

Links to Galaxy workflows and histories

- These workflows were developed as examples to show some of the common tools currently used in genome assembly and annotation.
- You can import these workflows and modify them to suit your own analysis.
- To import a workflow into Galaxy, you can click on the Galaxy workflow link and import from there. Or, you can choose a particular workflow here in Zenodo, download to your computer, then open Galaxy, go to Activity Bar, Workflows, Import, under “Archived Workflow File” click Browse, and choose the .ga file.
- We ran these workflows on some fungi data from BPA and NCBI (see the Data column for details).
- You can import/view the Galaxy histories to see how the tools worked and what the results look like (although note that some of these histories are quite large, so you may not wish to import them, only view them).
- To import a history into Galaxy, you can click on the Galaxy history link and import from there.
- Note that these histories are presented only to show examples of tool inputs and outputs, so the outputs should not be considered correct and final results (e.g. don't use an example genome assembly from here as input to a real analysis).

Workflow type	Workflow name	Galaxy workflow link	Workflow name in Zenodo	Data used in example history	Galaxy history link
Genome Assembly (with different data types)	Fungi: Illumina data QC and assembly	https://usegalaxy.org.au/u/anna/w/fungi-illumina-assembly	Galaxy-Workflow-Fungi_Illumina_data_QC_and_assembly_-_Version_1.ga	<i>Psilocybe subaeruginosa</i> BPA sample 465877	https://usegalaxy.org.au/u/anna/h/psilocybe-illumina-assembly
	Fungi: PacBio assembly	https://usegalaxy.org.au/u/anna/w/fungi-hifi-assembly	Galaxy-Workflow-Fungi_PacBio_HiFi_assembly_(from_TSI_workflow)_-_Version_1.ga	<i>Rhynchosporium commune</i> BPA sample 395386	https://usegalaxy.org.au/u/anna/h/rhynchosporium-pacbio-assembly
	Fungi: Nanopore assembly	https://usegalaxy.org.au/u/anna/w/fungi-nanopore-assembly	Galaxy-Workflow-Fungi_Nanopore_assembly_(from_TSI_workflow)_-_Version_1.ga	<i>Aspergillus fumigatus</i> NCBI SRR23337894 SRR23337893 SRR23337895	https://usegalaxy.org.au/u/anna/h/aspergillus-nanopore-assembly
Assembly QC	Fungi: Assembly QC, Blast, RagTag	https://usegalaxy.org.au/u/anna/w/fungi-assembly-qc	Galaxy-Workflow-Fungi_Assembly_QC,_Blast,_RagTag_-_Version_1.ga	<i>Psilocybe subaeruginosa</i> assembly from Illumina workflow Ref genome <i>P. cubensis</i> (has fewer contigs than ref genome for <i>P.</i>	https://usegalaxy.org.au/u/anna/h/psilocybe-assembly-qc

				<i>subaeruginosa</i>). Protein: psilocybin synthase	
Genome Annotation	Fungi: repeat masking, annotation with Helixer, Funannotate, Fgenesh	https://usegalaxy.org.au/u/anna/w/fungi-annotation	Galaxy-Workflow-Fungi_repeat_masking,_annotation_with_Helixer,_Funannotate,_Fgenesh_-_Version_1.ga	<i>Psilocybe subaeruginosa</i> assembly from Illumina workflow	https://usegalaxy.org.au/u/anna/h/repeat-masking-and-annotation---psilocybe
Combined	Combined workflow: Illumina assembly + QC + annotation	https://usegalaxy.org.au/u/anna/w/combined-fungi-assembly-and-annotation-workflow	Galaxy-Workflow-Combined_fungi_assembly_and_annotation_workflow_-_Version_1.ga	<i>Psilocybe subaeruginosa</i> BPA sample 465877 Ref genome <i>P. cubensis</i> Protein: psilocybin synthase	https://usegalaxy.org.au/u/anna/h/combined-fungi-workflows-illumina-psilocybe