Today

- Galaxy Introduction
- Get familiar with Galaxy
  - Upload data
  - Run tools
  - Perform analysis
- Create workflow

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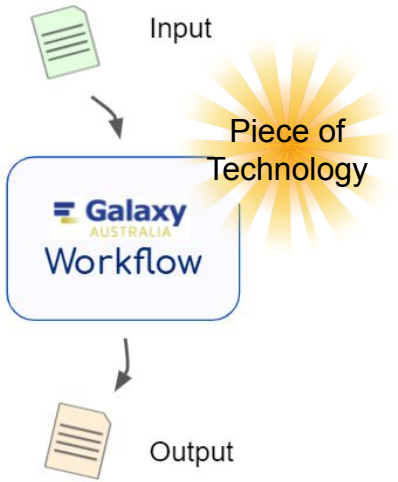

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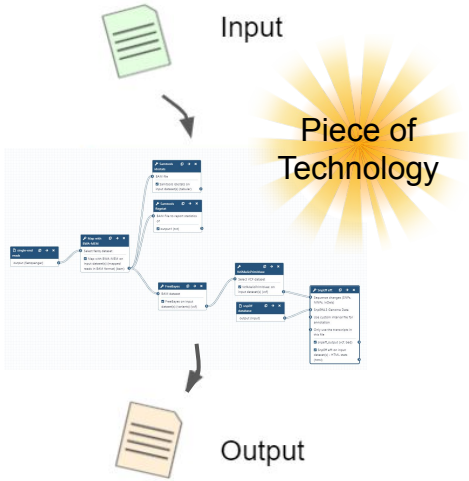

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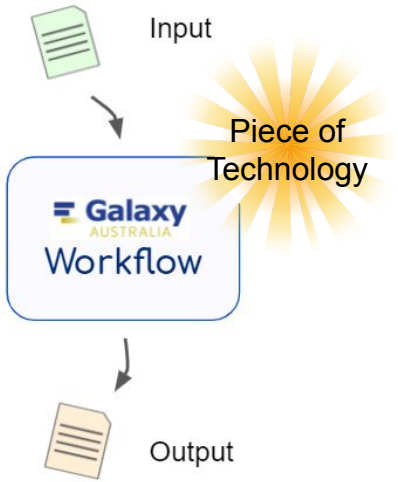

Today

Breakout 1:

- Login
- Upload data
- Data preprocessing (tools)

Breakout 2:

- Run analysis (tools)

Breakout 3:

- Convert analysis to workflow

Participants

Analysis	Count
RNAseq DE	11
RNAseq Transcriptome	2
Genome Assembly	3
Variant Calling	2
Metagenomics / Microbiomics	5
DNA Markers	3
Machine Learning	3

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AIM today:

Get comfortable with Galaxy so you can learn these areas using GTN!

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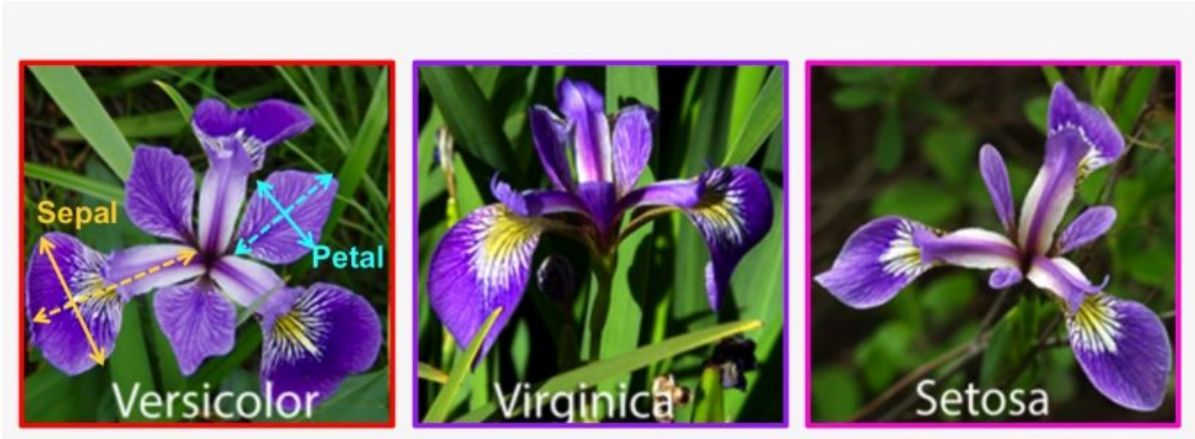
AIM today:

Get comfortable with Galaxy so you can learn these areas using GTN!

Get ready for other training sessions

Iris dataset



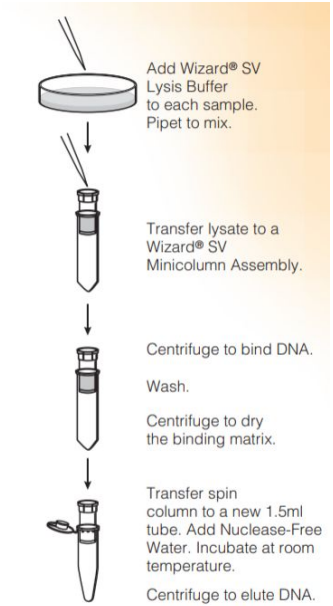
Ronald Fisher: 1936

- 50 samples of each species
- Sepal length, sepal width, petal length, petal width
- Classification problem

Workflows

Protocol

wet-lab



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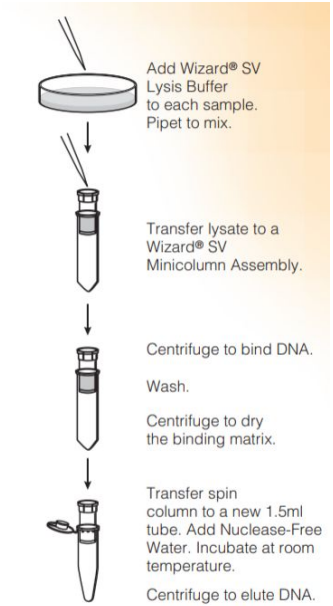
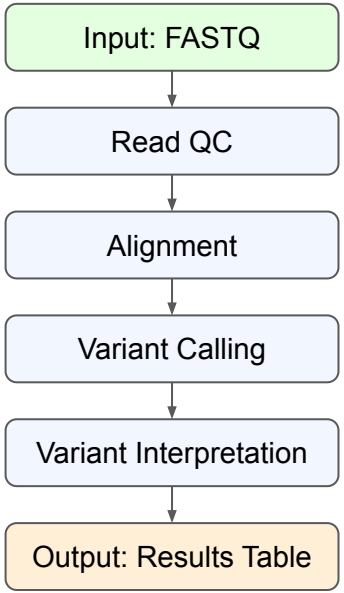


dry-lab



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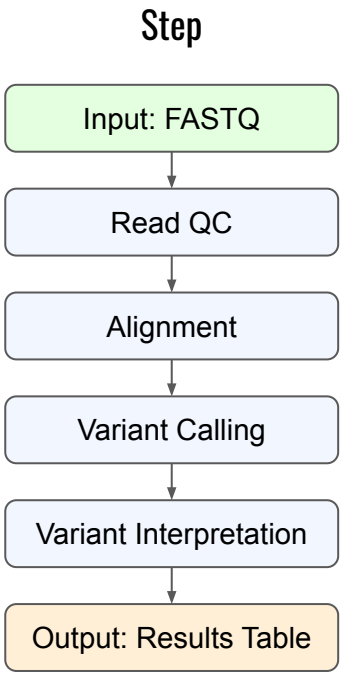
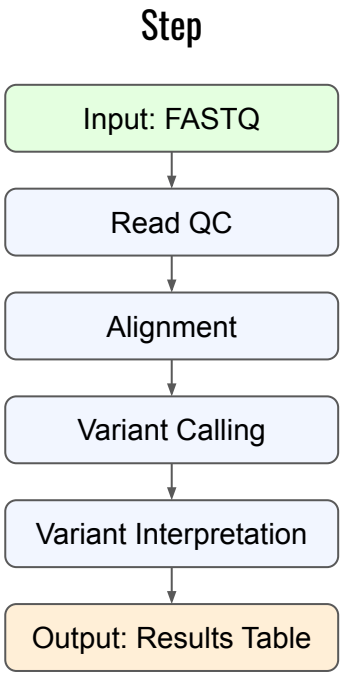

