

Galaxy Update

Dannon Baker
Galaxy Team
Emory University

Topics

- API
- Automatic Parallelization
- Tool Shed
- ?

API Overview

- RESTful API supporting CRUD operations
- Uses generated keys for per-user authentication
 - No username/password
 - No credential caching (via keys)
- Request parameters and responses are in JSON (JavaScript Object Notation)

Quickstart

Analyze Data

Workflow

Shared Data ▾

Cloud ▾

Admin

Help ▾

User ▾

Logged in as foo@foo.com

Preferences

Logout

Saved Histories

Saved Datasets

Saved Pages

API Keys

API Key

API key:

9fd51399610c93d44ab96aba8181

[Generate a new key now](#) (invalidates old key)

API key will allow you to access Galaxy via its web API (documentation forthcoming). Please note that this key is tied to your account, and should be treated with the same care as your login password.

Raw GET Example

```
>> GET /api/histories?key=966354fc14c9e427cee380ef50a72a21
<< [
<<   {
<<     'url': '/api/histories/d0bfe935d0f5258d',
<<     'id': 'd0bfe935d0f5258d',
<<     'name': 'Demo History 1'
<<   }
<< ]
```

Making the Calls

per methods exist (in /scripts/api/) to make calls easier

`scripts/api/{action}.py <api key> http://<ip>/api/{module}/[id]`

create | display | update | delete

y: obtained from the UI

e: datasets | forms | histories | libraries | permissions | quotas
ts | roles | samples | tools | users | visualizations | workflows

dataset_id / history_id / library_id / ...

Sample Invocations

get a history

```
python <api_key> https://localhost:8080/api/histories name="from API"
```

get all histories

```
python <api_key> https://localhost:8080/api/histories
```

get information about a history

```
python <api_key> https://localhost:8080/api/histories/6b5cf7e7ef797b21
```

get datasets in a given history

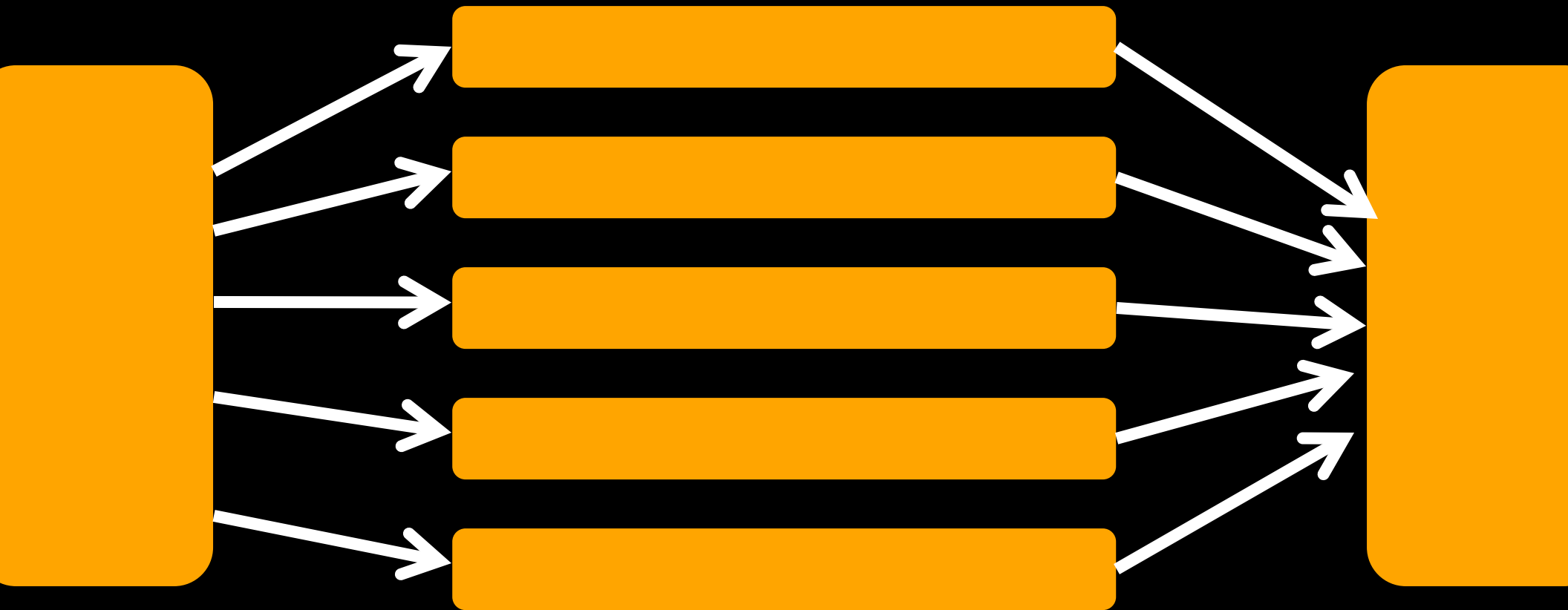
```
python <api_key> https://localhost:8080/api/histories/6b5cf7e7ef797b21/datasets
```

delete a history

End-to-end pipelines

- Push data from instruments to Galaxy
- Execute a workflow
- Associate with a user or add to a Data Library
- Export outputs
- Or a totally custom interface to Galaxy

