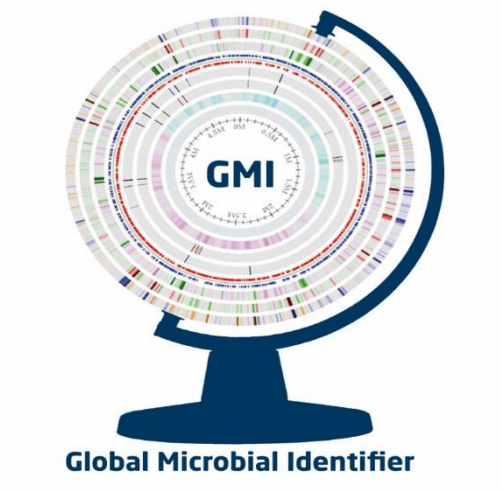
10th Global Microbial Identifier 2017



15th May to 17th May 2017
Sheraton Hotel, Cabo San Lucas, Mexico

Jorgen Schlundt

Biography:
Jørgen Schlundt is Michael Fam Chair Professor in Food Science and Technology at Nanyang Technological University, Singapore and Director NTU Food Technology Centre (NAFTEC), Singapore. He has worked at NTU since 2015, but is a Danish citizen with a Ph.D. from the Royal Veterinary University in Denmark in 1983. He has worked nationally on food safety 1983-99, including 3 years in Zimbabwe. From 1999-2010 he was Director Department for Food Safety and Zoonoses at the World Health Organization HQ in Geneva. 2011-14 Director National Food Institute in Denmark.

JS has participated in the international development of food safety Risk analysis principles and has overseen the creation of the WHO International Food Safety Authorities Network (INFOSAN) and the initiation of the first-ever estimation of the global burden of foodborne diseases. JS also initiated international evaluations of the importance of antibiotic use in agriculture, and the creation of the WHO list of critically important antibiotics for human health. JS chairs the Global Microbial Identifier, an international initiative suggesting a global database of DNA-sequences of all microorganisms. Throughout his professional life, JS has advocated the lowering of human health risk through effective, science-based action in food production systems.

Dra Lourdes Simental Oceguera

GMI Perspectives in developing countries

Abstract:
GMI is a powerful tool where you can share data, which translates to the decoding of any living being's DNA having an impact on all production sectors. Mexico is a developing country that uses this tool in different fields of science, but there are still many challenges; science must be solving the needs of society as well as projecting the solution of daily problems, such as diseases, the overuse of medications, vaccines, forensic medicine, in others in the field of medicine. Decoding also gift added value to primary production, that helps in safe global export, as well as the improvement of species and organisms intentionally used in food production, as well as the entire supplying industry helping to take care of our environment. Long term programs that include standardized techniques and beneficial molecules are needed. GMI 10th is a window to Latin America where researchers feel comfortable sharing their science.

Biography:
Oceanology, Autonomous University of Baja California. Master in Marine Biology and Aquaculture, University of Santiago de Compostela, Spain. Doctorate in Marine Biology and Aquaculture University of Santiago de Compostela, Spain. Head of the Department of Epidemiological Microbiology of the State Public Health Laboratory of Sinaloa. Director of the Center for Epidemiological Research of Sinaloa (CIES), General Hospital of Culiacán, Bernardo J. Gastelum., Secretary of Health of the State of Sinaloa. State Coordinator of Agri-Food Safety of the State Committee of Plant Protection of the State of Sinaloa (SAGARPA). Operational Director of the Regional Laboratory of Food Safety of the State of Sinaloa LARIA. Operative Director of Technology and Services in Food Safety S.A. Of C.V. (Tecsia®). Operating Director of INOQUOTECH. Stay at FDA in 2008, College Park, MD. USA Stay at the First Meeting "Disease Outbreak Detection in the Genomic Era: a Roadmap Forward" Food and Drugs Administration (FDA) USA. Arlington Virginia. Responsible for the project "Integral Plan for the Application of Systems to Reduce Risks of Contamination in the Primary Production of Fruits and Vegetables in the State of Sinaloa.

Georgius Ricardo Gotsis Fontes

Biography:
Georgius is the current Chairman of Eleven Rivers Board for the period 2016-2019, comes from a family of farmers with Greek roots; with him Agrícola Gotsis, S.A. de C.V. operates with the fourth generation in the farm business; Is an economist graduated from Pomona College, California; He has taken several courses in Oratory and leadership in various institutions. Since childhood he has been very involved with the activity, which has made him feel a great love for agriculture.

