
GenomeSpace Guide for Galaxy Users and Developers Documentation

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For Users

1.1 Associate your account with GenomeSpace's OpenID

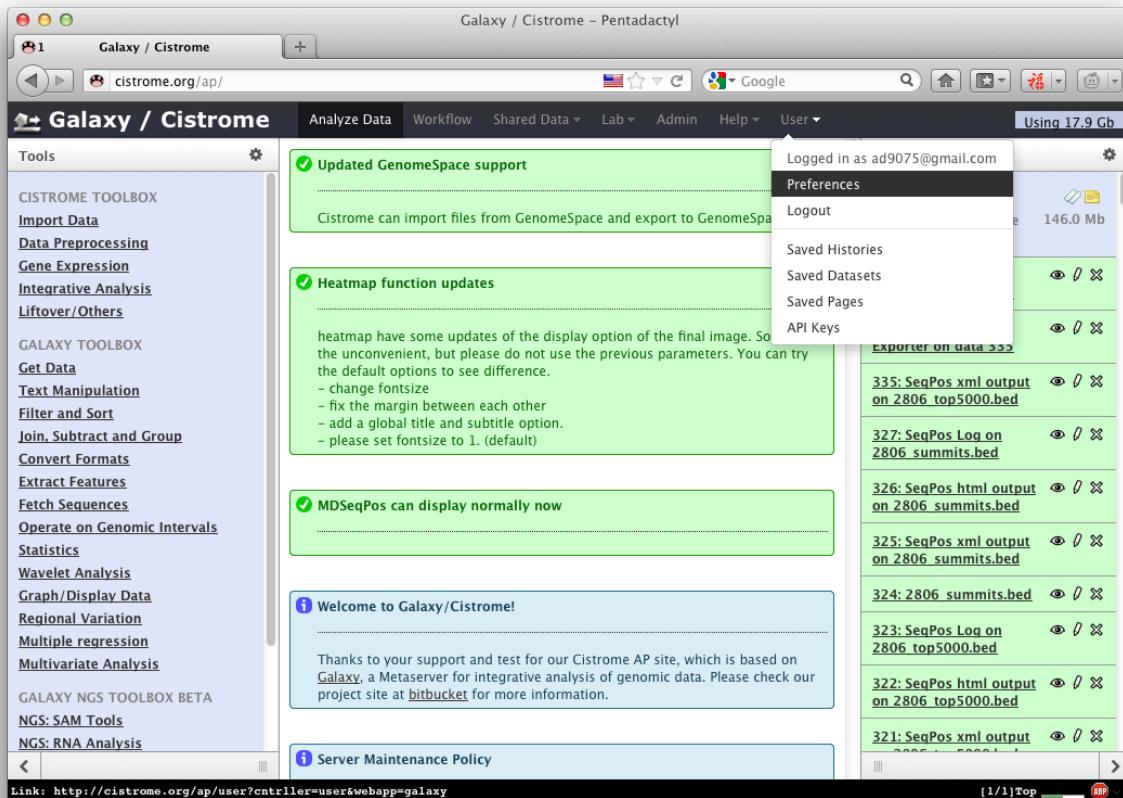


Fig. 1.1: Log in Galaxy/Cistrome. Then click User -> Preferences in the Navigation Toolbar

