

• Plug Apollo into your workflow

https://toolshed.g2.bx.psu.edu/view/gga/suite_apollo/

<https://pypi.org/project/apollo/>

<http://gonramp.wustl.edu/>

@erasche @abretaud

@luke-c-sargent @Yating-L



```
pip install pyarrow
pip install apollo
```



```
$arrow groups create_group university
$arrow users get_users | \
  jq '[] | select(.username | \
contains("@tam.u.edu")) | .username' | \
  xargs -nl arrow users add_to_group
university
```

```
from apollo import ApolloInstance
wa = ApolloInstance('https://fqdn/apollo',
                    'jane.doe@fqdn.edu', 'password')
orgs = wa.organisms.add_organism(
    "Yeast",
    "/path/to/jbrowse/data")
```

Full-screen view admin@galaxy.org

Annotations Tracks Ref Sequence

Annotation Name

ctgA

1-1 of 1

Name	Type	Length	Updated
No results			

History

search datasets

Unnamed history

6 shown, 2 deleted

13.6 MB

7: WA2: Annotate on data 6

6: WA2: Add Organism on data 3

5: WebApollo Credentials

2 lines

format: txt, database: 2

Username: admin@galaxy.org



Free on Galaxy Server

<https://annotation.usegalaxy.eu/>

Track and Variant Services

