

GEPAS

Microarray Data Analysis Differential Gene Expression

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Javier Santoyo-Lopez

jsantoyo@cipf.es

<http://bioinfo.cipf.es>

*Bioinformatics and Genomics Department
Centro de Investigacion Principe Felipe (CIPF)
Valencia, Spain*



Analysis of Differential Gene Expression

GEPAS 4.0 - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://gepas.bioinfo.cipf.es/

GEPAS
GENE EXPRESSION PATTERN ANALYSIS SUITE

You are using the new GEPAS 4.0, previous version v3.1 here
For GEPAS v4.0, your browser has to accept cookies

Tools Documentation Datasets News About us

Bioinformatics Depart

Lastest News

October 2007
New release GEPAS v4.0, projects and jobs management, new tools...

July 2007
A new ID converter tool was added to the GEPAS package

June 2007
New beta version: GEPAS v4.0, including new user-interface, session, project and jobs management,...

September 2006
A new tool was added to the GEPAS

Normalization
Preprocessing
Clustering
Differential expression
Predictors
Viewers
Pipeliner
InSilicoArray CGH
Babelomics Suite

remove missing values, standardize...

- Clustering**
Hierarchical (SOTA, UPGMA, WPGMA...), non-hierarchical (SOM, K-means)
- Differential expression**
T-Rex (t-test, Bayes, data adaptive, CLEAR, ANOVA, Pearson's test,

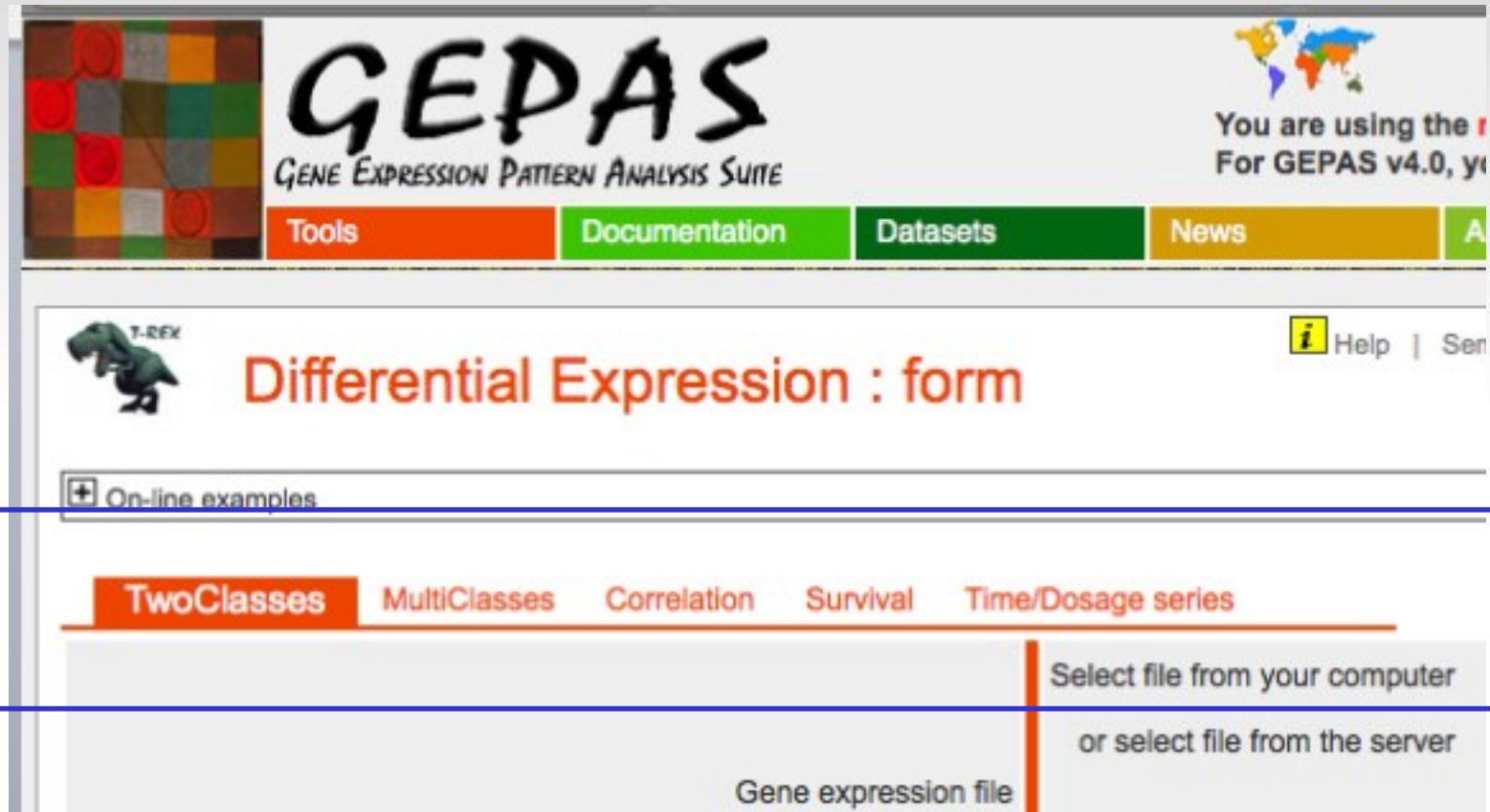
in microarray analysis, it is composed of the following interconnected tools :

Two-colour arrays
Affymetrix arrays
Raw data
Preprocessor
Prophet
T-Rex
Multi classes
Survival
Correlation
Two classes
KNN
DLDA
SVM
PAM
SOM
CAAT
SOTA
Hierarchical
K-means
SOM
ISAGGH
Normalization
Two sets of genes
FatiGO+
Marmite
TMT
FatiGO
Babelomics
GSEA
FatiScan
Blocks of genes

javascript:handleTool('/cgi-bin/t-rex.cgi',null,'TwoClasses');

start 2007_10_cambridge2 Normalization.ppt DifferentialGeneEx... GEPAS 4.0 - Mozilla ... ES 8:19

Different scenarios



The screenshot displays the GEPAS (Gene Expression Pattern Analysis Suite) web interface. At the top, the GEPAS logo is prominently featured in a large, stylized font, with the full name 'GENE EXPRESSION PATTERN ANALYSIS SUITE' written below it. To the right of the logo, a world map icon is accompanied by the text 'You are using the r' and 'For GEPAS v4.0, y'. Below the logo and map, a horizontal navigation bar contains five colored buttons: 'Tools' (orange), 'Documentation' (green), 'Datasets' (dark green), 'News' (yellow), and 'A' (light green).

Below the navigation bar, the main content area features a small 'T-REX' dinosaur icon on the left and a yellow information icon followed by 'Help | Sen' on the right. The central heading 'Differential Expression : form' is displayed in a large, orange font. Underneath this heading, there is a section titled 'On-line examples' with a plus sign icon.

A blue rectangular box highlights a specific part of the interface: a horizontal menu with five tabs labeled 'TwoClasses', 'MultiClasses', 'Correlation', 'Survival', and 'Time/Dosage series'. The 'TwoClasses' tab is currently selected and highlighted in orange. Below this menu, there is a large, light gray input area. On the right side of this area, there is a vertical orange line and a text box containing the instructions 'Select file from your computer' and 'or select file from the server'. At the bottom of this input area, the text 'Gene expression file' is visible.

Input: data entry (1/4)

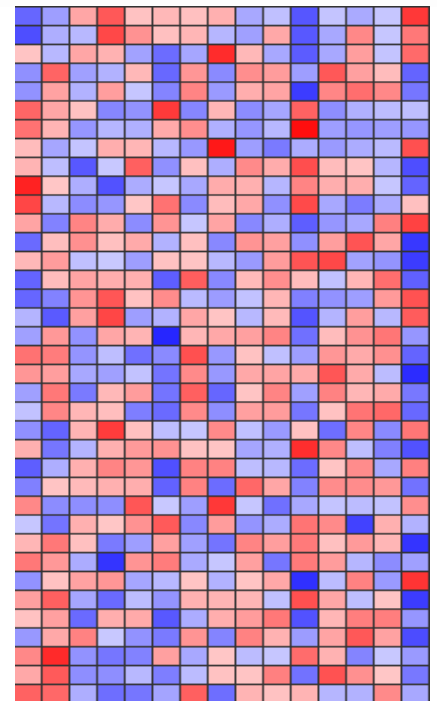
- Gene normalized intensities
- Gene names or gene identifiers

- Microarray information
 - In an independent text file
 - Using special lines and reserved words within the text file containing gene intensity measurements

Normalized Data

- Tab delimited file with numerical values (intensity)
- Genes in rows – samples in columns
- No class assigned to the samples (arrays)

gene1	10.23	9.98	10.41	10.55	10.65	9.69
gene2	10.51	9.74	10.65	10.63	10.43	10.35
gene3	9.89	10.02	9.89	11.03	10.21	10.77
gene4	10.25	10.83	8.94	10.16	10.49	10.46
gene...



Input: data entry (2/4)

File with ID and intensity measurements

gene1	10.23	9.98	10.41	10.55	10.65	9.69
gene2	10.51	9.74	10.65	10.63	10.43	10.35
gene3	9.89	10.02	9.89	11.03	10.21	10.77
gene4	10.25	10.83	8.94	10.16	10.49	10.46
gene...

Class file

```
#CLASS classA classB classA classA classB classA
```

Intensity file with special line for microarray class

```
#CLASS classA classB classA classA classB classA
gene1 10.23 9.98 10.41 10.55 10.65 9.69
gene2 10.51 9.74 10.65 10.63 10.43 10.35
gene3 9.89 10.02 9.89 11.03 10.21 10.77
gene4 10.25 10.83 8.94 10.16 10.49 10.46
gene... .....
```

Text files
tab delimited

Input: data entry (3/4)

- Reserved words

 - #NAMES

 - #CLASS

 - #INDEPENDENT_VARIABLE

 - #TIME_VARIABLE

 - #CENSORING_VARIABLE

 - #CONTIN

 - #SERIES

- Comment lines #

- Better do not use empty lines, spaces, weird symbols or funny characters ...