Saúl Beltrán Fernández

Epidemiological Research in Sinaloa

Abstract:
At the Center for Epidemiological Research of Sinaloa as of 2009 are stored and maintained clinical strains, water, food and environmental of interest from public health institutions (IMSS, ISSSTE, HGC and CSUC) and private (Clinical, water and food lab) in the State of Sinaloa, as well as institutions such as agricultural companies, fruit and food producers and processors in the State of Sinaloa and other states, for the purpose of determining their antibiotic resistance, epidemiological markers, and therefore the Data Analysis to obtain the Incidences, Antibiotic Resistance Patterns. As well as, Temporal variations, entries of new clones of each pathogen through protocols standardized by the CDC and FDA of the United States of America as well as the CDC of Europe. Studies on the prevalence of multi-resistant clinical strains of antibiotics from different public health institutions (IMSS, ISSSTE, HGC, IMSS YCSUC) and Private (clinical laboratory). Analysis of feces samples from HGC, IMSS, ISSSTE, IMSS and CSUC, for the identification of resistance clones of *Salmonella spp., Shigella spp., Vibrio parahaemolyticus, Vibrio cholerae and Escherichia coli O157: H7.* Determination and / or identification of resistance clones of clinical strains (*Pseudomonas, Escherichia coli, Klebsiella, Staphylococcus, Anicetobacter* among others) n Hospitals of the Public and Private Health Sector of the State of Sinaloa and the Northwest of Mexico.Performs isolates for its molecular characterization to obtain the restriction patterns by means of the PFGE technique which are analyzed with the Bionumerics software to establish the degree of similarity that exists between the strains obtained in the consecutive year.

Biograpghy:
Biomedical Chemist from Autonomous University of Sinaloa (UAS) Master of Science in Environmental and Sustainable Development, UAS Founder of the Sinaloa State Public Health Laboratory (1994) working in several Deparments like as Head of Department of sample reception, Water treatment plant, Chromatography and last Subdirector. Professor of the Master's Degree in Health, Safety and Sustainable Work Hygiene at the Faculty of Medicine of the UAS. Head of the Ceparium of the Center for Epidemiological Research of Sinaloa, General Hospital of Culiacán "Dr. Bernardo J. Gastelum ". Specialties in: Environmental Management of Hospitals; Quality and Productivity of Industrial Processes; Environmental Control and Regulation. Environmental Audit; Health, Safety and Environmental Protection. Stay at FDA in 2008, College Park, MD. USA He is currently Head of the Epidemiological Research Center of Sinaloa. Advisor of 6 research projects in Clinical Bacteriology.

Gabriela Olmedo-Alvarez

Microevoltion and trait diversity in members of a microbial community: When a genotype is not enough to predict a phenotype

Abstract:
My group (with many great collaborators) has been studying microbial diversity at the valley of Cuatrocienegas, Coahuila. This valley is a desert characterized by extremely low levels of phosphorus, where scattered ponds harbor a great microbial diversity in sediment communities. To explore the evolution, ecology and genetics of the microbial communities we have recurred to the simplicity of study and resolution of a single genus, Bacillus. Previous characterization of the interactions between the Bacillus spp. co-ocurring in the sediment communities revealed that antagonism influences the structure of the community. These interactions have been modeled through "cell automaton" to understand how diversity is maintained. The phenotypic analysis of hundreds of isolates has revealed the multiplicity of traits and a distribution of functions (genes) that seems to explain co-existence of different Bacillus spp. taxonomic groups. The genomic analysis of some groups has revealed that even at species level there is a 30% difference in gene content and numerous mobile genetic elements. Finally, our work has allowed us to describe how the sediment communities participate in the cycling of phosphorus in its different redox states, and how bacteria sample genes to adapt to the different available substrates. This sediment community is a great model to test genomic predictions about microbial interactions in different microbiomes.

Valeria Souza

Vibrio comparative genomics from an extraordinary oasis in Mexico: Can we explain the origins of pathogenicity?

Abstract:
The genomes of bacterial pathogens were compared with those of free-living close relatives from the Cuatro Ciénegas Basin (CCB), an ultra-oligotrophic site that contrasts with human-associated environments. CCB is a hyper-diverse oasis in the Chihuahuan desert in Mexico, where bacteria that forms microbial mats and stromatolites is the bases of the food web. In order to demonstrate adaptation to oligotrophy and enrichment experiment was performed by adding N and P to both water and sediment. Fifty-nine genomes were analyzed from *Vibrio*, *Photobacterium* and compared with *Pseudomonas*, and *Aeromonas*, including 8 reference strains, 45 free-living strains from Vibrionacea of CCB in un-riched sites and 6 stains from the enrichment experiment. Herein 15 virulence-related genes are described, common to all strains obtained from the wild or from the enrichment experiment and to reference pathogenic strains, observing that early horizontal gene transfer (HGT) events involving virulence genes distorted the phylogeny, as compared with a neutral 16S rDNA phylogeny. Wild strains had an average of 90 virulence genes, including those for the production and resistance of antibiotics and several ancestral types of secretion systems; but none of the genomes from wild strains had pathogenic islands, while integrons were few and rare. The wild strains were rich in CRISPR genes but did not present insertion sequences or prophages. Understanding the evolution of virulence as a mechanism of survival of colonizers opens a door to fresh evolutionary ideas on how to understand and treat bacterial diseases.

