

(Federating) Bioinformatics tools and resources

Providing bioinformatics infrastructure to the scientific community: Examples of networked tools and resources as well as their applications.

Provision of distributed bioinformatics infrastructure is on the rise, but how to leverage existing small tools and resources that are nevertheless widely used or foster interactions of tool and resource providers across national borders? How to mitigate risks such as personnel turnover or funding gaps? There are obviously no general solutions, but a few approaches will be discussed.

At the symposium there will be exciting talks from successful bioinformatics infrastructure providers and participants can enjoy nice food and networking in coffee breaks and at lunch.

[Sign up here!](#)

Symposium venue:

Novo Nordisk Foundation
Tuborg Havnevej 19 - 2900 Hellerup
NB! The symposium will be live streamed

On Thursday, 9 June 2022 the Novo Nordisk Foundation will host a workshop with the aim of bringing together the research community for an exciting day of knowledge sharing and networking around the topic of bioinformatics tools and resources. We will discuss on how to go beyond existing national bioinformatics infrastructures and how to leverage also smaller yet very useful resources.

Due to the exponentially increasing number of data in life sciences, Bioinformatics tools and resources become increasingly important for biomedical research. In Europe, in addition to services that are offered by the European Bioinformatics Institute (EBI) or the federated bioinformatics infrastructure ELIXIR, which taps into various national schemes, many other valuable bioinformatics services have been developed that are not on the radar of national or international infrastructures. The symposium will present a few and will enable discussions on how valuable and well-used tools and resources that started with little or still receive limited funding can be provided efficiently. One way is to federate them flexibly by being embedded in research groups, yet being interoperable and synergizing, evolving with new scientific challenges and discoveries. Some examples are discussed at the symposium.

Programme

09:15-09:45 Registration and coffee

09:45-10:00 Welcome by Senior Vice President Claus Felby, Novo Nordisk Foundation and Professor Bernard Henrissat, Chair of the Committee on the Novozymes Prize

10:00-10:25 Introduction by Peer Bork (EMBL-HD, DE) – Federated bioinformatics infrastructures and their applications

Keynote

10:25-10:55 Jo McEntyre (EMBL-EBI, UK) – Data resources at EMBL-EBI and their role in the ecosystem of European bioinformatics infrastructure and tools

10:55-11:25 Coffee break

Networks and data mining

11:25-11:50 Christian von Mering (Univ. Zurich, CH) - STRING and MicrobeAtlas: interaction networks at two distinct levels of organisation

11:50-12:15 Lars Juhl Jensen (CPR, DK) - Biomedical text mining: from literature to knowledge graphs

12:15-12:40 Takuji Yamada (Tokyo Univ., JP) – iPath and Enteropathway: Manually curated pathway diagram to interpret microbial function

12:40-13:40 Lunch

Organising molecular functions

13:40-14:05 Daniel Mende (Amsterdam UMC, NL) – One million microbial genomes and counting: challenges of big microbiology (Progenomes + specl)

14:05-14:30 Jaime Huerta Cepas (CSIC, ES) – Functional annotation and orthology assignments at the metagenomics scale (eggNOG-based resources)

14:30-14:55 Luis Pedro Coelho (Fudan Univ. CN/LU) – Analysing the microbiome at a global scale (GMGC & SemiBin)

Bioinformatics in population genetics and Cancer

14:55-15:20 Thea van Rossum (EMBL, DE) – Curated metadata catalogue of >66k metagenomes enables SNV-based subspecies detection (metalog & metaSNV)

15:20-15:45 Coffee break

15:45-16:20 Shamil Sunyaev (US) - Tools to predict the rate and the effect of mutations: multiple layers of tools and annotations.

16:20-16:45 Francesca Ciccarelli (UK) – Computational tools for a spatially resolved analysis of clinical samples

16:45-17:10 Jan Korbel (DE) - Data Science and AlphaDesign - de novo protein design based on AlphaFold

Examples of federated infrastructures

17:10-17:35 Roland Krause (Luxembourg Centre for Systems Biomedicine, University of Luxembourg) – Distributed genomics infrastructures for global research collaborations of the epilepsies

17:35-18:00 Rebecca Wade (Univ., Heidelberg, DE) – Distributed bioinformatics for the human brain project

18:00-18:10 Wrap up

18:10-19:00 Cocktails and discussion

Further information on the Novozymes Prize can be found [here](#).