



Department of Population Health  
and Reproduction

University of California, Davis



# Development of Stream Bacteria Transport Model for SWAT

**Pramod Pandey, PhD**

**Faculty/Specialist**

*Department of Population Health and Reproduction*

*School of Veterinary Medicine*

*University of California, Davis, USA*

**Coauthors in this research:**

**Drs Michelle Soupir, and Chris Rehmann**

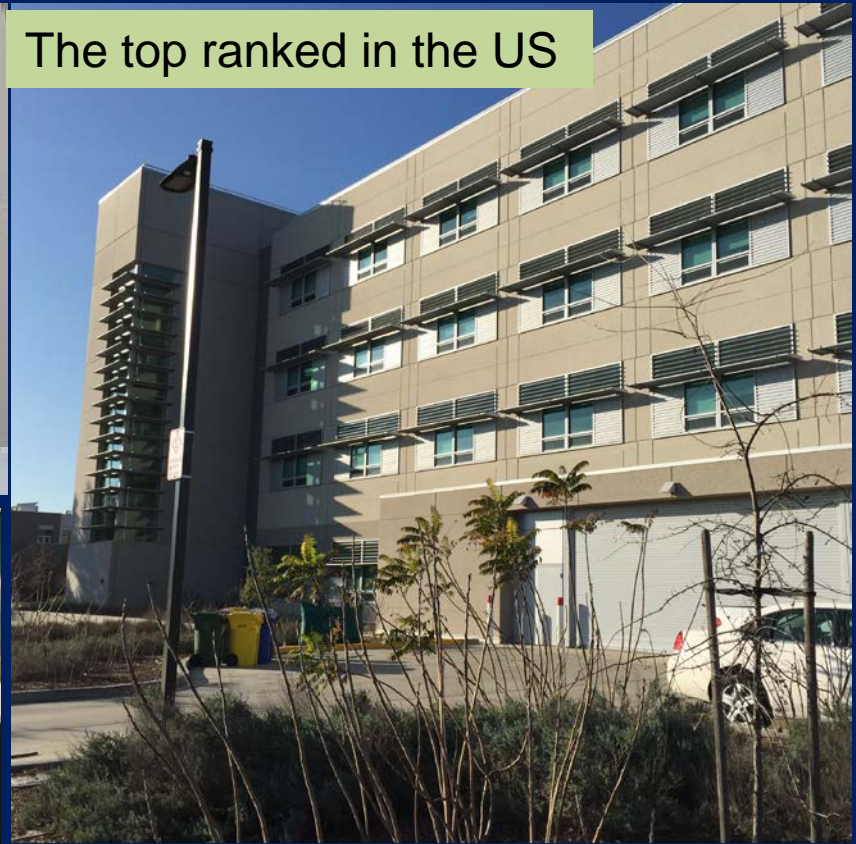
***Iowa State University, Ames, Iowa***

International Soil and Water Assessment Tool Conference  
Beijing Normal University, China  
July 27- 29, 2016

# Brief Introduction – UC Vet Med School



The top ranked in the US



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# My research - water/bacteria/waste



Dairy farm



Dairy lagoon



Manure application

Yosemite National Park – Merced river



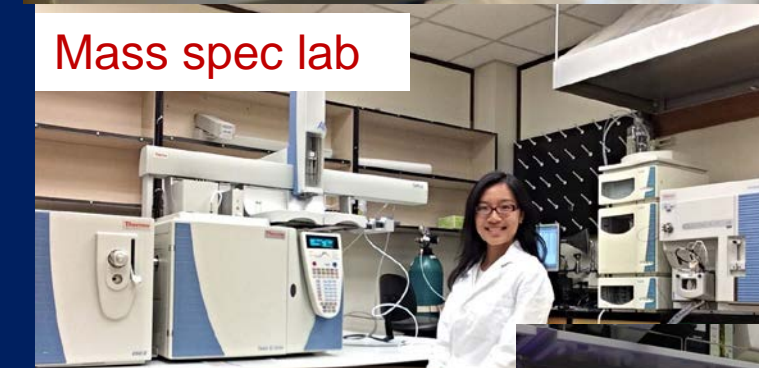
Water sampling

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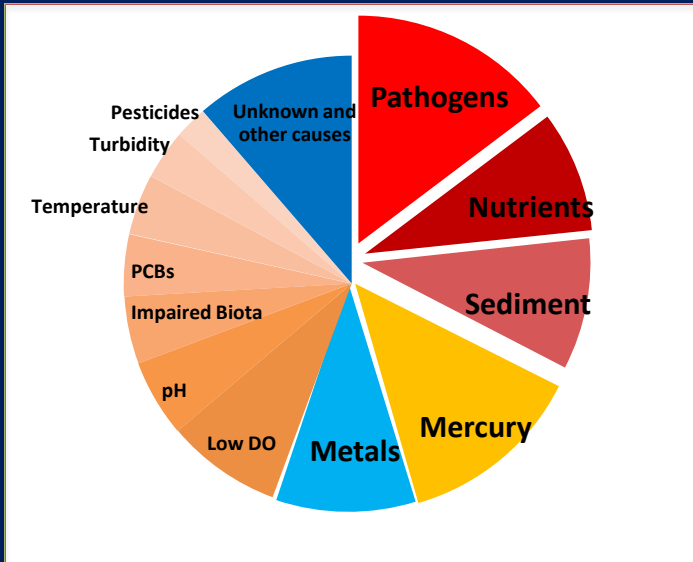


# My lab research- microbiology/mass spec



# Bacteria Contamination-Why an issue?

- Pathogen contamination is the leading cause of impairments.





