BASEL LIFE PRESS RELEASE 2019 – FOR IMMEDIATE RELEASE

Next generation molecular medicine: unlocking big data for precision oncology and infectious disease

Basel, Switzerland, 2 July 2019 – Join the international [BC]² conference and EMBO meeting at BASEL LIFE from 9–12 September: a unique opportunity for today’s scientists to get insights and share the latest discoveries, resources and approaches to make sense of genomic and health-related “big data” for molecular medicine – from precision oncology to infectious diseases.

Advances in next generation sequencing mean we are now enjoying the era of the sub-1000-dollar genome, and the world’s genomic databases are expanding exponentially with primary sequence data from more and more individuals daily. These terabytes of genomic data, alongside the growing wealth of digital health records and clinical trials, bring invaluable insights into the biological mechanisms of human health, aging and disease.

In order to fully exploit these data, it is essential to foster the cross-disciplinary connections between computational and experimental approaches, and the transfer of state-of-the-art knowledge between the two areas. This is what the [BC]² Basel Computational Biology conference at BASEL LIFE sets out to do, through a series of workshops and plenary sessions detailing the current level status of research, discoveries and computational methods on “Big Data in Molecular Medicine”.

The [BC]² conference highlights five focus areas, with invited experts and selected speakers: single-cell data, evolutionary medicine, clinical population genomics, systems biology of disease, and multi-level data integration. These focus areas converge into three key themes:

From single-cell data analysis to precision oncology. Being able to identify and interpret the consequences of mutations in the individual cells of a tumour is key to classify the tumour’s stage, and to apply adequate therapies. Keynote speaker Peter Kharchenko, from the Harvard Medical School (US), studies tumour heterogeneity, as well as the interactions between tumour cells and their microenvironment – his talk will provide new insights on the joint analysis of heterogenous single-cell data collections.

From pathogen sequencing to fighting infectious diseases. Many diseases are caused by rapidly mutating pathogens (bacteria, fungi, viruses) which can eventually become drug resistant. Understanding the molecular properties of pathogens is thus essential when designing drugs and vaccines, and when allocating resources for the monitoring of disease outbreaks. Keynote speaker Roy Kishony, from Technion (Israel Institute of Technology, IL) combines experimental and theoretical approaches
on the evolution of pathogens and antibiotic resistance, and will present the latest views on predicting antibiotic resistance.

**Biological big data analysis and methods.** Big data from basic research is made up of many different sources and formats, including (but not limited to) RNA or DNA sequencing, genome-wide association studies, and mass spectrometry. Extracting useful information from these data requires tailored tools and methods, such as algorithms derived from machine learning. Keynote speaker and systems biologist **Yves Moreau** (KU Leuven, BE) studies how the genetic variation in a person’s genome can influence the risk or severity of a disease – he will talk about Bayesian matrix factorization and deep learning data fusion to predict drug-target interaction.

Selected presentations and posters will further highlight research and efforts to facilitate data-driven precision medicine and give scientists an unprecedented opportunity to learn from one another. Practical sessions will include tutorials on machine learning in the context of DNA sequencing and drug sensitivity prediction models, pathogen genome analysis strategies, and reproducible data management, curation and analysis.

For the complete scientific programme and to register for [BC]$^2$, including tutorials and workshops, visit: [www.basellife.org/2019](http://www.basellife.org/2019).

[registration link] [https://profile.congrex.com/Congrex/basellife2019](https://profile.congrex.com/Congrex/basellife2019)

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Notes to editors:

About [BC]^2

The [BC]^2 Basel Computational Biology Conference is one of the major bioinformatics events in Europe which takes place in Basel, Switzerland, every two years. Organised by the SIB Swiss Institute of Bioinformatics, it unites scientists working in a broad range of disciplines, including bioinformatics, computational biology and systems biology. In 2019, the conference will take place from 9 to 12 September in the framework of BASEL LIFE with a thematic focus on “Big Data in Molecular Medicine”. Through workshops, tutorials, keynote lectures and poster sessions, the conference will feature the latest research results and highlight the importance of bioinformatics in analysing biological big data to improve our understanding of human diseases and contribute to the development of new and targeted treatments.

About BASEL LIFE

BASEL LIFE is Europe’s leading congress in the Life Sciences, at the intersection between basic life sciences research, medical research, and cutting-edge technologies. It brings together multi-disciplinary, specialist scientific programmes, including EMBO at BASEL LIFE and the [BC]^2 computational biology conference, and takes place in Basel, at the heart of European’s Life Sciences landscape. BASEL LIFE unites 1000s of established life sciences researchers, offering talented young scientists and innovative exhibitors the opportunity to present their research, bringing together basic molecular, biomedical and clinical research, computational biology, artificial intelligence applications and innovation, creating new synergies in translational medicine and across the life sciences.
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