GLOBAL MICROBIAL IDENTIFIER MEETING

DAVIS, CA
SEPTEMBER 10TH & 11TH

100K GENOME PROJECT

GMI
Global Microbial Identifier

Global Microbial Identifier Meeting #6

Agenda

When: September 10th and 11th, 2013 from 8:30 AM to 6:00 PM Daily

Where: Walter A. Buehler Alumni and Visitors Center, UC Davis Campus

Conveners

GMI • US Food & Drug Administration • UC Davis 100k pathogen genome project

Purpose

To determine a path forward for how to establish a globally distributed system and follow up on the previous GMI meetings. These meetings are primarily for collaboration and integration across international borders.

Discussions

Will focus on solutions to questions and challenges surrounding the deployment of next-generation genomic typing tools for public health and clinical disease cluster detection on a global scale. Specific topics for discussion will include: the working groups defined in earlier meetings; Political and financial challenges, Repository and storage of data, Analytical approaches, Ring trials and QA/QC and Pilot projects. Intermixed with the working groups reporting and updating a few examples will be presented on advances in the field since our last meeting in Copenhagen DK. Detailed instructions for breakout discussions will be provided prior to the meeting.

Agenda

AGENDA

Day #1 (September 10th, 2013)

Overview, Updates, Initiatives

08:30 AM	Welcome/Overview	Marc Allard and Bart Weimer
08:50 AM	Status and perspective of GMI meeting 5	Frank Aarestrup

Charter & Structure of GMI

09:05 AM	GMI Charter and Structure - An Introduction to the Discussion on Shared Principles	George Haringhuizen
09:20 AM	Discussion in Break-Out Sessions	
10:00 AM	Discussion in plenum	
10:30 AM	BREAK	

Status and Perspective of Each Working Group

11:00 AM	Political and financial challenges	Jorgen Schlundt
11:10 AM	Work Group 2 Update: Repository and Storage of Sequence and Meta-data	Bill Klimke
11:20 AM	Analytical approaches	Marc Allard
11:30 AM	Work Group 4 Update: Ring Trials and QA/QC	Rene Hendriksen
11:40 AM	An Update on Pilot Projects	Mark Wilson
11:50 AM	LUNCH BREAK	

GMI Resources

1:00 PM	FDA Genome Trakr database: details on dataflow from field labs to a public *Salmonella* reference database at NCBI	Ruth Timme

Focused Discussion to Review and Update Strategic Plan for Each Working Group

Working group 3 will continue with talks on software tools and standardization

1:15 PM	Focused Break-Out Sessions in working groups	Side Rooms
3:30 PM	BREAK	

Produce Written Update Strategic Plan for Each Working Group

3:34 PM	Focused Break-Out Sessions in working groups	Side Rooms
5:30 PM	QUESTIONS	
6:00 PM	ADJOURN DAY #1	

Day #2 (September 11th, 2013)

