Figure: Heatmap of Galaxy Tool Suites usage across Workflows, organised into categories (Visualisation, Sequencing quality control, Taxonomic classification, IA barcodi, Other) along the x-axis, with workflow groupings (Metagenomics, Microbiology, Taxonomy, Metagenomic sequencing, Other) along the y-axis.

Column group headers (top): Visualisation | Sequencing quality control | Taxonomic classification | IA barcodi | Other

Row group headers (right): Metagenomics | Microbiology | Taxonomy | Metagenomic sequencing | Other

Axis labels: Workflows (y-axis) | Galaxy Tool Suites (x-axis)

Top workflow rows:
- Taxonomy classification using Kraken2 and Bracken
- Analyses of shotgun metagenomics data with MetaPhlAn2
- GTN Training - Antibiotic Resistance Detection
- Taxonomy classification using Kraken2 and Bracken
- Analyses of shotgun metagenomics data with MetaPhlAn2

Lower workflow rows:
- 3: Plant virus exploration
- 2: Plant virus confirmation
- bacterial-genome-assembly/main
- Workflow 4: Staramr
- AMR-Pathfinder
- amr_gene_detection/main
- Copy Of GTN Training - Antibiotic Resistance Detection
- Flye-AMR workflow EMC/WMDI - v3.5 (imported from URL)
- MetaT: Metatranscriptomics data analysis
- ASaiM-MT: Metatranscriptomics Analysis of Microbes
- MetaG: Preparation, Building and Annotation of Metagenomics Assembled Genomes
- MAGs building with individual assembly
- Apollo Load Test
- Allele-based Pathogen Identification (release v0.1.2)
- Building an amplicon sequence variant (ASV) table from 16S data using DADA2
- From BAMs to drug resistance prediction with TB-profiler
- From Fastqs to VCFs and BAMs
- Workflow 3: Functional Information (quick)
- Workflow for Identifying MF from ITS2 sequencing using LotuS2 - tutorial example run'
- bacterial_genome_annotation/main
- metaquantome-function-worklow
- metaQuantome_datacreation_workflow
- Metaproteomics workflow
- Halophiles workup of Comparative gene analysis
- Comparative gene analysis
- MGnify's amplicon pipeline v5.0 - Quality control SE
- Cloud-Aerosole MT-MG Pre-Processing
- pAllori Blood RNA
- Cloud-Aerosole MT-MG Functional Profiling
- pox-virus-amplicon/main
- MGnify's amplicon pipeline v5.0 - Quality control PE
- Training: 16S rRNA Analysis with Nanopore Sequencing Reads
- Identification of the micro-organisms in a beer using Nanopore sequencing
- pAllori Amplicon 16S Pre-Processing and Taxonomy Classification
- Taxonomic Profiling and Visualization of Metagenomic Data
- Metagenomic Taxonomy and Functional Analysis
- quality-and-contamination-control/main
- Cloud Aerosol MT-MG Contamination Filtering
- WGS Part In ""Analyses Of Metagenomics Data - The Global Picture""
- 1: Plant virus detection with kraken2 (SE)
- 1: Plant virus detection with kraken2 (PE)
- MGnify's amplicon pipeline v5.0 - rRNA prediction
- MGnify's amplicon pipeline v5.0 - ITS
- 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
- 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]

Right-side category label (lower): Other