Swiss South African - Bioinformatics Workshop and Symposium

20-21st and 23rd February 2017

The National Research Foundation and Swiss National Science Foundation through their Swiss-South Africa programme, have funded a project entitled: A context-based knowledge resource integrating HIV and Mtb molecular biology with host-pathogen and drug-resistance data. The collaborative project includes joint workshops and meetings. As part of the project, the University of Cape Town Computational Biology Division is hosting a short workshop and mini symposium.

Workshop

The workshop is aimed at biologists with little technical knowledge as well as bioinformaticians who want to learn more about the biological aspects of databases and metabolic modelling. All practicals will be web-based. The workshop will take place in the Health Science Wolfson Computer Lab which is located on the 7th level of Health Science Library at the medical school campus.

Monday 20th February 2017: **Data, databases, and annotation**

Trainer: Marc Feuermann, Swiss Institute of Bioinformatics

Morning: lectures

1-Introduction

From Wikipedia to biological databases: internet or the « infosphere »

2- Focus on biological databases

After an overview of what kind of databases can be found and how they are linked, we will focus our attention on few examples:

A) UniProtKB/Swiss-Prot and the ViralZone portal

B) Lipids

C) Reactions, pathways and metabolisms

3- Manual annotation/biocuration

How annotation feeds a database: overview of the work of a biocurator through the dissection of a *M. tuberculosis* UniProt-Swiss-Prot entry.

4- The flood of data

A tremendous amount of data is produced which cannot all be handled manually. Automatization is required, but to keep control of quality, the eye of a biocurator is still required: the example of HAMAP

5- The necessity of a coherent ontology:

    A) What is GO

    B) LEGO: a dynamical way to annotate ontology

    C) PAINT: Phylogenetic propagation of GO

Afternoon: Practicals

- Participants are welcome to prepare questions and examples of data they would like to search for, allowing free playing with the various databases and search tools available online.

- Live annotations of M. tuberculosis (or other pathogen) proteins in UniProtKB/Swiss-Prot (participants are welcome to bring their favorite protein for annotation).

- Creation/improvement of the ontology for M. tuberculosis (creation of specific terms with a clear definitions and relevant references).

Tuesday 21st February 2017: Modeling – Logical formalism from knowledgebase to models (IOX)

Trainer: Marco Pagni, Swiss Institute of Bioinformatics

Genome-Scale Metabolic Network: AKA Stoichiometric models (MP, morning)

- Mathematical foundations

- Flux Balance Analysis

- Practical session online at MetaNetX.org

Genome-scale models construction, annotation and applications (MP, afternoon)

- Review of some of the concepts seen the first day and how they specifically apply for model construction with some emphasis on chemistry

- Model validation against experimental data

- Practical session online at MetaNetX.org

Thursday 23rd February 2017

The aim of the symposium is to provide the opportunity for short talks from the Swiss Institute of Bioinformatics trainers and local researchers to showcase their work in the genomics (and other "omics") of pathogens, with a particular focus on *Mycobacterium tuberculosis*.

To apply to attend the workshop and register for the symposium please go to:

https://docs.google.com/forms/d/e/1FAIpQLSelFyNL6RMyHzZzoRv8xc_Fs1QGEYRYtP-V74PekBmtUKzt4A/viewform?c=0&w=1

Attendance at the workshops is free, but no shows will be charged, as we will be paying lunch costs.