Agenda

08:30 AM	Welcome	Marc Allard and Bart Weimer

GMI Resources

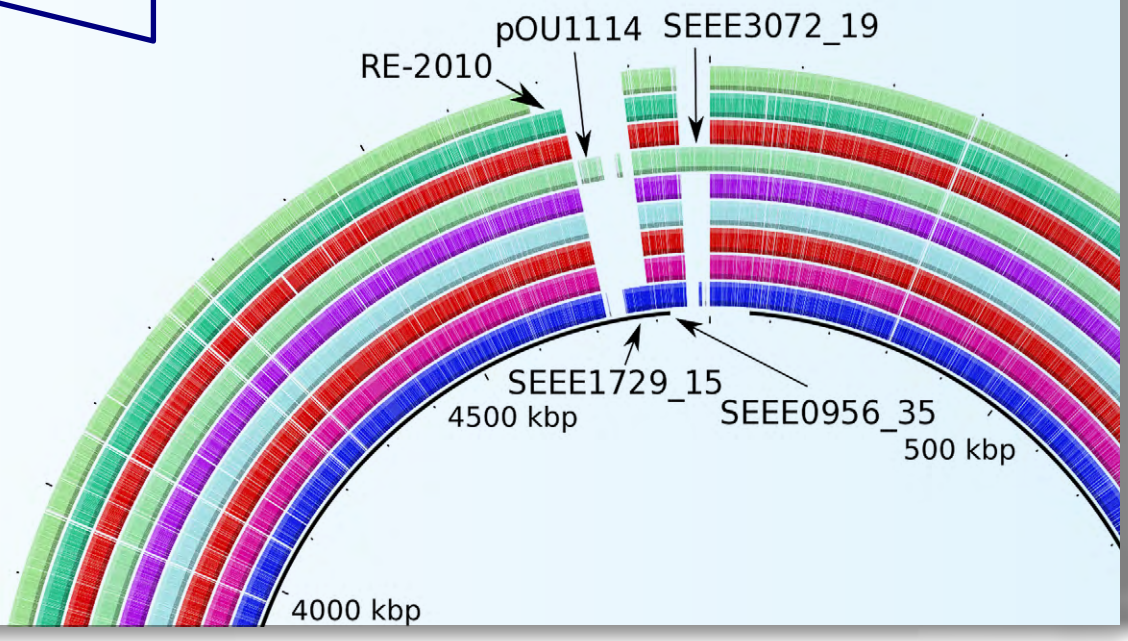
08:40 AM	Tomorrow's Genome: Complete Bacterial Genomes in <24 h for outbreak resposne	Ken Dewar
09:05 AM	U.S. Nation-wide Genome Sequencing-based *Listeria monocytogenes* Surveillance	John Besser
09:30 AM	100K Pathogen Genome Project	Bart Weimer
09:55 AM	Establishing Whole-genome based approaches as a Routine Tool in Reference Microbiology	Jonathan Green
10:20 AM	BREAK	

Identify Milestones and Responsible Volunteers to Accomplish Strategic Plan for each Working Group

10:35 AM	Focused Break-Out Sessions in working groups	Side Rooms
12:00 AM	LUNCH BREAK	
1:00 PM	Enabling Sequence-Based Technologies for Microbial Diagnostics	Heike Sichtig/ Uwe Scherf
1:25 PM	DTU software tools for NGS GMI data analysis	Ole Lund

Finalizing and Drafting Milestones to Accomplish Strategic Plan for Each Working Group

1:50 AM	Focused Break-Out Sessions in working groups	Side Rooms
3:30 PM	BREAK	
3:45 PM	(Generate final report from focused groups)	MAIN HALL/Side Rooms
4:45 PM	QUESTIONS and Discussions	
6:00 PM	ADJOURN DAY #2	



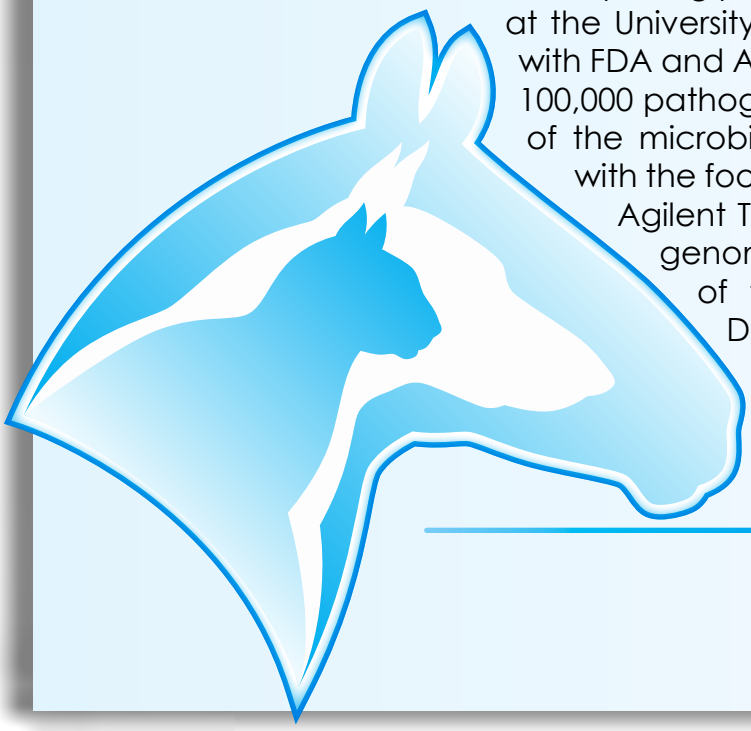
Speaker Biographies

Marc Allard, Ph.D.

