Maha Farhat

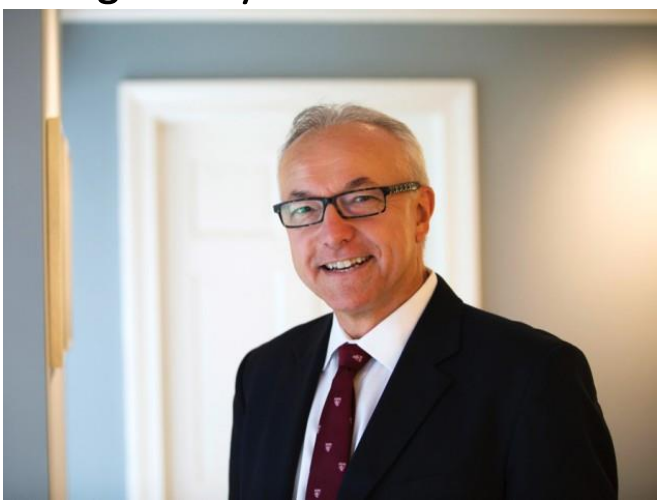
Maha Farhat holds an MD from the McGill University Faculty of Medicine and a MSc in biostatistics from the Harvard Chan School of Public Health. She is also a practicing physician at the Massachusetts General Hospital Division of Pulmonary and Critical Care Medicine.

Dr. Farhat's research focuses on the development and application of methods for associating genotype and phenotype in infectious disease pathogens, with a strong emphasis on translation to better diagnostics and surveillance in resource-poor settings. To date, Farhat's work has focused on the pathogen Mycobacterium tuberculosis and spans the spectrum from computational analysis to field studies. She is PI and Co-Investigator on several large projects funded by NIH including the NIAID and the BD2K initiative.

Michael Baym

Michael Baym received his PhD in Mathematics from MIT and was a postdoctoral fellow at Harvard Medical School in Systems Biology. Baym's research is centered around the problem of antibiotic resistance, at the intersection of experimental, theoretical and computational techniques. His work ranges from understanding the basic mechanisms of evolution to the development of algorithms for computation on massive biological datasets.

George Daley



George Q. Daley, MD, PhD, is Dean of Harvard Medical School, Caroline Shields Walker Professor of Medicine, and Professor of biological chemistry and molecular pharmacology at Harvard Medical School.

Daley's research focuses on stem cells, cancer and blood disorders. He received his bachelor's degree, *magna cum laude*, from Harvard (1982), a doctorate in biology from MIT (1989), where he worked with Nobel laureate David Baltimore, and his medical degree from Harvard Medical School (1991), *summa cum laude*.

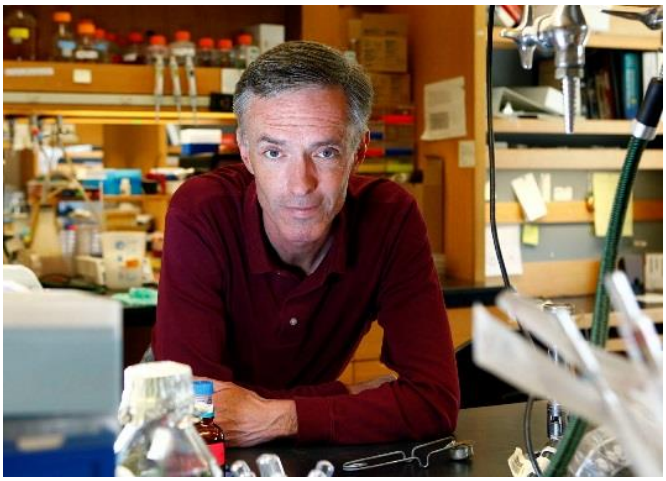
Daley pursued clinical training in internal medicine at Massachusetts General Hospital, where he served as chief resident (1994-1995), and a clinical fellowship in hematology/oncology at Brigham and Women's Hospital and Boston Children's Hospital.

He was a founding member of the executive committee of the Harvard Stem Cell Institute, and served as president of the International Society for Stem Cell Research from 2007 to 2008 and as its clerk from 2012 to 2015. He anchored the special task forces that produced the society's guidelines for stem cell research (2006) and clinical translation (2008) and their subsequent revisions and updates (2016).

Daley has been elected to the National Academy of Medicine, the American Society for Clinical Investigation, the American Association of Physicians, the American Pediatric Societies, the American Academy of Arts and Sciences and the American Association for the Advancement of Science.

