

## [BC]² Final report

### Index

1. [BC]² Conference summary .....	1
2. Scientific content .....	2
3. Travel fellowships .....	3

### 1. [BC]² Conference summary

The [BC]² Basel Computational Biology Conference is the main Swiss event in the area of Computational Biology and Bioinformatics. With its diverse programme featuring presentations of the latest scientific results, workshops, tutorials, poster sessions, and keynote lectures by international experts, it has also established itself as one of the major computational biology events in Europe uniting scientists from a diverse range of scientific domains and expertise.

In today's research environment, the interaction between Computational Biologists and Life Scientists has become key to the successful completion of scientific projects. Especially in the area of "Molecular and Precision Medicine", this interaction is indispensable. In 2019, the 14<sup>th</sup> edition of [BC]² has thus been organised as a pillar of BASEL LIFE - Europe's leading Congress in the Life Sciences - with a joined focus on "Advances in Molecular Medicine" and [BC]² itself highlighting the importance of "Big Data in Molecular Medicine".

[BC]² took place from 9-11 September 2019 at the Congress Center Basel. Together, around 430 international scientists from 30 countries were interested in joining [BC]². The event was organised by the Communication and Scientific Events Department of the SIB Swiss Institute of Bioinformatics, with Erik van Nimwegen (University of Basel & SIB) and Niko Beerenwinkel (ETHZ & SIB) as heads of the scientific committee.

The [BC]² scientific programme featured six keynote lectures by distinguished speakers, 30 presentations of selected abstracts, 85 poster presentations, seven tutorials, two workshops and two industry symposia. Together with this diverse programme, the joined lectures between the BASEL LIFE sister pillars [BC]², EMBO and Innovation Forums, and the possibility to easily switch between sessions of the different pillars, [BC]² 2019 has been a successful edition reflected by the high satisfactory level of participants. Furthermore, the organisation of joined industry symposia and the participation of several bioinformatics companies at the MipTec Industry Exhibition, show to which extent bioinformatic advances are important for Life Science research, and play an essential role in an applied context.

The complete conference programme can be found on the [\[BC\]² webpage](#) and the [BASEL LIFE webpage](#).

## 2. Scientific content

Organised under the main theme of “Big Data in Molecular Medicine”, the scientific programme has focused on three main key themes:

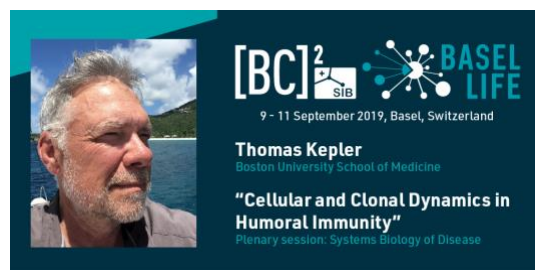
### 1. From single-cell data to precision oncology.

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. [BC]<sup>2</sup> thus featured a full session on “Single-cell Data” with [Peter Kharchenko](#), from the Harvard Medical School (USA) giving the opening lecture of this session.



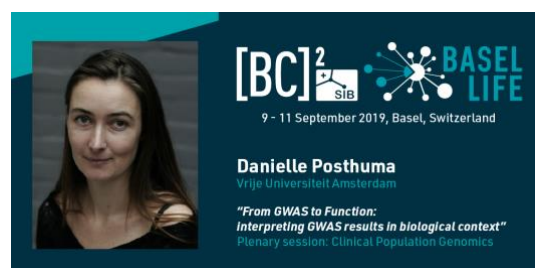
### 2. From pathogen sequencing to fighting infectious diseases.

Many diseases are caused by rapidly mutating pathogens (bacteria, fungi, viruses) which can eventually become drug resistant. Understanding the molecular properties of pathogens and how our body fights those is thus essential when designing drugs and vaccines, and when allocating resources for the monitoring of disease outbreaks. These aspects were addressed in the sessions on “Evolutionary Medicine” and “Systems Biology of Disease” with the respective opening lectures given by [Roy Kishony](#) (Technion – Israel Institute of Technology, ISR) and [Thomas Kepler](#) (Boston University School of Medicine, USA).