Input: file format (4/4)

Array names

Arrays

Tab separated file

genes

#NAMES	col1	col2	col3	col4	col5	col6	col7
YGR138C	-1.23	-0.81	1.79	0.78	-0.42	-0.69	0.58
YPR156C	-1.76	-0.94	1.16	0.36	0.41	-0.35	1.12
YOR230W	-2.19	0.13	0.65	-0.51	0.52	1.04	0.36
YAL018C	-1.22	-0.98	0.79	-0.76	-0.29	1.54	0.93
YBR287W	-1.47	-0.83	0.85	0.07	-0.81	1.53	0.65
YCL075W	-1.04	-1.11	0.87	-0.14	-0.80	1.74	0.48
YDR055w	-1.57	-1.17	1.29	0.23	-0.20	1.17	0.26
YOR358W	-1.53	-1.25	0.59	-0.30	0.32	1.41	0.77
YBR006W	-1.76	-0.72	0.13	-0.01	-0.23	1.30	1.28
YBR241C	-1.39	-0.42	-0.08	-0.29	-0.65	1.85	0.98
YCR021c	-1.52	-0.99	0.26	0.04	-0.42	1.43	1.19
YCR061W	-1.57	-0.39	0.33	-0.54	-0.51	1.59	1.09
YDL024c	-1.27	-1.14	0.57	-0.30	-0.47	1.46	1.14
YDR298C	-1.49	-0.87	0.41	-0.47	-0.25	1.38	1.29
YER141w	-1.69	-0.60	0.00	0.41	-0.62	1.45	1.05
.....							

Results (1/2)

The screenshot shows the GEPAS (Gene Expression Pattern Analysis Suite) web interface. At the top, there is a navigation bar with links for Tools, Documentation, Datasets, News, and About us. The main content area displays the results for a job named 'dif.expression_trained'. The results are organized into three sections: 'Input parameters', 'Output results', and 'Send results to...'. The 'Output results' section contains three links: 't_rex_out.txt', 't_rex_diff.txt', and 'image.7681.png'. The 'Send results to...' section contains two options: 'Send to FatiScan' and 'Send to FatiGO+ / Compare'.

Raw data

Output file, ordered genes
(Parameter estimates,
p-values,
adjusted p-values)

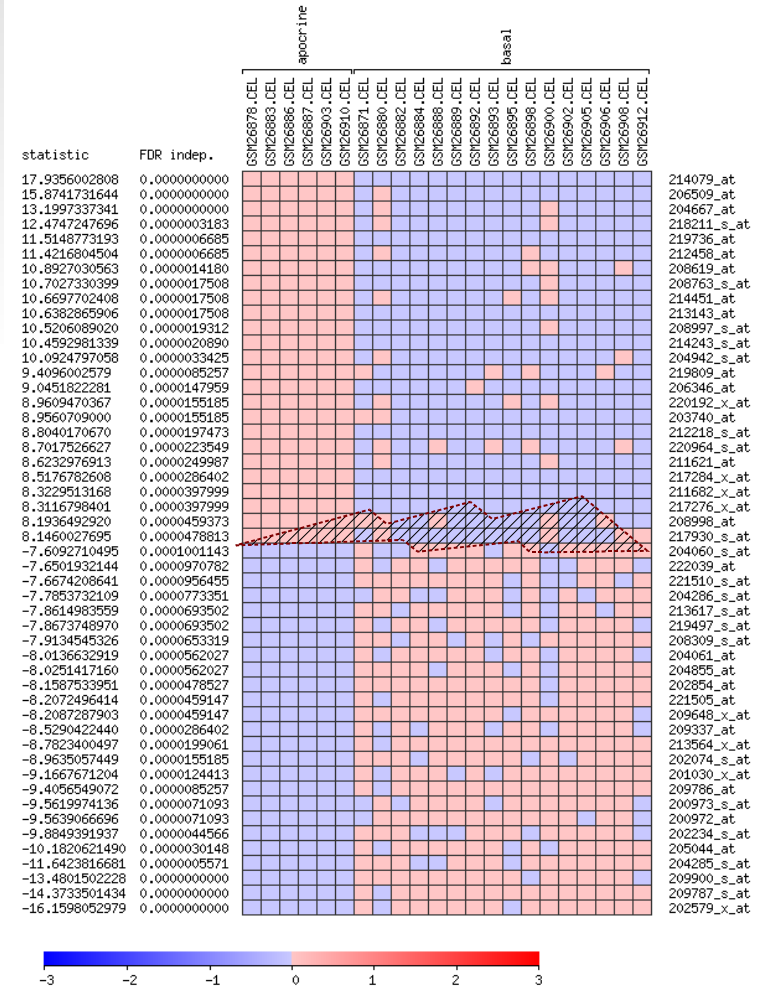
Graphic display of results
Ordered genes

Redirect output to
Babelomics

Results (2/2)

ALGORITHM #DESCRIPTION	t-test gene name	statistic	pvalue	fwer.holm	fdrBH	qvalue
202053_s_at	6.3181490898	8.70188e-05	1	0.34333944435125	0.257000064057149	
214959_s_at	5.464451313	0.0002751968	1	0.34333944435125	0.257000064057149	
218781_at	5.4459657669	0.0002824585	1	0.34333944435125	0.257000064057149	
217826_s_at	5.3622069359	0.000318031	1	0.34333944435125	0.257000064057149	
218363_at	5.3234291077	0.0003360978	1	0.34333944435125	0.257000064057149	
210018_x_at	5.2867088318	0.0003542212	1	0.34333944435125	0.257000064057149	
204987_at	5.2838191986	0.0003556911	1	0.34333944435125	0.257000064057149	
211024_s_at	5.2732758522	0.0003611098	1	0.34333944435125	0.257000064057149	
202974_at	5.1229920387	0.00044873	1	0.34333944435125	0.257000064057149	
205408_at	4.981192112	0.0005524519	1	0.34333944435125	0.257000064057149	
220075_s_at	4.8962396126	0.0006247507	1	0.34333944435125	0.257000064057149	
202809_s_at	4.8225498199	0.0006995474	1	0.34333944435125	0.257000064057149	
219321_at	4.7909593582	0.0007335332	1	0.34333944435125	0.257000064057149	
203357_s_at	4.7074847221	0.0008320683	1	0.34333944435125	0.257000064057149	
200793_s_at	4.6667556763	0.0008851652	1	0.34333944435125	0.257000064057149	
218582_at	4.6339182854	0.0009305915	1	0.34333944435125	0.257000064057149	
209749_s_at	4.6125841141	0.0009614255	1	0.34333944435125	0.257000064057149	
209137_s_at	4.6095442772	0.0009659064	1	0.34333944435125	0.257000064057149	
201303_at	4.605017662	0.00097262	1	0.34333944435125	0.257000064057149	
207891_s_at	4.5465116501	0.0010639882	1	0.34333944435125	0.257000064057149	
214541_s_at	4.5411777496	0.0010727592	1	0.34333944435125	0.257000064057149	
202453_s_at	4.4769094312	0.0011861788	1	0.34333944435125	0.257000064057149	
221025_x_at	4.4758839607	0.001186558	1	0.34333944435125	0.257000064057149	
36564_at	4.4685564041	0.0012001048	1	0.34333944435125	0.257000064057149	
216033_s_at	4.4133515358	0.0013075777	1	0.346881258832955	0.259651220408837	
220448_at	4.38676548	0.0013629247	1	0.346881258832955	0.259651220408837	
212872_s_at	4.3519635201	0.0014391437	1	0.348914934271717	0.261173488609104	
219753_at	4.3236727715	0.0015044184	1	0.348914934271717	0.261173488609104	
201504_s_at	4.2745676140	0.0016252496	1	0.358962494968317	0.271231138970159	
214879_x_at	4.2481431961	0.0016944702	1	0.362351460441905	0.272650999103575	
209006_s_at	4.234023571	0.0017327255	1	0.364248323740566	0.273329410664490	
209013_x_at	4.1964502335	0.0018390272	1	0.365154648216477	0.273329410664490	
208016_s_at	4.1860127449	0.0018697606	1	0.365154648216477	0.273329410664490	
208983_s_at	4.1770939827	0.0018964506	1	0.365154648216477	0.273329410664490	
217094_s_at	4.1725201607	0.0019102935	1	0.365154648216477	0.273329410664490	
205836_s_at	4.1524200439	0.0019724001	1	0.365154648216477	0.273329410664490	
206900_x_at	4.1388754845	0.002015447	1	0.365154648216477	0.273329410664490	
206953_s_at	4.093146801	0.0021682302	1	0.365154648216477	0.273329410664490	
208909_at	4.0697126389	0.0022512004	1	0.365154648216477	0.273329410664490	
217976_s_at	4.037735939	0.0023698353	1	0.365154648216477	0.273329410664490	
204160_s_at	4.034406662	0.002382559	1	0.365154648216477	0.273329410664490	

Ordered genes and ordered arrays



- We perform one hypothesis test for each gene
- There is an increased chance of finding false positives
- We need to adjust p-values to control
 - FWER (family-wise error rate)
 - FDR (false discovery rate)

Two class comparison

Two class comparison

On-line examples

TwoClasses MultiClasses Correlation Survival Time/Dosage series

Gene expression file

Select file from your computer or select file from the server (clean text-box) or enter your data

Sample info file (classes, indep., time, censored...)

