Doherty Institute | The University of Melbourne | The Royal Melbourne Hospital

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

Galaxy Workflows

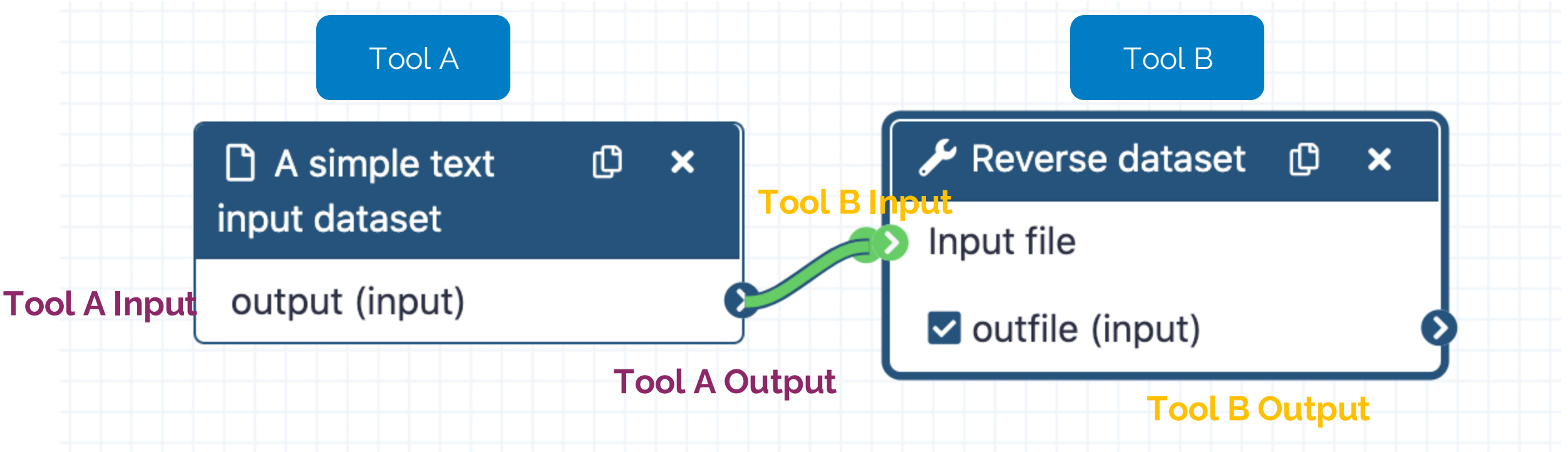
Presenter name

Objectives

- Introduction to Galaxy Workflows,
  - why they are useful and how they work
- Practice creating a tiny workflow in Galaxy
- How and where to find workflows
- Understand workflow outputs

Galaxy Workflows

Workflows are a powerful feature in Galaxy that allow you to link multiple steps of complex analysis.

