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Graz

*Pioneering Minds*

# Galaxy

Web-based Platform for  
Reproducible Data Analysis

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# What is Galaxy?

- ▶ Open Source web-based **data analysis** platform designed mostly for bioinformatics genomic analysis
- ▶ Cross-domain: chemistry, ecology, climate science, ..
- ▶ It's **easy to use** - doesn't require any programming knowledge
- ▶ Galaxy **Tool Shed** repository - 8000 ready to install tools
- ▶ Retains of all analysis details in **histories**
- ▶ Makes your research **reproducible and sharable**

# Galaxy World Wide

- ▶ **Big Community**, mainly located in Freiburg, Germany
- ▶ Three big Galaxy Instances: **Galaxy Main** ([usegalaxy.org](https://usegalaxy.org)), **Galaxy Europe** ([usegalaxy.eu](https://usegalaxy.eu)), **Galaxy Australia** ([usegalaxy.org.au](https://usegalaxy.org.au))
- ▶ Around **170 Galaxy Instances** - some of them domain specialized in particular types of analysis
- ▶ Extensive **tutorials** available for very different types of data analysis ([training.galaxyproject.org](https://training.galaxyproject.org) )

# Galaxy at MedUni Graz

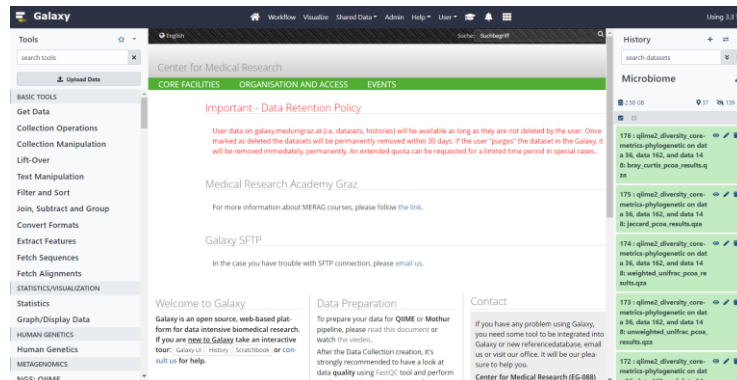


- ▶ [galaxy.medunigraz.at](https://galaxy.medunigraz.at) (Galaxy Austria [usegalaxy.at](https://usegalaxy.at))
- ▶ Accessible for MedUni members only, externals per request
- ▶ Data and analysis remain in-house and under your account
- ▶ Larger storage space
- ▶ It's extendable with custom tools and workflows (eg. Microbiome)
- ▶ Fast local support
- ▶ Easy to share with collaborators

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- The diagram illustrates a QIIME 2 workflow for analyzing sequencing data. It consists of 21 numbered steps, each represented by a blue box with a title and a list of options and requirements. The workflow is highly interconnected, with many steps having multiple inputs and outputs.
- 1. Mapping file**: output (input)
  - 2. Input dataset collection**: output (input)
  - 3. QIIME feature-classifier extract-reads**: QIIME feature-classifier extract-reads on input dataset(s); reads.qza (zqa)
  - 4. QIIME tools import**: Fastq pairs (collection); QIIME tools import on input dataset(s)
  - 5. Count sequences**: Fastq pairs (collection); Count sequences on input dataset(s); sequence
  - 6. QIIME feature-classifier fit-classifier-naive-bayes**: Reference reads; ARTACT FeatureData[Sequence] (required); -i class-weight: ARTACT FeatureTable[RelativeFrequency] (optional); QIIME feature-classifier fit-classifier-naive-bayes on input dataset(s); classifier.qza (zqa)
  - 7. QIIME demux summarize**: -i data: ARTACT SampleData[SequencesWithQuality]; PairedEndSequencesWithQuality; JoinedSequencesWithQuality; The demultiplexed sequences to be summarized. (required); QIIME demux summarize on input dataset(s); visualization.qza (item)
  - 8. QIIME dada2 denoise-paired**: Mapping file where 3rd and 4th columns must be forward and reverse primers respectively; Summary file; -i demultiplexed-seqs: ARTACT SampleData[PairedEndSequencesWithQuality]; The paired and demultiplexed sequences to be denoised (required); QIIME dada2 denoise-paired on input dataset(s); table.qza (zqa); QIIME dada2 denoise-paired on input dataset(s); representative-sequences.qza (zqa); QIIME dada2 denoise-paired on input dataset(s); denoising-table.qza (zqa)
  - 9. QIIME metadata tabulate**: -m input file 1 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (required); -m input file 2 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (optional); -i table: ARTACT FeatureTable[Frequency] RelativeFrequency; Pseudocounts: The feature table to be summarized. (required); -m metadata file 1 ~ -m: sample metadata file (multiple arguments will be merged). The sample metadata. (required); QIIME feature-table summarize
  - 10. QIIME feature-table summarize**: -i table: ARTACT FeatureTable[Frequency] RelativeFrequency; Pseudocounts: The feature table to be summarized. (required); -m metadata file 1 ~ -m: sample metadata file (multiple arguments will be merged). The sample metadata. (required); QIIME feature-table summarize
  - 11. QIIME feature-classifier classify-sklearn**: Reference classifier; -i reads: ARTACT FeatureData[Sequence] The feature data to be classified. (required); QIIME feature-classifier classify-sklearn on input dataset(s); classification.qza (zqa)
  - 12. QIIME alignment mafft**: -i sequences: ARTACT FeatureData[Sequence] The sequences to be aligned. (required); QIIME alignment mafft on input dataset(s); masked-alignment.qza (zqa)
  - 13. QIIME feature-table tabulate-seqs**: -i data: ARTACT FeatureData[Sequence] The feature sequences to be tabulated. (required); QIIME feature-table tabulate-seqs on input dataset(s); visualization.qza (item)
  - 14. Merge feature table and taxonomy**: Feature table; taxonomy; QIIME merge feature table and taxonomy on input dataset(s); biom\_and\_tax\_merged\_biom (zqa)
  - 15. QIIME metadata tabulate**: -m input file 1 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (required); -m input file 2 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (optional); -i table: ARTACT FeatureTable[Frequency] FeatureTable to visualize at various taxonomic levels. (required); -m metadata file (required); -m metadata file 1 ~ -m: metadata file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (required); -i table: ARTACT FeatureTable[Frequency] FeatureTable to visualize at various taxonomic levels. (required); QIIME metadata tabulate
  - 16. QIIME taxa export**: Reference database; -i table: ARTACT FeatureTable[Frequency] FeatureTable to visualize at various taxonomic levels. (required); -m metadata file (required); -m metadata file 1 ~ -m: metadata file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (required); QIIME taxa export
  - 17. QIIME alignment mask**: -i alignment: ARTACT FeatureData[AlignedSequence] The alignment to be masked. (required); QIIME alignment mask on input dataset(s); masked-alignment.qza (zqa)
  - 18. Convert BIOM to Tabular File**: Input table (BIOM); tabular\_biom2 (zqa)
  - 19. QIIME phylogeny feature-table**: -i alignment: ARTACT FeatureData[AlignedSequence] Aligned sequences to be used for phylogenetic reconstruction. (required); QIIME phylogeny feature-table on input dataset(s); tree.qza (zqa); -i path to input biom file (optional); output: fy (txt)
  - 20. QIIME phylogeny feature-table**: -i alignment: ARTACT FeatureData[AlignedSequence] Aligned sequences to be used for phylogenetic reconstruction. (required); QIIME phylogeny feature-table on input dataset(s); tree.qza (zqa); -i path to input biom file (optional); output: fy (txt)
  - 21. QIIME metadata tabulate**: -m input file 1 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (required); -m input file 2 ~ -m: input file: Metadata file or artifact viewable as metadata. This option may be supplied multiple times to merge metadata. The metadata to tabulate. (optional); -i tree: ARTACT Phylogeny[Unrooted] The phylogenetic tree to be rooted. (required); QIIME phylogeny midpoint-root on input dataset(s); root-tree.qza (zqa)

# Galaxy at MedUni Graz

Database/Storage System  
(Postgres, CEPH, SSD)



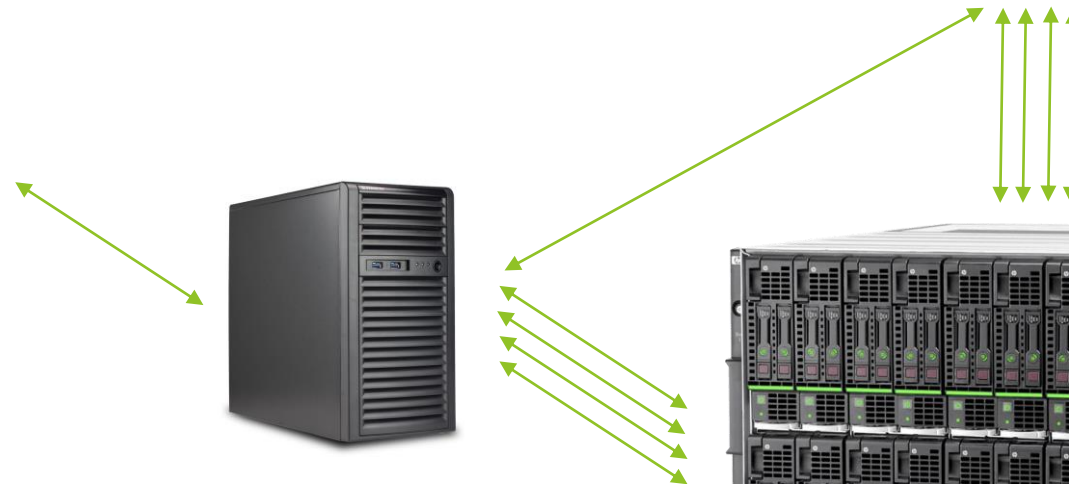
Web Interface  
(Chrome)



Web Server  
(Nginx)



Computing Nodes  
(SLURM)



# Live demo

- ▶ How to get into Galaxy
- ▶ Data importing and manipulation
- ▶ Analysis histories
- ▶ Creating and using workflows
- ▶ Creating pages
- ▶ Visualizations
- ▶ Data Sharing



Thank you 😊

Live demo...

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