Marc W. Allard received his Ph.D. in biology in 1990 from Harvard University (Cambridge, MA). Dr. Allard was the Louis Weintraub Associate Professor of Biology (and Genetics) at George Washington University (Washington, DC) for 14 years from 1994 to 2008. He has had appointments to the Visiting Scientists Program both at the Federal Bureau of Investigation's Counterterrorism and Forensic Science Research Unit (CTFSRU) and in the Chem.-Bio. Sciences Unit (CBSU) for approximately 8 years, where he assisted in the anthrax investigations as well as in human genetics data-basing. Dr. Allard joined the Office of Regulatory Science and the Division of Microbiology in November 2008 and he is using DNA sequence information from the genomes of food borne pathogens to identify unique single nucleotide polymorphisms (SNPs) and whole proteins to rapidly identify the various strains of bacteria, particularly *Salmonella, E. Coli, Shigella* and *Listeria*. Dr. Allard specializes in both phylogenetic analysis and bioinformatics methods, as well as the wet laboratory methods which generate this genetic information. mwallard@gmail.com, marc.allard@fda.hhs.gov.

Bart Weimer, Ph.D.

Dr. Weimer is a professor in UC Davis School of Veterinary Medicine since 2008 studying host/microbe interactions and foodborne pathogens. The primary thrust of his research program is the systems biology of microbial infection, host association, and bacterial survival in food and the environment. Using functional genomics and metagenomics, Dr. Weimer's program examines the interplay of genome evolution, gene regulation, and metabolomics to produce specific conditions needed for survival, infection, and host adaptation. The interplay between the host, the microbe, and the interdependent responses is a key question for his group. In addition to his faculty appointment Dr. Weimer was appointed as faculty assistant to the Vice Chancellor of Research to expand industry/university partnerships in the life sciences and co-director of BGI@UC Davis. Prior to joining UC Davis Dr. Weimer was a professor at Utah State University where he directed the Center for Integrated BioSystems and established the gene expression and bioinformatics core services. He also held positions with HyClone Laboratories (acquired by ThermoFisher) and AuroTech, Inc. (acquired by International Flavors and Fragrances) after completing postdoctoral training in genetics and biochemistry at the University of Melbourne. His group is currently partnered with FDA and Agilent Technologies to sequence the genome of 100,000 pathogens and is conducting metagenome sequence of the microbiome of chronic disease conditions associated with the food supply. Most recently he was honored with the Agilent Thought Leader Award and his work in microbial genomics received the HHSInnovate award as part of the 100K genome project. During his career Dr. Weimer mentored 26 graduate students, received 7 patents (3 pending), published over 90 peer-reviewed papers, contributed 17 book chapters, edited 3 books, and presented over 400 invited lectures.



George Haringhuizen, MA, LL.M.

George Haringhuizen (1954) studied Social Sciences (1983) and Law (2001). After a career as researcher and project leader in the field of welfare and refugees he entered the public health domain in 2001. Working at the Dutch Association of Public Health Services, George Haringhuizen was between 2001 and 2005 responsible for the taskforce to strengthen the national infrastructure for infectious disease control in The Netherlands. In 2006 he transferred to the newly established National Centre for Infectious Disease Control at RIVM, where he works as senior advisor to the director and as public health lawyer. He was responsible for the implementation of the International Health Regulations, was co-scribe of the revised Dutch Public Health Act (2008) and acts as liaison to WHO. George Haringhuizen published about law and infectious disease control in The Netherlands and European comparative public health law. He is guest-lecturer at the National School of Public and Occupational Health and at Erasmus University Rotterdam.

