Introduction to Babelomics 5

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GDA
International Course on
Genomic Data Analysis





Babelomics 5

Babelomics 5

Integrative open source platform with advanced functional profiling for the analysis of

- Transcriptomics
- Proteomics
- Genomics



http://www.babelomics.org

Babelomics 5





- Try it now: Enter as anonymous user
- Sign up: Create an identified user
- Log in: Log in as identified user



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- Sign up: Create an identified user
- Log in: Log in as identified user

Anonymous user

- Can access all functionalities and tools
- Data will be lost

Identified user

- Can access all functionalities and tools
- 10Gb of free disk

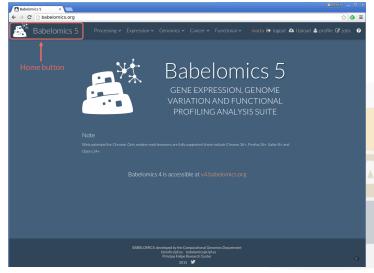
Exercise

Create a new account for yourself

- Go to Babelomics 5
- Create a new user

For help, ask or visit the logging in tutorial









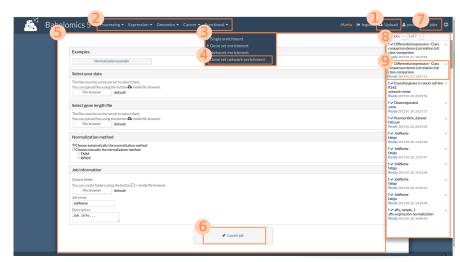






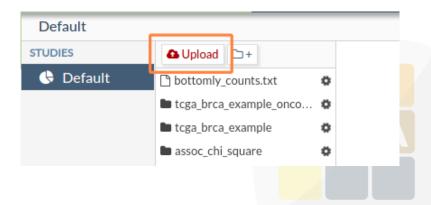


Workflow

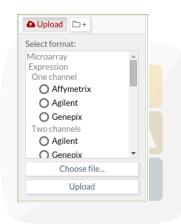








- Bioformat, more info
 - RNA-Seq: Data Matrix
- IMPORTANT: First row with rownames must begin with #NAMES
- We can remove files



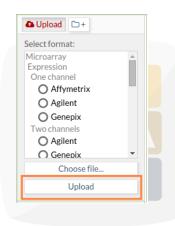
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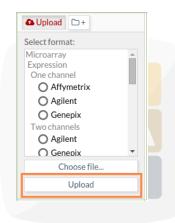
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Exercise

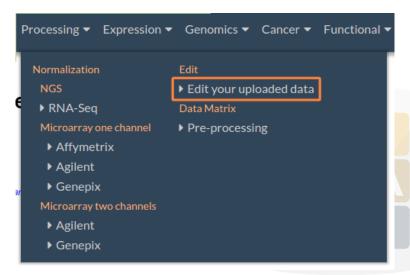
We will work with a breast cancer dataset from The Cancer Genome Atlas (TCGA). The expression matrix contains raw counts

- Go to the GDA 2016 wiki
- Oownload the brca_demo_counts_4babelomics.txt
- **6** Upload this file to Babelomics 5

For help, ask or visit the uploading data tutorial







Select your data

The files must be on the server to select them.

You can upload files using the button a inside file browser.

File browser

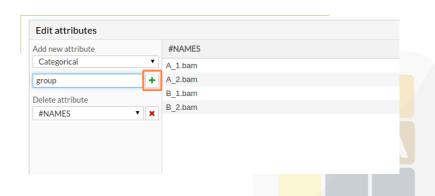
default/





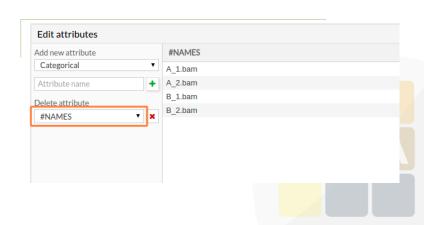


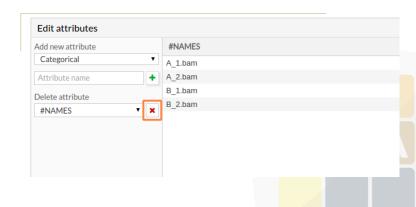


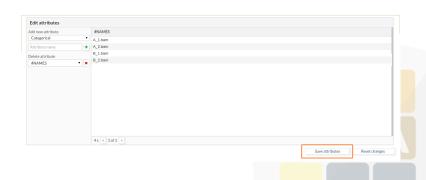


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		GDA









Exercise

The dataset of breast cancer contains healthy and tumor samples. Annotate to which class belongs each sample

- Go to the GDA 2016 wiki
- Oownload the BRCA_Normal-Basal_ED.txt
- 6 Edit the former file with the data in this experimental design

For help, ask or visit the editing data tutorial

Enjoy Babeblomics 5!

