A faint, light blue network diagram consisting of numerous small circles of varying sizes connected by thin grey lines, forming a complex web-like structure.

# PathAct

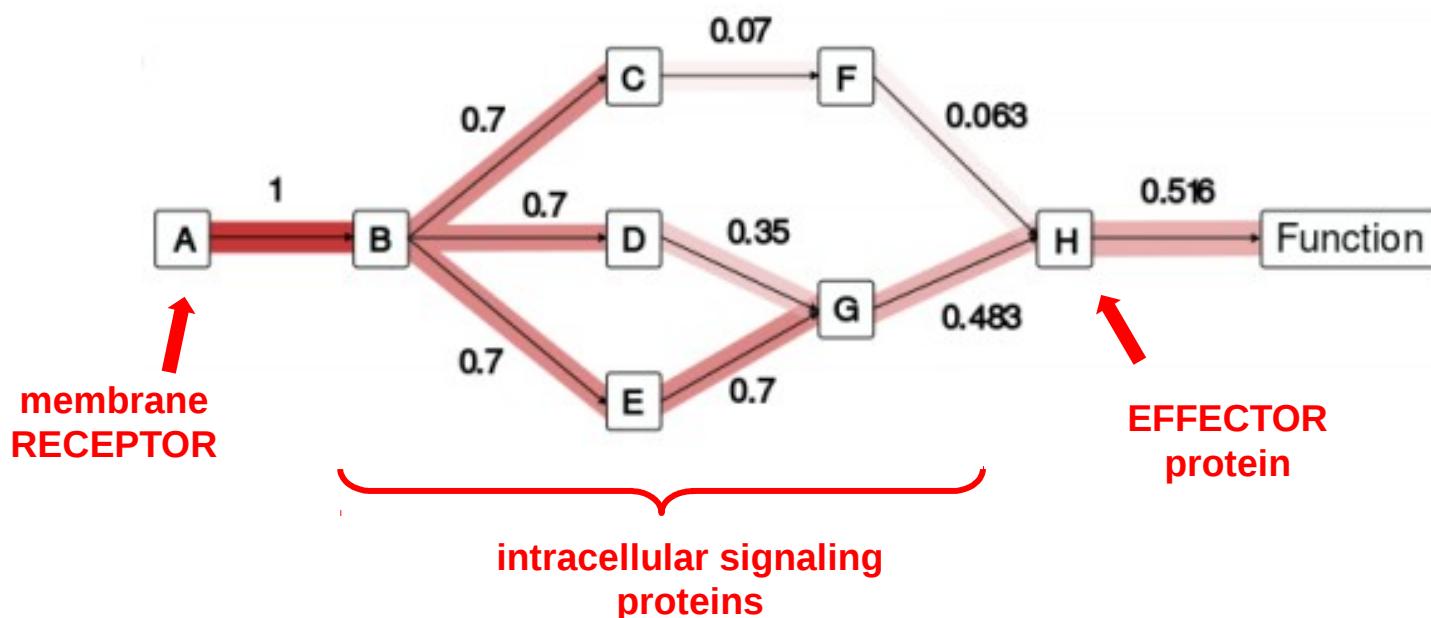
## In silico modulation of signal transduction