Select file from your computer or select file from the server (clean text-box) or enter your data

Tests

T-Test Bayes Data adaptive SAM CLEAR CLEAR test Significance level

Image parameters

Standardize Rows Scale

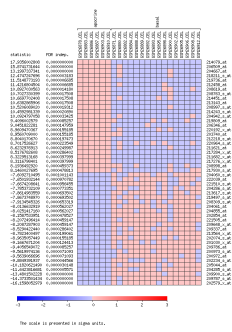
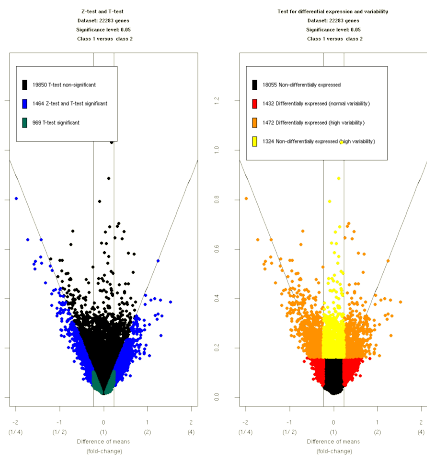
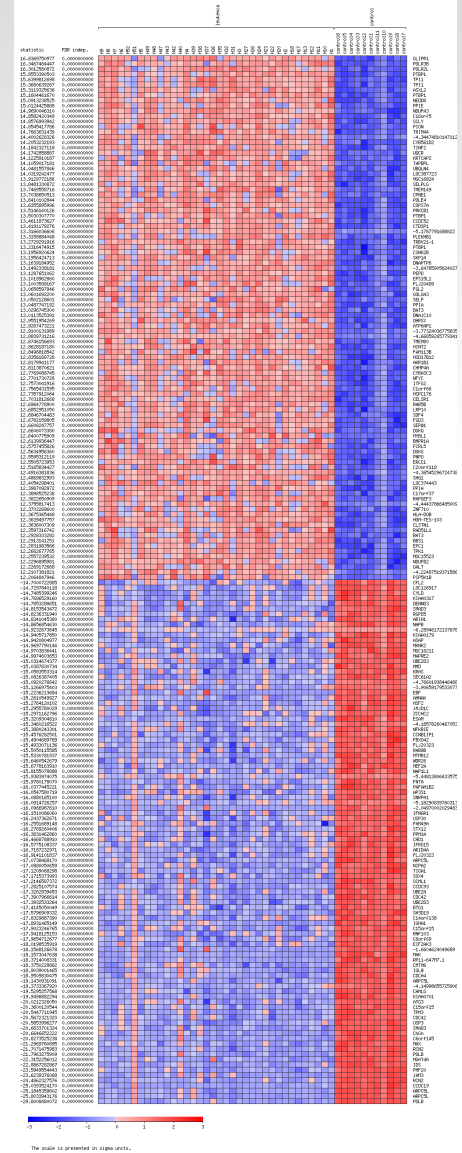
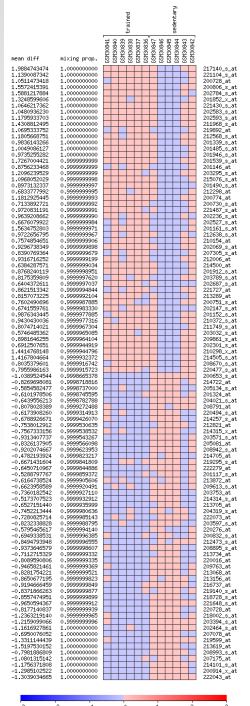
Job name

Submit

We can rank the genes according to a straightforward biological meaning

Two class comparison

- t-test
- data-adaptive statistic
- Empirical Bayes
- CLEAR test



t – test for a gene expression

For each gene, we check if its mean expression is equal or different across the **two** classes

$H_0: \mu_1 = \mu_2$ **Null hypothesis:** the mean expression is **equal** in both groups.

$H_a: \mu_1 \neq \mu_2$

$$T = \frac{\bar{Y}_1 - \bar{Y}_2}{\sqrt{s_1^2/N_1 + s_2^2/N_2}}$$

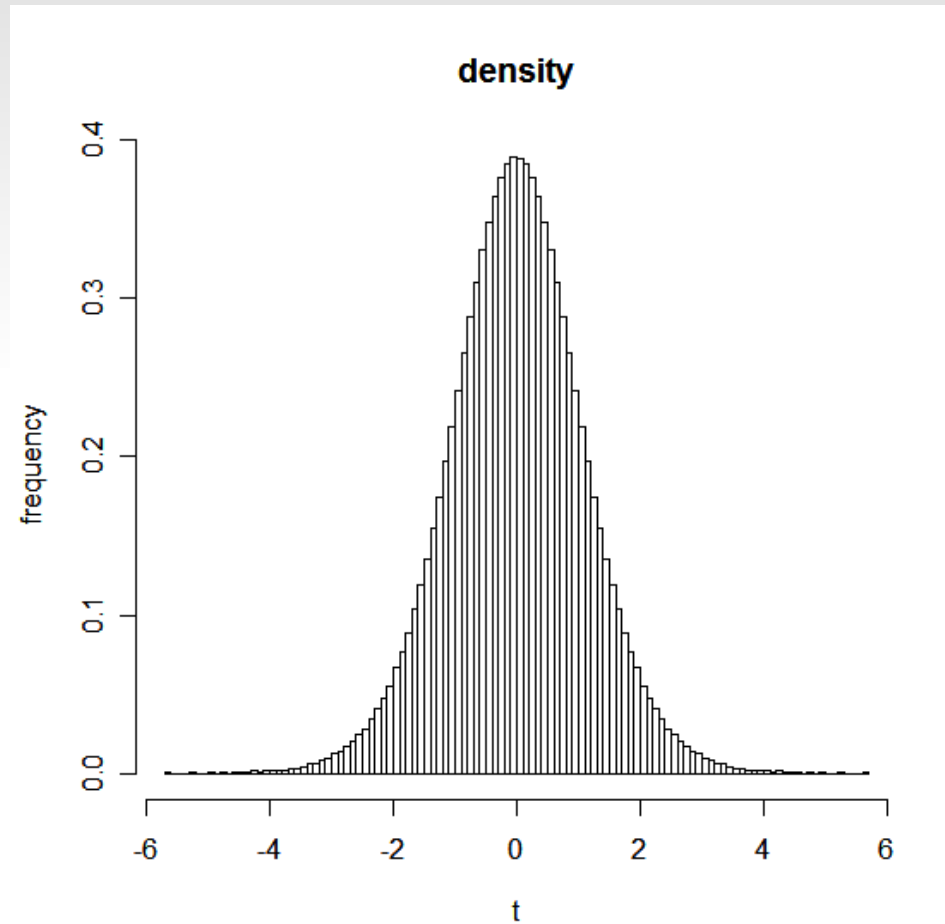
Mean in group 1

Mean in group 2

Estimation of the variability of the differences

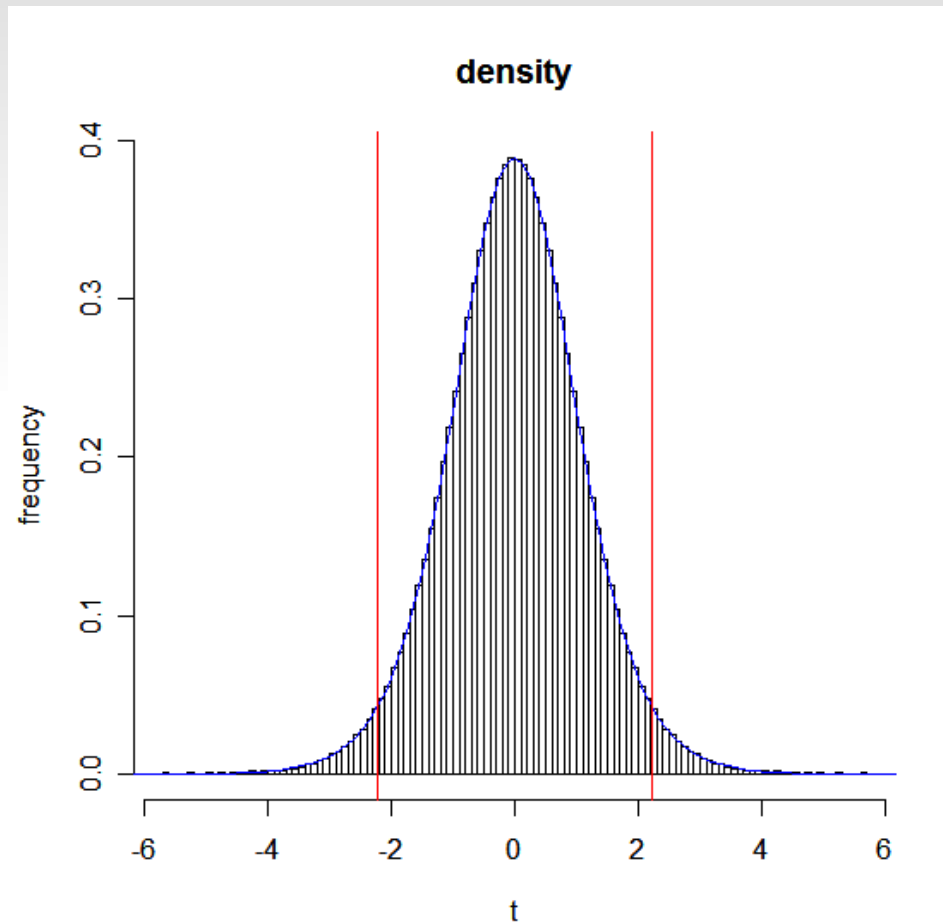
p - value

Under the **null** hypothesis



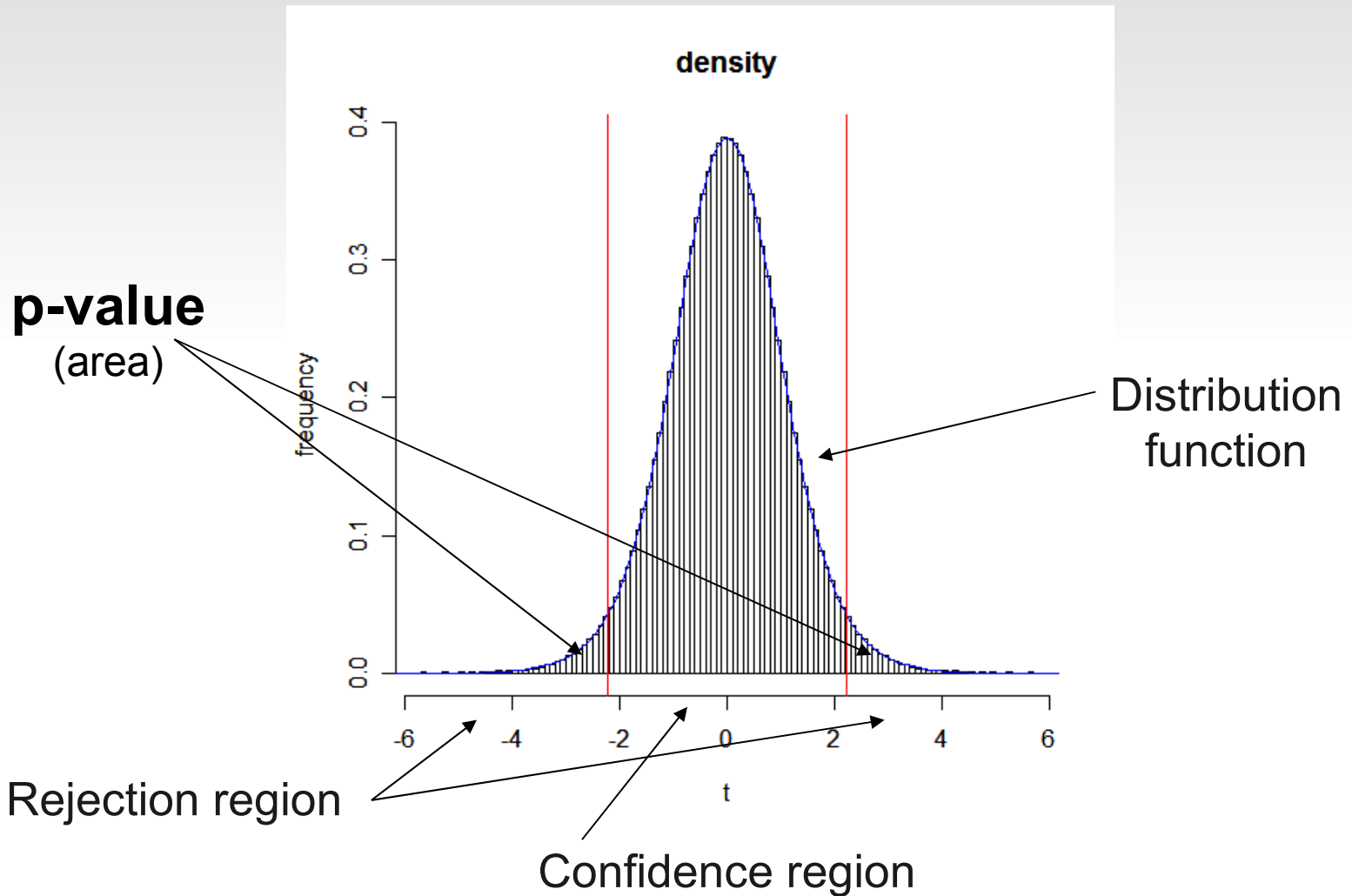
p - value

Under the **null** hypothesis



p - value

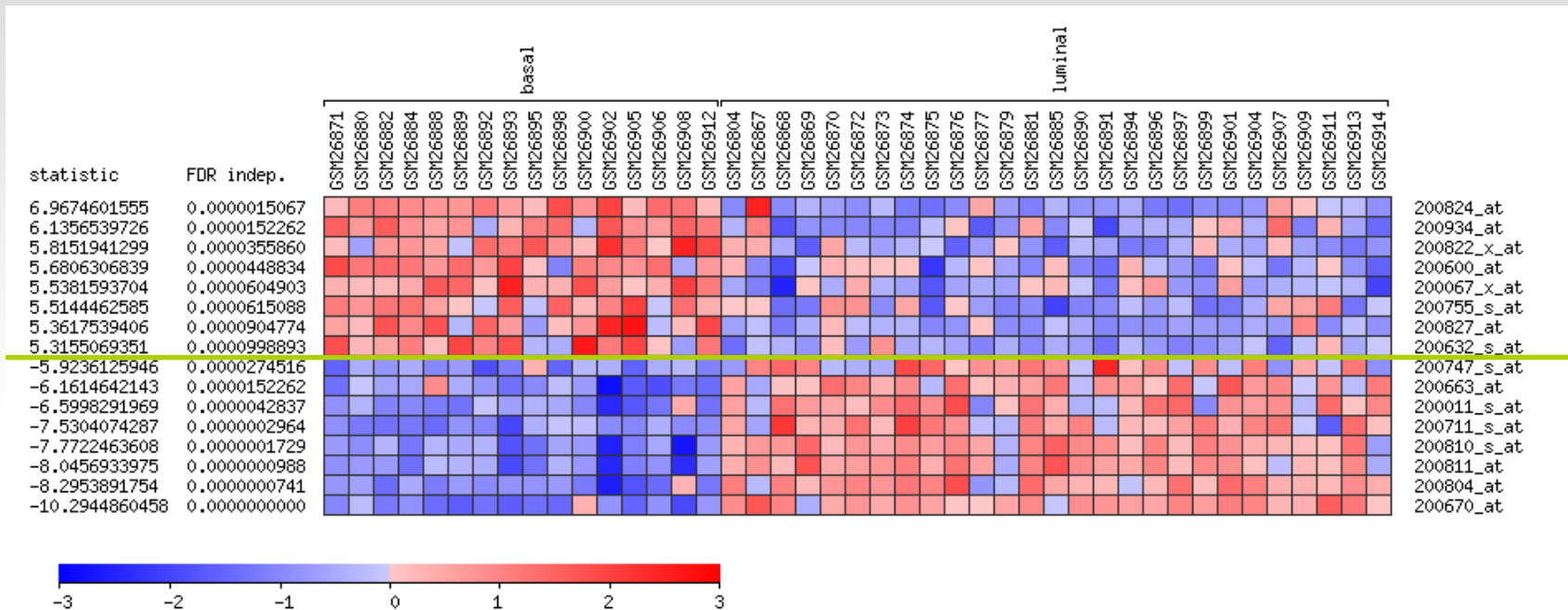
Under the **null** hypothesis



p - value

- If we reject when $p\text{-value} < 0.05$ there is a 5% chance of getting a **false positive**
- On average
 - If you test 100 hypotheses 5 will be false positives (appear significantly wrong)
 - If you test 10000 hypotheses 500 will appear as false positives
- **Multiple testing correction** is needed

Two class comparison



The scale is presented in sigma units.

#ALGORITHM	t-test	statistic	pvalue	fwer.holm	fdrBH	qvalue
#DESCRIPTION	gene name					
200824_at	6.9674601555	1.83e-08	8.9487e-06	1.5067e-06	5.74859921705511e-07	
200934_at	6.1356539726	2.774e-07	0.0001348164	1.52261777777778e-05	5.80933123064148e-06	
200822_x_at	5.8151941299	7.924e-07	0.0003835216	3.55859636363636e-05	1.35773174950655e-05	
200600_at	5.6806306839	1.2305e-06	0.000593101	4.48834285714286e-05	1.71246327964733e-05	
200067_x_at	5.5381593704	1.9592e-06	0.0009384568	6.04903e-05	2.30792122665049e-05	
200755_s_at	5.5144462585	2.1167e-06	0.0010117826	6.15088117647059e-05	2.34678109213897e-05	
200827_at	5.3617539406	3.4799e-06	0.0016564324	9.04774e-05	3.452036309824e-05	
200632_s_at	5.3155069351	4.0441e-06	0.0019209475	9.988927e-05	3.81113280224468e-05	

Redirecting to Babelomics

GEPAS 4.0 - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://gepas.bioinfo.cipf.es/ gepas

Heatmap visualization showing gene expression data. The color scale ranges from blue (low expression) to red (high expression). The heatmap is divided into two main clusters, one blue and one red, with a vertical line separating them.

Continue processing...

- Send to FatiScan
You can send your list of ordered genes to FatiScan
- Send to FatiGO+ / Compare

start 2007_10_cambridge2 DifferentialGeneExpr... GEPAS 4.0 - Mozilla Fi... ES 9:06

Multi-class comparison

Multi-class comparison

The screenshot shows the GEPAS 4.0 web interface in Mozilla Firefox. The browser address bar shows <http://gepas.bioinfo.cipf.es/>. The page has a navigation menu with tabs: TwoClasses, MultiClasses (selected), Correlation, Survival, and Time/Dosage series. The main content area is a form for multi-class comparison. It includes sections for:

