

# Introduction to Babelomics 5

Marta R. Hidalgo

September 29th, 2016



**GDA**

International Course on  
Genomic Data Analysis



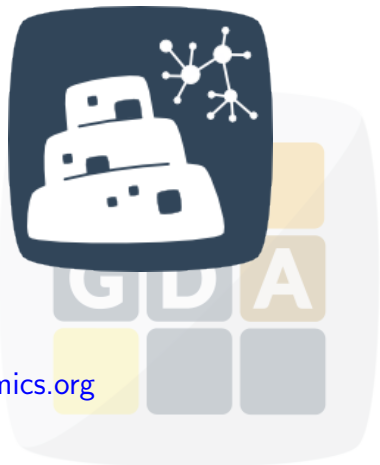
PRINCIPE FELIPE  
CENTRO DE INVESTIGACION

# Babelomics 5

## Babelomics 5

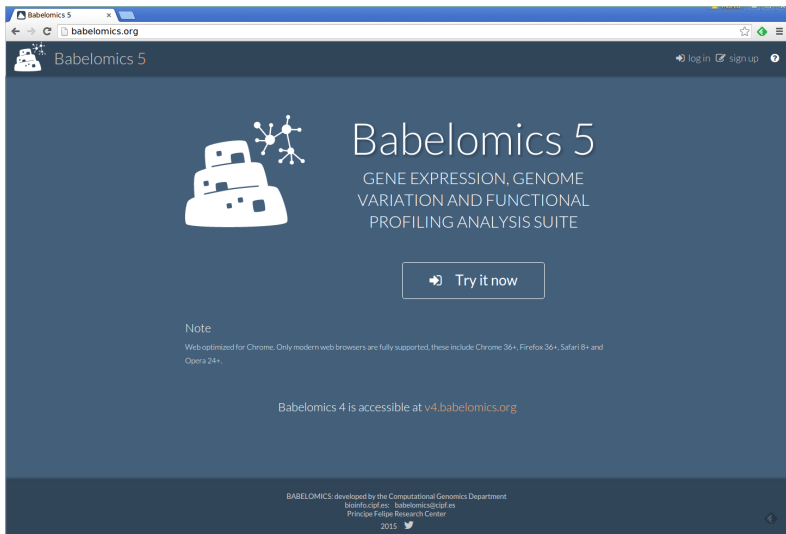
Integrative open source platform with advanced functional profiling for the analysis of

- Transcriptomics
- Proteomics
- Genomics



<http://www.babelomics.org>

# Babelomics 5



The screenshot shows the homepage of Babelomics 5. The browser address bar displays 'babelomics.org'. The page features a dark blue background with a white icon of a laboratory instrument and a network diagram. The main heading is 'Babelomics 5' followed by the subtitle 'GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE'. A 'Try it now' button is prominently displayed. A 'Note' section provides browser compatibility information. At the bottom, there is a footer with development details and a 2015 copyright notice.

Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

[Try it now](#)

Note

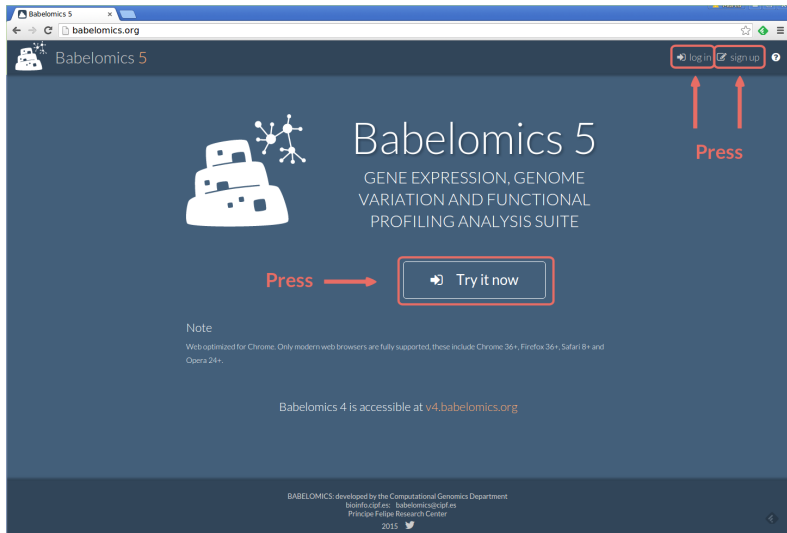
Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+.

Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)

BABELOMICS: developed by the Computational Genomics Department  
bioinfo.cipf.es: [babelomics@cipf.es](mailto:babelomics@cipf.es)  
Príncipe Felipe Research Center

2015

# Logging in



The screenshot shows the Babelomics 5 website interface. At the top right, there are two buttons: "log in" and "sign up", both highlighted with red boxes. Red arrows point from the word "Press" below to these two buttons. In the center of the page, there is a large "Try it now" button, also highlighted with a red box, with a red arrow pointing to it from the word "Press" on the left. The page features a dark blue background with a white icon of a microscope and a network diagram. The text "Babelomics 5" is prominently displayed, followed by "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE". A "Note" section at the bottom left provides browser compatibility information. At the bottom center, it states "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)". The footer contains the text "BABELOMICS: developed by the Computational Genomics Department. bioinfo.cif.es. babelomics@cif.es. Principe Felipe Research Center" and the year "2015" with a Twitter icon.

Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

Press → Try it now

Press → log in sign up

Note

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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

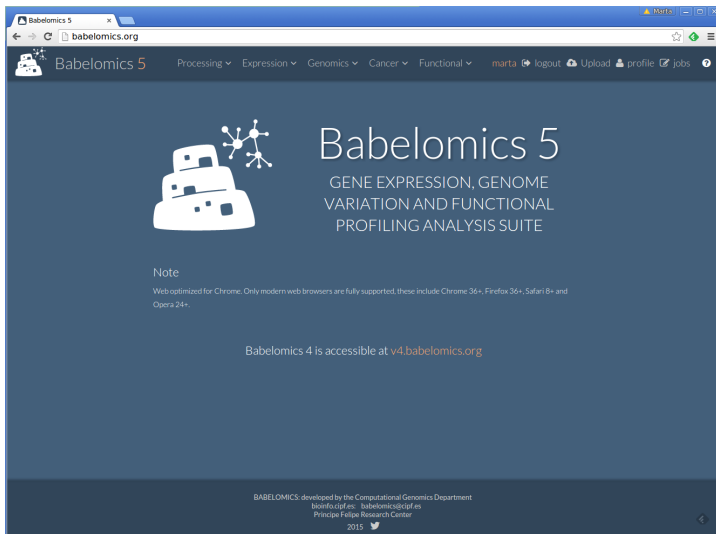
## Exercise

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



The screenshot shows the Babelomics 5 web application interface. The browser address bar displays `babelomics.org`. The navigation menu includes: Processing, Expression, Genomics, Cancer, Functional, **marta**, logout, Upload, profile, and jobs. The main content area features a white icon of a server tower with a network diagram above it. The title "Babelomics 5" is prominently displayed, followed by the subtitle "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE". A "Note" section states: "Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+." Below this, it says "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)". The footer contains the text: "BABELOMICS: developed by the Computational Genomics Department, bioinfo.cipf.es: babelomics@cipf.es, Principe Felipe Research Center, 2015".

