

	Sequencing quality control	Visualisation	Taxonomic classification	Statistical calculation	Other	
Pathogen detection from (direct Nanopore) sequencing data using Galaxy - Foodborne Edition						Sequence analysis
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)						
Comparative gene analysis in unannotated genomes						
Calling variants in non-diploid systems						
Building an amplicon sequence variant (ASV) table from 16S data using DADA2						
Essential genes detection with Transposon insertion sequencing						
Antibiotic resistance detection						
16S Microbial analysis with Nanopore data						
Identification of the micro-organisms in a beer using Nanopore sequencing						
Taxonomic Profiling and Visualization of Metagenomic Data						
Pathogen detection from (direct Nanopore) sequencing data using Galaxy - Foodborne Edition						Taxonomy
Metatranscriptomics analysis using microbiome RNA-seq data						
Metatranscriptomics analysis using microbiome RNA-seq data (short)						
Analyses of metagenomics data - The global picture						
16S Microbial Analysis with mothur (extended)						
16S Microbial Analysis with mothur (short)						
Metaproteomics tutorial						
metaQuantome 3: Taxonomy						
metaQuantome 1: Data creation						
Building an amplicon sequence variant (ASV) table from 16S data using DADA2						
16S Microbial analysis with Nanopore data						
Identification of the micro-organisms in a beer using Nanopore sequencing						
Taxonomic Profiling and Visualization of Metagenomic Data						
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Identification of AMR genes in an assembled bacterial genome						
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Genome annotation with Prokka						
Refining Genome Annotations with Apollo (prokaryotes)						
Tree thinking for tuberculosis evolution and epidemiology						
Making sense of a newly assembled genome						
Comparative gene analysis in unannotated genomes						
Calling variants in non-diploid systems						
Essential genes detection with Transposon insertion sequencing						Genomics
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						
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						
Bacterial Genome Annotation						
Identification of AMR genes in an assembled bacterial genome						
Microbial Variant Calling						
Genome annotation with Prokka						
Refining Genome Annotations with Apollo (prokaryotes)						
Tree thinking for tuberculosis evolution and epidemiology						
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