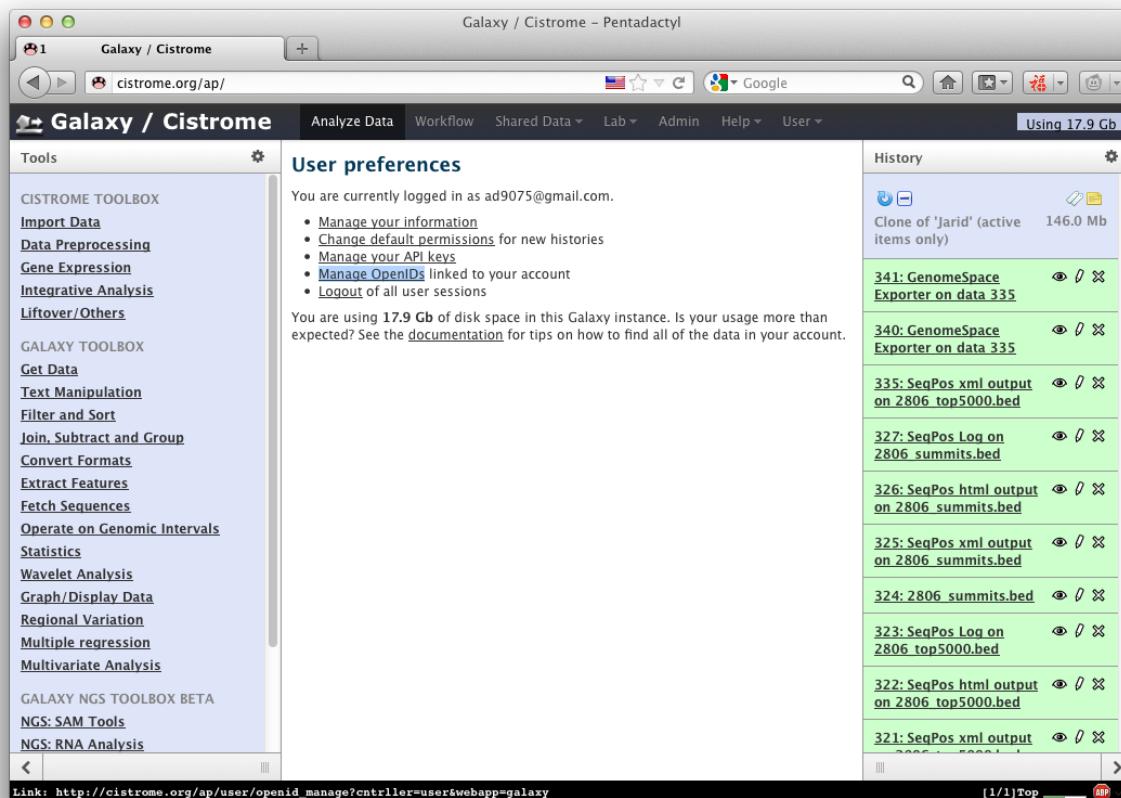


Fig. 1.2: In the new dialog, click Manage OpenIDs

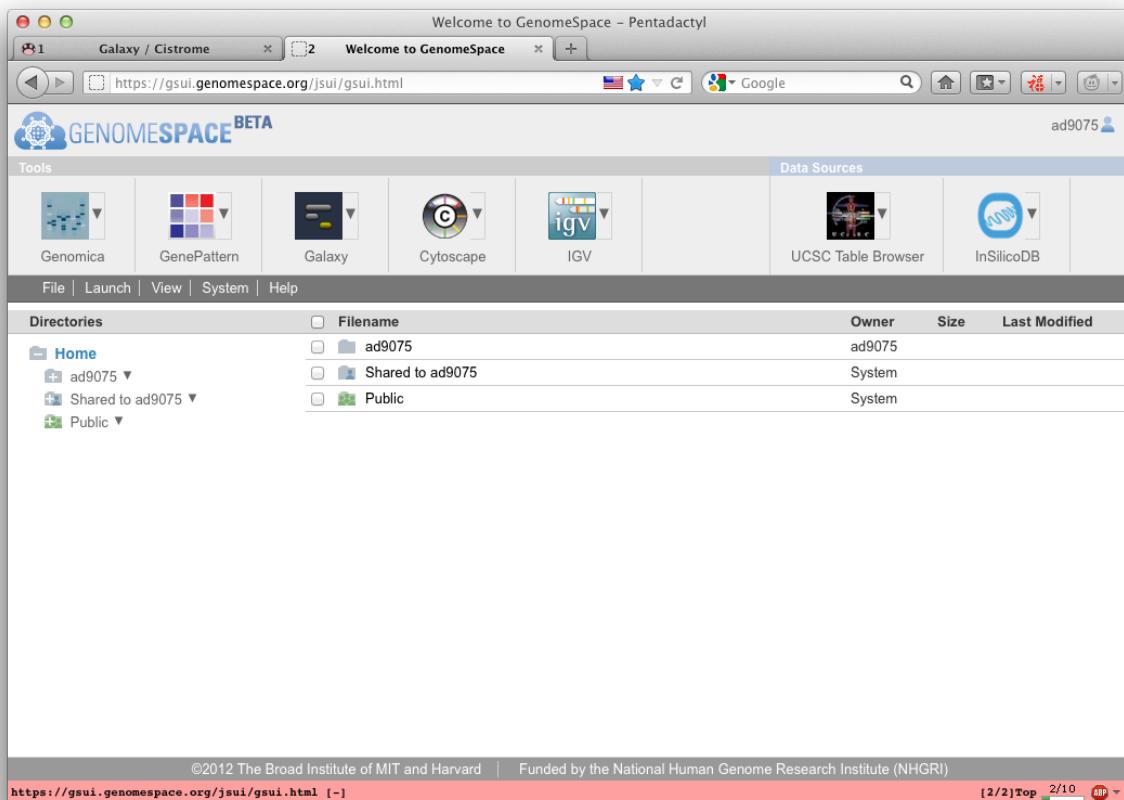


Fig. 1.3: Make sure you have already logged in GenomeSpace

