MetaDAG experiment example

Version beta 0.2

Invalid Date

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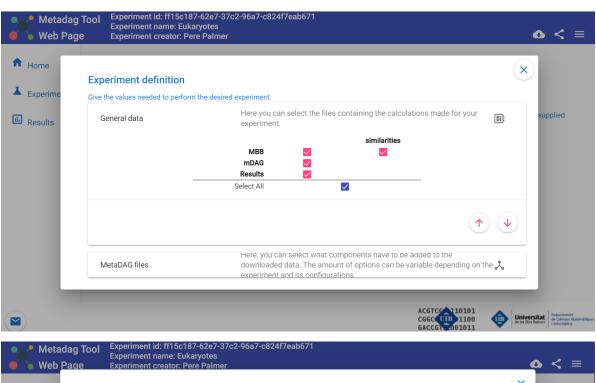
1 Load data MetaDag experiment

This is an example of an experiment of metaDag data with results.

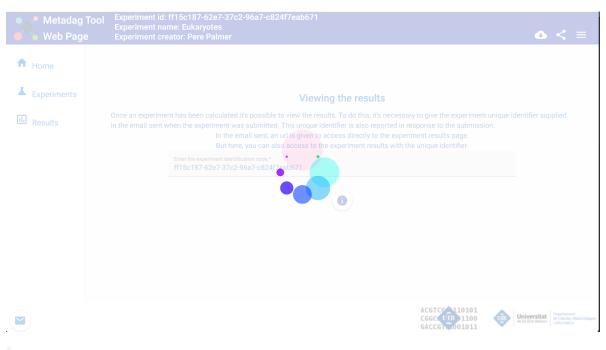
Hash: bb261b6e-95c6-3e39-b82b-b68eea80e30b

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)
```







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	netural	#nothrrows	Protists	Funci	Plants	Animals	Alveolates	Amoebozoa	Annelids
	natural	#pathways		Fungi				_	
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"