# In-stream contamination – Iowa work

In stream pollution



Stream sampling in Iowa



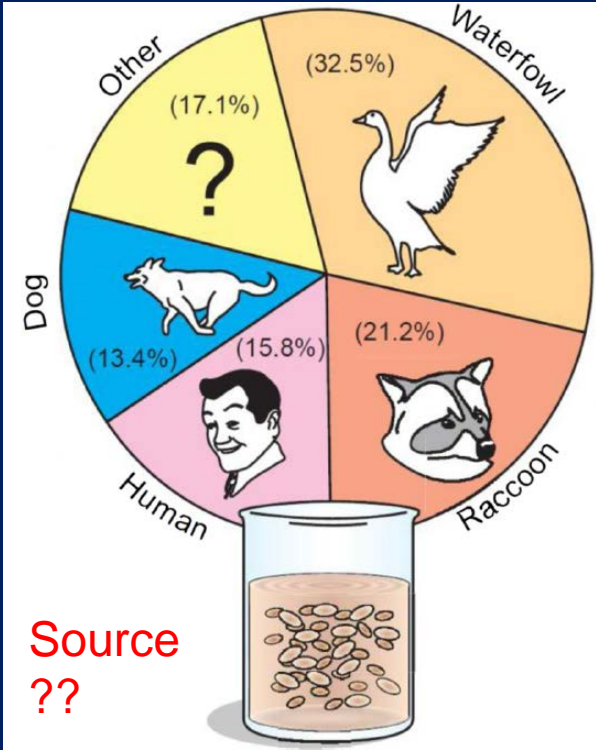
Dead fish in streams



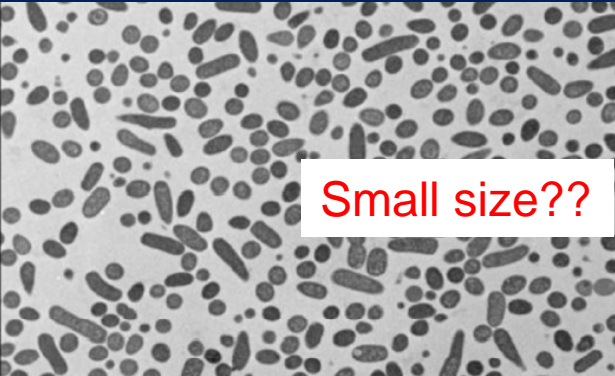
Heavy algae bloom



# Challenges in bacteria transport modeling

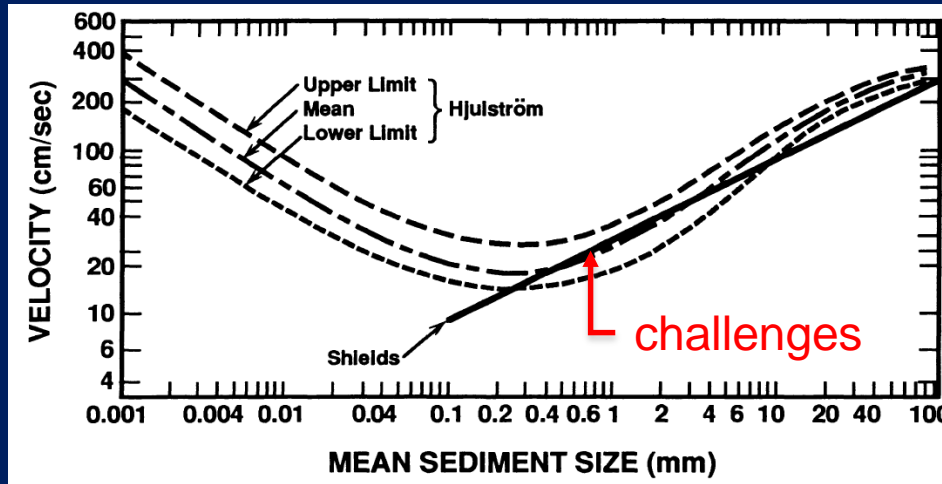
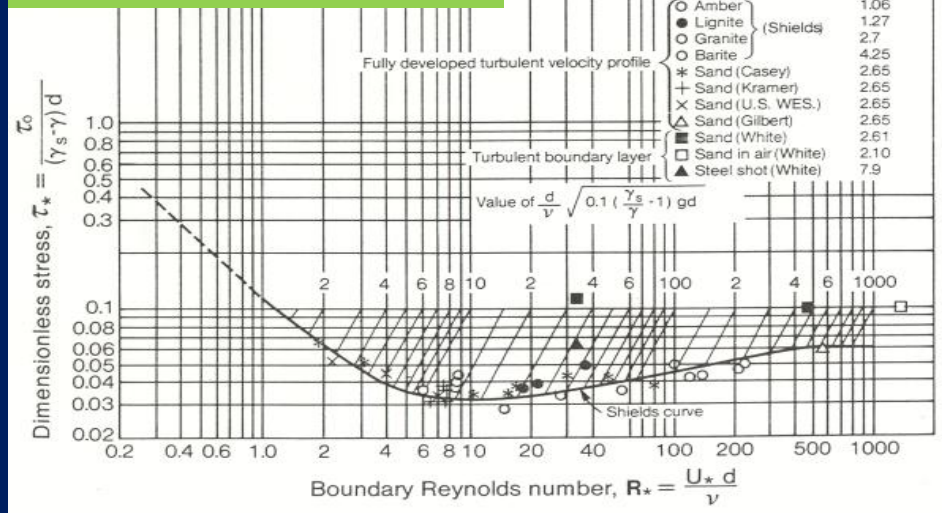


Malakoff (2002)



Pandey et al. (2014)

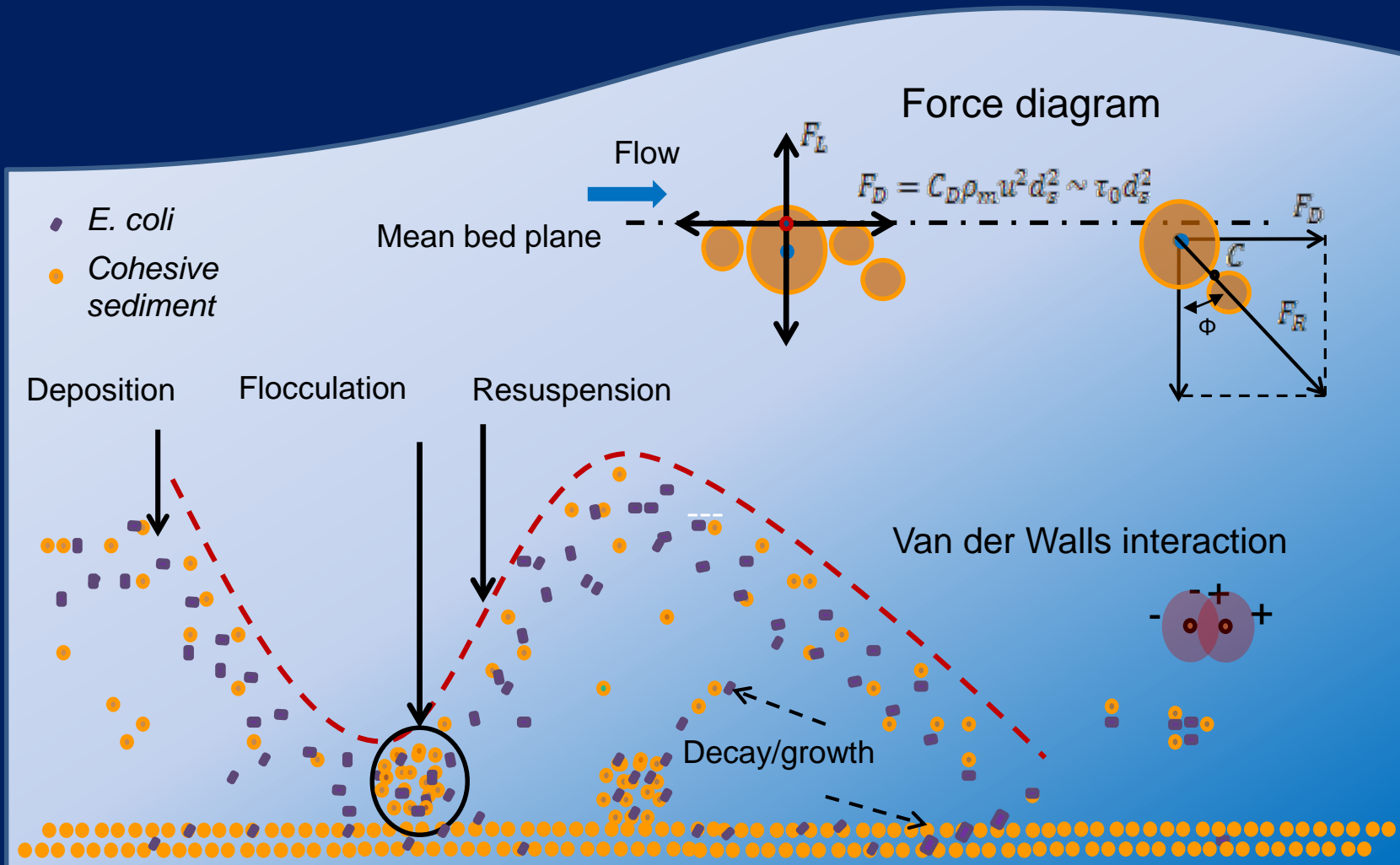
## Modelling complexity



Issue: poor performance for small sizes < 0.002 mm  
 Solution: need for new empirical approaches



# Conceptual bacteria dynamics in streams





# Bacteria modelling-new empirical formula

## New approach

$$\tau_c = \frac{C_2(F_c + F_g)}{C_1 d^2} \longrightarrow \tau_c = \left(1 + \frac{ae^{bp}}{d^2}\right) \tau_{cn}$$

$C_1 = \pi \rho_w C_d / 8C$   $C_2 = \text{constant}$   $F_g = \text{gravitational force}$   $F_c = \text{cohesive force}$   
 $\tau_c = \text{critical shear stress at cohesive and gravitational forces}$

$$E = 10^{-4} \left( \frac{\tau - \tau_{cn}}{\tau_c - \tau_{cn}} \right)^n \quad \text{and} \quad \tau_{cn} = 414 \cdot d; \quad d = \text{particle size}$$

