

# HiPathia

## Models of signaling pathway activity

Marta R. Hidalgo

March 10th, 2016



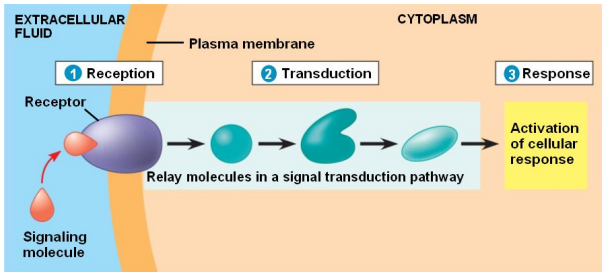
**GDA**

International Course on  
Genomic Data Analysis



**PRINCIPE FELIPE**  
CENTRO DE INVESTIGACION

# Signaling pathways



## Chemical signals

- Hormones
- Neurotransmitters
- Growth factors
- Cytokines
- Drugs

## Activation & Inhibition

- Phosphorilation
- Dephosphorilation
- Glycosylation
- Ubiquitination
- Methylation

## Cellular Function

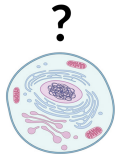
- Apoptosis
- Survival
- Growth
- Migration
- Proliferation



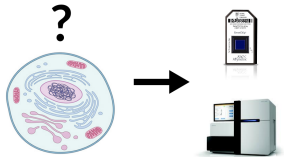
# HiPathia

Method

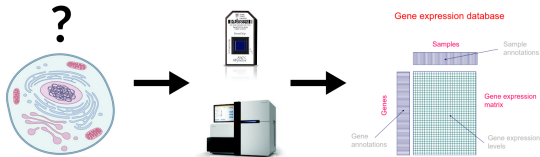
# From cell to pathways



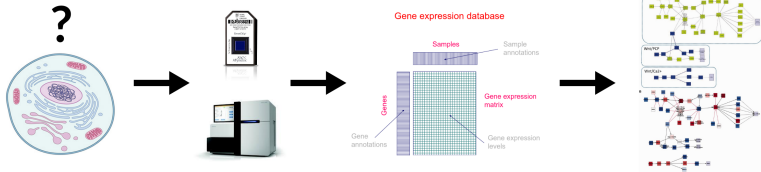
# From cell to pathways



# From cell to pathways



# From cell to pathways



# Pathway methods

- **DEGraph**: Based on DE
- **Clipper**: 2 test method
- **SPIA**: Impact factor
- **Sub-SPIA**: Find subnetwork by DE and apply SPIA
- **HiPathia**: Computes signal for each sample



# Pathway methods


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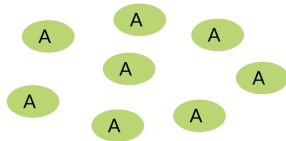
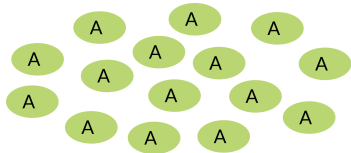
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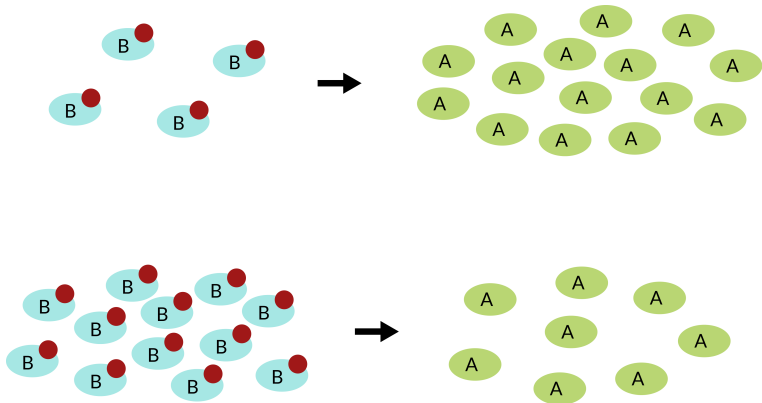
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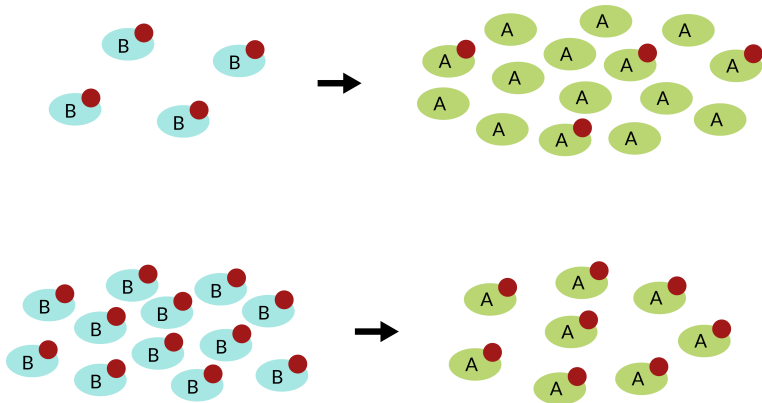
# Intuitive idea



