

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