

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