Introduction to Babelomics 5

Máster en Bioinformática y Biología Computacional

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PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Babelomics 5

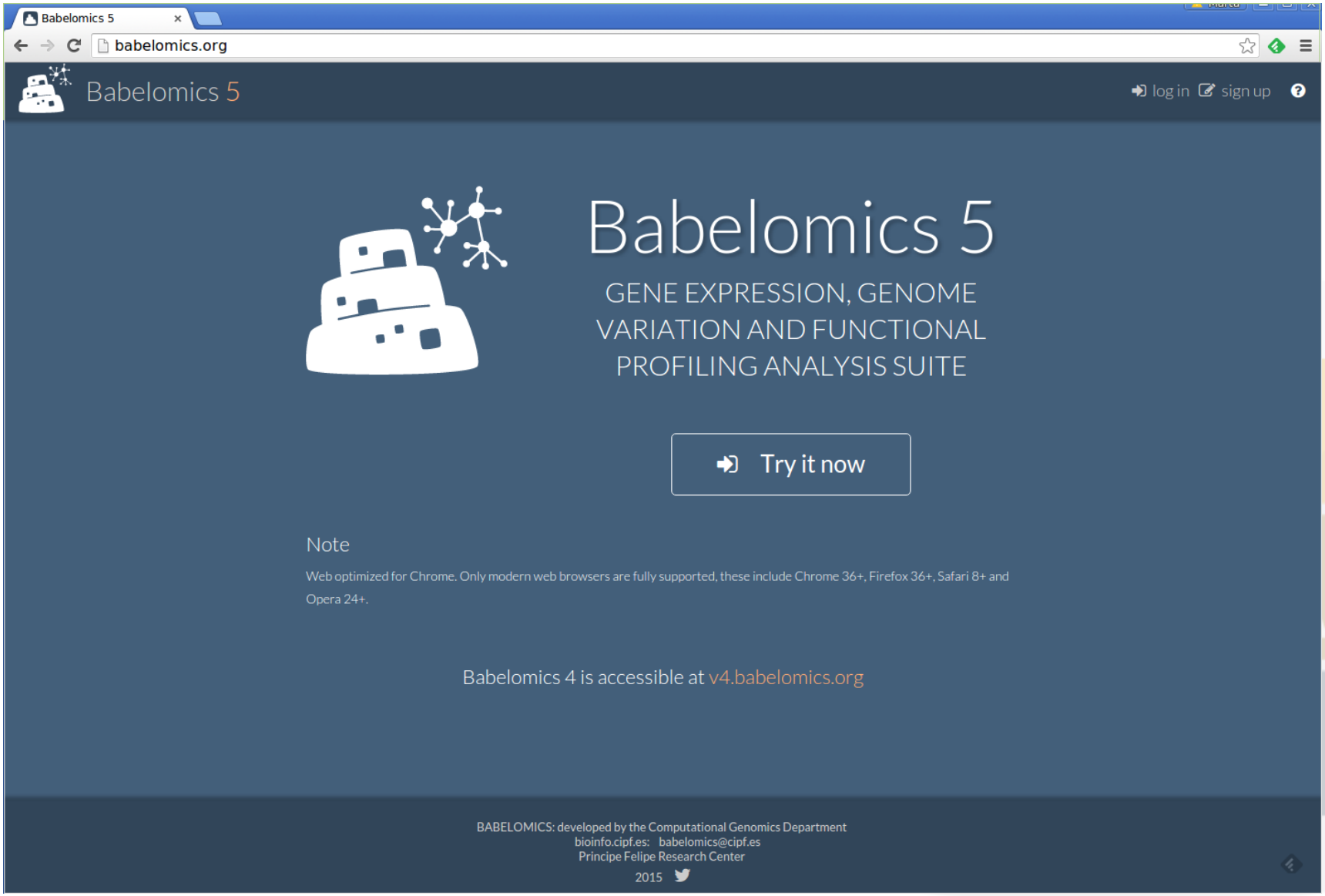
Babelomics 5

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

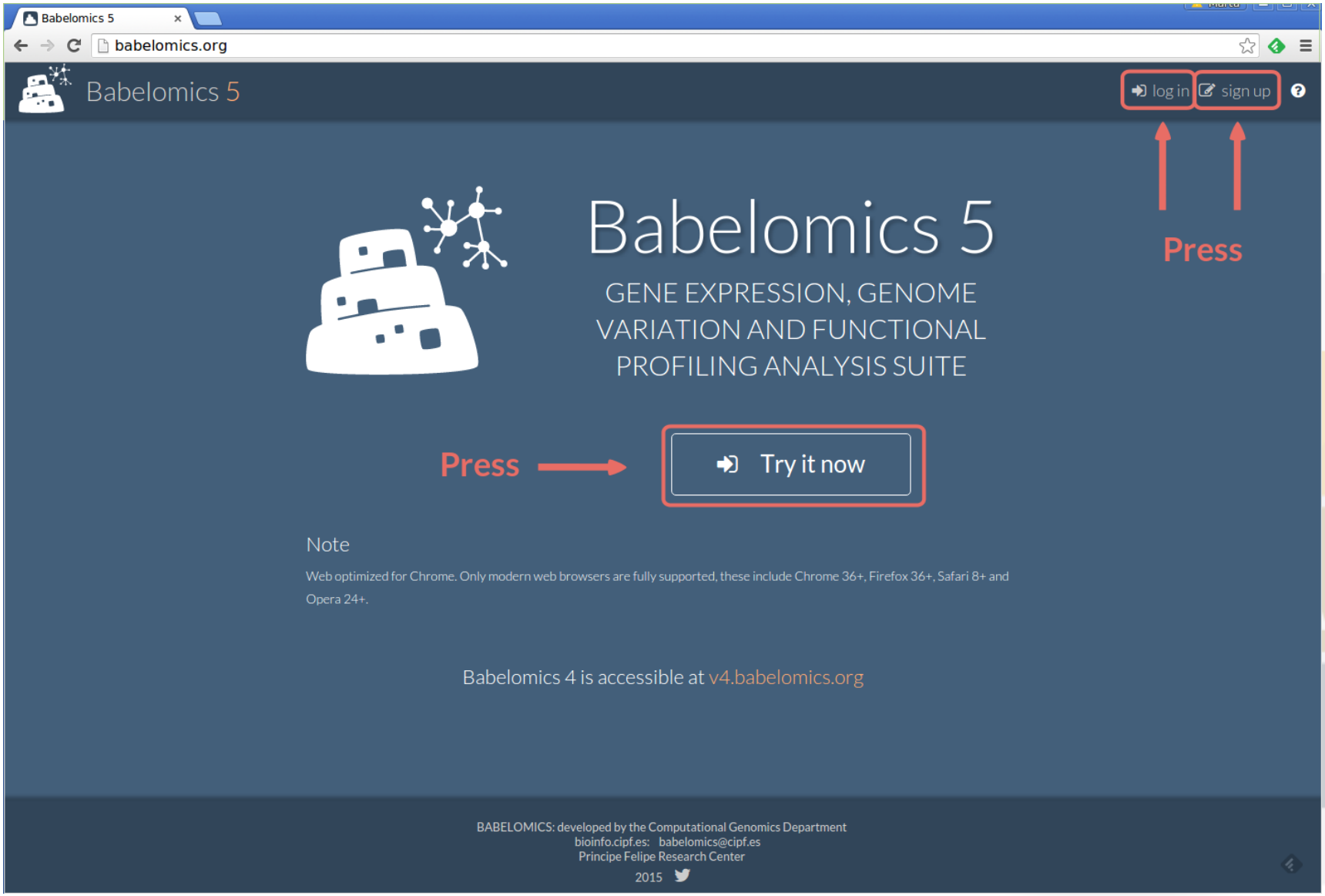
- Transcriptomics
- Proteomics
- Genomics

http://www.babelomics.org

Babelomics 5



Logging in


Babelomics 5
babelomics.org
Babelomics 5
log in
sign up
Press
Babelomics 5
GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE
Press
Try it now
Note
Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+.
Babelomics 4 is accessible at v4.babelomics.org
BABELOMICS: developed by the Computational Genomics Department
bioinfo.cipf.es: babelomics@cipf.es
Principe Felipe Research Center
2015

Logging in

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

Logging in

- **Try it now**: Enter as anonymous user
- **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

