Pathogen detection from (direct Nanopore) sequencing data using Galaxy - Foodborne Edition Metatranscriptomics analysis using microbiome RNA-seq data Metatranscriptomics analysis using microbiome RNA-seq data (short) Bacterial Genome Annotation Identification of AMR genes in an assembled bacterial genome Analyses of metagenomics data - The global picture 16S Microbial Analysis with mothur (extended) 16S Microbial Analysis with mothur (short) Microbial Variant Calling Genome annotation with Prokka Refining Genome Annotations with Apollo (prokaryotes) Metaproteomics tutorial Binning of metagenomic sequencing data Tree thinking for tuberculosis evolution and epidemiology metaQuantome 2: Function metaQuantome 3: Taxonomy Making sense of a newly assembled genome Comparative gene analysis in unannotated genomes Calling variants in non-diploid systems metaQuantome 1: Data creation Building an amplicon sequence variant (ASV) table from 16S data using DADA2 Essential genes detection with Transposon insertion sequencing Assembly of metagenomic sequencing data Antibiotic resistance detection Genome Assembly of MRSA from Oxford Nanopore MinION data (and optionally Illumina data) Genome Assembly of a bacterial genome (MRSA) sequenced using Illumina MiSeq Data Unicycler Assembly 16S Microbial analysis with Nanopore data Identification of the micro-organisms in a beer using Nanopore sequencing Taxonomic Profiling and Visualization of Metagenomic Data Checking expected species and contamination in bacterial isolate Quality and contamination control in bacterial isolate using Illumina MiSeq Data Identifying tuberculosis transmission links: from SNPs to transmission clusters M. tuberculosis Variant Analysis

Galaxy Tool Suites