Automatic Parallelism



input

BLAST/strip?

output

Parallelism

- Take maximum advantage of available resources
- Less costly fault recovery (spot instances)
- Overhead in splitting time
- Increased temporary storage requirement

Use it now

`use_tasked_jobs = True`

Tools supported:

BLAST, BWA, Bowtie

Yours?

Try it for your tool

<parallelism

method = "multi"

split_inputs = "query"

split_mode = "number_of_parts"

split_size = "4"

shared_inputs = "subject"

merge_outputs = "output1"

/>

Advanced Splitting

E

No disk write required

But it is slightly slower
to read

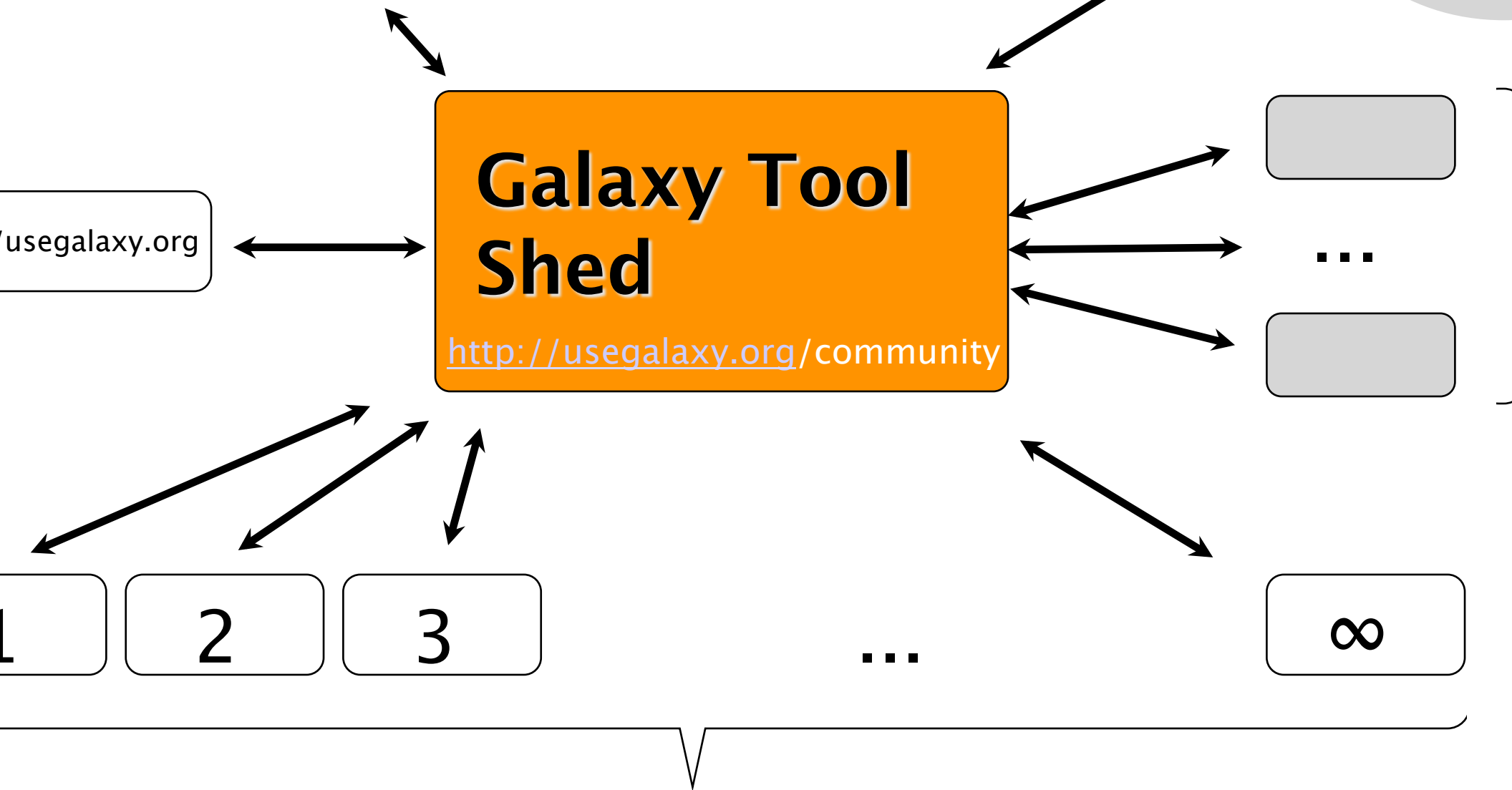
re splitters:

Chromosome based?

```
1 114 13 145 160 176 191 206 221 237 252 32 48
10 115 130 146 161 177 192 207 222 238 253 33 49
100 116 131 147 162 178 193 208 223 239 254 34 5
101 117 132 148 163 179 194 209 224 24 255 35 50
102 118 133 149 164 18 195 21 225 240 256 36 51
103 119 134 15 165 180 196 210 226 241 257 37 52
104 12 135 150 166 181 197 211 227 242 258 38 53
105 120 136 151 167 182 198 212 228 243 259 39 54
106 121 137 152 168 183 199 213 229 244 26 4 55
107 122 138 153 169 184 2 214 23 245 260 40 56
108 123 139 154 17 185 20 215 230 246 261 41 57
109 124 14 155 170 186 200 216 231 247 27 42 58
11 125 140 156 171 187 201 217 232 248 28 43 59
110 126 141 157 172 188 202 218 233 249 29 44 6
111 127 142 158 173 189 203 219 234 25 3 45 60
112 128 143 159 174 19 204 22 235 250 30 46 61
yoplait@gizmo ~/work/mountpoint cat all.seqs/99
>8
CGCAGGCCGCAATCTGGTGTGGATTATCTGCGTGCCCATCGTGCTCCTGTAC
GCTTCCTGCTGCTGCTGTTTCATGAATGACCCGCAGGGTCCGGCCATCGACAC
CTGCGCATCCTGTCTCCCTTCTATTTGTGGTGTGCTCAAGCTGGTCACTGA
GGCTGCGGCATGATGGTGCGC
>9
CAGCATCAGGCAGCCAACCAGGATGGCGGCATCGGGCAGGGTGAGGGAAACG
TGATCGGGAAGAGGATCTTCTCAGTCTTGGAAACCTTGCGCGGGCTTTCCAT
TCTTTTGTGGTG
>10
CAAGTACAGCAGATGCAGAAACAGCATGATACGCAAATCCACAATCTCAGAG
GGAACCTTGACATGAAAGAAAAGAACTGTACGGCTCGCCAGAATCATAGAC
GGTTTCCGGTATGTTTCAGGGAAA
>11
GTTGTTTGCCTATTTACAACATTCTATATTATGGTTGGATACCTGTAAGATT
TCCATCTGGTATTTCTTGATGCGTCTTTCTACGCTTTTTGGGTTTCGTGTTAC
GGACGGAATT
>12
GTAATTGACATGGTTTCGTGTGGCAACTTACGTGCACCAGATGCCTGCTGCAA
AGATGCCAAGGCACACAGGGGATAGG
>13
```

Galaxies on private clouds

Galaxies on public clouds



Tool Shed - Developer

Galaxy Tool Shed

Galaxy Tool Shed Repositories Help User

Galaxy Tool Shed

Repositories

- [Browse by category](#)
- [Browse all repositories](#)
- [Browse my repositories](#)
- [Create new repository](#)

Create Repository

Name:

Synopsis:

Detailed description:

Categories

- Fasta Manipulation
- Format Converters
- Graphics
- SAM
- Text Manipulation

Multi-select list - hold the appropriate key while clicking to select multiple categories.

Tool Shed - Developer

Galaxy Tool Shed

Galaxy Tool Shed

Repositories

Admin

Help

User

Tool Shed


Repositories

[View by category](#)

[View all repositories](#)

[View my repositories](#)

[Create new repository](#)




 The file '1filtering.tar' has been successfully uploaded to the repository

Browse filter

Clone this repository:

hg clone <http://greg@127.0.0.1:9009/repos/greg/filter>

Contents:

-  filter
 -  filtering.py
 -  filtering.xml

Click on a file to display its contents below. You may delete files from the repository by clicking the check box next to each file and clicking the **Delete selected files** button.

Message:

Deleted selected files

This is the commit message for the mercurial change set that will be created if you delete selected files.