## Semi - empirical approach

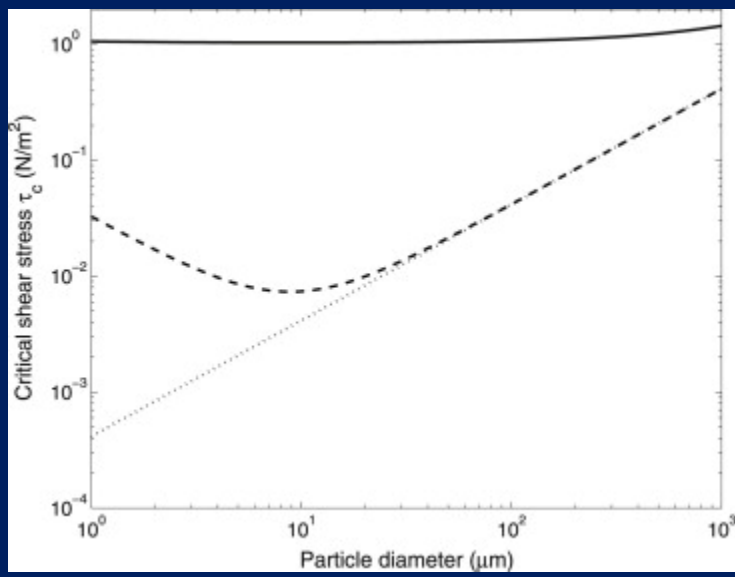
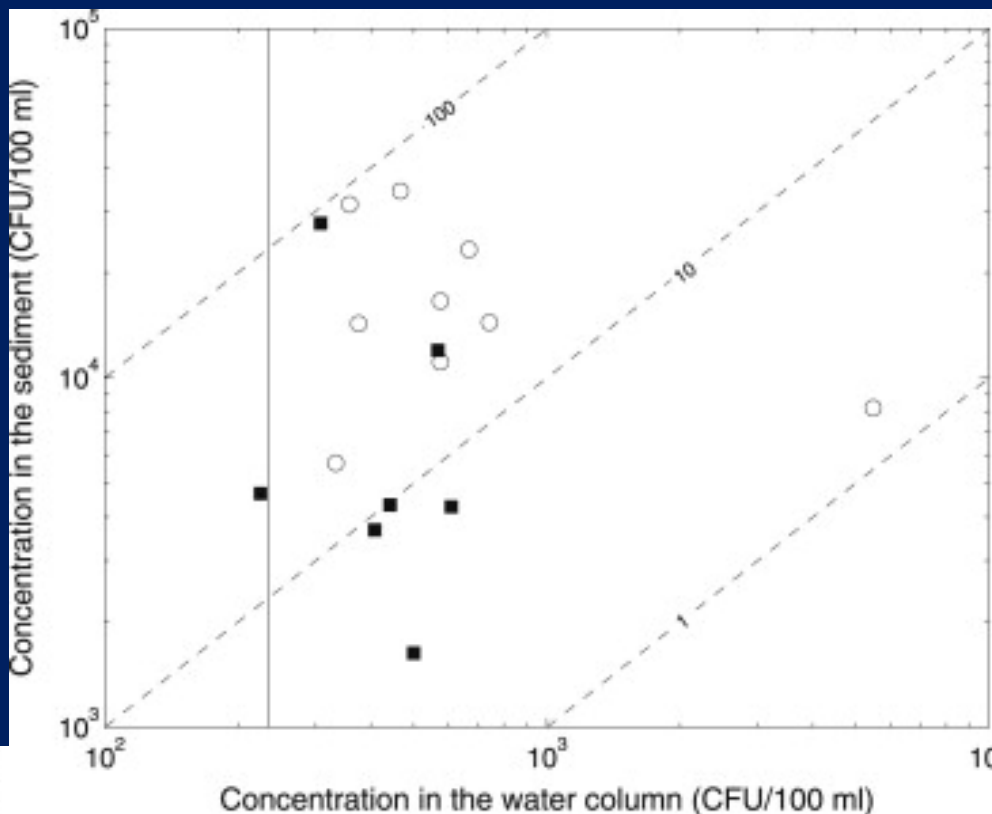
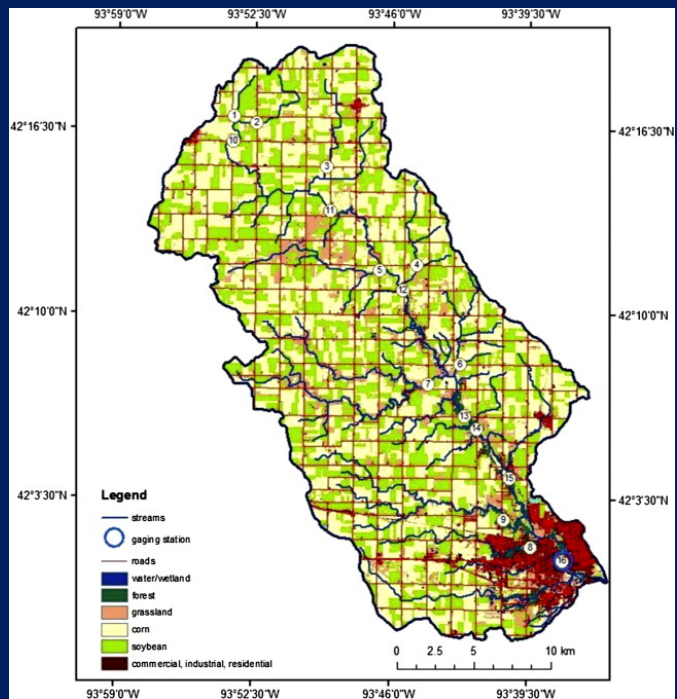
$\phi = \text{Repose angle}$

Shields parameter  $\downarrow$   $\tau_{cs}$

Cohesive parameter  $\downarrow$

$$\frac{\tau_{cs}}{g(\rho_{sf} - \rho)d} = \frac{\alpha_3 \tan \phi}{(\alpha_1 + \alpha_2 \tan \phi)} + \frac{F_c \tan \phi / (\alpha_1 + \alpha_2 \tan \phi)}{g(\rho_{sf} - \rho)d^3}$$