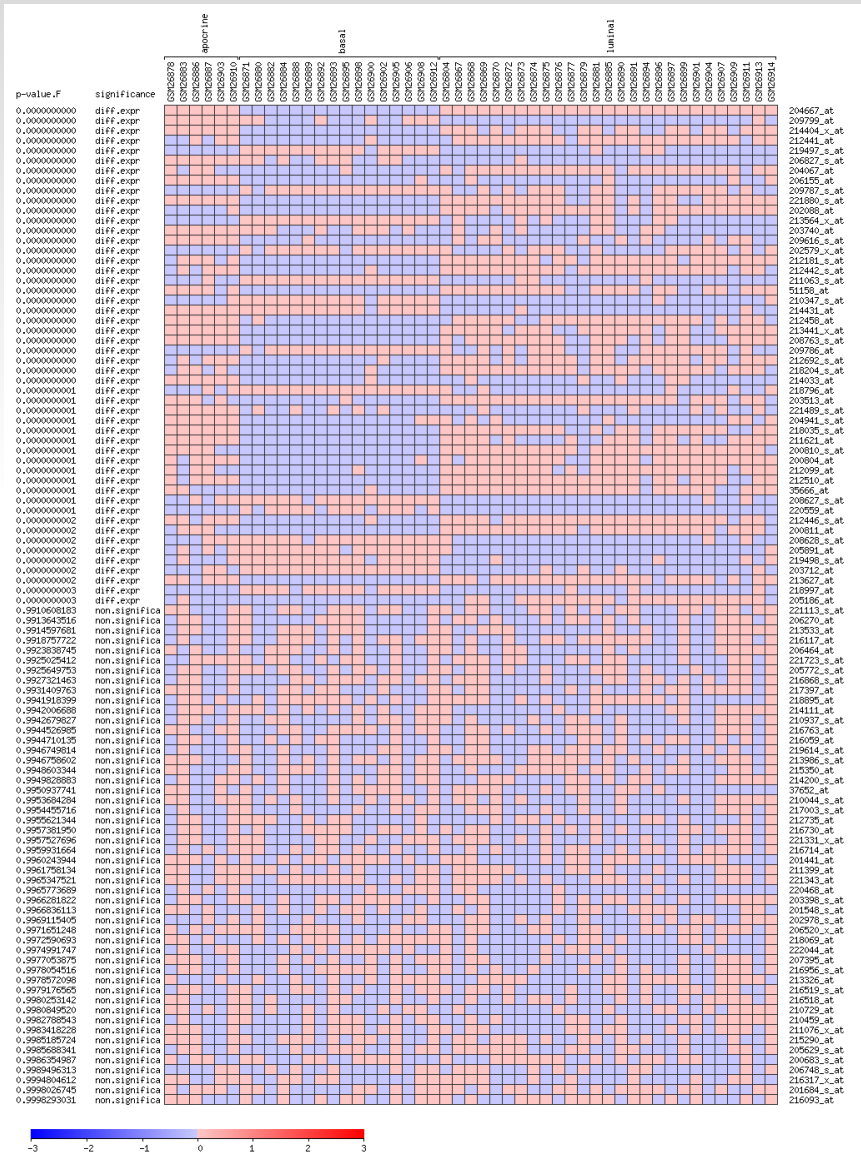
- Gene expression file:** Options to select a file from the computer or server, or enter data directly. Includes 'Browse...' buttons and a 'clean text-box' option.
- Sample info file (classes, indep., time, censored...):** Similar options to the gene expression file section.
- Test:** Radio buttons for 'Anova' (selected) and 'CLEAR'. A 'CLEAR test' section with a radio button and a 'Significance level' input field set to 0.05.
- Image parameters:** A 'Standardize' checkbox (checked), 'Rows' input field set to 100, and a 'Scale' dropdown menu set to '-3/+3'.
- Job name:** Input field containing 'multiclasses'.
- Submit:** A 'run' button.

At the bottom of the page, there is contact information for GEPAS, 2002-2007, Bioinformatics Department, CIPF, Avda. Autopista del Saler 16, 46013 Valencia, Spain, with a phone number +34 96 328 96 80. The browser's taskbar at the bottom shows the start button, open folders, and the current application window.

It is not clear how to arrange genes by their pattern across classes

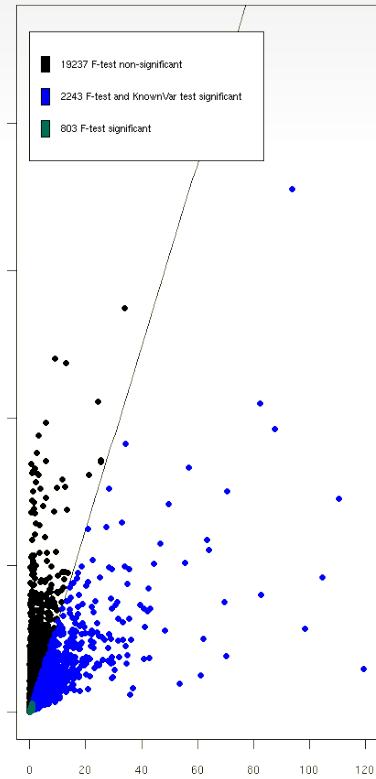
Multi-class comparison

- ANOVA
- CLEAR

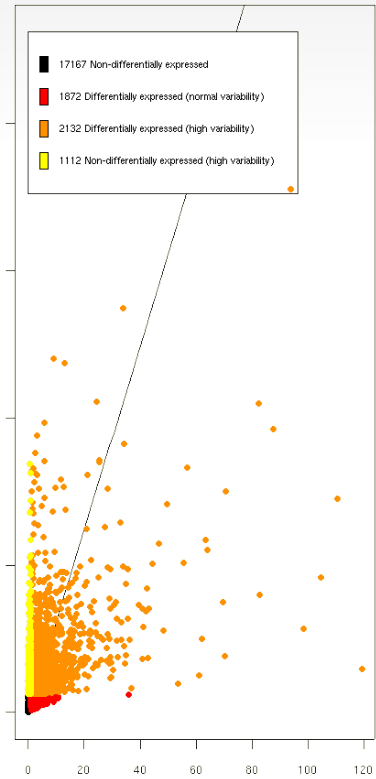


The scale is presented in sigma units.

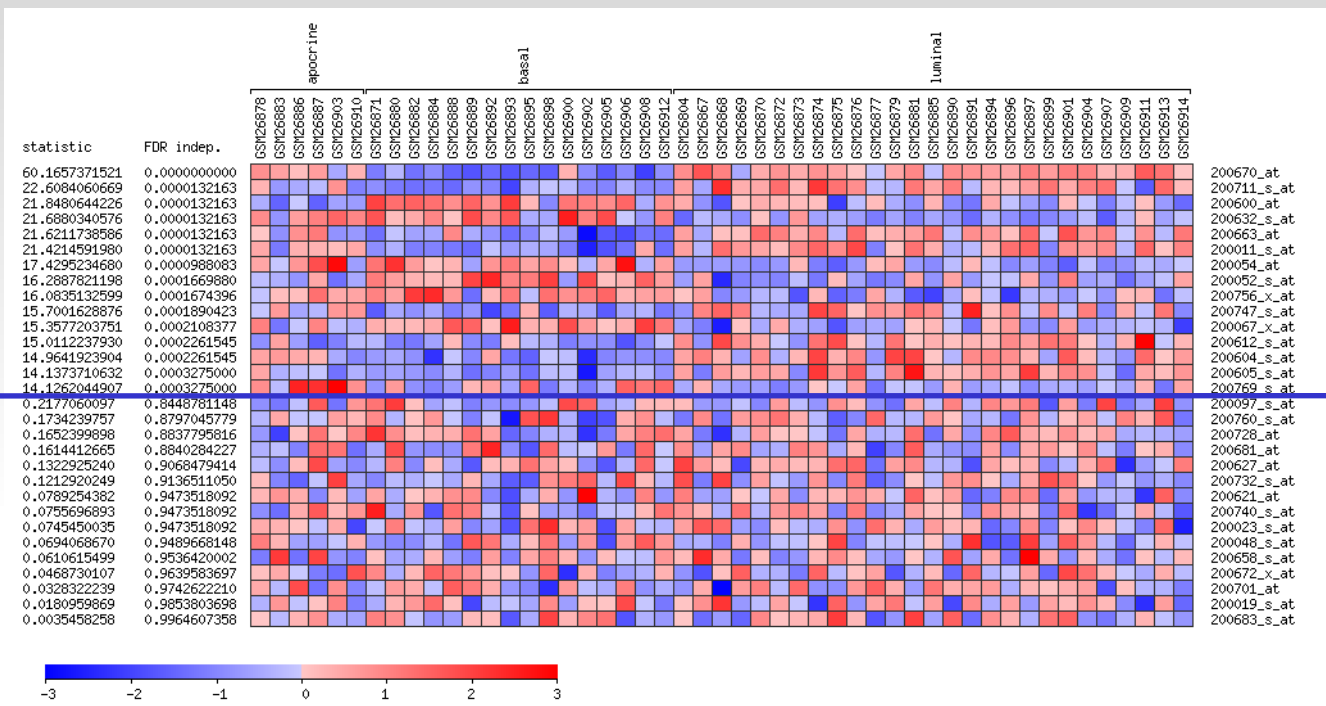
F-test and knownVar test
Dataset: 2283 genes
Significance level: 0.001



Test for differential expression and variability
Dataset: 2283 genes
Significance level: 0.001



Multi-class comparison



#ALGORITHM	anova	statistic	pvalue	fwer.holm	fdrBH	qvalue
#DESCRIPTION	genename					
200670_at	60.1657371521	0	0	0		
200711_s_at	22.6084060669	1.451e-07	4.30947e-05	1.32163e-05	3.37446090852385e-06	
200600_at	21.8480644226	2.136e-07	6.32256e-05	1.32163e-05	3.37446090852385e-06	
200632_s_at	21.6880340576	2.319e-07	6.84105e-05	1.32163e-05	3.37446090852385e-06	
200663_at	21.6211738586	2.4e-07	7.056e-05	1.32163e-05	3.37446090852385e-06	
200011_s_at	21.421459198	2.661e-07	7.79673e-05	1.32163e-05	3.37446090852385e-06	
200054_at	17.429523468	2.321e-06	0.000677732	9.88082857142857e-05	2.52282936662389e-05	
200052_s_at	16.2887821198	4.4829e-06	0.0013045239	0.000166988025	4.26363326009628e-05	
200756_x_at	16.0835132599	5.0569e-06	0.001466501	0.000167439577777778	4.27516256252393e-05	
200747_s_at	15.7001628876	6.3437e-06	0.0018333293	0.00018904226	4.82673453560378e-05	
200067_x_at	15.3577203751	7.7826e-06	0.0022413888	0.000210837709090909	5.3832283420473e-05	
200612_s_at	15.011223793	9.5889e-06	0.0027520143	0.000226154492307692	5.77430516543485e-05	

**Gene expression related to
a continuous variable:**

Correlation and Regression

Gene expression related to a continuous variable

On-line examples

TwoClasses MultiClasses **Correlation** Survival Time/Dosage series

Gene expression file

Select file from your computer Browse...
or select file from the server Browse... (clean text-box)
or enter your data

Sample info file (classes, indep., time, censored...)

