

METAGENOMICS AND METATRANSCRIPTOMICS WORKSHOP

Venue: Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa

Date: 22-26 October 2018

Presenters: Dr. Maria Vivas - FABI, University of Pretoria, South Africa
Dr. Martin Kemler - Ruhr-University Bochum, Germany
Dr. Richard Allen White III - Washington State University, USA

Monday 22 October 2018: Basic introduction

09:30 - 12:00 Introduction to Linux commands
Introduction R / ggplot / tidyverse, notebooks
12:00 - 13:30 Lunch break
13:30 - 16:30 Introduction python
Introduction to databases - SQL
Reproducible research

Tuesday 23 October 2018: Metabarcoding

08:30 - 12:00 Advantages and disadvantages of marker assisted community analysis
Short overview of library preparations for NGS community analysis
Quality control of NGS data for community analysis
Introduction to QIIME
12:00 - 13:30 Lunch break
13:30 - 16:30 OTU clustering and taxonomic assignment
Preparing OTU tables for downstream analysis

Wednesday 24 October 2018: Biodiversity analysis in R

08:30 - 12:00 What is biodiversity?
Relative abundance: common and rare species
Species richness
Diversity indices
Differences in species composition
12:00 - 13:30 Lunch break
13:30 - 15:30 Data analysis using Phyloseq and Vegan packages
16:00 - 17:30 Special seminar by Dr. Richard Allen White III

Thursday 25-10-2018: Genome (core/pan), metagenomic analyses

08:30 - 12:00 Genomic analysis - core/pan, assembly, annotation
12:00 - 13:30 Lunch break
13:30 - 16:30 Genome resolved metagenomic analysis

Friday 26-10-2018: Metatranscriptomic analysis

08:30 - 12:00 Metatranscriptomic analysis pipelines
12:00 - 13:30 Lunch break
13:30 - 16:30 Wrap-up and feedback