Disease Outbreak Detection in the Genomics Era: Global Road Map Meeting #3

Conveners: US Food & Drug Administration/Danish Technical University/National Center for Biotechnology Information

When: September 24th and 25th, 2012 from 8:00 AM to 6:00 PM daily

Where: NIH campus Lister Hill Center in Bethesda, MD

Purpose: To determine a path forward for how to establish a globally distributed system and follow up on the three previous meetings: 1) Brussels, Belgium 2011, 2) NIH, Bethesda, MD, USA, 2011, and 3) Arlington, VA, USA, 2012.

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: (i) implementing metadata requirements for clinical and outbreak isolates; (ii) computer resources/tools required for a global genome-based disease detection network; (iii) standards for bacterial identification and clustering; (iv) policy challenges (political, legal, and global health diplomacy) to sharing data on a global scale; (v) lessons learned regarding clinical utility and rapid detection; (vii) strategic sequencing targets and proof-of-concept case studies; and (vii) industry contributions toward a global genomic network. Detailed instructions for breakout discussions will be provided prior to the meeting.

Expected outcome: A series of draft road map statements focused on establishing a global disease outbreak detection system using a worldwide network of shared genomic information for bacterial, viral, and parasitic microorganisms AND a commitment from various institutions for working together on developing such a database.

Agenda:

Day #1 (September 24th, 2012)

Overview, Updates, Initiatives

8:00 AM Welcome/Overview M. Allard (FDA)/E. Brown (FDA)

8:20 AM Leadership panel comments S. Musser (FDA); D. Lipman (NCBI); J. Lindsy (USDA); A. Wotherspoon (UK FSA); S. Magnino (WHO); J. Schlundt (DFI)

Health Policy Needs (F. Aarestrup/E. Brown)

8:45 AM DFI update F. Aarestrup (DTU)

9:00 AM CDC update J. Besser (CDC)

9:15 AM 100K Pathogen Genome Project: A consortium and beyond B. Weimer (Agilent/UC-Davis)

9:25 AM Genome-in-a-Bottle Consortium: Reference Materials for Clinical Applications of Human Genome Sequencing M. Salit (NIST)

9:40 AM NGS Platform comparisons M. Pallen (University of Birmingham)

9:55 AM QUESTIONS

10:05 AM BREAK

10:15 AM Focused Break-Out Session 1 Side Rooms

11:55 AM LUNCH BREAK Sponsored by Illumina

Lessons learned from recent (updates) (D. Harmsen / H. den Bakker)

1:00 PM Strategies for successful integration of sequence data sets from multiple NGS platforms; an example from the *Salmonella* Montevideo -outbreak H. den Bakker (Cornell University)

1:15 PM Current experience with Whole Genome Cluster Analysis for *Salmonella* outbreak investigations in a State Health Department Laboratory W. Wolfgang (NY State Dept. Health)

1:30 PM DOD NGS pipeline S. Gibbons/N. Rosenzweig (DOD)

1:45 PM Automated assembly and annotation of ungapped bacterial chromosomes without manual finishing G. Harhay (ARS)

2:00 PM QUESTIONS

An IT Path Forward: Data Pipelines and Public Data Networking (W. Klimke/E. Strain)

2:15 PM NGS Metadata report W. Klimke (NCBI)

2:30 PM Update on NCBI pipeline R. Agarwala/M. Shumway (NCBI)

2:45 PM Datasharing for public health action: rules of the game? M. Koopmans (RIVM)

3:00 PM National Biodefense Analysis and Countermeasures Center A. Phillippy (DHS)

3:15 PM QUESTIONS

3:25 PM BREAK

3:35 PM Focused Break-Out Session 2 Side Rooms

6:00 PM ADJOURN DAY #1

Day #2 (September 25th, 2012)

Clinical Perspectives on NGS-based Pathogen Identification System (L. Bry/K. Frank)

8:00 AM Director, Center for Clinical and Translational Metagenomics L. Bry/G. Gerber (Harvard)

8:15 AM Use of Genomic Testing at the NIH Clinical Center K. Frank (NIH)

8:30 AM Using large-scale phenotype databases to detect and track new and emerging microbial strains J. Stelling (Harvard)

8:45 AM Rapid NGS for clinical and public health microbiology - challenges and opportunities D. Harmsen (Universit of Münster)

9:00 AM	QUESTIONS	
9:10 AM	Focused Break-Out Session 3	Side Rooms
11:10 AM	BREAK	
11:20 AM	(Generate report from focused groups)	MAIN HALL/Side Rooms
12:00 PM	LUNCH BREAK	Sponsored by Ion Torrent-Life Technologies
1:00 PM	(Generate report from focused group) (continue)	MAIN HALL/Side Rooms
1:30 PM	Plenary Session - Report from focus groups	MAIN HALL
2:30 PM	BREAK	
Industry solutions for global network		(M. Allard/C. Elkins)
2:40 PM	Hybrid assembly and methylation	J. Korlach (Pacific Biosciences)
2:50 PM	MiSeq overview	G. Smith (Illumina)
3:00 PM	DNA Sequencing on a Semi-conductor Chip: Applications in Infectious Diseases	M. Furtado (Ion Torrent)
3:10 PM	OpGen solution	R. Moore (OpGen)
3:20 PM	Biomatters solution	L. Brennan (Biomatters)
3:30 PM	Facilitating management and incorporating analysis of next generation genomic data combined with data derived from established subtyping methods	B. Pot (Bionumerics)
3:40 PM	Leveraging CLC bio software for fast, automated pathogen identification across the globe	C. Boysen (CLC Bio)
3:50 PM	Sequencing Solutions: 454 and Sequence Capture Applications	C. Matthews (Roche)
4:00 PM	QUESTIONS	
4:30 PM	Meeting Summary	
5:00 PM	MEETING ADJOURNED	