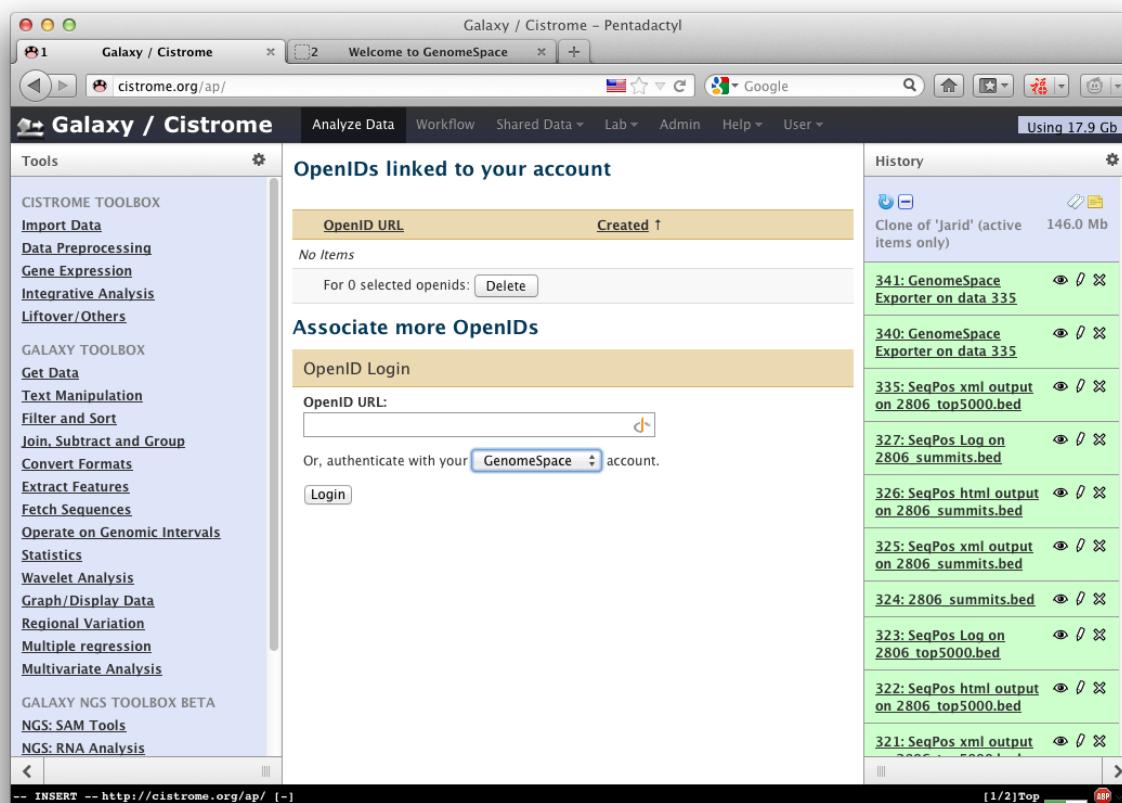


Fig. 1.4: Select GenomeSpace in the Combo box of Associate more OpenIDs section. Then click Login button in the bottom.