Marta R. Hidalgo  
January 11th, 2018



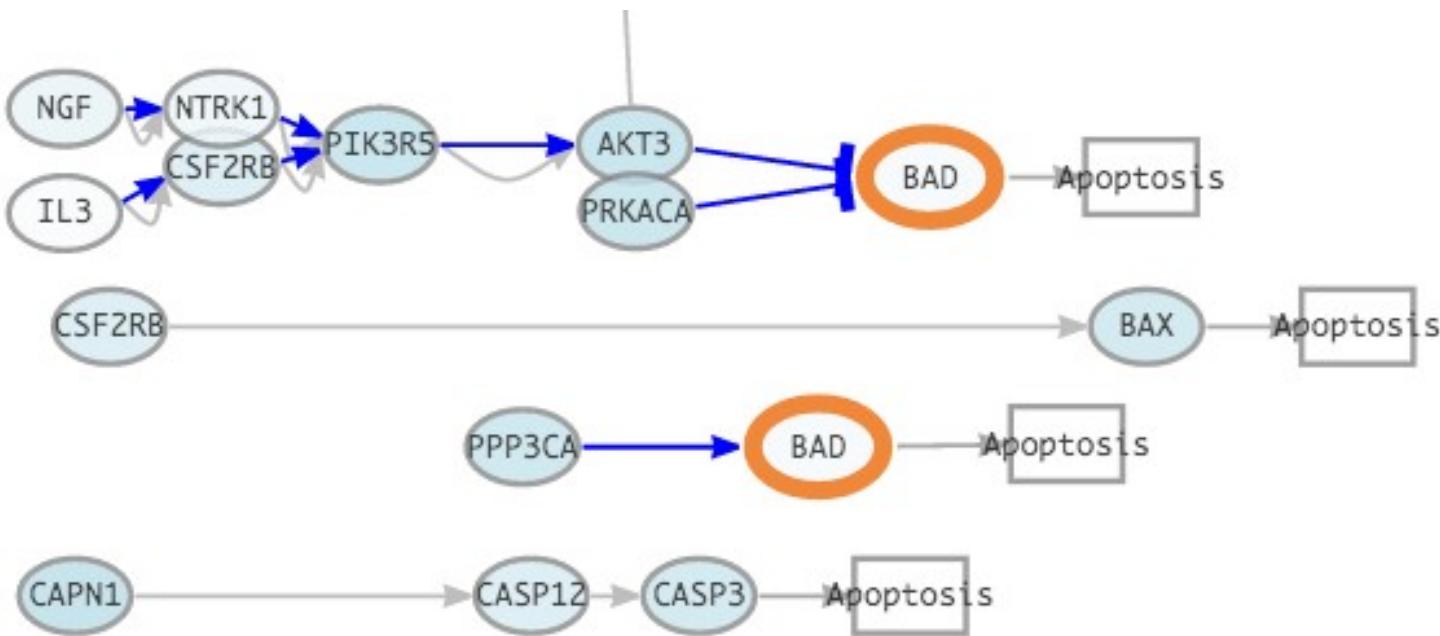
# Signal transduction modelling

In our model, signal transduction is usually modulated through all nodes between a membrane receptor and an effector protein



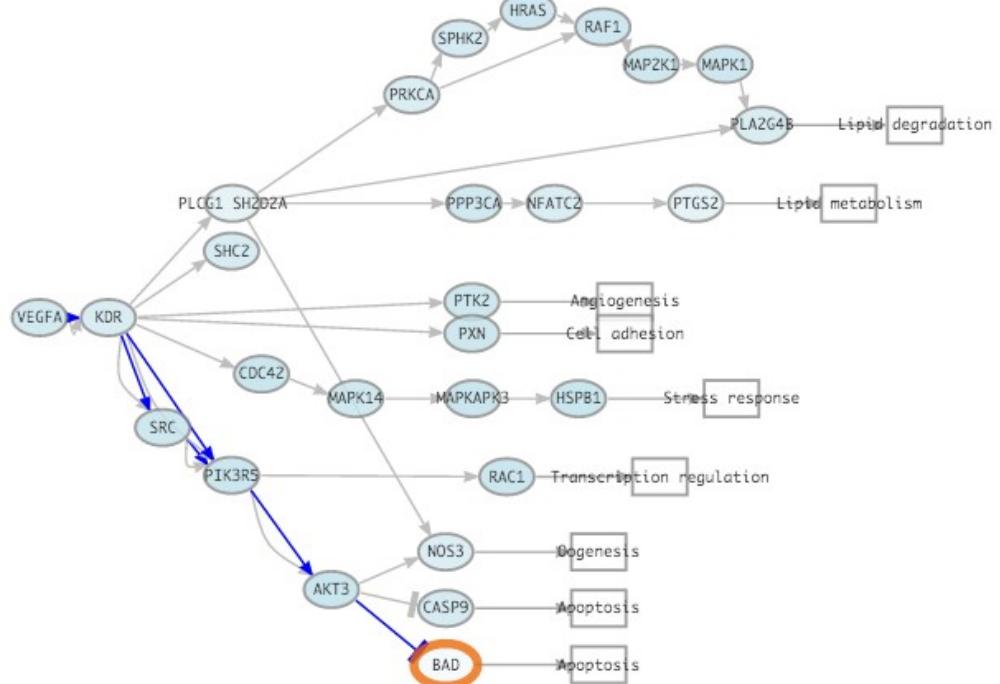
# Signal transduction modelling

We can use the same machinery to virtually explore the consequences of knocking out (or overexpress) a gene in signal transduction.



# Signal transduction modelling

This approach offers a powerful framework to design targeted therapies with minimum resources



# PathAct Web Tool



<http://pathact2.babelomics.org>



The screenshot shows the homepage of the PathAct web tool. At the top left is the PathAct logo and the text "Actionable pathway workshop". At the top right are "Login" and "Sign up" buttons. Below the header is a large orange circle containing the number "1" and a white "Start" button with a play icon. To the right of the button is the text "ACTIONABLE PATHWAY WORKSHOP". Above the "Start" button is the word "PathAct" in a large, white, sans-serif font. To the left of the "Start" button is a circular icon depicting a central node with a red lightning bolt and several white nodes connected by lines. At the bottom left is a "Notes" section with some text. At the bottom center is copyright information: "PathAct v1.1.0", "Created by Computational Genomics Department", "Principe Felipe Research Center, Valencia, Spain", and "2016".

