EDU session programme

Bioinformatic Team

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September 25th 2020

Microbiome Bioinformatics with MRC 16S rRNA Pipeline-A singularity version

Members of the bioinformatics team will teach a one-day workshop on bioinformatics tools for microbiome analysis. This workshop will introduce bioinformatic tools and concepts used for sequencing analysis using UNSW's computational Cluster, Katana. The workshop will include lectures covering QIIME 2 usage and theory, and interactive work with the MRC 16S rRNA Pipeline to perform microbiome analysis from raw sequence data through publication-quality statistics and visualizations.

Topics will include:

- Introduction to HPC and Linux commands
- Core microbiome concepts
- QIIME 2 types, formats, and metadata
- Quality control of Miseq Pair-end 16S sequences
- Taxonomic analysis

- Phylogenetic tree reconstruction
- Measuring alpha and beta diversity
- Differential abundance analysis

Required software

Prior to session please download the following SFTP tool:

1. Iterm (Mac) or mobaxterm (Windows)
2. Download SFTP client FileZilla (Windows and Mac)

Preparing for the workshop

Linux command line will be used during the hands-on portion of the workshop. Introduce yourself to basic linux command using an online course. A cheatsheet that might help on the day can be found here

Schedule	
	Introduction to Linux command lines and HPC katana
10:00 am - 10:30 am	Data transfer between sever and local computer
	Questions
	Introduction of important concepts for microbiome analysis
10:40 am - 12:00 am	High fat diet demo data set
	Quality assessment with fastp and control with dada2
Lunch break	
	Taxonomical annotation and phylogenetic tree construction
1:30 pm-2:30 pm	Rarefaction analysis, core alpha and beta diversity
short break	
2:40 pm - 3:00 pm	Differential abundant analysis with LEfSe