# Intuitive idea

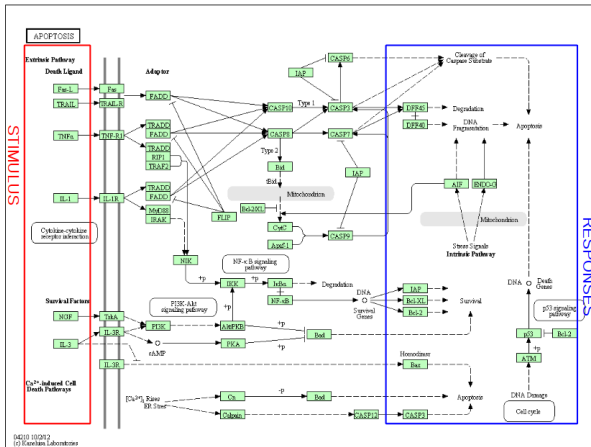


# Intuitive idea



# Pathways layout

Take pathways information from KEGG, [www.kegg.jp](http://www.kegg.jp)

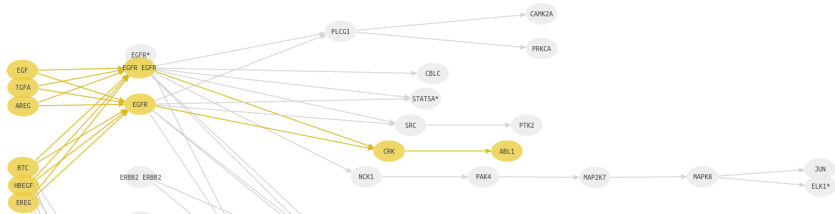




# Meaningful subpathways

## Effector subpathway

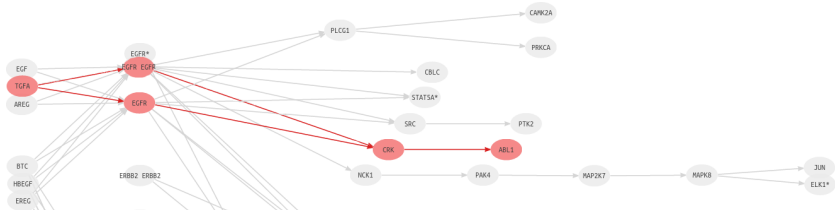
Subpathway including any node from any receptor to one effector protein



# Meaningful subpathways

## Decomposed subpathway

Subpathway including any node from one receptor to one effector protein



# Computing the signal

- 1 Compute a node score based on the expression
- 2 Compute signal passing through each node  $n$

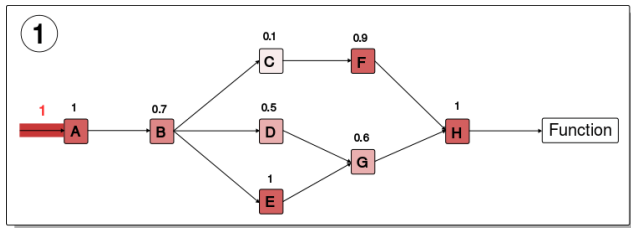
$$S_n = v_n \cdot \left(1 - \prod_{s_i \in A} (1 - s_i)\right) \cdot \prod_{s_j \in I} (1 - s_j)$$

