



EU-US Shortcourse lecturers



Jennifer F. Biddle

University of Delaware
College of Earth, Ocean, and Environment, USA

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Research

My research concentrates on the microbial populations and processes in subseafloor marine environments. This extreme environment comprises one of the largest biomes on Earth and mounting evidence suggests a large amount of microbial biomass lives in deep sediments. Initial geochemical and metagenomic investigations suggest that new metabolisms and species may exist. We have particular interest in groups of subsurface Archaea, biogeography within sediment and general adaptation to low energy environments.



Mya Breitbart

University of California, San Diego/San Diego State
University, USA

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Research

In every milliliter of surface seawater, there are 1 million bacteria and 10 million viruses. Microbes are very diverse, and play important roles in global carbon and nutrient cycling. The Breitbart lab uses molecular techniques (such as metagenomic sequencing) to examine the diversity, distribution, and ecological roles of viruses and bacteria in a wide range of environments - including seawater, marine animals, coral reefs, and reclaimed water.



Melody Clark

British Antarctic Survey, Cambridge, UK

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Research

My research interests involve the development of cross-disciplinary studies into the Environmental Genomics of Antarctic organisms. Molecular analyses of marine organisms' capacity to cope in stressful environments over timescales from days to years. Stresses include heat, hypoxia, ocean acidification, disturbance and sedimentation. These are being studied in a range of taxa, feeding guilds and developmental stages, with personal research concentrating on their limited heat-shock (stress) response and the application of 'Omics technologies to Environmental Science. Other research interests include: calcium regulation and shell deposition in marine molluscs.



Jed Fuhrmann

University of Southern California, Dept. Of Biological Sciences,
Los Angeles, USA

<http://dornsife.usc.edu/cf/faculty-and-staff/faculty.cfm?pid=1003269>

Research

Professor Fuhrman researches the roles of microorganisms in natural marine ecosystems and the cycling of matter in the ocean, from the microscopic scale to the global scale. He also measures human pathogenic viruses at recreational beaches as a potential health hazard, and works on innovative ways to make such measurements relatively easy and inexpensive. Professor Fuhrman is currently exploring global marine microbial biodiversity with molecular biological techniques, which has enabled him to identify major new taxonomic groups and make better estimates of the total diversity found in these communities and its role in ecosystem function. His team has discovered a major new group of Archaea inhabiting the deep sea and other novel microbial groups in coral reefs and other ocean habitats. Recently, his lab has determined patterns in diversity that help show how the microorganisms interact as a complex network. In the public health realm, his team has helped to link cases of illness to exposure to microbial and viral pathogens in the coastal zone.



Jack Gilbert

Argonne National Laboratory, Argonne, Illinois, USA

<http://www.bio.anl.gov/PI/gilbert.html>

Research

Microbial communities: temporal and biogeographic structure

Coming primarily from a marine background I have been very interested in how bacteria exist in such a fluid matrix. Specifically, what determines how microbes exist when the medium in which they live is moving around so much? My research site in the Western English Channel has demonstrated that even though the sampling location is flushed with new water every two weeks, the same communities of microbes appear year after year. This highlights that microbes exist in robust and well-defined communities in this ecosystem. My ongoing research is to determine how true this is for all ecosystems around the planet.



Frank Oliver Glöckner

Microbial Genomics & Bioinformatics Group, Max Planck for Marine Microbiology, Bremen, Germany

www.microbial-genomics.de

Jacobs University gGmbH, School of Engineering & Science – SES Life Sciences, Bremen, Germany

Research

The Microbial Genomics and Bioinformatics Research Group develops enabling technologies to transform the wealth of sequence- and metadata from the environment into biological knowledge. Techniques are whole genome and metagenome analysis, sequence classification, phylogenetic inference as well as software and database development for integrated data analysis. An integrated view on the complex interplay of organisms, genes and the environment surrounding them is the first step towards the statistical analysis and modelling of complex metabolic processes and networks (ecosystems biology). It will help to reveal the key genes involved in central processes in the ecosystem and provide hints to discovering their potential functions. The results will not only generate a better understanding of the marine environment and its impact on human welfare in times of global climate change, but also deliver new targets for medical and biotechnological applications.