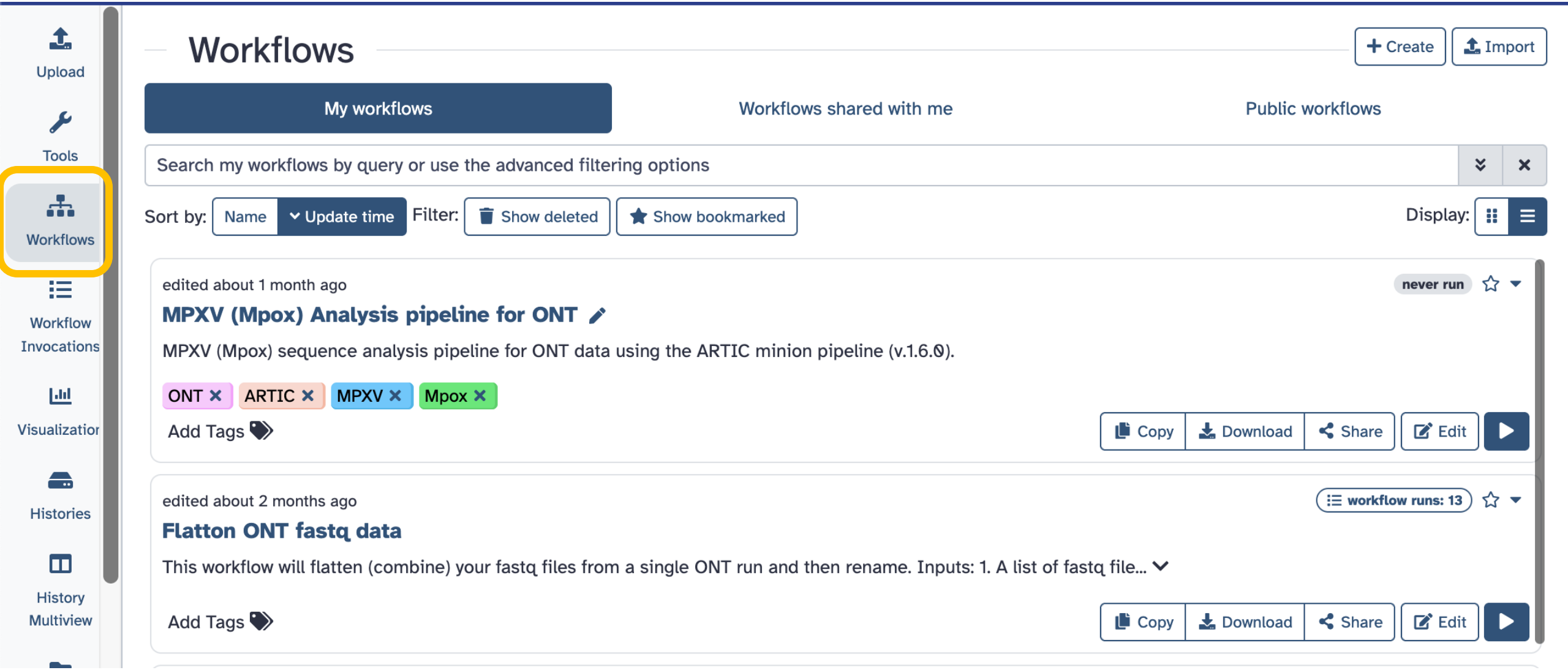


Galaxy Workflows

Workflows are a powerful feature in Galaxy that allow you to link multiple steps of complex analysis.

Connections can be made by clicking on an output terminal and dragging the cursor to an input terminal. Input terminals that are compatible with the current output are highlighted in green, while input terminals that can't be connected are highlighted in Orange.

Finding Workflows – In Galaxy



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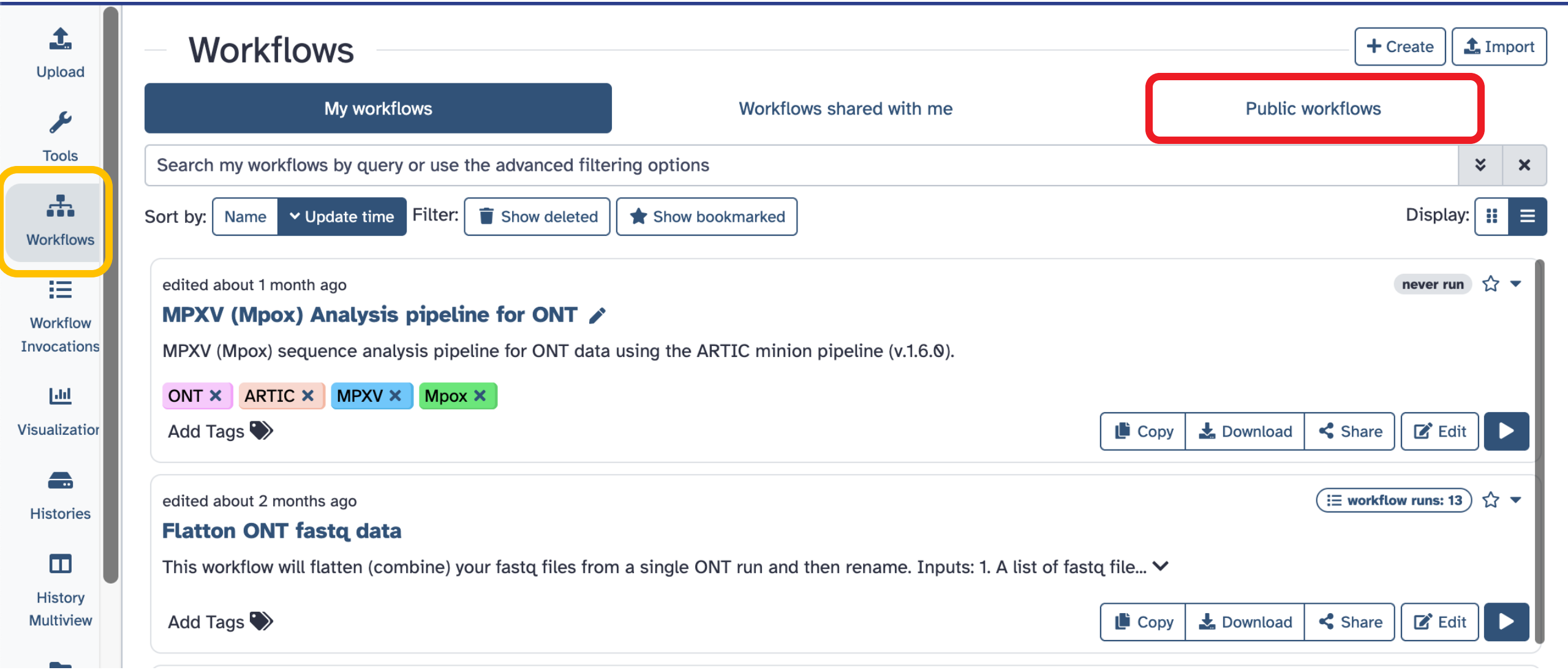