Biography:
Full Professor, Member of the national system of Researchers level III Department of Evolutionary Ecology, Instituto de Ecología, UNAM. Born in 1958; Bachelor in Biology (1983), Master in Sciences (1985) and PhD in Ecology (1990), all from Universidad Nacional Autonoma de México. Two postdoctoral research positions with Richard Lenski, both in UCI and MSU. I was hired as an assistant Professor in 1993 at the Instituto de Ecología, UNAM, where I am working in understanding the rules of evolution and ecology that can explain diversification and coexistence. I got a MacArthur fellowship in 1994; the National award on ecology and Conservation in 2006; the Love for the Planet award given by VW in 2010; I am a Aldo Leopold Fellow since 2011. I have co-edited several books, including a text book for high schools and 14 book chapters. I have 99 papers in international journals in the ISI, 4 of them accepted and in revisions, with more than 2800 citations and I have been invited to more than 65 conferences internationally.My students have got the honor degree in Biology (9), Masters in Science (6) PhD (12); besides I have 7 students in the process of getting their degree.

William Klimke

The NCBI Pathogen Detection Isolates Browser and Rapid Typing of Listeria and Salmonella

Abstract:
The NCBI Pathogen Detection pipeline is a completely automated pipeline that ingests raw sequencing data from laboratories sequencing food and clinical pathogen isolates. The pipeline takes the raw sequencing data, assembles, annotates, and clusters the isolates based on SNP analysis (single-linkage clustering with a 50 SNP distances threshold). For each cluster phylogenetic trees are reconstructed using maximum compatibility. The annotated assemblies are checked for the presence of antimicrobial resistance genes/proteins. The cluster membership and links to phylogenetic trees, isolate metadata, and antimicrobial resistance gene content are made available in a web interface that allows easy access to the information to aid outbreak and traceback investigations by public health labs without the need for local bioinformatics expertise and expensive computational infrastructure at every lab doing the sequencing. NCBI is also exploring a rapid assembly and typing system using a new de Bruijn graph assembler and rapid wgMLST typing. A pilot project for Listeria and Salmonella has been used as a testbed for automated generation of wgMLST schemas.

Biograpghy:
William Klimke is the NCBI Pathogen Detection Team Leader at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, and Department of Health and Human Services. William Klimke received his Ph.D from the University of Alberta in 2002, and has been at NCBI since that time. He has been involved with RefSeq microbial genomes, various annotation projects to improve functional annotation, and has helped to create the NCBI Protein Clusters database. Dr. Klimke's has received numerous awards for his work on the Pathogen Detection pipeline.

Swaine Chen

The Genome Institute of Singapore GERMS Bacterial Genome Browser Platform - bringing integration and intuitiveness to non-genomics collaborators

Abstract:
The Genome Institute of Singapore has a dedicated GERMS (GIS Efficient and Rapid Microbial Sequencing) Platform which focuses on protocols and analyses relevant to microbes, including bacteria, viruses, and eukaryotic pathogens. We have developed an integrated genome sequence browser over the last two years that helps us manage the data flow and collaborator demands. The Genome Browser Platform is focused on enabling our collaborators, who are mostly busy hospital clinicians, to answer the questions they want (Do we have an outbreak? What is the source of this infection?) without having to wade through the sea of G's, A's, T's, and C's. I will show some of our integration features which help drive intuitive interaction with data, even for those who are not genomics analysis specialists. All the data is kept private for each collaborator, while the code is open source. We estimate that we can keep pace with global data sets through at least the next 3 years with our current hardware, so we are eager to expand our collaborations to the region and internationally.

Genomic insights into an outbreak of Group B Streptococcus

Abstract:
In 2015, the largest outbreak of invasive Group B Streptococcal infection occurred in Singapore. Initial epidemiology linked infections to the consumption of raw fish. I will describe the contribution of bacterial genomics to the multi-agency investigation of this outbreak. I will also highlight some lessons we learned about the value and execution of genomics, which we are now incorporating into future preparedness plans.

Biography:
Dr. Swaine Chen is an Assistant Professor of Medicine at the National University of Singapore and a Senior Research Scientist at the Genome Institute of Singapore. His research interests include the application of genomics to understanding molecular mechanisms of urinary tract infection, particularly those caused by Escherichia coli. He specializes in the bacterial genetics and manipulation of wild type clinical isolates, which helps in understanding pathogenesis and antibiotic resistance as well as in creating new tools for synthetic biology. In addition, he has expertise in the application of genomics to the investigation of outbreaks of bacterial disease.

Paul Kielm

Focused Amplicon Sequencing for Clinical Applications: Drug Susceptibility Testing of Mycobacterium tuberculosis from Patient Specimens

Abstract:
Tuberculosis (TB) is one of the world's most threatening infectious diseases, infecting 2-3 billion people and representing one of the top ten causes of global mortality. While antibiotic therapy can be effective, drug resistance is prevalent with multiple drug resistance (MDR) and extreme drug resistance (XDR) creating particularly critical challenges. Culture methods to determine drug resistance can take weeks and then fail to correctly phenotype minor subpopulations in hetero-resistant infections. In the absence of rapid and accurate diagnostics, empiric therapeutic approaches are common. We have been applying focused amplicon sequencing to diagnostic and detection problems using Next-Generation DNA sequencing platforms. This involves multiplexed PCR targeting of high-value genomic regions. Several innovations have been developed to decrease sequencing error rates, decrease optical contamination, and allow multiple specimen analysis during a single sequencing run. A specialized analysis pipeline (Amplicon Sequencing Analysis Pipeline – ASAP) allows deconvolution of specimens, mapping of reads and the generation of reports targeted at specific expert levels (researcher to clinician), which makes this technology feasible for wide applications. For TB, this approach has involved DNA extracted directly from sputum, with PCR targeted at genome locations with known drug resistance mutations. Single Molecule Overlapping Read (SMOR) analysis decreases the sequencing error to less than 0.1% and allows the detection of even minor mutant drug resistant populations with confidence. Overall, amplicon-based sequencing for DST is highly concordant with the phenotypic DST, and much faster.

Biography:
Paul Keim, PhD, is the executive director of The Pathogen and Microbiome Institute, which uses genomic tools for understanding infectious diseases and the microbiome. This is a joint institute between TGen and Northern Arizona University, where Dr. Keim holds the Cowden Endowed Chair in Microbiology. His work has employed genetic and genomic analyses for understand bacterial pathogen population structure and evolution for more than 30 years. Linking the populations to their ecology has also been a critical part of his program. His laboratory served as the evidence repository and genetic analysis lab for the FBI during the 2001 anthrax-letter investigation. He has been a leader in the field of microbial forensics which uses evolutionary analysis to understand close relationships among pathogen isolates. This work was foundational for his pursuit in public health investigations and the development of novel clinical diagnostic tests. He is an elected fellow of both the American Association for the Advancement of Science and the American Academy for Microbiology. The National Institutes of Health appointed him to the National Science Advisory Board for Biosecurity in 2004 and served as its chairman for two years. He has published over 400 scientific research articles that have been cited over 20,000 times.

Duncan MacCannell

Implementation of genomics in public health - US Advanced Molecular Detection Program

Abstract:
Advances in laboratory and information technologies are transforming public health microbiology. In particular, next-generation sequencing (NGS) and bioinformatics are enhancing our ability to investigate and control outbreaks, detect emerging infectious diseases, develop vaccines, and combat antimicrobial resistance—all with increased accuracy, timeliness, and efficiency. The Centers for Disease Control and Prevention (CDC)'s Advanced Molecular Detection (AMD) program is helping to drive the coordinated and sustainable implementation of NGS and other emerging and innovative technologies in routine practice throughout the US public health laboratory system. In addition to a range of applied projects and strategic collaborations, the AMD program directly supports a number of cross-cutting efforts, such as: 1) building shared IT and laboratory capacity for genomics, proteomics, bioinformatics and next-generation diagnostic testing—including standardization of workflows, data systems and quality management processes; 2) developing training in bioinformatics and other essential skills, including fellowships and career paths for public health laboratory staff; and 3) supporting continued innovation and coordinated application of genomics and other emerging technologies to meet public health challenges. This presentation will describe the AMD initiative, including a brief overview of current projects and successes, and will discuss both priorities and challenges for the future.