Jørgen Schlundt, Ph.D.

Dr. Jørgen Schlundt is the Director at the National Food Institute, Technical University of Denmark. Dr. Schlundt has a veterinary degree as well as a Ph.D. from the Veterinary University in Copenhagen, Denmark. He worked at national level on environmental and food safety issues from 1983 to 1999, during which period he headed the Bacteriology Department at the Veterinary Research Laboratory in Harare, Zimbabwe for three years. From 1999-2010 Dr. Schlundt was Director of the Department of Food Safety and Zoonoses at WHO, Geneva. During the years, he participated in a number of international bodies, including OECD expert groups, WHO and FAO Expert Consultations, EU Scientific Committees, and the FAO/WHO Codex alimentarius Commission. Dr. Schlundt has participated in the international development of Risk analysis principles, including the use of scientific risk assessment as the basis for food safety management decisions. As part of this, he has overseen major new international initiatives, including the creation of the Joint WHO/FAO Joint Expert meeting on Microbiological Risk Assessment (JEMRA) and the International Food Safety Authorities Network (INFOSAN), the build-up of the Global Foodborne Infections Network (GFN), the initiation of the first-ever estimation of the global burden of foodborne diseases, and the development of a major consumer education programme on the Five Keys to Safer Food.

William Klimke, Ph.D.

Dr. William Klimke is a staff scientist at the National Center for Biotechnology Information (NCBI), part of the US National Library of Medicine, National Institutes of Health. He has been involved in projects related to prokaryotic genome sequencing, annotation and analysis in GenBank, the Reference Sequence (RefSeq) project, and the bacterial pathogen analysis pipeline. Dr. Klimke received his BSc and PhD from the University of Alberta.

Speaker Biographies

Rene Hendriksen, Ph.D.

In 1993, Dr. Rene Hendriksen was employed at the National Veterinary Institute as laboratory technologist. In 1999, the institute was appointed as WHO Collaborating Centre and his duties and responsibility were transferred to building up laboratory capacity in relation to the WHO Global Foodborne Infections Network (WHO GFN). In 2006, the institute was also appointed as European Union Reference Laboratory (EURL) in antimicrobial resistance for which he is daily responsible. He has facilitated and conducted more than 25 international laboratory training courses for more than 500 scientists from more than 50 countries; primarily in Southeast and central Asia, China, Eastern Africa, the Middle East, and Europe. He is also responsible for conducting national and international (WHO / EURL) proficiency test programs (External Quality Assurance Systems).

In 2010, he defended his PhD thesis "Global epidemiology of non-typhoidal *Salmonella* infections in humans". Currently, he works as senior scientist at the Technical University of Denmark, National Food Institute (DTU Food), Division of Bacterial Genomics and Epidemiology, Research Group of Bacterial Genomics and Antimicrobial Resistance and act as deputy for the reference centres. He represents the institute in the WHO Global Foodborne Infections Network (WHO GFN) and the WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR) network. Additionally, he chair working group 4 of the Global Microbial Identifier. Dr. Rene Hendriksen is INFOSAN and ECDC focal. His main focus is research in global epidemiology, surveillance, antimicrobial resistance, and population structure of mainly foodbone pathogens. Dr. Rene Hendriksen is author of 57 peer-reviewed published and accepted articles in international refereed journals.

Mark R. Wilson, Ph.D.