Logging in

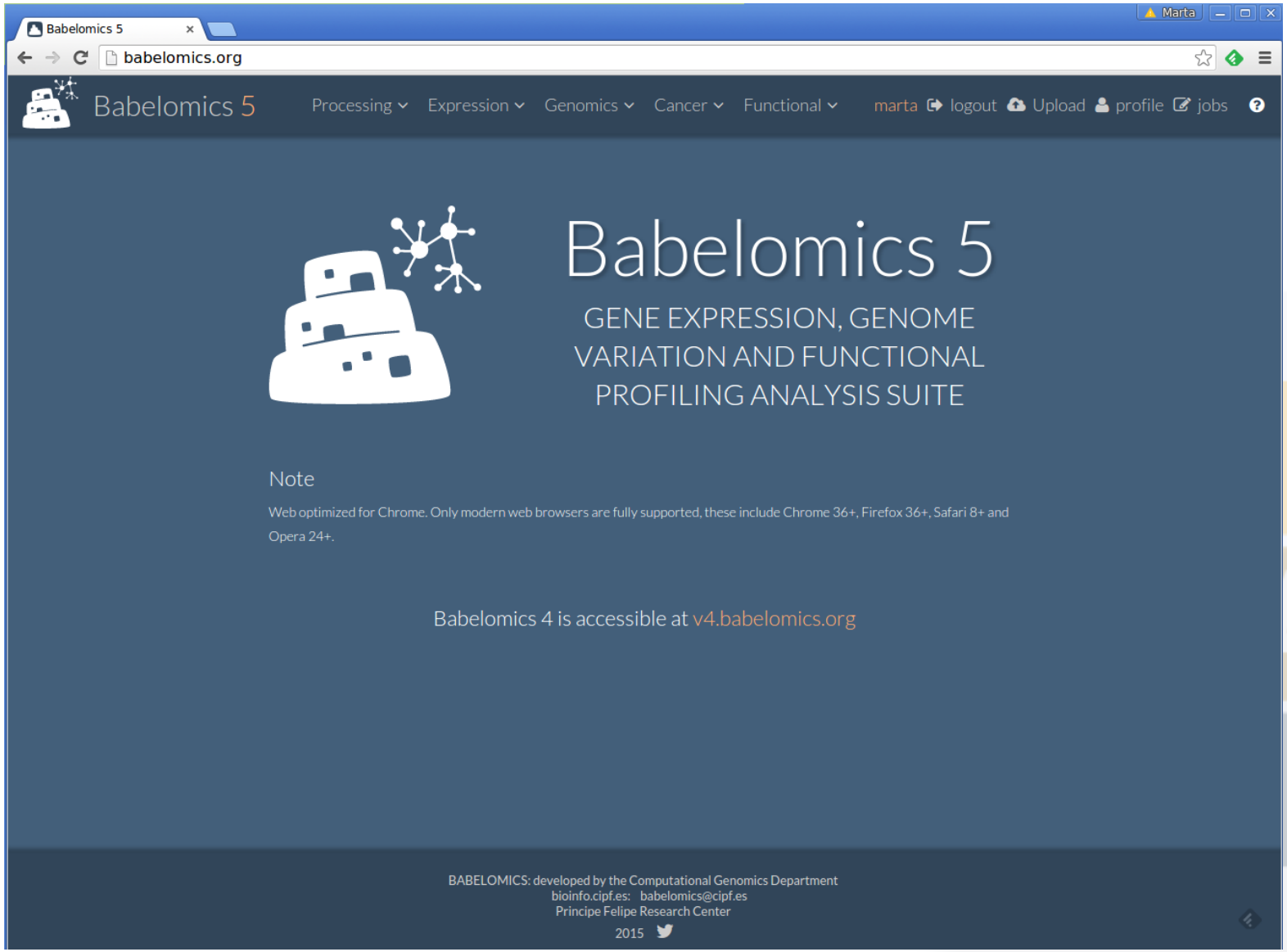
Exercise

Create a new account for yourself

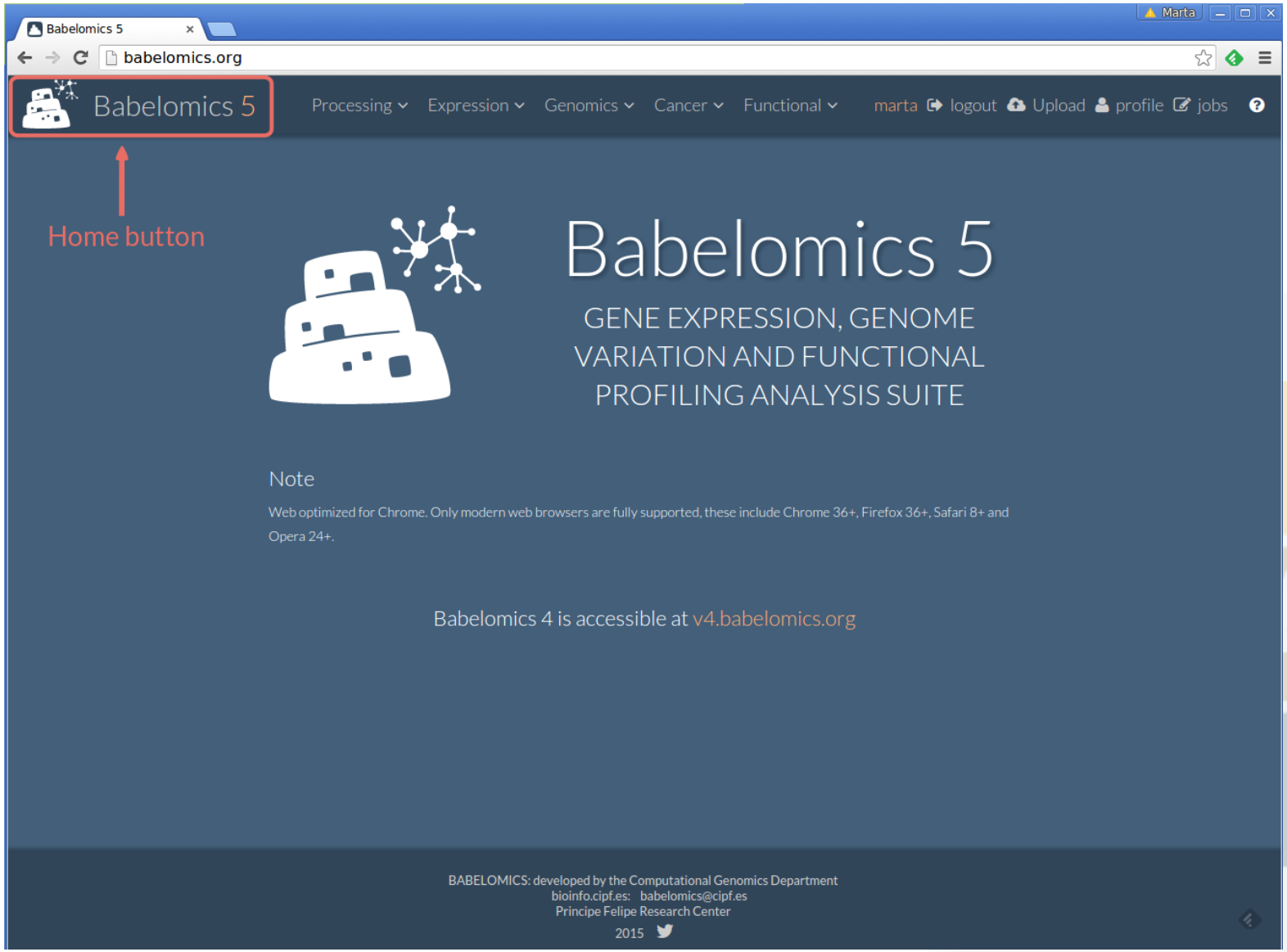
1. Go to Babelomics 5
2. Create a new user

For help, ask or visit the logging in tutorial

Web structure



Web structure



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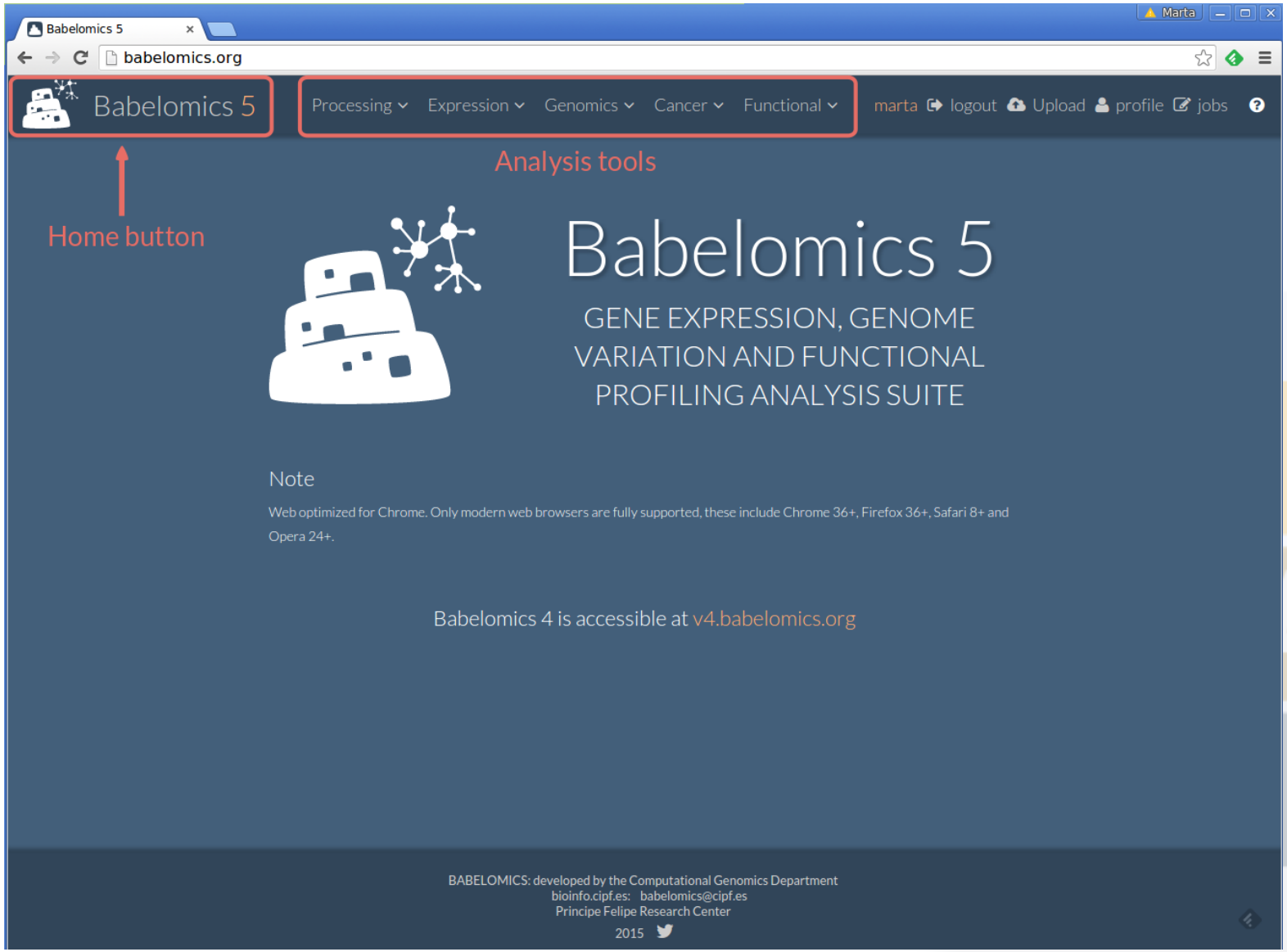
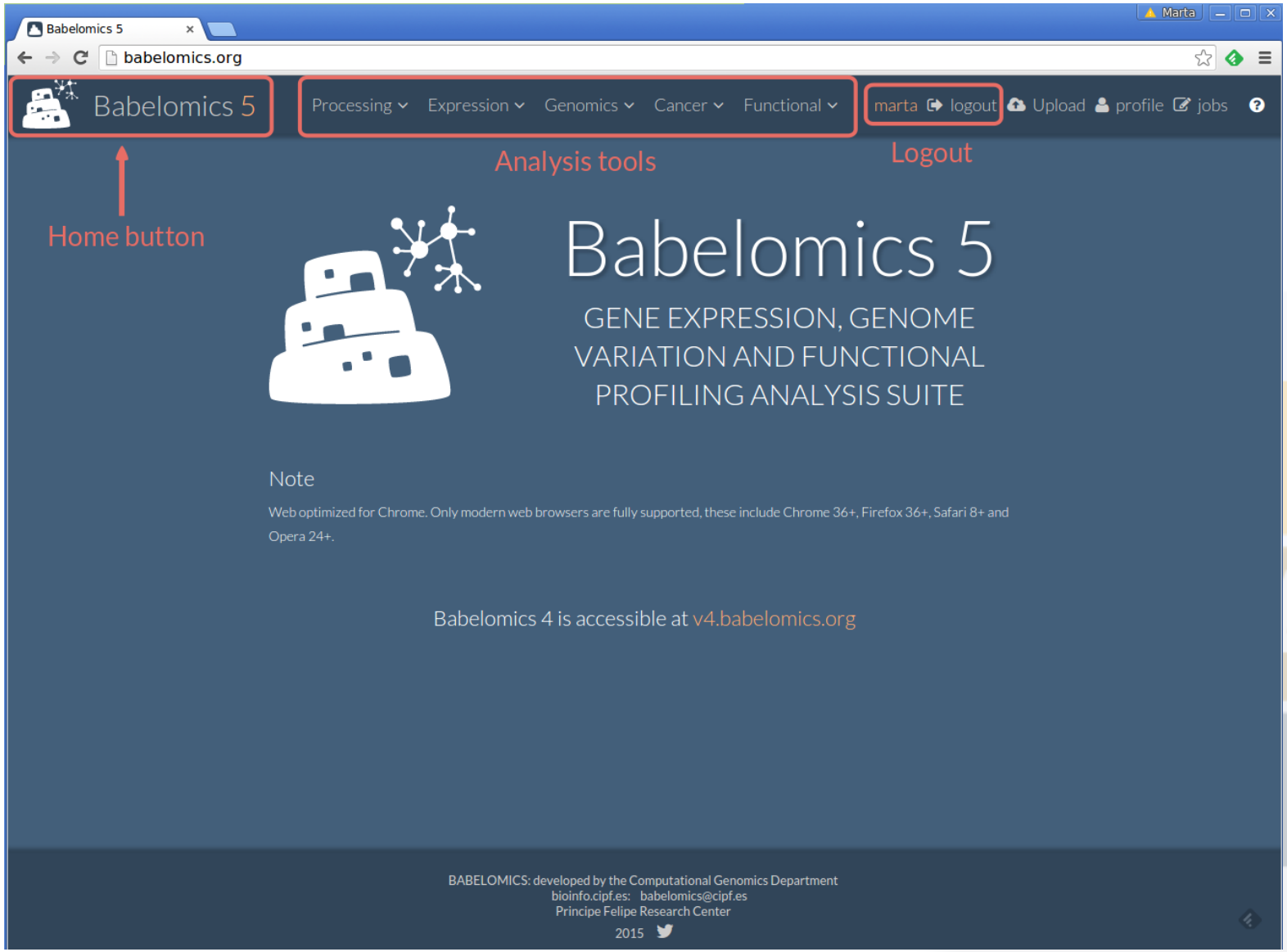