# Bacteria modelling – 1. Resuspension in stream





Water Research

Volume 46, Issue 1, 1 January 2012, Pages 115–126



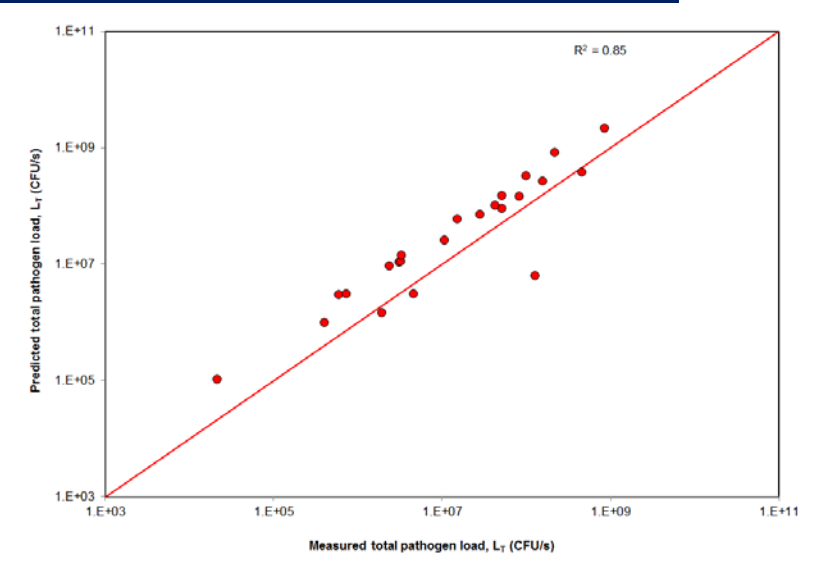
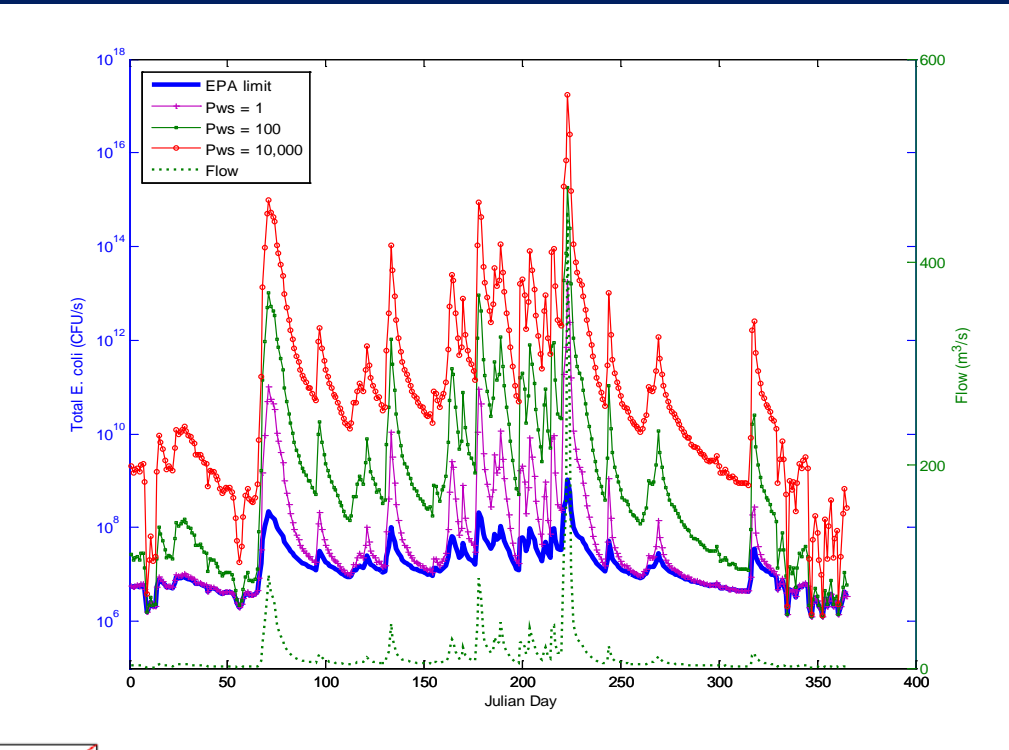
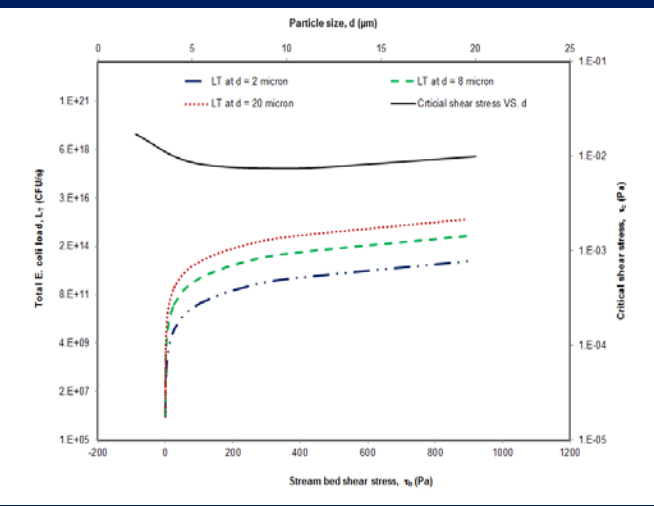
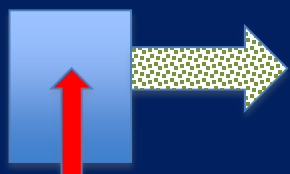
**A model for predicting resuspension of *Escherichia coli* from streambed sediments**

Prasad K. Pandey<sup>a</sup>, Michelle L. Soupir<sup>a</sup>, Chris R. Rehmann<sup>b</sup>  





# Bacteria modelling- 2. Pathogen Load



Technical Paper

**Assessing the Impacts of *E. coli* Laden Streambed Sediment on *E. coli* Loads over a Range of Flows and Sediment Characteristics**

Pramod K. Pandey Postdoctoral scholar and Michelle L. Soupir Assistant Professor

Version of Record online: 21 JUN 2013  
 DOI: 10.1111/jawr.12079  
 © 2013 American Water Resources Association

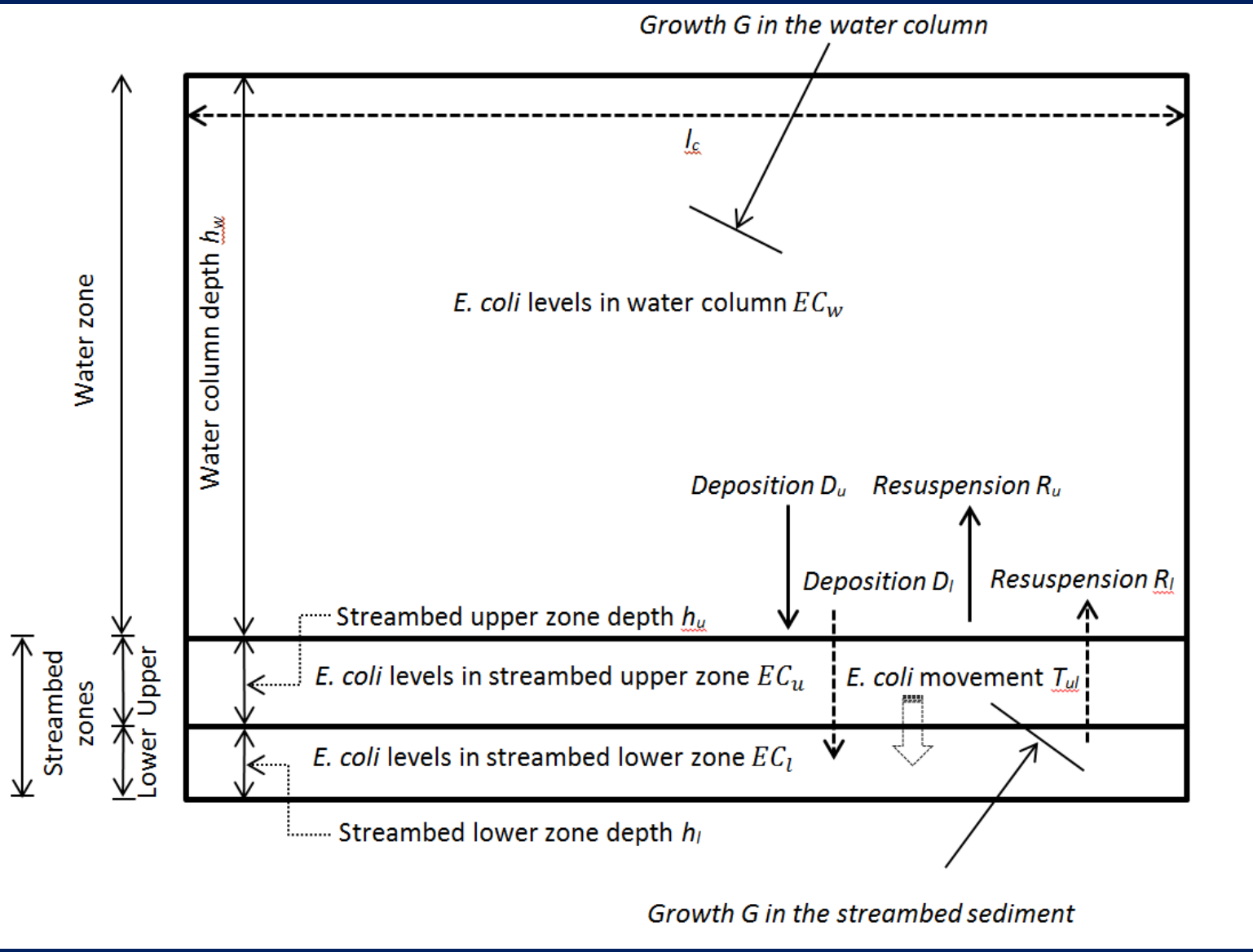
Issue

**JAWRA**  
 DECEMBER 2013

JAWRA Journal of the American Water Resources Association  
 Volume 49, Issue 6, pages 1261–1269, December 2013

