Clinical bioinformatics for microbial genomics and metagenomics

Lausanne, Switzerland
9 – 12 September 2019

Target Audience
Clinical microbiologists and other professionals working in the field with little or no programming background.

Faculty Members
Claire Bertelli, Lausanne, Switzerland
João Carriço, Lisboa, Portugal
Eric Claas, Leiden, Netherlands
David Dylus, Lausanne, Switzerland
Adrian Egli, Basel, Switzerland
Gilbert Greub, Lausanne, Switzerland
Hassan Hartman, London, United Kingdom
Aitana Lebrand, Geneva, Switzerland
Jacob Moran-Gilad, Beit Kama, Israel
John W. A. Rossen, Groningen, Netherlands
Etienne Ruppé, Paris, France
Helena Seth-Smith, Basel, Switzerland
Daniel Wüthrich, Basel, Switzerland

Course Objective
Next generation sequencing (NGS) is being increasingly used and implemented at clinical microbiology laboratories, heavily relying on bioinformatics for data processing, analysis and interpretation. This course aims at providing participants with the essential tools to understand the output of bioinformatics analysis pipelines, interpret the results for making better-informed clinical recommendations, recognise the main challenges and limitations when using NGS bioinformatics analysis pipelines in clinical settings, and acquire a common language to foster multidisciplinary discussions of results with clinical bioinformaticians in their team. It will cover the essential bioinformatics concepts on NGS data management and processing for typing and phylogenetics, resistance and virulence prediction, and metagenomics-based taxonomic classification.
Course Programme

Monday, 9 September 2019
08:00–09:00 Registrations

Session 1: NGS Clinical applications
09:00–09:15 Welcome & Introduction to the course
Gilbert Greub, Patricia Palagi, Aitana Lebrand
09:15–09:45 [From the clinic] The changing profession of the clinical microbiologist
Jacob Moran-Gilad
09:45–10:15 [From the clinic] Clinical genomics and metagenomics: when to go for one or the other and what to expect
John Rossen
10:15–11:00 Coffee break

Session 2: NGS technologies and data pre-processing
11:00–11:45 2nd and 3rd generation NGS technologies and their limitations
Eric Claas
11:45–12:30 Bioinformatics pipeline overview for genomics and metagenomics
Aitana Lebrand
12:30–14:00 Lunch break
14:00–16:00 Hands-on: Pre-processing of course datasets
16:30–22:00 Social event and dinner

Tuesday, 10 September 2019
Session 3: Alignment and assembly
08:45–09:30 Alignment and blast: basic principles and limitations to keep in mind for downstream analyses
David Dylus
09:30–10:15 Genome assembly (mapping-based and de novo): basic principles and quality control
Hassan Hartman
10:15–11:00 Coffee break
11:00–12:30 Hands-on: Genome assembly (incl. public repositories for reference genomes)
12:30–14:00 Lunch break

Session 4: Typing and phylogenetics
14:00–14:45 Typing the beast: gene-by-gene, (cg/ wg)MLST & SNP calling
Helena Seth-Smith
14:45–15:30 How to read and build a tree (incl. ML and bootstrap)
Daniel Wüthrich
15:30–16:00 Coffee break
16:00–17:30 Hands-on: SNP calling and phylogenetics
17:30–18:15 Student presentations, debriefing and quiz

Wednesday, 11 September 2019
Session 5: Resistance and virulence
08:45–09:45 Predicting resistance and virulence: overview of methodologies
Claire Bertelli
09:45–10:15 [From the clinic] NGS resistance and virulence predictions: potential and challenges compared to other lab techniques
Gilbert Greub
10:15–11:00 Coffee break
11:00–12:30 Hands-on prediction of resistance (incl. genome browsing)
12:30–14:00 Lunch break

Session 6: Metagenomics taxonomic classification
14:00–15:00 Overview of metagenomics methods (amplicon vs. shotgun, mapping vs. k-mer-based)
Aitana Lebrand
15:00–15:30 [From the clinic] Metagenomics for pathogen discovery
Etienne Ruppé
15:30–16:00 Coffee break
16:00–17:30 Hands-on: Pathogen metagenomics
17:30–18:15 Students presentation, debriefing

Thursday, 12 September 2019
Session 7: Bioinformatics capacity building
08:45–09:15 Data management: standards, storage, computing
Job Coens
09:15–09:45 [From the clinic] On the importance of standardized data for spatio-temporal molecular surveillance platforms
Adnan Eglı
09:45–10:15 Setting-up bioinformatics ring trials for NGS bacterial typing and viral metagenomics: towards harmonized best practices
Aitana Lebrand
10:15–11:00 Coffee break
11:00–11:30 Developing a streamlined tool for routine NGS analyses, from sample to report speaker to be confirmed
11:30–12:15 [Group discussion] NGS reports: what I need out of the bioinformatics pipeline as a clinical microbiologist in order to critically/confidently interpret the data
Panel of speakers
12:15–12:30 Concluding remarks
Gilbert Greub, Patricia Palagi, Aitana Lebrand
12:30–13:15 Students presentation, debriefing

Organisation

Course Venue
University of Lausanne, Dominy Campus

Registration Procedure
The registration portal can be found on the ESCMID website at www.escmid.org/education. Please complete the course registration by the deadline of 30 July 2019.

Registration Fee
EUR 600 for ESCMID members
EUR 750 for all others

The fee includes the course, tea and coffee during the course, lunch during the 4 days, a dinner on Monday evening and the social event. Travel and accommodation are not included.

Attendance Grants
ESCMID provides a number of attendance grants for ESCMID «young scientist members». The grant covers the registration fee, but not travel or accommodation costs. Please apply via the ESCMID website at www.escmid.org/education before 30 April 2019. Applicants will be informed about their acceptance by 15 May 2019.

CME Accreditation
The organiser of the course will apply for European CME accreditation through EACCME and for the FAMH accreditation through the Swiss Society of Microbiology accreditation.