The Journal of Open Source Software

MicroBenthos: a modeling framework for microbial benthic ecology

Arjun Chennu[1]

1 Max Planck Institute for Marine Microbiology

DOI: 10.21105/joss.00674

Software

- Review
- Repository
- Archive

Submitted: 04 April 2018
Published: 12 April 2018

Summary

Microbial benthic habitats, such as microbial mats and sediments, exhibit extremely steep gradients in the physical, chemical and biotic parameters within the space of a few millimeters. These micro-environments drive the localization and exploitation of physico-chemical niches by a variety of microbial groups, such as cyanobacteria, sulfur-oxidizing bacteria, etc (Van Gemerden 1993). Studies of biogeochemistry and microbial ecology in these systems use various sensors to profile micro-environments and infer the local budgets and productivities of the microbial groups and metabolisms (Revsbech et al. 1983). Microbenthic habitats are typically modeled as diffusive-reactive systems (Wit, Ende, and Gemerden 1995), i.e. the dominant mass transport mode is physical diffusion of solutes within the porespaces of the sediment matrix. The "reactive" aspect refers to the presence of a large number of local sources and sinks within the mat system.

MicroBenthos is a modeling framework to study *in silico* microbenthic habitats. The main perspective is to recognize that while modeling physical diffusion is straightforward, the larger challenge is to have a flexible way to define, compose and study various microbial metabolisms under dynamic conditions. MicroBenthos enables this by providing a high-level abstraction to compose and simulate microbenthic systems in terms of solar irradiance, chemical solutes, microbial groups and chemical or metabolic processes. While the software is written in python, with a modular structure for ease of extensibility, it can be used without programming through a (YAML) structured text file as the interface. This allows the user to focus on specifying the constitutive relations between environmental parameters and processes as a simple mathematical formula, which is then symbolically cast (using sympy (Meurer et al. 2017)) into a set of coupled partial differential equations for the full model. Using a simple command, the equations can be numerically solved (using fipy (Guyer, Wheeler, and Warren 2009)) to study the evolution of the various model variables.

MicroBenthos provides several useful features:

- Modular and extensible abstractions to create microbenthic systems
- Non-programming interface to define processes and model structure
- On-line visualization of running simulations and video export
- Stateful simulations that can be interrupted and resumed
- Export of detailed model data in open archival format
- Open-source software (MIT license): https://github.com/achennu/microbenthos
- Detailed documentation and tutorials: https://microbenthos.readthedocs.io

References

Guyer, Jonathan E., Daniel Wheeler, and James A. Warren. 2009. "FiPy: Partial Differential Equations with Python." *Computing in Science & Engineering* 11 (3). Institute of Electrical; Electronics Engineers (IEEE):6–15. https://doi.org/10.1109/mcse.2009.52.

Meurer, Aaron, Christopher P. Smith, Mateusz Paprocki, Ondřej Čertík, Sergey B. Kirpichev, Matthew Rocklin, AMiT Kumar, et al. 2017. "SymPy: Symbolic Computing in Python." *PeerJ Computer Science* 3 (January). PeerJ:e103. https://doi.org/10.7717/peerj-cs.103.

Revsbech, Niels Peter, Bo Barker Jørgensen, T Henry Blackburn, and Yehuda Cohen. 1983. "Microelectrode Studies of the Photosynthesis and O2, H2S, and pH Profiles of a Microbial Mat." *Limnology and Oceanography* 28 (6):1062–74. https://doi.org/10.4319/lo.1983.28.6.1062.

Van Gemerden, Hans. 1993. "Microbial Mats: A Joint Venture." *Marine Geology* 113 (1). Elsevier:3–25. https://doi.org/10.1016/0025-3227(93)90146-M.

Wit, Rutger de, Frank P. van den Ende, and Hans van Gemerden. 1995. "Mathematical Simulation of the Interactions Among Cyanobacteria, Purple Sulfur Bacteria and Chemotrophic Sulfur Bacteria in Microbial Mat Communities." *FEMS Microbiology Ecology* 17 (2). Oxford University Press (OUP):117–36. https://doi.org/10.1111/j.1574-6941.1995.tb00136.x.