$S_n$ : Signal value through  $n$

$v_n$ : Node value

$A$ : Activation edges

$I$ : Inhibition edges



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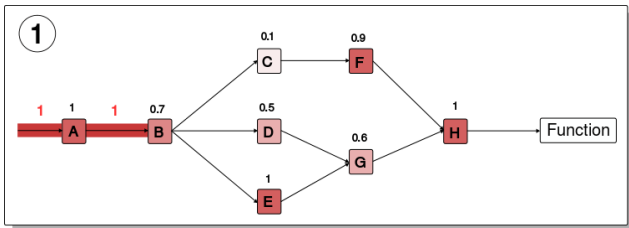
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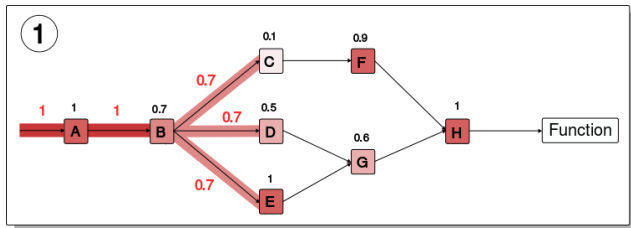
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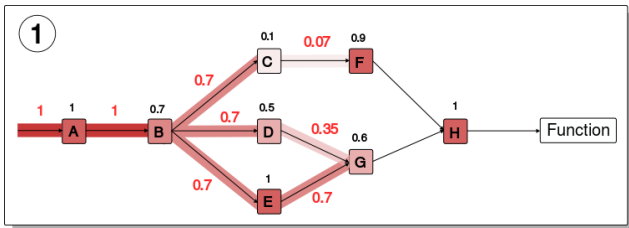
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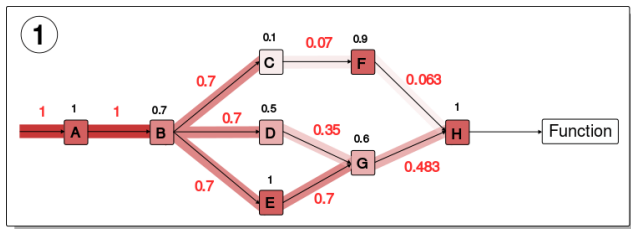
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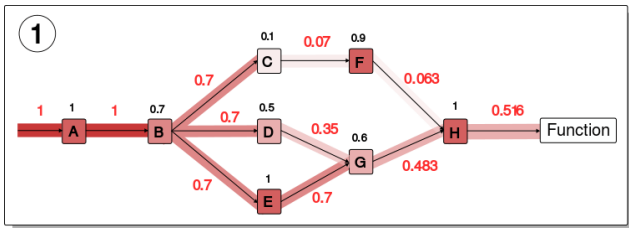
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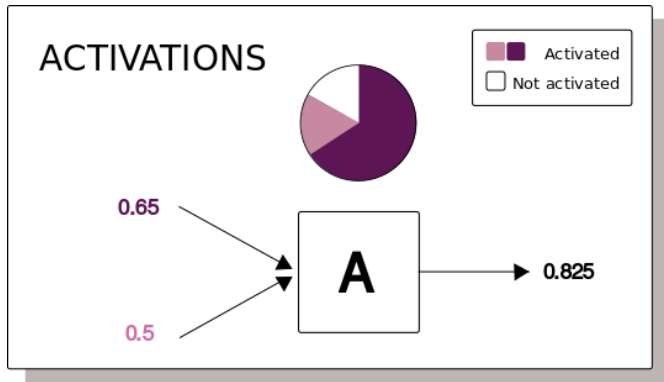
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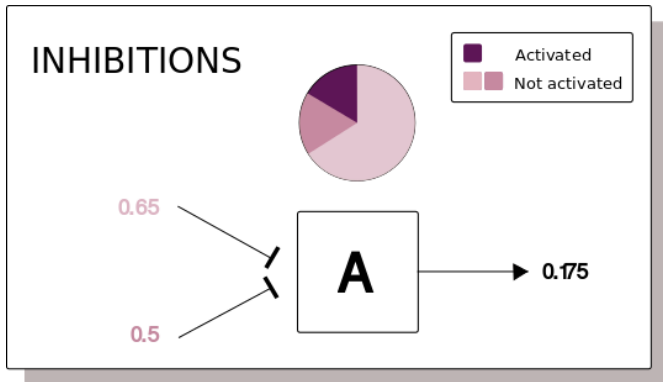




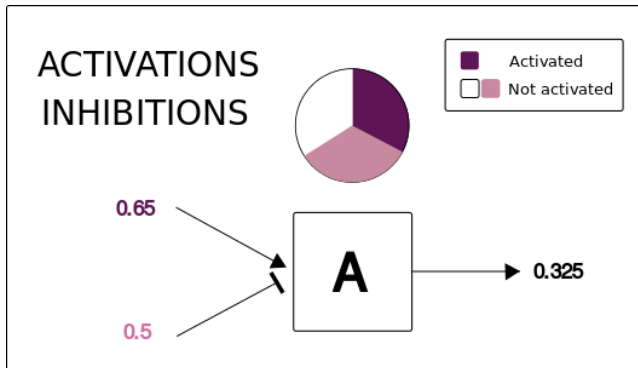
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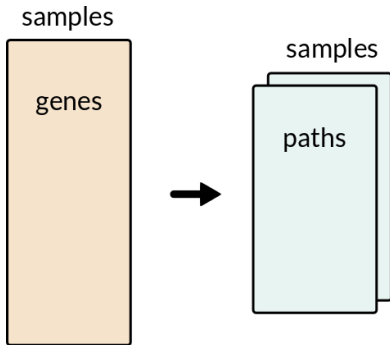
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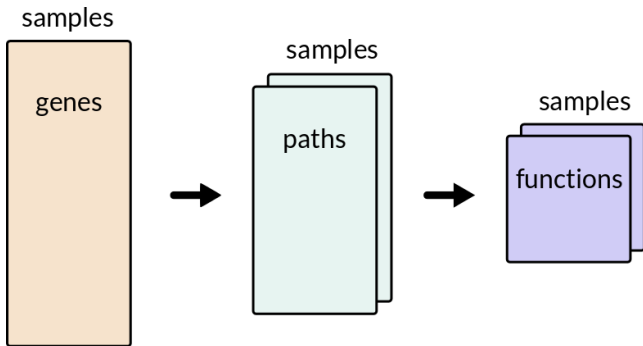
# Functional annotation



# Functional annotation

We annotate each effector protein to a function

- Uniprot keywords
- GO annotation





# HiPathia

Web tool

# Logging in

[hipathia.babelomics.org](http://hipathia.babelomics.org)

hiPathia Pathways analysis suite Differential signaling Prediction Login Sign up

## hiPathia

HIGH THROUGHPUT PATHWAY  
INFERENCE ANALYSIS

1 Start

2 3

hiPathia is a web tool for the interpretation of the consequences of the combined changes of gene expression levels and/or genomic mutations in the context of signalling pathways. hiPathia transforms uninformative gene expression and/or genomic variation data into signalling circuit activities, which carry information on the different cell functionalities triggered by them. Such signalling activities not only account for the underlying molecular mechanisms of diseases or the mode of action of drugs but they can also be used as mechanistic features for the prediction of complex phenotypes.

Note:

hiPathia web application makes an intensive use of the HTML5 standard and other cutting-edge web technologies such as Web Components, so only modern web browsers are fully supported.

hiPathia v1.1.0  
Created by Computational Genomics Department  
Príncipe Felipe Research Center, Valencia, Spain  
2016

# Upload data

The screenshot shows the hiPathia web application interface. The top navigation bar includes links for 'Differential signaling', 'Prediction', and 'My data' (highlighted with an orange box and labeled '1'). The left sidebar shows a file browser for 'gta2016ciberer' with an 'Upload' button (highlighted with an orange box and labeled '3'). The main content area displays the 'hiPathia' logo and the text 'HIGH THROUGHPUT PATHWAY INFERENCE ANALYSIS'. A table lists a file named 'Exercise\_1' with a size of '-' and a date of 'Sep 26, 2016'. The bottom of the page contains a 'Note' section and the version information 'hiPathia v1.1.0'.