Babelomics 5

Processing Expression Genomics Cancer Functional **marta** logout Upload profile jobs



## Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

Note

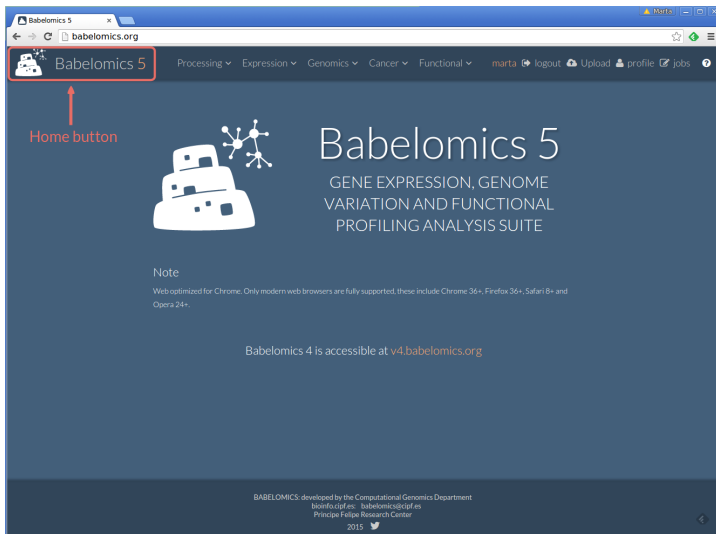
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Principe Felipe Research Center  
2015



# Web structure




The screenshot shows a web browser window with the address bar displaying `babelomics.org`. The page header features a navigation menu with items: Processing, Expression, Genomics, Cancer, Functional, marta, logout, Upload, profile, and jobs. A red box highlights the 'Babelomics 5' logo in the top left, with a red arrow pointing to it and the text 'Home button' below. The main content area has a dark blue background and includes a white icon of a server tower and a network diagram. The title 'Babelomics 5' is prominently displayed, followed by the subtitle 'GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE'. A 'Note' section states: 'Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+'. Below this, it says 'Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)'. The footer contains the text: 'BABELOMICS: developed by the Computational Genomics Department, bioinfo.cipf.es: babelomics@cipf.es, Principe Felipe Research Center, 2015'.

Babelomics 5

Processing Expression Genomics Cancer Functional marta logout Upload profile jobs

Home button



# Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

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2015

# Web structure

The screenshot shows the Babelomics 5 web application in a browser. The browser's address bar displays `babelomics.org`. The application's navigation bar includes a logo and the text "Babelomics 5", which is highlighted with a red box and labeled "Home button" with an orange arrow. To the right of the logo are several dropdown menus: "Processing", "Expression", "Genomics", "Cancer", and "Functional". Further right are user options: "marta", "logout", "Upload", "profile", and "jobs".

The main content area features the heading "Analysis tools" in orange. Below this is a large white icon of a laboratory instrument (a sequencer) with a network diagram above it. To the right of the icon, the text reads "Babelomics 5" in a large font, followed by "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE" in a smaller font.

A "Note" section below the icon states: "Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+."

At the bottom of the main content area, it says "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)".

The footer contains the text: "BABELOMICS: developed by the Computational Genomics Department  
bioinfo.cipf.es: babelomics@cipf.es  
Principe Felipe Research Center  
2015" followed by a Twitter icon.

# Web structure


The screenshot shows the Babelomics 5 web application interface. The browser address bar displays `babelomics.org`. The navigation bar includes a logo, the text "Babelomics 5", a menu with categories like "Processing", "Expression", "Genomics", "Cancer", and "Functional", and user options "marta" and "logout". Below the navigation bar, the main content area features the text "Analysis tools" and "Logout" in orange. A red arrow points to the "Babelomics 5" logo with the label "Home button". The main heading is "Babelomics 5" in large white font, followed by the subtitle "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE". A "Note" section states: "Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+." Below this, it says "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)". The footer contains the text: "BABELOMICS: developed by the Computational Genomics Department, bioinfo.cipf.es: babelomics@cipf.es, Principe Felipe Research Center, 2015".

Babelomics 5

Processing ▾ Expression ▾ Genomics ▾ Cancer ▾ Functional ▾ marta logout Upload profile jobs

Analysis tools Logout

Home button



# Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

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# Web structure

The screenshot shows the Babelomics 5 web application interface. The browser address bar displays `babelomics.org`. The navigation bar includes a logo, the text "Babelomics 5", a menu with categories: "Processing", "Expression", "Genomics", "Cancer", and "Functional", and user options: "marta", "logout", "Upload", "profile", and "jobs".

