Automating work in Galaxy

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There are two main approaches to automating work in Galaxy:

- Running one tool on lots of inputs
- Creating and running workflows
Multiple inputs in one tool

Some tools, such as FastQC, support multiple inputs. Note that these will run as separate, unrelated jobs!

Click on “Run tool in parallel..”

Use the shift and control keys to toggle or select many inputs at once.

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Introduction to workflows

Workflows encapsulate an entire histories worth of work. They can be created by:

- Building from scratch
- Extracting from history
- Importing from shared workflow
Building workflows

Create a new workflow and annotate it with something you will remember a year from now!
Building workflows

Each step is created by choosing tools to build the pipeline. Here is an example input with a dataset collection.
Building workflows

Outputs from one tool can be clicked and dragged into the input of another tool. This process can be extended until the entire pipeline is created.

- from SAM or BAM files
  - Cutadapt: Remove adapter sequences from Fastq/Fasta
  - Tabular to FASTQ converter
  - FASTQ Quality Trimmer by sliding window
  - FASTQ Trimmer by column

The bottom right side has an overview panel to allow the entire board to be scrolled by clicking and dragging.

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Extracting workflows

An entire history can be converted into a workflow for easy sharing and to reproduce work. Make sure you are in the history that you want to extract from.

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Extracting workflows

As always, a descriptive name will help in the long run!

Create Workflow when done

Input files are chosen later.

You can skip steps you don’t need

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

<table>
<thead>
<tr>
<th>Tool Name</th>
<th>Include in Workflow</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unknown</td>
<td></td>
</tr>
<tr>
<td>Unknown</td>
<td></td>
</tr>
<tr>
<td>FastQC:Read QC</td>
<td></td>
</tr>
<tr>
<td>FASTQ Quality Trimmer</td>
<td></td>
</tr>
<tr>
<td>FASTQ Quality Trimmer</td>
<td></td>
</tr>
</tbody>
</table>

History items created:

1: TB_1.fq (Treat as input dataset)
2: TB_2.fq (Treat as input dataset)
3: FastQC_TB_1.fq.html
4: FASTQ Quality Trimmer on data 1
5: FASTQ Quality Trimmer on data 2

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Importing workflows

Sharing workflows makes it easy for others to reproduce your work and for you to run new inputs through the same procedure.

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Running workflows

The inputs are the only thing you need to set up in order to run the workflow.

For a cleaner history, send results to a new history:
Sharing workflows makes it easy for others to reproduce your work and for you to run new inputs through the same procedure.
Future directions

There are other methods in development that will add even more flexibility to running massive numbers of jobs and increasing throughput:

- API calls for advanced use
- Dataset collections
- Nested workflows

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Thanks for watching!
Questions and comments:
Email help@ncgas.org

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