



EU-US Shortcourse lecturers



Jennifer F. Biddle

University of Delaware

College of Earth, Ocean, and Environment, Lewes, US

<http://www.ceoe.udel.edu/people/profile.aspx?jfbiddle>

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.



Guy Cochrane

European Bioinformatics Institute, Hinxton, Cambridge,
UK

http://www.ebi.ac.uk/Information/Staff/person_maintx.php?s_person_id=207

Research

The European Nucleotide Archive team develops nucleotide sequence archive data services, as part of the nucleotide section of Protein and Nucleotide Database ([PANDA](#)) Group. The team provides data repositories and services in the nucleotide sequencing domain, from raw read data, through assembled sequence to submitted functional annotation. Serving both as a public-facing resource and as a key infrastructure to other EBI services, the team's work includes the provision of submission services and data access tools and represents the European arm of the [International Nucleotide Sequence Database Collaboration](#)



Dawn Field

Department of Zoology, University of Oxford, Oxford, UK

http://www.zoo.ox.ac.uk/staff/academics/field_d.htm

Research

Key Research Interests include molecular evolution, comparative genomics, metagenomics, standards and ontologies, bioinformatics, data sharing, and science policy.

Activities

Director of the NERC Environmental Bioinformatics Centre (<http://nebc.nox.ac.uk>), founding member and President of the Genomic Standards Consortium (<http://gensc.org>), founding member of the BioSharing initiative (<http://biosharing.org>), Visiting Fellow at the European Bioinformatics Institute (EMBL-EBI), Advisory Board of the Earth Microbiome Project (<http://www.earthmicrobiome.org/>)



Frank Oliver Glöckner

Microbial Genomics & Bioinformatics Group, Max Planck Institute 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.



Christopher Hunter

European Bioinformatics Institute, Hinxton, Cambridge, UK

<https://www.ebi.ac.uk/>

Research

InterPro is an integrated documentation resource for protein families, domains and functional sites. The project integrates protein signatures from Pfam, PRINTS, PROSITE, ProDom, TIGRFAMs, PIRSF, SUPERFAMILY, Gene3D, PANTHER and HAMAP. As well as grouping together related signatures, InterPro adds biological annotation and provides links to external databases such as GO, PDB, SCOP, CATH and ENZYME. All InterPro matches to UniProt proteins are calculated monthly using the InterProScan software (<http://www.ebi.ac.uk/Tools/InterProScan/>), and displayed in InterPro entries in various formats. InterPro has a number of important applications, including protein functional classification and automatic annotation of proteins for UniProtKB and genome annotation projects.



Ivaylo Kostadinov

Institute of Marine Sciences, Marine Biology and Oceanography,
Barcelona, Spain

<http://www.cmima.csic.es/en/content/staff-detail?idpersonal=4365>

Research

I am a bioinformatician working in the field of marine ecological genomics. I am currently involved in comparative genomics of selected marine taxa and the analysis of large metagenomic datasets with focus on ecologically relevant functional genes. I am also interested in the application of relational databases for high-throughput data analysis.



Renzo Kottmann

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

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

Main 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 workpackage “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).



Adam Martiny

Adam Martiny Lab, Department of Earth System Science and
Ecology & Evolutionary Biology, University of California, Irvine,
CA, US

<http://ess.uci.edu/researchgrp/amartiny/home>

Research

The main objectives of our research is to (1) understand how bacteria adapt to different environmental conditions and (2) how the resulting diversity influences global biogeochemical cycles. Most of the work is done on the unicellular marine cyanobacteria *Prochlorococcus* and *Synechococcus*, but we are also interested in other organisms. The goal is to understand the relationship between variation in the physical environment, genome composition and phylogeny - and how that all ties to together in shaping biogeochemical cycles.



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 trained as a computer scientist 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 of 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.



Alex Mitchell

European Bioinformatics Institute, Hinxton, Cambridge, UK

<http://www.ebi.ac.uk/>

Research

InterPro is an integrated documentation resource for protein families, domains and functional sites. The project integrates protein signatures from Pfam, PRINTS, PROSITE, ProDom, TIGRFAMs, PIRSF, SUPERFAMILY, Gene3D, PANTHER and HAMAP. As well as grouping together related signatures, InterPro adds biological annotation and provides links to external databases such as GO, PDB, SCOP, CATH and ENZYME. All InterPro matches to UniProt proteins are calculated monthly using the InterProScan software (<http://www.ebi.ac.uk/Tools/InterProScan/>), and displayed in InterPro entries in various formats. InterPro has a number of important applications, including protein functional classification and automatic annotation of proteins for UniProtKB and genome annotation projects.



Jörg Peplies, CEO
Ribocon GmbH, Bremen, Germany

<http://www.ribocon.com/>

Research

Jörg Peplies is the technical head of the private bioinformatics company Ribocon in Bremen, Germany. He gained his PhD in Microbiology for his work on DNA microarrays for the rRNA-based detection and identification of Bacteria from complex environmental samples. A subsequent two-year follow-up postdoctoral period has moved him more and more into the bioinformatics aspects of rRNA data processing as well as bacterial genomics which have been established at that time within the Microbial Genomics and Bioinformatics Research Group at the MPI Bremen. During that phase, he and his colleagues realized the strong demand for bioinformatics support and services in Microbiology which evidently could not be satisfied by academia alone anymore, resulting in the formation of the independent spin-off company Ribocon in the year 2005. Since then he is transferring bioinformatics knowledge and solutions into science and industry on a professional level. Moreover, he provides his expertise in (rRNA) sequence analysis, phylogeny, and especially the widely-used software package ARB by regular workshops with more than 400 participants from all over the world within in the last 8 years.



