



2nd edition of

Advanced de novo Assembly and Resolving Complex Genomic Regions

Monday, 1 June 2015 - Wednesday, 3 June 2015

Leiden University Medical Center
Albinusdreef 2, 2333ZA Leiden, the Netherlands

Keynote Speakers

Mark Chaisson, University of Washington, Seattle, USA
Alexandre de Kochko, Centre IRD de Montpellier, France

Confirmed Speakers

Ken Kraaijeveld, VU Amsterdam, the Netherlands | **Jean-François Flot**, University College London, UK
Hendrik-Jan Megens, Wageningen University, the Netherlands | **Christoph Konig**, Pacific Biosciences, Germany
Gabino Sanchez Perez, Wageningen University, the Netherlands | **Phillip Lobb**, Pacific Biosciences, UK
Hans Jansen, ZF-screens, the Netherlands | **Yavuz Ariyurek**, Leiden University Medical Center, the Netherlands
Sandra Smits, Wageningen University, the Netherlands | **Derek Butler**, BaseClear, the Netherlands
Thomas Otto, Wellcome Trust Sanger Institute, UK | **Tyler Alioto**, CNAG, Spain

Organizers

Yahya Anvar, Leiden University Medical Center, the Netherlands
Johan den Dunnen, Leiden University Medical Center, the Netherlands

For more information and registration please visit the [BioSB website](#) or send an email to [BioSB Office](#).



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FINAL PROGRAMME

Monday, 1 June 2015

Session 1	Introduction Lecture Hall 3 Chair: TBA
9:00 - 9:30	Registration
9:30 - 9:45	Welcome and general remarks Yahya Anvar, <i>Leiden University Medical Center, the Netherlands</i>
9:45 - 10:45	What should every biologist know about de novo assembly? Relevance and misconceptions Ken Kraaijeveld, <i>VU Amsterdam, the Netherlands</i>
10:45 - 11:00	Coffee Break
11:00 - 12:00	Genome architecture and genome assembly Hendrik-Jan Megens, <i>Wageningen University, the Netherlands</i>
12:00 - 13:00	Lunch Break
Session 2	Technologies Lecture Hall 3 Chair: TBA
13:00 - 13:30	Traditional approaches (Sanger Sequencing and BACs) TBA, <i>TBA, the Netherlands</i>
13:30 - 14:00	Advent of high-throughput sequencing technologies Hans Jansen, <i>ZF-screens, the Netherlands</i>
14:00 - 14:15	Coffee Break
14:15 - 15:00	Single-molecule long-read sequencing technologies Christoph Konig, <i>Pacific Biosciences, Germany</i>
15:00 - 15:45	Optical mapping to bridge between micro and macro genomic variations Gabino Sanchez Perez, <i>Wageningen University, the Netherlands</i>
15:45 - 16:00	Coffee Break
16:00 - 17:00	Keynote: Sequencing and assembling the genome of the allotetraploid <i>Coffea arabica</i> Alexandre de Kochko, <i>Evolution du Génome des Caféiers, Centre IRD de Montpellier, France</i>

Tuesday, 2 June 2015

Session 3	Methodologies, tricks and common mistakes Lecture Hall 3 Chair: TBA
9:00 - 9:30	Sampling strategies Yavuz Ariyurek, <i>Leiden University Medical Center, the Netherlands</i>
9:30 - 10:00	Data quality assessment without a reference genome (old and new) Yahya Anvar, <i>Leiden University Medical Center, the Netherlands</i>
10:00 - 10:15	Coffee Break
10:15 - 11:00	The evolution of assembly strategies (old and new) Phillip Lobb, <i>Pacific Biosciences, UK</i>
11:00 - 11:30	Mind the gap: quality assessment, scaffolding and gap filling strategies Thomas Otto, <i>Wellcome Trust Sanger Institute, UK</i>
11:30 - 12:00	From sequence to biology: annotation and comparative genomics Sandra Smits, <i>Wageningen University, the Netherlands</i>
12:00 - 13:00	Lunch Break
Session 4	Achievements, Novel Discoveries and Current Limitations Lecture Hall 3 Chair: TBA
13:00 - 13:45	From single bacteria assembly to resolving complex microbiomes Yahya Anvar, <i>Leiden University Medical Center, the Netherlands</i>
13:45 - 14:15	Defeating heterozygosity in de novo genome assembly Jean-François Flot, <i>University College London, UK</i>

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- 14:15 - 14:30 Coffee Break
- 14:30 - 15:00 Optimal NGS-based analysis of metagenomic samples
Derek Butler, *BaseClear, the Netherlands*
- 15:00 - 15:45 De novo genome assembly using diverse data types
Tyler Alioto, *CNAG, Spain*
- 15:45 - 16:00 Coffee Break
- 16:00 - 17:00 **Keynote:** Resolving the complexity of the human genome by single-molecule sequencing
Mark Chaisson, *University of Washington, USA*

Wednesday, 3 June 2015

Session 5 **Practicals and hands-on sessions**
J01-82/83 | Chair: TBA

- 9:00 - 16:00 Sampling strategy, data quality assessment and best practices for study design
Choosing the right assembler, how to interpret the results and what is the next step
From sequence to biology: making sense of the genomic information
- 10:30 - 10:45 Coffee Break
- 12:30 - 13:30 Lunch Break
- 15:00 - 15:15 Coffee Break
- 16:00 - 17:00 QA and open discussion