PathAct is a web tool that enables the study of the consequences that Knockouts(KOs) or over-expressions of genes can have over signalling pathways. PathAct implements robust models of signalling pathways within an advanced graphical interface that provide a unique interactive working environment in which actionable genes, that could become potential drug targets, can be easily assayed alone or in combinations. Also the effect of drugs with known targets over the different signalling pathways can be studied. Since signals trigger functions across the pathways, the direct and long-distance functional consequences of interventions over genes can be straightforwardly revealed through this actionable pathway scenario.

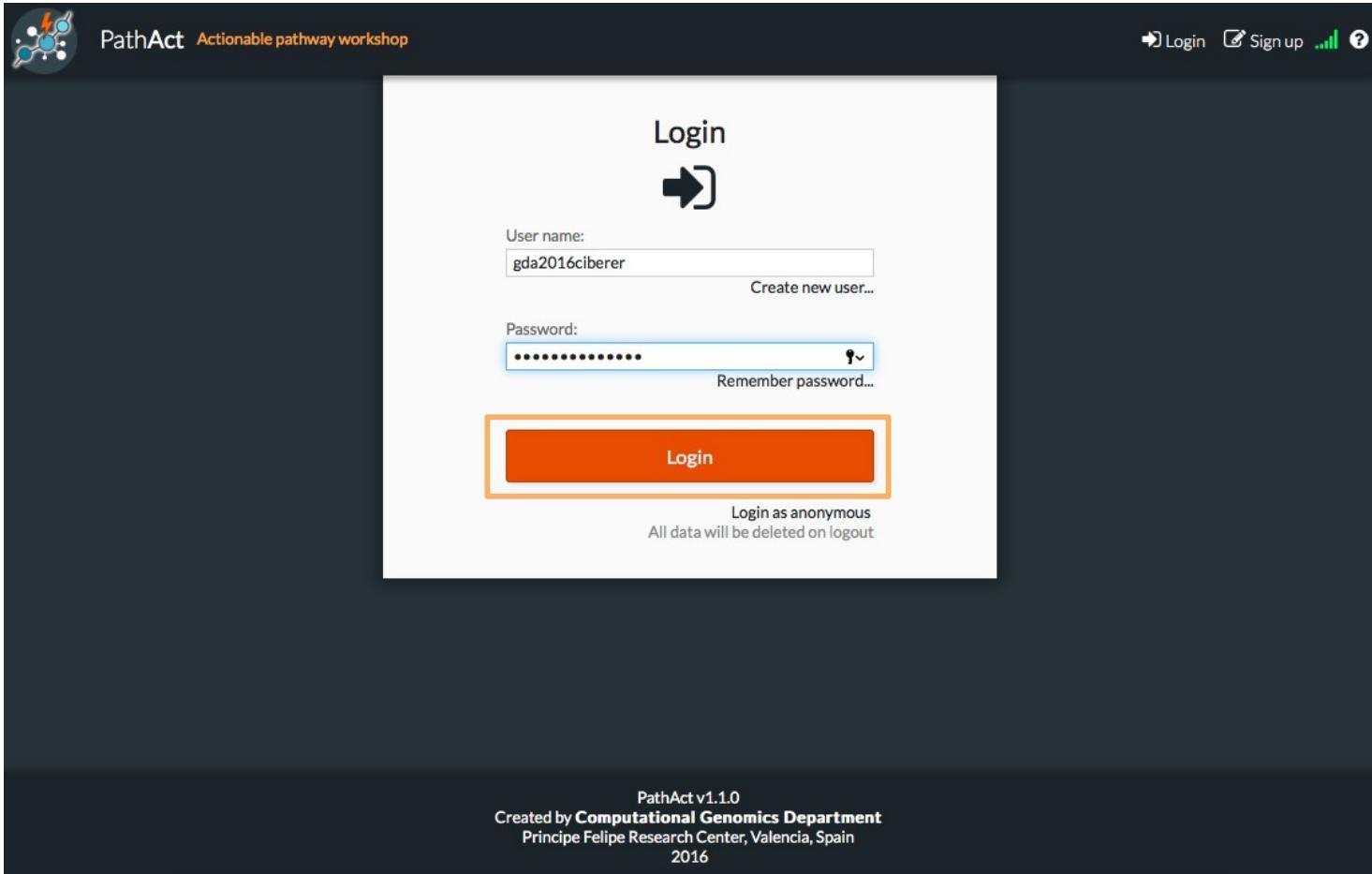
Notes

PathAct v1.1.0  
Created by Computational Genomics Department  
Principe Felipe Research Center, Valencia, Spain  
2016

# PathAct Web Tool



<http://pathact2.babelomics.org>



The screenshot shows the login interface of the PathAct Web Tool. At the top left is the PathAct logo with the text "Actionable pathway workshop". At the top right are links for "Login" (with a key icon), "Sign up" (with a person icon), and a gear icon. Below the header is a large white rectangular login form. The form has a "Login" title at the top center with a right-pointing arrow icon. It contains two input fields: "User name:" with the value "gda2016ciberer" and "Password:" with a masked value. To the right of the password field is a dropdown menu icon and a "Remember password..." link. A large orange "Login" button is centered below the inputs. At the bottom of the form is a link "Login as anonymous" with the note "All data will be deleted on logout". The footer of the page includes the text "PathAct v1.1.0", "Created by Computational Genomics Department", "Principe Felipe Research Center, Valencia, Spain", and the year "2016".