Web structure



Web structure

Babelomics 5

babelomics.org

Processing Expression Genomics Cancer Functional

marta logout Upload profile jobs

Analysis tools

Logout

Upload

Home button

Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

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Web structure

Babelomics 5

babelomics.org

Babelomics 5 | Processing | Expression | Genomics | Cancer | Functional | marta | logout | Upload | profile | jobs

Home button

Analysis tools

Logout

Upload

Settings

Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

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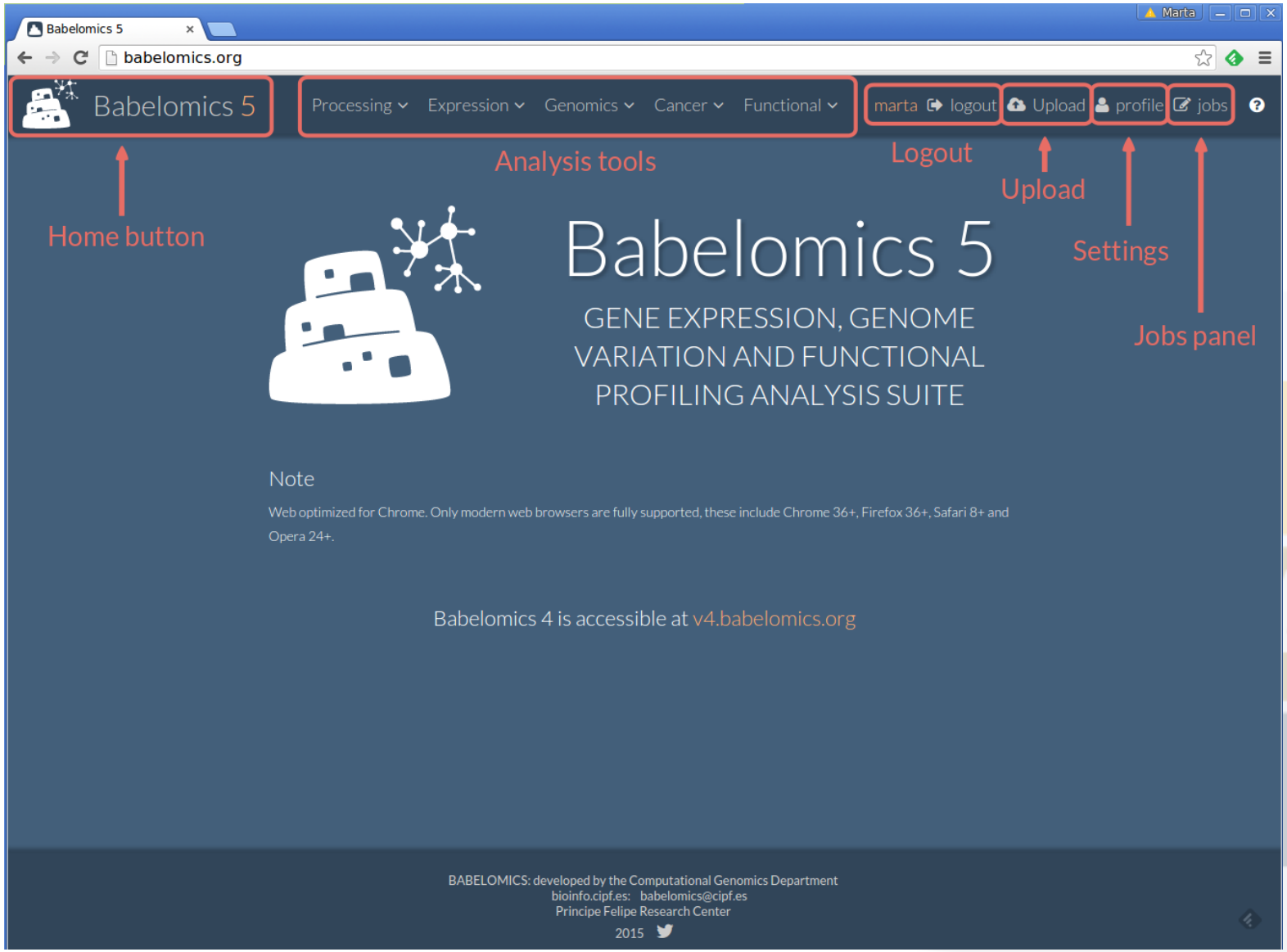
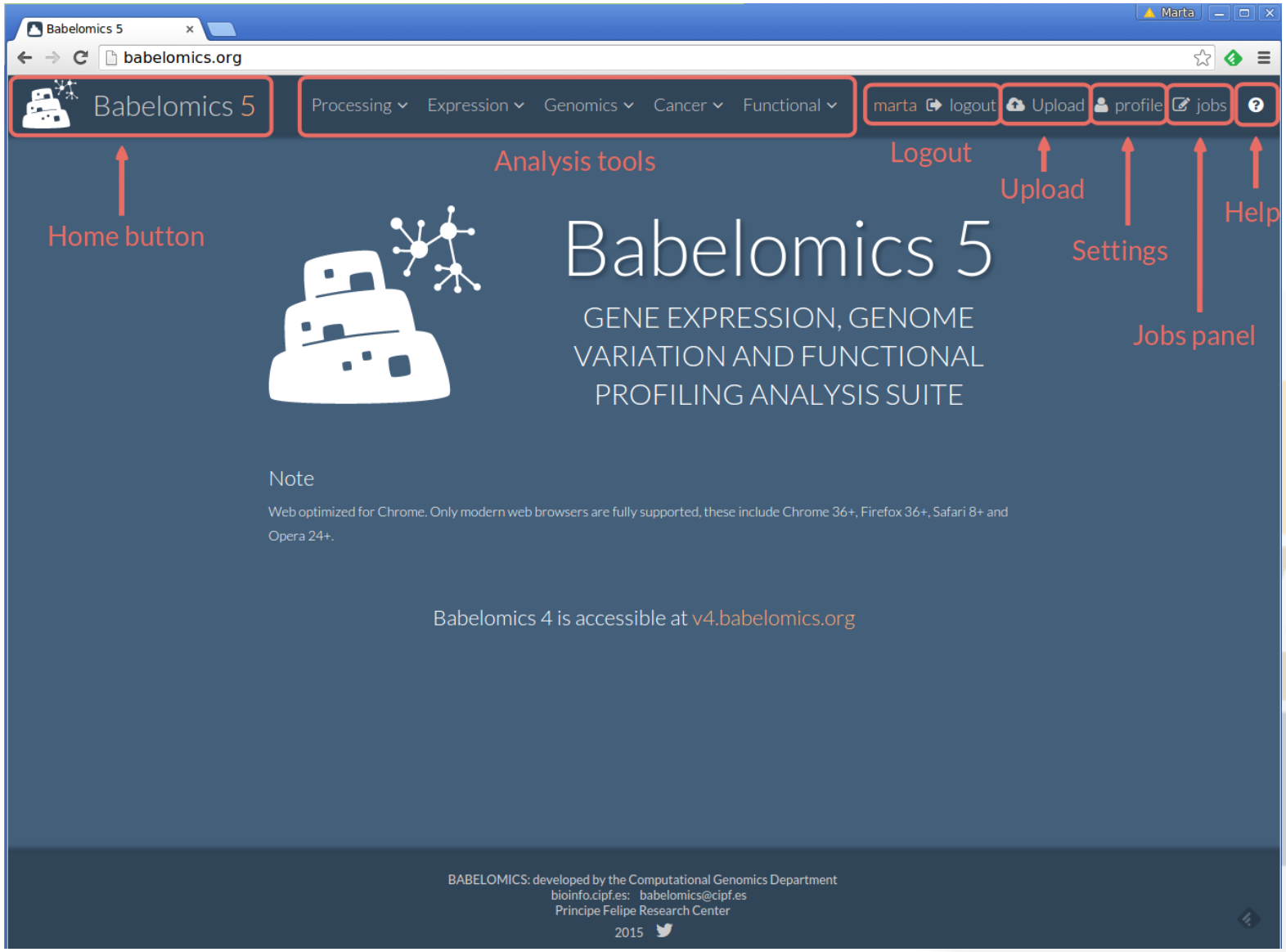
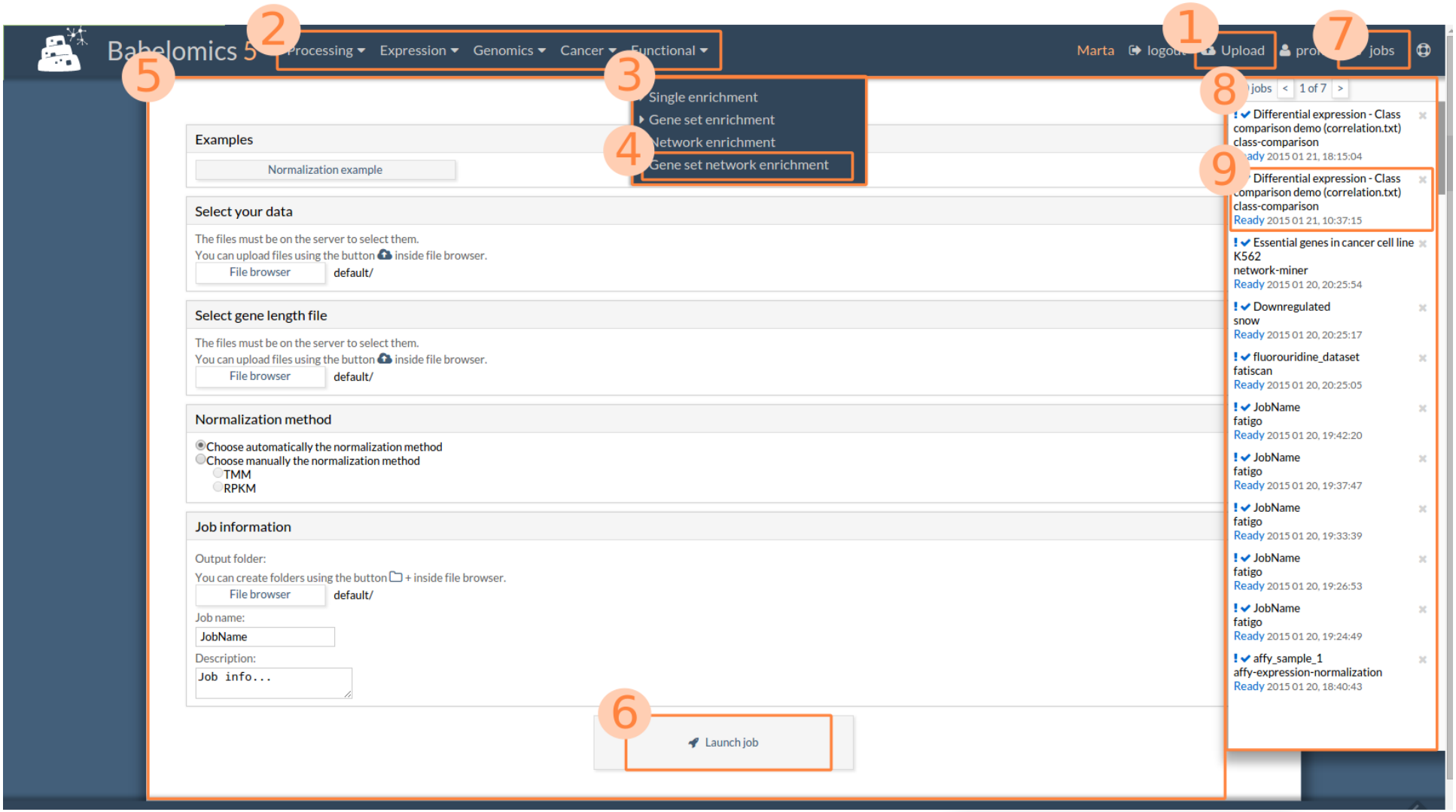


