Tutorials (y-axis):
- 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

X-axis label: Galaxy Tool Suites