John F. Heidelberg

University of Southern California, Los Angeles, USA

<http://dornsife.usc.edu/cf/faculty-and-staff/faculty.cfm?pid=1012506&CFID=6236164&CFTOKEN=46404263>

Research

Dr. John Heidelberg's research interests are the field of microbial genomics. Specifically, he is studying the metabolic potential of the common and abundant marine bacteria by sequencing these organisms' DNA. Because we are unable to bring the vast majority of bacteria into a pure culture, we are unable to use more common microbiological techniques to study these uncultured bacteria. Therefore, Dr. Heidelberg employs one of the newest DNA sequencers to look at the genomes of these bacteria without the need of first growing the bacteria in pure culture.



Renzo Kottmann

Max Planck Institute for Marine Microbiology, Microbial Genomics and Bioinformatics Group, Bremen, Germany

http://www.mpi-bremen.de/Renzo_Kottmann.html

Research

I use my combined expertise in computer science and marine microbiology to investigate optimal solutions in data integration, analysis, and visualization in the field of microbial environmental genomics. I gained experience in integration and analysis of (meta) genome and environmental data. I am leading the megx.net project (<http://www.megx.net>) as well as the work package "Bioinformatics and Data Integration" of the Micro B3 project (www.microb3.eu), and I am an executive board member of the Genomic Standards Consortium (GSC).



Folker Meyer

Argonne National Laboratory, Mathematics and Computer Science Division and Institute for Genomics and Systems Biology, Illinois, US

<http://www.mcs.anl.gov/~folker/>

Research

Folker Meyer is a computational biologist at Argonne National Laboratory and a senior fellow at the Computation Institute at the University of Chicago. He is also associate division director of the Institute of Genomics and Systems Biology.

He trained as a computer scientists and started to work with biologists early on in his career. It was that exposure to interesting biological problems that sparked his interest in building software systems to tackle biological problems, mostly in the field of genomics or post-genomics. In the past he has been best known for his leadership role in the development of the GenDB genome annotation system, he has also played an active role in the design and implementation of several high-performance computing platforms.

His current work focuses on the analysis of **shotgun metagenomics** data sets and on the [MG-RAST](#) community resource for metagenomics. Shotgun metagenomics is benefitting directly from the current advances in sequencing technology, leading to dramatic growth in the number scientists using this approach and the number and size of the data sets being produced. He also has an interest in microbial genomics and the analysis of complete microbial genomes and is a member of the [RAST](#) project.



William Orsi

Woods Hole Oceanographic Institution, Dept. of Geology & Geophysics, Woods Hole, Massachusetts, USA

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Research

Phytoplankton, Oceanography, Biogeography, Remote Sensing, Ocean Observing
Phytoplankton Physiology, Phytoplankton Evolution, Genome Evolution



Shawn W. Polson

University of Delaware, Delaware Biotechnology Institute, Newark, USA

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Research

My research interests lie at the intersection of genomics and microbial ecology, examining the ways in which microorganisms and viruses affect and are affected by their environments. While I admit a preference for marine research, I also research a broad range of other environments from soils and agriculture to the extreme environments of hot springs and deep sea hydrothermal vents. The data intensive nature of my research has led me to specialize in bioinformatic aspects, identifying creative solutions to visualize and analyze microbial community data.



Alban Ramette

Max-Planck-Institute for Marine Microbiology, HGF MPG joint research group for deep sea ecology and technology, Bremen, Germany

http://www.mpi-bremen.de/en/Habitat_group.html

Research

The Joint Research Group on Deep-Sea Ecology and Technology was co-founded in December 2008, the by the [Alfred-Wegener-Institute for Polar and Marine Research](#) of the Helmholtz (HGF) Society and the Max-Planck-Institute for Marine Microbiology, with Antje Boetius as the group leader. This Joint Research Group comprises the expertise of the MPI in the area of marine microbial ecology and biogeochemistry, development of new molecular-biological and in situ analytical methods (former Microbial Habitat Group, 2003-2010) together with the capacity of AWI to conduct research in polar environments and to carry out long-term observation in the deep sea (former Deep-Sea Research group). The goal is to contribute significantly to the study of global change effects on deep-sea ecosystems and to the exploration of extreme and unknown deep-sea habitats.



