

[BC]² BASEL COMPUTATIONAL BIOLOGY CONFERENCE 2021

13 – 15 September
Congress Center Basel, Switzerland

*Harnessing biological data:
from molecular processes to human health*

Conference programme



Organised by:
SIB Swiss Institute of Bioinformatics
www.sib.swiss

MONDAY, 13 SEPTEMBER

Registration for the ELIXIR Forum

Congress Center Basel
8:15 – 9:00

Registration for the Tutorials & Workshops

University of Basel
(tutorials and workshops are organised at different places,
please check our webpage for the exact location)
8:15 – 9:00

ELIXIR Forum

Building the learning ecosystem of health: from data tracking to preventive medicine

Parallel Track A
Congress Center Basel, Room Montreal
9:00 – 16:45

Session chair
Daniel Stekhoven

| Time | Talk |
|---------------|---|
| 9:00 – 9:30 | <i>Welcome words and introduction to the day</i> Daniel Stekhoven NEXUS Personalized Health Technologies, ETH Zurich, CH |
| 9:30 – 10:15 | KEYNOTE SPEAKER Serena Scollen ELIXIR Europe, UK |
| 10:15 – 10:45 | Coffee break |
| 10:45 – 12:15 | SELECTED PRESENTATIONS <i>Curation and integration of single-cell RNA-Seq data for cross-study analysis and interpretation</i> Nebion AG (CH) |

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| | <p><i>Hematocrit self-testing for Polycythaemia vera patients at home - A collaboration of physicians, device manufacturer Nova Biomedical and Novartis</i> Novartis (CH)</p> <p><i>Integrating relevant phenotype and genomic data in EHR with SNOMED CT, LOINC and other Genomic Standards</i> BITAC (ES)</p> <p><i>NFL/NBA 2020-2021 Sports Season COVID-19 Monitoring</i> IQVIA (UK)</p> |
| 12:15 – 13:15 | Lunch break |
| 13:15 – 14:25 | <p>SELECTED PRESENTATIONS</p> <p><i>Pill Protect: an innovative and integrated tool for the benefit of patients</i> Gene Predictis (CH)</p> <p><i>Bringing the world's health knowledge to research and medical decision makers.</i> HealthECCO (DE)</p> <p><i>MyPharmaGenes: Pharmacogenetics in clinical practice</i> HeartGenetics, Genetics and Biotechnology SA (PT)</p> |
| 14:25 – 15:10 | <p>KEYNOTE SPEAKER</p> <p>Nicolas Loeillot Groupe Mutuel, CH</p> |
| 15:10 – 15:55 | <p>KEYNOTE SPEAKER</p> <p>Bogi Eliassen Copenhagen Institute for Future Studies, DK</p> |
| 15:55 – 16:45 | Panel discussion |

Tutorials & Workshops

Parallel Track B
University of Basel
9:00 – 16:00

Tutorials (Kollegienhaus, University of Basel)

- Inferring gene regulatory networks from high-throughput data

- Semantic representation of clinical data in RDF
- Understanding protein and glycoprotein structure - activity relationship
- Beyond the usual Docker tutorial - Web apps & CI
- Defining genomic signatures with non-negative matrix factorization
- Deep learning on biological sequences: from HMMs to RNNs
- Publication Perfect: Painlessly creating powerful plots

Workshops (Biozentrum, University of Basel)

- Toward a common framework for annotated, accessible, reproducible and interoperable computational models in biology
- Federating computational analyses with GA4GH standards
- BioNetVisA: biological network reconstruction, data visualization and analysis in biology and medicine

Registration for [BC]²

Congress Center Basel
16:00 – 17:00

[BC]² Welcome words & Opening lecture

Joined session
Congress Center Basel, Room Montreal
17:00 – 18:15

| Time | Talk |
|---------------|------------------------|
| 17:10 – 17:15 | Welcome words |
| 17:15 – 18:15 | OPENING LECTURE |

[BC]² Welcome Apéro & Dinner

Open to all participants
KLARA's Restaurant (see webpage for exact location)
18:30 – 22:30

– END OF THE DAY –

TUESDAY, 14 SEPTEMBER

Artificial intelligence, machine learning and computer vision: expanding the bioinformatics toolkit

