

March. 4		Kingkey Palace Hotel
14:00-22:00	Registration	
March. 5Ballroom I & II, -1F, Kingkey Palace Hotel		
Keynote and Introduction to GSC and the Importance of Standards in Megasequencing Projects		
Chair: Dr. Jack A Gilbert (University of Chicago/Argonne National Laboratory, USA)		
08:30-09:15	Keynote Talk: The Role of Contextual Data in Making Sense of Genomes and Metagenomes Rita Colwell (University of Maryland, USA).	
09:15-09:45	The Genomic Standards Consortium (GSC) Dawn Field (Centre for Ecology and Hydrology, UK)	
09:45-10:00	Sequencing, Sequencing, and Sequencing Jun Wang (BGI, China)	
10:00-10:30	Group Photo & Coffee Break	
MegaGenome Projects I: Animal and Plant Megagenomics		
Chairs: Linda Amaral-Zettler (Marine Biology Laboratory, USA) & Tatiana Tatusova (National Center for Biotechnology Information, USA)		
5 min introduction by chair		
10:30-12:00	Genome Assembly and Functional Study of Oyster Xiaodong Fang (BGI, China)	
	The International Oryza Map Alignment Project Rod Wing (Arizona Genomic Institute, USA)	
	Rice reference genome assembly and database services in Japan Takeshi Itoh (National Institute of Agrobiological Sciences, Japan)	
	The BGI Plant Reference Genomes Project Xun Xu (BGI, China)	
12:00-13:30	LunchFeast Restaurant, 1F, Kingkey Palace Hotel	
MegaGenome Projects II: Viral Megagenomics		
Chair: Hui Wang (Centre for Ecology and Hydrology, UK) & Yiming Bao (National Center for Biotechnology Information, USA)		
5 min introduction by chair		
13:30-15:40	Clinical Metagenomics for Diagnosis and Discovery of Viral Pathogens Charles Chiu (University of California, San Francisco, USA)	
	Uncovering the Plant Virome: Problems and Solutions Ulrich Melcher (Oklahoma State University, USA)	
	Standardizing Metadata Associated with NIAID Genome Sequencing Center Projects and their Implementation in NIAID Bioinformatics Resource Centers Richard Scheuermann (U.T. Southwestern Medical Center, USA)	

	Viral metagenomic analysis of several bat populations and fresh water samples Zhengli Shi (<i>Wuhan Institute of Virology, CAS, China</i>)
	Viral high-throughput next generation sequencing at JCVI Timothy Stockwell (<i>J. Craig Venter Institute, USA</i>) ²²
	Viral discovery by metagenomics sequencing of clinical samples Gane Ka-Shu Wong (<i>University of Alberta, Canada</i>)
15:40-16:00	Coffee Break
MegaGenome Projects III: Fungal Megagenomics. Chair: Linda Amaral Zettler (<i>Marine Biological Laboratory, USA</i>) 5 min introduction by Chair	
16:00-17:30	Bioinformatic Portal System for Fungal Functional, Comparative and Evolutionary Genomics Jaeyoung Choi (<i>Seoul National University, Korea</i>)
	Exploring the microbial world multiple cells at a time! Patrick Chain (<i>Los Alamos National Laboratory, USA</i>)
	Fungi Indoors: Creating the Appropriate Databases for Fungal Research Jason Stajich (<i>University of California, Riverside, USA</i>)
	UNITE database for molecular identification of fungal communities in metagenomic studies. Kessy Abarenkov (<i>University of Tartu, Estonia</i>)
17:30-17:50	Coffee Break
17:50-18:50	Evening Lecture: Genomics, Metagenomics and Data Standards James Tiedje (<i>Michigan State University, USA</i>), introduced by Dr. Dawn Field (<i>CEH, UK</i>)
19:30	Banquet <i>Ballroom III & IV, -1F, Kingkey Palace Hotel</i>
March. 6 <i>Ballroom I & II, -1F, Kingkey Palace Hotel</i>	
08:30-09:00	Morning Lecture: Confronting the Rare Biosphere Mitchell Sogin (<i>Marine Biological Laboratory, Woods Hole, USA</i>), introduced by Dr. Frank Oliver Glöckner (<i>Max Planck Institute for Marine Microbiology, Germany</i>)
Interactions Host-associated Biome Projects Chair: Ilene Karsch-Mizrachi (<i>National Center for Biotechnology Information, USA</i>) 5 min introduction by chair	
9:00-10:00	PanOCT: Automated Clustering of Orthologs Using Conserved Gene Neighborhood for Pan-Genomic Analysis of Bacterial Strains and Closely Related Species Granger Sutton (<i>J. Craig Venter Institute, USA</i>)
	MetaHIT: Exploring the Human Microbiome Junjie Qin (<i>BGI, China</i>)