Daley was an inaugural winner of the National Institutes of Health Director's Pioneer Award for highly innovative research and has received the Judson Daland Prize from the American Philosophical Society for achievement in patient-oriented research, the E. Mead Johnson Award from the American Pediatric Society for contributions to stem cell research, and the E. Donnall Thomas Prize of the American Society of Hematology for advances in human induced pluripotent stem cells.

Jim Collins



James J. Collins is the Termeer Professor of Medical Engineering & Science and Professor of Biological Engineering at MIT, as well as a member of the Harvard-MIT Health Sciences & Technology Faculty. He is also a Core Founding Faculty member of the Wyss Institute for Biologically Inspired Engineering at Harvard University, and an Institute Member of the Broad Institute of MIT and Harvard. He is one of the founders of the field of synthetic biology, and his research group is currently focused on engineering cells to serve as living diagnostics and living therapeutics.

Professor Collins' patented technologies have been licensed by over 25 biotech, pharma and medical devices companies, and he has helped to launch a number of companies, including Synlogic (NASDAQ: SYBX), EnBiotix, Sample6 Technologies, and Senti Biosciences. He has received numerous award and honors, including a Rhodes Scholarship, a MacArthur "Genius" Award, an NIH Director's Pioneer Award, the Sanofi-Institut Pasteur Award, as well as several teaching awards.

Professor Collins is an elected member of all three national academies – the National Academy of Sciences, the National Academy of Engineering, and the National Academy of Medicine – as well as the American Academy of Arts & Sciences, the National Academy of Inventors, and the World Academy of Sciences.

Synthetic biology-based diagnostics for infectious diseases

Synthetic biology is bringing together engineers, physicists and biologists to model, design and construct biological circuits out of proteins, genes and other bits of DNA, and to use these circuits to rewire and reprogram organisms, as well as create paper-based diagnostics and other tools. In this talk, we highlight recent efforts to create synthetic gene networks and programmable cells, and discuss how these technologies are being used to develop next-generation diagnostics for infectious diseases.

Romney Humphries

Romney Humphries, PhD D(ABMM) received her PhD in bacterial pathogenesis from the University of Calgary, Calgary Alberta Canada. She completed a clinical and public health microbiology CPEP fellowship at UCLA, and served as the Section Chief of Clinical Microbiology for UCLA for 6 years. She is currently the Chief Scientific Officer at Accelerate Diagnostics.

Dr. Humphries serves as a member of the Clinical and Laboratory Standards Institute (CLSI) Antibiotic Susceptibility Testing (AST) Subcommittee, and chairs several working groups for the CLSI. She is a member of the College of American Pathologists (CAP) Microbiology Resource Committee, a member of the American Society for Microbiology (ASM)/ Association for Public Health Laboratories (APHL) Antibiotic Resistance Laboratory Working Group, the chair of the Clinical and Public Health Microbiology track for the ASM Microbe Meeting, and a member of the professional practices group of the ASM. She has served as a consultant for several diagnostic companies on the development of antimicrobial susceptibility test systems.

Using better data to perform more sophisticated determinations of antibiotic susceptibility and resistance

At the frontlines of detecting antibiotic resistance are clinical laboratories. However, the tools available to laboratories to detect resistance are varied and based on principles developed over 50 years ago. This talk will explore up-and-coming methodologies for the rapid and accurate detection of antibiotic resistance (and susceptibility), and discuss advantages and pitfalls of different approaches. After this talk you will be able to describe the current landscape of antibiotic susceptibility in the United States, discuss strategies to improve timeliness and accuracy of susceptibility testing, and compare genotypic and phenotypic approaches to susceptibility testing.

Bill Hanage

Bill Hanage is Associate Professor of Epidemiology in the Center for Communicable Disease Dynamics at Harvard T.H. Chan School of Public Health. He was a Royal Society University Research Fellow and Reader at Imperial before moving to the Chan School. His honors include the Fleming prize from the Microbiology Society, and a young investigator award from the American Society for Microbiology. His research combines theoretical and empirical methods, with a recent focus on genomics, and has produced important discoveries about the epidemiology and evolution of many pathogens. But he is especially interested in the pneumococcus.

