



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

# Galaxy Workflows

—  
Presenter name

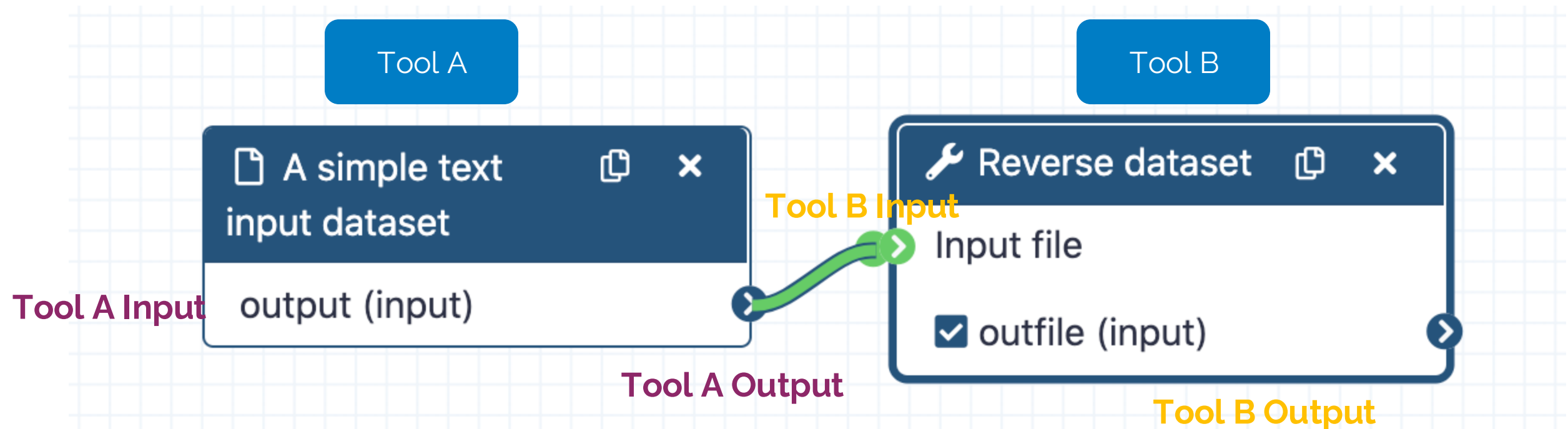
# Objectives

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- 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

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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

Upload

Tools

Workflows

Workflow Invocations

Visualizations

Histories

History Multiview

## Workflows

My workflows

Workflows shared with me

Public workflows

Search my workflows by query or use the advanced filtering options

Sort by: 

Name

Update time

 Filter: 

Show deleted

Show bookmarked

Display:

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☆

**MPXV (Mpx) Analysis pipeline for ONT**

MPXV (Mpx) sequence analysis pipeline for ONT data using the ARTIC minion pipeline (v.1.6.0).

ONT

ARTIC

MPXV

Mpx

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workflow runs: 13

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**Flatton ONT fastq data**

This workflow will flatten (combine) your fastq files from a single ONT run and then rename. Inputs: 1. A list of fastq file...

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# Finding Workflows – In Galaxy



## Workflows

[+ Create](#)

[↑ Import](#)

My workflows

Workflows shared with me

Public workflows

Search published workflows by query or use the advanced filtering options

⌵ ×

Sort by:

Name

▼ Update time

Display:

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≡

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maxcummins

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**Genomic Assembly and analysis - RDH**

Type isolates from a collection of paired raw Illumina paired reads

Salmonella

serotyping

Illumina

raw

reads

Link to Workflow

Download

Import

edited about 6 hours ago

iwc

⌵

**Allele-based Pathogen Identification (release v0.1.4)**

Microbiome - Variant calling and Consensus Building

#Collection

#microGalaxy

#PathoGFAIR

#IWC

Link to Workflow

Download

Import

Copy link to workflow

edited about 6 hours ago

iwc

⌵

**Generate Nx and Size plots for multiple assemblies (release v0.1.3)**



Link to Workflow

Download

Import

# 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.

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**Allele-based Pathogen Identification (release v0.1.4)**

Microbiome - Variant calling and Consensus Building

**#Collection** **#microGalaxy** **#PathoGFAIR** **#IWC**

[Link to Workflow](#) [Download](#) [Import](#) 

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**Generate Nx and Size plots for multiple assemblies (release v0.1.3)**

[Link to Workflow](#) [Download](#) [Import](#) 



# 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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## MPXV (Mpox) Analysis pipeline for ONT

MPXV (Mpox) sequence analysis pipeline for ONT data using the ARTIC minion pipeline (v.1.6.0).