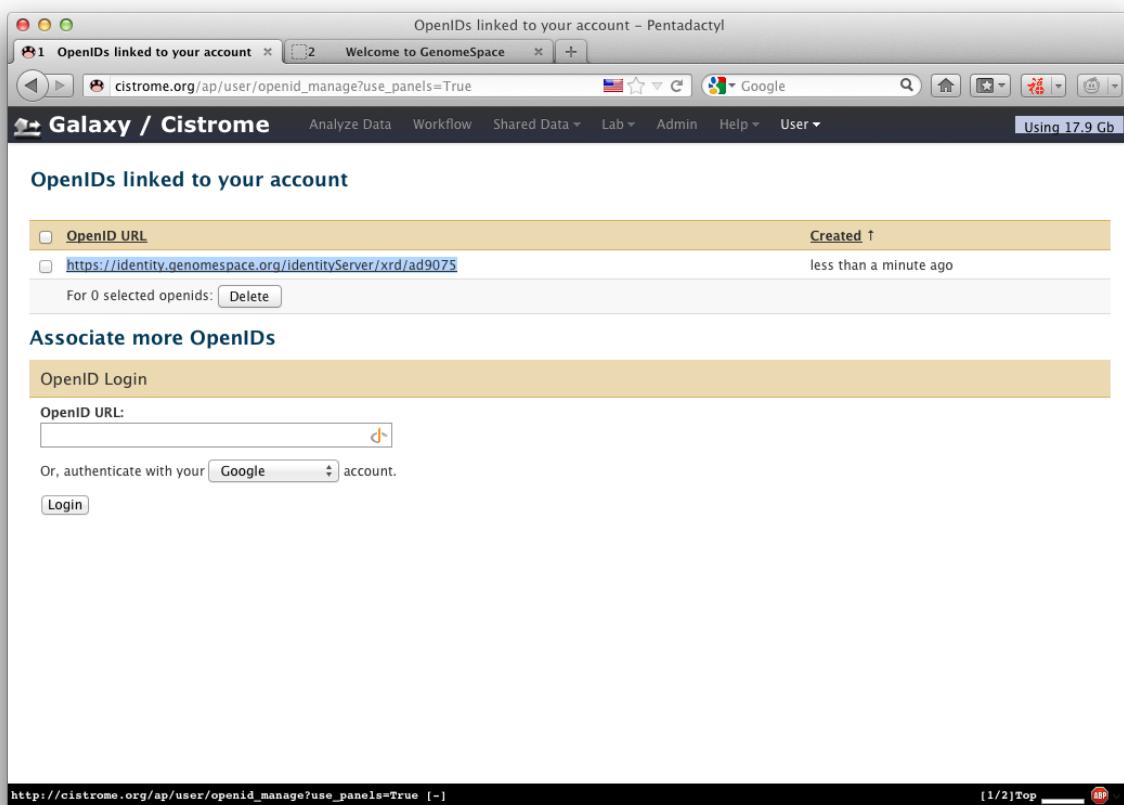


Fig. 1.5: Congratulations! Your Galaxy/Cistrome account is linked to the OpenID of GenomeSpace now and you can use everything GenomeSpace provides for Galaxy/Cistrome now.