Web structure

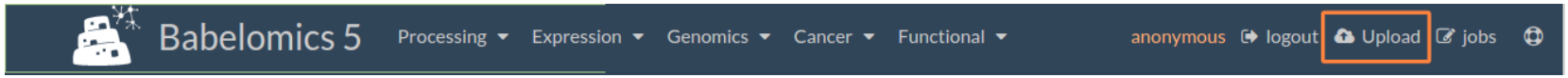


Workflow


Babelomics 5
Processing
Expression
Genomics
Cancer
Functional
Marta
logout
Upload
jobs
Single enrichment
Gene set enrichment
Network enrichment
Gene set network enrichment
Examples
Normalization example
Select your data
The files must be on the server to select them.
You can upload files using the button inside file browser.
File browser
default/
Select gene length file
The files must be on the server to select them.
You can upload files using the button inside file browser.
File browser
default/
Normalization method
Choose automatically the normalization method
Choose manually the normalization method
TMM
RPKM
Job information
Output folder:
You can create folders using the button + inside file browser.
File browser
default/
Job name:
JobName
Description:
Job info...
Launch job
jobs
1 of 7
Differential expression - Class comparison demo (correlation.txt)
class-comparison
Ready 2015 01 21, 18:15:04
Differential expression - Class comparison demo (correlation.txt)
class-comparison
Ready 2015 01 21, 10:37:15
Essential genes in cancer cell line K562
network-miner
Ready 2015 01 20, 20:25:54
Downregulated
snow
Ready 2015 01 20, 20:25:17
fluorouridine_dataset
fatiscan
Ready 2015 01 20, 20:25:05
JobName
fatigo
Ready 2015 01 20, 19:42:20
JobName
fatigo
Ready 2015 01 20, 19:37:47
JobName
fatigo
Ready 2015 01 20, 19:33:39
JobName
fatigo
Ready 2015 01 20, 19:26:53
JobName
fatigo
Ready 2015 01 20, 19:24:49
affy_sample_1
affy-expression-normalization
Ready 2015 01 20, 18:40:43
1
2
3
4
5
6
7
8
9

Uploading data

Uploading data tutorial



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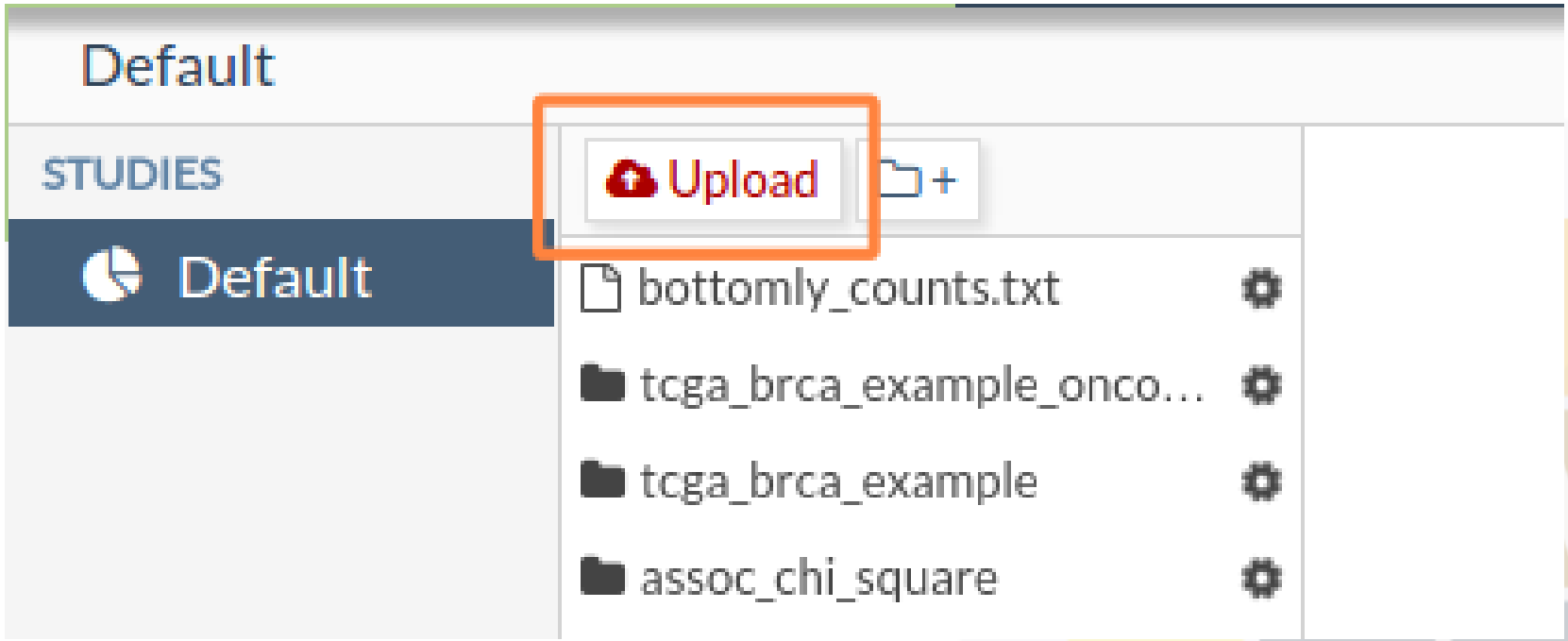
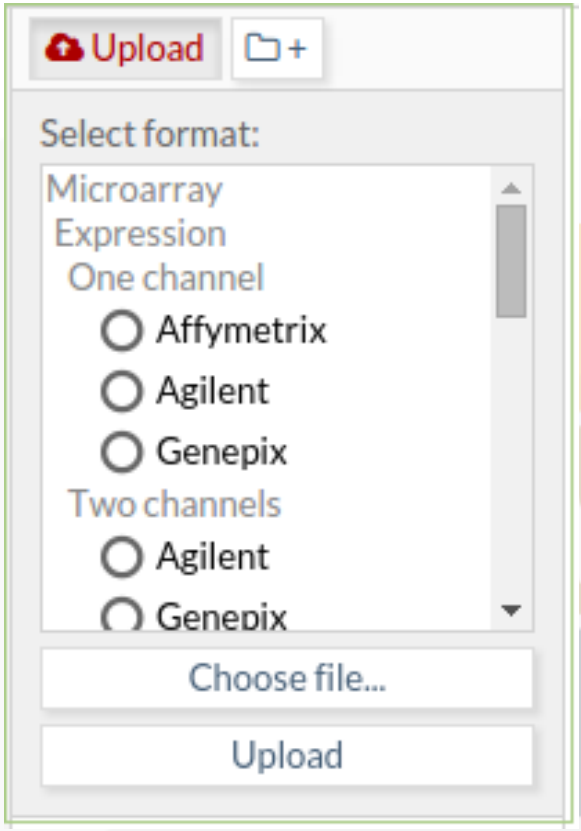