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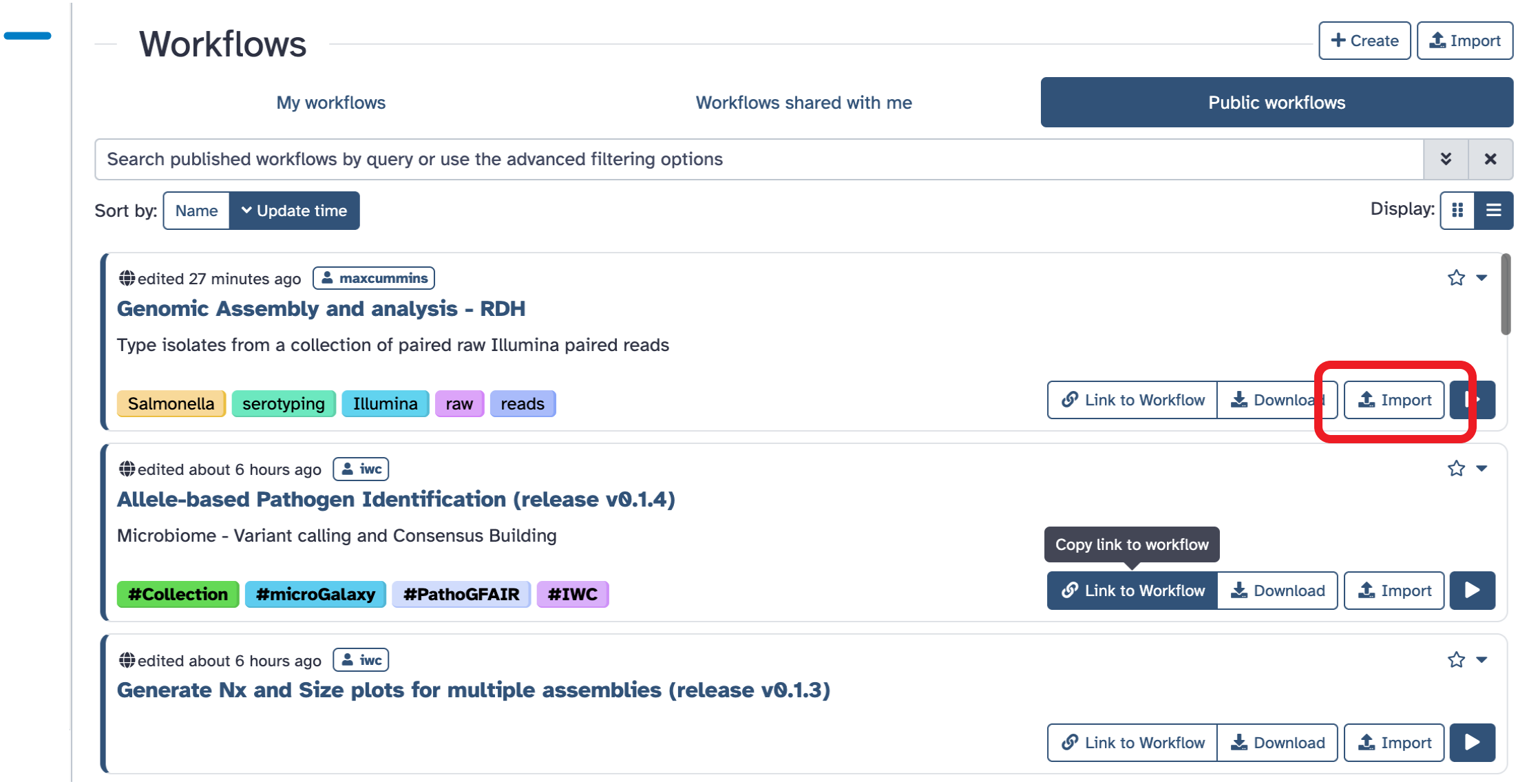

IWC – Intergalactic Workflow Commission

- IWC Workflows: Curated collection of **ready-to-use**, **open-source** analysis workflows designed to help researchers make progress quickly and reliably.

IWC – Intergalactic Workflow Commission

- Available through Galaxy via the "Workflows" tab
  - Website: https://iwc.galaxyproject.org
- Each workflow comes with sample datasets, clear documentation, and links to training materials to streamline learning and application.

- Tips:
  - Read the workflow description to understand the inputs/outputs
  - Import and run the workflow, read the inputs
  - Workflows will run on Dataset Collections
  - Each outputs will be collated by type per sample in Dataset Collection

Workflow Inputs/Outputs

Each workflow has a different requires for input files and will output different things.

