

# **MetaDAG experiment example**

Version beta 0.2

Invalid Date

## **Table of contents**

# 1 Load data MetaDag experiment

This is an example of an experiment of [metaDag](#) data with results.

Hash: bb261b6e-95c6-3e39-b82b-b68eea80e30b

URL: <http://bioinfo.uib.es/metadag/results?uuid=bb261b6e-95c6-3e39-b82b-b68eea80e30b>

```
library(tidyverse)
library(igraph)
library(ComplexHeatmap)
library(viridis)
library(circlize)
library(plotly)
library(randomcoloR)
library(factoextra)
library(RColorBrewer)
library(kableExtra)
library(igraph)
library(GGally)
```

Metadag Tool

Web Page

Experiment id: ff15c187-62e7-37c2-96a7-c824f7eab671  
Experiment name: Eukaryotes  
Experiment creator: Pere Palmer

Home

Experiment

Results

### Experiment definition

Give the values needed to perform the desired experiment.

General data

Here you can select the files containing the calculations made for your experiment.

MBB	<input checked="" type="checkbox"/>	similarities	<input checked="" type="checkbox"/>
mDAG	<input checked="" type="checkbox"/>		
Results	<input checked="" type="checkbox"/>		
Select All	<input checked="" type="checkbox"/>		

MetaDAG files

Here, you can select what components have to be added to the downloaded data. The amount of options can be variable depending on the experiment and its configurations.

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MetaDAG files

Here, you can select what components have to be added to the downloaded data. The amount of options can be variable depending on the experiment and its configurations.

	type		format		representation		Select row
	core	pan image	svg data	graphml data	raw mDAG	Essential Reaction Compound	
Global	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Categories	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Individuals	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Select column	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

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 Home  
 Experiments  
 Results


### Viewing the results






Once an experiment has been calculated it's possible to view the results. To do this, it's necessary to give the experiment unique identifier supplied in the email sent when the experiment was submitted. This unique identifier is also reported in response to the submission.

In the email sent, an url is given to access directly to the experiment results page.

But here, you can also access to the experiment results with the unique identifier.

Enter the experiment identification code \*  
 ff15c187-62e7-37c2-96a7-c824f7eab671



```

experiment=
  "result_bb261b6e-95c6-3e39-b82b-b68eea80e30b"
path_exp=paste0("data/",experiment,"/data/")
knitr::kable(data.frame(Directory_files_and_folders=dir(path_exp),
                        Type=c(rep("Data file",2),
                              rep("Directory",2),
                              rep("Data file",5),
                              "Directory"))))

```

Directory_files_and_folders	Type
Different_MBB.csv	Data file
Different_mDAG.csv	Data file
Global	Directory
Individuals	Directory
Results.csv	Data file
Similarities_MBB_MSAMethod.csv	Data file
Similarities_MBB_MunkresMethod.csv	Data file
Similarities_mDAG_MSAMethod.csv	Data file
Similarities_mDAG_MunkresMethod.csv	Data file
TaxonomyLevels	Directory

```
MBB=read_csv(paste0(path_exp,"Different_MBB.csv"),show_col_types = FALSE)
mDAG=read_csv(paste0(path_exp,"Different_mDAG.csv"),show_col_types = FALSE)
Results=read_csv(paste0(path_exp,"Results.csv"),show_col_types = FALSE)
save(MBB,mDAG,Results,file="MBB_mDag_Results.Rdata")
```

## 1.1 MBB

In this experiment MBB is a table with 5112 rows and 4106 columns.

```
knitr::kable(MBB[1:20,1:100]) %>%   scroll_box(width = "100%", height = "200px")
```

MBB Id	natural	#pathways	Protists	Fungi	Plants	Animals	Alveolates	Amoebozoa	Annelids
0	0	0	0	0	0	0	0	0	0
0.0	0	0	0	0	0	0	0	0	0
0.0.0	1	1	1	0	0	0	0	0	0
0.0.0.0	1	1	1	0	0	0	0	0	0
0.0.1	1	1	1	0	0	0	0	0	0
0.0.1.0	1	86	2	77	1	6	1	0	0
0.0.1.1	1	86	2	77	1	6	1	0	0
0.0.1.2	1	15	15	0	0	0	12	0	0
0.0.1.3	1	5	5	0	0	0	0	4	0
0.0.1.4	0	0	0	0	0	0	0	0	0
0.0.1.4.0	1	609	14	128	128	339	1	3	1
0.0.1.4.1	1	609	14	128	128	339	1	3	1
0.0.1.4.2	1	322	6	92	133	91	1	0	0
0.0.1.4.3	1	322	6	92	133	91	1	0	0
0.0.1.4.4	1	1	0	0	1	0	0	0	0
0.0.1.4.5	1	1	1	0	0	0	0	1	0
0.0.1.5	0	0	0	0	0	0	0	0	0
0.0.1.5.0	1	5	5	0	0	0	0	4	0
0.0.2	1	1	1	0	0	0	0	0	0
0.0.3	1	1	1	0	0	0	0	1	0

## 1.2 mDAG

Abstract/unique mDAG's in this experiment

```
dim(mDAG)
```

```
[1] 884 5224
```

```
kable(mDAG[1:20,1:100]) %>% scroll_box(width = "100%", height = "200px")
```

mDAG Id	#Categories	Animals	Plants	Fungi	Protists	Alveolates	Amoebozoa	Annelids	Arthr
0001	3	1	0	0	0	0	0	0	
0002	2	0	0	1	0	0	0	0	
0003	2	1	0	0	0	0	0	0	
0004	3	1	0	0	0	0	0	0	
0005	3	1	0	0	0	0	0	0	
0006	3	0	1	0	0	0	0	0	
0007	2	0	1	0	0	0	0	0	
0008	3	0	1	0	0	0	0	0	
0009	3	0	1	0	0	0	0	0	
0010	3	1	0	0	0	0	0	0	
0011	3	1	0	0	0	0	0	0	
0012	3	0	0	0	1	0	0	0	
0013	3	1	0	0	0	0	0	0	
0014	3	0	0	0	1	1	0	0	
0015	2	0	0	1	0	0	0	0	
0016	3	0	0	0	1	0	1	0	
0017	3	1	0	0	0	0	0	0	
0018	3	1	0	0	0	0	0	0	
0019	3	1	0	0	0	0	0	0	
0020	3	1	0	0	0	0	0	0	

```
dim(mDAG)
```

```
[1] 884 5224
```

```
names(mDAG)[1:6]
```

```
[1] "mDAG Id"      "#Categories" "Animals"      "Plants"      "Fungi"
[6] "Protists"
```

```
head(names(mDAG)[7:(dim(mDAG)[2]-1150)])# 28 to 1213 code MBB: 1 if MBB in mDAG 0
```

```
[1] "Alveolates"      "Amoebozoa"      "Annelids"
[4] "Arthropods"      "Ascomycetes"    "Basal angiosperms"
```