Step
Input: FASTQ
Read QC
Alignment
Variant Calling
Variant Interpretation
Output: Results Table

Protocol



Step	Tools
Input: FASTQ	
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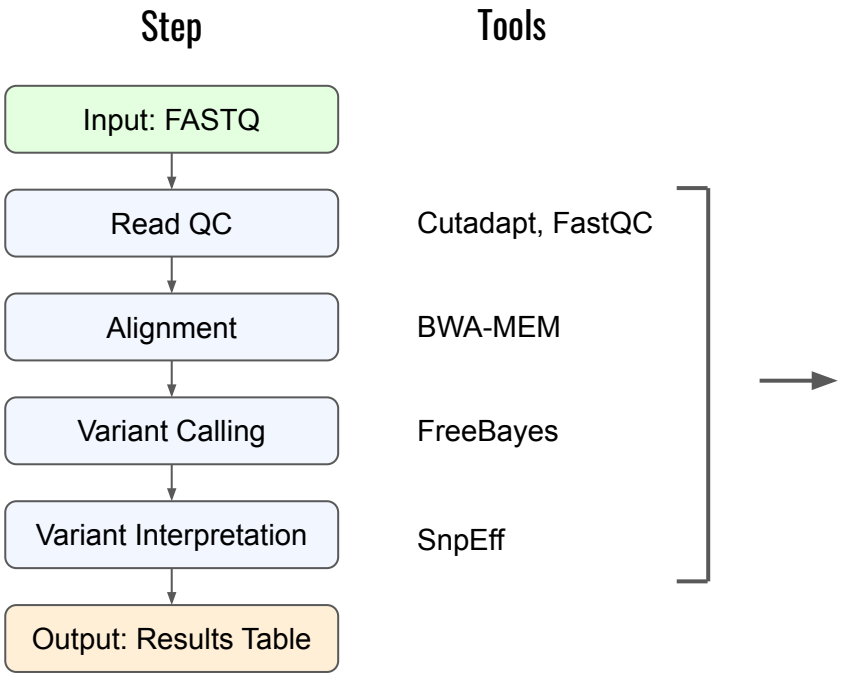
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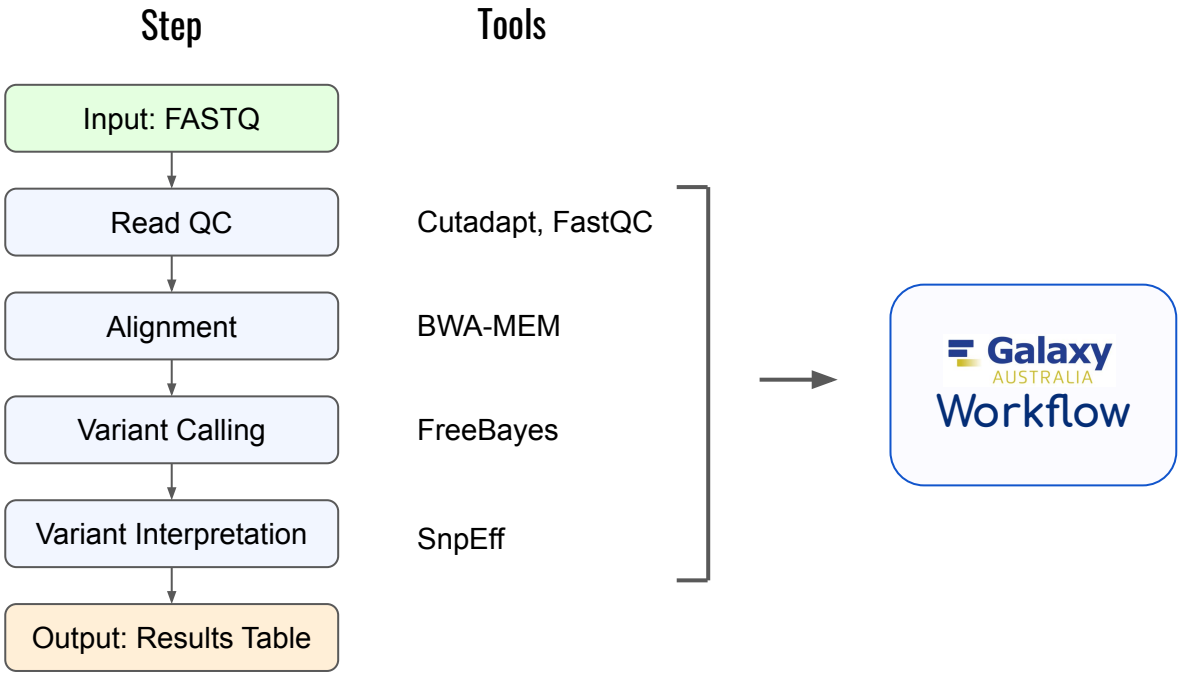
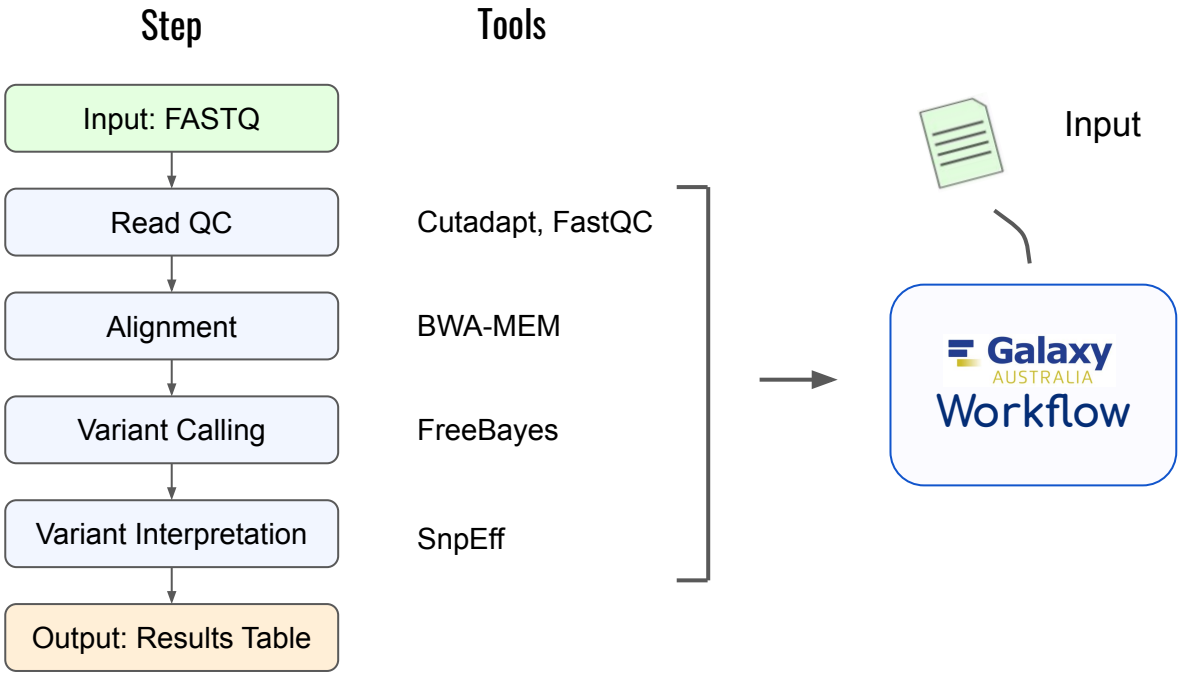
Convert to Workflow



