Making Galaxy User Interface Pluggable with Webhooks

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#usegalaxy

30JUN17
What do we do?
What do we have?
### Single-end or paired-end reads

- **Single-end**

**RNA-Seq FASTQ/Fasta file**

- 11: CSM61182_untreant_single_chr4.fastq

**Custom or built-in reference genome**

- Use a built-in index
- Built-ins were indexed using default options

**Reference genome with or without an annotation**

- Use genome reference without built-in gene-model
- Must the index have been created WITH a GTF file (if not you can specify one afterward).

**Select reference genome**

- No options available
- If your genome of interest is not listed, contact the Galaxy team (---genomeDir)

**Gene model (.gtf/.gtf2) file for splice junctions**

- Nothing selected
- Exon junction information for mapping splices (---sjdbGTFfile)

**Length of the genomic sequence around annotated junctions**

- 100

**Count number of reads per gene**

- Yes

**Other parameters (seed, alignment, and chimeric alignment)**

- Use Defaults

**Job Resource Parameters**

- Use default job resource parameters

### What it does

**STAR** is an ultrafast RNA-seq aligner.

**Extra SAM attributes**

The standard option includes the following four attributes:
Expectation: Rich user experience

- Galaxy’s user interface (UI) did not allow the features familiar for users of services like Facebook, Gmail, GitHub.
- This has changed in recent years and we are starting to leverage that.
  - Drag & Drop datasets
  - Propagating tags
  - Tours
Problem: One Galaxy does not fit all

- The community reaches far and wide in their interests.
- Instances use different data structures, processes, tooling, paradigms.
Galaxy Webhooks
Inspiration

- GMail Labs
- Browser plugins
- Google Drive extensions
Approach

- Pre-defined ‘high interest’ entry points
  - Top menu
  - Tool menu
  - Tool/Workflow submission page
  - History menu
Menu webhooks
Create a Docker flavour of this instance:

The text area on the right shows the list of installed tools on this Galaxy instance. You can use it to build a custom Galaxy flavour based on the same tools. Keep in mind that this list only contains tools which can be installed from a toolshed.

1. Save this list as a `.yaml` file and edit it according to your needs. You might want to add or remove tools.
2. Follow this guide on how to create a new Galaxy Docker flavour. Don’t forget to add and install the tool list with:

ADD my_tool_list.yml $GALAXY_ROOT/my_tool_list.yml

and

RUN install-tools $GALAXY_ROOT/my_tool_list.yml

$ ansible-playbook tools.yml -i "my.awesome.galaxy.org --extra-vars galaxy_tools_api_key=<secret>"
Tool menu webhooks
Submission webhooks
1 job has been successfully added to the queue – resulting in the following datasets:

145: Cut on data 3

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.
1 job has been successfully added to the queue – resulting in the following datasets:

92: Cut on data 80

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

Price Calculator
You're using 0.000082 GB of data, this would cost you 0.0000025 $/month on Amazon S3

Amount of standard file storage you need.

Total Price: 30.97 $/month
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**Runtime Plot**

Cut1’s observed runtime

![Runtime Plot Graph](image)
Related publications:

**Faster single-end alignment generation utilizing multi-thread for BWA.**
Jo H, Koh G.
PMID: 28405948
Similar articles

**Verification and validation of bioinformatics software without a gold standard: a case study of BWA and Bowtie.**
Giannoulatou E, Park SH, Humphreys DT, Ho JW.
PMID: 25521810 Free PMC Article
Similar articles

**Fast and accurate short read alignment with Burrows-Wheeler transform.**
Li H, Durbin R.
PMID: 19451168 Free PMC Article
Similar articles
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How do you like using this tool in Galaxy?

⭐⭐⭐⭐⭐

How experienced are you using this tool?

- first time user
- beginner
- intermediate
- advanced
- expert

Any feedback you have for us?
Envisioned effects

- Specialized instance-specific features.
- Rapid prototyping that enables experiments.
- Diverse and accelerated contributions to the interface.
Future direction

- Monitor community's efforts in webhook development.
- Evaluate the entry points and design new if there is a demand.
- Adopt proven webhooks to the codebase.
Webhooks alter the user interface and provide custom features.

Building a webhook is faster and easier than contributing to the codebase.

Check out training.galaxyproject.org to get started.
Thank you
Galaxy Community & Team

Core Team

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