

Two postdoctoral research scientist positions in microbial evolution and ecology

Summary

Two postdoctoral positions are available in Dr. Stepanauskas' laboratory. One position is focused on the deep evolution of Bacteria and Archaea and the genome content of the "microbial dark matter". Another position is focused on chemolithoautotrophy in the deep ocean and hydrothermal systems. The hired scientists will be engaged in large, collaborative projects, and will employ single cell genomics and other advanced molecular biology and biogeochemistry research tools. Anticipated employment duration: 2 years, with potential extension. Bigelow Laboratory's new campus is located in scenic, coastal Maine with abundant opportunities for outdoor and cultural activities. It is about an hour drive from Portland and a 3-hour drive from Boston.

Responsibilities

Hired scientists will be responsible to lead computational analyses of large single cell genomics, community "omics" and biogeochemical data sets, prepare manuscripts, supervise undergraduate students, and assume gradually increasing responsibilities in project management. These positions also include opportunities for field expeditions and laboratory analytical work.

Requirements

Candidates must have a PhD degree in microbiology, evolutionary sciences, bioinformatics, computational biology, or a related field. Prior experience in computational analyses of large microbial genomic data sets will be necessary for this opportunity. Candidates interested in these positions must be highly motivated, willing to learn and demonstrate initiative in assigned tasks. Excellent written and verbal communication skills and willingness to work in teams composed of field, laboratory and computational scientists are crucial.

Research overview: Deep evolution of Bacteria and Archaea

Hired scientist will be engaged in a major effort to improve our understanding of the genealogy of the Bacteria and Archaea by a large-scale genomic analysis of those deep evolutionary branches (phyla) that contain no cultivated representatives. Popularly referred to as Microbial Dark Matter (MDM), these enigmatic limbs near the base of the tree of life constitute a large fraction of biological diversity on our planet; yet, we learned of their existence only in 1990's. Current knowledge about MDM is mostly limited to sequences of its small subunit ribosomal RNA genes, primarily due to former technology limitations. Recent advances in single cell genomics technology, however, have enabled us to bridge this knowledge gap - one that is essential to the genealogy of life - by providing access to the complete genomic blueprints of microorganisms without the need for cultivation. The following, general hypotheses will be tested: 1) The extant number of major (phylum-level) evolutionary branches of Bacteria and Archaea is significantly greater than the current consensus; 2) Extant cellular life forms three distinct domains: Bacteria, Archaea and Eukaryotes; 3) The early evolution of Bacteria and Archaea followed a progression of bifurcating divergences rather than a single radiation from the last universal common ancestor; 4) Inter-domain and inter-phylum horizontal gene transfer (HGT) had a significant impact on the early evolution of Bacteria and Archaea; 5) Evolutionary divergence in the early history of Bacteria and Archaea co-occurred with the colonization of and adaptations to novel environments; 5) The habitable subsurface is a repository for early evolutionary history of Bacteria and Archaea. Primary field study sites include the Kaapvaall Craton of South Africa; the Sanford Underground Research Facility in South Dakota; and the Death Valley Regional Flow System in Nevada.

Research overview: Chemolithoautotrophy in the dark ocean

An increasing body of evidence suggests the significance of chemolithoautotrophy in the dark ocean water column and hydrothermal systems. However, the specific energy sources, metabolic pathways and microbial taxonomic groups remain poorly understood.

The hired scientist will assume a leading role in a) A global inventory of chemoautotrophs in the dark ocean water column; and b) An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents. The following general hypotheses will be tested: 1) Multiple prokaryote taxonomic groups found in the dark ocean contain chemoautotrophic metabolic pathways; 2) Both known and previously unrecognized chemoautotrophy pathways are present in dark ocean's prokaryotes; 3) Dark ocean

chemoautotrophs are broadly distributed around the globe, with biogeographic patterns determined by the isopycnal movement of water masses, water mass age, and the downward flux of organic matter; 4) Diverse chemoautotrophy pathways are expressed in the dark ocean. During the course of the project, single amplified genomes (SAGs) will be generated from several diffuse-flow hydrothermal systems and from all major intermediate and deep water masses around the globe, representing most major taxonomic groups of bacteria and archaea that are known to be present in the dark ocean. Whole genome sequencing will be performed on a subset of SAGs, enabling detailed annotation of chemoautotrophy pathways. Metagenomic and metatranscriptomic fragment recruitment will be used to determine global patterns of chemoautotroph distribution and chemoautotrophy pathway expression.

How To Apply

Please visit www.bigelow.org for more information and method of application, position reference # PD-2015-1 for the Ecology position and PD-2015-2 for the Evolution position. Application deadline: February 1, 2015.