# PathAct Web Tool

PathAct Actionable pathway workshop

Create a new job

1. In order to create a job, a file must be selected from the server, if the file is not already in the server it should be uploaded first, both actions can be performed using the following button.

Please click [here](#) to read more about the input file format.

1

hcc4006\_mutant\_dmso.txt

2. Now select a sample from your expression matrix file.

Log<sub>e</sub> transform data matrix

hcc4006\_mutant\_dmso

3. To finish, set a name for your job, and press the run button.

Jobs

Settings gda2016ciberer Profile Logout

Use an existing job

Search by name...

<input checked="" type="checkbox"/>	HCC4006 mutant dmso-hcc4006_mutant_dmso.txt Pathact-Init Done 28/9/2016 12:14:59	<input type="button" value="Delete"/> <input type="button" value="Download"/>
<input checked="" type="checkbox"/>	HCC4006_mutant_dmso-hcc4006_mutant_dmso.txt Pathact-Init Done 28/9/2016 12:11:39	<input type="button" value="Delete"/> <input type="button" value="Download"/>
<input checked="" type="checkbox"/>	Example Pathact-Init Done 28/9/2016 11:54:27	<input type="button" value="Delete"/> <input type="button" value="Download"/>

Total: 3

Enable job notifications

# PathAct Web Tool

PathAct Actionable pathway workshop

Jobs Settings gda2016ciberer Profile Logout ?

Create a new job Use an existing job

Run example

Select Expression Matrix File...

/ PathAct\_Exercises /

1. In order to create a job, you must upload an expression matrix file that is not already in the service. You can upload a file by clicking the "Upload" button below. You can also perform using the following steps:

Please click [here](#) to learn more about how to upload files.

2. Now select a sample from the dropdown menu below.

Upload

Name Example

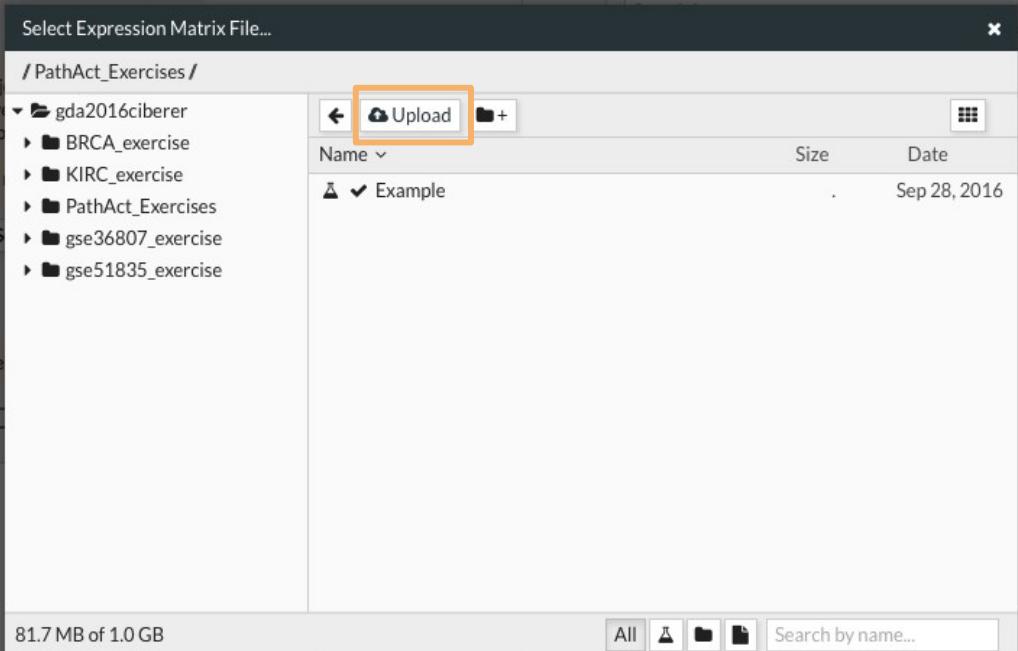
Size Date

81.7 MB of 1.0 GB

All Search by name...

Total: 1

Enable job notifications



# PathAct Web Tool

The screenshot shows the PathAct Web Tool interface for creating a new job. The main navigation bar includes links for 'Jobs', 'Settings', 'Profile', and 'Logout'. Below the navigation, there are two main sections: 'Create a new job' and 'Use an existing job'. A modal window titled 'Upload File' is open, guiding the user through the process:

- Step 1:** 'File upload:' with a 'Choose file...' button. The selected file is 'hcc4006\_mutant\_dmso.txt'. An orange circle with the number '1' highlights this step.
- Step 2:** 'Bioformat:' with a radio button selected for 'Data matrix expression' (indicated by an orange circle with the number '2').
- Step 3:** 'Upload' button at the bottom of the modal (indicated by an orange circle with the number '3')).

