Introduction to Pan-genomics

Lake Como School of Advanced Studies, July 4-8, 2022

Home

We are very proud to announce the PhD school *Introduction to Pangenomics*.

Graph based data structures have been pointed out to have disruptive benefits over traditional sequence based structures when representing pan-genomes, sufficiently large, evolutionarily coherent collections of genomes. This idea has its immediate justification in the laws of genetics: evolutionarily closely related genomes vary only in relatively little amounts of letters, while sharing the majority of their sequence content. The fundamental task in computational biology of capturing genetic variations largely benefit from graph-based pangenome representations: they summarize redundancies without discarding individual differences and graphs lend themselves to data structures and algorithms for pangenome analysis.

This school is an opportunity for interacting with the computational pangenomics community of two European Research Networks, ALPACA and PANGAIA. The school provides a forum for being exposed to novel approaches on how to push the shift from sequence to graph-based representations of genomes.

The expected audience consists of PhD students and young researchers that are interested in the new field of computational pangenomics and that are eager to learn from world-renowned scientists.

This school will start on Monday July 4th and end on Friday July 8th.

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Board

The school is supervised by

- Paola Bonizzoni (Univ. Milano-Bicocca)
- Gianluca Della Vedova (Univ. Milano-Bicocca)
- Alex Schoenhuth (Univ. Bielefeld, Germany)

Lecturers

The current preliminary list of speakers include:

- Jasmijn Baaijens (Assistant Professor at TU Delft, the Netherlands)
- Christina Boucher (Associate Professor at Univ. Florida, USA)
- Rayan Chikhi (Group Leader at Institut Pasteur, France)
- Evan Eichler (Professor of Genome Sciences at Univ. of Washington, USA)
- Mareike Fischer (Associate Professor at Univ. Greifswald, Germany)
- Shilpa Garg (Assistant Professor at Univ. of Copenhagen, Denmark)
- Erik Garrison (Assistant Professor at Univ. Tennessee, USA)
- Zamin Iqbal (Group Leader at EMBL)
- Veli Mäkinen (Professor at Univ. Helsinki, Finland)
- Pjotr Prins (Assistant Professor at Univ. Tennessee, USA)
- Alex Schoenhuth (Univ. Bielefeld, Germany)
- Jouni Sirén (Assistant Research Scientist at Univ. California Santa Cruz Genomics Institute, USA)
- Tomáš Szemes (Director at Geneton, Slovakia)

Organizers

- **Paola Bonizzoni**
- **Simone Ciccolella**
- **Gianluca Della Vedova**
- **Luca Denti**
- **Yuri Pirola**
- **Raffaella Rizzi**

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Sponsors

ALgorithms for PAngenome Computational Analysis (ALPACA)

This project has received funding from the European Union's Horizon 2020 Innovative Training Networks programme under the Marie Skłodowska-Curie grant agreement No. 956229

Pangenome Graph Algorithms and Data Integration (PANGAIA)

This project has received funding from the European Union's Horizon 2020 Research and Innovation Staff Exchange programme under the Marie Skłodowska-Curie grant agreement No. 872539

Schedule

Schedule

Time	Mon 4/7	Tue 5/7	Wed 6/7	Thu 7/7	Fri 8/7
9:00-10:30		Jouni Siren	Jouni Siren	Veli Makinen	Shilpa Garg
10:30-11:00	Welcome and registration	Coffee break			
11:00-12:30		Zamin Iqbal	Evan Eichler	Christina Boucher	Alex Schoenhuth
12:30-14:00		Lunch			
14:00-15:30	Veli Makinen	Mareike Fischer	Rayan Chikhi	Jasmijn Baaijens	Departures
15:30-16:00		Coffee break			
16:00-18:00	Pjotr Prins	Tomáš Szemes	Erik Garrison	Alex Schoenhuth	

Lecture plan

Monday 4/7

14:00-15:30	Veli Makinen (Univ Helsinki) *Alignments on pangenome representations*
16:00-18:00	Pjotr Prins (Univ. Tennessee) *Why free software matters for Science and what to do*

Tuesday 5/7

9:00-10:30	Jouni Siren (Univ. California Santa Cruz) *Pangenome graphs with haplotype paths*
11:00-12:30	Zamin Iqbal (EMBL) *Analysis of genetic variation with genome graphs*
14:00-15:30	Mareike Fischer (Univ. Greifswald) *How future-proof are phylogenetic methods?*
16:00-18:00	Tomáš Szemes (Geneton) *Bioinformatics driven genomic biotechnologies and how they help in solving biomedical challenges*

Wednesday 6/7

9:00-10:30	Jouni Siren (Univ. California Santa Cruz) *Pangenome graphs with haplotype paths*
11:00-12:30	Evan Eichler (Univ. of Washington) *Long-read sequencing and the structural diversity of human genomes*
14:00-15:30	Rayan Chikhi (Institut Pasteur) *Introduction to sequence graphs representations*
16:00-18:00	Erik Garrison (Univ. Tennessee) *Building and understanding pangenome variation graphs*

Thursday 7/7

9:00-10:30	Veli Makinen (Univ Helsinki) *Alignments on pangenome representations*
11:00-12:30	Christina Boucher (Univ. of Florida) *Understanding the details behind Moni Align*
14:00-15:30	Jasmijn Baaijens (TU Delft) *Viral quasispecies assembly*
16:00-18:00	Alex Schoenhuth (Univ. Bielefeld) *Introduction to Capsule networks*

Friday 8/7

9:00-10:30	Shilpa Garg (Univ. of Copenhagen) *Chromosome-scale haplotype-resolved assembly*
11:00-12:30	Alex Schoenhuth (Univ. Bielefeld) *Introduction to Capsule networks*