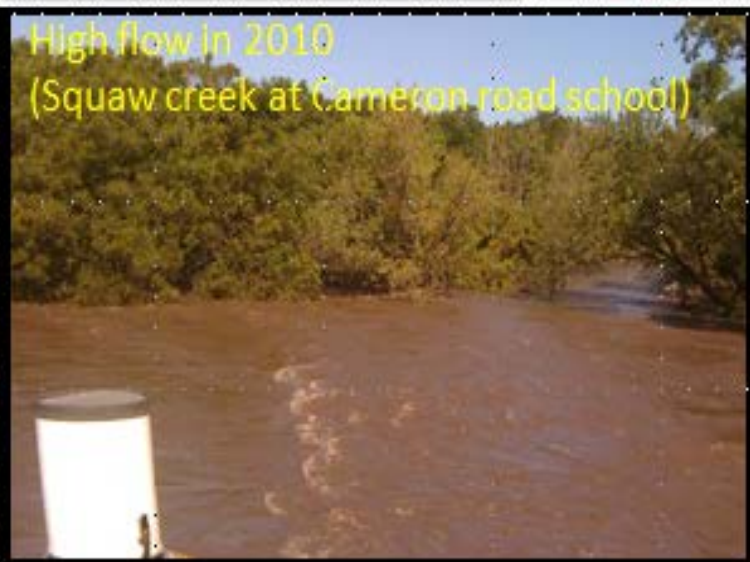


# Bacteria modelling- 3. SWAT model





# Bacteria (*E. coli*) monitoring in stream



# Subroutines for SWAT bacteria transport

The screenshot displays the Microsoft Visual Studio IDE with the following components:

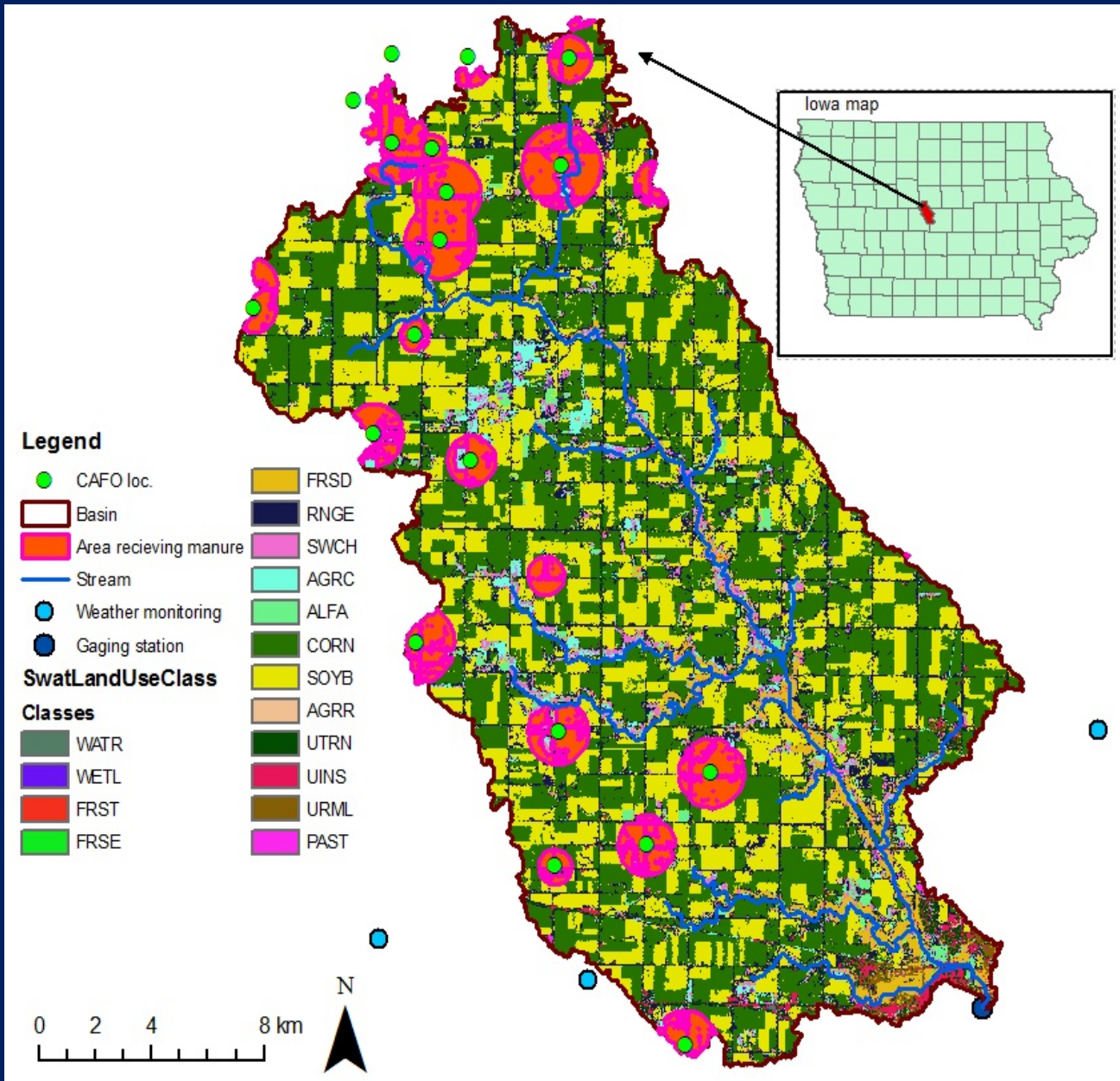
- Code Editor:** Shows Fortran code for the `rtbact1.f90` file. The code includes a list of subroutines and functions called, such as `Intrinsic: Exp, Max, Sqrt, Min` and `SWAT: netgrowth_wat, netgrowth_sed`. It also contains a `use parm` block with numerous `real, external` and `integer` declarations for variables like `netgrowth_sed`, `netgrowth_wat`, `ii`, `jrch`, `initotwatecoli`, `inibedsedecoli`, `insussed`, `netwtr`, `tday`, `totwatecoli`, `atcwatecoli`, `atcwatecolicon`, `uatcwatecoli`, `sussedmass`, `bedsedmass`, `bedsedvol`, `acbedsedvol`, `acbedsedmass`, `taub`, `tauc`, `taunc`, `Eoa`, `na`, `resvel`, `setvel`, `ressedmass`, `setsedmass`, `resedecoli`, `setecoli`, `fa`, `fua`, `bedsedecoli`, `bedseddep`, `acbedseddep`, `wetp`, `chz`, `chn`, `chs1`, `c3`, `c5`, `gr`, `sr`, `a`, `b`, `dp`, `rows`, `roww`, `mu`, `wtmp`, `hydr`, `pi`, `kp`, `sedin`, `qdin`, `sussedcon`, `bedsedecolicon`, `totbactp`, `totbactlp`, `ressedcon`, `initotwatlp`, `initotwatp`, `inibedsedlp`, `inibedsedp`, `atcwatlp`, `atcwatp`, `uatcwatlp`, `uatcwatp`, `uatcwatlpcon`, `uatcwatpcon`, `reslp`, `resp`, `setlp`, `setp`, `bedsedlpcon`, `bedsedpcon`, `bedsedlp`, `bedsedp`, `totwatlp`, `totwatp`, `atcwatecolicon`, `atcwatlpcon`, `atcwatpcon`, `uatcwatecoli`, `reachwatr`, `wtrin`, `totbactecoli`, `insussedmass`, `isedlp_conc`, `watvol`, `insussedcon`, `inwatlp_conc`, `watlp_conc`, `insedlp_conc`, `sussedmass_bf`, `dtl`, `dbl`, `bedsedmass_tl`, `bedsedmass_b1`, `bsen_tl`, `bsen_b1`, `bsec_tl`, `bsec_b1`, `res_f`, `nres_f`, `res_ecn_tl`, `res_ecn_b1`, `ressedmass_tl`, `ressedmass_b1`, `ibsen_tl`, `ibsen_b1`, `ibsec_tl`, `ibsec_b1`, `ibsec`, `ibsen`, `bsen`, `bsec`, `wen`, `wec`, `in_bedseden`, `bedseden`, `in_bedsedec`, `bedsedec`, `sussedcon_b1`.
- Solution Explorer:** Lists various subroutines and functions in the project, including `subday.f`, `submon.f`, `substor.f`, `subwq.f`, `subyr.f`, `sumhyd.f`, `sumv.f`, `sunglaser.f`, `sunglass.f`, `sunglasu.f`, `surface.f`, `surfst_h2o.f`, `surfstor.f`, `surq_daycn.f`, `surq_greenampt.f`, `swbl.f`, `sweep.f`, `swu.f`, `tair.f`, `telobjre.f`, `telobs.f`, `telpar.f`, `tgen.f`, `theta.f`, `tillfactor.f`, `tillmix.f`, `tmeas.f`, `tran.f`, `transfer.f`, `tstr.f`, `ttcoef.f`, `urb_bmp.f`, `urban.f`, `varint.f`, `vbl.f`, `virtual.f`.
- Output Window:** Shows the output from the Intel Parallel Debugger Extension.
- Properties Window:** Shows the file properties for `rtbact1.f90`.



