



Galaxy dataset collections

Introduction

Collections in Galaxy can be useful when you have to deal with large numbers of datasets. Examples of when you might use collections include when you have many DNA sequencing samples (e.g. .fastq files) or when you have many genome assembly contigs (e.g. .fasta files). Dataset collections allow you to not only organize these datasets but they also allow you to manipulate them in a single batch operation.

Activity

Estimated time: 45 min

Instructions

1. Review the “Datasets versus collections” FAQ
 - training.galaxyproject.org/training-material/faqs/galaxy/histories_datasets_vs_collections.html
2. Complete the “Using dataset collections” hands-on tutorial
 - training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/collections/tutorial.html

Grading Criteria

- Submit URL to your shared Galaxy history on Canvas

Footnotes

Resources

- [Google Doc](#)
- Using Galaxy and Managing your Data [[topic](#)]

Contributions and Affiliations

- Frederick Tan, Johns Hopkins University

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