

A Guide to Interpreting the Results of MetaDAG Analysis

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1 Introduction

As an illustrative example for interpreting [metaDAG](#) results, we consider here the Eukaryotes test presented in Section 2.5. Namely, we consider all Eukaryotes from the KEGG database. [Experiment github](#).

First of all, results must be downloaded from:

Hash: [0a845f74-826e-3b46-aed9-e7ecf74db262](#)

URL: (https://bioinfo.uib.es/metadag/handleExperiment/result_0a845f74-826e-3b46-aed9-e7ecf74db262)

and saved in the folder:

“data/result_0a845f74-826e-3b46-aed9-e7ecf74db262”.

```
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

mDAG

Results

Select All

similarities

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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	type		format		representation		
	core	pan image	svg data	graphml data	raw mDAG	Essential Reaction Compound	Select row
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










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2 Load data

```
experiment=  
  "result_0a845f74-826e-3b46-aed9-e7ecf74db262/"  
path_exp=paste0("data/",experiment)  
knitr::kable(data.frame(  
  Directory_files_and_folders=dir(path_exp),  
  Type=c(rep("Data file",2),  
         rep("Directory",3),  
         rep("Data file",6),  
         "Directory")))
```

Directory_files_and_folders	Type
Different_MBB.csv	Data file
Different_mDAG.csv	Data file
Global	Directory
Groups	Directory
Individuals	Directory
Report.pdf	Data file
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)
```

2.1 Load metadata

Organisms are sorted by Kingdom, Phylum and Class:

```
path_exp
```

```
[1] "data/result_0a845f74-826e-3b46-aed9-e7ecf74db262/"
```

```
Results=read_csv(paste0(path_exp, "Results.csv"))
#rename MetaDaG variables
names(Results)[c(1,2,3,4,5)]=c("Organism", "Categories", "Groups", "mDAG_Id", "Full_Name")
taxo=Results %>% select(Organism:Full_Name)
meta_taxo=taxo %>% separate(Categories, into=c("Kingdom", "Phylum", "Class"))
index=which(is.na(meta_taxo$Class))
meta_taxo$Class[index]=paste(meta_taxo$Phylum[index])
rm(taxo)
aux=table(meta_taxo$Kingdom)
Freq_Kingdom=tibble(Kingdom=names(aux), Freq_Kingdom=aux)
aux=table(meta_taxo$Phylum)
Freq_Phylum=tibble(Phylum=names(aux), Freq_Phylum=aux)
aux=table(meta_taxo$Class)
Freq_Class=tibble(Class=names(aux), Freq_Class=aux)

meta_taxo = meta_taxo %>%
  left_join(Freq_Kingdom) %>%
  left_join(Freq_Phylum) %>%
  left_join(Freq_Class)
meta_taxo = meta_taxo %>%
  arrange(desc(Freq_Kingdom),
           desc(Freq_Phylum),
           desc(Freq_Class))
```

```
#arrange metaxto by frequencies of kingom phylum and class
```

```
knitr::kable(head(meta_taxo))
```

Organism	Kingdom	Phylum	Class	Groups	mDAG_Id	Full_Name
aamp	Animals	Vertebrates	Mammals	Cluster 1	0313	Arvicola amphibius (Eurasian water vole)
afz	Animals	Vertebrates	Mammals	Cluster 1	0143	Antechinus flavipes (yellow-footed mouse)
ajm	Animals	Vertebrates	Mammals	Cluster 1	0221	Artibeus jamaicensis (Jamaican fruit bat)
aju	Animals	Vertebrates	Mammals	Cluster 1	0224	Acinonyx jubatus (cheetah)
aml	Animals	Vertebrates	Mammals	Cluster 1	0279	Ailuropoda melanoleuca (giant panda)
anu	Animals	Vertebrates	Mammals	Cluster 1	0310	Arvicanthis niloticus (African grass rat)

```
table(meta_taxo$Kingdom) %>% kable %>%
  kable_styling("striped", full_width = F, position="left")%>%
  scroll_box(width = "400px", height = "200px")
```

Var1	Freq
Animals	535
Fungi	154
Plants	139
Protists	56

```
table(meta_taxo$Phylum,meta_taxo$Kingdom) %>% kable %>%
  kable_styling("striped", full_width = F,position="left")%>%
  scroll_box(width = "500px", height = "500px")
```