Uploading data

Uploading data tutorial

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



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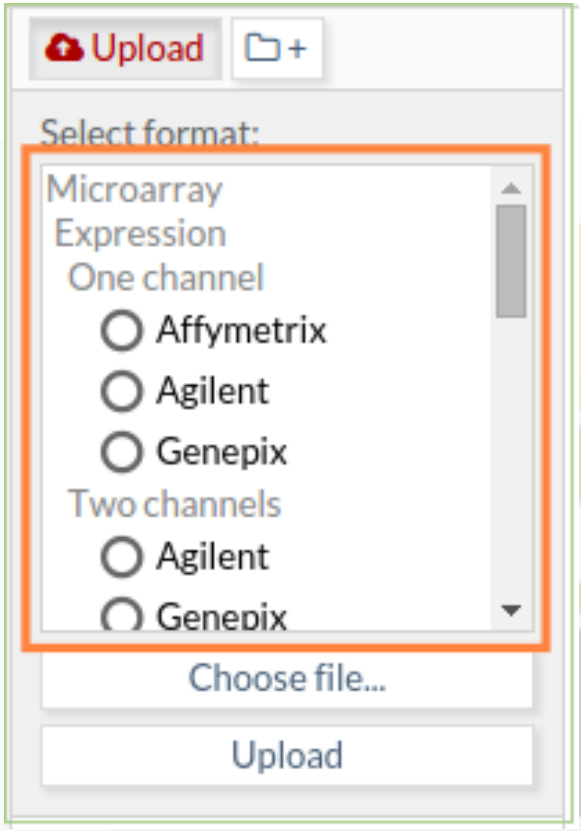

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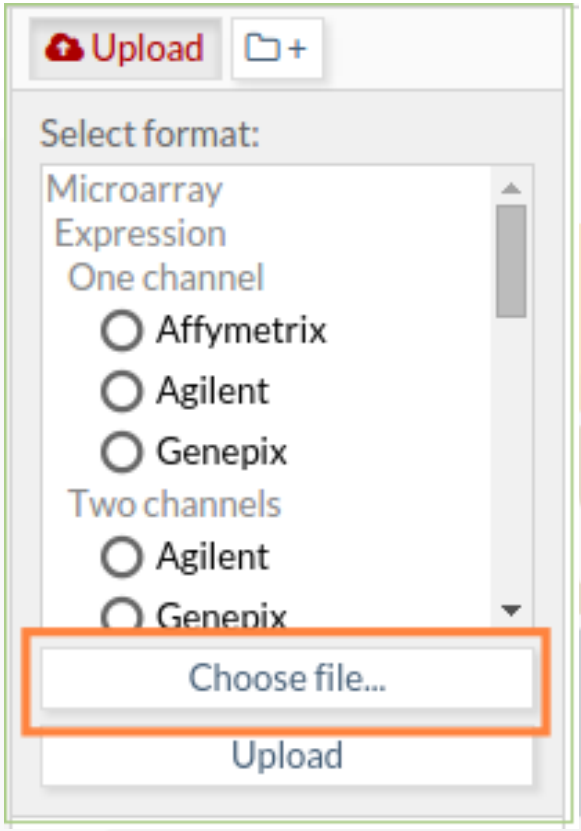

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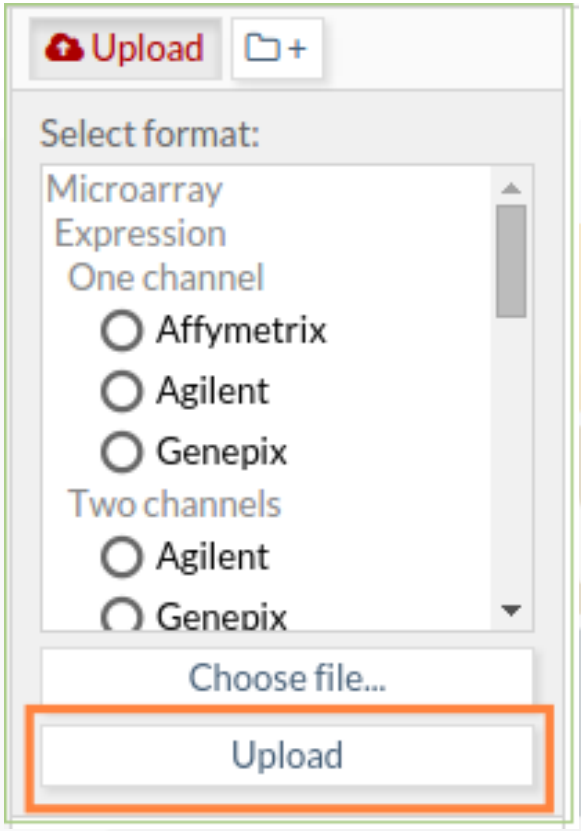

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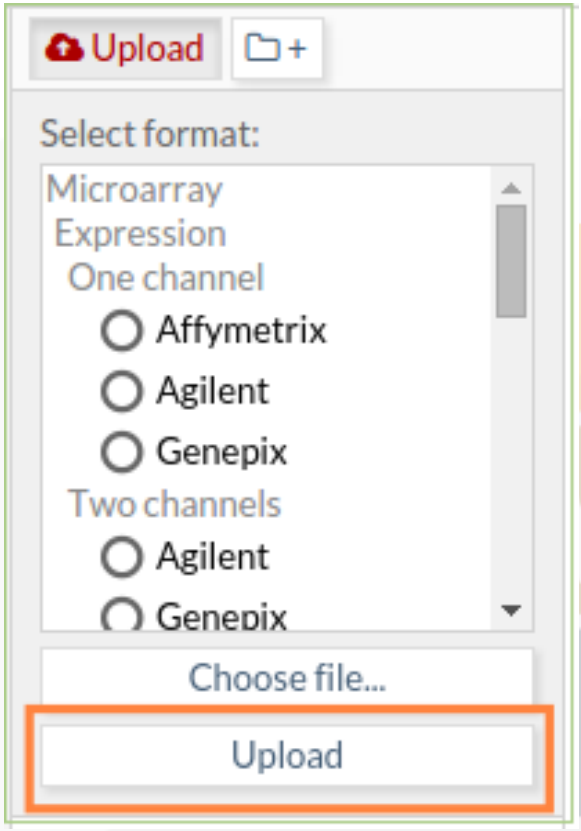