	The Merlot Microbiome Project: Exploring the Relationship Between Plant Associated Microbes and the Health and Wealth of Merlot Vines Jack Gilbert (<i>University of Chicago/Argonne National Laboratory, USA</i>)
	Ant Microbiome: Exploring the Host-associated Microbiome of Ant Species Corrie Moreau (<i>Field Museum of Natural History, USA</i>)
10:00-10:30	Coffee Break
Microbial Metagenomics Projects Chair: Folker Meyer (<i>Argonne National Laboratory, USA</i>) 5 min introduction by chair	
10:30-12:30	Utra High-throughput Microbial Ecology: Software, Sequencing and Practice for Studying Tens of Thousands of Environments Greg Caporaso (<i>University of Northern Arizona, USA</i>)
	The Earth Microbiome Project: A New Paradigm in Geospatial and Temporal Studies of Microbial Ecology Jack Gilbert (<i>University of Chicago/Argonne National Laboratory, USA</i>)
	Mining Soil Metagenomes for Meaning James Tiedje (<i>Michigan State University, USA</i>)
	Cryptic Drivers of Soil Microbial Diversity Jacob Parnell (<i>NEON INC, USA</i>)
	Plankton community genomics in the Tara-Oceans expedition Patrick Wincker (<i>Genoscope, France</i>)
	Microbes Thriving in the Hot Subsurface Australian Aquifers Bharat Patel (<i>Griffith University, Australia</i>)
12:30-13:30	Lunch <i>Feast Restaurant, 1F, Kingkey Palace Hotel</i>
Towards a Genomic Observatories Network Chair: Dawn Field (<i>Centre for Ecology and Hydrology, UK</i>) 10 min introduction by chair	
13:30- 15:00	The Moorea Genomic Observatory Neil Davies (<i>UC Berkeley - Moorea, USA</i>)
	The L4 Genomic Observatory Jack Gilbert (<i>University of Chicago/Argonne National Laboratory, USA</i>)
	The Promise of 'Site-based' Research: MIRADA -LTER Project Linda Amaral-Zettler (<i>Marine Biological Laboratory, Woods Hole, USA</i>)
	The Micro B3 Project: Biodiversity, Bioinformatics, Biotechnology Frank Oliver Glöckner (<i>Max Planck Institute for Marine Microbiology, Germany</i>)
	Building Linkages Between Genomic Observatories and GEO BON Makiko Mimura (<i>Kyushu University, Japan</i>)
	Open Discussion with Speakers in Panel session <ul style="list-style-type: none"> What is the special value of 'site-based' genomic research? How do we define a 'genomic observatory'?

	<ul style="list-style-type: none"> How should we build the Network?
15:00-15:30	Coffee Break
Policies and Standards for Reproducible Research: From Theory to Practice Chairs: Susanna-Assunta Sansone (<i>University of Oxford, UK</i>) & Scott Edmunds (<i>GigaScience, BGI, China</i>)	
15:30-17:30	An Overview of the Evolving Portfolio of Data Sharing Enablers: BioSharing Susanna-Assunta Sansone (<i>University of Oxford, UK</i>)
	Revolutionizing Data Dissemination: GigaScience Scott Edmunds (<i>GigaScience, BGI, China</i>)
	Funders:
	The US National Science Foundations Perspective Rita Colwell (<i>University of Maryland, USA</i>)
	Case Study: Alfred P. Sloan Foundation's Microbiology of the Built Environment Program Paula J. Olsiewski (<i>Alfred P. Sloan Foundation, USA</i>)
	Breaching the Single Bio-domain
	Share Reproducible Research, Transcending Individual Life Science Domains: ISAcommons Philippe Rocca-Serra (<i>University of Oxford, UK</i>)
	Sharing and Not Sharing, the MG-RAST Experience Folker Meyer (<i>Argonne National Laboratory, USA</i>)
	From Open Data Sharing to Insights Via Community Participation: A Structural Genomics Case Study Srikrishna Subramanian (<i>Institute of Microbial Technology, India</i>)
	" AppStore" in Life Science with OMICS Data Content, BGI-GeneBank Project Yong Zhang (<i>BGI, China</i>)
	Editors
	TBA
	Clare Garvey (<i>Genome Biology/BioMed Central</i>)
	Perspective from <i>Nature Biotechnology</i> on data standards and policies Craig Mak (<i>Nature Biotechnology/Nature PG</i>)
17:30-19:00	BGI Visit (OPTIONAL)
18:30	Dinner <i>Feast Restaurant, 1F, Kingkey Palace Hotel</i>
March. 7 <i>Ballroom I & II, -1F, Kingkey Palace Hotel</i>	
The Alfred P Sloan Foundation Microbiology of the Built Environment Session Chair: Jack A. Gilbert (<i>University of Chicago/Argonne National Laboratory, USA</i>) 5 min introduction by Program Officer –Paula J. Olsiewski (<i>Alfred P. Sloan Foundation</i>)	