	Animals	Fungi	Plants	Protists
Alveolates	0	0	0	25
Amoebozoa	0	0	0	7
Annelids	1	0	0	0
Arthropods	158	0	0	0
Ascomycetes	0	113	0	0
Basal	0	0	2	0
Basidiomycetes	0	36	0	0
Brachiopodas	1	0	0	0
Cephalochordates	2	0	0	0
Choanoflagellates	0	0	0	2
Cnidarians	10	0	0	0
Cryptomonads	0	0	0	1
Echinoderms	3	0	0	0
Eudicots	0	0	98	0
Euglenozoa	0	0	0	9
Ferns	0	0	1	0
Flatworms	4	0	0	0
Green	0	0	11	0
Haptophyta	0	0	0	1
Hemichordates	1	0	0	0
Heterolobosea	0	0	0	1
Metamonada	0	0	0	2
Microsporidians	0	5	0	0
Mollusks	14	0	0	0
Monocots	0	0	23	0
Mosses	0	0	1	0
Nematodes	6	0	0	0
Placozoans	1	0	0	0
Poriferans	1	0	0	0
Red	0	0	3	0
Stramenopiles	0	0	0	8
Tunicates	2	0	0	0
Vertebrates	331	0	0	0

2.2 Table of MBBs

In this example MBB is a table with 5149 rows and 4122 columns. It displays, for every MBB, the selected groups (Kingdoms, families, etc.) to which it belongs.

```
#100
```

```
knitr::kable(MBB[1:20,1:10]) %>%  
  scroll_box(width = "100%", height = "200px")
```

MBB Id	natural	#pathways	Protists	Fungi	Plants	Animals	Alveolates	Amoebozoa	Annelid
0	0	0	0	0	0	0	0	0	0
0.0	0	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	0	0	0	1	0	0	0
0.0.0.0.0	1	1	0	0	0	1	0	0	0
0.0.0.0.0.0	1	1	0	0	0	1	0	0	0
0.0.0.1	1	1	0	0	0	1	0	0	0
0.0.0.2	1	1	0	0	0	1	0	0	0
0.0.1	0	0	0	0	0	0	0	0	0
0.0.1.0	1	1	0	0	0	1	0	0	0
0.0.1.1	1	1	1	0	0	0	0	0	0
0.0.1.1.0	1	1	1	0	0	0	0	0	0
0.0.1.2	1	1	0	0	0	1	0	0	0
0.0.1.3	1	1	0	0	0	1	0	0	0
0.0.1.4	1	1	0	0	0	1	0	0	0
0.0.1.4.0	1	1	0	0	0	1	0	0	0
0.0.1.4.0.0	1	1	0	0	0	1	0	0	0
0.0.1.5	1	1	1	0	0	0	0	0	0
0.0.1.6	1	4	3	0	0	1	0	0	0
0.0.1.6.0	1	3	0	0	3	0	0	0	0

2.3 Table of m-DAGs

In this example `mDAG` is a table with 1132 rows and 5278 columns. It displays, for every m-DAG, the selected groups (Kingdoms, families, etc.) in which it belongs.

```
kable(mDAG[1:20,1:10]) %>%   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] 1132 5278
```

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

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

```
head(names(mDAG)[7:(dim(mDAG)[2]-1150)])
```

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

```
# 28 to 1213 code MBB: 1 if MBB in mDAG 0
```

2.4 Results Table

The **Results** table contains for every organism (row) the following information: its category (taxonomy), selected group, Full name, m-DAG id and all reactions name id with their corresponding enzyme. When a reaction is present in the corresponding m-DAG, the MBB to which it belongs is displayed in this column.

```
kable(Results[1:20,1:10])%>%
  row_spec(0, angle = 0) %>%
  scroll_box(width = "300%", height = "1000px")
```

Organism	Categories	Groups
aaf	Protists Stramenopiles Pelagophytes	MSA Cluster 3 MUN Cluster 3
aag	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
aalb	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
aali	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
aalt	Fungi Ascomycetes Dothideomycetes	Fungui and Algae MSA Cluster 3 MSA Fungui and Nemat
aam	Animals Vertebrates Birds	Cluster 1
aamp	Animals Vertebrates Mammals	Cluster 1
aang	Animals Vertebrates Fishes	Cluster 1
aara	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
abe	Fungi Ascomycetes Eurotiomycetes	Fungui and Algae MSA Cluster 3 MSA Fungui and Nemat
abp	Fungi Basidiomycetes	Fungui and Algae MSA Cluster 3 MSA Fungui and Nemat
abv	Fungi Basidiomycetes	Fungui and Algae MSA Cluster 3 MSA Fungui and Nemat
acan	Protists Amoebozoa Acanthamoeba	MSA Cluster 3 MUN Cluster 3
acar	Animals Vertebrates Birds	Cluster 1
acep	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
acer	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2
achc	Animals Vertebrates Birds	Cluster 1
ache	Fungi Ascomycetes Eurotiomycetes	Fungui and Algae MSA Cluster 3 MSA Fungui and Nemat
achl	Animals Vertebrates Birds	Cluster 1
acoz	Animals Arthropods Insects	MSA Cluster 2 MUN Cluster 2

```
dim(Results)
```

```
[1] 1132 3998
```

```
names(Results)[1]# organisms kegg id class representant of mDAG
```

```
[1] "Organism"
```

```
names(Results)[2]# taxonomy separate by /
```

```

[1] "Categories"

names(Results)[3]# groups

[1] "Groups"

names(Results)[4]# mDAG_Id

[1] "mDAG_Id"

names(Results)[5]# Full name representant

[1] "Full_Name"

names(Results)[6:36]# columns 6 to 3998

[1] "R00005(3.5.1.54)" "R00009(1.11.1.6)" "R00010(3.2.1.28)"
[4] "R00014(1.2.4.1)" "R00014(4.1.1.1)" "R00021(1.4.7.1)"
[7] "R00022(3.2.1.52)" "R00024(4.1.1.39)" "R00028(3.2.1.20)"
[10] "R00031(1.10.3.1)" "R00032(1.13.11.63)" "R00036(4.2.1.24)"
[13] "R00045(1.10.3.1)" "R00066(2.5.1.9)" "R00068(1.10.3.3)"
[16] "R00073(1.14.99.1)" "R00075(2.5.1.43)" "R00078(1.16.3.1)"
[19] "R00084(2.5.1.61)" "R00086(3.6.1.15)" "R00086(3.6.1.5)"
[22] "R00087(3.6.1.9)" "R00093(1.4.1.14)" "R00095(1.6.5.4)"
[25] "R00100(1.6.2.2)" "R00102(3.2.2.5)" "R00102(3.2.2.6)"
[28] "R00103(3.6.1.22)" "R00103(3.6.1.9)" "R00104(2.7.1.23)"
[31] "R00111(1.14.13.39)"