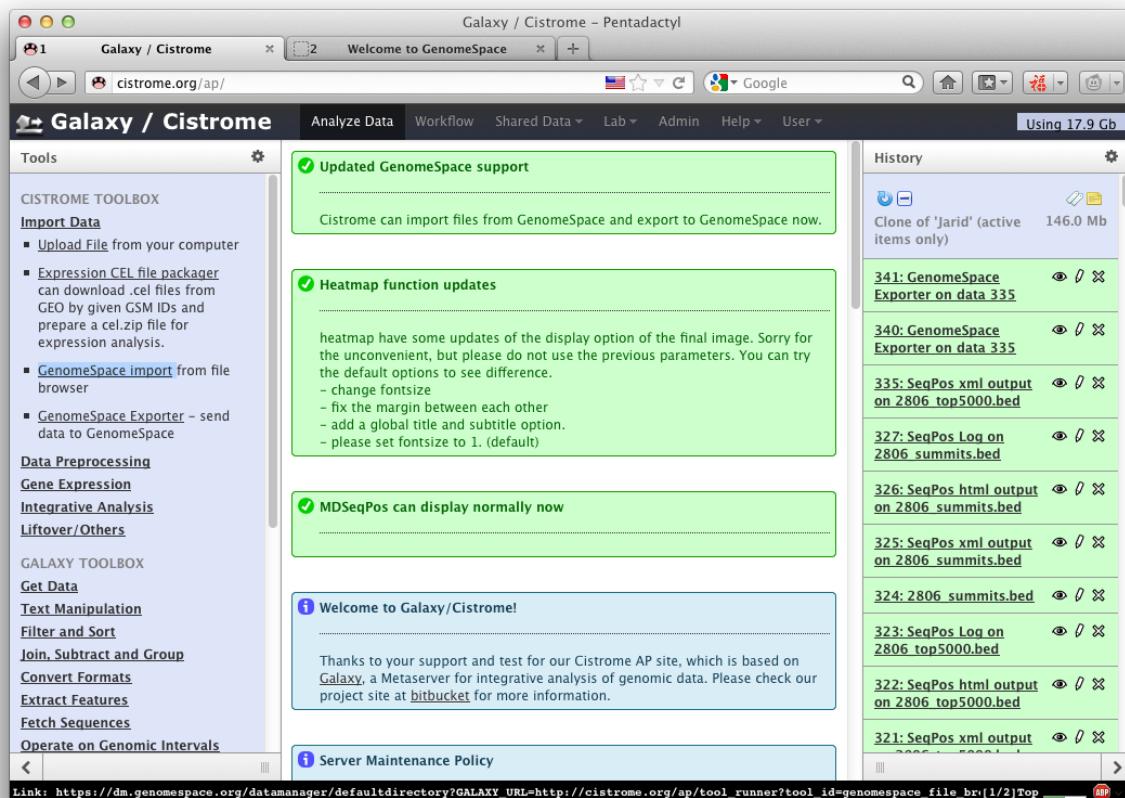


Fig. 1.6: In the Toolbox panel, click Import Data -> GenomeSpace import

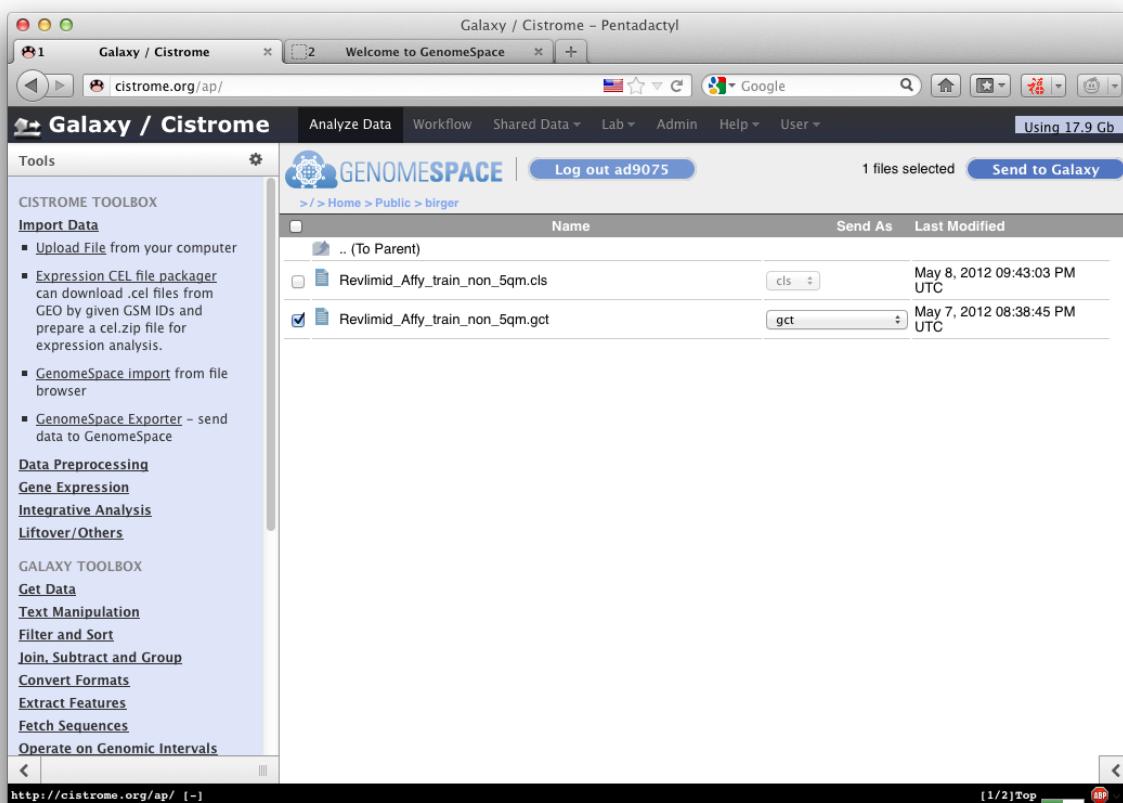


Fig. 1.7: Select one or more data in the GenomeSpace