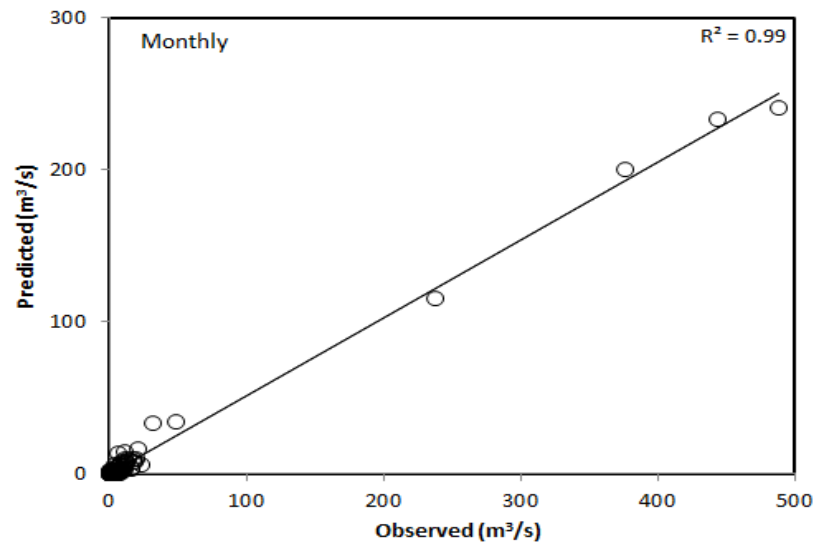
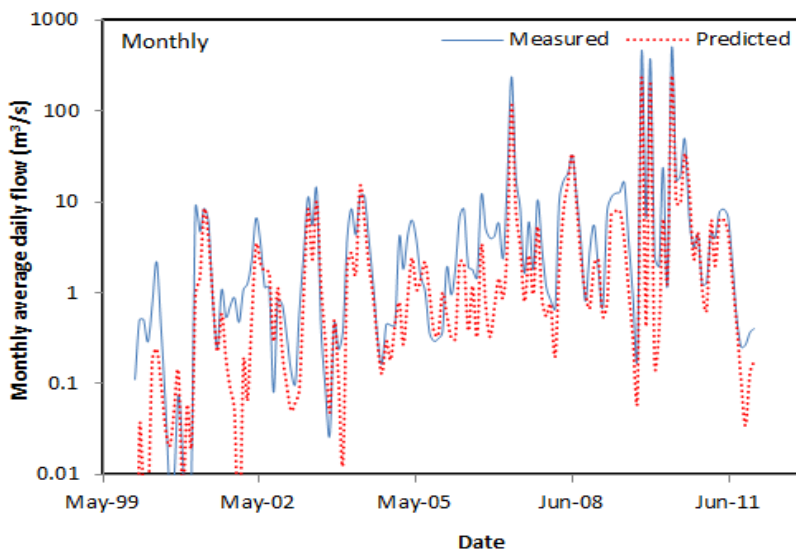
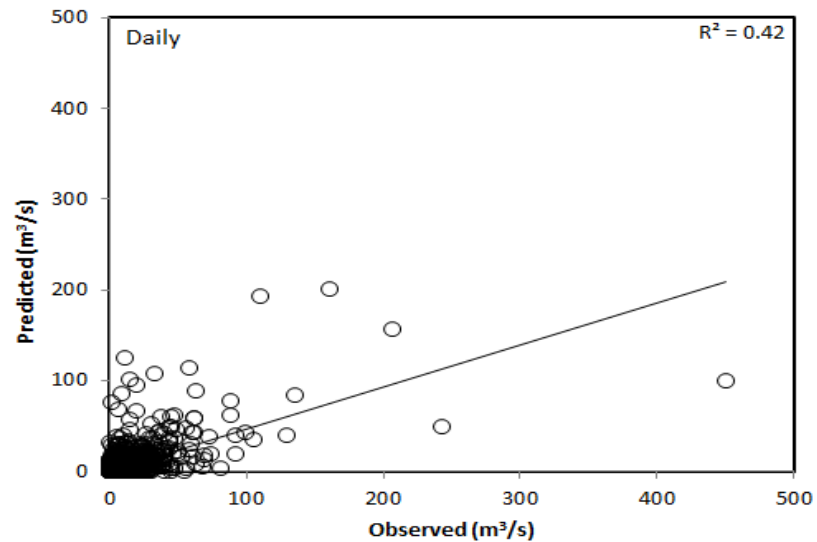
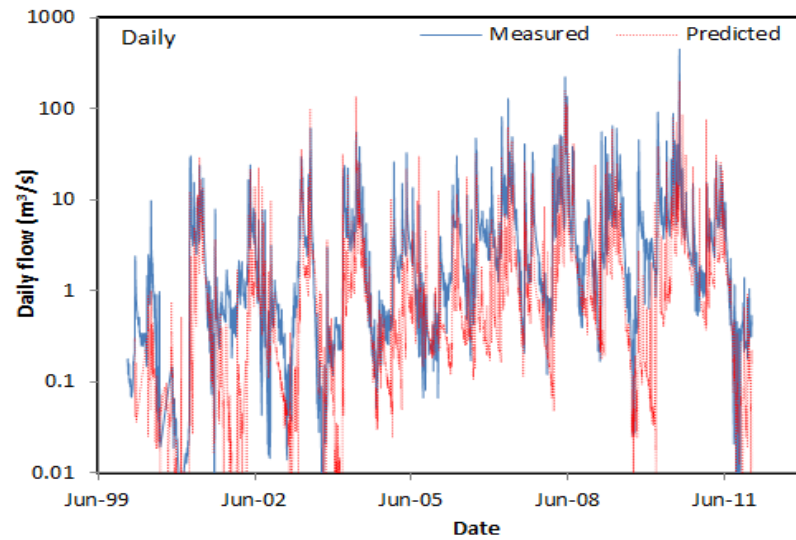
My background/experience in programming of ROTO model did help; challenges were in GIS interphase