Annotations with red arrows point to:

- Home button**: Points to the Babelomics 5 logo.
- Analysis tools**: Points to the menu categories.
- Logout**: Points to the "logout" link.
- Upload**: Points to the "Upload" button.

The main content area features the Babelomics 5 logo (a stylized white building) and the text:

## Babelomics 5

GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

**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](http://v4.babelomics.org)

At the bottom, the footer contains: BABELOMICS: developed by the Computational Genomics Department, [bioinfo.cipf.es](mailto:bioinfo.cipf.es), [babelomics@cipf.es](mailto:babelomics@cipf.es), Principe Felipe Research Center, 2015.

# Web structure

The screenshot shows the Babelomics 5 web interface. The browser address bar displays `babelomics.org`. The navigation bar includes a logo, the text "Babelomics 5", and a menu with categories: "Processing", "Expression", "Genomics", "Cancer", and "Functional". On the right side of the navigation bar, there are buttons for "marta", "logout", "Upload", "profile", and "jobs".

Annotations with red arrows point to the following elements:

- Home button**: Points to the Babelomics 5 logo.
- Analysis tools**: Points to the menu categories.
- Logout**: Points to the "logout" button.
- Upload**: Points to the "Upload" button.
- Settings**: Points to the "profile" button.

The main content area features the Babelomics 5 logo (a stylized white building) and the text "Babelomics 5" in large font, followed by "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE". Below this is a "Note" section stating: "Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+." At the bottom of the main area, it says "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)".

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# Web structure

The screenshot shows the Babelomics 5 web interface. The browser address bar displays `babelomics.org`. The navigation bar includes a logo, the text "Babelomics 5", and a menu with items: "Processing", "Expression", "Genomics", "Cancer", and "Functional". On the right side of the navigation bar, there are buttons for "marta", "logout", "Upload", "profile", and "jobs".

Annotations with red arrows point to the following elements:

- Home button**: Points to the Babelomics 5 logo.
- Analysis tools**: Points to the menu items (Processing, Expression, Genomics, Cancer, Functional).
- Logout**: Points to the "logout" button.
- Upload**: Points to the "Upload" button.
- Settings**: Points to the "profile" button.
- Jobs panel**: Points to the "jobs" button.

The main content area features the Babelomics 5 logo (a stylized white building) and the text "Babelomics 5" in large font, followed by "GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE". Below this is a "Note" section stating: "Web optimized for Chrome. Only modern web browsers are fully supported, these include Chrome 36+, Firefox 36+, Safari 8+ and Opera 24+." At the bottom of the main area, it says "Babelomics 4 is accessible at [v4.babelomics.org](http://v4.babelomics.org)".

The footer contains the text: "BABELOMICS: developed by the Computational Genomics Department, bioinfo.cipf.es: babelomics@cipf.es, Principe Felipe Research Center, 2015" with a Twitter icon.

# Web structure

The screenshot shows the Babelomics 5 web interface. The browser address bar displays "babelomics.org". The navigation bar includes a "Babelomics 5" logo, a menu with "Processing", "Expression", "Genomics", "Cancer", and "Functional", and user options for "marta", "logout", "Upload", "profile", "jobs", and a help icon. Red arrows point to these elements with labels: "Home button" (pointing to the logo), "Analysis tools" (pointing to the menu), "Logout" (pointing to the "logout" button), "Upload" (pointing to the "Upload" button), "Settings" (pointing to the "profile" button), "Jobs panel" (pointing to the "jobs" button), and "Help" (pointing to the help icon). The main content area features the Babelomics 5 logo, the text "Babelomics 5 GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE", a "Note" section, and a footer with contact information and the year 2015.

