ABSTRACT: Our goal is to develop a Genome-Enabled Watershed Simulation Capability (GEWaSC) which will provide a predictive framework for understanding how genomic information stored in a subsurface microbiome affects biogeochemical watershed functioning, how watershed-scale processes affect microbial functioning, and how these interactions co-evolve. This calls for dramatically new simulation capabilities that couple microbial functional distribution with a suite of biogeochemical and hydrologic processes. These new simulation capabilities will go beyond conventional watershed models by ultimately integrating surface hydrologic, biogeochemical, and microbial processes (e.g., those taking place in the soil and surface waters) with the subsurface flow, transport, and reaction in a formal manner to provide a complete description of carbon, biogeochemical, and nutrient cycles within a catchment. A novel feature of the GEWaSC will be the coupling of microbial functional distributions inferred from trait-based models that are parameterized using site-specific “omic” data with a comprehensive simulation of biogeochemical networks. In addition, the GEWaSC model for flood plain to watershed scale cycling will rely on model development and quantification of vertical carbon and nutrient fluxes from the vegetative canopy, soil zone, and deeper vadose zone to the water table. These will provide boundary conditions for water flow and carbon/nutrient flux to the groundwater, and the basis for process models that can quantify these fluxes dynamically. Detailed process models for the interactions of organic matter and mineral surfaces and their effect on carbon and electron fluxes, along with data on organic carbon speciation and biogeochemical reaction rates, will be used to further refine the fate of organic carbon and nutrients within the flood plain and ultimately the watershed. In addition, new methods for treating the multiscale nature of the watersheds will be necessary, since fully resolved methods are not computationally feasible in all cases. In the later phases of this project, a new multiscale framework will be developed that can incorporate parameters and processes from the microscale (whether defined in terms of pore-scale soil processes, or in terms of subcatchment vegetation, exposure, and soil-type zones) into watershed-scale simulations. The guiding principle for the GEWaSC is that surface and subsurface hydrology provides the basis for model discretization because of its control of biophysical and biogeochemical connectivity. In this respect, surface and subsurface flow of water control the transport of organic carbon, nutrients, and the various electron acceptors and thus provide the first-order basis for definition of numerical model units. Despite the inability to completely resolve all of the relevant scales at the flood plain to watershed scale, high-resolution reactive transport modeling based on High Performance Computing (HPC) will be an important part of the GEWaSC effort. This framework will be used to develop an interpretive and predictive capability for the quasi-steady state biogeochemical and microbial functional zonation within a subsurface aquifer, as influenced by lateral groundwater flow and vertical inputs from the vadose zone.