# SWAT setup - Bacteria modeling



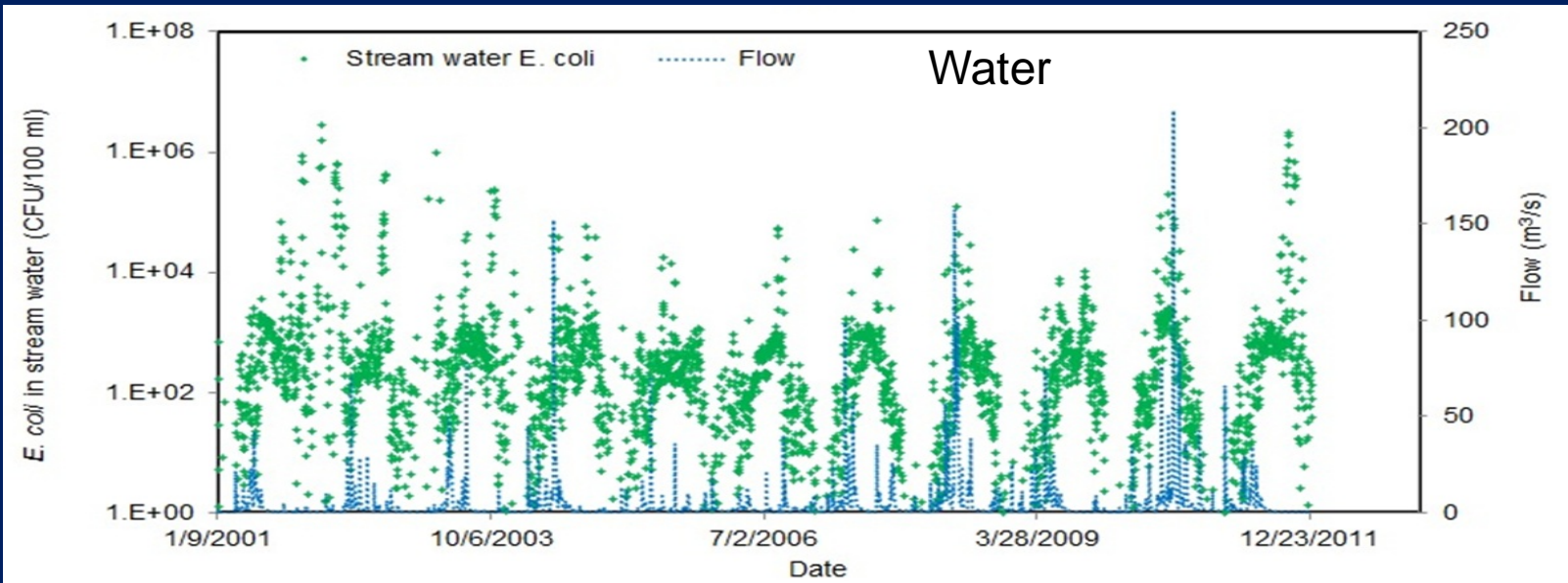
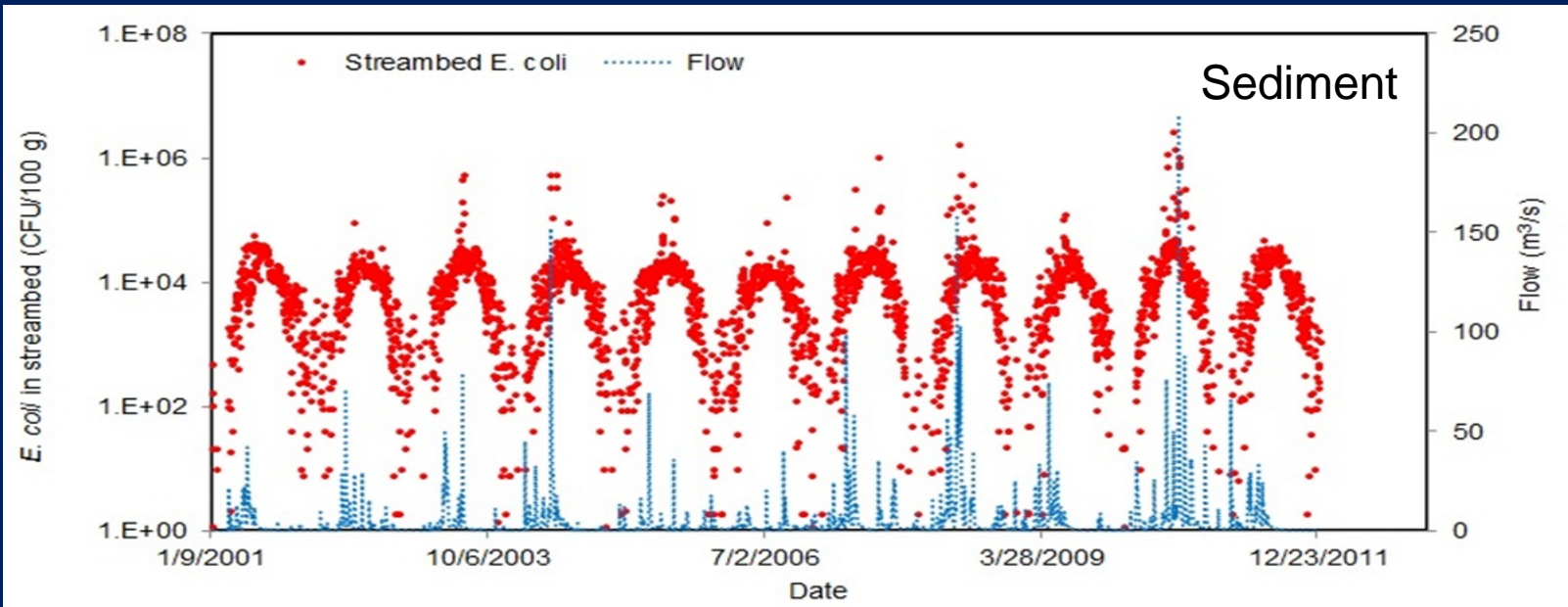
# SWAT in-stream flow (observ./pred.)



