GENOPOLE

Genopole Summer School

Bioinformatic and biostatistic tools in medical genomics

4-7 JULY 2017, Châteauform Les Berges de Seine (Seine-Port 77)

http://summerschool.genopole.fr

Summary

The programme will cover statistical methodologies and bioinformatic tools used in genomics and metagenomics in the context of a comprehension approach of pathological mechanisms.
The course will include lectures and a round table with scientific leaders as well as hands-on computer sessions* with experts in the field.

*Participants are asked to bring their own laptop.

The course is intended **for researchers, engineers and PhD** already involved or planning to start their research projects in the field of genomics for medical research.
It is **limited to 20 participants,** in order to ensure the highest quality in the to the interactions and to the practical sessions. For this reason, registration will include a selection step by the organizing committee.

This is a **residential summer school**. Hence, all sessions will take place in the Campus of Chateauform' Les Berges de Seine, in a nature area close to Paris. Participants will be hosted in the campus with **accommodation and meals all included in the registration fees as well as the scientific sessions.**

Prerequisites

The programme of the practical sessions requires a working knowledge of UNIX system (use of UNIX commands, create and modify files…). In order to ensure a homogeneous level among the participants **a short test is included in the registration form** (script language and statistics).

Speakers and guests

- Mathieu ALMEIDA, University of Maryland
- Christophe AMBROISE, Université d'Evry-Val d'Essonne
- Jacques BECKMANN, Swiss Institute of Bioinformatics Switzerland
- Johann BEGHAIN, Genoscope, CEA
- Hervé CHNEWEISS, Chair of the ethics committee of Inserm
- Karine CLEMENT, Université Pierre et Marie Curie and ICAN institute
- Stéphane CRUVEILLER, Genoscope, CEA
- Adrien JOSSO, Genoscope, CEA
- Yves LEVY, Chair and CEO of Inserm, Chair of AVIESAN
- Valentin LOUX, French national institute for agricultural research
- Vincent MEYER, National Center for genotyping, CEA
- Guillem RIGAILL, French national institute for agricultural research
- Todd TREANGEN, University of Maryland, US
- Daniel ZERBINO, EMBL-EBI, UK

Scientific committee

- Roxane BRACHET Genopole (scientific coordinator)
- Jean-François DELEUZE, Institute of Genomics, CEA
- Pierre LE BER, Institute of Genomics, CEA
- Victoria DOMINGUEZ DEL ANGEL, French Institute of Bioinformatics
- Claudine MEDIGUE, Institute of Genomics, CEA
- Francis QUETIER, University of Evry Val d'Essonne
- Pierre TAMBOURIN, Genopole

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GUEST AND SPEAKERS

UNIVERSITY OF MARYLAND 1856

ICAN Institute of Cardiometabolism And Nutrition

Inserm

SIB Swiss Institute of Bioinformatics

EMBL-EBI

PROGRAMME

DAY 1 – July 4
Key note lectures
14:00 – 18:00

13:00 – 14:00 Welcome and Registration

14:00 – 18:00 Key notes session

14:00 - 14:10 The Genopole Biocluster in the era of genomics and precision medicine - JM GROGNET, CEO Genopole (10 min)

14:10 – 15:10 Think Globally, process locally: laying the bioinformatic infrastructure for clinical genomics - Daniel ZERBINO, EMBL-EBI (45 min + 15 min questions)

15 :10 – 16 :10 Gut microbiome : challenges in cardiometabolic disorders - Karine CLEMENT, ICAN Université Pierre et Marie Curie (45 min + 15 min questions)

16:10 – 16:20 Coffee break

16:20 – 17:40 Partners session

France Genomique Infrastructure - P. Le Ber, CEA (20 min)

GenMed programme - JF. Deleuze CEA (20 minutes)

Cloud computing support and development - V.Dominguez Del Angle, IFB (20 min)

Questions and discussion : 20 min

19:00 – 20:30 Dinner

DAY 2 – July 5
Bioinformatic tools

7:00 – 8:45 BREAKFAST

9:00 – 12:30 Practical session – including coffee break

Generation and analysis of data
Vincent Meyer, CNG-CEA ; Valentin Loux, Inra

- Genome assembly, local and global alignment, annotation

12:30 – 13:45 LUNCH

13:45 – 16:45 Practical session – including coffee break

Variation in the human genome (SNPs, CNV…)
Vincent Meyer, CNG-CEA

- Exome sequence analysis: alternative of Whole Exome Sequencing versus Whole Genome Sequencing as a strategy to identify the genetic bases of common Mendelian disorders and rare diseases.

16:45 – 18:00 FREE TIME Several sport activities are proposed on the campus site

18:00 – 19:30 Poster session
Special session assigned to the participants upon submission of poster

19:30 – 21:00 DINNER

DAY 3 – July 6
Statistical methods

7:00 – 8:45 BREAKFAST

9:00 – 12:30 Practical session - including coffee break

Statistical methods
Christophe Ambroise, Université d'Evry-Val d'Essonne and Guillem Rigaill, Inra

- Transcriptome / RNA-Seq analysis (Whole Transcriptome Sequencing): quantification and differential expression
- How to choose the appropriate statistical methodologies: detecting bias and troubleshoots and interpreting statistical results

12:30 – 13:45 LUNCH

13:45 – 16:45 Practical session - including coffee break

Statistical methods
Christophe Ambroise, Université d'Evry-Val d'Essonne and Guillem Rigaill, Inra

- Statistical inference /hypothesis testing
- Quantitative genetics

17:00 – 18:00 SOCIAL SESSION Hiking on the « circuit des villages briards » OR free time for sport activities on the campus

18:30 – 20:00 Cocktail-Round table

Nationwide strategies for translating genomic approaches into clinical decision making: impact on health care systems, massive data management and ethics

Chairs: J.F. Deleuze, Director of the National Center for Genotyping, CEA ; P.Tambourin, former CEO of Genopole

Speakers
J. Beckmann (Swiss institute of Bioinformatics)
Y.Levy (Chairman and CEO of Inserm and Chairman of Aviesan)
J.Béranger (Founder of ADEL label and associate scientist Inserm U1027)
Hervé Chneiweiss (Director of research, and Chair of the ethics committee of Inserm)

20:00 – 21:30 DINNER

DAY 4 – July 7
Metagenomics applied to human diseases
'Strategies for exploring microbiota'

7:00 – 8:45 BREAKFAST

9:00 – 12:00 **Practical session** (including coffee break)
Stéphane Cruveiller, Adrien Josso, Johann Beghain - Genoscope CEA

PathoTRACK project : bioinformatics strategies for the study of microbial communities in the scope of human health

12:15 – 13:30 LUNCH

13:45 – 16:00 **Practical session** (including coffee break)
Mathieu Almeida, University of Maryland

Use of marker genes tools for detection of known and unknown micro-organisms in whole genome human intestinal tract metagenomic samples

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Todd James Treangen, University of Maryland

Title TBC

16:30 – 16:45 CLOSING TALK, END OF THE SUMMER SCHOOL