

	Visualisation	encing quality co	omic classifi	tistical calculat	Validation	ontaminati	omposition	netic a	arc	re-proc	ence trim	Formatting	a :4	Other	
GTN Training - Antibiotic Resistance Detection TB Variant Analysis v1.0															Microbiology
Analyses of shotgun metagenomics data with MetaPhlAn2 Taxonomy classification using Kraken2 and Bracken															Metagenomics
Taxonomy classification using Kraken2 and Bracken															Taxonomv
Analyses of shotgun metagenomics data with MetaPhlAn2															Metagenomic sequencing
TB Variant Analysis v1.0															Genetic variation
TB Variant Analysis v1.0															Infectious disease
TB Variant Analysis v1.0															Public health and epidemiology
TB Variant Analysis v1.0															Sequence assembly
Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 2: Community profile WGS Part In ""Analyses Of Metagenomics Data - The Global Picture"" 1: Plant virus detection with kraken2 (SE) 1: Plant virus detection with kraken2 (PE) Taxonomic Profiling and Visualization of Metagenomic Data taxonomy-profiling-and-visualization-with-krona/main Identification of the micro-organisms in a beer using Nanopore sequencing Metagenomic Taxonomy and Functional Analysis Calculating diversity from microbiome taxonomic data quality-and-contamination-control/main Quality and contamination control in bacterial isolate using Illumina MiSeq Data bacterial-quality-and-contamination-control-post-assembly/main Cloud Aerosol MT-MG Contamination Filtering Checking expected species and contamination in bacterial isolate MGnify's amplicon pipeline v5.0 - ITS (release v0.2) MGnify's amplicon pipeline v5.0 - ITS (release v0.1) mgnify-amplicon-pipeline-v5-its/main MGnify's amplicon pipeline v5.0 - ITS mgnify-amplicon-pipeline-v5-rrna-prediction/main MGnify's amplicon pipeline v5.0 - rRNA prediction From Fastqs to VCFs and BAMs From BAMs to drug resistance prediction with TB-profiler Workflow 1: AbrisAMR clinicalmp-database-generation/main clinicalmp-verification/main metaquantome-function-workflow pox-virus-tiled-amplicon-ref-masking pAllori Amplicon 16S Pre-Processing and Taxonomy Classification Workflow for Identifying MF from ITS2 sequencing using LotuS2 - tutorial example run' bacterial-genome-assembly/main Assembly of metagenomic sequencing data bacterial_genome_annotation/main MetaT: Metatranscriptomics data analysis MetaG: Preparation, Building and Annotation of Metagenomics Assembled Genomes dada2/main Building an amplicon sequence variant (ASV) table from 16S data using DADA2 Refining Genome Annotations with Apollo (prokaryotes) Apollo Load Test Halophiles workup of Comparative gene analysis Comparative gene analysis mgnify-amplicon-pipeline-v5-complete/main MGnify's amplicon pipeline v5.0 Workflow 3: Functional Information (quick) Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 3: Functional Information metaQuantome_datacreation_workflow Metaproteomics workflow clinicalmp-data-interpretation/main clinicalmp-quantitation/main clinicalmp-discovery/main Metatranscriptomics analysis using microbiome RNA-seq data ASaiM-MT: Metatranscriptomics Analysis of Microbes Metatranscriptomics analysis using microbiome RNA-seq data - Workflow 1: Preprocessing Workflow 4: Staramr AMR-Pathfinder amr_gene_detection/main Workflow 3: AMR - SeqSero2/SISTR 3: Plant virus exploration 2: Plant virus confirmation Taxonomic Analysis of eDNA gene-based-pathogen-identification/main Flye-AMR workflow EMC/WMDI - v3.5 (imported from URL) Copy Of GTN Training - Antibiotic Resistance Detection Allele-based Pathogen Identification (release v0.1.4) Allele-based Pathogen Identification (release v0.1.3) allele-based-pathogen-identification/main Training: 16S rRNA Analysis with Nanopore Sequencing Reads Nanopore Preprocessing (release v0.1) TB Variant Analysis v1.0 MGnify's amplicon pipeline v5.0 - Quality control PE (release v0.1) MGnify's amplicon pipeline v5.0 - Quality control PE MGnify's amplicon pipeline v5.0 - Quality control PE (release v0.2) mgnify-amplicon-pipeline-v5-quality-control-paired-end/main sars-cov-2-pe-illumina-wgs-variant-calling/COVID-19-PE-WGS-ILLUMINA pox-virus-amplicon/main generic-non-segmented-viral-variant-calling/main sars-cov-2-pe-illumina-artic-ivar-analysis/SARS-COV-2-ILLUMINA-AMPLICON-IVAR-PANGOLIN-NEXTCLADE influenza-isolates-consensus-and-subtyping/main MGnify's amplicon pipeline v5.0 - Quality control SE Cloud-Aerosole MT-MG Pre-Processing MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.1) MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.2) MGnify's amplicon pipeline v5.0 - Quality control SE (release v0.3) mgnify-amplicon-pipeline-v5-quality-control-single-end/main pAllori Blood RNA Cloud-Aerosole MT-MG Functional Profiling Workflow7: Beta Diversity [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 7 : Beta Diversity [16S Microbial Analysis With Mothur] Training: 16S rRNA Sequencing With Mothur: Main Tutorial pathogen-detection-pathogfair-samples-aggregation-and-visualisation/main Workflow 1: Further Quality Control [16S Microbial Analysis With Mothur] Amplicon Tutorial Workflow 1: Quality Control [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 2: Data Cleaning And Chimera Removal [16S Microbial Analysis With Mothur] Workflow 2: Data Cleaning And Chimera Removal [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 3: Classification [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 4: Mock OTU Clustering [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 5: OTU Clustering [16S Microbial Analysis With Mothur] Workflow 5: OTU Clustering [Galaxy Training: 16S Microbial Analysis With Mothur] Workflow 6: Alpha Diversity [16S Microbial Analysis With Mothur] Workflow 6: Alpha Diversity [Galaxy Training: 16S Microbial Analysis With Mothur]															Other