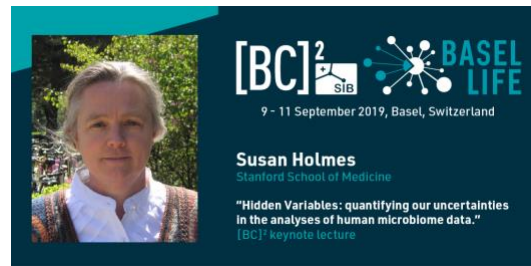


### 3. Biological big data analysis and methods.

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. The [BC]<sup>2</sup> sessions “Clinical Population Genomics” and “Multi-level Data Integration” with the keynote speakers [Danielle Posthuma](#) (Vrije Universiteit Amsterdam, NLD) and [Yves Moreau](#) (KU Leuven, BEL) touched on several of these aspects, further



discussed in the [BC]<sup>2</sup> keynote lecture on statistical challenges in microbiome data given by [Susan Holmes](#) (Stanford School of Medicine, USA).



In addition to the [BC]<sup>2</sup> plenary sessions, several joined sessions with the other pillars of BASEL LIFE were organised and included for example the opening and closing lectures, the poster session and flash talks as well as a joined session with EMBO on “Computational Biology, Artificial Intelligence and Machine Learning in Precision Medicine”.

The [BC]<sup>2</sup> programme includes traditionally also a tutorial and workshop programme, which is aimed at both beginner and advanced bioinformaticians. The field of bioinformatics is moving fast and making sure that researchers are trained in different methods belongs to one of SIB’s and [BC]<sup>2</sup>’s key missions to ensuring high-quality science. In 2019, seven tutorials and two workshops were organised covering a wide range of topics from data management, machine learning, pathogen genomes to single-cell analysis. They took place on Monday, 9 September at the Kollegienhaus at the University of Basel and attracted 169 participants.

**Feedback:** With 90% of participants rating the scientific content of BASEL LIFE either of excellent or good quality and almost 40% of participants joining exclusively [BC]<sup>2</sup> (data from the BASEL LIFE feedback survey), [BC]<sup>2</sup> has once again demonstrated its strength in assembling a diverse scientific programme at the edge of current research.

*“I came to attend this Bioinformatics Conference to update myself about the latest trends in this field.”*

Qaaifah Gillani Syed, PhD Student at University of Kashmir, India

*“The [BC]<sup>2</sup> Conference is highly timely.”*

Roy Kishony, Professor at Technion – Israel Institute of Technology, Israel

### 3. Travel fellowships

We would like thank ISB for supporting the 14<sup>th</sup> edition of the [BC]<sup>2</sup> conference by providing two travel fellowships. The fellowships allowed two early career researchers to attend the conference and to present their research in front of an international audience.

The two Laureates are:

- Qaaifah Gillani Syed, PhD Student at University of Kashmir, India ([Tweet](#))

Qaaifah presented her research on “*PCTAIRE1 kinase overcomes PolST induced mitotic arrest and cell death*” as **Flash Talk** and at the **Poster** session on Tuesday, 10 September.



- Zannatun Nayema, PhD Student at Kanazawa University, Japan ([Tweet](#))

Zannatun presented a poster entitled “*Genome-wide association study in Japanese cohort identifies variants near amylase genes associated with serum amylase level*” at the **Poster session** on Tuesday, 10 September.



We were able to meet Qaaifah and Zannatun in person at the [BC]<sup>2</sup> conference and both of them expressed their gratitude to ISB and the financial support that allowed them to participate at [BC]<sup>2</sup>.

Qaaifah is also featured in the [\[BC\]<sup>2</sup> video](#), which was produced at the conference.