Todd J. Treangen

National Biodefense Analysis and Countermeasures Center (NBACC), Maryland, USA

<http://cbcb.umd.edu/~treangen/>

Research

Dr. Todd Treangen is a Senior Bioinformatics Scientist at the National Biodefense Analysis and Countermeasures Center. His current work focuses on rapid nucleic acid diagnostics and microbial forensics using next generation sequencing. Before joining NBACC, he held positions as a postdoctoral fellow at the McKusick–Nathans Institute of Genetic Medicine at Johns Hopkins University (JHU), at the Center for Bioinformatics and Computational Biology at the University of Maryland, and also at the Pasteur Institute in Paris, France. He received his Ph.D. in Computer Science in 2008 from the Polytechnic University of Catalonia, Barcelona, Spain, where his work focused on novel data structures, algorithms and software for large-scale comparisons of closely-related bacterial genomes.



Colomaban de Vargas

Station Biologique de Roscoff, France

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Research

Colomaban's main interest is to better understand evolutionary dynamics in open ocean micro-plankton. What is the extent of gene flow and adaptations among oceanic planktonic species with worldwide distributions? When did contemporary species originate? and through which speciation process(es) ? Colomaban pursues those "species-level" questions using molecular, morphological, and paleontological tools to study the pelagic protists having the best-known morphologies in both the modern and past oceans the coccolithophores and the foraminifers. He is currently coordinating two large projects: BioMarks and Tara-Oceans.



Eric Wommack

Department of Plant and Soil Sciences
Graduate College of College of Earth, Ocean, and Environment,
Delaware Biotechnology Institute, Newark, USA

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Research

The varied research interests of my lab are connected through the creative use of molecular genetic tools to investigate population-level processes occurring in microbial communities. Primary among these interests are investigations on the role of viruses and viral infection in microbial communities. Current projects seek to understand to what extent viral infection influences the composition and diversity of bacterial and phytoplankton host communities. In the course of this research we are examining virus populations in estuarine and coastal waters as well as deep-sea hydrothermal environments. Additional research projects include microbial degradation of chiral organic pollutant compounds in soils and water and development of in situ molecular detection methods for free living nitrogen fixing bacteria. Peer-reviewed publications reporting Dr. Wommack's research can be found in Nature, Applied and Environmental Microbiology, Limnology and Oceanography, and Microbial and Molecular Biology Reviews.



Cathy Wu

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Biology, Newark, USA

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Research

Systems integration is becoming the driving force for the 21st century biology. Researchers are systematically tackling gene functions and complex regulatory processes by studying organisms at different levels of organization, from genomes, transcriptomes and proteomes to metabolomes and interactomes. To fully realize the value of such high-throughput data requires advanced bioinformatics for integration, mining, comparative analysis, and functional interpretation. My group conducts bioinformatics and computational biology research and has developed a bioinformatics resource at the Protein Information Resource with integrated databases and analytical tools to support genomics, proteomics and systems biology research [Wu et al., 2003]. PIR is a member of the UniProt Consortium to provide the central international resource on protein sequence and function [Wu et al., 2006]. The PIR web site and the UniProt web site at PIR are accessible by researchers worldwide with over 4 million hits per month from over 100,000 unique sites.

Our research encompasses protein evolution-structure-function relationships, biological text mining, protein ontology, proteomic bioinformatics, computational systems biology, and bioinformatics cyberinfrastructure. The protein-centric bioinformatics framework we are developing connects data mining, text mining and ontology for functional analysis of genes and proteins in the systems biology context. The integrative approach reveals hidden relationships among the various components of the biological systems, allows researchers to ask complex biological questions and gain better understanding of disease processes, and facilitates target discovery. We will further establish a new Center for Bioinformatics and Computational Biology at University of Delaware to foster collaborative interdisciplinary research and to offer graduate degree programs in Bioinformatics and Computational Biology to train the next generation of researchers and educators.