2 hiPathia Pathways analysis suite

1 My data

3 Upload

gta2016ciberer

Name	Size	Date
Exercise_1	-	Sep 26, 2016

0B of 1.0 GB

hiPathia

HIGH THROUGHPUT PATHWAY  
INFERENCE ANALYSIS

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2016



# Upload data

The screenshot shows the hiPathia web application interface. The main window displays a file browser for the user 'gda2016ciberer'. An 'Upload File' dialog box is open in the foreground. The dialog has three main sections:

- File upload:** Contains a 'Choose file...' button (highlighted with callout 5) and a 'Revalidate' button.
- Bioformat:** Contains three radio button options: 'Data matrix expression' (selected, highlighted with callout 4), 'Variant (VCF)', and 'Experimental design'.
- File validation log:** Contains a table with columns 'Line', 'Type', and 'Message'. Below the table, it shows 'Errors: 0', 'Warning: 0', 'Info: 0', and 'Lines: 0'. A 'Stop' button is also present.

At the bottom of the dialog is an 'Upload' button (highlighted with callout 6). The background shows the hiPathia logo and navigation links like 'My data', 'My jobs', 'Profile', and 'Logout'.

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hiPathia v1.0  
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2016

# Workflow

The screenshot shows the hiPathia web application interface. The top navigation bar includes the text "2 hiPathia Pathways analysis suite" and two tabs: "Differential signaling" and "Prediction". On the right side of the navigation bar, there is a "My data" button (annotated with a red circle 1), a "My jobs" link, a user profile icon, and a "Logout" link. The main content area on the left is titled "Browse My Data" and shows a file browser for the user "gda2016ciberer". It contains a table with columns "Name", "Size", and "Date". A file named "Exercise\_1" is listed with a size of "-" and a date of "Sep 26, 2016". The browser also shows "0B of 1.0 GB" and a search bar. The main content area on the right features the "hiPathia" logo, the subtitle "HIGH THROUGHPUT PATHWAY INFERENCE ANALYSIS", and a paragraph of text. A red circle 3 is placed over the top navigation bar, and a red circle 1 is placed over the "My data" button. A red circle 3 is also placed over the "Differential signaling" tab.

2 hiPathia Pathways analysis suite

Differential signaling Prediction

My data My jobs gda2016ciberer Profile Logout

Browse My Data

gda2016ciberer

Upload

Name	Size	Date
Exercise_1	-	Sep 26, 2016

0B of 1.0 GB

Search by name...

# hiPathia

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INFERENCE ANALYSIS

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2016

# Workflow

The screenshot displays the hiPathia Pathways analysis suite interface. The top navigation bar includes the hiPathia logo, the text "Pathways analysis suite", and tabs for "Differential signaling" and "Prediction". On the right side of the navigation bar are links for "My data", "My jobs", "Subscribers", "Profile", and "Logout".

Four numbered callouts highlight specific interface elements:

- 4**: Points to the "Function level analysis" section, which contains checkboxes for "Gene ontology" and "Uniprot keywords".
- 5**: Points to the "Launch Job" button at the bottom of the "Job information" section.
- 6**: Points to the "My jobs" link in the top navigation bar.
- 7**: Points to the "My data" link in the top navigation bar.
- 8**: Points to the "Differential signaling example" job entry in the "My jobs" panel.

The main content area is divided into two panels. The left panel, titled "Color nodes by differential expression", contains two sections: "Function level analysis" and "Pathways". The "Pathways" section lists various biological pathways with checkboxes, all of which are currently checked. The right panel, titled "Browse My Jobs", shows a list of jobs with columns for "Select tool", "Job name", and "Status". It lists two jobs: "Prediction train example" and "Differential signaling example". The "Differential signaling example" job is highlighted with a red box and callout 8. At the bottom of the right panel, it shows "Total: 2" and a checkbox for "Enable job notifications".

