



Modeling Non-point Source Contributions of Host-specific Fecal Contamination in San Pablo Bay

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This project focuses on coupling microbial source tracking, pathogen analysis, and validated ultrafiltration technology with a solid 3-D modeling approach for a case study of San Pablo Bay. A major outcome of the project is to provide a tool for decision makers to maximize financial resources. End users may include water control boards, wastewater treatment facilities, managers of recreational lands and natural resources, and others involved in water quality monitoring.

The four objectives of the project are:

Objective 1: Develop sea bird (especially seagull) – specific molecular PCR assays to quantify their contribution to bacterial fecal loads in San Pablo Bay and its tributaries.

Objective 2: Monitor 5 locations in the 3 tributaries for *Bacteroidales* and a suite of pathogens during 4 events reflecting both dry and wet weather conditions.

Objective 3: Demonstrate the utility of a combination of theoretical/numerical modeling and innovative molecular PCR assays to determine experimentally, and then forecast, the extent of fecal contamination of a water body, and for the identification of the sources of that contamination.

Objective 4: Initiate development of quantitative tools that could help stakeholders in making decisions to minimize public health risks in San Pablo Bay, e.g., best management practices aimed at reducing source-specific contamination determined by *Bacteroidales*-based assays.

During the first phase of this project, we have made progress for each objective:

Objective 1: Our published method for quantitative universal *Bacteroidales* PCR (qPCR), the assay BacUni-UCD, did amplify *Bacteroidales* in mixed seagull feces, although fewer gene copies were determined relative to feces from other warm-blooded animals. Therefore, non-*Bacteroidales* 16S rRNA target sequences will need to be identified for development of a seagull-specific qPCR assay.

Objective 2: Locations for water sampling were selected to best represent the fecal contamination contributed to San Pablo Bay from fresh water sources. Sample sites include the Napa River, Sonoma Creek, the Petaluma River, the Napa Sonoma Marsh, Suisun Bay, Gallinas Creek near China Camp State Park, and inside the Bay. The first field measurement and sampling event is planned in October 2007. Exploratory numerical tests with Si3D are helping to determine the best sampling locations in San Pablo Bay. Moreover, preliminary experiments were performed to determine decay rates of host-specific *Bacteroidales* cells and their DNA in the environment. Stool samples of cows, dogs, and humans were used. The decay rates will be used in the mathematical/numerical models being developed.

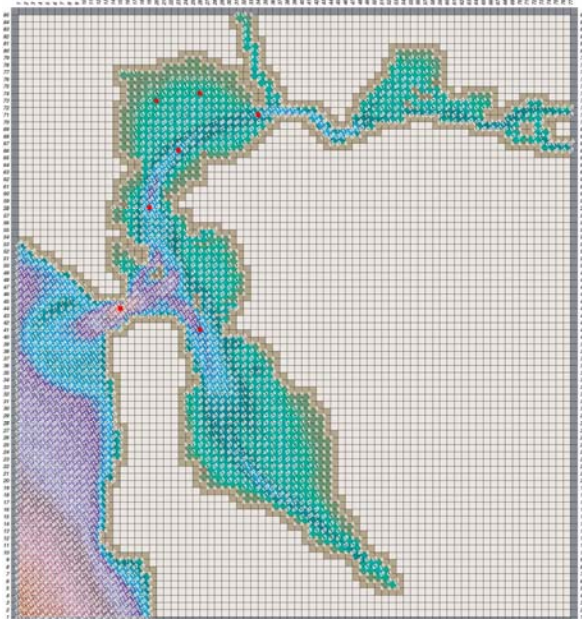
Objective 3: One- and two-dimensional (1-D and 2-D) mathematical/numerical models of the fate and transport of *Bacteroidales* in

water bodies were developed. The models have been validated via comparison with analytical solutions and via assessing the correctness of the model solution under diverse scenarios of interest. These 1- and 2-D numerical solutions will become crucial in obtaining dispersion coefficients and decay rates from observations in different rivers and estuaries.

The first analyses with the Si3D code were performed for all of San Francisco Bay, and preliminary results, including the ADR transport equation for *Bacteroidales* in Si3D, were obtained. An assessment of the impact of grid resolution into the numerical result in terms of flow and transport of *Bacteroidales* is underway. Grid sizes of 200 to 1,000 meters are being tested.

Moreover, a comprehensive list of Internet resources was compiled for water quality, flow, and weather data in the San Francisco Bay and Estuary. These data are crucial for a sound modeling of San Pablo Bay.

Objective 4: Modeling of *Bacteroidales* concentration within the San Pablo Bay will be accomplished after a set of localized concen-



Grid spacing and bathymetric data for the computational domain of the San Francisco Bay and Estuary, indicating the seven locations in which velocity profiles obtained from the numerical solution are shown. (This run corresponds to a grid size of 1,000 m.)

trations of *Bacteroidales* has been obtained. Preliminary runs are currently underway to optimize placement of sampling locations.

Selected Publications

Santo Domingo, J.W., D.G. Bambic, T.A. Edge and S. Wuertz, Quo Vadis Source Tracking? Towards a Strategic Framework for Environmental Monitoring of Fecal Pollution, *Water Research*, 2007, 41: 3539-3552.

Kildare, B.J., C.M. Leutenegger, B.S. McSwain, D.G. Bambic, V.B. Rajal and S. Wuertz, 16S rRNA-based Assays for Quantitative Detection of Universal, Human-, Cow- and Dog-Specific Fecal *Bacteroidales*: A Bayesian Approach, *Water Research*, 2007, 41:3701-3715.

Rajal, V.B., B.S. McSwain, D.E. Thompson, C.M. Leutenegger, B. Kildare, and S. Wuertz, Validation of Hollow Fiber Ultrafiltration and Real Time PCR Using Bacteriophage PP7 as Surrogate for the Quantification of Viruses from Water Samples, *Water Research*, 2007, 41:1411-1422.

Collaborative Efforts

Dr. Drew M. Talley and Ms. Marina Psaros at Romberg Tiburon Center, San Francisco National Environmental Research Reserve (NERR) have provided assistance with site selection for field measurements and public outreach, e.g., workshop planning and maintenance of a project website, respectively.

End users are providing input on the research as it progresses.

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