Babelomics 5

Processing ▾ Expression ▾ Genomics ▾ Cancer ▾ Functional ▾

marta logout Upload profile jobs

Home button

Analysis tools

Logout

Upload

Settings

Jobs panel

Help

**Babelomics 5**  
GENE EXPRESSION, GENOME VARIATION AND FUNCTIONAL PROFILING ANALYSIS SUITE

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2015

# Workflow

The screenshot displays the Babalomics 5.0 web interface. The top navigation bar includes the logo, the text "Babalomics 5.0", and a menu with items: Processing, Expression, Genomics, Cancer, and Functional. On the right, there are links for "Marta", "login", "Upload", "pro", and "jobs".

The main content area is divided into several sections:

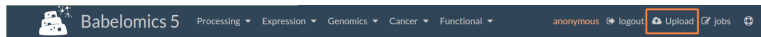
- Examples:** A "Normalization example" button is highlighted with callout 5.
- Select your data:** A "File browser" button is highlighted with callout 2. A dropdown menu is open, showing options: "Single enrichment", "Gene set enrichment", "Network enrichment", and "Gene set network enrichment". Callouts 3 and 4 point to the "Gene set enrichment" and "Network enrichment" options respectively.
- Select gene length file:** A "File browser" button is highlighted with callout 6.
- Normalization method:** Radio buttons for "Choose automatically the normalization method" (selected), "Choose manually the normalization method", "TMM", and "RPKM" are present.
- Job information:** Includes an "Output folder:" section with a "File browser" button (callout 6), and input fields for "Job name:" (containing "JobName") and "Description:" (containing "Job info...").
- Launch job:** A button at the bottom center is highlighted with callout 6.

On the right side, a "Jobs" panel shows a list of job entries. Callout 1 points to the "Upload" button in the top right. Callout 7 points to the "Jobs" button in the top right. Callout 8 points to the "Jobs" panel header. Callout 9 points to a job entry: "Differential expression - Class comparison demo (correlation.txt) class-comparison", which is highlighted with a red box. Other job entries include "Essential genes in cancer cell line K562 network-miner", "Downregulated snow", "fluorouridine\_dataset fatiscan", and "affy\_sample\_1 affy-expression-normalization".



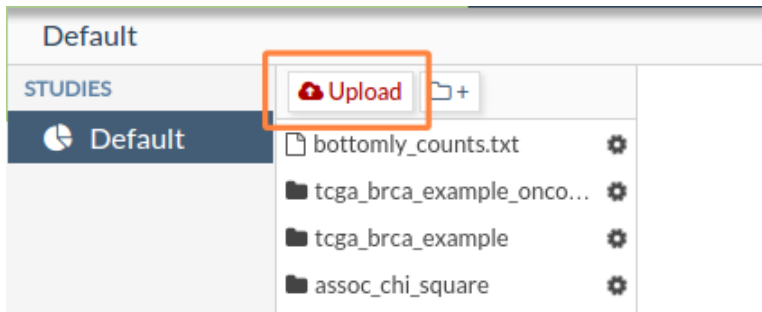
# Uploading data

## Uploading data tutorial



# Uploading data

## Uploading data tutorial



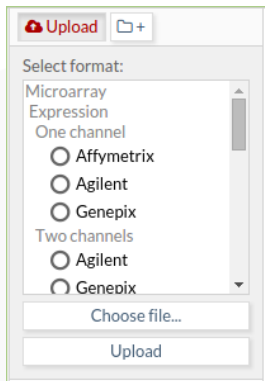
The screenshot displays a software interface with a sidebar on the left and a main content area on the right. The sidebar is titled "Default" and contains a "STUDIES" section with a "Default" study selected, indicated by a pie chart icon. The main content area shows a list of files and folders, each with a gear icon for settings. An orange box highlights the "Upload" button, which features a red cloud icon and the text "Upload". To the right of the "Upload" button is a folder icon with a plus sign. The list of items includes:

- bottomly\_counts.txt
- tcga\_brca\_example\_onco...
- tcga\_brca\_example
- assoc\_chi\_square