Mark R. Wilson currently is the Director of the Forensic Science Program at Western Carolina University (WCU) in Cullowhee, N.C. He received a Bachelor of Science degree in Biology and Chemistry from Azusa-Pacific University, an M.S. degree in Biology from California State University, Fullerton, and a Ph.D. in Biosciences from George Mason University. Dr. Wilson is a retired Supervisory Special Agent of the FBI, and spent the majority of his 23-year FBI career in the Laboratory Division developing and implementing new DNA typing techniques and transitioning them into casework. Dr. Wilson was the first qualified forensic mitochondrial DNA examiner in the country, and was also a qualified microscopist in the Trace Evidence Unit of the FBI Laboratory. He has analyzed over 400 forensic cases, and has testified in international, Federal, and State courts on the topics of trace evidence analysis and human mitochondrial DNA typing. He has published over 48 articles in peer-reviewed journals on topics related to DNA typing and microbial forensics. He received the FBI Director's Award in Information Management and Scientific and Technical Merit in 1996 and 2009. Wilson helped to establish and manage the new Chemical Biological Sciences Unit of the FBI Laboratory in Quantico, Virginia. This Unit included a new research effort dedicated to integrating traditional forensic examinations with the emerging threats of biological, chemical and radiological agents. While there, he initiated the Unit's research efforts into the forensic characterization of microbial evidence, and served as chair of the Scientific Working Group on Microbial Genetics and Forensics (SWGMGF). As the Director of the Forensic Science Program at WCU, Wilson oversees an active DNA research program, and also teaches or co-teaches courses in Forensic DNA Typing, Physical Methods, Principles of Systematics, Population Genetics, and Scientific Method.

Ruth Timme, Ph.D.

Dr. Timme is a Research Microbiologist at the FDA's Office of Regulatory Science. She received her PhD in 2006 in Plant Biology at The University of Texas at Austin. Her research background is focused mainly on utilizing comparative genomics and phylogenetics methods to answer evolutionary questions. Although her training is in botany, her published research spans a diversity of organisms, including sunflowers (*Helianthus*), Dinoflagellates, Charophyte green algae, and *Salmonella*. At the FDA she is implementing phylogenomic methods for tracking foodborne pathogens through the US food supply.

Darcy Hanes, Ph.D.

Dr. Hanes is a research microbiologist in the Division of Virulence Assessment, Office of Applied Nutrition, Center for Food Safety and Applied Nutrition (CFSAN) at the Food and Drug Administration. She obtained her undergraduate degree in Biology from St. Bonaventure University and her doctoral degree in microbiology from the State University of New York at Buffalo. Dr. Hanes joined the FDA in 1988 and in 1990 became a Commissioned Officer in the United States Public Health Service (PHS). Dr. Hanes leads a research team developing methods for the isolation, identification and molecular characterization of *Salmonella enterica.* She is also the director of the Special Pathogens Laboratory that develops methods for the isolation of biothreat agents from food. Her work is conducted as part of the joint FDA-USDA Food Emergency Response Network (FERN).

Ken Dewar, Ph.D.

Dr. Ken Dewar holds a joint position of Associate Professor in the Departments of Human Genetics and Experimental Medicine at McGill University. Dr. Dewar obtained his PhD from Université Laval in 1995 studying the genome structure of the Dutch elm disease fungus, *Ophiostoma ulmi*. After completing post-doctoral work at the University of Pennsylvania participating in the genome mapping and sequencing of the model plant *Arabidopsis thaliana*, Dr. Dewar joined the Whitehead Institute/MIT Center for Genome Research in 1997 as part of the Human Genome Project, where he led teams for genome mapping and chromosome closure. In 2002, Dr. Dewar joined the Department of Human Genetics at McGill University. The Dewar laboratory combines leading edge DNA sequencing technologies and bioinformatics to better understand genome structure and variation. Past projects funded by Genome Quebec and Genome Canada included the comparisons of epidemic and non-epidemic isolates of the hospital pathogenic bacterium *Clostridium difficile*; the development of genomic resources for complex trait analysis in the biomedical primate model, the vervet monkey; and the genome sequencing and analysis of cellulose degrading fungi. Current projects focus on technological advances for rapid sequencing of microbial genomes, and the development of new approaches for the sequencing and assembly of multiple species comprising intestinal microbiomes. The Dewar lab is situated in the McGill University and Genome Quebec Innovation Centre and works closely with the Innovation Centre in the implementation of new DNA sequencing technologies and analysis procedures.

Speaker Biographies

John Besser, Ph.D.