On the right side of the modal, there is a 'File validation log' section showing one warning message:

Line	Type	Message
19766	warning	Empty line.

At the bottom of the validation log, it says 'Errors: 0 Warning: 1 Info: 0 Lines: 19766'.

# Select data

gene expression data

<http://bioinfo.cipf.es/gda16ciberer>

## File format

Columns: GeneIDs + Sample

Rows: EntrezGene (id)

## Example

Non-small cell lung cancer (NSCLC)

EGFR mutant

Not treated with Erlotinib (TKIs)

geneID	hcc4006_mutant_dmso
1	5.99830927735415
10	4.26909388237212
100	7.90281107406193
1000	8.46383745767134
10000	5.82801370891263
100009676	5.95028396323201
10001	9.24054483957849
10002	4.50114481512442
10003	2.84739433259492
10004	4.59393709385877
100048912	3.2801596933055
10005	7.61874234203795
10006	8.67399667422145
10007	9.68407263257293
10008	4.72208873889579
10009	8.67753823201646
100093630	9.99164686804014
100093698	2.90650126505663
1001	11.4324736716045
10010	8.27543394593235
100101467	5.19948516713951
100101938	4.20778055144368
10011	9.43505129657583
100113407	3.3861342172626
100124700	4.55907367543182
100125288	5.92518975661431
100126784	5.23839965772242

# Select data

PathAct Actionable pathway workshop

Create a new job

[Run example](#)

1. In order to create a job, a file must be selected from the server, if the file is not already in the server it should be uploaded first, both actions can be performed using the following button.

Please click [here](#) to read more about the input file format.

1  hcc4006\_mutant\_dmso.txt

2. Now select a sample from your expression matrix file.

Log<sub>e</sub> transform data matrix

2 hcc4006\_mutant\_dmso

3. To finish, set a name for your job, and press the run button.

3 My HCC4006 mutant dims analysis

4

Jobs

Settings gda2016ciberer Profile Logout

Use an existing job

5

Search by name...

HCC4006 mutant dmso-hcc4006\_mutant\_dmso.txt  
Pathact-Init Done 28/9/2016 12:14:59

HCC4006\_mutant\_dmso-hcc4006\_mutant\_dmso.txt  
Pathact-Init Done 28/9/2016 12:11:39

Example  
Pathact-Init Done 28/9/2016 11:54:27

Total: 3

Enable job notifications

# Overexpression

**PathAct Actionable pathway workshop**

Jobs    Settings    gda2016ciberer    Profile    Logout

6    4    5    2    1    3

**ErbB signaling pathway (hsa04012)**

Add genes: Gene search (min 2 char)

Select gene related drugs:

Add drugs: Drug search (min 3 char)