# Tools

## ① Differential signaling

- Compare signal activity between two conditions
- Correlate path value with a continuous variable

## ② Prediction

- Construct a predictor from a dataset
- Predict classes from new dataset using the predictor

# Tools

## ① Differential signaling

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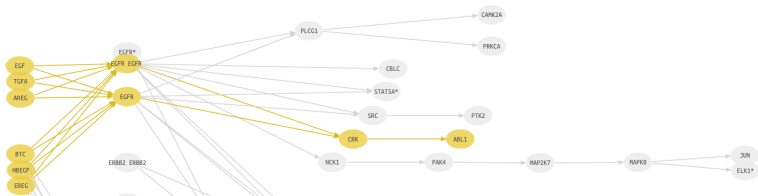
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# Parameters

## 1 Parameters

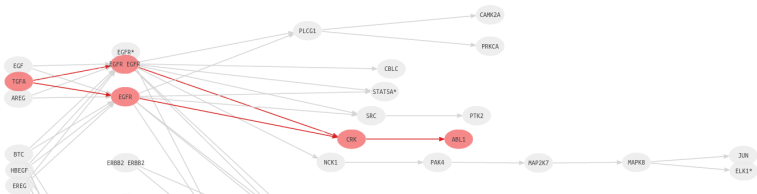
- Decompose paths
- Color nodes by differential expression



## Parameters

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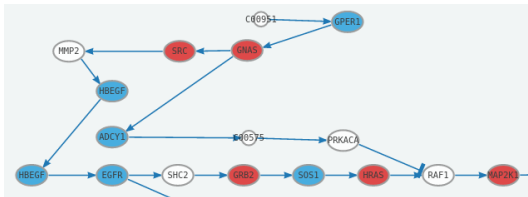
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# Parameters

## ① Parameters

- Decompose paths
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# Parameters

## ① Parameters

- Decompose paths
- Color nodes by differential expression

## ② Function level analysis

Perform analysis with the following functional annotations:

- Gene ontology
- Uniprot keywords



# HiPathia

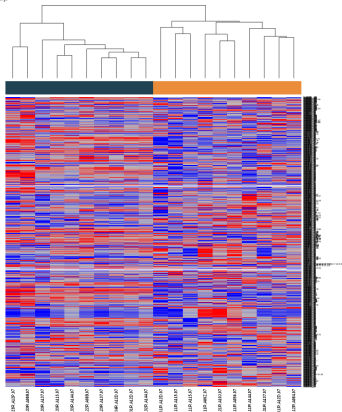
Results

# Heatmap

Graphical representation of data where values in a matrix are represented as colors

Path values

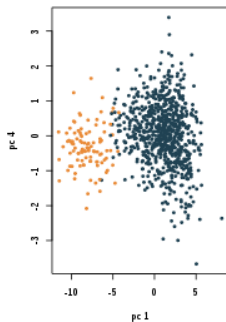
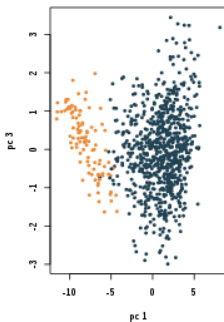
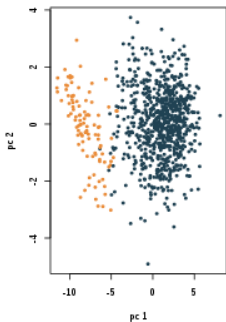
- Path values
- Heatmap



# Principal Components Analysis (PCA)

Statistical procedure to convert a set of observations into a set of values of linearly uncorrelated variables

 PCA 



## Results table

- Table of results for the comparison.
- Ordered by the FDR p-value.

