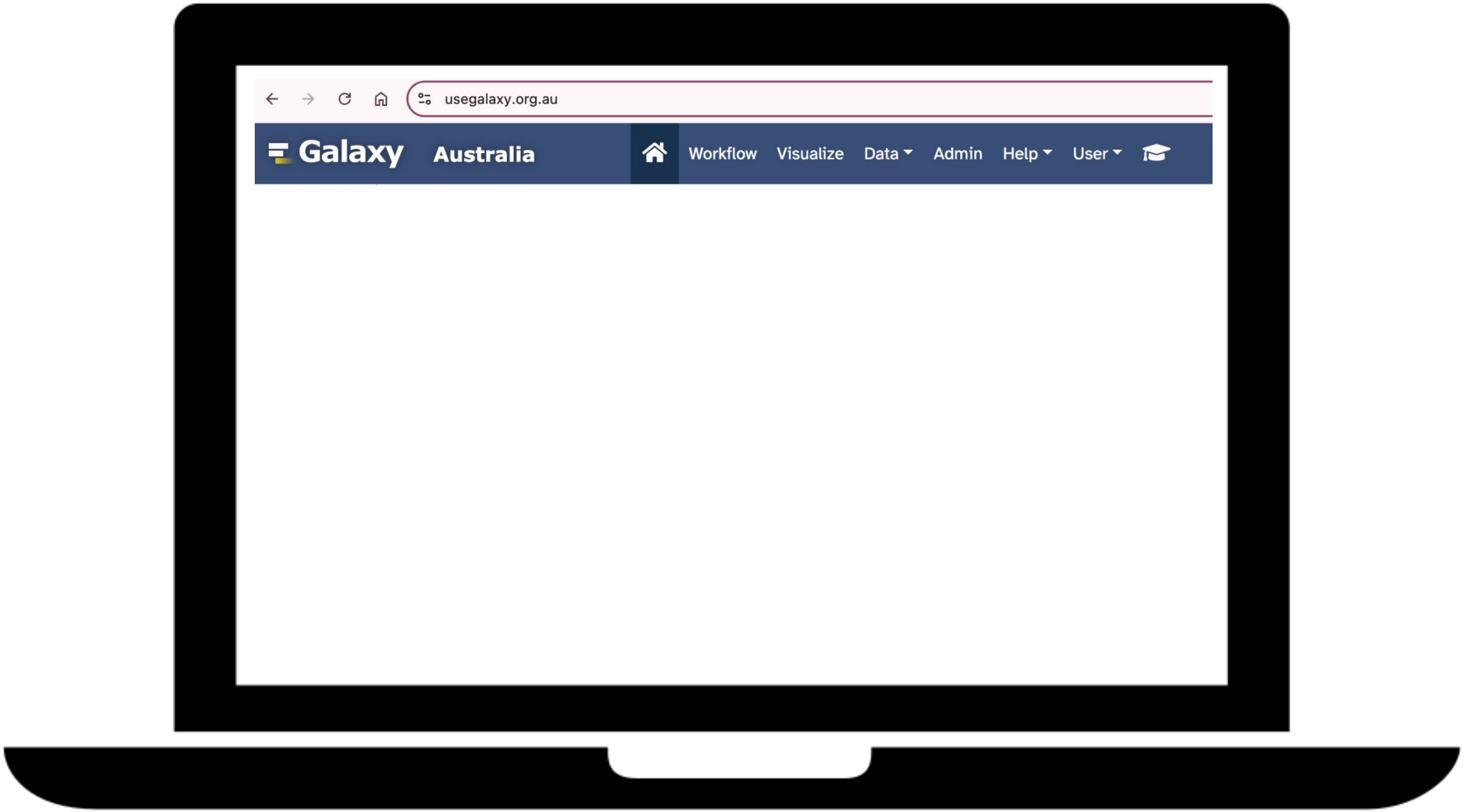
Galaxy tutorials: overview

Fungi Bioinformatics Workshop, Canberra, October 2024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