



## Capacity-building Workshop

# Whole Genome Sequencing for clinical microbiology and infection prevention

October 12<sup>th</sup> – 14<sup>th</sup>, 2016, UMCG Groningen

### Organisers

- ESCMID Study Group for Genomic and Molecular Diagnostics
- ESCMID Study Group for Epidemiological Markers
- Department of Medical Microbiology and Infection Prevention (UMCG)

### Supporters

- University Medical Center Groningen (UMCG)
- University of Groningen
- SeqNet.org
- EurHealth-1Health

### Sponsors

- Illumina, Inc.

### Course Coordinators

- Alexander Friedrich, Groningen, The Netherlands
- Ruud Deurenberg, Groningen, The Netherlands
- John Rossen, Groningen, The Netherlands
- Dag Harmsen, Münster, Germany

**Course Objectives**

- Provide microbiologists engaged in reference diagnostic services with basic knowledge about the generation and analysis of whole genome data sets.
- Engender discussions about the opportunities and challenges posed by novel whole genome sequencing technology.
- Providing a forum for data exchange and mining of large scale databases

**Target Audience**

- Experts engaged in the identification and epidemiological typing of bacteria with respect to clinical and veterinary microbiology and/or infection prevention.

**Course Venue**

Department of Medical Microbiology  
University Medical Center Groningen  
Hanzeplein 1  
9713 GZ Groningen  
The Netherlands

**Registration Fee**

EUR 500 for ESCMID members  
(Full Membership /Young Scientist Membership)  
EUR 600 for all others  
The fee includes coffee, lunches and the social dinner.  
Travel costs and accommodation are not included.

**Contact Person (Scientific Programme)**

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**Administrative Secretariat**

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## Preliminary Course Programme

Wednesday, 12<sup>th</sup> October 2016

Meeting room: Traversezaal/ Laboratory room: 3214.0214

*Practical day – Wet laboratory*

**Time**                      **Subject**

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8.30                              Registration and coffee

9.00 – 9.05                      Opening of the course, welcome (*John Rossen*)

9.05 – 9.35                      Next generation epidemiology in modern infection prevention and control  
(*Alex Friedrich*)

9.35 – 10.05                      Theoretical aspects of library preparation (*Erwin Raangs*)

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10.05 - 10.30                      *Coffee Break (in de Hal bij de Keuningzaal)*

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10.30 - 11.30                      DNA Quantification

11.30 - 12.30                      Tagmentation and Index PCR

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12.30 – 13:15                      *Lunch (in de Hal bij de Keuningzaal)*

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13.15 - 14:15                      PCR Cleanup

14.15 – 15.15                      Library Normalization and Pooling

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15.15 - 15.45                      *Coffee Break (in de Hal bij de Keuningzaal)*

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15.45 - 17.15                      “Got sequences and what now?” (*Dag Harmsen*)

## Thursday, 13<sup>th</sup> of October

Meeting room: Ronde zaal

### *Scientific talks*

<b>Time</b>	<b>Subject</b>
09.00 - 09.35	WGS for global surveillance and monitoring of high risk clones ( <i>David Aanensen</i> )
09.35 - 10.10	Software solutions for bacterial typing based on WGS data ( <i>Henrik Hasman</i> )
10.10 - 10.45	From reads to profiles to trees: challenges and solutions in high throughput sequencing data analysis ( <i>João André Carriço</i> )
10.45 - 11.15	<i>Coffee Break</i>
11.15 - 11.55	WGS for Acinetobacter and Legionella ( <i>Jacob Moran Gilad</i> )
11.55 - 12.30	About 16-23S sequencing, WGS and more... ( <i>Artur Sabat</i> )
12.30 - 13.30	<i>Lunch</i>
13.30 - 14:15	Detection of resistance genes - application of WGS and Metagenomics ( <i>Silke Peter</i> )
14:15- 15:00	Metagenomics in routine clinical microbiology and infection prevention – are we already there? ( <i>Robert Schlaberg</i> )
15:00 - 15.30	<i>Coffee Break</i>
15.30 - 16:15	Analysis of the dissemination of plasmids by whole genome sequencing ( <i>Willem van Schaik</i> )
16:15 -17:00	Personalized microbiology during outbreaks - unique marker and <i>in silico</i> screening approaches ( <i>John Rossen</i> )
18.00 - 22.30	<i>Dinner and Social Programme</i>



## Friday, 14<sup>th</sup> of October

Meeting room lokaal 6 LM4 (Triade)

### *Practical day – Computer analysis*

<b>Time</b>	<b>Subject</b>
08.30 - 09.15	Introduction to data-analyses using commercial and open source software tools in a clinical microbiology lab ( <i>Dag Harmsen</i> )
09.15 – 10.00	Illumina basespace tools ( <i>Illumina representative</i> )
10.00 - 10.30	<i>Coffee Break</i>
10.30 - 11.30	Sequence data analysis in daily clinical practice – assembly, epi – and pathotyping ( <i>Sigrid Rosema</i> )
11:30 – 13:00	PHYLOViZ: phylogenetic inference and data visualization for sequence based typing methods ( <i>João André Carriço</i> )
13.00 – 13.45	<i>Lunch</i>
13.45 – 15.15	Whole Genome Sequence Analysis (WGSA): free and open tools from the Centre for Genomic Pathogen Surveillance ( <i>Corinna Glasner</i> )
15.15 – 15.30	<i>Fresh-up</i>
15.30- 16.45	Annotation (RAST) and visualization (Artemis, ACT) ( <i>Monika Chlebowicz</i> )
16.45 – 17.00	Final remarks and closure

## Confirmed Faculty Members

- Willem van Schaik, Utrecht, The Netherlands
- Dag Harmsen, Münster, Germany
- John Rossen, Groningen, The Netherlands
- Alexander Friedrich, Groningen, The Netherlands
- Erwin Raangs, Groningen, The Netherlands
- Monika Chlebowicz, Groningen, The Netherlands
- Corinna Glasner, Groningen, The Netherlands
- João André Carriço, Portugal
- Henrik Hasman, Denmark
- Jacob Moran Gilad, Israel
- Artur Sabat, Groningen, The Netherlands
- Silke Peter, Tuebingen, Germany
- Robert Schlaberg, Utah, USA
- Sigrid Rosema, Groningen, The Netherlands
- David Aanensen, London, United Kingdom

## Course Registration

Please register on-line using the URL below:

[https://docs.google.com/forms/d/1ZJlcfgg\\_1ZPT9loRFxOeG6H5NDeZGexuAHof9IKg0tY/edit](https://docs.google.com/forms/d/1ZJlcfgg_1ZPT9loRFxOeG6H5NDeZGexuAHof9IKg0tY/edit)

We will confirm your participation within 5 working days.

Please book your accommodation **only** after confirmation.



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