```

reactions name id with its enzyme.

```

reactions=names(Results)[-c(1:5)]
reverse_reactions=stringr::str_detect(reactions,"rev")
reverse_reactions=table(reverse_reactions)
dimnames(reverse_reactions)$reverse_reactions=
  c("Non reverse reaction","Reverse reaction")
reverse_reactions %>% kable %>%
  kable_styling("striped", full_width = F,position="left")

```

reverse_reactions	Freq
Non reverse reaction	3399
Reverse reaction	594

3 Metabolic Graphs

```
load(file='metadag_work_space.RData')
```

We present here some analysis examples of the metabolic graphs generated in GraphML format.

3.1 Metabolic graphs for each organism

Read the individual metabolic graphs generated for Homo sapiens (KEGG id: hsa) in the directory(Individuals/hsa)

```
experiment=
  "result_0a845f74-826e-3b46-aed9-e7ecf74db262/"
path_exp=paste0("data/",experiment)
files_hsa=dir(paste0(path_exp,"Individuals/hsa"))
files_hsa
```

```
[1] "hsa_mDAG.graphml"      "hsa_mDAG.pdf"          "hsa_mDAG.svg"
[4] "hsa_mDAG_adj.csv"      "hsa_mDAG_biggerDAG.pdf" "hsa_mDAG_biggerDAG.svg"
[7] "hsa_mDAG_nl.csv"       "hsa_mDAG_structure.csv" "hsa_R_adj.csv"
[10] "hsa_R_nl.csv"          "hsa_RC.graphml"        "hsa_RC.pdf"
[13] "hsa_RC.svg"            "hsa_summary.txt"
```

files_Individual_hsa	Description
hsa_mDAG.graphml	m-DAG GraphML format
hsa_mDAG.pdf	m-DAG pdf graphic
hsa_mDAG.svg	m-DAG svg graphic
hsa_mDAG_adj.csv	csv file with the adjacency matrix of the m-DAG
hsa_mDAG_biggerDAG.pdf	pdf graphic with the biggest conected componet of the m-DAG
hsa_mDAG_biggerDAG.svg	svg graphic with the biggest conected componet of the m-DAG
hsa_mDAG_nl.csv	csv file with the node (MBBs) labels of the m-DAG
hsa_mDAG_structure.csv	csv file with all connected components of the m-DAG
hsa_R_adj.csv	csv file with the adjacency matrix of the reaction graph
hsa_R_nl.csv	csv file with the node (reactions) labels of the reaction graph
hsa_RC.graphml	reaction graph GraphML format
hsa_RC.pdf	reaction graph pdf graphic
hsa_RC.svg	reaction graph svg graphic
hsa_summary.txt	text summary file with the number of MBBs, reactions, etc. in the previous g

3.2 Pan & core metabolic graphs

Pan and core metabolic graphs for every group were generated. For instance, one can read the pan and core metabolic graphs generated for the group Algae in the directory (Groups/Algae).

```
files_Algae=dir(paste0(path_exp,"Groups/Algae"))
files_Algae
```

```
[1] "core" "pan"
```

The global core reaction graph, which is the core of all the organisms' reaction graphs in this Eukaryotes test, is empty.

```
graph_core_RC=read.graph(
  paste0(path_exp,
    "Global/core/core_RC.graphml"),
  format = "graphml")
summary(graph_core_RC)
```

```
IGRAPH 8182f78 D--- 0 0 --
+ attr: color (v/c), label (v/c), id (v/c)
```

The global core reaction graph has 0 vertex and 0 edges. It is an empty graph.

The core reaction graph for the Algae group is: