediment concentration in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O)
$conc_{sed,ch,mx}$	the maximum concentration of sediment that can be transported by the water (ton sediment/m^3 H_2O or kg sediment/L H_2O)

$conc_{sed,dep}$	the concentration of sediment deposited in water in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O)
$conc_{sed,sus}$	the concentration of sediments suspended in water in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O)
day	the day of year
sed_{deg}	the amount of sediment reentrained in the reach segment (metric tons)
sed_{dep}	the amount of sediment deposited in the reach segment (metric tons)
C_{ch}	the channel cover factor which is defined as the ratio of degradation from a channel with a specified vegetative cover to the corresponding degradation from a channel with no vegetative cover
K_{ch}	the channel or soil erodibility factor (cm/hr/Pa) which is a function of properties of the bed or bank materials
K_p	the linear partitioning coefficient of bacteria between the sediments and water (m^3 H_2O/ton sediment or L H_2O/kg sediment)
V_{ch}	the volume of water in the reach segment (m^3 H_2O)

1. Background

Streambed sediment has been increasingly attracting attention as a reservoir of bacteria, including pathogenic strains. Streambed microorganisms can be released to water in substantial amounts as sediments resuspend (Byappanahalli et al., 2003; Muirhead et al., 2004; Giddings and Oblinger, 2004; Cinotto, 2005). Streambed sediment provides a favorable chemical and biological environment for bacteria (Gannon et al., 1983), and can protect bacteria from protozoan predators (Davies et al., 1995). Therefore, sediment-associated bacteria release and settling model was developed and the code was added to the current SWAT bacteria module.

2. Model development

In sediment channel routing, the maximum concentration of sediment that can be transported by the water, $conc_{sed,ch,mx}$, (ton/m^3 or kg/L) is compared to the concentration of sediment in the reach at the beginning of the time step, $conc_{sed,ch,i}$ (Neitsch et al., 2005).

If $conc_{sed,ch,i} < conc_{sed,ch,mx}$, resuspension is the dominant process in the reach segment and the net amount of sediment reentrained is calculated:

$$sed_{deg} = \left(conc_{sed,ch,mx} - conc_{sed,ch,i}\right) \cdot V_{ch} \cdot K_{ch} \cdot C_{ch} \qquad [1]$$

where sed_{deg} is the amount of sediment reentrained in the reach segment (metric tons), $conc_{sed,ch,mx}$ is the maximum concentration of sediment that can be transported by the water (ton sediment/m^3 H_2O or kg sediment/L H_2O), $conc_{sed,ch,i}$ is the initial sediment concentration in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O), V_{ch} is the volume of water in the reach segment (m^3 H_2O), K_{ch} is the channel or soil erodibility factor (cm/hr/Pa) which is a function of properties of the bed or bank materials, and C_{ch} is the channel cover factor which is defined as the ratio of degradation from a channel with a specified vegetative cover to the corresponding degradation from a channel with no vegetative cover. When sediment resuspends, both bacteria in sediment solution and on sediment particles are released, and the net amount of bacteria released from streambed is calculated:

$$bact_{deg} = sed_{deg} \cdot conc_{bact,sed} \qquad [2]$$

where $bact_{deg}$ is the amount of bacteria released from streambed in the reach segment (# cfu), sed_{deg} is the amount of sediment reentrained in the reach segment (metric tons), and $conc_{bact,sed}$ is the concentration of bacteria in the upper layer of streambed in the reach segment (# cfu/ton sediment). Bacteria concentration in streambed is calculated by the empirical regression equation, logarithmic sine function of the days of year:

$$\log(conc_{bac,sed}) = bsc_1 \cdot \sin\left(bsc_2 \cdot \frac{day - bsc_3}{366} \cdot \pi \right) + bsc_4 \qquad [3]$$

where $conc_{bac,sed}$ is the concentration of bacteria in the upper layer of streambed (# cfu/ton sediment), day is the day of year, and bsc_1 through bsc_4 are the regression coefficients in streambed bacteria concentration equation.