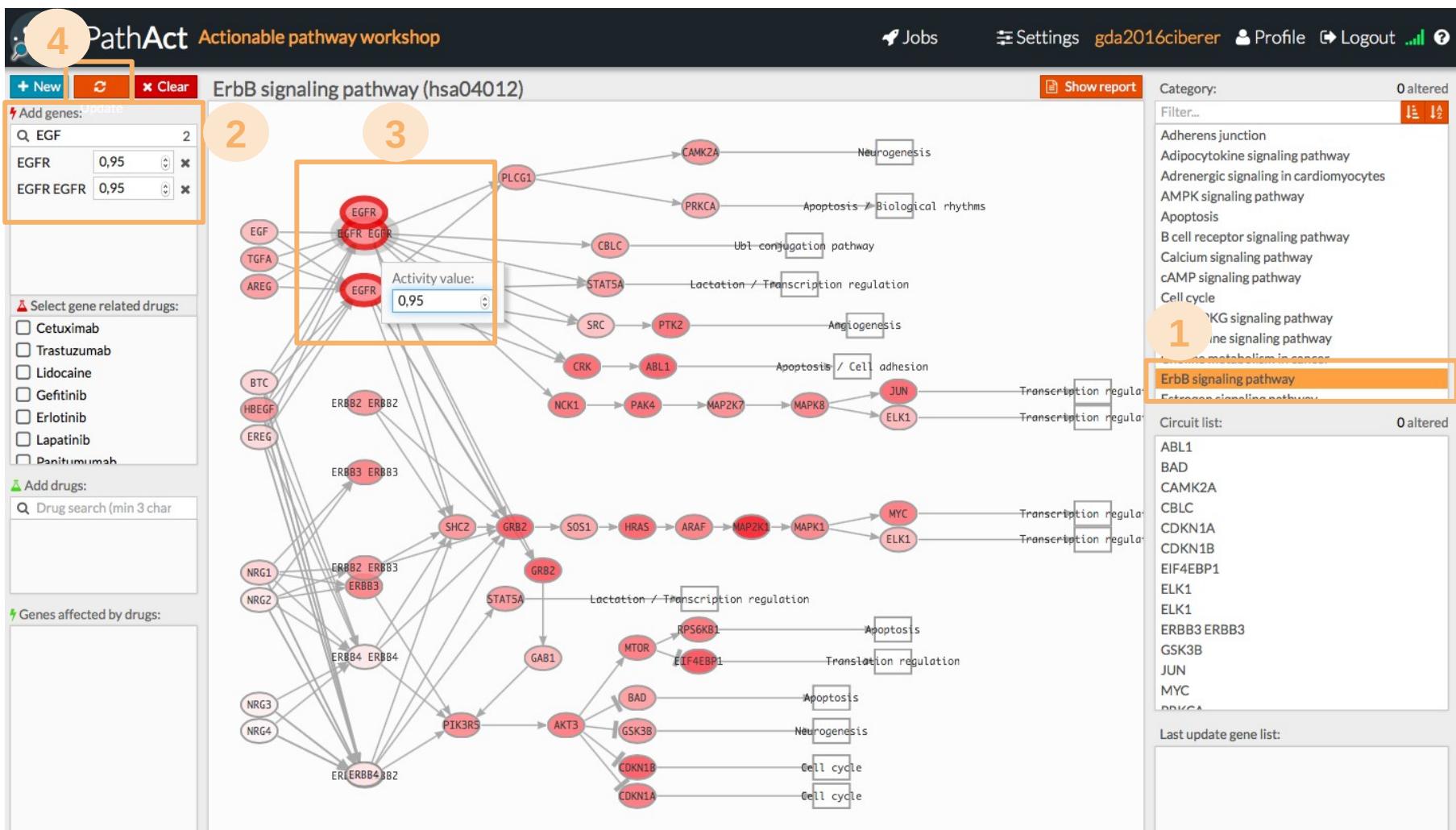
Genes affected by drugs:

Category: Filter... Adherens junction, Adipocytokine signaling pathway, Adrenergic signaling in cardiomyocytes, AMPK signaling pathway, Apoptosis, B cell receptor signaling pathway, Calcium signaling pathway, cAMP signaling pathway, Cell cycle, cGMP-PKG signaling pathway, Chemokine signaling pathway, Choline metabolism in cancer, ErbB signaling pathway, Estrogen signaling pathway.

Circuit list: ABL1, BAD, CAMK2A, CBLC, CDKN1A, CDKN1B, EIF4EBP1, ELK1, ERBB3 ERBB3, GSK3B, JUN, MYC, PRKCA

Last update gene list:

# Overexpression



# Overexpression

**PathAct Actionable pathway workshop**

Jobs    Settings    gda2016ciberer    Profile    Logout

Add genes:  Update

Q: EGF    2  
EGFR    0,95  
EGFR EGFR    0,95

Select gene related drugs:  
 Cetuximab  
 Trastuzumab  
 Lidocaine  
 Gefitinib  
 Erlotinib  
 Lapatinib  
 Panitumumab

Add drugs:

Genes affected by drugs:

**ErbB signaling pathway (hsa04012)**

Category: 14 altered  
Filter...

- ↑ Adherens junction
- ↑ Choline metabolism in cancer
- ↑ ErbB signaling pathway **1**
- ↑ Estrogen signaling pathway
- ↑ Focal adhesion
- ↑ Gap junction
- ↑ HIF-1 signaling pathway
- ↑ MAPK signaling pathway
- ↑ Oxytocin signaling pathway
- ↑ Pathways in cancer
- ↑ PI3K-Akt signaling pathway
- ↑ Proteoglycans in cancer
- ↑ Rap1 signaling pathway
- ↑ Ras signaling pathway

Circuit list: 16 altered

- ↑ ABL1
- ↓ BAD
- ↑ CAMK2A
- ↑ CBLC
- ↓ CDKN1A
- ↓ CDKN1B
- ↓ EIF4EBP1
- ↑ ELK1
- ↑ ELK1
- ↓ GSK3B
- ↑ JUN
- ↑ MYC
- ↑ PRKCA
- ↑ PTK2

Last update gene list:  
 gene - w - origin  
 EGFR - 0.95 - user

1

2

4

# Overexpression

**PathAct Actionable pathway workshop**

Jobs Settings gda2016ciberer Profile Logout

+ New Clear Add genes: /update

Q: EGF 2  
EGFR 0,95  
EGFR EGFR 0,95

Select gene related drugs:  
 Cetuximab  
 Trastuzumab  
 Lidocaine  
 Gefitinib  
 Erlotinib  
 Lapatinib  
 Panitumumab

Add drugs:  
 Drug search (min 3 char)

Genes affected by drugs:

**ErbB signaling pathway (hsa04012)**

Show report

Category: 14 altered

Filter...