Uploading data

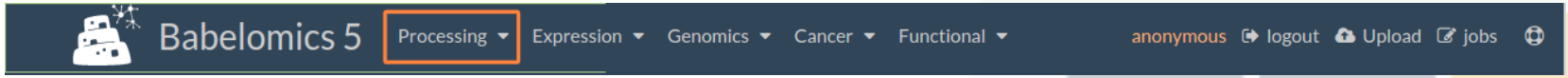
Exercise

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

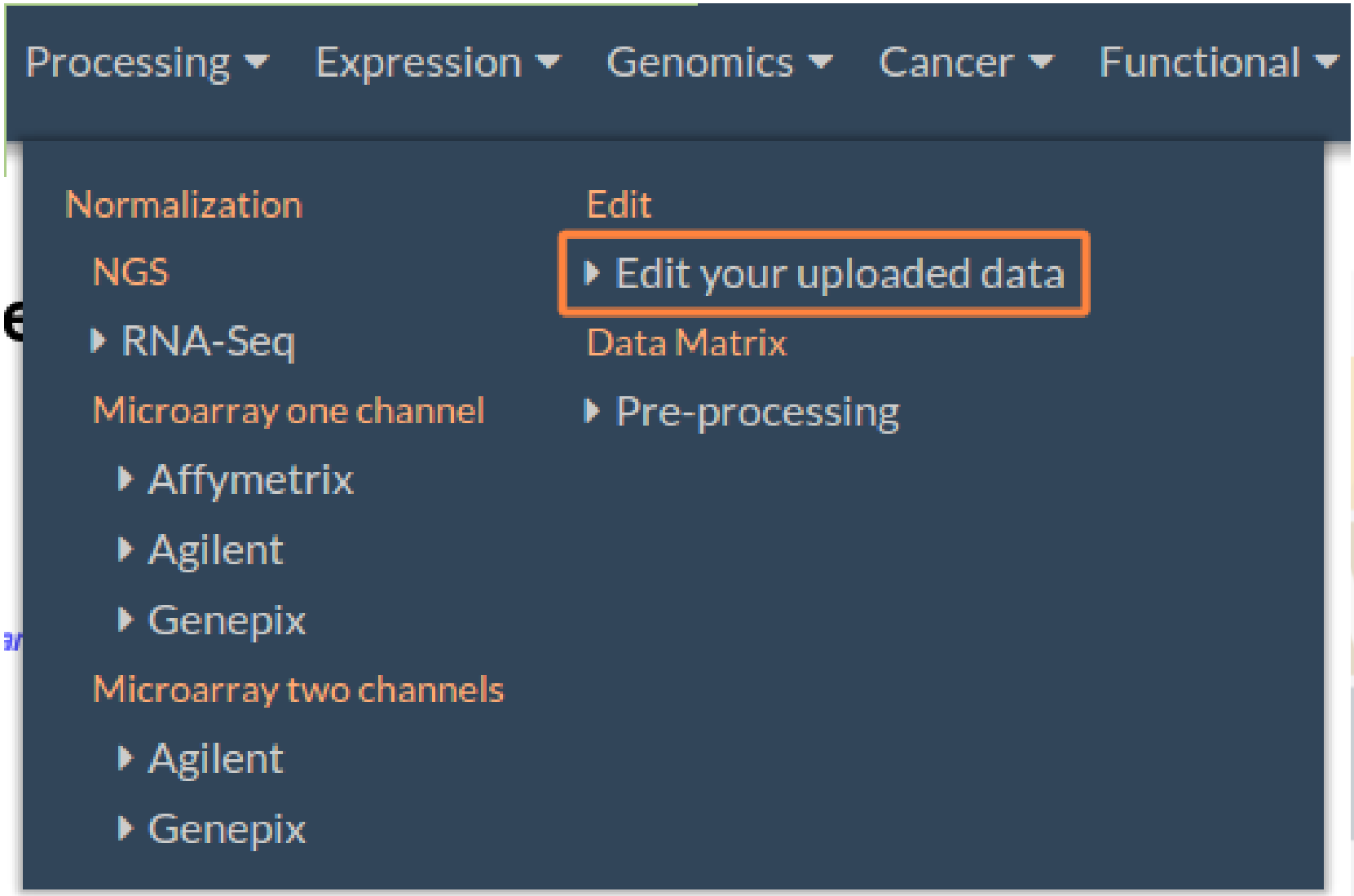
1. Go to the GDA 2016 wiki
2. Download the *brca_demo_counts_4babelomics.txt*
3. Upload this file to Babelomics 5

For help, ask or visit the uploading data tutorial

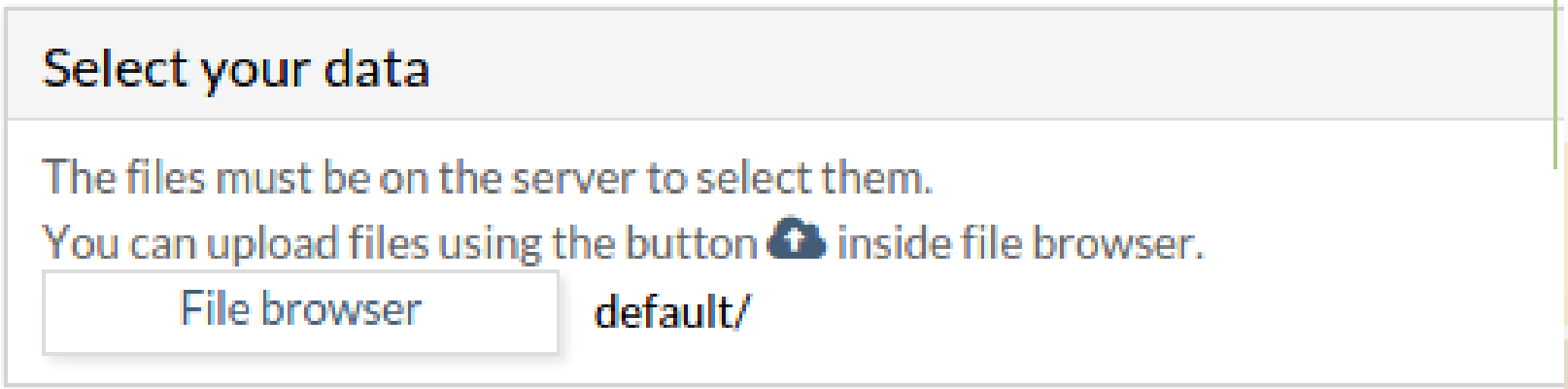
Editing data



Editing data



Editing data



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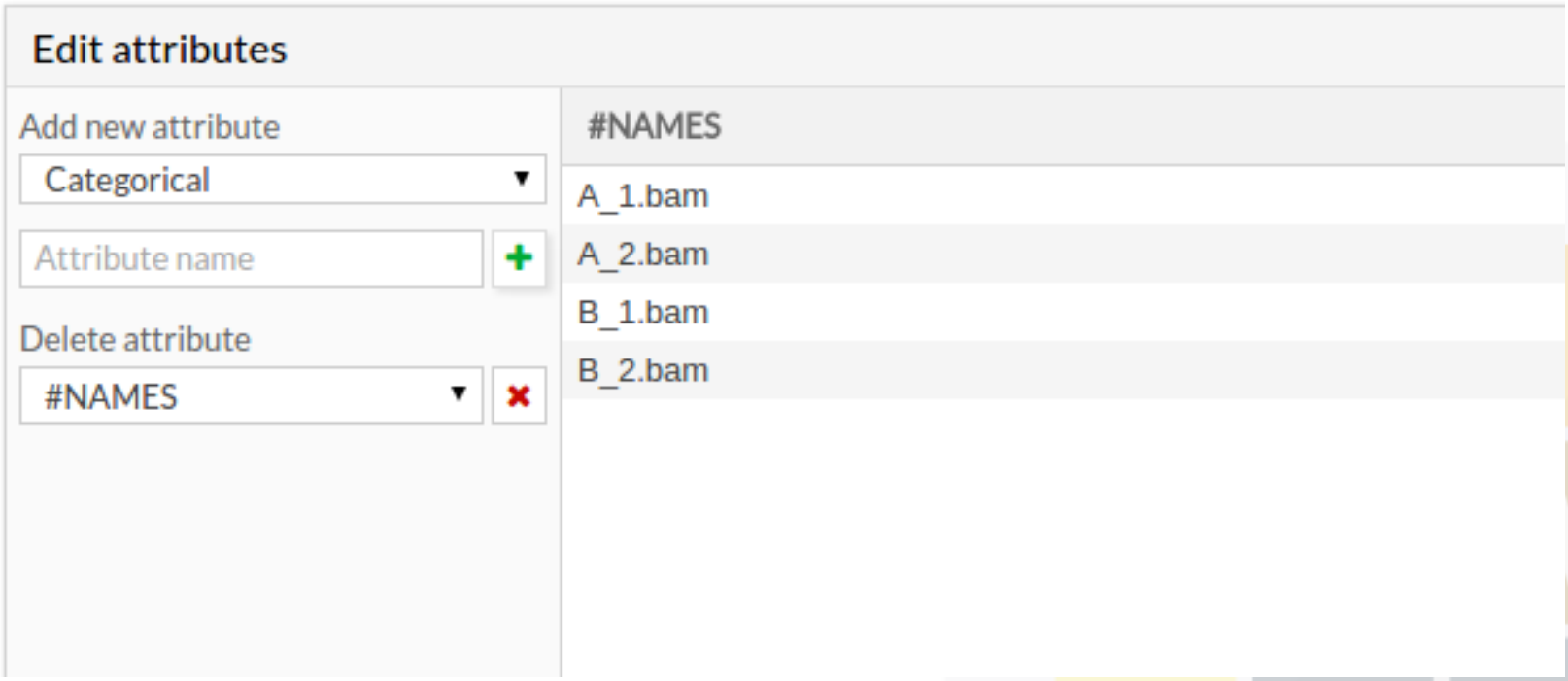

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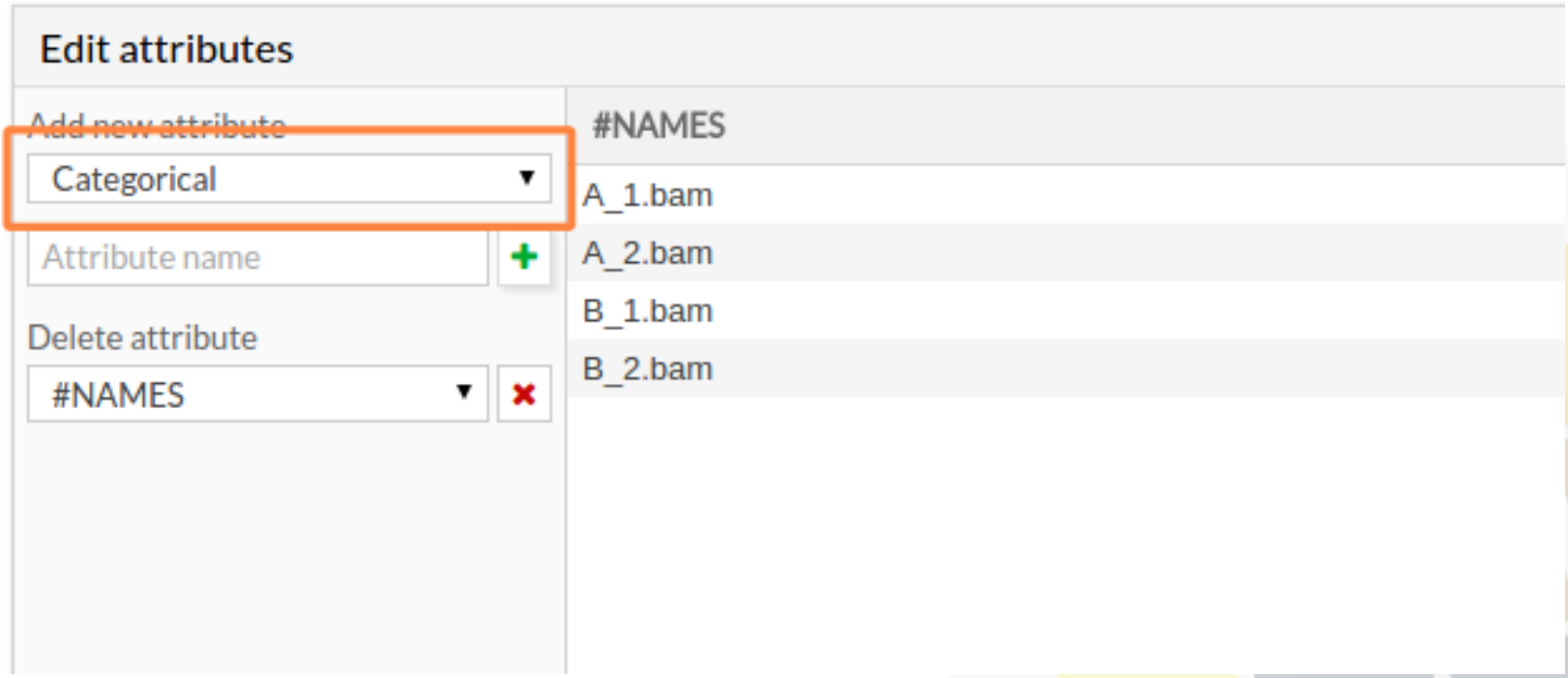