John Besser has been the Deputy Chief of the Enteric Diseases Laboratory Branch at the U.S. Centers for Disease Control and Prevention (CDC) since July 2009, where he has been involved in national and global programs to detect, characterize, and track enteric diseases. Prior to CDC he directed infectious disease laboratory activities at the Minnesota Department of Health for 19 years. John received his MS and PhD degrees from the University of Minnesota.

Jonathan Green, Ph.D.

Professor Jonathan Green leads on infectious disease bioinformatics for Public Health England Microbiology Services. Initially training as a clinical scientist in virology, Jon studied for an MSC in Medical Microbiology at the University of Surrey and in 1993 he obtained a PhD, also at Surrey, investigating transmission of human papillomavirus. Following this, he lead the molecular group within the Enteric Virus Unit, HPA Colindale where the emphasis as on molecular approaches for the detection, characterisation and molecular epidemiological studies of gastroenteric viruses, particularly noroviruses and rotaviruses. During this period, the need for specific bioinformatics developments to support the exponential developments in molecular diagnostics and typing was identified and Jon was placed in charge of a new Bioinformatics Unit in 2000. The unit provides training, support and R&D to staff across the Agency and to external collaborators. A particular current focus is the translation of NGS technologies for public health purposes. He has had a key role in the establishment of a centralised Next Generation Sequencing Service at Colindale, especially in establishing the high performance computing resources to underpin the service, plus the development and delivery of bioinformatics pipelines and resources to end users. He has recently been appointed as Honorary Professor in the Department of Clinical Infection, Microbiology and Immunology, University of Liverpool.

Heike Sichtig, Ph.D.

Dr. Sichtig is a subject matter expert and premarket reviewer within the Division of Microbiology Devices in the Office of In -vitro Diagnostics and Radiological Health (OIR), Center for Devices and Radiological Health at the U.S. Food and Drug Administration (FDA). She is the lead technical scientist for microbial diagnostic devices related to high throughput sequencing and bioinformatics. She is developing approaches to use alternative analytical models for assessing safety and effectiveness for these novel sequence-based diagnostic devices. She has significant experience developing methods and computational tools for bioinformatics with the biologist in mind. Prior to joining the FDA, Dr. Sichtig developed and assessed a novel adaptive computational modeling platform for transcription factor binding site detection and discovery using machine learning techniques (artificial spiking neural networks and genetic algorithms) at the Department of Molecular Genetics and Microbiology at University of Florida, Gainesville, Florida. She received her Ph.D. (2009) in Biomedical Engineering from Binghamton University, Binghamton, New York, her M.Sc. (2004) in Computing, Statistics and Math and her B. Sc. (2003) in Computer Science from Kean University, Union, NJ. She has experience in teaching courses such as Bioinformatics, Complex Biological Systems, Autonomous Agents, Probabilistic Systems and Biological Networks. She is Part-Editor for the Handbook of Bio – and Neuroinformatics and is on the Advisory Board for the Springer Series in Bio-Neuroinformatics. She is a member of the CLSI Consensus Committee on Molecular Methods and many professional societies including IEEE CIS,