High risk resistant clones, and how to find them

There is great interest in using sequence data to detect the presence of antibiotic resistance pathogens, by detecting the genes conferring resistance using modern methods for rapid sequencing. Identifying the species present in a metagenomic sample by matching to a database of known genome sequences, is well established, but a similar approach to identifying the specific resistance lineages or clones within a sample has not been attempted. We have developed an approach that constructs a lossless k-mer index from a database of known genomes, together with resistance metadata (the Resistance Associated Sequence Element or RASE database). This can be used in combination with an Oxford Nanopore device, to match the sequence of the emerging read to the RASE database, and rapidly identify which lineage is present, within 5 minutes, even with a metagenomic sample. This approach may be helpful in the surveillance of resistance, and the very rapid lineage calling approach may have application in diagnostics.

John Brownstein

John Brownstein, PhD is Professor of Biomedical Informatics at Harvard Medical School and is the Chief Innovation Officer at Boston Children's Hospital. He also directs the Computational Epidemiology Lab and the Innovation and Digital Health Accelerator both at Boston Children's. He was trained as an epidemiologist at Yale University.

Overall, his work aims to have translation impact on the surveillance, control and prevention of disease. He has been at the forefront of the development and application of data mining and citizen science to public health. His efforts are in use by millions each year including the CDC, WHO, DHS, DOD, HHS, and EU, and has been recognized by the National Library of Congress and the Smithsonian. In addition to research achievements, this translational impact comes from playing an advisory role to numerous agencies on real-time public health surveillance including HHS, DHS, CDC, IOM, WHO and the White House.

He was awarded the Presidential Early Career Award for Scientists and Engineers, the highest honor bestowed by the United States government to outstanding scientists and the Lagrange Prize for international achievements in complexity sciences. Dr. Brownstein is also Uber's healthcare advisor and co-founder of digital health companies Epidemico and Circulation. He has authored over 200 peer-reviewed articles on epidemiology and public health. This work has been reported on widely including pieces in the New England Journal of Medicine, Science, Nature, New York Times, The Wall Street Journal, CNN, National Public Radio, and BBC.

Open data and the future of antibiotic resistance surveillance

Over the past twenty years, Internet technology has significantly changed the landscape of public health surveillance and epidemic intelligence gathering. Disease and outbreak data is disseminated not only through formal online announcements by government agencies, but also through informal channels such as social networking sites, blogs, chat rooms, Web searches, local news media and crowdsourcing platforms. These data streams have been credited with decreasing the time between an outbreak and formal recognition of an outbreak, allowing for an expedited response to the public health threat. Collectively, these online sources create an image of global public health that is fundamentally different from the one produced by traditional public health surveillance infrastructure. Dr. Brownstein will discuss the current capabilities and future directions in the use of the non-traditional data sources for the purposes of public health surveillance and rapid detection of infectious diseases, with a specific focus on antibiotic resistance.

Céire Costelloe

Céire is a Lecturer at the NIHR funded Health Protection Research (HPRI) in Healthcare associated infection and antimicrobial resistance, at Imperial College London. The HPRU is a partnership between Imperial College London, Public Health England, Cambridge University Veterinary School, the Wellcome Trust Sanger Institiute and Imperial College Health Partners North West London Academic Health Science Network. The Unit was funded to bring Universities to work in partnership with Public Health England to support excellent health protection research relevant to the healthcare needs of the UK population.

Dr. Costelloe has a background in Immunology and Medical Statistics which she has applied to the investigation of the risk factors associated with antimicrobial resistant infection and to developing and evaluating interventions to target antimicrobial resistance.

Céire has a track record in producing research which leads to direct policy changes and her work is highly cited, contributing towards both UK and European antibiotic stewardship guidelines. Building on previous NIHR funded research, Dr. Costelloe has recently been awarded a prestigious NIHR Career Development Fellowship. This will allow expansion of her research team and will focus on developing a framework for evaluating intervention targeting antimicrobial resistance using routinely collected clinical data and novel statistical causal inference methods. The research addresses repeated calls from the Department of Public Health, to utilize routinely collected data to evaluate clinical and public health interventions for the UK NHS and will demonstrate the benefits of using these data to shape future healthcare policy and practice.