Biography:
Duncan MacCannell is the chief science officer for the CDC's Office of Advanced Molecular Detection (OAMD), where he coordinates the implementation and support of pathogen genomics, bioinformatics, high-performance computing and other innovative laboratory technologies across the CDC's four infectious disease centers. With a broad focus on laboratory science and strategic innovation, he directs the agency's high-performance computing center of excellence, and works to integrate standardized, sustainable capacity for advanced laboratory technologies and scientific computing into routine public health practice.
Previously, as a public health microbiologist and molecular epidemiologist, Duncan worked with the PulseNet program on the development and validation of next-generation subtyping and characterization methods for Shiga-toxin producing Escherichia coli (STEC), as a general subject matter expert on bacterial molecular epidemiology and antimicrobial resistance, and as the CDC laboratory surveillance team lead for healthcare-associated pathogens, such as methicillin-resistant Staphylococcus aureus (MRSA) and Clostridium difficile. His research interests include the application of comparative pathogen genomics and metagenomics to public health microbiology, and the development, validation and standardization of molecular diagnostics, next-generation straintyping and bioinformatics for pathogen identification, outbreak investigation and large-scale molecular surveillance.

Randall Olsen

Use of NGS in clinical microbiology

Abstract:
Our clinical laboratory has validated whole genome sequencing of microbes as a routine clinical test. We use whole genome sequencing in the clinical laboratory to 1) provide taxonomic assignments for slow growing, difficult to cultivate, or difficult to identify organisms; 2) investigate nosocomial infections and possible outbreaks; 3) study the molecular basis of severe, unusual, or interesting infections; and 4) understand bacteria strain genotype – patient disease phenotype relationships. To date, we have sequenced more than 15,000 genomes. I will use a case based approach to illustrate how whole genome sequencing has been used in our health care system. Obstacles to implementation and lessons learned will also be discussed.

Biography:
Randall Olsen is Medical Director of the Molecular Diagnostics Laboratory, Microbiology Laboratory, and Special Testing Laboratory at Houston Methodist Hospital in Houston, Texas, USA. He also has appointments at Tecnologico de Monterrey, Weill Cornell Medical College, and Texas A and M Health Science Center. Randall earned a Ph.D. (Pathology and Microbiology) and M.D. from the University of Nebraska and completed clinical pathology residency training at Baylor College of Medicine. The overarching goal of his research is to translate new discoveries in basic science to improve patient care. He uses an integrated molecular approach, including whole genome sequencing, genome-wide transcript analysis (RNA sequencing), in vitro and ex vivo assays, and mouse and monkey models to test hypotheses bearing on bacterial virulence and host-pathogen interactions. Most recently, he has used whole genome sequencing to study the population genetic structure and molecular basis of epidemics of Klebsiella pneumoniae, Staphylococcus aureus, and Streptococcus pyogenes.

Maria Hoffmann

The role of NGS in driving modern functional genomic studies of pathogens/microorganisms

Abstract:
Genetic adaptations observed in Salmonella and other foodborne pathogens associated with food production and processing environment, causing foodborne illnesses have become a public health concern. The persistent emergence of outbreaks attributed to certain serovars demonstrates adaptive characteristics of these organisms in certain food commodities. This highlights the probability of evolutionary changes in these pathogens, in which a selective advantage was conferred for survival, persistence and even growth within food matrices and in the environment, increasing their propensity for morbidity and mortality. For example, the consumption of fresh tomatoes has been linked to numerous foodborne outbreaks involving specifically S. Newport. Moreover, S. Newport strains associated with tomato and tomato-growing environment mostly belong to S. Newport lineage III. By integration of whole genome sequencing (WGS) data and transcriptomic data, genes and other elements capable of conferring adaptive advantages to foodborne and environmental Salmonella were identified. Our results showed the differing response of S. Newport lineages that may indicate the fitness of lineage III in tomato and the tomato-growing environment. This study provided insights into how S. Newport adapts to this unique niche and acquires increased virulence. Staphylococcus food poisoning (SFP) ranks fifth among pathogens associated with foodborne illness in the U.S. To date, 23 staphylococcal enterotoxins and enterotoxin-like enterotoxins have been identified, but commercially available immunological assays detect only five of the enterotoxins (SEA-SEE). A joint analysis of transcriptomic data and mass spectrometry (MS) data enables us to pinpoint the time during staphylococcus growth when enterotoxins (SEC, SEG, SEH, and SEI) are produced. These results are helpful to develop accurate assays to detect these enterotoxins in the food chain. Taken together, as WGS takes over as the primary tool for bacterial characterization, it is important for FDA to continue development and application of this tool and continue with plans to harmonize with global partners and provide preventive measures to support the U.S. food supply.