Automated analysis



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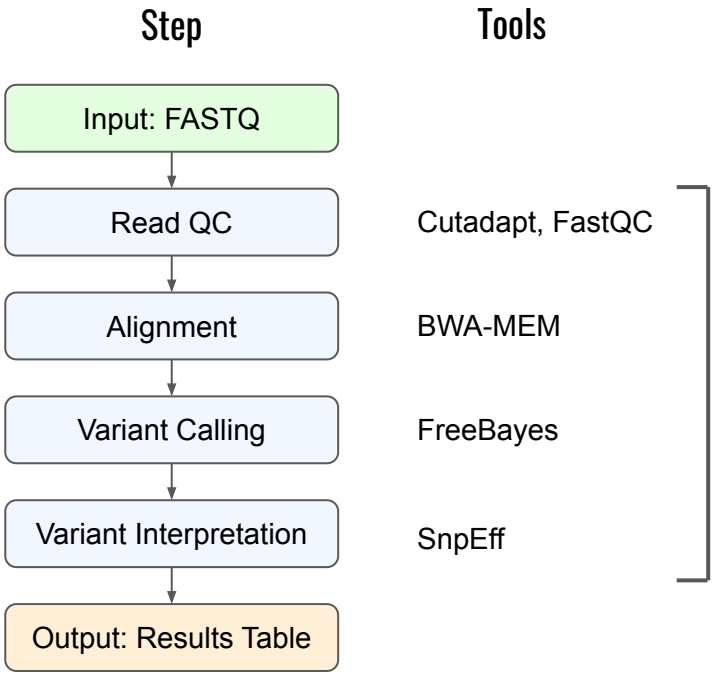

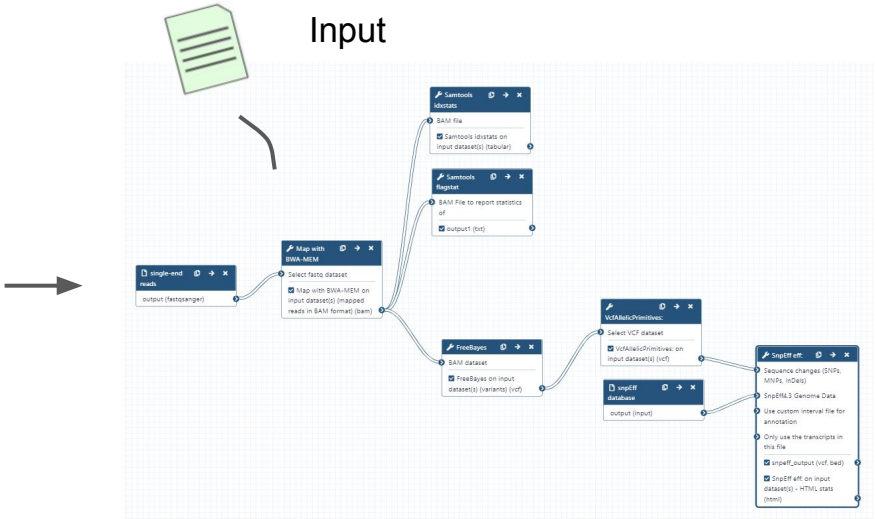

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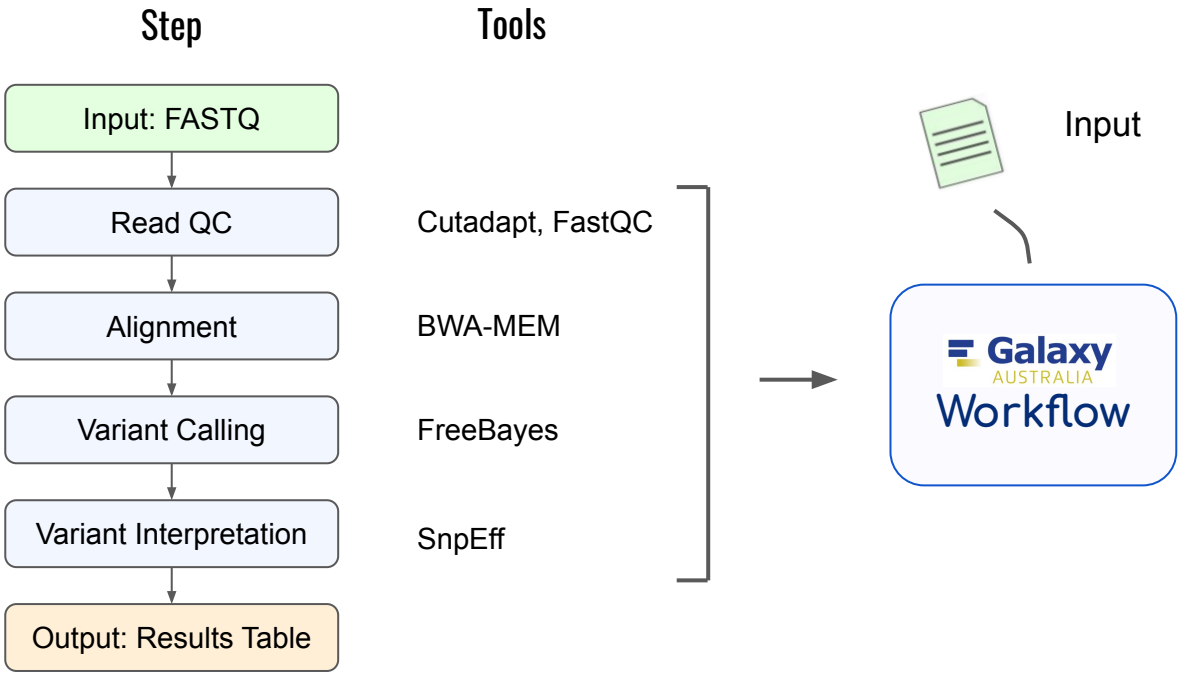

