Next-generation sequencing in routine clinical microbiology and infectious diseases

Lørenskog, Norway
7 - 10 December 2020

Target Audience
Technicians, [molecular] biologists, medical [molecular] microbiologists, infectious diseases specialists, public health specialists and bioinformaticians who would like an introduction and an update on how to use next-generation sequencing in routine diagnostics of infectious diseases.

Faculty Members
Hege Vangstein Aamot, Lørenskog, Norway
Ola Bøghildud, Oslo, Norway
Patricia Campbell, Lørenskog, Norway
João André Caricó, Lisbon, Portugal
Natacha Couto, Groningen, Netherlands
Adrian Egli, Basel, Switzerland
Nicole Fischer, Hamburg, Germany
Stefan Green, Chicago, IL, United States
Gilbert Greub, Lausanne, Switzerland
André Ingebretsen, Oslo, Norway
Mirjam Kooistra-Smid, Groningen, Netherlands
Sonja Lagström, Lørenskog, Norway
Attila Lebrand, Geneva, Switzerland
Jacob Moran-Gilad, Beer Sheva, Israel
Paula Mölling, Örebro, Sweden
Justin O’Grady, London, UK
Helena Seth-Smith, Basel, Switzerland
Silke Peter, Tuebingen, Germany
John W.A. Rossen, Groningen, Netherlands
Henrik Westh, Hvidovre, Denmark

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Course Objectives
With a multitude of benefits, Next-Generation Sequencing (NGS) technology is revolutionizing microbiological diagnostics and NGS is on the way on becoming the new gold standard. The workshop will highlight opportunities and challenges with this technology and present how it can be used in clinical diagnostic settings. As bioinformatics is a known challenge for most non-bioinformaticians, a practical e-lab will be included where we focus on data processing, analysis and interpretation of data.
Monday, December 7, 2020
08:00 Registration
09:00 Welcome to Norway
09:10 Welcome to the course
John W.A.Rossen
Session 1: Introduction to NGS
Chairs: John W.A. Rossen, Hege Vangstein Aamot
09:15 NGS: the basics
Stefan Green
10:15 Sequencing technologies and platforms
Ailara Leibrand
11:15 Coffee break
11:45 Sample preparation and sequencing
Stefan Green
12:30 Bioinformatics for non-bioinformaticians
Ola Brynhildsrud
13:15 Lunch
14:15 QC of the bioinformatic pipelines
Jacob Moran-Gilad
15:00 Analyses and visualisation of metagenomic data
André Ingebretsen
15:45 Coffee break
16:15 Added value of long read sequencing
Justin O’Grady
17:15 Welcome reception (drinks and bites)
Tuesday, December 8, 2020
Session 2: Clinical applications – Part 1
Chairs: Stefan Green and Natacha Couto
NGS from a clinical view
08:30 Challenges with current microbiological diagnostics and opportunities with NGS to provide some insight on patients prognosis by looking at the virulome
Gilbert Breuk
09:30 Translating NGS to the clinic: challenges and opportunities
Henrik Westh
10:30 Coffee break
Amplicon sequencing
11:00 Amplicon sequencing of human papillomavirus – possible markers for cervical cancer
Sanja Logstrøm
11:45 Added clinical value of 16S–23S amplicon-based sequencing in a clinical setting
Mirjam Kooistra-Smid
12:30 Lunch
13:30 The use of WGS in a hospital setting
André Ingebretsen
14:15 The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria
Silke Peter
15:00 Coffee break
15:30 NGS for outbreak detection – there is more than the core genome!
Helena Seth-Smith
16:00 Social event and dinner
Wednesday, December 9, 2020
Session 3: Clinical applications – Part 2
Chairs: Patricia Campbell, Henrik Westh
Metagenomic sequencing
09:00 Shotgun metagenomic sequencing of infected tissue
Hege Vangstein Aamot
09:45 When dealing with difficult to culture microbes – identification of Neisseria gonorrhoeae in throat samples
Patricia Campbell
10:30 Coffee Break
11:00 Application of metagenomics for bacteremia
Paula Mölling
11:45 Metagenomics for typing
Natacha Couto
12:30 Lunch
13:30 The pros and cons of metagenomic sequencing for infectious disease diagnosis – is the juice worth a squeeze?
Nicol Fischer
14:15 Machine learning in microbiology diagnostics
Adrian Egli
15:00 Coffee Break
15:30 Integrative and machine learning metagenomic approaches
John W.A. Rossen
16:15 Farewell to participants not attending the practicals
Thursday, December 10, 2020
Session 3: Bioinformatics – e-lab
Trainers: Natacha Couto, Hege Vangstein Aamot, John W.A. Rossen, Sanja Logstrøm, Helena Seth-Smith
08:30 Practicals on
– 16:00
• Quality control
• Assembly and annotation
• Pipelines
• Visualization tools
• Virulence and resistance markers
Course Venue
Akershus University Hospital
Sykehusveien 25
1478 Lørenskog, Norway
Registration Procedure
Register on the ESCMID website at www.escmid.org/education. Registration closes on 25 October 2020
Registration Fee
EUR 400 for ESCMID members
EUR 500 for all others
The fee includes the course, coffee, lunches, welcome reception and the social dinner. Travel and accommodation are not included. Attendees participating in the bioinformatics practicals will be charged an extra fee of 100 EUR (members) or 150 EUR (non-members).
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 registration website by 1 March 2020. Applicants will be informed about their acceptance by 15 March 2020.
CME Accreditation
The organiser of the course will apply for European CME accreditation through EACCME.
Recommended Accommodation
Thon Hotel Arena
Nesgata 1, 2004 Lillestrøm, Norway
https://www.thonhotels.com/event/escmid-workshop/
Phone: +47 66 93 6000
E-Mail: arena@olavthon.no
Registration closes on 25 October 2020