Using electronic Healthcare record data to inform and evaluate interventions targeting healthcare associated infection across the healthcare economy

Healthcare associated infections (HCAIs) are considered to be the most frequent adverse event that threatens patients' safety, costing the UK National Health Service (NHS) approximately £1 billion per year. During hospitalization, patients visit many procedural and diagnostic common areas, presenting opportunities for infection transmission. However, these potential exposures are not typically captured in analyses evaluating disease transmission. Routinely available electronic health record (EHR) data allow us to track patients in time and space, but to date these data have not been applied to infection control or quality improvement efforts. My talk will focus on how these data are being used to inform intervention development and targeting of infection control measures within Imperial College Healthcare Trust using data visualization and predictive analytics.

In addition, I will describe the comparative effectiveness research methods currently being developed by my group to make use of these HER, alongside routine clinical data to evaluate interventions across the healthcare economy. We are currently developing a framework for evaluating interventions targeting Antimicrobial resistance (AMR), focusing on interventions recently introduced to reduce antibiotic prescribing in primary care in the UK. With the growing availability of quantitative observational data derived from non-randomized sources, it is important to recognize the potential of this data for clinical decision-making and policy development for public health issues such as AMR.

Gerry Wright

Gerry Wright is the Director of the Michael G. DeGroote Institute for Infectious Disease Research (since 2007). He is a Professor in the Department of Biochemistry and Biomedical Sciences, an Associate member in the Departments of Chemistry and Chemical Biology and of Pathology and Molecular Medicine.

Dr. Gerry Wright received his BSc in Biochemistry (1986) and his PhD in Chemistry (1990) from the University of Waterloo. He holds the Michael G. DeGroote Chair in Infection and Anti-Infective Research and a Tier 1 Canada Research Chair in Antibiotic Biochemistry. From 2001-2007 Gerry served as Chair of the Department of Biochemistry and Biomedical Sciences at McMaster.

Gerry was elected as a Fellow of the Royal Society of Canada (2012) and a fellow of the American Academy of Microbiology (2013). He is the recipient of the Canadian Institutes of Health Research Scientist (2000-2005), Medical Research Council of Canada Scholar (1995-2000), Killam Research Fellowship (2011-2012), R.G.E Murray Award for Career Achievement of the Canadian Society of Microbiologists (2013), NRC Research Press Senior Investigator Award from the Canadian Society for Molecular Biosciences (2016), Premier's Research Excellence (1999) and the Polanyi Prize (1993). In 2016 he was named a McMaster Distinguished University Professor, the highest academic honor at the university.

Gerry has served on grant panel advisory boards and Chaired grant panels for a number of funding agencies in Canada, the US, and Europe and consults widely for the pharmaceutical and biotech sectors.

He is the author of over 250 manuscripts and is a member of the editorial boards of several peer-reviewed journals including *mBio*, *Antimicrobial Agents Chemotherapy*, *Cell Chemistry and Biology* and the *Journal of Antibiotics.* He is an Associated Editor of *ACS Infectious Diseases* and Editor of *Annals of the New York Academy of Sciences, Antimicrobial Therapeutics Reviews*. He has filed a number of patents and is the co-founder of Symbal Therapeutics. In 2016 he was named McMcaster University's Innovator of the Year.

Mining the antibiotic resistome for new drug discovery opportunities

The antibiotic resistome is the collection of resistance genes in both pathogens and benign bacteria. It is now well established that the latter are the prime source of new resistance elements that emerge, usually through lateral gene transfer, in pathogens. The vast genomic and mechanistic diversity of the resistome reflects its ancient origins and broad distribution in bacteria across the globe. Exploring this diversity offers several useful tools in antibiotic discovery. These include insight into the potential resistance liabilities of new antibacterial agents under investigation, the development of molecular diagnostics to identify sources of resistance elements, and as targets for antibiotic adjuvants. Examples of how the resistome can inform on these aspects of drug discovery will be presented.

Deborah Hung

Dr. Deborah Hung is an associate professor in the Department of Molecular Biology at Massachusetts General Hospital and in the Department of Genetics at Harvard Medical School, and the director of the Infectious Disease Program and Microbiome at the Broad Institute of MIT and Harvard. She also holds positions as an infectious disease physician at Brigham and Women's Hospital. She has been awarded the American Society for Microbiology Merck Irving S. Sigal Memorial Award, a Pew Scholars Award in the Biomedical Sciences, Kavli fellowship from the National Academy of Sciences, and a Doris Duke Foundation Clinical Scientist Development Award. She has served on the Scientific Advisory boards of the New England Center for Excellence in Biodefence, of the Pew Foundation Initiative in Antibiotic Resistance, and contributed to the President's Council of Advisors on Science and Technology report on Combatting Antibiotic Resistance. She has chaired the Boston Area Antibiotic Resistance Network Symposium and a Keystone meeting on the Challenges of Antibiotic Resistance.