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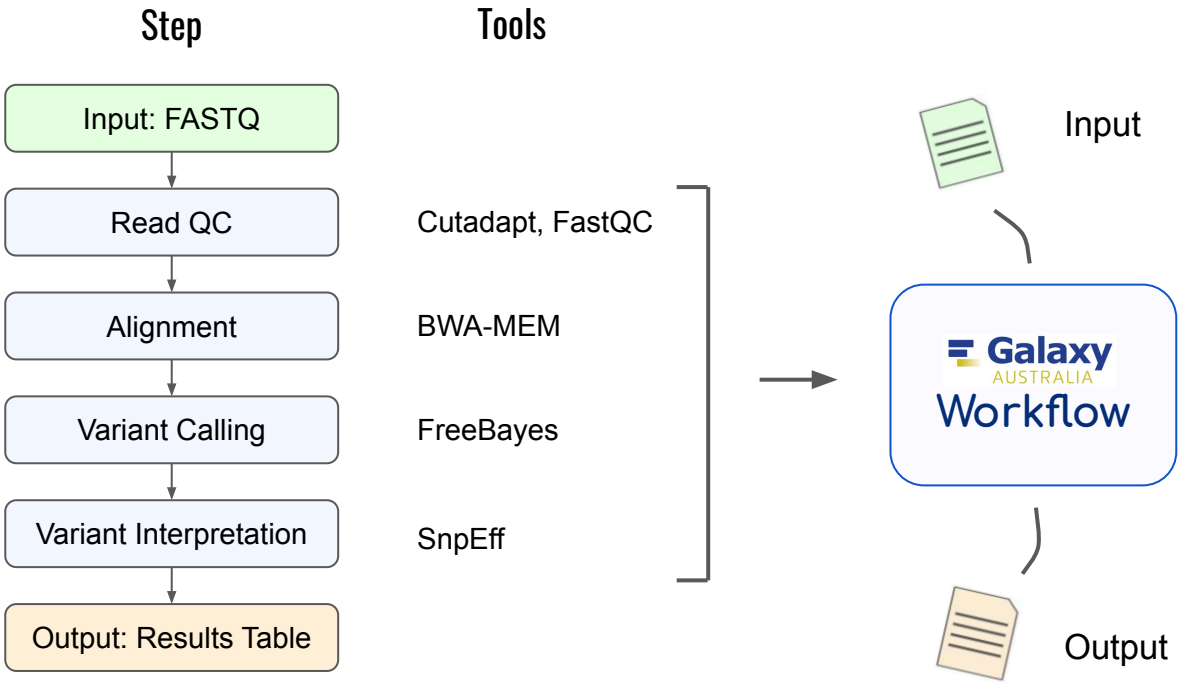

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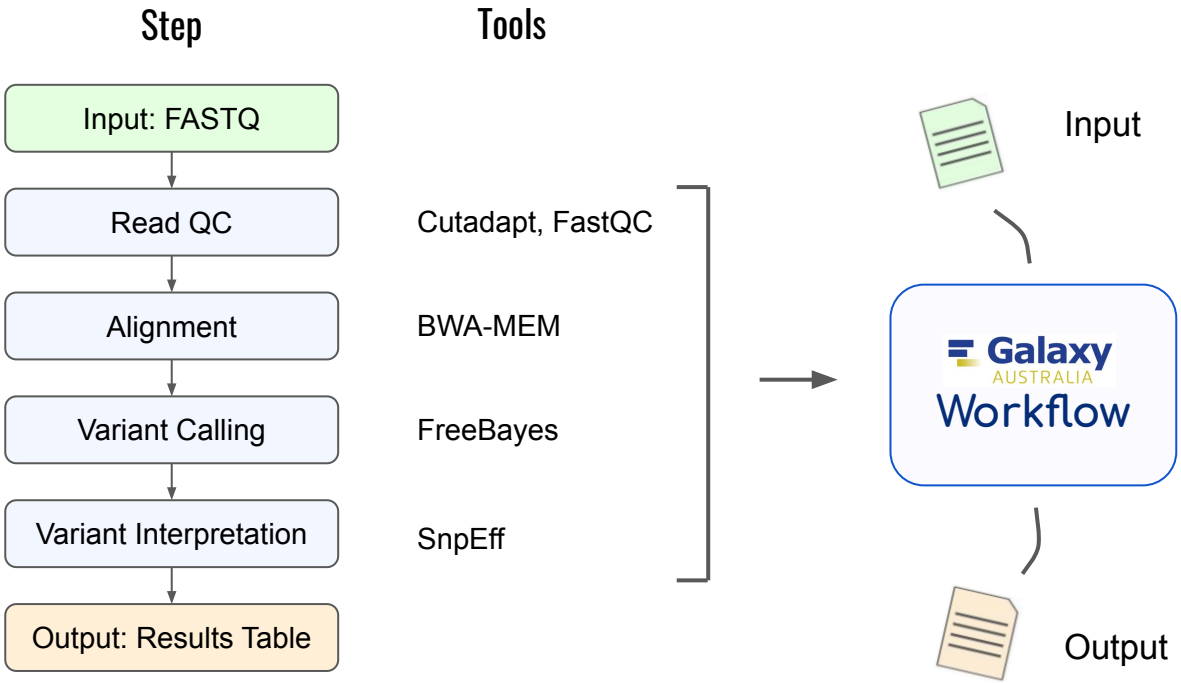

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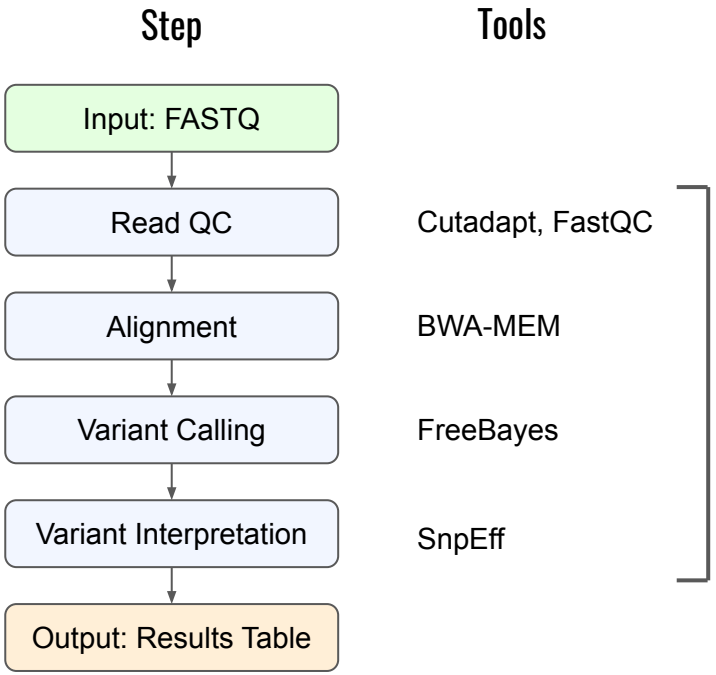