If $conc_{sed,ch,i} > conc_{sed,ch,mx}$, deposition is the dominant process in the reach segment and the net amount of sediment deposited is calculated:

$$sed_{dep} = (conc_{sed,ch,i} - conc_{sed,ch,mx}) \cdot V_{ch} \qquad [4]$$

where sed_{dep} is the amount of sediment deposited in the reach segment (metric tons), $conc_{sed,ch,i}$ is the initial sediment concentration in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O), $conc_{sed,ch,mx}$ is the maximum concentration of sediment that can be transported by the water (ton sediment/m^3 H_2O or kg sediment/L H_2O), and V_{ch} is the volume of water in the reach segment (m^3 H_2O). When suspended sediment deposits, bacteria on settling sediment particles are deposited, and the bacteria in the stream water are partitioned into 3 phases based on the Bai and Lung's (2005) linear adsorption assumption:

$$\frac{bact_{free} + bact_{sus} + bact_{dep}}{bact_{ch,i}} = \frac{1 + K_p \cdot conc_{sed,sus} + K_p \cdot conc_{sed,dep}}{1 + K_p \cdot conc_{sed,ch,i}} \qquad [5]$$

where $bact_{ch,i}$ is the amount of bacteria in the stream water in the reach segment at the beginning of the time period (# cfu), $bact_{free}$ is the amount of free-floating bacteria in the stream water in the reach segment (# cfu), $bact_{sus}$ is the amount of bacteria attached on the suspended sediments in the stream water in the reach segment (# cfu), $bact_{dep}$ is the amount of bacteria attached on the deposited sediments in the stream water in the reach segment (# cfu), K_p is the linear partitioning coefficient of bacteria between the sediments and water (m^3 H_2O/ton sediment or L H_2O/kg sediment), and $conc_{sed,ch,i}$ is the initial sediment concentration in the reach (ton sediment/m^3 H_2O or kg sediment/L H_2O). Here, $conc_{sed,ch,i}$ is the sum of $conc_{sed,sus}$ which is the concentration of sediments suspended in water in the reach and $conc_{sed,dep}$ which is the concentration of sediment deposited in water in the reach.

Therefore, using the variables used in the sediment computation, the net amount of bacteria settled from stream water is calculated as:

$$bact_{dep} = bact_{ch,i} \cdot \frac{K_p \cdot sed_{dep}}{V_{ch} + K_p \cdot \left(conc_{sed,ch,i} \cdot V_{ch}\right)} \qquad [6]$$

where $bact_{dep}$ is the amount of bacteria settled from stream water in the reach segment (# cfu), $bact_{ch,i}$ is the amount of bacteria in the stream water in the reach segment at the beginning of the time period (# cfu), K_p is the linear partitioning coefficient of bacteria between the sediments and water (m^3 H_2O/ton sediment or L H_2O/kg sediment), sed_{dep} is the amount of sediment deposited in the reach segment (metric tons), V_{ch} is the volume of water in the reach segment (m^3 H_2O), and $conc_{sed,ch,i}$ is the initial sediment concentration in the reach (ton sediment/m^3 H_2O or kg sediment/L

H_2O). The linear partitioning coefficient is calculated from the empirical regression equation (Pachepsky et al., 2006):

$$K_p = 10^{-1.6} \cdot clay^{1.98} \qquad [7]$$

where K_p is the linear partitioning coefficient of bacteria between the sediments and water (m^3 H_2O/ton sediment or L H_2O/kg sediment) and *clay* is the percentage of clay in suspended sediment in stream water in the reach segment (%). *clay* normally varies between 2 and 50%.

Once the amount of bacteria released and settled has been calculated, the final amount of sediment in the reach is determined:

$$bact_{ch} = bact_{ch,i} + bact_{deg} - bact_{dep} \qquad [8]$$

where $bact_{ch}$ is the amount of bacteria in the stream water in the reach segment (# cfu), $bact_{ch,i}$ is the amount of bacteria in the stream water in the reach segment at the beginning of the time period (# cfu), $bact_{deg}$ is the amount of bacteria released from streambed in the reach segment (# cfu), and $bact_{dep}$ is the amount of bacteria settled from stream water in the reach segment (# cfu).

The final bacteria concentration in the reach is calculated:

$$conc_{bact,ch} = \frac{bact_{ch}}{V_{ch}} \cdot 10^{-4} \qquad [9]$$

where $conc_{bact,ch}$ is the concentration of bacteria in the stream water in the reach segment (# cfu/100 mL), $bact_{ch}$ is the amount of bacteria in the stream water in the reach segment (# cfu), and V_{ch} is the volume of water in the reach segment (m^3 H_2O).