# Uploading data

## Uploading data tutorial

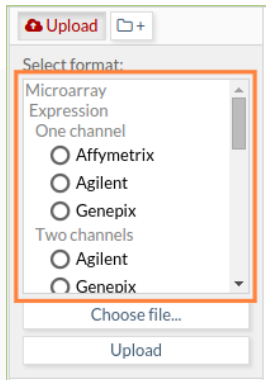
- Bioformat, [more info](#)
  - RNA-Seq: Data Matrix
- **IMPORTANT:** First row with rownames must begin with #NAMES
- We can remove files



# Uploading data

## Uploading data tutorial

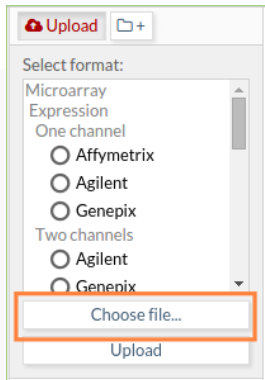
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## Uploading data tutorial

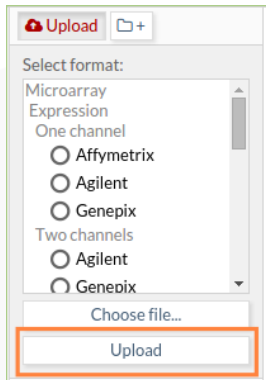
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## Uploading data tutorial

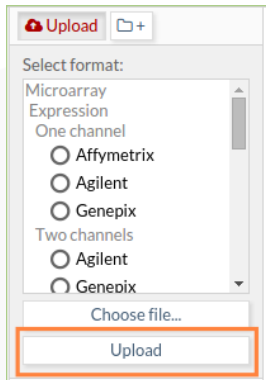
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# Uploading data

## Uploading data tutorial

- Bioformat, [more info](#)
  - RNA-Seq: Data Matrix
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# Uploading data

## Exercise

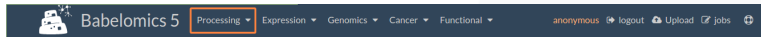
We will work with a breast cancer dataset from The Cancer Genome Atlas (TCGA). The expression matrix contains raw counts

- 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

Processing ▾ Expression ▾ Genomics ▾ Cancer ▾ Functional ▾

## Normalization

### NGS

▶ RNA-Seq

### Microarray one channel

▶ Affymetrix

▶ Agilent

▶ Genepix

### Microarray two channels

▶ Agilent

▶ Genepix

## Edit

▶ Edit your uploaded data


## Data Matrix

▶ Pre-processing

# Editing data

## 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/

# Editing data

**Edit attributes**

Add new attribute

Categorical ▼

Attribute name  +

Delete attribute

#NAMES ▼ ✖

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute

Categorical

Attribute name  +

Delete attribute

#NAMES

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute

Categorical ▼

Attribute name  +

Delete attribute

#NAMES ▼ ✕

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute  
Categorical ▼

group +

Delete attribute  
#NAMES ✕

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute	#NAMES	group
Categorical	A_1.bam	
Attribute name <input type="text"/> +	A_2.bam	
Delete attribute	B_1.bam	
#NAMES <input type="text"/> x	B_2.bam	



# Editing data

**Edit attributes**

Add new attribute

Categorical

Attribute name

+

Delete attribute

#NAMES

×

#NAMES	group
A_1.bam	0
A_2.bam	0
B_1.bam	1
B_2.bam	

G D A

Navigation icons: back, forward, search, etc.

# Editing data

**Edit attributes**

Add new attribute

Categorical ▼

Attribute name  +

Delete attribute

#NAMES ▼ ✕

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute

Categorical ▼

Attribute name  +

Delete attribute

#NAMES ▼ ✖

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

# Editing data

**Edit attributes**

Add new attribute  
Categorical

Attribute name  +

Delete attribute  
#NAMES

#NAMES
A_1.bam
A_2.bam
B_1.bam
B_2.bam

4s < 1 of 1 >

Save attributes Reset changes

# 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](#)

Enjoy Babebloemics 5!