Parallel session 1, Track A
Congress Center Basel, Room Montreal
9:15 – 10:45

Session chairs
Karsten Borgwardt
Julia Vogt

| Time | Talk |
|---------------|---|
| 9:15 – 9:45 | INVITED SPEAKER Thomas Fuchs Memorial Sloan Kettering Cancer Center, US |
| 9:45 – 10:00 | SELECTED PRESENTATION <i>Interpretable deep learning approach enables detection of phosphorylated peptides based on their tandem mass spectra</i> Tom Altenburg Hasso-Plattner-Institut, DE |
| 10:00 – 10:15 | SELECTED PRESENTATION <i>A morphometric framework for the embryo-wide quantification of tissue organisation at single cell resolution</i> Max Brambach Department of Molecular Life Sciences, University of Zurich, CH |
| 10:15 – 10:30 | SELECTED PRESENTATION <i>Improving Cancer Survival Prediction With Multitask Neural Networks</i> Daniel Rowson ETH Zurich, CH |
| 10:30 – 10:45 | POSTER PITCHES <i>Mapping high-resolution cell states in single-cell RNA-seq data</i> Pascal Grobecker Biozentrum, University of Basel, CH |

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| | <p><i>DEPICTION: an interpretability toolbox for computational biologists</i></p> <p>An-phi Nguyen IBM Research Europe, CH</p> <p><i>Genome-Wide Association Studies of retinal vessel tortuosity identify 173 novel loci, capturing genes and pathways associated with disease and vascular tissue pathomechanics</i></p> <p>Mattia Tomasoni Jules-Gonin Eye Hospital, Dept of Ophthalmology, UNIL, CH</p> |
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Evolutionary dynamics and ecology: where organisms, time and space interplay

Parallel session 1, Track B
Congress Center Basel, Room Singapore
9:15 – 10:45

Session chairs
Jérôme Goudet
Sara Mitri

| Time | Talk |
|---------------|--|
| 9:15 – 9:45 | <p>INVITED SPEAKER</p> <p>Tami Lieberman MIT - Massachusetts Institute of Technology, US</p> |
| 9:45 – 10:00 | <p>SELECTED PRESENTATION</p> <p><i>Evolutionary profiling identifies insect immune gene families that function in concert</i></p> <p>Robert Waterhouse University of Lausanne, CH</p> |
| 10:00 – 10:15 | <p>SELECTED PRESENTATION</p> <p><i>Bacterial trade-offs between translational efficiency and proline-induced ribosomal stalling</i></p> <p>Tess Brewer UZH, Institute of Evolutionary Biology and Environmental Sciences, CH</p> |
| 10:15 – 10:30 | <p>SELECTED PRESENTATION</p> |

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| | <p><i>Ecological diversification and incipient speciation in an eco-evolutionary model of resource competition</i></p> <p>Massimo Amicone Instituto Gulbenkian de Ciencia, PT</p> |
| 10:30 – 10:45 | <p>POSTER PITCHES</p> <p><i>Imputation of ancient genomes</i></p> <p>Barbara Mota University of Lausanne, CH</p> <p><i>A long-lived population of stem cells under neutral competition shapes the clonal composition of cerebral organoids</i></p> <p>Florian Pflug University of Vienna, Center for Integrative Bioinformatics (CIBIV), AT</p> <p><i>New models for the spatial distribution of fossil taxa demonstrate size-dependent dispersal and cooling-driven extinction of carnivores</i></p> <p>Torsten Hauffe Department of Biology, University of Fribourg, CH</p> |

Coffee break

Congress Center Basel, Foyer
10:45 – 11:15

SIB Bioinformatics Awards Ceremony

Joined session
Congress Center Basel, Room Montreal
11:15 – 12:30

| Time | Talk |
|---------------|---|
| 11:15 – 11:40 | <p>Bioinformatics Graduate Paper Award Announcement of Awardee and presentation of paper</p> |
| 11:40 – 12:05 | <p>Early Career Bioinformatician Award Announcement of Awardee and presentation of research</p> |
| 12:05 – 12:30 | <p>Bioinformatics Resource Innovation Award Announcement of Awardee and presentation of resource</p> |

Lunch break

Congress Center Basel, Foyer
12:30 – 13:30

Pathogens, immune systems and host-pathogen interactions: an arms race with infectious agents

Parallel session 2, Track A
Congress Center Basel, Room Montreal
13:30 – 15:00

Session chairs
Jacques Fellay
Richard Neher

| Time | Talk |
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| 13:30 – 14:00 | INVITED SPEAKER Aleksandra Walczak Laboratoire de Physique - Ecole Normale Supérieure, FR |
| 14:00 – 14:15 | SELECTED PRESENTATION <i>Genome-to-genome analysis identifies hepatitis B virus escape mutations induced by NTCP variation and HLA class I restriction</i> Zhi Ming Xu EPFL, CH |
| 14:15 – 14:30 | SELECTED PRESENTATION <i>Determinants of SARS-CoV-2 transmission to guide vaccination strategy in a European urban area</i> Sarah Brüningk ETHZ, D-BSSE, CH |
| 14:30 – 14:45 | SELECTED PRESENTATION <i>Robust prediction of HLA class II epitopes</i> Julien Race University of Lausanne, CH |
| 14:45 – 15:00 | POSTER PITCHES |