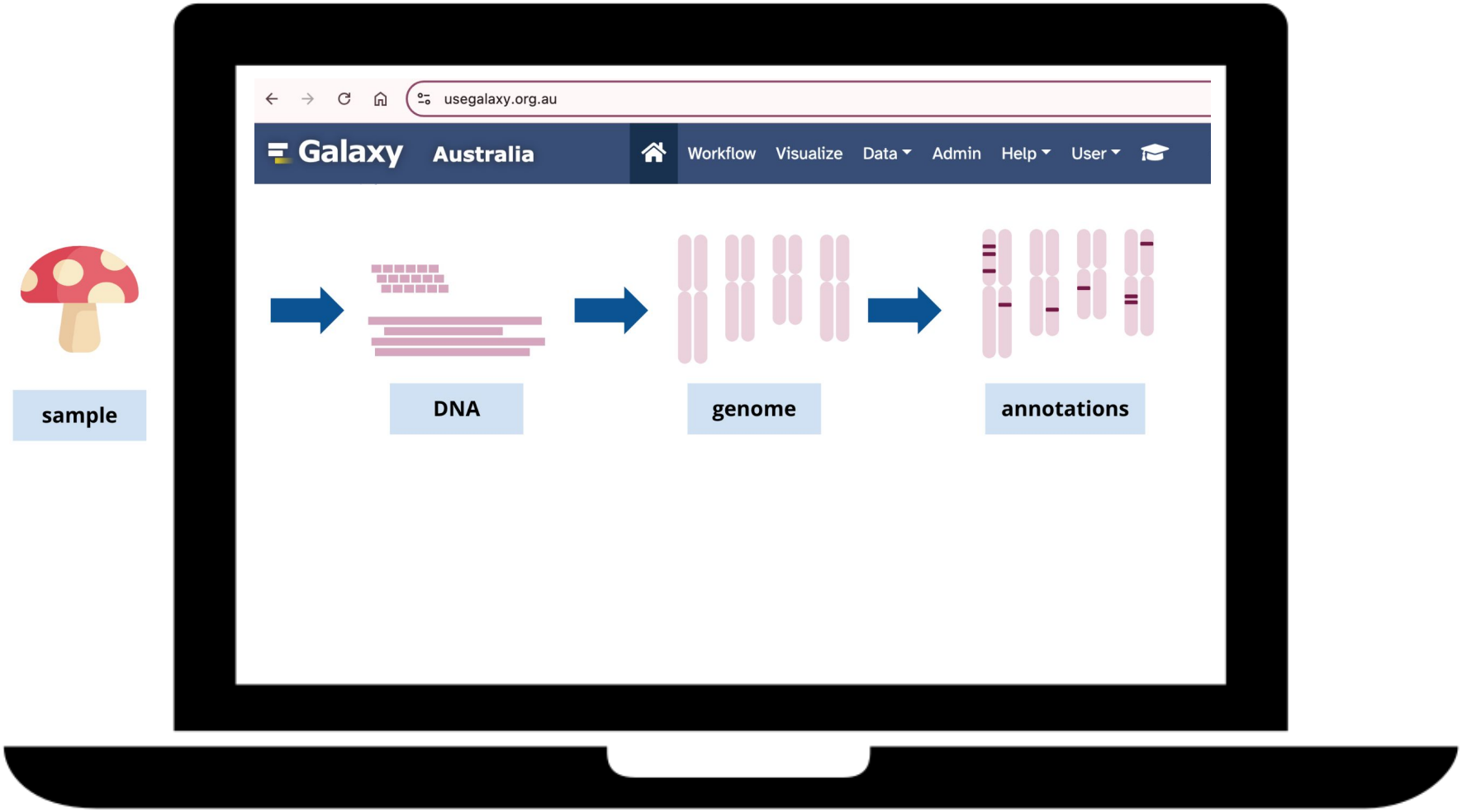
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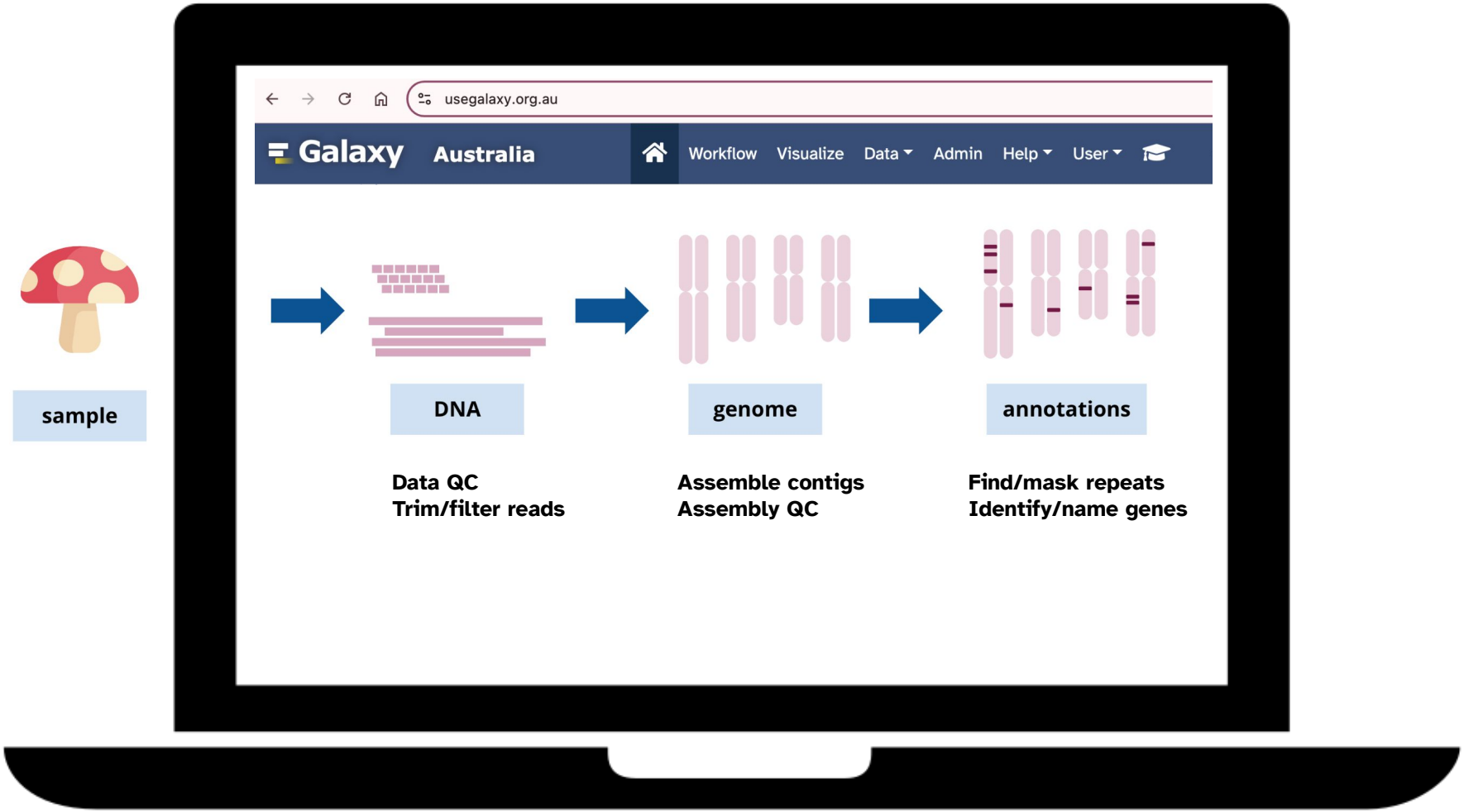