Select file from your computer Browse...
or select file from the server Browse... (clean text-box)
or enter your data

Test

Pearson's correlation
Spearman correlation
regression

Image parameters

Standardize
Rows
Scale

Job name

Submit

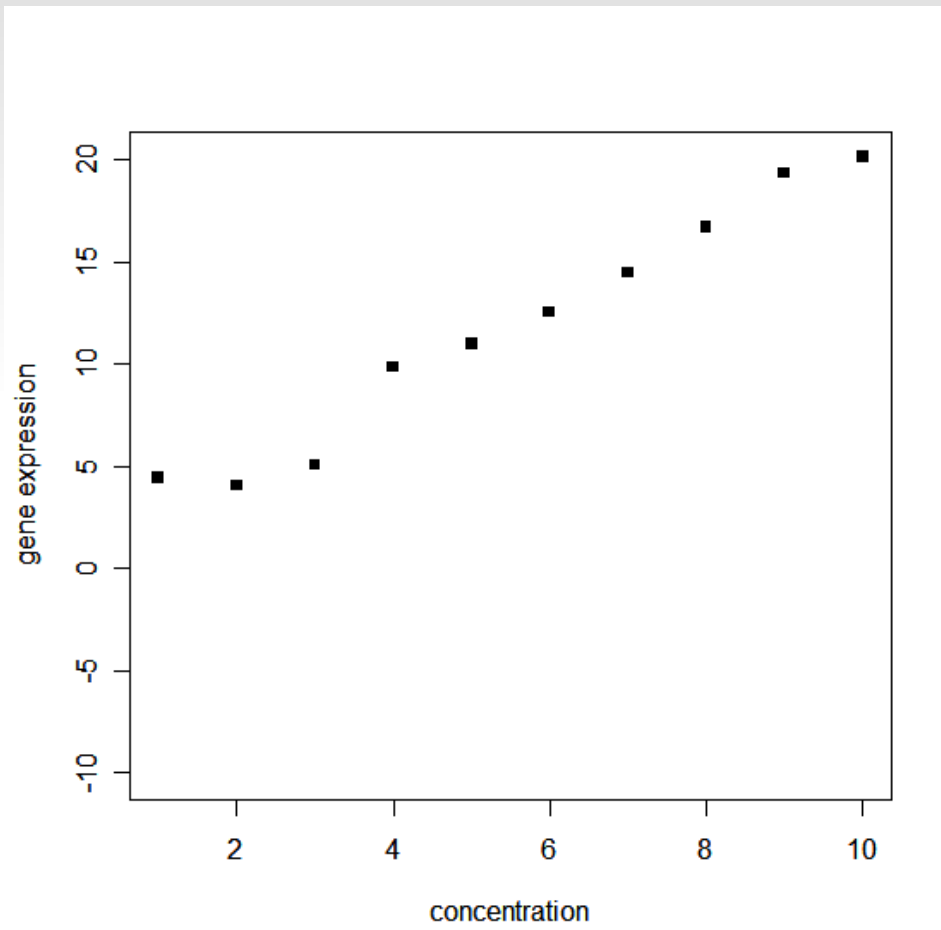
Expression data

Continuous Variable

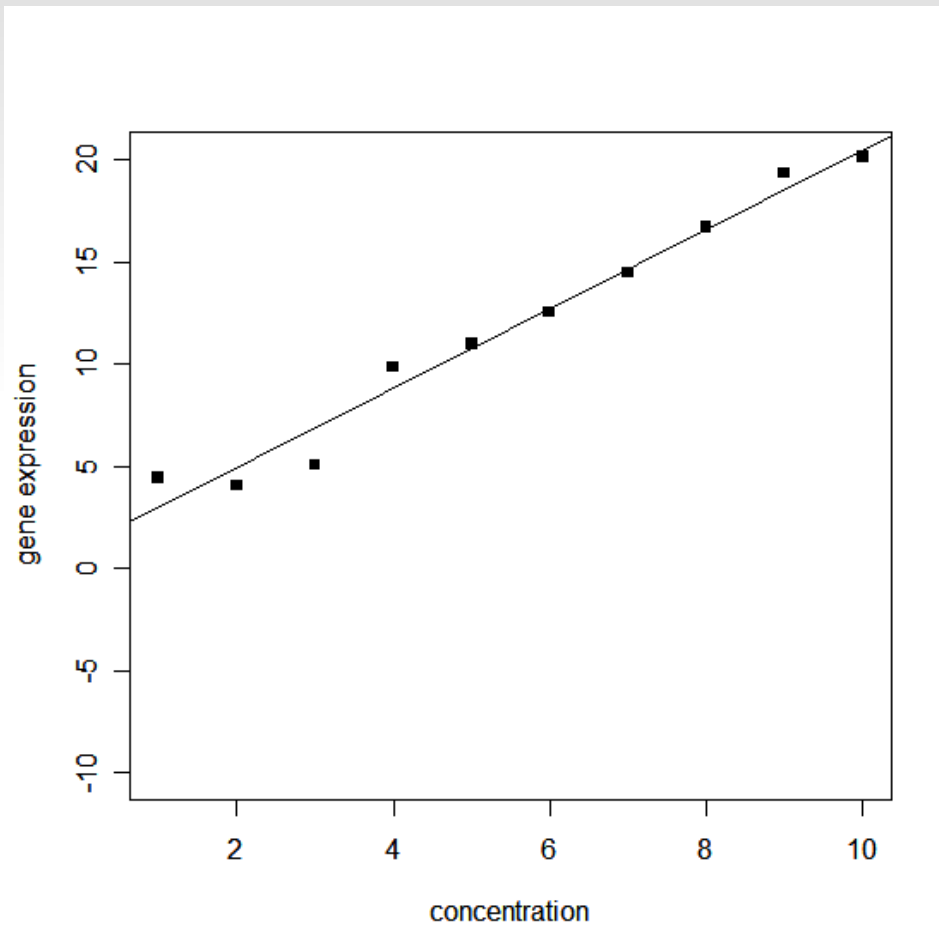
#INDEPENDENT_VARIABLE

Assessing linear relationships

Regression

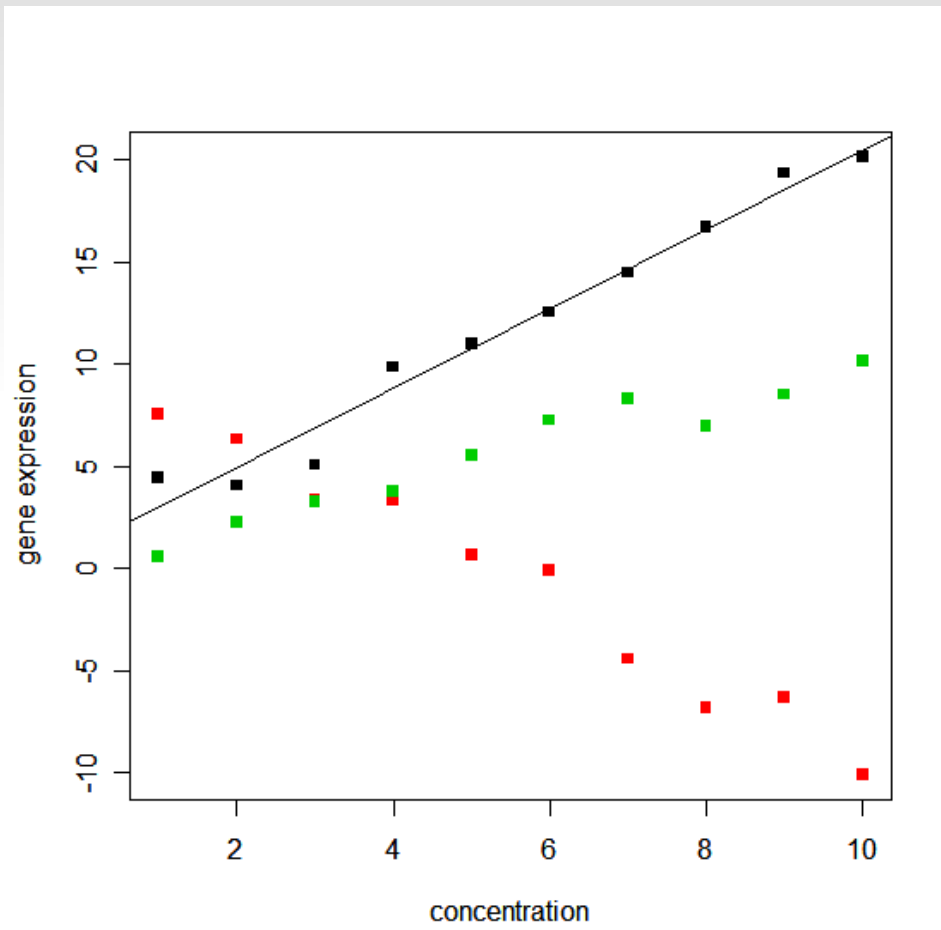


Regression



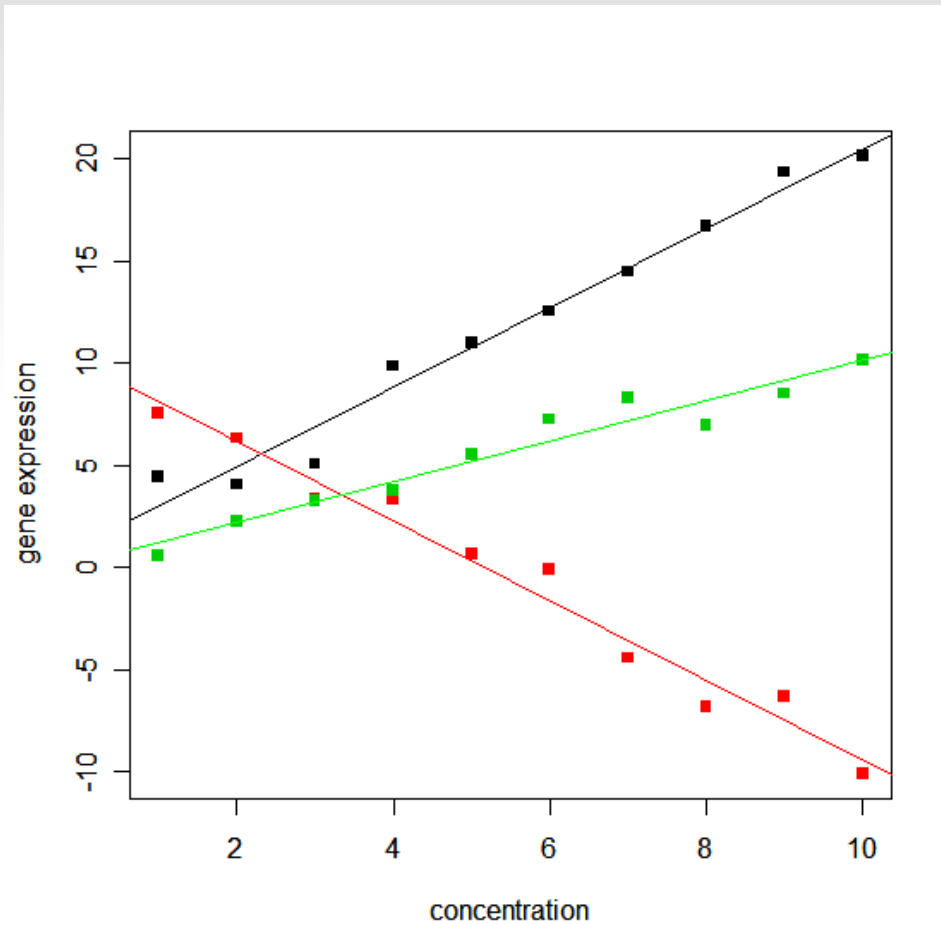
gene1 slope

Regression



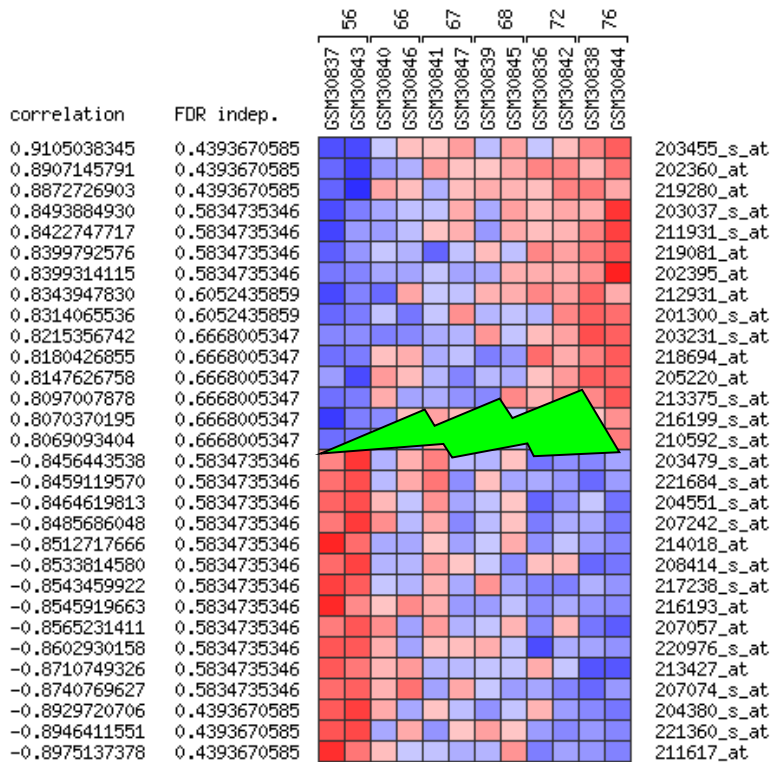
gene1 slope

Regression



gene1 slope
gene2 slope
gene3 slope
...

Correlation



- Pearson correlation coefficient
- Spearman correlation coefficient
- Linear regression

Arrays ranked according to the independent variable

Genes ranked by correlation to the continuous variable



The scale is presented in sigma units.

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Heatmap visualization showing gene expression data. The color scale ranges from blue (low expression) to red (high expression). The heatmap is divided into two main vertical sections, one blue and one red, with a color scale legend below it.

Continue processing...

- Send to FatiScan
You can send your list of ordered genes to FatiScan
- Send to FatiGO+ / Compare

start 2007_10_cambridge2 DifferentialGeneExpr... GEPAS 4.0 - Mozilla Fi... ES 9:06

Survival data

Survival data

On-line examples

TwoClasses MultiClasses Correlation **Survival** Time/Dosage series

Gene expression file

Select file from your computer Browse...
or select file from the server Browse... (clean text box)
or enter your data

Sample info file (classes, indep., time, censored...)

Select file from your computer Browse...
or select file from the server Browse... (clean text box)
or enter your data

Test Cox

Standardize

Image parameters

Rows 100

Scale -3/+3

Job name survival

Submit run

Expression

Survival times & Censoring indicator

#TIME_VARIABLE
#CENSORING_VARIABLE

Cox proportional hazards regression model

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PRINCIPE FELIPE CENTRO DE INVESTIGACION INB

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Heatmap visualization showing gene expression data. The color scale ranges from blue (low expression) to red (high expression). The heatmap is divided into two main vertical sections, each with a color scale below it.