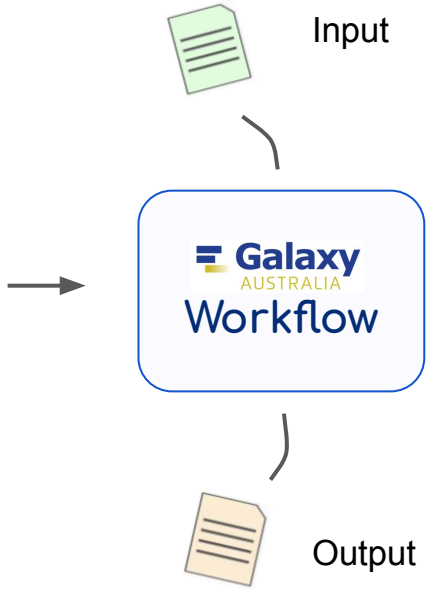

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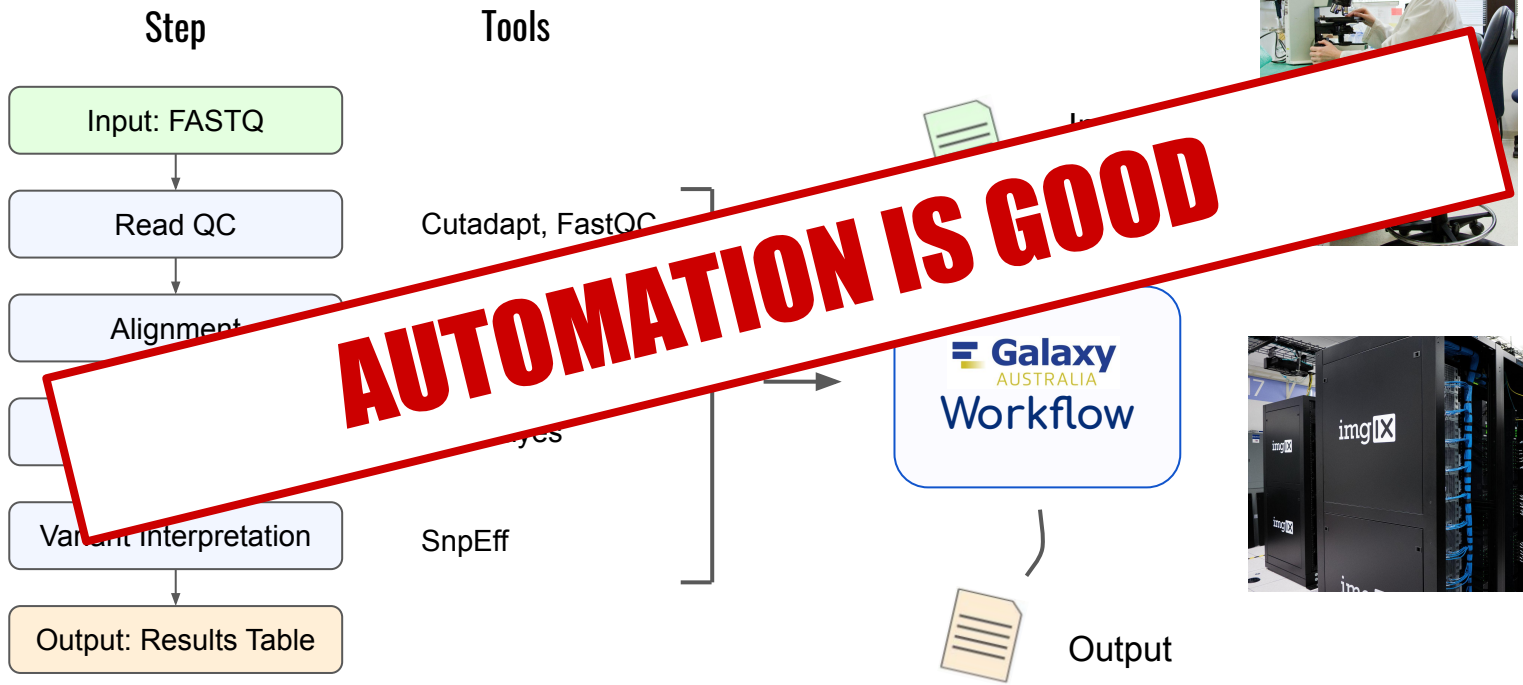
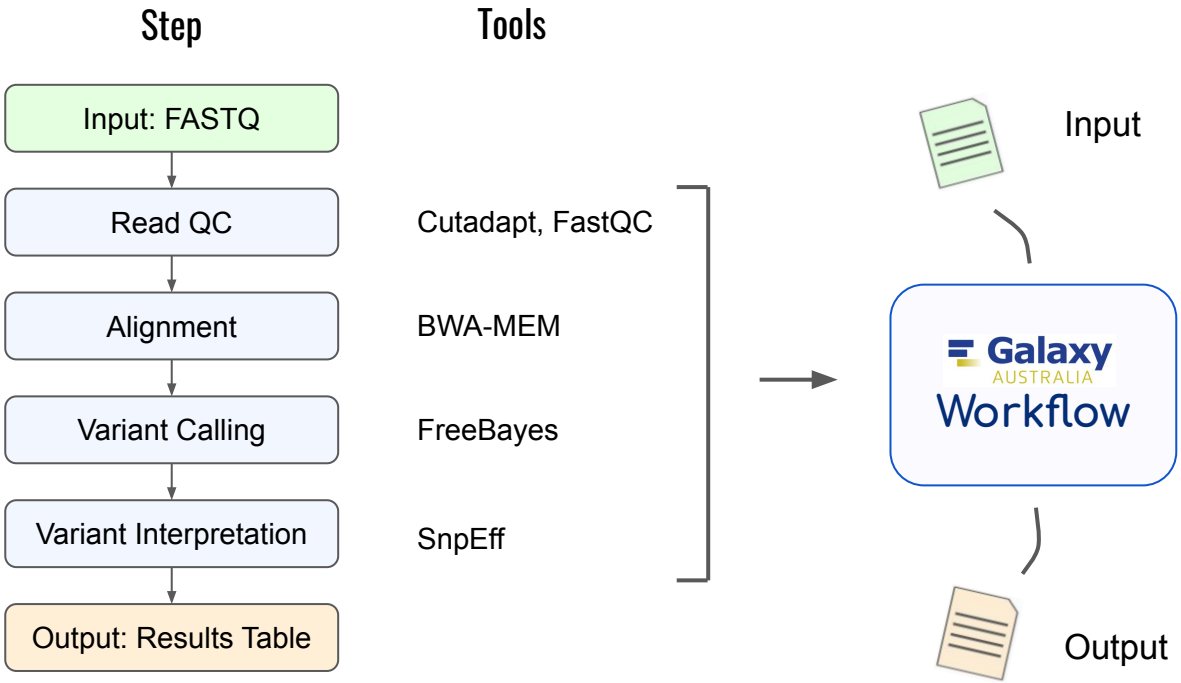
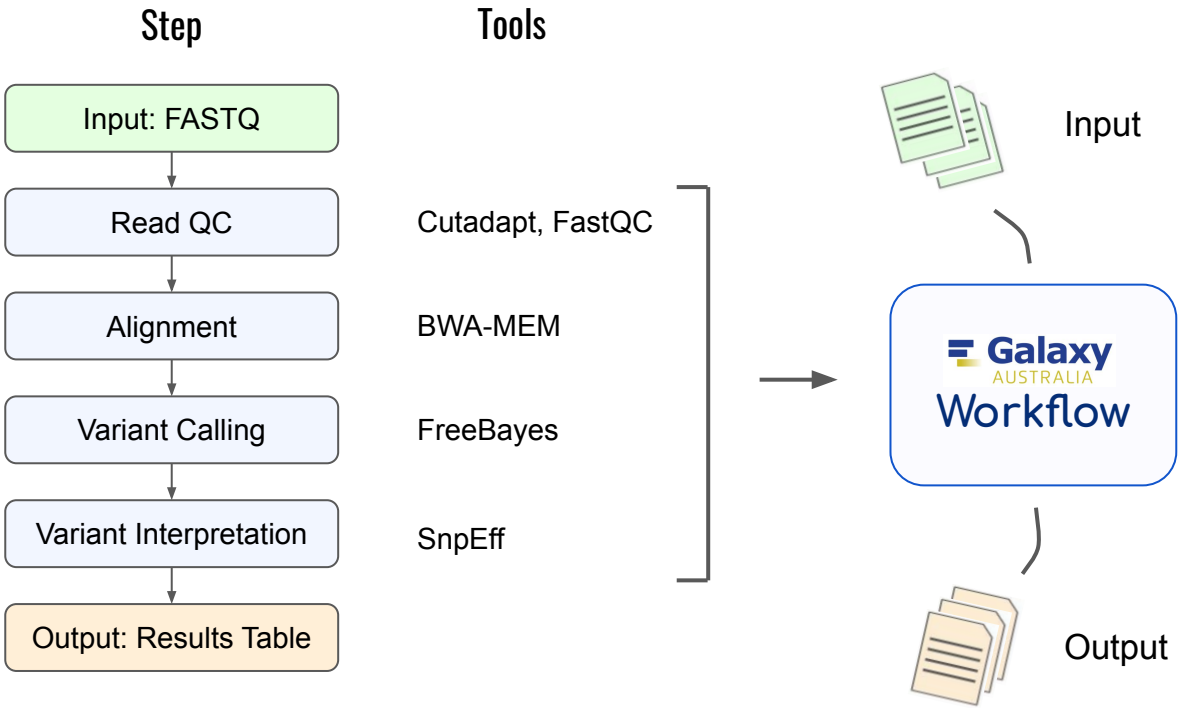