3. SWAT input variables that pertain to bacteria release and settling in the stream

Variable Name	Definition	SWAT Input File

CLAY	$clay$: the percentage of clay in suspended sediment in stream water in the reach segment (%)	.bsn
BSC1 through BSC4	bsc_1 through bsc_4 : the regression coefficients in streambed bacteria concentration equation	.bsn

4. Model limitations and further developments

The developed model uses the measured dynamics of bacteria in streambed that is approximated with Eq. [3]. Also the model does not take into account the distribution of bacteria in sediment with depth. Further work will be performed to overcome these limitations.

5. References

Bai, S.; Lung, W.S., 2005. Modeling sediment impact on the transport of fecal bacteria. Water Research, 39(20): 5232-5240.

Byappanahalli, M.; Fowler, M.; Shively, D.; Whitman, R., 2003. Ubiquity and persistence of *Escherichia coli* in a midwestern coastal stream. Applied and Environmental Microbiology, 69(8): 4549-4555.

Cinotto, P.J., 2005. Occurrence of fecal-indicator bacteria and protocols for identification of fecal-contamination sources in selected reaches of the West Branch Brandywine Creek, Chester County, Pennsylvania: U.S. Geological Survey Scientific Investigations Report 2005-5039, pp 91.

Davies, C.M.; Long, J.A.H.; Donald, M.; Ashbolt, N.J., 1995. Survival of fecal microorganisms in marine and fresh-water sediments. Applied and Environmental Microbiology, 61(5): 1888-1896.

Gannon, J.J.; Busse, M.K.; Schillinger, J.E., 1983. Fecal coliform disappearance in a river impoundment. Water Research, 17(11): 1595-1601.

Giddings, E.M.; Oblinger, C.J., 2004. Fecal-indicator bacteria in the Newfound Creek watershed, western North Carolina, during a high and low streamflow condition, 2003: U.S. Geological Survey Scientific Investigations Report 2004–5257, accessed January 18, 2005, at http://pubs.water.usgs.gov/sir2004-5257.

Muirhead, R.W.; Davies-Colley, R.J.; Donnison, A.M.; Nagels, J.W., 2004. Faecal bacteria yields in artificial flood events: quantifying in-stream stores. Water Research, 38: 1215-1224.

Neitsch, S.L.; Arnold, J.G.; Kiniry, J.R.; Williams, J.R., 2005. Soil and Water Assessment Tool Theoretical Documentation (Version 2005).

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: 81-92.

6. Algorithm implementation and computer code listing

The SWAT model was compiled with COMPAQ VISUAL FORTRAN 6.0 and run using the input files (watershed topography, soils, landuse, etc.) generated from AVSWATX interface.

The new model is embedded in SWAT's bacteria routing module ('rtbact.f'). In the following Table 1, the new variables/parameters used in this module are related to variables in equations used in the model description. Sediment routing-related variables are taken from the SWAT Fortran common field.

Table. Parameter synchronization

in codes	in equations
con_bact_sed	$conc_{bact,sed}$
kp	K_p
clay	$clay$
bsc1 through bsc4	bsc_1 through bsc_4
sedin	$conc_{sed,ch,i} \cdot V_{ch}$
deg	sed_{deg}
dep	sed_{dep}

6.1. Project configuration settings

In the FORTRAN workspace,

Click on **Project / Settings / Fortran** tab

Click on the **Category** drop down menu and set the following:

Floating point – Floating Point Exception: **0**

Optimizations – Math Library: **Fast**

Run time – check the box next to the following:

Array & String Bounds

Floating Point Underflow

Integer Overflow

Flawed Pentium

Click **OK**.

Click on **Project / Settings / Debug** tab

Set the **Working directory** as the directory which includes the SWAT input files.