frame within Galaxy/Cistrome page, then click Send to Galaxy button in the top right.

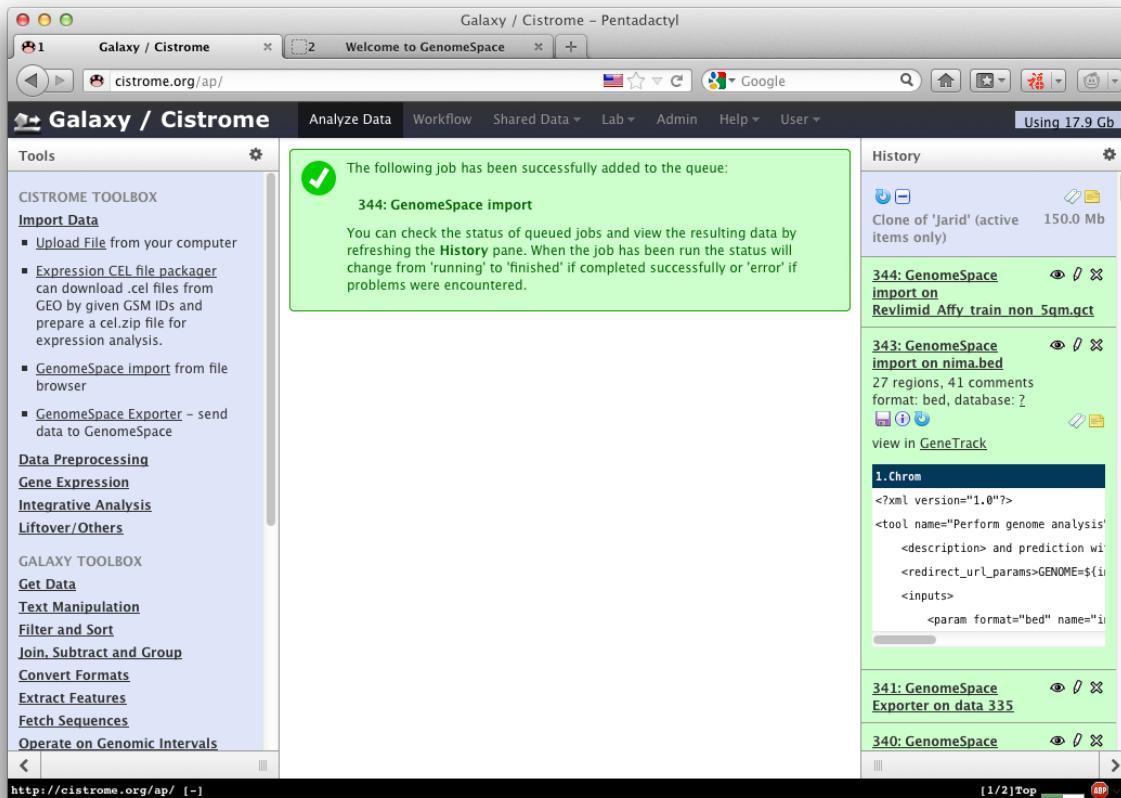


Fig. 1.8: Then your data will be imported to Galaxy/Cistrome successfully.