AUTOMATION IS GOOD

Automated analysis



Analyse new datasets!



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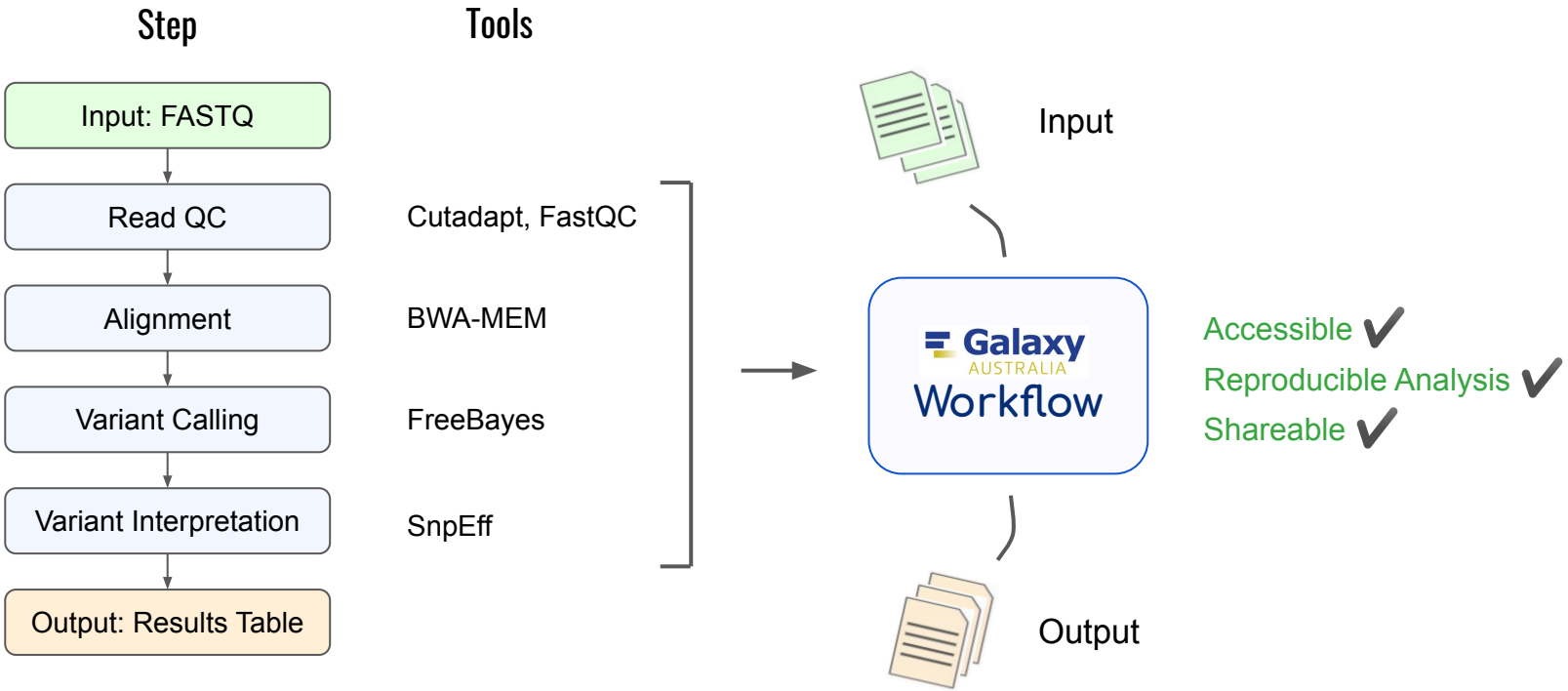


Share with the world

Share with the world

Your Boss

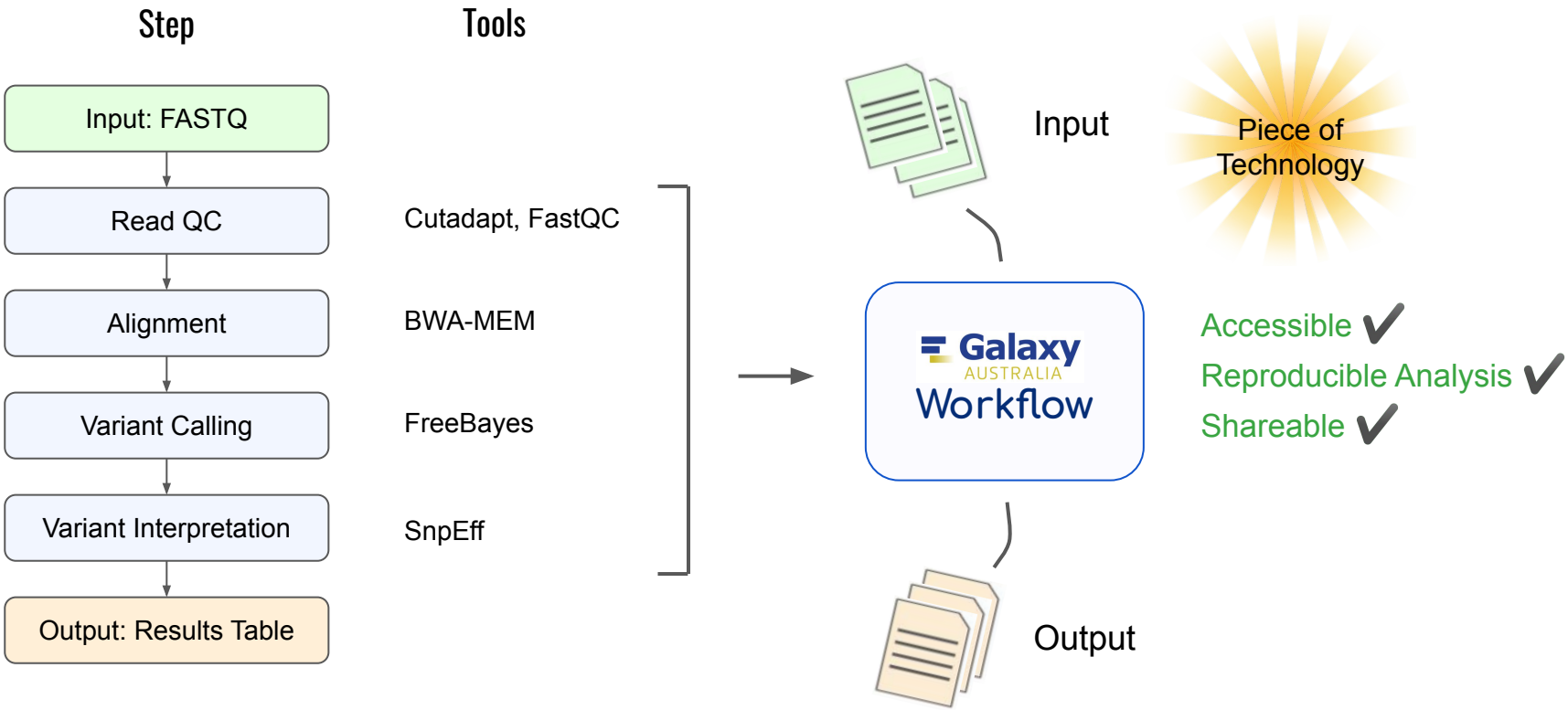
Share with the world

Your Boss

Research
Community

Graveyard

Analyse new datasets!



