

|   | Visualisation | Sequencing quality control | Taxonomic classification | Statistical calculation | Other |
|---|---------------|----------------------------|--------------------------|-------------------------|-------|
| pathogen-detection-pathogfair-samples-aggregation-and-visualisation/main<br>mgnify-amplicon-pipeline-v5-quality-control-single-end/main<br>influenza-isolates-consensus-and-subtyping/main<br>sars-cov-2-pe-illumina-artic-ivar-analysis/SARS-COV-2-ILLUMINA-AMPLICON-IVAR-NG-variant-calling/main<br>generic-non-segmented-viral-variant-calling/main<br>pox-virus-amplicon/main<br>sars-cov-2-pe-illumina-wgs-variant-calling/COVID-19-PE-WGS-ILLUMINA<br>mgnify-amplicon-pipeline-v5-quality-control-paired-end/main<br>allele-based-pathogen-identification/main<br>gene-based-pathogen-identification/main<br>amr_gene_detection/main<br>clinicalmp-discovery/main<br>clinicalmp-quantitation/main<br>clinicalmp-data-interpretation/main<br>mgnify-amplicon-pipeline-v5-complete/main<br>dada2/main<br>bacterial_genome_annotation/main<br>bacterial_genome-assembly/main<br>clinicalmp-verification/main<br>clinicalmp-database-generation/main<br>mgnify-amplicon-pipeline-v5-rna-prediction/main<br>mgnify-amplicon-pipeline-v5-fits/main<br>bacterial-quality-and-contamination-control-post-assembly/main<br>quality-and-contamination-control/main<br>taxonomy-profiling-and-visualization-with-krona/main  |               |                            |                          |                         |       |
| Workflow 6: Alpha Diversity [16S Microbial Analysis With Mothur]<br>Workflow 5: OTU Clustering [16S Microbial Analysis With Mothur]<br>Workflow 3: Classification [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 2: Data Cleaning And Chimera Removal [16S Microbial Analysis With Mothur]<br>Workflow 1: Further Quality Control [16S Microbial Analysis With Mothur]<br>Workflow 7: Beta Diversity [16S Microbial Analysis With Mothur]<br>TB Variant Analysis v1.0<br>2: Plant virus confirmation<br>3: Plant virus exploration<br>Workflow 3: AMR - SeqSero2/SISTR<br>AMR-Pathfinder<br>Workflow 4: Saramr<br>Refining Genome Annotations with Apollo (prokaryotes)<br>Workflow 1: AbritAMR<br>Taxonomy classification using Kraken2 and Bracken<br>1: Plant virus detection with kraken2 (PE)<br>1: Plant virus detection with kraken2 (SE)<br>Analyses of shotgun metagenomics data with MetaPhlAn2  |               |                            |                          |                         |       |
| Cloud-Aerosole MT-MG Functional Profiling<br>pAlori Blood<br>MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.3)<br>MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.2)<br>MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.1)<br>Cloud-Aerosole MT-MG Pre-Processing<br>MGnify's amplicon pipeline v5.0 - Quality control PE (release v0.2)<br>MGnify's amplicon pipeline v5.0 - Quality control PE (release v0.1)<br>Nanopore Preprocessing (release v0.3)<br>Allele-based Pathogen Identification (release v0.4.3)<br>Allele-based Pathogen Identification (release v0.4.4)<br>Flye-AMR workflow EMC/WMDI - v3.5 (imported from URL)<br>ASaiM-MT: Metatranscriptomics Analysis of Microbes<br>MetaProteomics workflow<br>metaQuantome_datacreation_workflow<br>Comparative gene analysis<br>Halophiles workup of Comparative gene analysis<br>Apollo Load test<br>MetaG: Preparation, Building and Annotation of Metagenomics Assembled Genomes<br>MetaT: Metatranscriptomics data analysis<br>pAlori Amplicon 16S Pre-Processing and Taxonomy Classification<br>metaquantome-function-workflow<br>From BAMs to drug resistance prediction with TB-profiler<br>From Fastqs to VCFs and BAMs<br>MGnify's amplicon pipeline v5.0 - ITS (release v0.1)<br>MGnify's amplicon pipeline v5.0 - ITS (release v0.2)<br>Cloud Aerosol MT-MG Contamination Filtering<br>Metagenomic Taxonomy and Functional Analysis   |               |                            |                          |                         |       |
| Workflow 6: Alpha Diversity [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 5: OTU Clustering [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 4: Mock OTU Clustering [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 3: Classification [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 2: Data Cleaning And Chimera Removal [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Workflow 1: Quality Control [Galaxy Training: 16S Microbial Analysis With Mothur]<br>Amplicon Tutorial<br>Training: 16S rRNA Sequencing With Mothur: Main Tutorial<br>Workflow 7: Beta Diversity [Galaxy Training: 16S Microbial Analysis With Mothur]<br>MGnify's amplicon pipeline v5.0 - Quality control SE<br>MGnify's amplicon pipeline v5.0 - Quality control PE<br>TB Variant Analysis v1.0<br>Training: 16S rRNA Analysis with Nanopore Sequencing Reads<br>Copy Of GTN Training - Antibiotic Resistance Detection<br>GTN Training - Antibiotic Resistance Detection<br>taxonomic Analysis of eDNA<br>Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 1: Preprocessing<br>Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 3: Functional Information (quick)<br>Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 3: Functional Information (quick)<br>MGnify's amplicon pipeline v5.0<br>Building an amplicon sequence variant (ASV) table from 16S data using DADA2<br>Assembly of metagenomic sequencing data<br>Workflow for Identifying MF from ITS2 sequencing using Lotus2 - tutorial example run<br>pox-virus-tied-amplicon-ref-masking<br>MGnify's amplicon pipeline v5.0 - rRNA prediction<br>MGnify's amplicon pipeline v5.0 - ITS<br>Checking expected species and contamination in bacterial isolate<br>Quality and contamination control in bacterial isolate using Illumina MiSeq Data<br>Calculating diversity from microbiome taxonomic data<br>Identification of the micro-organisms in a beer using Nanopore sequencing<br>Taxonomic Profiling and Visualization of Metagenomic Data<br>WGS Part I in "Analyses Of Metagenomics Data - The Global Picture"<br>Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 2: Community profile |               |                            |                          |                         |       |

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