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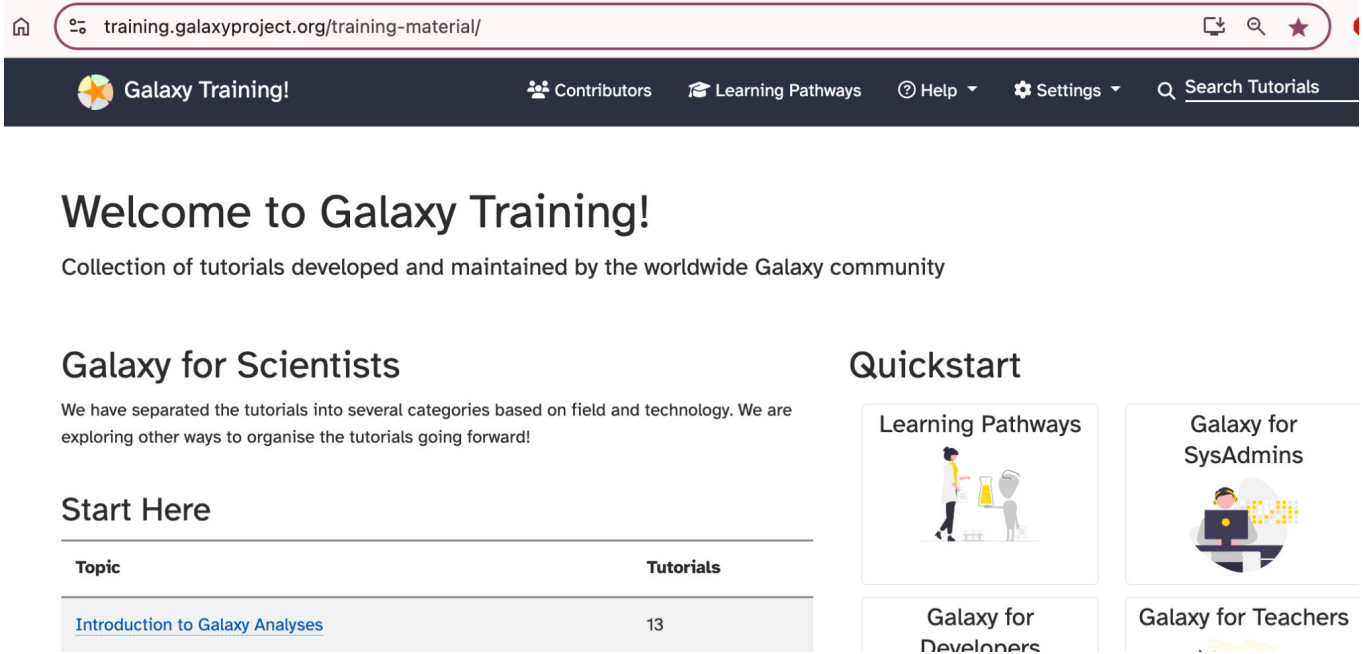
Data QC
Trim/filter reads
Assemble contigs
Assembly QC
Find/mask repeats
Identify/name genes