Analysis Development

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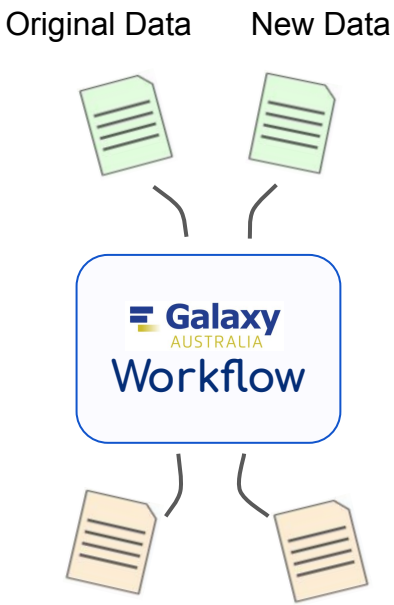

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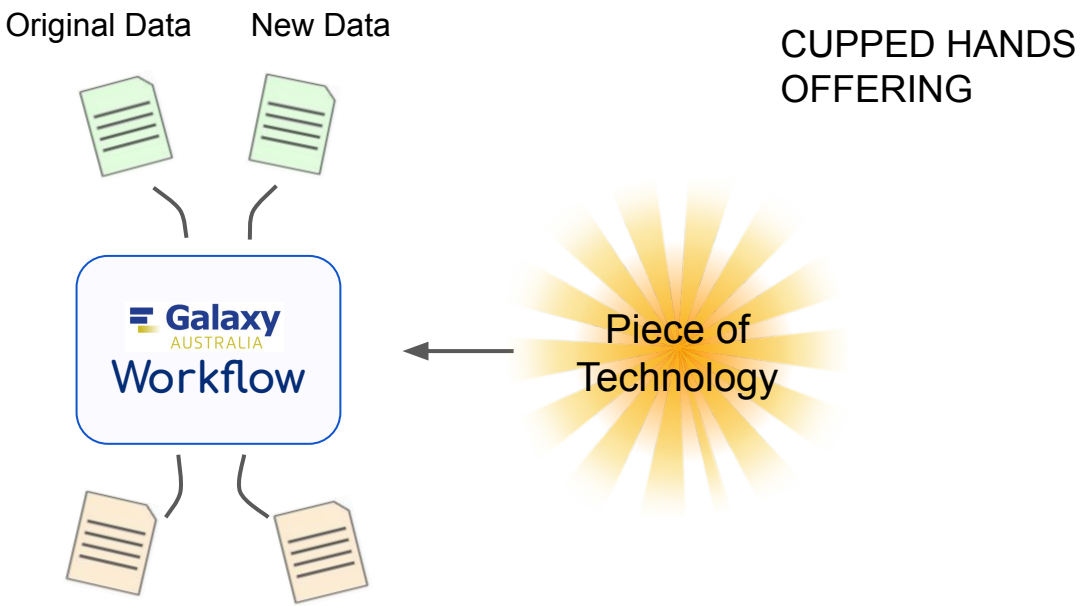

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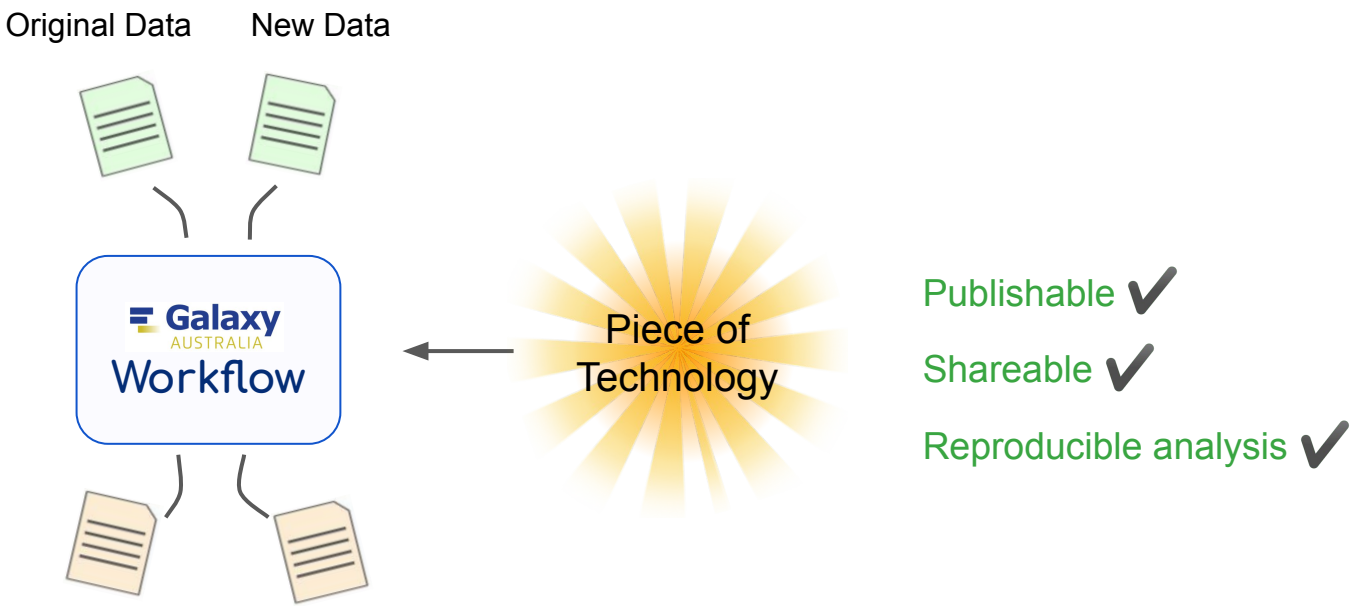

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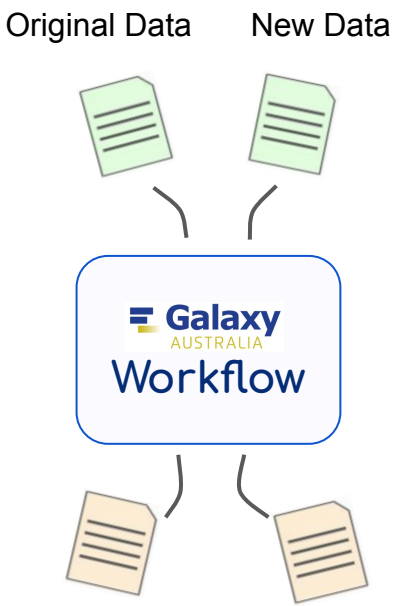
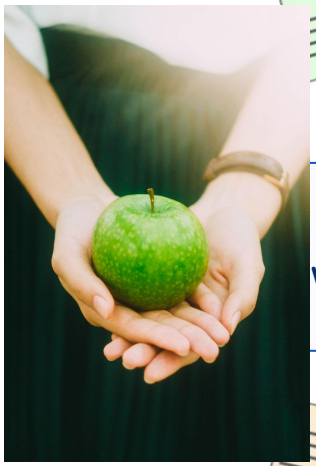


