

# OMIC TOOLS 1/30

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# Today's contents

- **Bicoverlapper2**
- MORPHIN

# Bicoverlapper2

- What can we do with Bicoverlapper2?
  - Visualization of gene expression matrices as heatmaps
  - Calculation DEGs from raw microarray data
  
- Good
  - GUI-based easy operation
  - Sophisticated graphics

# Bicoverlapper2

## ■ How to use?

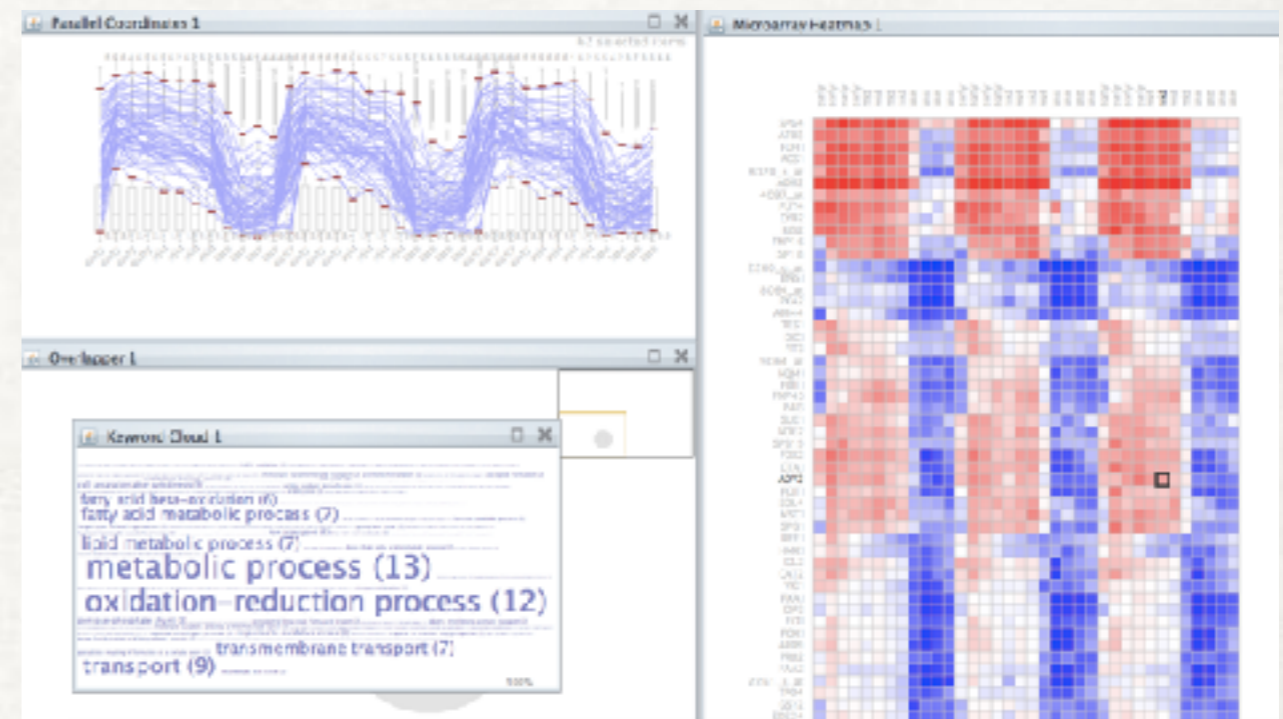
### ① R package installation

```
1 install.packages("rJava") #needed for starting
2 source("https://bioconductor.org/biocLite.R")
3 biocLite("ygs98.db") #annotation DB for sample data
```