Biography:
Dr. Maria Hoffmann received her master degree in Food Chemistry at the University of Hamburg in 2007. In 2012 she received her PhD degree "Development of a Molecular Subtyping Method and Phylogenetic Analysis of Vibrio associated with Sponge Microcosms" from the University in Hamburg. She did a postdoctoral fellowship at FDA/CVM (Center for Veterinary Medicine) and at the University of Maryland. Currently Dr. Hoffmann is a Research Genomics Microbiologist at FDA/CFSAN. She uses next generation molecular genetic detection, identification, and traceback technologies to study and survey foodborne pathogens in produce.

Greg Paoli

Development of a Model of Public Health and Economic Benefits of GMI-related Technology and Information Sharing to Support Decision-making for Preventative and Rapid Response

Abstract:
The development and deployment of novel technologies and capabilities is often premised on qualitative characterizations of the benefits of the technology. While these qualitative characterizations can be compelling, there may be contexts in which a quantitative assessment of benefits associated with the technology are either necessary or provide more compelling evidence to relevant decision-makers (international agencies, governments, donors). Quantitative outcomes can include formal cost-benefit analysis (Societal Net Benefit), cost-effectiveness analysis (e.g., Disability-Adjusted Life Years Saved per Dollar Spent). The means to provide such quantitative estimates include the development of simulation models of a baseline scenario, implementation of model elements that cause a change in the baseline conditions to the benefit of public health, and the valuation of the benefits of the change in public health using standardized techniques of benefits valuation. The key model elements that are required include: a) the baseline conditions in the absence of the specific technologies being evaluated, b) the nature of the change (the presence/absence, the quality, or the timeliness of information need to trigger actions or decisions). A simulation model that predicts the benefits of enhanced laboratory and outbreak detection capacity applied to foodborne outbreaks is provided as an example of the types of models which could be expanded to include the variety of public health benefits that NGS technology may provide across different decision-support contexts.

Biography:
Greg Paoli is the Co-Founder and Principal Risk Scientist at Risk Sciences International, Inc. He has been a consultant specializing in risk assessment methodology in the field of public health and public safety for 23 years. He holds a Master of Applied Science Degree in Systems Design Engineering from the University of Waterloo. He specializes in probabilistic risk assessment methods, uncertainty analysis, the development of risk-based decision-support tools and comparative risk assessment. He has served on more than ten expert committees convened by the World Health Organization and the Food and Agriculture Organization. For over a decade, Greg has led the technical team responsible for the development of the FDA-iRISK on-line risk assessment tool (irisk.foodrisk.org) for food safety risk assessment for both microbial and chemical hazards. He has served as Councilor of the Society for Risk Analysis (SRA) and on the Editorial Board of Risk Analysis, and was awarded the Sigma Xi – SRA Distinguished Lecturer Award. Greg recently served on a U.S. National Academy of Sciences (NAS) Committee on the Design and Evaluation of Safer Chemical Substitutions. He previously served on the NAS Committee on Improving Risk Analysis Approaches Used by the US Environmental Protection Agency, which issued the 2009 report, Science and Decisions: Advancing Risk Assessment (NRC, 2009). Greg has recently been invited to join the Science Advisory Committee for the Chemicals Management Plan in Canada.

Eric Brown

An important and current role for WGS in augmenting the US FDA food safety effort

Abstract:
GenomeTrakr is an open source WGS database for foodborne and other bacterial pathogens where public health agencies collect and publically share WGS data in real time. This high-resolution, rapidly growing database is actively being used in outbreak investigations at the state, national, and international level. The GenomeTrakr network demonstrates how desktop WGS data can be used in concert with traditional epidemiology for source tracking of foodborne pathogens. Along with the paradigm shift in technology this new "open data" model allows greater transparency between federal/state agencies, our industry partners, academia, and international partners. Ten new labs were added to the network in 2016 in an effort to grow and diversify the foodborne pathogen database. Two new surveillance efforts were added to collect food and environmental isolates of Escherichia coli and Campylobacter. And multiple data analysis pipelines were tested on benchmark datasets in an effort to validate our analysis methods. NCBI is currently producing daily cluster results for ten pathogen surveillance efforts: Salmonella enterica, Listeria monocytogenes, E. coli, Campylobacter, Acinetobacter, Klebsiella, Serratia, Elizabethkingia, Providencia and Morganella, all of which are publically available. The high-resolution WGS data in concert with solid epidemiological evidence has drastically enhanced our ability to identify the food source of current outbreaks for Listeria monocytogenes, for which the CDC is also contributing clinical isolates in real time. These results demonstrate that WGS is a high-resolution subtyping tool and the global benefits of having an open data model cannot be overstated.