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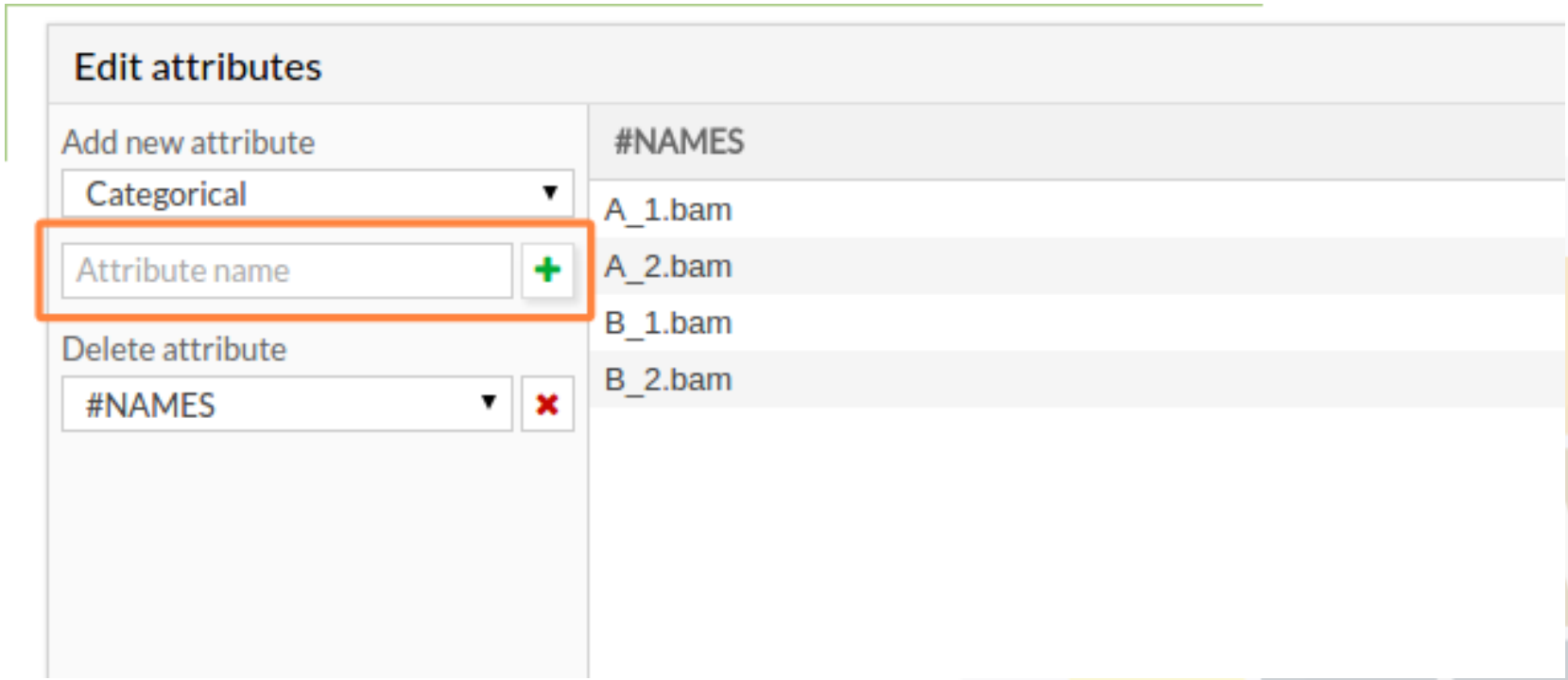

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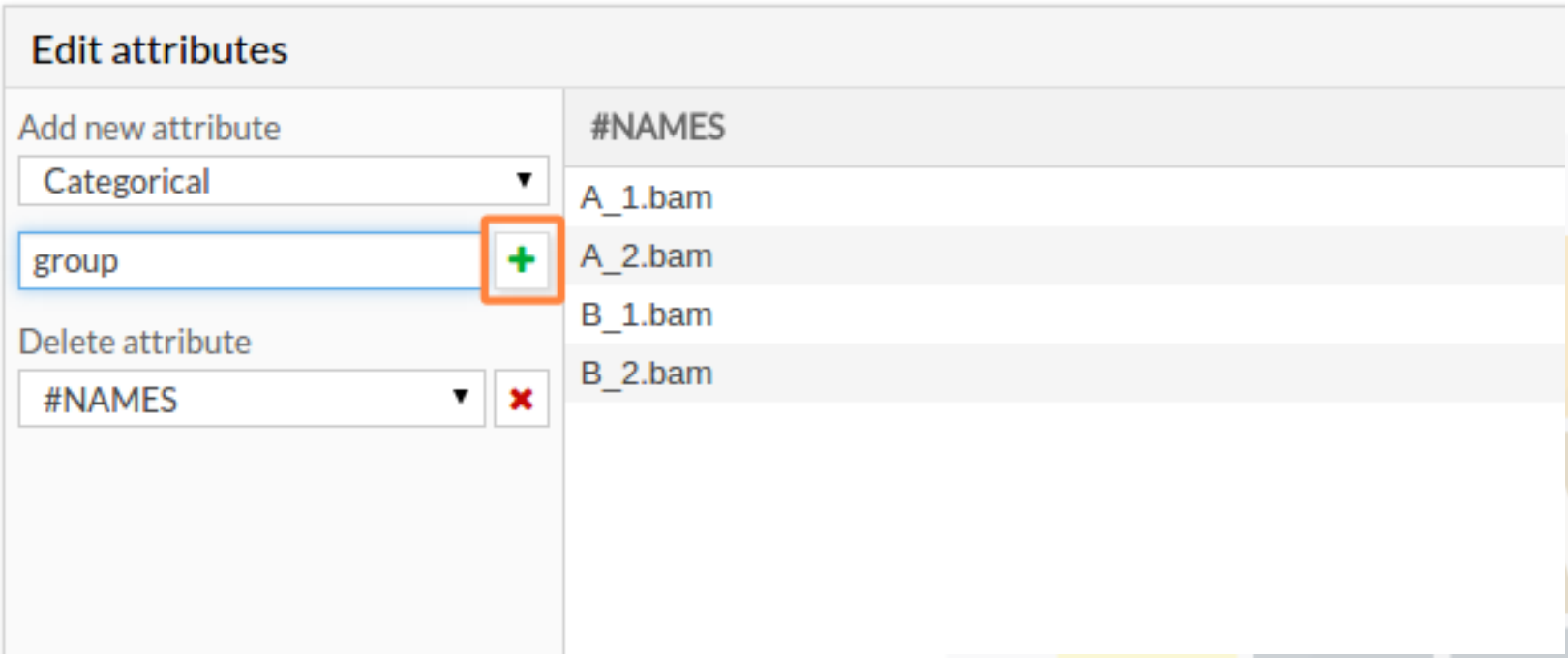