She received her AB from Harvard University, PhD from Harvard University, and MD from Harvard Medical School. She completed a residency in internal medicine and fellowships in infectious disease and critical care medicine at Brigham and Women's Hospital and Massachusetts General Hospital.

Innovations in high throughput technologies for new antibiotic development

With multi-drug resistant tuberculosis (MDR-TB) prevalence on the rise, new drugs and regimens are needed against Mycobacterium tuberculosis (Mtb). Despite recent efforts, the number of promising new compounds is still limited. Using a systems chemical biology strategy we have coupled large-scale mutagenesis of essential bacterial targets with chemical screening to identify new small molecule candidates with rapid prediction of their mechanisms of action (MOA), thereby demonstrating a strategy to rapidly increase the numbers of candidates with development potential against Mtb.

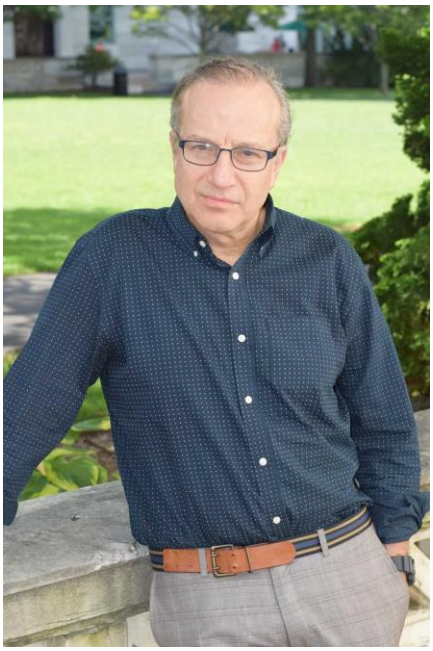
Alita Miller

Alita Miller is a Senior Director and Head of Bioscience at Entasis Therapeutics, a small biotech focused on the discovery and development of novel antibiotics to treat serious Gram-negative infections. Alita holds a BA in Chemistry from Kalamazoo College and a PhD in Biochemistry & Molecular Biology from the University of Chicago. Her postdoctoral work was on bacterial pathogenesis at the University of Michigan with Vic DiRita. Alita spent over a decade in the Pfizer Antibacterials Unit where she worked on both large and small molecule anti-infective projects. Alita joined AstraZeneca in 2013 as an Associate Director of Infection and was a founding member of Entasis when it was spun out of AstraZeneca Infection in May of 2015. Alita serves on several scientific advisory and editorial boards and is a permanent member of the NIH grant review panel for Drug Discovery and Resistance. Her current research interests include understanding the molecular drivers of bacterial antibiotic uptake.

Omics Approaches for Antibacterial Discovery

Antibiotic resistance is a serious public health crisis. As resistance to antibiotics grows, it becomes increasingly difficult to effectively manage a wide range of infections, which often results in poor outcomes for patients and escalating healthcare costs. Our vision at Entasis is to improve patients' health and outcomes by creating innovative, life-saving medicines to treat serious infectious diseases caused by drug-resistant Gram-negative bacteria, including *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacteriaceae*, and *Neisseria gonorrhoeae*. Our discovery efforts include TNseq and RNAseq platforms that are routinely used for target characterization, mechanism of action, uptake and resistance studies. Several examples of these types of studies at Entasis plus their implications for future directions will be presented.

Isaac Kohane



Isaac (Zak) S. Kohane, MD, PhD, is the inaugural Chair of the Department of Biomedical Informatics and the Marion V. Nelson Professor of Biomedical Informatics at Harvard Medical School. He served as co-author of the Institute of Medicine Report on Precision Medicine that has been the template for national efforts. He develops and applies computational techniques to address disease at multiple scales: from the whole healthcare systems as “living laboratories” to the functional genomics of neurodevelopment with a focus on autism.

Over the last 30 years, Zak’s research agenda has been driven by the vision of what biomedical researchers could do to find new cures, provide new diagnoses and deliver the best care available if data could be converted more rapidly to knowledge and knowledge to practice. In doing so, Kohane has designed and led multiple internationally adopted efforts to “instrument” the healthcare enterprise for discovery and to enable innovative decision-making tools to be applied to the point