ONT  ARTIC  MPXV  Mpox 

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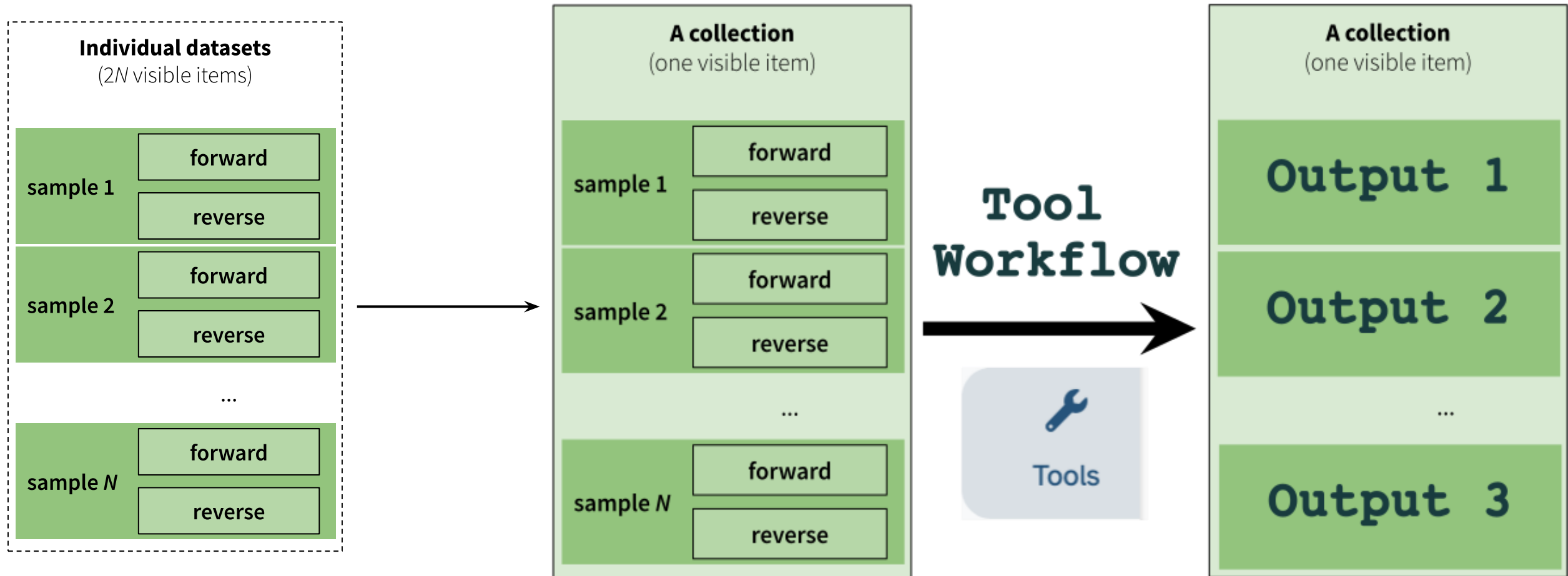
# Workflow Inputs/Outputs

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

- Workflows will run on Dataset Collections
- Each outputs will be collated by type per sample in Dataset Collection

# Workflow Inputs/Outputs - Collections



# Let's import the MPXV workflow - Tutorial

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1. In Galaxy, navigate to Workflows tab



Workflows

# Let's import the MPXV workflow - Tutorial

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1. In Galaxy, navigate to Workflows tab
2. Click on 'Public Workflows' - enter 'mpxv'

The screenshot shows the Galaxy Public Workflows search interface. At the top, there are three tabs: 'My workflows', 'Workflows shared with me', and 'Public workflows'. The 'Public workflows' tab is selected and highlighted in dark blue. Below the tabs is a search bar containing the text 'mpxv'. To the right of the search bar are two small icons: a downward arrow and a close 'x' icon. Below the search bar, on the left, is a 'Sort by:' label followed by two buttons: 'Name' and 'Update time'. On the right, there is a 'Display:' label followed by two icons: a grid icon and a list icon.

My workflows      Workflows shared with me      Public workflows

mpxv

Sort by: Name    Update time

Display:



# Let's import the MPXV workflow - Tutorial

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

 edited less than a minute ago

 aaziz

### MPXV (Mpox) Analysis pipeline for ONT

MPXV (Mpox) pipeline for ONT platform. Using the L... 

ONT


MPXV

3 more...





 Import



# Workflow MPXV for ONT

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ONT ✕ ARTIC ✕ MPXV ✕ Mpox ✕

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- 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>