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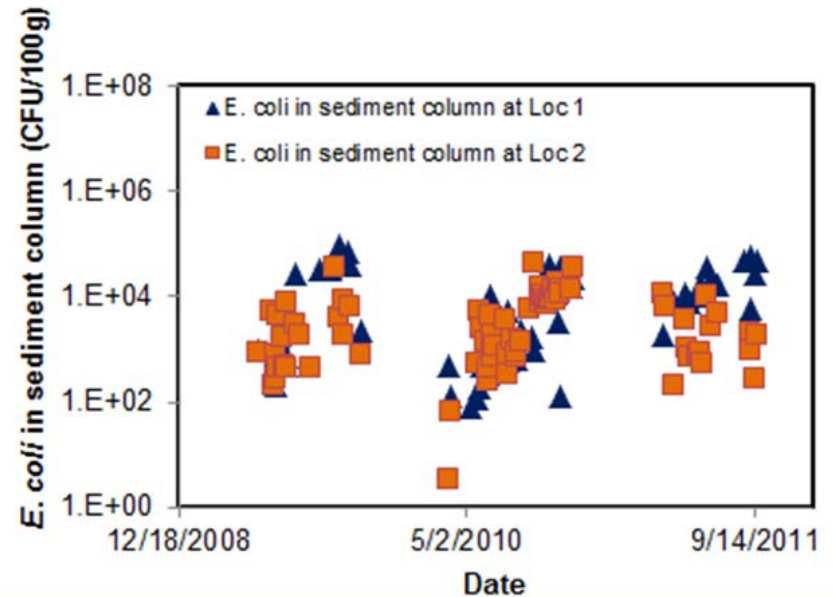
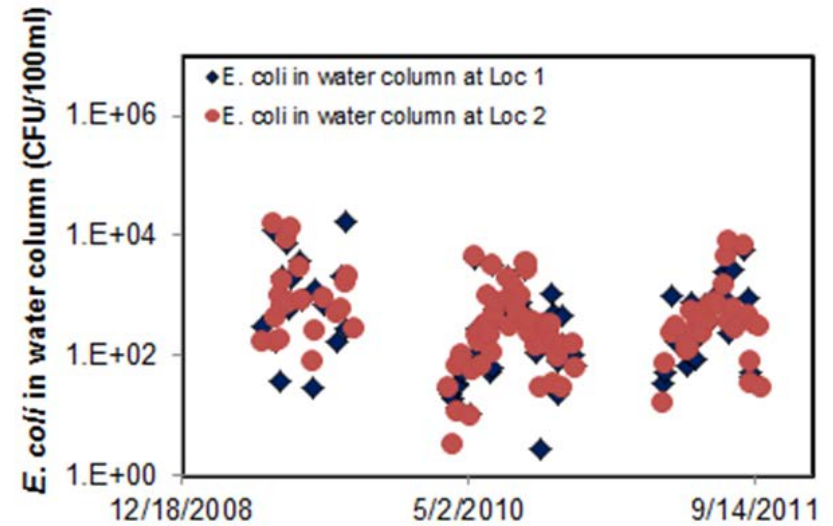
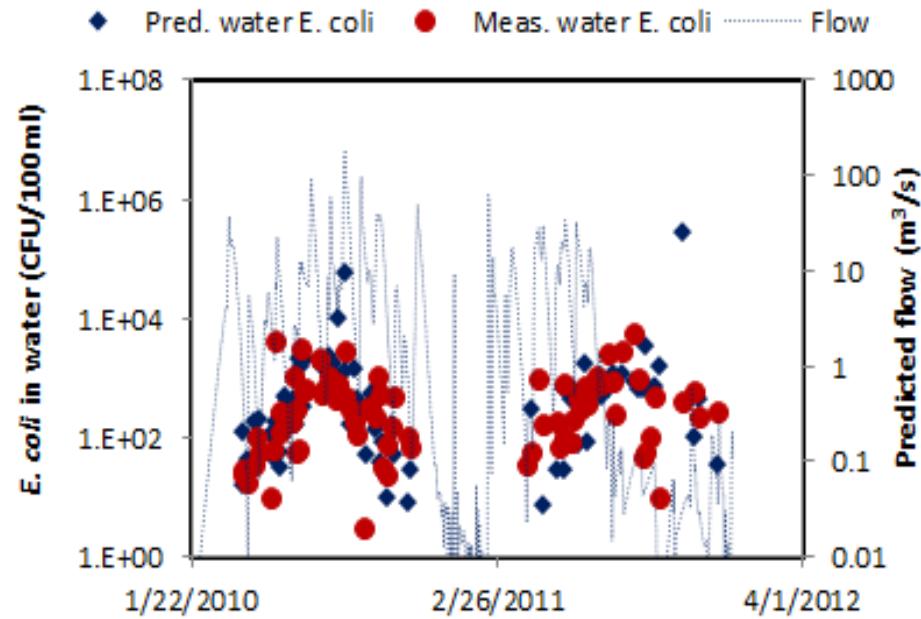


# SWAT bacteria predictions





# Pathogen modelling in stream



Bacteria field work – relatively expensive

Technical Paper

Predicting Streambed Sediment and Water Column *Escherichia coli* Levels at Watershed Scale<sup>†</sup>

Pramod K. Pandey Assistant Specialist<sup>1</sup>,  
Michelle L. Soupir Associate Professor<sup>2</sup>,  
Charles D. Ikenberry Graduate Student<sup>2</sup>  
and Chris R. Rehmann Professor<sup>3</sup>

Version of Record online: 18 DEC 2015

DOI: 10.1111/1752-1688.12272

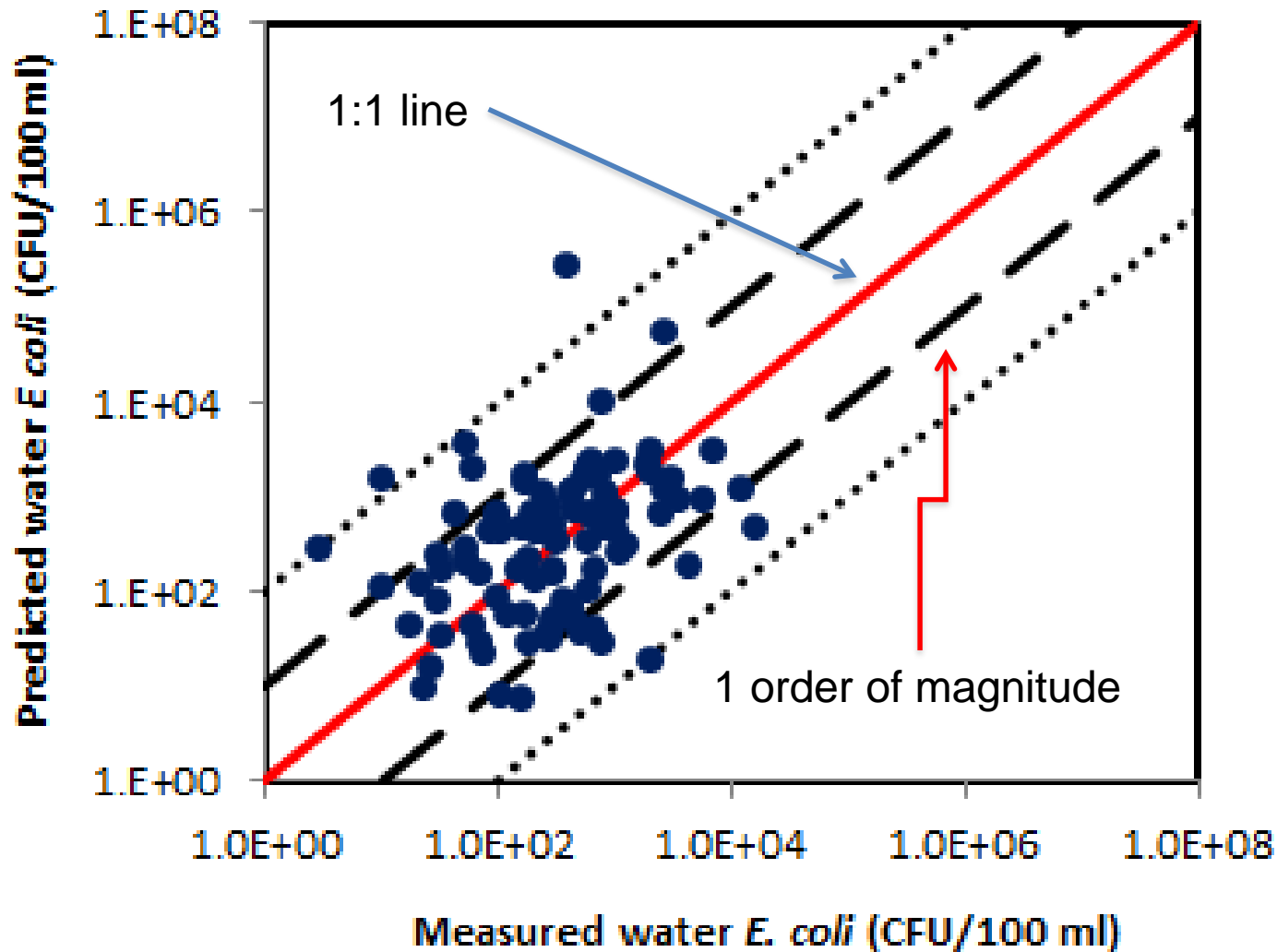
Issue



JAWRA Journal of the  
American Water Resources  
Association

Volume 52, Issue 1, pages  
184–197, February 2016

# SWAT bacteria predictions and observations (predictability estimation)



# Conclusions of this bacteria modelling

- Modified SWAT model can improve the estimation of bacteria transport at watershed scale.
- This will be the first model to understand bacteria dynamics in streambed sediment (not found reported yet)
- This model predicts pathogen concentrations in the sediment bed as well as in water column simultaneously.
- The predictions were verified in the Squaw Creek Watershed, Iowa; and approximately 82% of the water column predictions and 62% of the streambed sediment bacteria predictions fall within 1 order of magnitude of bacteria measured data.





# Acknowledgments



Funding for this study was provided by:

- National Science Foundation (NSF)
- Environmental Protection Agency (EPA)

*Thank you*



Question please ??



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