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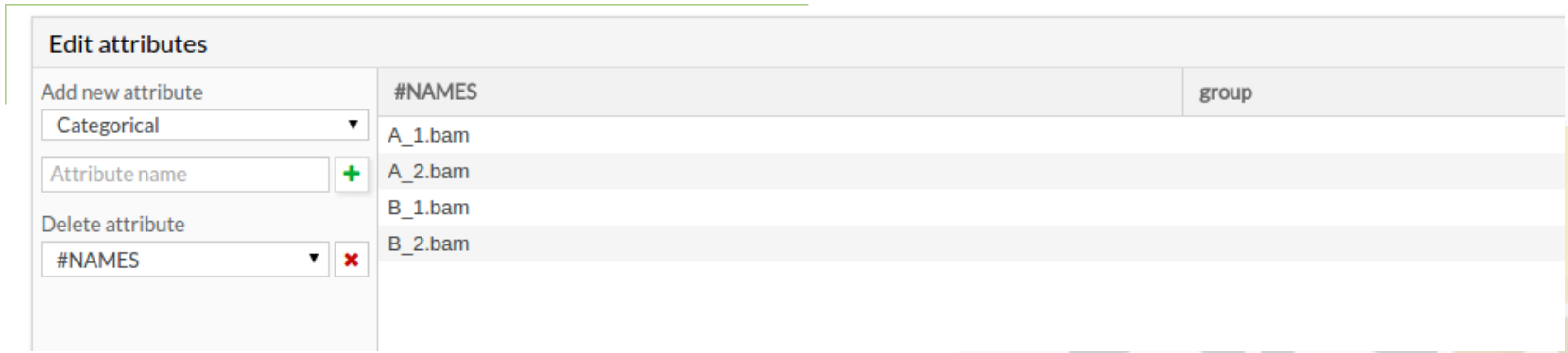
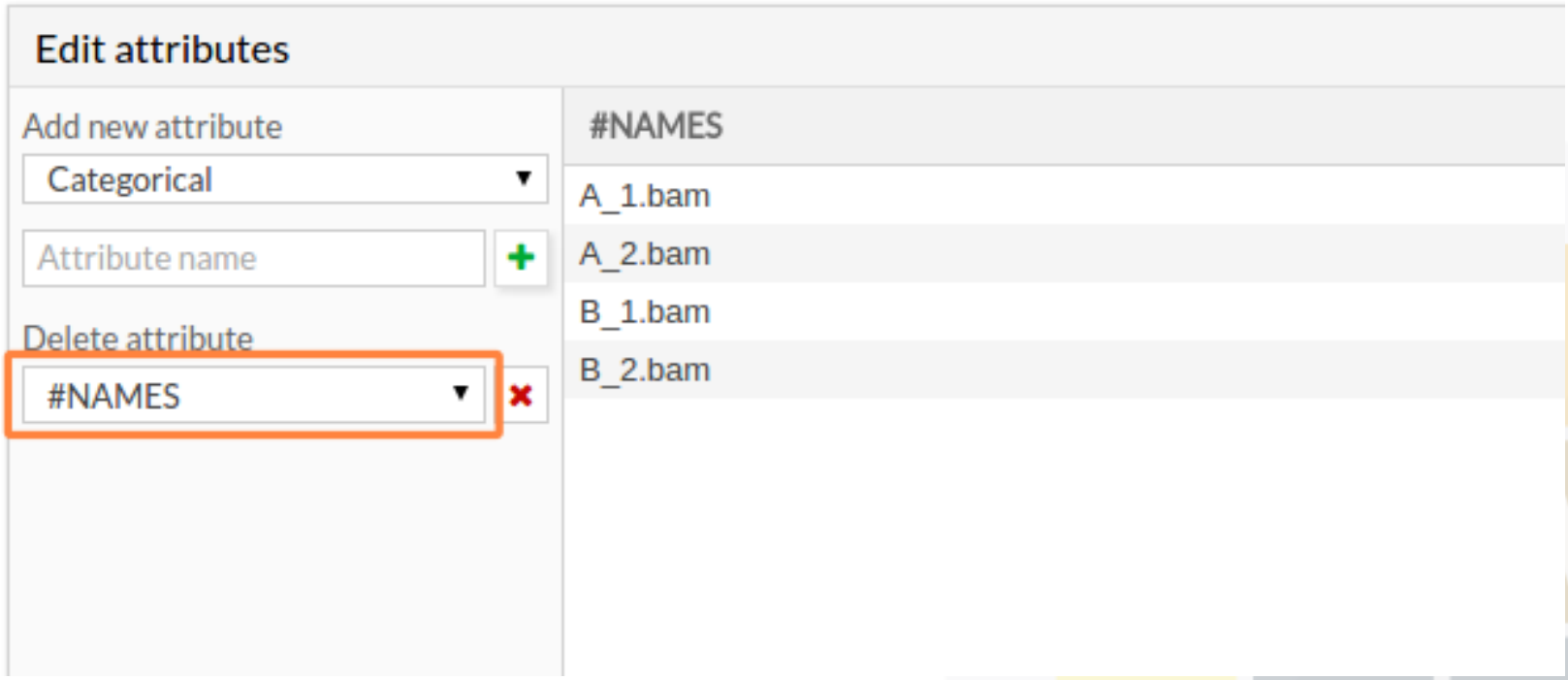


Editing data

Editing data



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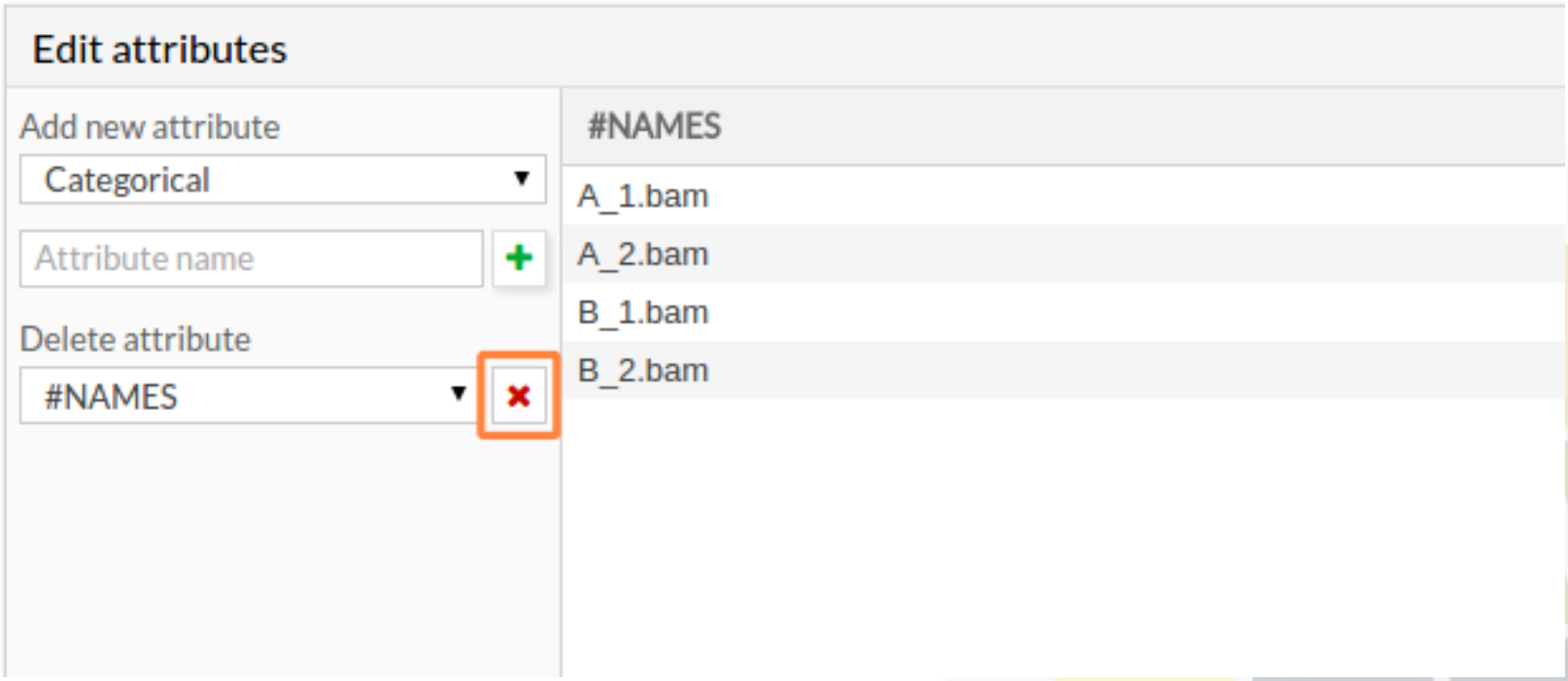

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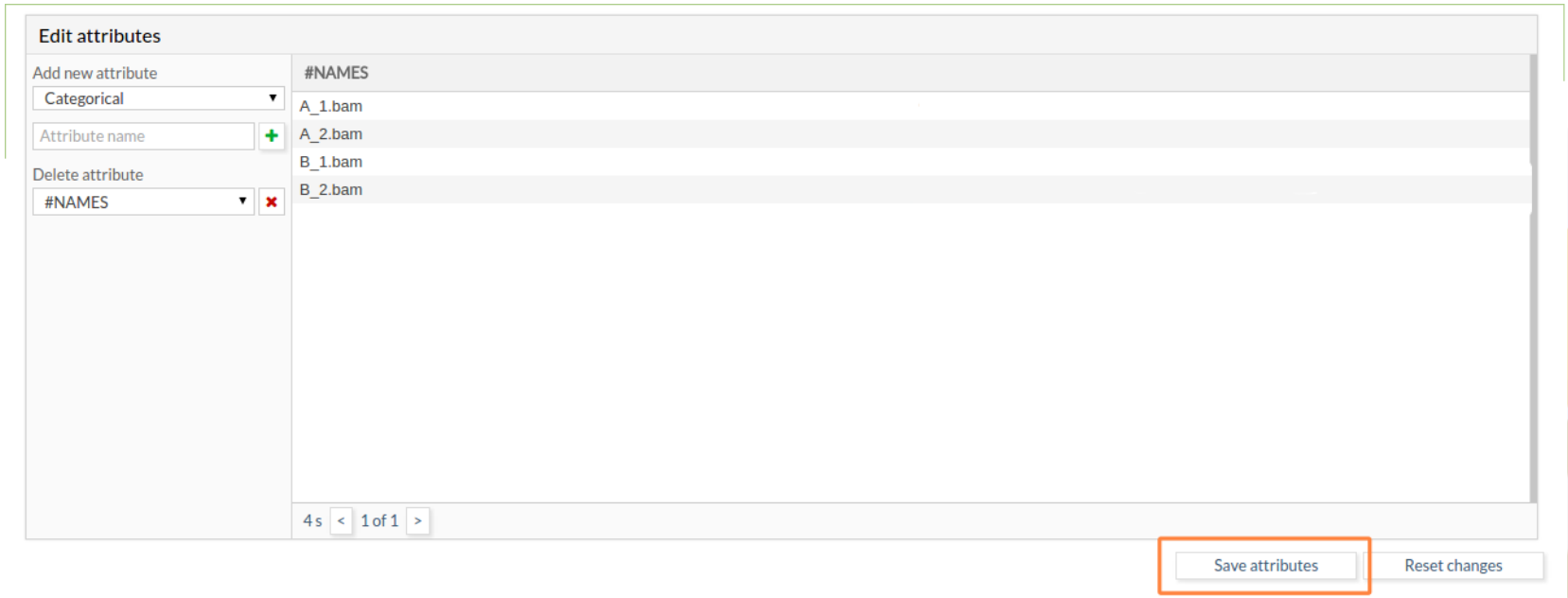

Editing data

Exercise

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

1. Go to the GDA 2016 wiki
2. Download the *BRCA_Normal-Basal_ED.txt*
3. Edit the former file with the data in this experimental design

For help, ask or visit the editing data tutorial