Biography:
Dr. Eric W. Brown has been with the Food and Drug Administration's Center for Food Safety and Applied Nutrition (CFSAN) since 1999 and currently serves as Director of the Division of Microbiology in the Office of Regulatory Science. Here, he oversees a group of 60 food safety microbiology researchers and support scientists engaged in a multi-parameter research program to develop and apply microbiological and molecular genetic strategies for detecting, identifying, and differentiating bacterial foodborne pathogens such as Salmonella, Listeria, and shiga-toxin producing E. coli. Recently, his laboratory has been instrumental in adapting next-generation sequencing technologies to augment foodborne outbreak investigations and to ensure preventive control and compliance standards at the FDA including the establishment of the GenomeTrakr whole-genome sequencing network for food safety. Dr. Brown received his M.Sc. in Microbiology from the National Cancer Institute/Hood College joint program in the biomedical sciences in 1993 and his Ph.D. in Microbial Genetics from The Department of Biological Sciences at The George Washington University in 1997. He has conducted research in microbial evolution and genetics as a research fellow at the National Institutes of Health, the U.S. Department of Agriculture, and as an Assistant Professor of Microbiology at Loyola University of Chicago. He has been a member of the American Society for Microbiology since 1994 and was recently inducted as a Fellow of the American Academy of Microbiology in 2015. He has co-authored more than 150 refereed publications and book chapters on the molecular differentiation, evolutionary genetics, and ecological persistence of bacterial pathogens.

Xu Jianguo

The Metataxonomics with full-length 16s rRNA sequencing as a new tool for etiological investigation

Abstract:
16S rRNA sequencing is the most widely used technique for microbial identification and diversity analysis. Metataxonomics is defined as the use of high-throughput 16s rRNA amplicon sequencing along with the phylogenetic analysis to characterize the entire microbiota of a given sample. The major problem with most of current studies is that they rely on the use of platforms like Illumina MiSeq or Roche 454 that generate only partial 16S rRNA gene sequences mostly from hypervariable regions of no more than 600 bp in length, and in general <400 bp. An accurate 16S rRNA gene analysis can only be done by using the almost full-length gene sequence.The PacBio platform offers the possibility to sequence the almost full-length 16S rRNA gene amplicons with some restrictions due to the error rate higher than the other platforms. However, contrarily to most research done with NGS that is based on clustering sequences at a given identity threshold in Operational Taxonomic Units (OTUs), we use the Operational Phylogenetic Unit (OPU) approach that is based on the phylogenetic inference after a treeing approach which, among other benefits, diminishes the influence of sequence errors and indels.

We integrated the high-throughput almost full-length 16s rRNA sequencing technology, with the operational phylogenetic units (OPU) assessment strategy, to characterize the entire microbiota of old world vultures. With this approach, we detected 314 OPUs (with a mean of 78 ±49.6 per vulture) that could be assigned to individual species. A total of 102 OPUs represented known species, 50 putative new yet un-described species belonging to known genera, and 161 uncultured new lineages. The results suggested that Clostridium perfringens and Peptostreptococcus russellii were the top two most abundant species present in all vultures tested. This finding was supported by isolation of Clostridium perfringens from all nine vultures. In addition, the analysis of the New World dataset confirmed that the American vultures also contained C. perfringens as a major microbial component. Finally, the PacBio + OPU tandem approach seems to be a very accurate system to reveal species composition of microbiomes.

The Metataxonomics with full-length 16s rRNA sequencing is a comprehensive and accurate approach to address etiological investigations or to be used as a diagnostic tool for infectious diseases caused by bacterial pathogens. Our results reveal that vultures are important animal reservoirs for C. perfringens, which may have established a mutualistic relation. Vultures may also be animal reservoirs for many other pathogens since 45 of 102 species identified belong to medical significant bacteria.

Biography:
Jianguo Xu is the director and Professor of State Key Laboratory for Infectious Diseases Prevention and Control, National Institute of Communicable Disease Control and Prevention, China CDC; Chairman, division of Capacity building, State Key Project for Aids, Infectious Hepatitis and other major infectious disease, National Health and Family Planning Commission China; Vice President, China Association of Microbiology; Member, steering committee, China Association of Medicine. Member of Chinese Academy of Engineering.

DR. Xu's team conducted the etiological investigations of outbreaks in China caused by Escherichia coli O157:H7 in 1999, by Streptococcus suis sequence type 7 2005, by Anaplasma phagocytophilum in 2006, by Neisseria meningitides sequence type 4821 complex in 2005. Recently, his team identified the emerging new serotype of Shigella flexneri Xv, the cytotoxic and aggregative Citrobacter freundiiin and Streptococcus lutetiensis as potential enteric pathogen.