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| | <p><i>metaGCcorrect: Correcting GC Bias Improves Accuracy and Comparability in Metagenomic Abundance Estimation</i> Laurenz Holcik Max Perutz Labs, AT</p> <p><i>cDR3AM: A Curated Database of Immune Repertoires</i> Deniz Tosoni FHNW University of Applied Sciences and Arts Northwestern, CH</p> <p><i>Deep generative selection models of T and B cell receptor repertoires with soNNia</i> Giulio Isacchini École normale supérieure, FR</p> |
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Spatiotemporal gene expression dynamics and single-cell approaches: zooming in to better scale up

Parallel session 2, Track B
Congress Center Basel, Room Singapore
13:30 – 15:00

Session chairs
Bart Deplancke
Charlotte Sonesson
Michael Stadler

| Time | Talk |
|---------------|--|
| 13:30 – 14:00 | <p>INVITED SPEAKER</p> <p>Barbara Treutlein ETH Zurich, CH</p> |
| 14:00 – 14:15 | <p>SELECTED PRESENTATION</p> <p><i>Niche-specific gene expression using PICseq analysis during mouse embryonic development</i> Kyoung Won University of Copenhagen, DK</p> |
| 14:15 – 14:30 | <p>SELECTED PRESENTATION</p> <p><i>distinct: a novel approach to differential distribution analyses</i> Simone Tiberi</p> |

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| | UZH, Institute of Molecular Life Sciences, CH |
| 14:30 – 14:45 | <p>SELECTED PRESENTATION</p> <p><i>Cell cycle gene regulation dynamics revealed by RNA velocity and deep-learning</i> Andrea Riba IGBMC, FR</p> |
| 14:45 – 15:00 | <p>POSTER PITCHES</p> <p><i>Inferring single-cell trees alongside cell-state transitions from lineage tracing and RNAseq data</i> Sophie Seidel D-BSSE, CH</p> <p><i>Model-based robustness and bistability analysis for methylation-based, epigenetic memory systems</i> Viviane Klingel Institute for Systems Theory and Automatic Control, University of Stuttgart, DE</p> <p><i>Latenta: unified, probabilistic and interpretable modelling of single-cell omics data</i> Wouter Saelens EPFL, CH</p> |

Coffee break

Congress Center Basel, Foyer
15:00 – 15:30

Poster session 1, Industry exhibition and “Boost your career corner”

Congress Center Basel, Foyer
15:30 – 17:00

| Time | Talk |
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| 15:30 – 17:00 | <p>Poster session 1 Discuss your science with your peers in front of your poster!</p> |

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| | <i>*More details on the different posters will be published in the beginning of September</i> |
| 15:30 – 17:00 | Industry exhibition Get in touch with different companies and institutions working with bioinformatics! |
| 16:30 – 17:00 | INVITED SPEAKER “Boost your career”-Corner <i>Ten simple rules for doing a postdoc in pharma</i> Jitao David Zhang Roche, CH |

Treasure hunt

Start point: Congress Center Basel
17:15 – 19:30

Apéro & Winner’s ceremony

Markthalle, Basel
19:30 – 20:30

– END OF THE DAY –

WEDNESDAY, 15 SEPTEMBER

Cancer biology and precision medicine: deepening our understanding towards tailored treatments

Parallel session 3, Track A
Congress Center Basel, Room Montreal
9:15 – 10:45

Session chairs
Valentina Boeva
David Gfeller

| Time | Talk |
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| 9:15 – 9:45 | INVITED SPEAKER Olivier Elemento Weill Cornell Medicine, US |
| 9:45 – 10:00 | SELECTED PRESENTATION <i>The molecular underpinnings of wild-type Von Hippel–Lindau clear cell renal cell carcinomas</i> Aashil Batavia Department of Biosystems Science and Engineering, ETH & Institute of Pathology and Molecular Pathology, USZ, CH |
| 10:00 – 10:15 | SELECTED PRESENTATION <i>Seeing beyond the target: Leveraging off-target reads in targeted clinical tumor sequencing to identify prognostic biomarkers</i> Serghei Mangul University of Southern California, US |
| 10:15 – 10:40 | SELECTED PRESENTATION <i>Variomes: a high recall search engine to support the curation of genetic variants</i> Emilie Pasche SIB Swiss Institute of Bioinformatics, CH |
| 10:30 – 10:45 | POSTER PITCHES <i>DNA damage repair proteins synergistically affect the cancer prognosis and resistance</i> Meetal Sharma CSIR-Institute of Himalayan Bioresource Technology, IN |

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| <p><i>protti: an R package for comprehensive analysis of peptide- and protein-centric bottom-up proteomics data</i></p> <p>Jan-Philipp Quast Institute of Molecular Systems Biology, CH</p> <p><i>Integration of single cell RNA-sequencing data across tissues and cancer types reveals pathways leading to dendritic cell activation</i></p> <p>Bhavesh Soni Roche Pharma Research and Early Development, Pharmaceutical Sciences, Roche Innovation Center Basel, CH</p> |
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Population genomics in human health: connecting genotypes to phenotypes