Manage repository

Upload files to repository

View change log

Download as a .tar.gz file

Download as a .tar.bz2 file

Download as a zip file

Tool Shed - User

The screenshot displays the Galaxy Administration web interface. At the top, the title bar reads "Galaxy Administration". Below it is a navigation bar with the "Galaxy" logo and several menu items: "Analyze Data", "Workflow", "Shared Data", "Admin" (which is highlighted), "Help", and "User".

On the left side, there is a sidebar menu with the following sections:

- Administration
- Security
 - Manage users
 - Manage groups
 - Manage roles
- Data
 - Manage quotas
 - Manage data libraries

The main content area is titled "Accessible Galaxy tool sheds". It contains a dropdown menu currently set to "Bx tool shed". A tooltip is visible over the dropdown, listing the following actions:

- Browse valid repositories
- Search for valid tools
- Search for workflows

Administration

Security

- [Manage users](#)
- [Manage groups](#)
- [Manage roles](#)

Data

- [Manage quotas](#)
- [Manage data libraries](#)

Server

- [Reload a tool's configuration](#)
- [Profile memory usage](#)
- [Manage jobs](#)
- [Manage installed tool shed repositories](#)

Tool sheds

- [Search and browse tool sheds](#)

Form Definitions

- [Manage form definitions](#)

Sample Tracking

- [Manage sequencers and external services](#)
- [Manage request types](#)
- [Sequencing requests](#)
- [Find samples](#)

Valid repositories

Name ↓	Synopsis	Revision	Owner
abyss_toolsuite ▼	This suite contains Abyss and Abyss-PE config files and wrappers for Galaxy	0:92636934a189	edwar
agile_wrapper ▼	Quickly match reads to a reference genome or sequence file	0:d6a426afaa46	simor
assemblystats ▼	Summarise an assembly (e.g. N50 metrics)	0:6544228ea290	konra
bam_to_bigwig ▼	Calculates coverage from a BAM alignment file	1:0ff100a057ef	brad-
bam_to_fastq ▼	Convert BAM file to fastq	0:5a9ada9a3191	brad-
barcode_splitter ▼	Moves selected barcode files into your history.	0:bc23f6946bb8	jjohns
blast ▼	Modified Galaxy wrappers add support for makeblastdb files and add dustmasker	0:f3ac34855f5e	edwar

Tool Shed

Galaxy Administration

galaxy

Analyze Data

Workflow

Shared Data

Admin

Help

User

Administration

[Add users](#)

[Add groups](#)

[Add roles](#)

[Add quotas](#)

[Add data libraries](#)

[View a tool's configuration](#)

[View memory usage](#)

[View jobs](#)

Install to local Galaxy

Tool Shed Actions

Repository filter

Revision:

1:10456b4659aa

Preview tools and inspect metadata by tool version

Tools - click the name to preview the tool and use the pop-up menu to inspect all metadata

name	description	version	requirements
Filter ▼	data on any column using simple expressions	1.0.1	none

Tool Shed - User

Galaxy Administration

Galaxy Analyze Data Workflow Shared Data **Admin** Help User

Administration

- [Manage users](#)
- [Manage groups](#)
- [Manage roles](#)
- [Manage quotas](#)
- [Manage data libraries](#)
- [Load a tool's configuration](#)
- [Manage file memory usage](#)
- [Manage jobs](#)
- [Manage installed tool shed repositories](#)
- [Search and browse tool sheds](#)

Definitions

✓ Revision 10456b4659aa of repository filter has been loaded into tool panel section Filter and Sort.

⚠ The core Galaxy development team does not maintain the contents of many Galaxy tool shed repositories. Some repository tools may include code that produces malicious behavior, so be aware of what you are installing.

If you discover a repository that causes problems after installation, contact [Galaxy support](#), sending all necessary information, and appropriate action can be taken.

[Contact the repository owner](#) for general questions or concerns.

⚠ Installation may take a while, depending upon the size of the repository contents. Wait until a message is displayed in your browser after clicking **Install** button below.

Load tools into tool panel

Tool panel section:

- Get Data
- Filter and Sort
- Short read mapping

Tool Shed

Simple installation to galaxy of tools, workflows

- Dependencies

Automatic update notifications

Multiple Tool Versions installed

Tool Shed References

- Main Tool Shed: usegalaxy.org/toolshed
- ISMB Tech Track w/ Greg – Sunday, TT10

if more_time:

- S3ObjectStore
- Documentation
 - `<galaxy_dir>/doc – `make html``
- Join us in [#galaxyproject](#) on [irc.freenode.net](#)
- Acknowledgements:
 - Galaxy Team, Community, people who send pull requests