He found that some outbreaks occurred in China in last ten years could be prevented by changing the social and personal behaviour. His current research field is new pathogen discovery and microbiome of wild life.

Jennifer Beal

WGS in US Foodborne Outbreak Detection and Response and the Rise of Retrospective Outbreak Investigations

Abstract:
Foodborne outbreak detection and response in the United States is a collaborative effort among local, state and federal public health and regulatory agencies. For the past 20 years in the United States, Pulsed-Field Gel Electrophoresis (PFGE) bacterial subtyping has been the cornerstone for detection of foodborne outbreaks due to major bacterial pathogens, including Listeria monocytogenes, shiga-toxin producing E. coli (STEC), and Salmonella enterica Serovars, among others. The U.S. is currently transitioning from PFGE-based surveillance and outbreak detection to a system based on Whole Genome Sequencing (WGS). The use of WGS as a subtyping method in foodborne outbreak detection and response allows for greater certainty in identifying clusters of human cases related to a common food source, and provides a higher level of confidence in laboratory linkages between isolates from clinical cases and food or environmental samples. The increased resolution that WGS provides for relationships between clinical and nonclinical isolates is also driving an alternative approach to identifying and solving outbreaks, in which bacterial isolates collected from food or environmental samples (from food manufacturing facilities) are linked "retrospectively" to clinical isolates (collected from patients). These WGS linkages can then be further evaluated using traditional epidemiologic investigative tools to confirm whether a specific food (or food from a specific firm) was the vehicle for those illnesses. Robust sampling of food and food production environments, combined with the high resolution of WGS, are facilitating the detection of more "retrospective" outbreaks than in previous years and driving responses to these nontraditional outbreaks.

Biography:
Jennifer Beal is the senior epidemiologist in the US Food and Drug Administration's Coordinated Outbreak Response and Evaluation (CORE) Network. FDA created the CORE Network in 2011 to manage FDA's activities for outbreak detection/surveillance, response and post-response prevention efforts related to incidents involving multiple illnesses linked to FDA-regulated human food and cosmetic products. In the past six years with CORE, Jennifer has worked on many high profile investigations, including outbreaks of Listeria monocytogenes in ice cream, caramel apples, cantaloupe, and cheese; Cyclospora in cilantro and bagged salad; Hepatitis A in frozen pomegranate arils, frozen strawberries, and scallops; multiple Salmonella enterica serovars in peanut butter, tuna sushi and various produce items; and shiga-toxin producing E. coli in leafy greens, sprouts, flour and soy butter. Prior to her work in CORE, Jennifer served as an epidemiologist in the FDA's Office of Regulatory Affairs (ORA) from 2008-2011, where she was responsible for providing emergency response and epidemiologic expertise on all foodborne outbreak investigations that FDA conducted during that time. Jennifer earned a Master's of Public Health in Epidemiology from the George Washington University School of Public Health in 2008 and a Bachelor of Arts in Biology from Colby College in 2004.

Robert Schlaberg

Metagenomics, from Research Tool to Routine Diagnostics

Abstract:
Current infectious disease molecular tests are largely pathogen-specific, requiring test selection based on the patient's symptoms. For many common syndromes caused by a large number of viral, bacterial, fungal, and parasitic pathogens this necessitates large panels of tests and has limited yield. In contrast, metagenomics can be used for detection of both expected and unexpected pathogens. While proof-of-concept has been extensively shown, implementation of metagenomics tests in routine diagnostic practice is challenging. We have performed extensive performance evaluation of a metagenomics test for use in a large reference laboratory setting. This presentation will provide an overview of remaining challenges, potential solutions, and lessons learned. The need for organized efforts to overcome limitations of reference databases, quality control programs, and standardization of protocols will be discussed.

Biography:
Robert Schlaberg, MD, Dr Med, MPH, is a medical director at ARUP Laboratories, an assistant professor of Pathology at the University of Utah, and a co-founder of IDbyDNA Inc. He completed his Clinical Pathology residency and Master of Public Health training at Columbia University, and a Medical Microbiology fellowship at ARUP Laboratories. His research is focused on next-generation sequencing-based infectious disease diagnostics and is supported in part by the Bill & Melinda Gates Foundation. He has co-developed Taxonomer, an ultrafast, user-friendly, web-based metagenomics data analysis tool, and a diagnostic version (TaxonomerDx) with the goal of facilitating adoption of metagenomic testing in routine diagnostic practice. He is board-certified in Clinical Pathology and Medical Microbiology by the American Board of Pathology. He is a member of the College of American Pathologists' Microbiology Resource Committee and Standard Committee.