1.2 Import data from GenomeSpace

1.3 Export data to GenomeSpace

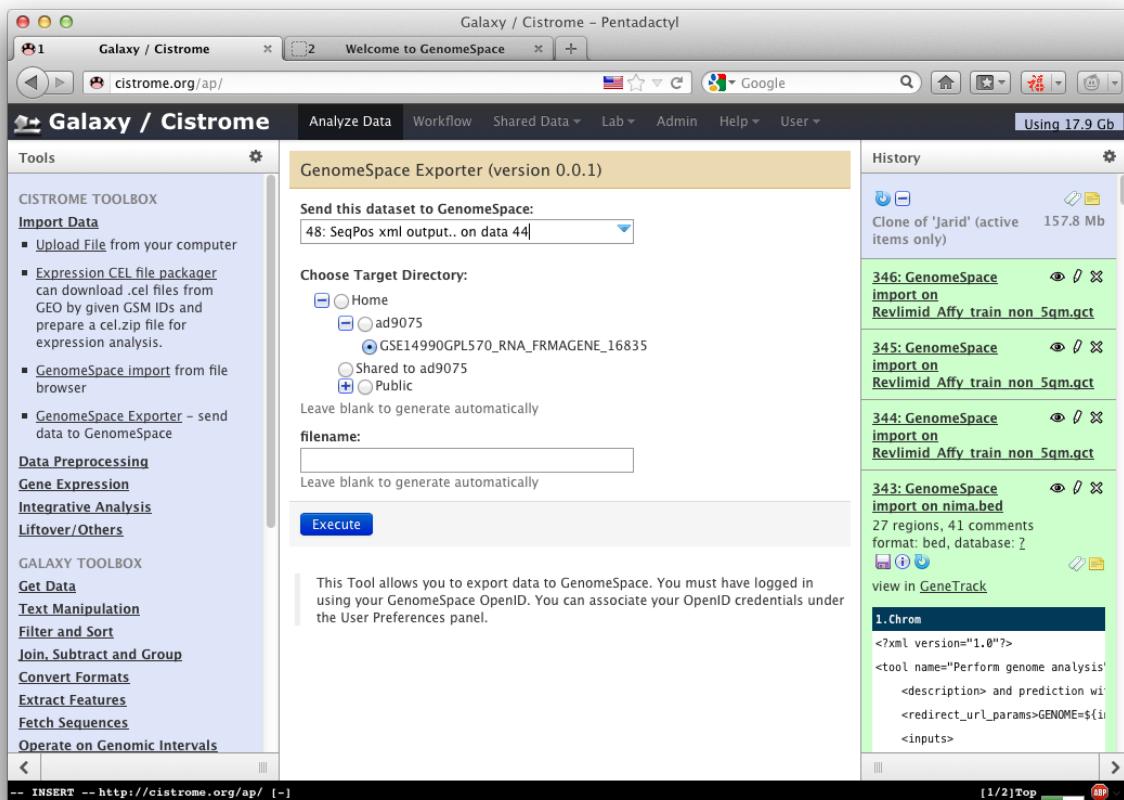


Fig. 1.9: To export data to GenomeSpace is also easy. Click Import Data -> GenomeSpace Exporter, select your data to send and Target Directory, then click Execute.

For Developers

If anyone want to enable the GenomeSpace functions, following these steps:

1. Pull the changesets from [Galaxy Distribution](#) and update your repository.
2. Add GenomeSpace tool to the Toolbox (see details below)
3. Activate OpenID in the Configuration file
4. Restart your Galaxy instance, and these tools will be loaded automatically.

2.1 Add GenomeSpace tool to the Toolbox

Add these lines into the section you want to add the GenomeSpace tools:

```
<tool file="genomespace/genomespace_file_browser_prod.xml" />
<tool file="genomespace/genomespace_importer.xml" />
<tool file="genomespace/genomespace_exporter.xml" />
```

such as:

```
<?xml version="1.0"?>
<toolbox>
  <section name="Import Data" id="dataimporting">
    <tool file="data_source/upload.xml"/>
    <tool file="genomespace/genomespace_file_browser_prod.xml" />
    <tool file="genomespace/genomespace_importer.xml" />
    <tool file="genomespace/genomespace_exporter.xml" />
  </section>
</toolbox>
```

2.2 Activate OpenID in the Configuration file

In the `universe_wsgi.ini` file, enable the OpenID authenticatio like this

```
# Enable authentication via OpenID. Allows users to log in to their Galaxy
# account by authenticating with an OpenID provider.
enable_openid = True
```