Parallel session 3, Track B
Congress Center Basel, Room Singapore
9:15 – 10:45

Session chairs
Sven Bergmann
Olivier Delaneau

| Time | Talk |
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| 9:15 – 9:45 | <p>INVITED SPEAKER</p> <p>Lude Franke Utrecht University, NL</p> |
| 9:45 – 10:00 | <p>SELECTED PRESENTATION</p> <p><i>Parent-of-origin inference for biobank scale datasets</i></p> <p>Robin J. Hofmeister UNIL, Department of Computational Biology, CH</p> |
| 10:00 – 10:15 | <p>SELECTED PRESENTATION</p> <p><i>At least a third of DNA methylation-to-complex trait effects are mediated by transcript levels</i></p> <p>Marie Sadler Unisanté, CH</p> |
| 10:15 – 10:30 | <p>SELECTED PRESENTATION</p> <p><i>From menarche to menopause: the impact of reproductive factors on the metabolome of over 65,000 women</i></p> <p>Maria Carolina Borges</p> |

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| | University of Bristol, UK |
| 10:30 – 10:45 | <p>POSTER PITCHES</p> <p><i>A comprehensive framework for low-coverage whole genome sequencing imputation across human populations</i> Simone Rubinacci UNIL, Department of Computational Biology, CH</p> <p><i>Estimation of age-specific marker effects for time-to-diagnosis traits</i> Sven Erik Ojavee UNIL – DBC, CH</p> <p>Investigating scenarios regulating gene expression in the immune system Diana Avalos UniGE, Campus Biotech, CH</p> |

[BC]² Highlights Session

Joined session
 Congress Center Basel, Room Montreal
 11:15 – 12:45

Session chairs
 Erik van Nimwegen
 Zoltán Kutalik

| Time | Talk |
|---------------|--|
| 11:15 – 11:30 | <p>SELECTED PRESENTATION</p> <p><i>Discovering Novel Cell Types across Heterogeneous Single-cell Experiments</i> Maria Brbic Stanford University, US</p> |
| 11:30 – 11:45 | <p>SELECTED PRESENTATION</p> <p><i>Neandertal population history from cave sediment DNA</i> Benjamin Vernot Max Planck Institute for Evolutionary Anthropology, DE</p> |
| 11:45 – 12:00 | <p>SELECTED PRESENTATION</p> |

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| | <p><i>Detection and surveillance of SARS-CoV-2 genomic variants in wastewater</i></p> <p>David Dreifuss Department of Biosystems Science and Engineering, ETH Zurich, CH</p> |
| 12 :00 – 12 :15 | <p>SELECTED PRESENTATION</p> <p><i>Embryo multiplexing enables quantitative investigation of global chemokine-scavenger interactions</i></p> <p>Marvin Albert Universitaet Zuerich, CH</p> |
| 12:15 – 12:30 | <p>SELECTED PRESENTATION</p> <p><i>Inference of clonal evolution from longitudinal single cell data</i></p> <p>Davide Maspero University of Milano - Bicocca, IT</p> |
| 12:30 – 12:45 | <p>SELECTED PRESENTATION</p> <p><i>The impact of copy number variants on complex human traits</i></p> <p>Chiara Auwerx University of Lausanne, CH</p> |

Lunch break

Congress Center Basel, Foyer
12:45 – 13:45

Poster session 2, Industry exhibition and “Boost your career corner”

Congress Center Basel, Foyer
13:45 – 15:15

| Time | Talk |
|---------------|---|
| 13:45 – 15:15 | <p>Poster session 2 Discuss your science with your peers in front of your poster!</p> <p><i>*More details on the different posters will be published in the beginning of September</i></p> |
| 13:45 – 15:15 | Industry exhibition |

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| | Get in touch with different companies and institutions working with bioinformatics! |
| 14:45 – 15:15 | <p>INVITED SPEAKER</p> <p>“Boost your career”-Corner</p> <p><i>How to present your skillset when applying to industry</i></p> <p>Dala Egger SIB Swiss Institute of Bioinformatics, CH</p> |

Coffee break

Congress Center Basel, Foyer
15:15 – 15:45

[BC]² Closing Lecture and words

Congress Center Basel, Room Montreal
15:45 – 17:00

| Time | Talk |
|---------------|--|
| 15:45 – 16:45 | <p>KEYNOTE SPEAKER</p> <p>Nikolaus Rajewsky Max Delbrück Center for Molecular Medicine, DE</p> |
| 16:45 – 17:00 | Poster prize and closing words |

– END OF THE DAY –