Continue processing...

- Send to FatiScan
You can send your list of ordered genes to FatiScan
- Send to FatiGO+ / Compare

start 2007_10_cambridge2 DifferentialGeneExpr... GEPAS 4.0 - Mozilla Fi... ES 9:06

Time course analysis / Dose analysis

Time course analysis / Dose analysis Inputs

On-line examples

TwoClasses MultiClasses Correlation Survival **Time/Dosage series**

Gene expression file

Select file from your computer Browse...
or select file from the server Browse... (clean text box)
or enter your data

Meta-data file (series, time, dosage,...)

Select file from your computer Browse...
or select file from the server Browse... (clean text box)
or enter your data

Polynomial degree

Significance level for gene selection

Multiple testing adjustment

Significance level for model variable

Clustering

Cluster method

Number of clusters

Job name

Submit

Expression data

Time variable and series classification

#CONTIN
#SERIES

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Time course analysis / Dose analysis: Example

- ✓ Arabidopsis.
- ✓ 4 series: **control and 3 treatments**
(cold, salt, heat).
- ✓ 3 time points.
- ✓ 3 replicates.

What do we want?

Time course analysis / Dose analysis.

Output: list of significant genes

Control

#genes	cluster
STMEQ29	1
STMID05	2
STMGB57	1
STMEY09	3
STMHY68	4
STMGI03	5
STMCU02	1
STMGB35	6
STMDI90	1
STMJI76	7
STMJO83	8
STMCS44	1
STMIA31	3
STMJF53	1
STMIQ37	4
STMJC14	9
STMCM86	2
STMGQ83	3
STMCK87	1
STMCU87	1
STMHN19	9
STMED61	3
STMIC27	5
STMCH79	6
STMDU84	8
STMIO93	9
STMEG09	1
STMIX47	9
STMIP63	6
STMEV77	4

Cold vs Control

#genes	cluster
STMJH42	1
STMDE66	2
STMHZ45	1
STMGL58	3
STMIF71	1
STMEG62	4
STMFB37	5
STMEQ29	1
STMDW06	6
STMEL85	5
STMEG74	1
STMCO26	7
STMHX33	3
STMDV94	3
STMID12	1
STMCV66	2
STMGH56	2
STMEJ16	5
STMCD46	1
STMIT95	1

Salt vs Control

#genes	cluster
STMJH42	1
STMDE66	2
STMHZ45	1
STMGL58	3
STMIF71	1
STMEG62	4
STMEQ29	1
STMDW06	5
STMEG74	1
STMCO26	6
STMID05	5
STMID12	1
STMDH27	7
STMEJ16	1
STMCD46	1
STMIT95	3
STMHJ39	1
STMGB57	3
STMIT31	1
STMEZ42	1
STMIM44	5
STMHN16	5
STMEY09	2
STMCE01	1
STMIY82	2
STMEU24	8
STMHH10	1
STMGQ20	5
STMGI03	9
STM CY10	5
STMHV34	5
STMHY91	2
STMJN05	1
STMEF65	1

Heat vs Control

#genes	cluster
STMJH42	1
STMDE66	2
STMHZ45	1
STMGL58	3
STMIF71	1
STMEG62	4
STMFB37	5
STMEQ29	1
STMDW06	6
STMEL85	5
STMEG74	1
STMCO26	7
STMHX33	3
STMDV94	3
STMID12	1
STMCV66	2
STMGH56	2
STMEJ16	5
STMCD46	1
STMIT95	1
STMJE19	2
STMHJ39	1
STMGU26	5

