Swiss South African Symposium on Pathogen Genomics
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 symposium on pathogen genomics. 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*.

Agenda

9:00	Welcome
09:20	**Ioannis Xenarious, Swiss Institute of Bioinformatics** Title TBD
09:45	**Gaston Mazandu CBIO, University of Cape Town, AIMS** A graph-based functional analysis of tuberculosis predicted targets using human and pathogen protein-protein interactions
10:10	**Ruben Cloete, South African National Bioinformatics Institute** Predicting the functional effect of variant in the TB drug metabolizing enzyme, NAT1.
10:35	Coffee break
11:00	**Alan Christoffels, South African National Bioinformatics Institute** COMBAT-TB- computational bacterial analytical toolkit for Tuberculosis research.
11:25	**Anzaan Dippenaar, Stellenbosch University** Investigating recurrence of tuberculosis due to relapse and reinfection using whole genome sequencing
11:50	**Jon Ambler, CBIO, University of Cape Town** Variant calling in the context of graph genomes
12:15	**Ruth McNerney, honorary position as Associate Professor in the Division of Pulmonology, Department of Medicine, University of Cape Town** Towards NGS as a reliable diagnostic tool for drug resistance
12:40	Lunch
13:45	**Marisa Klopper, Stellenbosch University** Hidden ethionamide resistance as a drives beyond-XDR-TB epidemic in a high burden setting.
14:10	**Marc Feuermann, Swiss Institute of Bioinformatics** M. tuberculosis annotation at SIB

14:35	**Nelson Soares, University of Cape Town**
	Mycobacterial phosphoproteome profiling for the discovery of novel Ser/Thr protein kinases substrates
15:00	**Matthys Potgieter, CBIO, University of Cape Town**
	Multistrain proteogenomic analysis of lab strains and clinical isolates of *Mycobacterium tuberculosis* - comparing H37Rv to a clinical isolate
15:25	Coffee break
15:50	**Anastasia Koch, CIDRI, University of Cape Town**
	The impact of HIV-1 on the evolution of *Mycobacterium tuberculosis*.
16:15	**Tulio de Oliviera, University of Kwazulu Natal, Africa Centre**
	Title TBD
16:40	**Marco Pagni, Swiss Institute of Bioinformatics**
	Recent advances in fungal Bioinformatics to bring together genome, transcriptome and metabolism
17:05	Wrap up and discussion