- ↑ Adherens junction
- ↑ Choline metabolism in cancer
- ↑ ErbB signalling pathway **1**
- ↑ Estrogen signalling pathway
- ↑ Focal adhesion
- ↑ Gap junction
- ↑ HIF-1 signalling pathway
- ↑ MAPK signalling pathway
- ↑ Oxytocin signalling pathway
- ↑ Pathways in cancer
- ↑ PI3K-Akt signalling pathway
- ↑ Proteoglycans in cancer
- ↑ Rap1 signalling pathway
- ↑ Ras signalling pathway

Circuit list: 16 altered

- ↑ ABL1
- ↓ BAD
- ↑ CAMK2A
- ↑ CBLC
- ↓ CDKN1A
- ↓ CDKN1B
- ↓ EIF4EBP1
- ↑ ELK1
- ↑ ELK1
- ↓ GSK3B **1**
- ↑ JUN **1**
- ↑ MYC
- ↑ PRKCA
- ↓ PTK2

Last update gene list:  
 gene - w - origin  
 EGFR - 0,95 - user

# Results interpretation

Configure fold change:  2

Configure drug action weight:

Acetylation:	0,1	Activator:	1
Adduct:	0,1	Agonist:	1
Allosteric Modulator:	0,1	Antagonist:	0,1
Antibody:	0,1	Binder:	0,1
Binding:	0,1	Blocker:	0,1
Chaperone:	0,1	Chelator:	0,1
Cleavage:	0,1	Cofactor:	0,1
Component Of:	0,1	Conversion Inhibitor:	0,1
Cross-Linking/Alkylation:	0,1	Desensitize The Target:	0,1
Inactivator:	0,1	Incorporation Into And Destabilization:	0,1
Inducer:	1	Inhibitor:	0,1
Inhibitor, Competitive:	0,1	Inhibitory Allosteric Modulator:	0,1
Intercalation:	0,1	Inverse Agonist:	0,1
Ligand:	0,1	Metabolizer:	0,1
Modulator:	0,1	Multitarget:	0,1
Negative Modulator:	0,1	Neutralizer:	0,1
Other:	0,1	Other/Unknown:	0,1
Partial Agonist:	0,5	Partial Antagonist:	0,5
Positive Allosteric Modulator:	1	Positive Modulator:	1