### ② Data preparation and import

	A	B	C	D	E	F	G	H	I	
1	Saccharomyces	GSM77298	GSM77299	GSM77300	GSM77301	GSM77302	GSM77303	GSM77304	GSM77305	GSM77306
2	Interval	T1	T2	T3	T4	T5	T6	T7	T8	T9
3	Cycle	C1	C1	C1	C1	C1	C1	C1	C1	C1
4	IntervalGroup	early	early	early	early	mid	mid	mid	mid	late
5	10000_at	0.078088701	0.102978462	0.16390807	0.077404509	0.043068726	0.037232906	0.018635717	0.126912122	0.12
6	10001_at	1.582230608	1.488402042	1.120130514	1.102561811	0.956440591	0.948812563	0.878584011	1.048180769	2.07
7	10002_at	2.849542737	2.741045989	3.124838417	3.184457096	3.221871908	3.078746706	2.96399504	3.286677326	3.58
8	10003_at	4.555598907	3.594244748	4.381594569	4.209409486	4.186115751	4.276996171	4.35453713	4.643795871	5.67
9	10004_at	0.00816468	0.006656044	0.070311346	0.019343689	0.006462251	0.043346028	0.009347949	0.012010018	0.01
10	10005_at	1.687152244	1.539212543	1.751304697	1.507741117	1.451016812	1.516300882	1.424773575	1.591480344	2.06
11	10006_at	0.728754452	0.710030016	0.727769935	0.930178585	1.089461634	1.000785574	1.049170033	1.01648816	1.96
12	10007_at	2.119753691	2.258510181	2.192498564	2.253128297	2.051295997	2.139573678	1.875179388	1.820432488	1.14
13	10008_at	0.037180754	0.041105202	0.253175394	0.209584941	0.02567712	0.055495109	0.043114691	0.090663218	0.15
14	10009_at	0.395666637	0.123026924	0.224029062	0.116849733	0.253286449	0.211575538	0.351936974	0.438587655	0.50
15	10010_at	4.95007011	4.790036815	5.051673306	4.552896077	4.059379452	3.547684268	3.995695135	3.753267459	3.87
16	10011_at	0.338535304	0.159323063	0.226830412	0.203960394	0.200718388	0.107476367	0.217247518	0.13928404	0.23
17	10012_at	1.370553789	2.075146721	2.238679877	2.222160545	2.338349976	2.372272326	2.379232791	1.984464615	1.28
18	10013_at	0.765823688	0.923803186	1.039572642	0.958012779	0.956440591		0.985074073	0.997736955	1.27
19	10014_at	2.377503532	2.41524597	2.196427056	2.275422776	2.3000663	2.101263363	2.064945499	2.165395366	1.40
20	10015_at	2.572352936	3.326257893	3.920258528	3.334531084	3.371269491	2.932848393	2.664280605	2.926951237	3.7
21	10016_at	2.108405769	1.819977975	1.981048087	2.004051463	1.874027594	1.677285067	1.903352857	2.138257111	1.83

### ③ Result



# Bicoverlapper2

- Bad
  - Updated at last in 2014 and only available for microarray data.
  - Annotation database as R package is needed.

# Today's contents

- Bicoverlapper2
- **MORPHIN**

# MORPHIN

- What can we do with MORPHIN?
  - Web-based study for human diseases with model organism genes.
  - Calculation DEGs from raw microarray data
  
- Good
  - It can convert input genes to human orthologs, annotate to the human gene network and detect disease-related pathways.
  - Very easy to use

# MORPHIN

## How to use?

### ① Data submission

Here is a precomputed example using 5 worm genes modulating dauer inductions, [show](#)

You may run MORPHIN with your choice of pathway/disease database only (check your choice below).

GOBP  KEGG  GWASCAT  DO  OMIM  GAD  HPO

Model Species

Inparalog score threshold (bigger than or equal to)  
\* Default threshold value is recommended.

Input a set of model organism genes for a function/pathway/phenotype. (Max=500).  
Each gene name must be separated by comma, tab, white space or new line.  
Expected calculation time : 10 ~ 20 minutes.

Prrs  
Trp13  
Lix1  
Pia2g4e  
Fcgbo  
LOC103880006  
Arimts17  
Acan  
Fanci  
Tsur

For a test run, you may submit a toy example of each species by selecting [Examples](#) below.