Your Boss

Analysis Development

Original Data

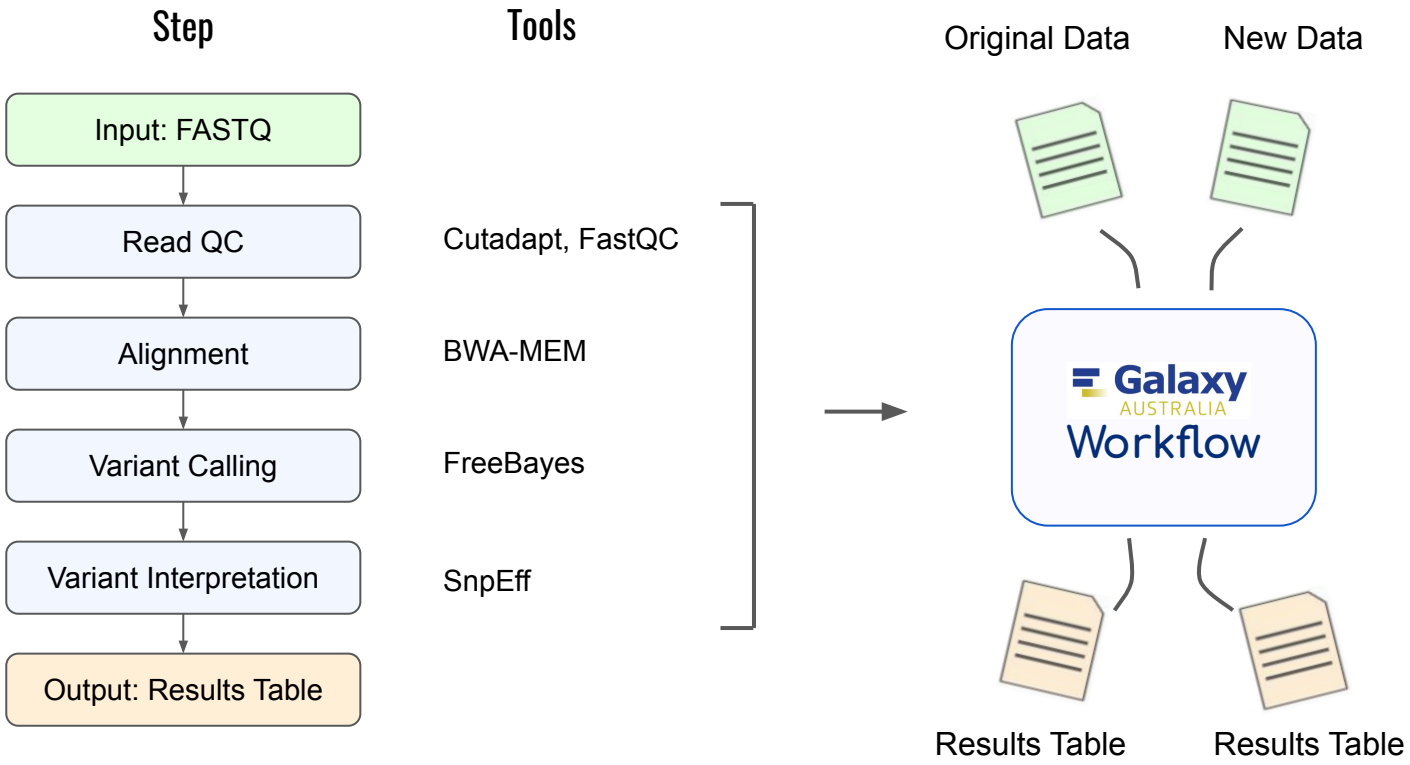
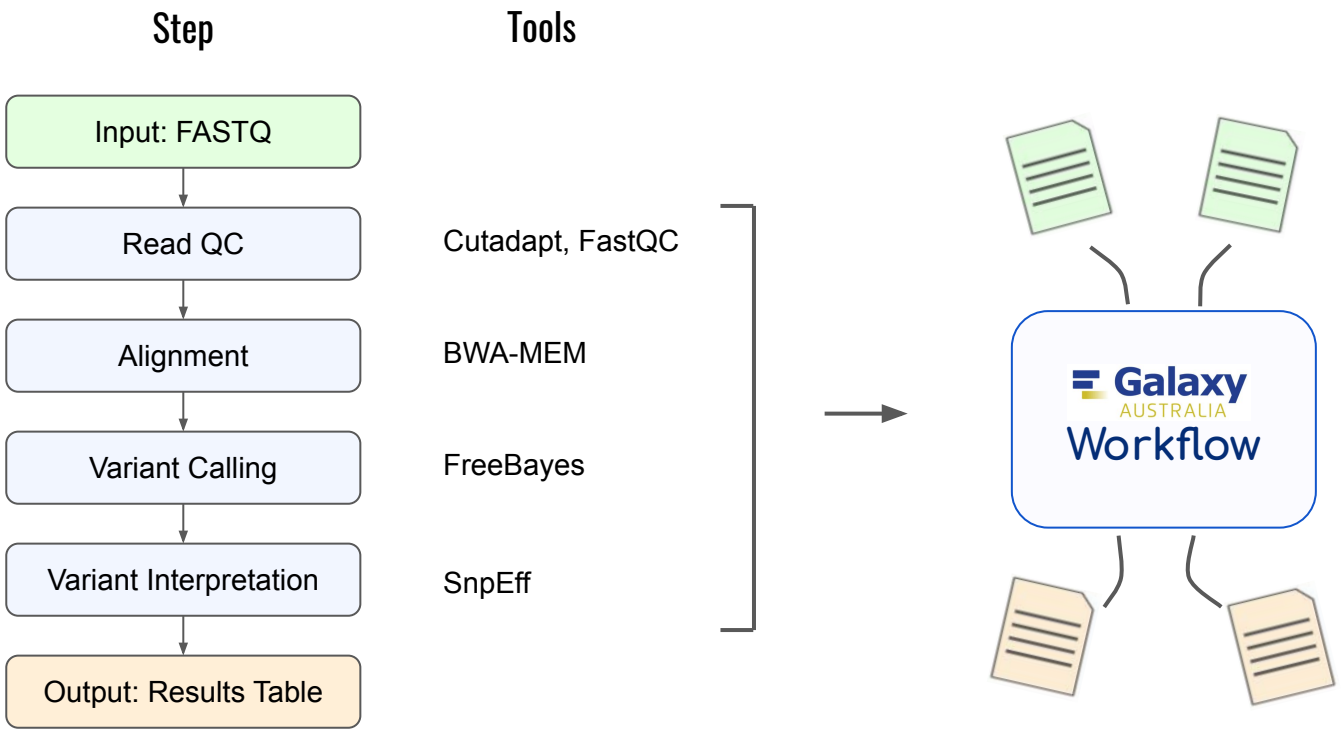
New Data



Your Boss

Research Community

Analysis Development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