08:30 - 10:30	The Indoor Standards - What Parameters Do We Need to Record? Jeffrey Siegel (<i>University of Texas at Austin, USA</i>)
	Minimal Metadata for the Built Environment: A MIxS Extension Lynn Schriml (<i>University of Maryland, USA</i>)
	The Home Microbiome Project: Unraveling the Relationship Between Human-associated and Home-associated Microbial Signatures. Jack Gilbert (<i>University of Chicago/Argonne National Laboratory, USA</i>)
	The Indoor Virome! Scott Kelley (<i>San Diego State University, USA</i>)
	The Role of VAMPs in the MoBEDAC Initiative Mitchell Sogin (<i>Marine Biological Laboratory, Woods Hole, USA</i>)
	MoBEDAC - Handling Fungal Data From MicroBE Jason Stajich (<i>University of California, Riverside, USA</i>)
	MoBeDAC - Integrated data and analysis for the indoor and built environment Folker Meyer (<i>Argonne National Laboratory, USA</i>)
10:30-11:00	<i>Coffee Break</i>
The RCN4GSC GSC Biodiversity Working Group (GBWG) Session Chairs: Bob Robbins (<i>UC San Diego, USA</i>) & Norman Morrison (<i>University of Manchester, UK</i>)	
11:00 - 12:30	GBWG Meeting Updates, to Include: 1) Update on GBWG Session at TDWG, 2) Update on Dwc / MiXS Alignment Meeting at JGI, Walnut Creek. 3) Update on GBIF / GSC Meeting at OERC, Oxford. Followed by Future Directions, Including Roadmap for Upcoming Meetings and Event Bob Robbins (<i>UC San Diego, USA</i>)
	The BioVeL Project and the Role to Play by Megasequencing Projects Norman Morrison (<i>University of Manchester, UK</i>)
	The MicroB3 Project Frank-Oliver Glöckner (<i>Max Planck Institute for Marine Microbiology, Germany</i>)
	TBA James Tiedje (<i>Michigan State University, USA</i>)
	How Can We Coordinate Megasequencing Projects to Our Advantage. Thoughts on Model Ecosystems Neil Davies (<i>UC Berkeley - Moorea, USA</i>)
	Beyond the Census of Marine Life: The Life in a Changing Ocean Initiative Linda Amaral-Zettler (<i>Marine Biological Laboratory, USA</i>)
	Discussion - 'Agile' discussion topics are to be put forward by the session chairs. Possible discussion topics include: Microbial Biodiversity: Ecosystem Puppeteers or Marionettes? Are taxonomies still relevant with the rapid progression of megasequencing projects? The biodiversity discussion sessions are lively and we encourage you to join in.

12:30-14:00	Lunch <i>Feast Restaurant, 1F, Kingkey Palace Hotel</i>
GSC Projects and Activities Chair: Pieter Sterk (<i>University of Oxford, UK</i>) & Lynn Schriml (<i>University of Maryland, USA</i>)	
14:00-15:30	The MlxS Family of GSC Standards Pieter Sterk (<i>University of Oxford, UK</i>) & Lynn Schriml (<i>University of Maryland, USA</i>)
	GSC's eJournal Standards in Genomic Sciences (SIGS) George Garrity (<i>Michigan State University, USA</i>)
	The GSC MlxS Compliance and Interoperability Group Pieter Sterk (<i>University of Oxford, UK</i>)
	The M5 (Metagenomics, Metadata, MetaAnalysis, Models and MetaInfrastructure) Working Group Folker Meyer (<i>Argonne National Laboratory, USA</i>)
	The GSC Biodiversity Working Group Bob Robbins (<i>UC San Diego, USA</i>) & Norman Morrison (<i>University of Manchester, UK</i>)
15:30-16:00	Coffee Break
16:00-17:30	Hands On and Parallel Sessions
	a) MlxS Working Group Chair: Pieter Sterk (<i>University of Oxford, UK</i>) & Lynn Schriml (<i>University of Maryland, USA</i>) In this session we will give a brief introduction to the MlxS checklists. In addition, we will give an overview of curation and data submission tools and discuss further needs of researchers to generate MlxS compliant reports.
	b) M5 Working Group -- Towards Better Standards for Computed Results Chair: Folker Meyer (<i>Argonne National Laboratory, USA</i>) The data deluge (or data bonanza) has created a series of novel problems in biology. Simply exchanging sequence data is not sufficient. The community has to work towards standards that enable exchanging higher level data products, the results of computational analyses. We will be describing the current state of the "ecosystem", open issues and the current plan for the path forward. Existing standards will be discussed.
17:30-17:40	c) Virus Standards Working Group Chair: Yiming Bao (<i>NCBI, USA</i>) & Hui Wang (<i>CEH, UK</i>) This session will discuss ways to harmonize community based viral metadata standards with MIGS/MIMS and those of other resources such as the NCBI's BioSample database; what type of NGS data should be captured, where and how they should be captured; whether it is necessary to give special isolate names for viruses whose sequences are generated through meta-genomics, and if so how such names should be formed and standardized.
	Coffee Break

17:40-18:00	Closing Session: Handing Over GSC13 to GSC14 Jack Gilbert & Dawn Field
18:00-19:00	GSC Board Meeting