

ExomeAI

- ✓ WES data
- ✓ Only tumor samples are required
- ✓ BAF or VCF file
- ✓ detecting AI (including LOH) segments shared among all or some of the tumor samples
- ✓ Removing false positives using a large internal control database

Registering at ExomeAI

- only email address is required
- use all features: managing your data , space, results, histories, ...
- come back to previous sessions after logout
- ...

The image shows a web interface for ExomeAI. At the top is a dark navigation bar with the 'ciLab' logo and links for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The 'User' dropdown menu is open, showing 'Login' and 'Register' options. Below the navigation bar is a registration form titled 'Create account'. The form contains the following fields and text:

- Email address:** A text input field containing 'myemail@gmail.com'.
- Password:** A text input field with masked characters (dots).
- Confirm password:** A text input field with masked characters (dots).
- Public name:** A text input field containing 'user-123'.
- A paragraph of text: 'Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least four characters in length and contain only lower-case letters, numbers, and the '-' character.'
- Subscribe to mailing list:** A checkbox that is currently unchecked.
- A link: 'See [all Galaxy project mailing lists](#).'
- A 'Submit' button at the bottom.

Using the simulated dataset

Galaxy / MajewskiLab

Analyze Data Workflow Shared Data Visualization Help User

Published Histories

search name, annotation, owner, and tags

Advanced Search

Name	Annotation	Owner	Community Tags
Test_Dataset_AI_1		javad	

Data Libraries

Data Libraries Beta

Published Histories

Published Workflows

Published Visualizations

Published Pages

Galaxy / MajewskiLab

Analyze Data Workflow Shared Data Visualization Admin Help User

Using 162.3 MB

Tools 1 Load Data

search tools

1 Get Data

ExomeAI

2 Detection of AI on batch of tumor samples

Workflows

- All workflows

Detection of AI on batch of tumor samples (version 1.0)

Vcf Names:

Selection is Optional

[required] Min of BAF: 0.05

[required] Min of |BAF-0.5|: 0.0

[required] Min Proportion of variants with AI: 0.15

[required] Max Frequency in Control db: 0.005

[required] FileType: 1= VCF, 2= BAF: 2

[required] Input File1: 1: Sample1.BAF

[required] Input File2: 2: Sample2.BAF

History

Test_Dataset 763.5 KB

- 10: PerSamplePlots.tar.gz
- 9: Recurrent.txt
- 8: Recurrent.pdf
- 7: Segments.txt
- 2: Sample2.BAF
- 1: Sample1.BAF

Some results for the simulated data

ExomeAI detects a recurrent segment, the blue rectangle, shared between the two samples at about 15-20 Mb (length ~ 5Mb).