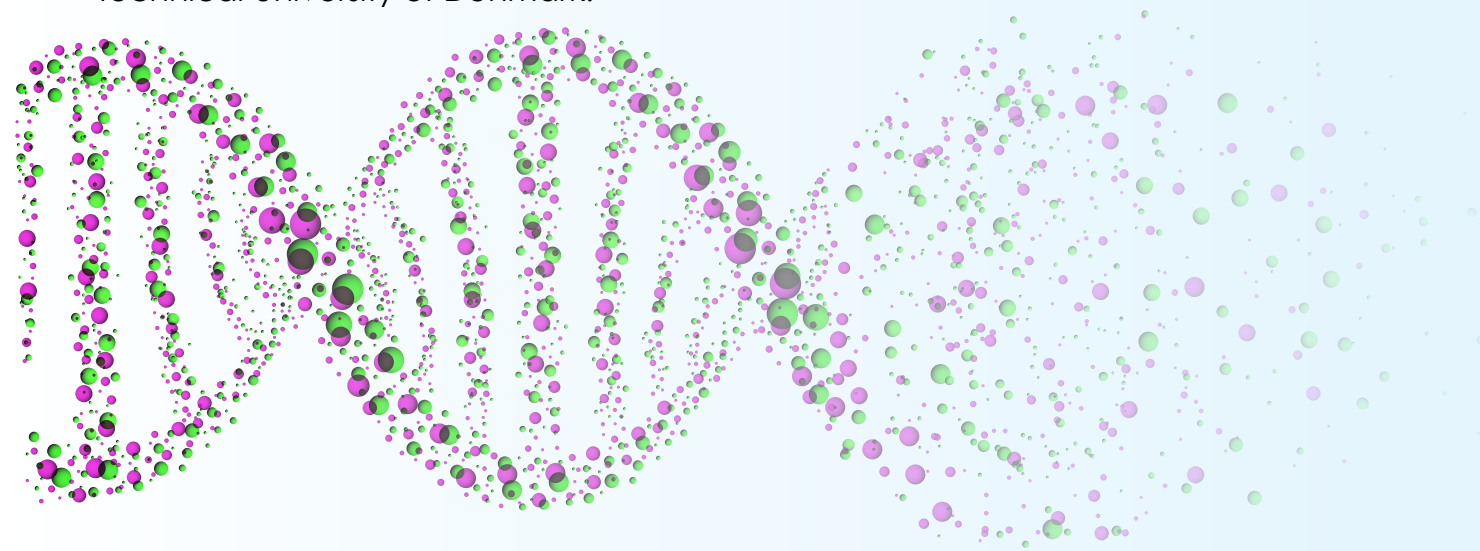
INNS, ASM and ASEE. She is the current chair of the IEEE CIS Chapters Sub-Committee and is a member of the Bioinformatics and Bioengineering Technical Committee. Her diverse background spanning from computer science and engineering to molecular biology and bioinformatics requires superior communication skills to navigate between research fields.

Uwe Scherf, Ph.D.

Uwe Scherf, M.Sc., Ph.D., is the Deputy Director in the Division of Microbiology Devices in the Office of *In Vitro* Diagnostics and Radiological Health (OIR) in FDA's Center for Devices and Radiological Health (CDRH) since August 2011. Dr. Scherf has extensive regulatory experiences. He approves/clears premarket applications (PMAs) and notifications (510ks), by determining the safety and effectiveness of these devices for marketing in the US. This includes the scientific supervision and workload management of subject matter experts and consumer safety officers to assure a timely response, processing, and approval of IVD application. Dr. Scherf is also serving as a member of the Board of Directors of the Clinical and Laboratory Standards Institute (CLSI) and is very interested in standard development. Prior to joining the U.S. Food and Drug Administration in 2004, Dr. Scherf was Senior Director for Genomics Research & Development in a genomic gene expression profiling company. Before his experience in industry, he worked for several years at the National Cancer Institute/NIH and developed with Dr. John Weinstein and collaborators a gene expression database for the molecular pharmacology of cancer on the NCI 60 human cancer cell lines. Dr. Scherf received his M. Sc. and Ph.D. in Microbiology/Biochemistry from the University of Marburg, Germany.

Ole Lund, Ph.D.

Dr. Ole Lund has worked in the fields of mathematical biology and bioinformatics since 1992. In this period he has contributed in a number of diverse areas: simulation of biological systems on a cell level, predictions of protein sequence motifs (glycosylations and MHC binding), protein structure prediction, genomics of humans and bacteria. This work has been described in more than 100 peer-reviewed papers in scientific journals, which has been citied more than 3000 times (h-index: 32). Currently his research focus is to make geno- to pheno-type associations based on whole genome sequences and use the derived phenotypes in simulations of the temporal behavior of biological systems. Dr. Lund received his M.Sc. and Ph.D. in Mathematical Biology/Bioinformatics from the Technical University of Denmark.



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