Click **OK.**

Click **File / Save Workspace**

6.2. Modification of source codes (based on SWAT2005)

6.2.1. 'modparm.f' (external dependency file)

Add new parameters and variables used in common. To compile the SWAT code, delete the 'modfparm.f' file from the project list in the FORTRAN workspace.

```
=================================================================================================
       module parm

!!     sediment-associated bacteria (Kim et al., 2009)
       real :: clay, bsc1, bsc2, bsc3, bsc4
       real :: sedin, deg, dep

       real :: wshd_sw, wshd_snob, wshd_pndfr, wshd_pndv, wshd_pndsed
       real :: wshd_wetfr, wshd_resfr, wshd_resha, wshd_pndha, percop

…
=================================================================================================
```

6.2.2. 'readbsn.f'

Add statements to read new parameters.

```
=================================================================================================
…

       read (103,*,iostat=eof) dorm_hr
       if (eof < 0) exit

!!     sediment-associated bacteria (Kim et al., 2009)
       read (103,*,iostat=eof) clay
       if (eof < 0) exit
       read (103,*,iostat=eof) bsc1
       if (eof < 0) exit
       read (103,*,iostat=eof) bsc2
       if (eof < 0) exit
       read (103,*,iostat=eof) bsc3
       if (eof < 0) exit
       read (103,*,iostat=eof) bsc4
       if (eof < 0) exit

       exit
       end do

…
=================================================================================================
```

Optionally, set the default values of the parameters.

```
=======================================================================================================
…

       if (bactminp <= 0.) bactminp = 0.
       if (cn_froz <= 0.) cn_froz = .000862

!!     sediment-associated bacteria (Kim et al., 2009)
       if (clay <= 0.) clay = 20.
       if (bsc1 <= 0.) bsc1 = 1.543
       if (bsc2 <= 0.) bsc2 = 2.194
       if (bsc3 <= 0.) bsc3 = 187.
       if (bsc4 <= 0.) bsc4 = 3.870

       call caps(petfile)
       call caps(wwqfile)

…
=======================================================================================================
================
```

6.2.3. ‘rtsed.f’ (in-stream sediment routing module)

Remove the variables set in ‘modparm.f’ as common variables in the specification statement.

```
=======================================================================================================
…

       use parm

       integer :: jrch
!      real :: qdin, sedin, vc, cyin, cych, depnet, deg, dep
       real :: qdin, vc, cyin, cych, depnet
       real :: depdeg, dot

…
=======================================================================================================
```

6.2.4. ‘rtbact.f’ (in-stream bacteria routing module)

Specify new variables and parameter, and add new sediment-associated bacteria module after computing bacteria die-off (applied for only less-persistent bacteria).

```
=======================================================================================================
…

       use parm
       implicit none

!!     sediment-associated bacteria (Kim et al., 2009)
       real :: kp, con_bact_sed
       real, parameter :: pi = 3.1416

       real, external :: Theta

…

       totbactlp = totbactlp * Exp(-Theta(wdlprch,thbact,wtmp)*tday)
       totbactlp = Max(0., totbactlp)

!!     sediment-associated bacteria (Kim et al., 2009)
!!     considering only less persistent bacteria(totbactlp)
```

```
        con_bact_sed = 1e6 * 10**(bsc1*sin(bsc2*pi*(tday-bsc3)/366)+bsc4)  !! cfu/ton
        totbactlp = totbactlp + con_bact_sed * deg / 1e4  !! resuspension

        kp = (10**(-1.6)) * (clay**(1.98))
        totbactlp = totbactlp * (1 - (kp*dep)/(netwtr+kp*sedin))  !! deposition

!!      new concentration
        netwtr = 0.

...
====================================================================================================
```

6.3. Modification of input data file (based on SWAT2005)

6.3.1. ‘basins.bsn’

Add the values of new parameters.

```
====================================================================================================
Basin DATA           .bsn file Tue Feb 17 17:49:00 2009 AVSWATX2003 - SWAT interface MDL
Modeling Options: Land Area
Water Balance:
           1.000    | SFTMP : Snowfall temperature [ºC]
           0.500    | SMTMP : Snow melt base temperature [ºC]
           4.500    | SMFMX : Melt factor for snow on June 21 [mm H2O/ºC -day]

...

           0.000    | GDRAIN_BSN
           0.000    | CN_FROZ
           0.000    | DORM_HR
          20.000    | CLAY(%)
           1.543    | BSC1
           2.194    | BSC2
         187.000    | BSC3
           3.870    | BSC4
====================================================================================================
```