Currently, MORPHIN takes the following nine model organisms:

Model organism	Gene names recognized by MORPHIN
<i>Saccharomyces cerevisiae</i> (yeast)	ORF ID (e.g., YAL002W) or gene symbol (e.g., YPS6)
<i>Caenorhabditis elegans</i> (worm)	Gene ID (e.g., AC23.6) or gene symbol (e.g., col-151)
<i>Drosophila melanogaster</i> (fly)	Flybase ID (e.g., FBgn0037137) or gene symbol (e.g., CG16874)
<i>Danio rerio</i> (zebrafish)	Ensembl ID (e.g., 30582) or gene symbol (e.g., tp53)
<i>Mus musculus</i> (mouse)	Ensembl ID (e.g., 22059) or gene symbol (e.g., Trp53)
<i>Rattus norvegicus</i> (rat)	Ensembl ID (e.g., 24842) or gene symbol (e.g., Trp53)
<i>Schistosoma mansoni</i> (blood fluke)	Parasite ID (e.g., SMNS029110.10) or gene symbol (e.g., smp21)
<i>Glycocalyx obscurus</i> (cell-living amoeba)	Dicylex ID (e.g., DIC5_GDPB1007) or gene symbol (e.g., cdk2)
<i>Xenopus laevis</i> (cloned frog)	Uniprot Entry name (e.g., HAN01_XENLA) or gene symbol (e.g., p53)

Available species

### ② Waiting



Navigation: [About MORPHIN](#) [Submit New Query](#) [Tutorial](#)

Your query is running now

Query ID: ml24jvz2mgoznl0w0mzdunkd2

Query has been under processing for 0 min 4 sec and now.

Bookmark this page to see your query status and results later.

[Go to main page](#)

Input genes




# MORPHIN

## ■ Result


### ① Associated pathway by Fisher's test

#### 2. Associated human disease pathways by Fisher's exact test

P-value : Fisher's exact test p-value, Q-value : adjusted p-value by false discovery rate  
 m : # query gene human orthologs, n : # disease pathway genes, k : # genes for intersection

 : A network between human orthologs of query genes and disease genes and prioritized human orthologs of query genes for each disease pathway.

[Download a tab-separated table list](#)


Rank	Pathway DB	Description	P-value	Q-value	m	n	k	
1	GOBP	<a href="#">mitotic cell cycle</a>	1.609e-17	6.582e-14	344	879	88	
2	GOBP	<a href="#">microtubule-based movement</a>	6.098e-12	1.117e-8	344	24	10	
3	KEGG	<a href="#">Cell cycle - Homo sapiens (human)</a>	1.082e-9	2.098e-7	344	124	16	
4	KEGG	<a href="#">Viral carcinogenesis - Homo sapiens (human)</a>	1.513e-8	2.098e-7	344	205	20	
5	KEGG	<a href="#">Alcoholism - Homo sapiens (human)</a>	6.330e-9	4.858e-7	344	180	18	
6	KEGG	<a href="#">Esophageal leiomyomatosis - Homo sapiens (human)</a>	5.254e-9	4.858e-7	344	138	16	
7	GOBP	<a href="#">mitosis</a>	1.118e-7	1.379e-4	344	33	8	
8	GOBP	<a href="#">G1/S transition of mitotic cell cycle</a>	1.275e-6	1.177e-3	344	135	13	
9	GOBP	<a href="#">mitotic M phase</a>	1.636e-6	1.210e-3	344	6	4	
10	DO	<a href="#">retinoblastoma</a>	1.267e-6	1.736e-3	344	114	12	

### ② Associated pathway by RIDDLE method












#### 3. Associated human disease pathways by RIDDLE

FDR : False discovery rate calculated by RIDDLE

m : # query gene human orthologs, n : # disease pathway genes,

 : A network between human orthologs of query genes and disease genes and prioritized human orthologs of query genes for each disease pathway.