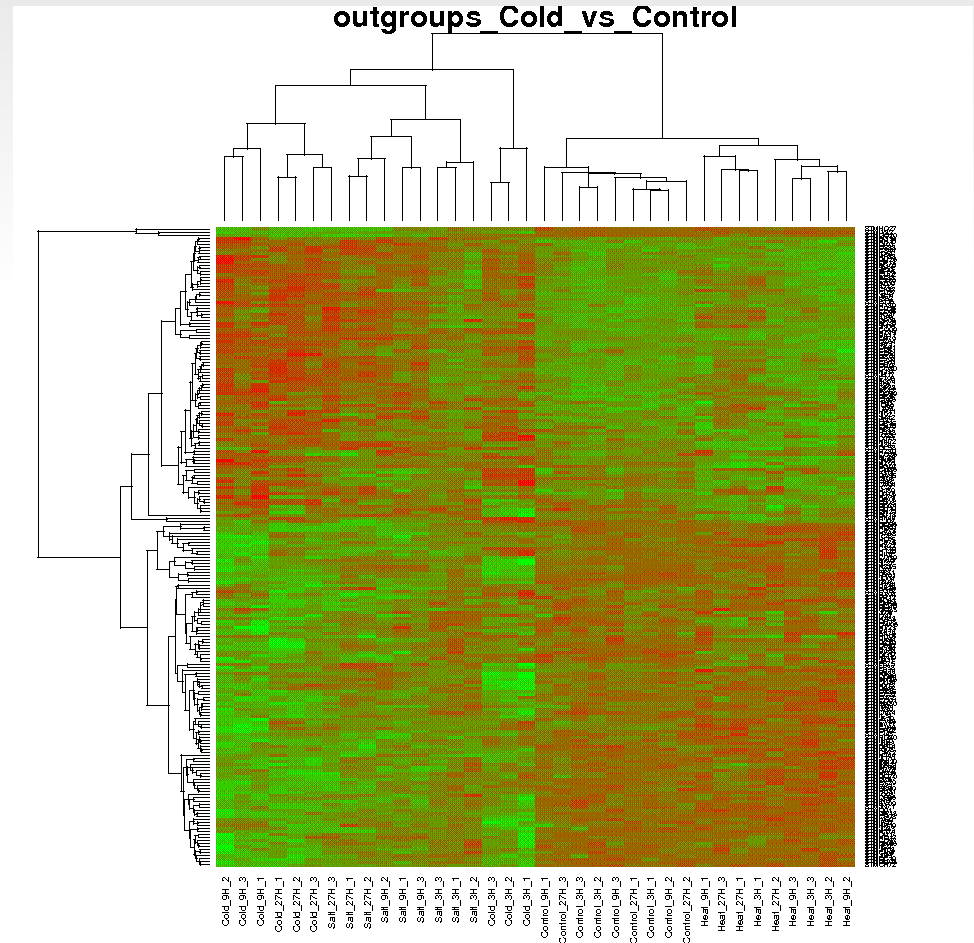
Time course analysis / Dose analysis.

Output: visualization

Cold vs Control

Heatmap

```
#genes cluster
STMJH42 1
STMDE66 2
STMHZ45 1
STMGL58 3
STMIF71 1
STMEG62 4
STMF37 5
STMEQ29 1
STMDW06 6
STMEL85 5
STMEG74 1
STMCO26 7
STMHX33 3
STMDV94 3
STMID12 1
STMCV66 2
STMGH56 2
STMEJ16 5
STMCD46 1
STMIT95 1
...
```



210 significant genes

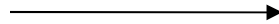
Time course analysis / Dose analysis.

Output: visualization

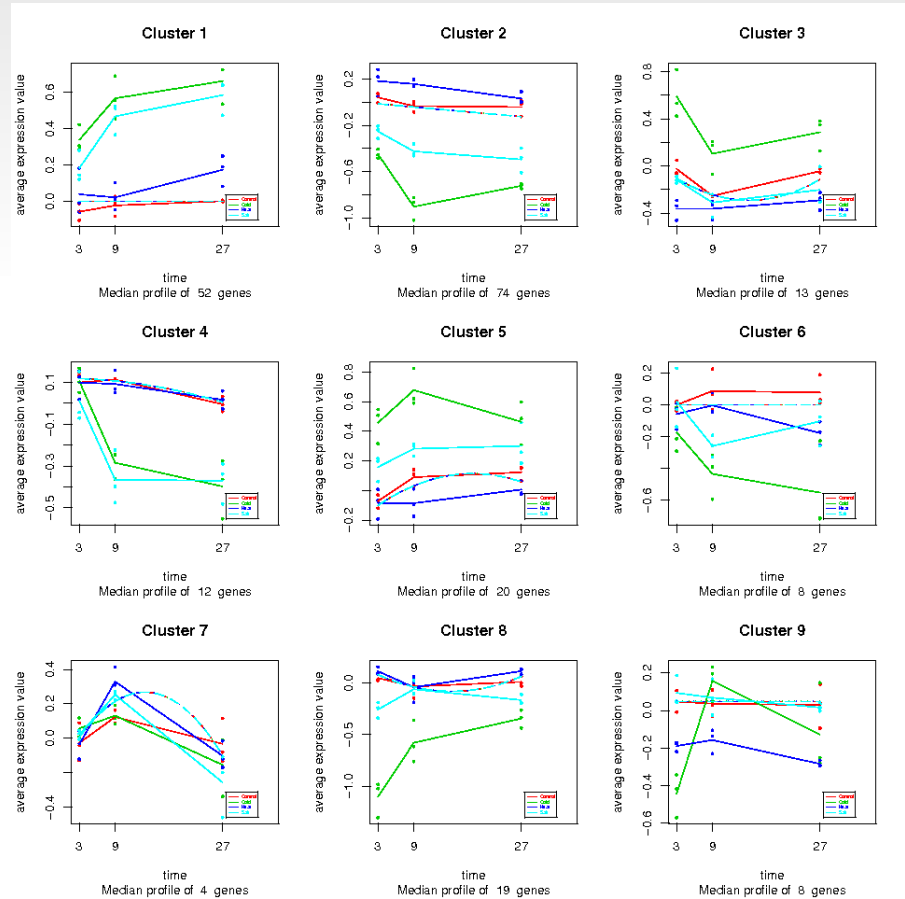
Cold vs Control

Groups plot

```
#genes cluster
STMJH42 1
STMDE66 2
STMHZ45 1
STMGL58 3
STMIF71 1
STMEG62 4
STMTFB37 5
STMEQ29 1
STMDW06 6
STMEL85 5
STMEG74 1
STMCO26 7
STMHX33 3
STMDV94 3
STMID12 1
STMCV66 2
STMGH56 2
STMEJ16 5
STMCD46 1
STMIT95 1
...
```



210 significant genes



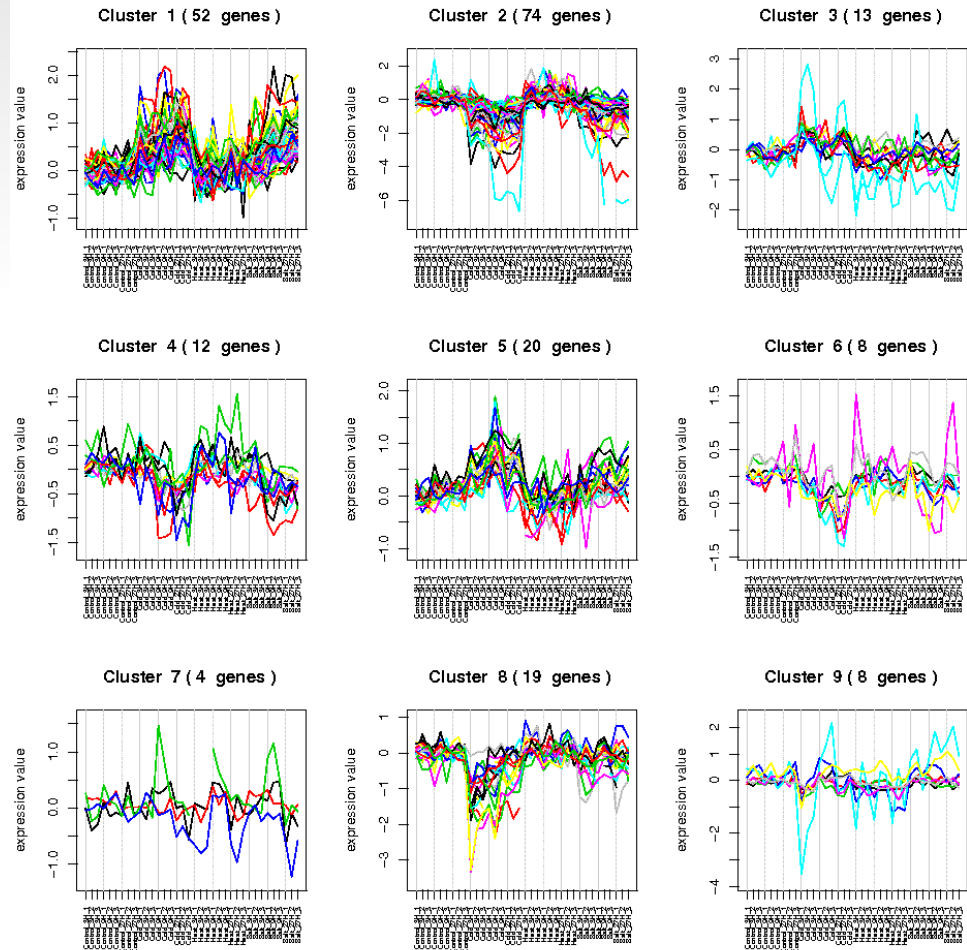
Time course analysis / Dose analysis.

Output: visualization

Profiles plot

Cold vs Control

```
#genes cluster
STMJH42 1
STMDE66 2
STMHZ45 1
STMGL58 3
STMIF71 1
STMEG62 4
STMFB37 5
STMEQ29 1
STMDW06 6
STMEL85 5
STMEG74 1
STMCO26 7
STMHX33 3
STMDV94 3
STMID12 1
STMCV66 2
STMGH56 2
STMEJ16 5
STMCD46 1
STMIT95 1
...
```



210 significant genes

Time course analysis / Dose analysis.

Redirecting to Babelomics

Send results to...

By series

Select one list to send to FatiGO in order to compare it against all your genes

- [outgroups_summary_Cold_vs_Control.txt](#)
- [outgroups_summary_Salt_vs_Control.txt](#)
- [outgroups_summary_Control.txt](#)
- [outgroups_summary_Heat_vs_Control.txt](#)

Cold vs Control:
210 significant genes

STMJH42
STMDE66
STMHZ45
STMGL58
STMIF71
STMEG62
STMPB37
STMEQ29
STMW06
STMEL85
STMEG74
STMCO26
STMHX33
STMDV94
STMID12
STMCV66
STMGH56
STMEJ16
STMCD46

→ Babelomics

Remember...

- ✓ GEPAS allows us to analyze Differential Expression in different experimental scenarios.
- ✓ This module needs normalized data from GEPAS or other tool.
- ✓ Results can be functional interpreted from Babelomics.

The End

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