Workflows in Galaxy

Demo: Importing, creating and modifying workflows in Galaxy
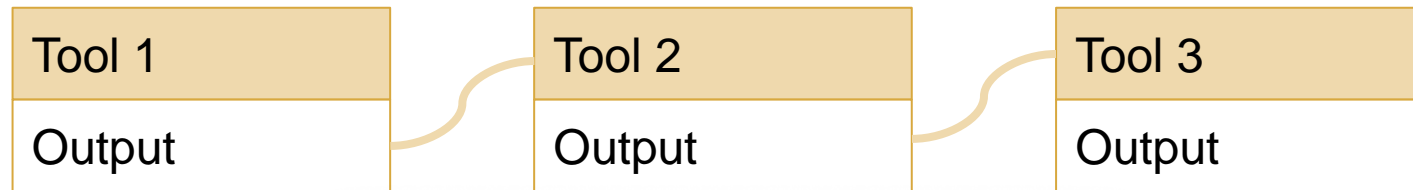
Erik Hjerde

Workflows in Galaxy

Galaxy is a workflow manager with a graphical user interface

Workflows in Galaxy are strings of tools connected in the correct order so that the output from one tool becomes the input for the next tool

Tool 1
Output

Tool 2
Output

Tool 3
Output

```
fp3-ntf-m0053:exercise2 service$ /location/of/tool1 -input [FILE] -parameterA [INT] -para
meterB [INT] -output [FILE] | /location/of/tool2 -input [FILE] -parameterA [INT] -paramet
erB [INT] -output [FILE] | /location/of/tool3 -input [FILE] -parameterA [INT] -parameterB
 [INT] -output [FILE] > result.txt
```

Workflows in Galaxy

Create workflow

Modify workflow

Share workflow

Run workflow

Documenting workflow

Live demo – feel free to join

Finding existing workflows in Galaxy

Modifying workflows in Galaxy

Sharing workflows in Galaxy

Constructing new workflows in Galaxy

Running workflows in Galaxy

The remaining slides are repetition of the most important things from the demo for later use when you go home and have forgotten everything you learned☺

Workflows in Galaxy

Create, import or upload a workflow

NeLS galaxy-uit.bioinfo.no   Analyze Data   Workflow   Shared Data   Visualization   Admin   Help   User   ⠿   Using 48%

Tools   ⬆

search tools   ⊗

GENERAL GALAXY TOOLS

Get Data

Send Data

Collection Operations

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

Extract Features

Metagenomics

Statistics

NGS: QC and Manipulation

NGS: Picard

NGS: Mapping and Sequence analysis

NGS: GATK Tools

Assembly and Validation

Transcriptomics

NGS: SAM-tools

Genome Diversity

Workflows

- All workflows

Your workflows

Workflow page

search for workflow...   +   ⬆

Name	Tags	Owner	# of Steps	Published	Show in tools panel
My first workflow ▾	🏷	You	0	No	☐

Edit
Run
Share
Download
Copy
Rename
View
Delete

Context menu

Details panel

Details

Edit Workflow Attributes

Name:
My first workflow

Tags:
🏷

Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

Workflows in Galaxy

NeLS   galaxy-uit.bioinfo.no   Analyze Data   Workflow   Shared Data ⌄   Visualization ⌄   Admin   Help ⌄   User ⌄   Using 48%

Tools

search tools

GENERAL GALAXY TOOLS

Get Data
Send Data
Collection Operations
Text Manipulation
Filter and Sort
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Metagenomics
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NGS: QC and Manipulation
NGS: Picard
NGS: Mapping and Sequence analysis
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Transcriptomics
NGS: SAM-tools
Genome Diversity

Workflows
▪ All workflows

Workflow Canvas | My first workflow

Details

Edit Workflow Attributes

Name:
My first workflow

Tags:

Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow

Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

Tools

Canvas navigation

Workflows in Galaxy

Workflows in Galaxy

Workflows in Galaxy

Sharing a workflow in Galaxy

Go back to Workflows List

Workflow ' My first workflow'

Share

This workflow is currently restricted so that only you and the users listed below can access it.

Make Workflow Accessible via Link

Generates a web link that you can share with other people so that they can view and import the workflow.

Make Workflow Accessible and Publish

Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's Published Workflows section, where it is publicly listed and searchable.

You have not shared this workflow with any users yet.

Share with a user

Export

Download   workflow as a file so that it can be saved or imported into another Galaxy server.

This workflow must be accessible. Please use the option above to "Make Workflow Accessible and Publish" before receiving a URL for importing to another Galaxy.

Create image   of workflow in SVG format

Export to the www.myexperiment.org site.

myExperiment username:

username

myExperiment password:

password

Export to myExperiment

Import shared history

Histories shared by other users can be copied into your history

Accessing the documentation

The documentation in Pages can accessed by users under the "Pages" tab

Accessing the documentation

The description of the workflow including an embedded overview is available