

A Guide to Interpreting the Results of MetaDAG Analysis

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1 Load data

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.

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	<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.

ACGTCT 110101
CGGC 1100
GACCGT 001011

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	type		format		representation		Select row
	core	pan image	svg data	graphml data	raw Essential mDAG	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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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_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)
Results=read_csv(paste0(path_exp,"Results.csv"),
                 show_col_types = FALSE)
save(MBB,mDAG,Results,
      file="MBB_mDag_Results.Rdata")

```

1.1 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

1.2 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
```

1.3 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

reverse_reactions
Non reverse reaction      Reverse reaction
              3399              594

```

2 Metabolic Graphs

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

2.1 Metabolic graphs for each organism

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

```
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

2.2 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 dcda4dc 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:

```
knitr::include_graphics(
  paste0(path_exp,"Groups/MSA_Cluster_3/core/MSA_Cluster_3_core_RC.pdf"))
```

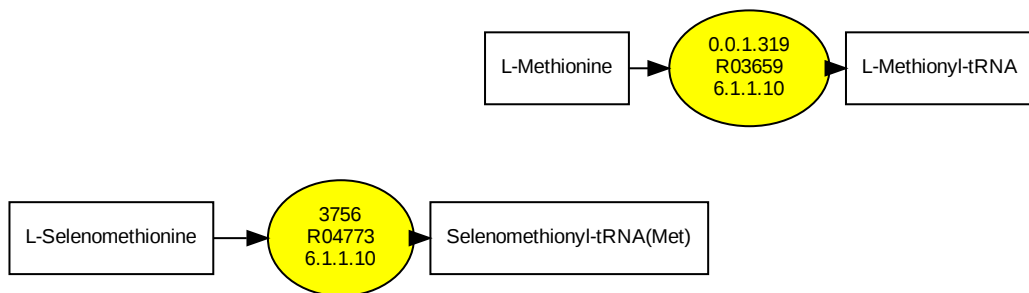


Figure 2.1: Algae core reaction graph