$|\log FC| > \log(2) = 0.693$

# Report

Circuit impact  $|\log FC| > \log(2) = 0.693$

Report

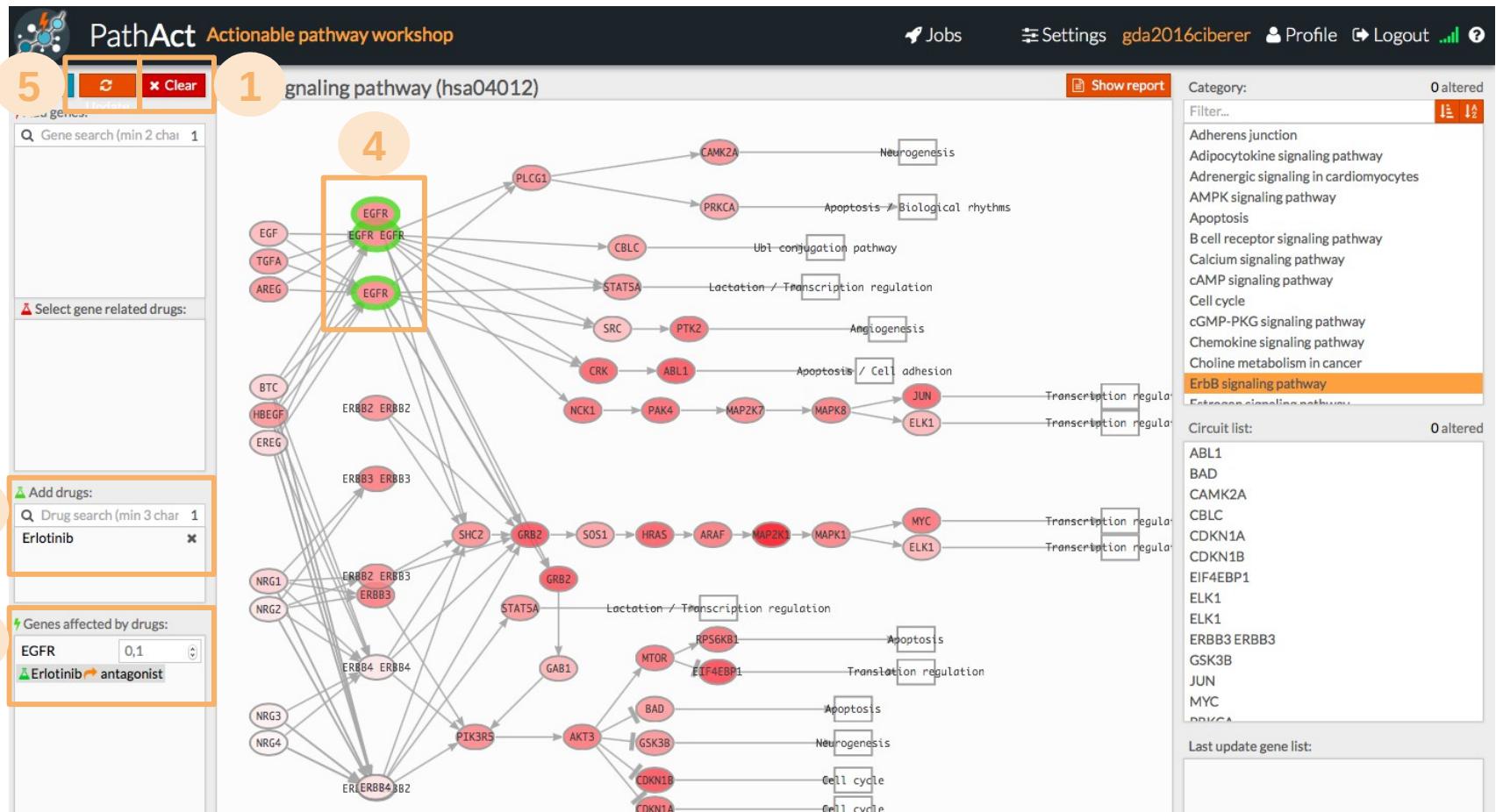
Circuit changes

circuit	log_fold_change	sig
Adherens junction: CTNND1	-1.665	TRUE
Adherens junction: LEF1 CTNNB1	-1.665	TRUE
Estrogen signaling pathway: AKT3*	0.708	TRUE
ErbB signaling pathway: JUN	0.708	TRUE
ErbB signaling pathway: ELK1*	0.708	TRUE
ErbB signaling pathway: CBLC	0.708	TRUE
Oxytocin signaling pathway: CDKN1A	0.708	TRUE
Estrogen signaling pathway: ESR1 C00951	0.708	TRUE
Estrogen signaling pathway: ESR1 FOS	0.708	TRUE
Estrogen signaling pathway: ESR1 C00951*	0.708	TRUE

« < Page 1 of 15 > »

Close

# Drug action



# Drug action

**PathAct Actionable pathway workshop**

**ErbB signaling pathway (hsa04012)**

**3**

**Category:** 10 altered

**Filter...**

- ↑ ↓ Adherens junction
- ↑ ↓ Choline metabolism in cancer
- ↓ ErbB signaling pathway**
- ↑ ↓ Estrogen signaling pathway
- ↑ ↓ Gap junction
- ↑ ↓ HIF-1 signaling pathway
- ↑ ↓ MAPK signaling pathway
- ↑ ↓ Oxytocin signaling pathway
- ↑ ↓ Pathways in cancer
- ↑ ↓ Proteoglycans in cancer

Adipoctokine signaling pathway  
Adrenergic signaling in cardiomyocytes  
AMPK signaling pathway  
Apoptosis

**Circuit list:** 16 altered

- ↓ ABL1**
- ↑ BAD
- ↓ CAMK2A
- ↓ CBLC
- ↑ CDKN1A
- ↑ CDKN1B
- ↑ EIF4EBP1
- ↓ ELK1
- ↓ ELK1
- ↑ GSK3B
- ↓ JUN
- ↓ MYC
- ↓ PRKCA
- ↓ PTK2

Last update gene list:  
gene - w - origin  
EGFR - 0.1 - drug

**Add genes:** Update

**Gene search (min 2 char)** 1

**Select gene related drugs:**

**Add drugs:**

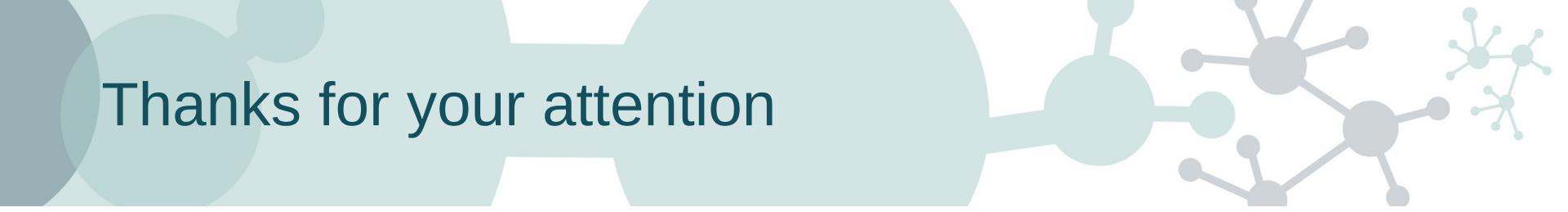
**Drug search (min 3 char)** 1

Erlotinib

**Genes affected by drugs:**

EGFR 0,1

Erlotinib antagonist



Thanks for your attention

Any questions?