 Path significance 

circuit/term	UP/DOWN	statistic	p.value	FDRp.value
ErbB signaling pathway: STAT5A	DOWN	-16.076	0.000	0.000
Adrenergic signaling in cardiomyocytes: SCN1B	DOWN	-15.987	0.000	0.000
Thyroid hormone signaling pathway: RCAN1	DOWN	-15.966	0.000	0.000
cGMP-PKG signaling pathway: PDE2A	DOWN	-15.909	0.000	0.000
cGMP-PKG signaling pathway: C00144	DOWN	-15.786	0.000	0.000
AMPK signaling pathway: LEPR	DOWN	-15.761	0.000	0.000
Hippo signaling pathway: FGF1	DOWN	-15.728	0.000	0.000
Adherens junction: SMAD4 SMAD2	DOWN	-15.727	0.000	0.000
Adipocytokine signaling pathway: PTPN11	DOWN	-15.727	0.000	0.000
p53 signaling pathway: CDK1 CCNB3	UP	15.693	0.000	0.000

«

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Page 1

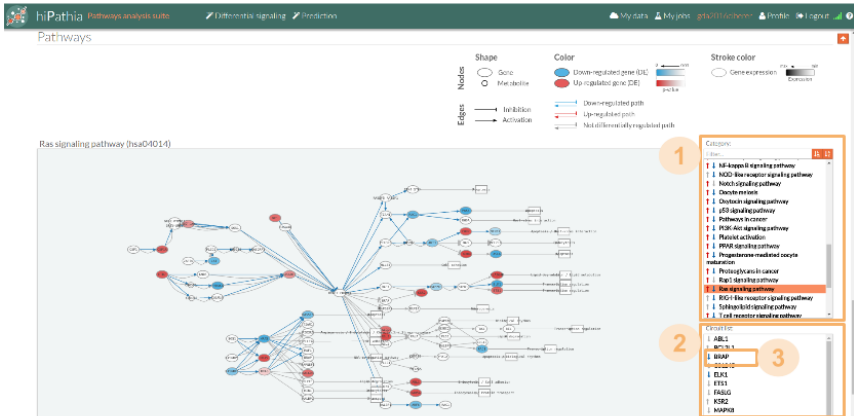
of 102

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1 - 10 of 1014

# Viewer



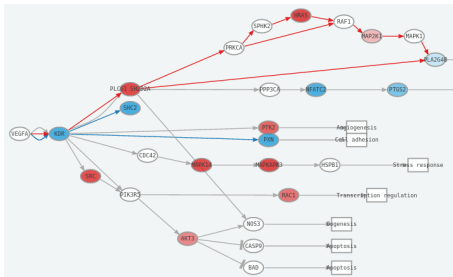
Viewer

# Viewer





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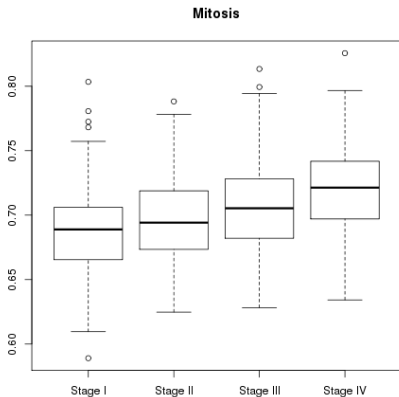


# HiPathia

Further analysis

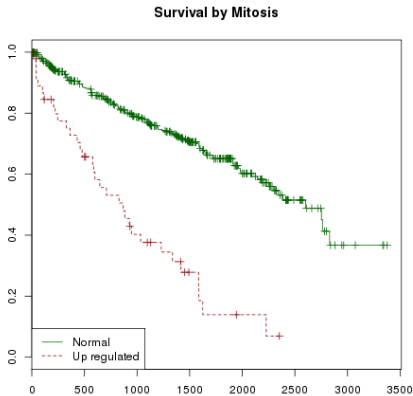
# Disease progression analysis

Search for features which increase with the progression of the disease



# Survival analysis

Analysis of time duration until one or more events happen





# Exercises



# HiPathia exercises

## Exercise 1

Do the [Differential signaling worked example](#)

## Exercise 2

Do the Prediction worked example

- ① Train a predictor following [these steps](#)
- ② Test a new dataset following [these steps](#)

## Exercises 3,4,...

Do the [Differential signaling exercises](#)