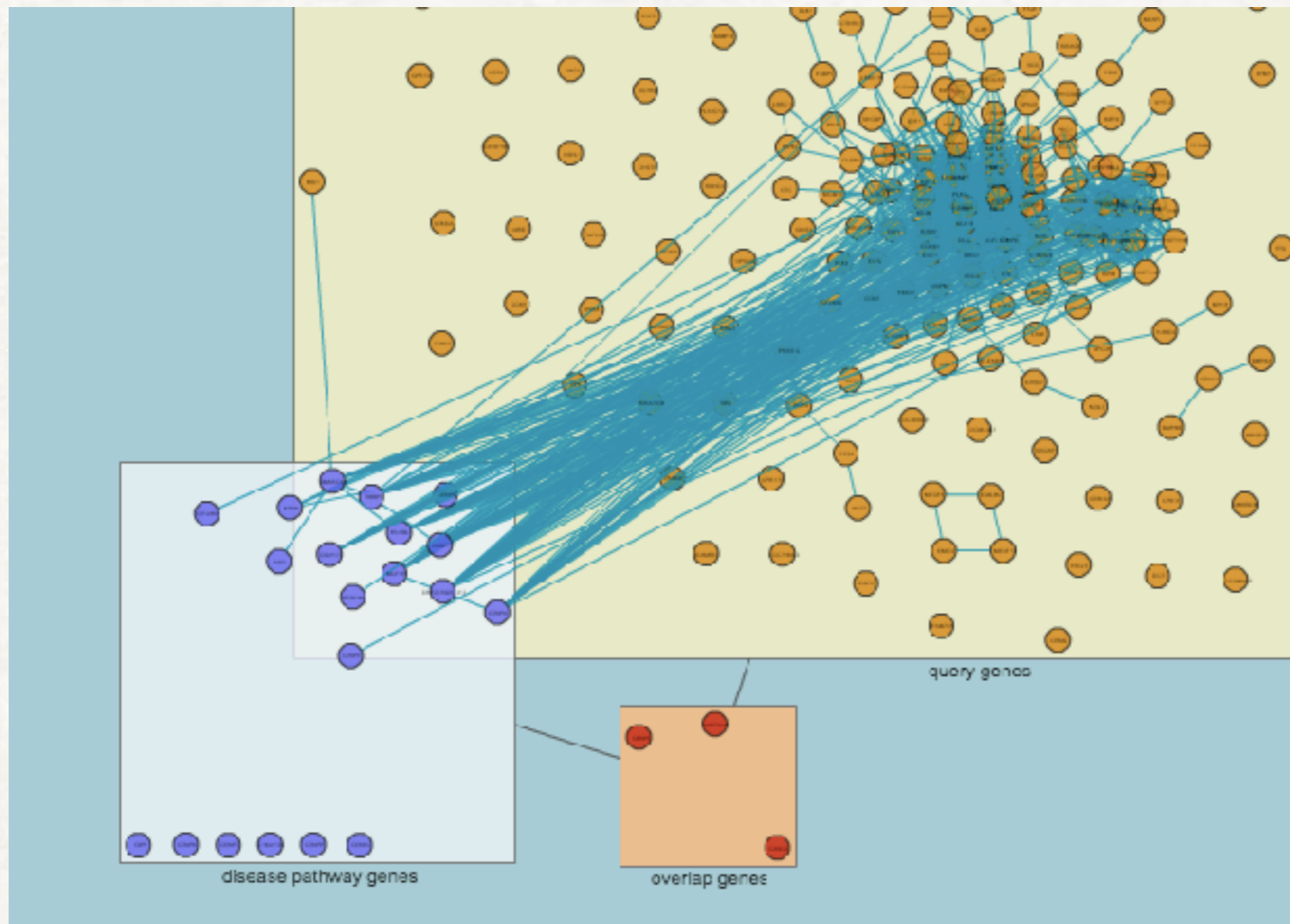
[Download a tab-separated table list](#)

Rank	Pathway DB	Description	FDR	m	n	
1	GOBP	<a href="#">CCND-A containing nucleosome assembly at centromere</a>	4.553e-1	344	23	
2	GOBP	<a href="#">nucleosome assembly</a>	4.604e-1	344	26	
3	GAD	<a href="#">HIV-1</a>	4.646e-1	344	57	
4	GAD	<a href="#">Hemochromatosis</a>	4.735e-1	344	28	
5	GAD	<a href="#">Factor VII</a>	4.759e-1	344	19	
6	GOBP	<a href="#">mitotic cell cycle checkpoint</a>	4.826e-1	344	24	
7	GAD	<a href="#">Thyrotropin</a>	4.833e-1	344	50	
8	DO	<a href="#">multiple epiphyseal dysplasia</a>	4.845e-1	344	4	
9	GOBP	<a href="#">double-strand break repair</a>	4.853e-1	344	48	
9	GWASCAT	<a href="#">Bipolar disorder and schizoaffective disorder</a>	4.853e-1	344	56	

# MORPHIN

- Result

- ③ Network plot



Each blue line show functionally relational genes.

# MORPHIN

- Bad

- The version of database is old (updated in 2013~2014)

- No remarkable advantages to use this website.