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

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

Main Interests

Development of the SILVA software suite / databases and associated work on the fully automated classification of TAG / BULK DNA sequences.



Christopher Quince

School of Engineering, Glasgow University
Glasgow, UK

<http://userweb.eng.gla.ac.uk/christopher.quince/>

Research

The computational microbial genomics group at the University of Glasgow was created in December 2009 as the result of an award of an EPSRC Career Acceleration Fellowship worth over £800K to Dr Christopher Quince: "[Pioneering the New Genomics Era in Environmental Microbiology for Engineering Design](#)". The aim of the group is to build on the prior success of Dr Quince's research, and develop novel algorithms for the analysis of next-generation sequencing data that are capable of accurately determining microbial community structure. This data will then be used in both statistical models, that allow diversity patterns to be correlated with environmental parameters, and mathematical models that can predict community dynamics. There is an emphasis within the group on communities associated with engineering systems, and there are ongoing projects on the genomics of slow sand filters and microbial fuel cells, but the algorithms are universal, and are being applied through international collaborations, to a whole range of environments and organisms, from marine metazoans to HIV.



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.



Lucas Stal

Royal Netherlands Institute for Sea Research, Yerseke,
the Netherlands

<http://www.ceme.nioo.knaw.nl/content/prof-dr-lucas-j-stal>

Research

An important part of my research interests is in the field of the ecology, functional diversity and physiology of (marine) cyanobacteria. Cyanobacteria can be found in almost any environment. My research has focussed on benthic cyanobacteria that form microbial mats in coastal environments, and on planktonic cyanobacteria that form waterblooms in marine and semi-marine systems. To a lesser extent I have studied cyanobacteria from extreme and other unusual environments such as hypersaline ponds, hot springs and deserts. Aspects of cyanobacterial ecophysiology that I have studied include N_2 fixation, photosynthesis, anaerobic metabolism and functional diversity. I maintain a large collection of (axenic) cyanobacteria that my group has isolated during our studies of a large variety of different environments.



Shulei Sun

UC San Diego, Center For Research on Biological
System, La Jolla, California, US

<http://act.ucsd.edu/directory/search?jlinkevent=Redirect&entry=shulei+sun>

Research

Shulei Sun's major research interests include metagenomic analysis, sequence quality control, assembly, gene prediction, annotation, functional and comparative genomics applications, as well as tool development and integration.



Hanno Teeling

Max-Planck-Institute for Marine Microbiology, Department of Molecular Ecology, Bremen, Germany

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

Research

The analysis of collectively sampled and sequenced microbial genomes has emerged as one of the key technologies in the field of microbial ecology. In particular the field of marine microbial metagenomics has in recent years become a major contributor to the growth of the INSDC public sequence databases. While earlier studies were restricted to merely analyzing a part of a habitat's microbial gene inventory, recent studies have become much more sophisticated, and combine metagenomic data with expression data, environmental data, single cell sequencing approaches and knowledge from isolates (pure culture studies, whole genome sequencing). In order to transform this wealth of data into meaningful biological knowledge, techniques are required that cluster metagenomes in taxonomic coherent bins, as well as dedicated pipelines for data analysis and data integration. Current research interests are bioinformatic methods for integrative metagenome data analysis, phytoplankton – bacteria interrelations with a focus on carbon turnover, as well as microbial communities in extreme habitats.



Luke Ursell

Knight Lab, University of Colorado at Boulder, Colorado, US

<http://chem.colorado.edu/knightgroup/>

Research

We are developing new methods to test factors that make environments more or less similar in terms of the phylogenetic diversity of the organisms they contain. For example, in hot springs in Yellowstone, the driving factors might be temperature, pH, hydrogen sulfide, or any of a number of other physical and chemical factors. In our own human bodies, the microbial symbionts we carry with us outnumber our so-called human cells by as much as an order of magnitude, and these microbial communities have profound implications for health and disease.



Colomban de Vargas
Station Biologique de Roscoff, France

<http://www.sb-roscoff.fr/>

Research

Colomban'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) ? Colomban 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.



Daniel Vaultot
Station Biologique de Roscoff, France

<http://www.sb-roscoff.fr/>

Research

My current research interests are focused on the analysis of 18S clone libraries in various marine systems to assess eukaryotic diversity and on the application of metagenomics to determine the functional adaptations of specific picoplankton groups. Daniel also supervises the Roscoff Culture Collection (RCC).



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

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

Scientific Interests and Goals

My main research interests can be summarized as follows:

- standardization of contextual meta (data) for nucleic acid sequences
- data integration
- bio-curation

The over-arching theme of these efforts is to enable large scale meta-analysis of meta (genomic) datasets, in order to obtain an integrated of organisms, genes and the environment.