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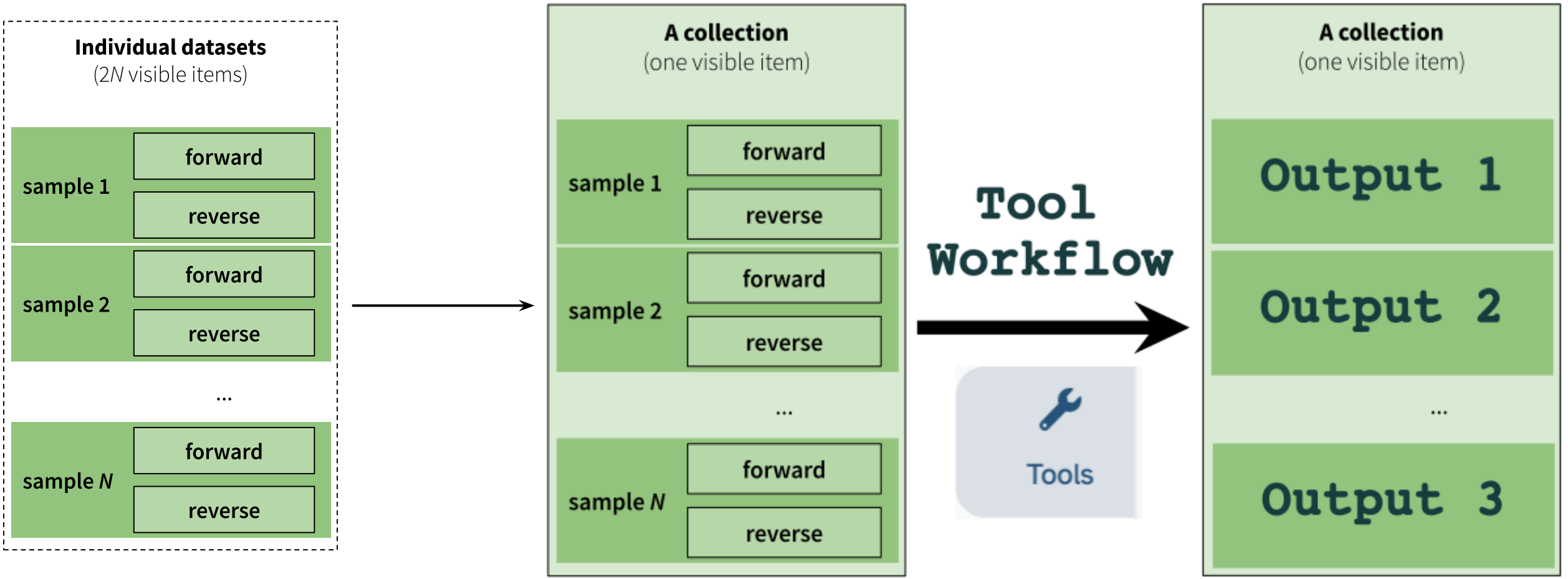
Workflow Inputs/Outputs - Collections



Let's import the MPXV workflow - Tutorial

1. In Galaxy, navigate to Workflows tab

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1. In Galaxy, navigate to Workflows tab
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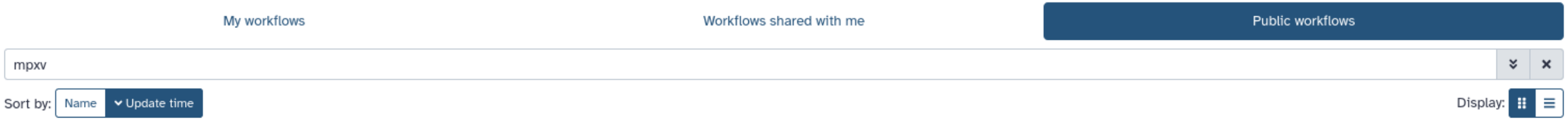

Let's import the MPXV workflow - Tutorial

1. In Galaxy, navigate to Workflows tab
2. Click on 'Public Workflows' - enter 'mpxv'
3. Find and import the MPXV pipeline:

Workflow MPXV for ONT

- Created by specifically for this workshop by Ammar Aziz and Tristan Reynolds (Melbourne Bioinformatics)
- Based on nf-artic-mpxv pipeline
  - https://github.com/artic-network/artic-mpxv-nf

Questions? + Resources

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- Tutorial Feature: Easier launching of WorkflowHub & Dockstore Workflows
  - https://training.galaxyproject.org/training-material/news/2023/12/12/tutorial-run-wfh-ds.html
- Galaxy Training Network – Collections
  - https://galaxyproject.github.io/training-material/topics/galaxy-interface/tutorials/collections/tutorial.html