training.galaxyproject.org/training-material/
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Welcome to Galaxy Training!
Collection of tutorials developed and maintained by the worldwide Galaxy community
Galaxy for Scientists
We have separated the tutorials into several categories based on field and technology. We are exploring other ways to organise the tutorials going forward!
Start Here
Topic
Tutorials
Introduction to Galaxy Analyses
13
Quickstart
Learning Pathways
Galaxy for SysAdmins
Galaxy for Developers
Galaxy for Teachers

Galaxy tutorials

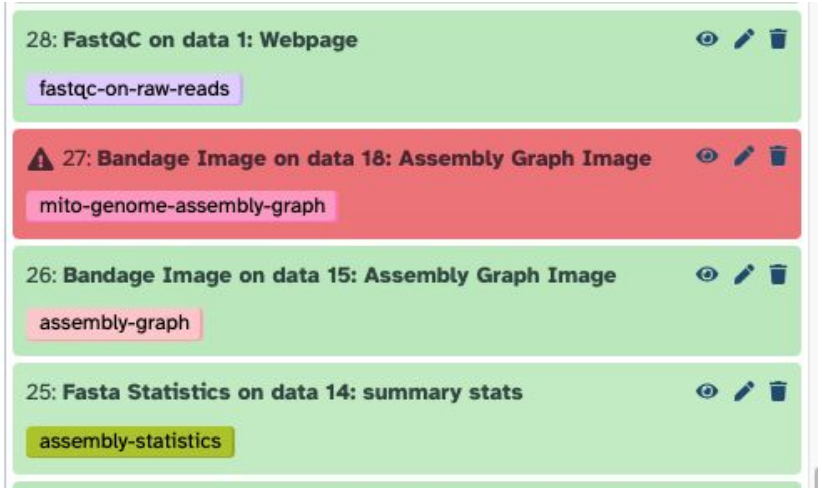
- Using material from the Galaxy Training Network
  - A global set of tutorials for using Galaxy: https://training.galaxyproject.org/
  - We will use some of these tutorials
  - Some tutorial sections will be skipped for time

- Will cover main tools and concepts that are presented in the theory sections
  - We will provide links to other relevant tutorials

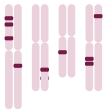
- Will be relevant for real analysis
  - Tutorials use smaller sets of test data so they run in time
  - The same workflows and tools should work on real-sized (large) data sets
  - We have tested on some real fungi data and will provide some links

Bugs, fails and troubleshooting

- Part of bioinformatics - to be expected at times
- Will show how to investigate or report bugs



Main topics covered in tutorials



- How to use Galaxy
  - Find and use tools, analyse data and view results
- Genomic data QC
  - Check quality of sequencing reads, trim and filter reads
- Genome assembly
  - Join reads to create contigs
- Genome annotation
  - Identify and name features ➜ annotated genome for further analyses

Tutorial: A short introduction to Galaxy

- Open Galaxy Australia, register, log in
- Join TIaaS by clicking on the link
- Open tutorial: https://gxy.io/GTN:T00190