

Metagad experiment example

MetaDag Team

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Introduction

This is a example of experiment whith results of metaDag data <https://http://bioinfo.uib.es/metadag/>.

The screenshot shows the Metadag Tool web interface. At the top, there are two tabs: "Metadag Tool" (selected) and "Web Page". Below the tabs, the experiment details are listed: Experiment id: ff15c187-62e7-37c2-96a7-c824f7eab671, Experiment name: Eukaryotes, and Experiment creator: Pere Palmer. On the right side of the header are icons for cloud storage, sharing, and more. The main content area has a sidebar with "Home", "Experiments", and "Results" links. The "Results" link is selected. The main content area is titled "Viewing the results". It contains instructions about using the unique identifier sent in the email and provides a text input field where the identifier "ff15c187-62e7-37c2-96a7-c824f7eab671" is entered. A blue info icon is located below the input field. At the bottom right, there are logos for Universitat de les Illes Balears, Departament de Ciències Matemàtiques i Informàtica, and UTB.

1 Load data MetaDag experiment

```
library(tidyverse)

-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr     1.1.2     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.2     v tibble    3.2.1
v lubridate 1.9.2     v tidyr    1.3.0
v purrr    1.0.1

-- Conflicts -----
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become non-conflicting

experiment=
  "results_ff15c187-62e7-37c2-96a7-c824f7eab671"
path_exp=paste0("data/",experiment,"/data/")
dir(path_exp)

[1] "Different_MBB.csv"
[2] "Different_mDAG.csv"
[3] "Global"
[4] "Individuals"
[5] "Results.csv"
[6] "Similarities_MBB_MSAMethod.csv"
[7] "Similarities_MBB_MunkresMethod.csv"
[8] "Similarities_mDAG_MSAMethod.csv"
[9] "Similarities_mDAG_MSAMethod_MunkresMethod.csv"
[10] "Similarities_mDAG_MunkresMethod.csv"
[11] "Similarities_mDAG_MunkresMethod_MSAMethod.csv"
[12] "Similarities_mDAGOOnReaction.csv"
[13] "TaxonomyLevels"
```

```
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)
```

1.1 MBB

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

```
library(knitr)
library(kableExtra)
```

Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':

```
group_rows
```

```
#add_header_above(c("a" = 5, "b" = 18,"last"=2752-23)) %>%
# kable_paper() %>%
kable(MBB[1:20,1:30]) %>% 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

Manual columnas MBB

```
#definition_cols=data.frame(col_number,col_name,col,definition)
```

1.2 mDAG

Abstract/unique mDAG's in this experiment

```
dim(mDAG)
```

```
[1] 884 5224
```

```
kable(mDAG[1:20,1:30]) %>% 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"
```

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

```
[1] "Alveolates"           "Amoebozoa"
[3] "Annelids"             "Arthropods"
[5] "Ascomycetes"          "Basal_angiosperms"
[7] "Basidiomycetes"        "Brachiopoda"
[9] "Cephalochordates"     "Choanoflagellates"
[11] "Cnidarians"           "Cryptomonads"
```

[13]	"Echinoderms"	"Eudicots"
[15]	"Euglenozoa"	"Ferns"
[17]	"Flatworms"	"Green algae"
[19]	"Haptophyta"	"Hemichordates"
[21]	"Heterolobosea"	"Metamonada"
[23]	"Microsporidians"	"Mollusks"
[25]	"Monocots"	"Mosses"
[27]	"Nematodes"	"Placozoans"
[29]	"Poriferans"	"Red algae"
[31]	"Stramenopiles"	"Tunicates"
[33]	"Vertebrates"	"Acanthamoeba"
[35]	"Acanthus family"	"Amaranth family"
[37]	"Amborella family"	"Amphibians"
[39]	"Apicomplexans"	"Asparagus family"
[41]	"Banana family"	"Beech family"
[43]	"Birds"	"Bittersweet family"
[45]	"Buckthorn family"	"Caper family"
[47]	"Cartilaginous fishes"	"Chelicerates"
[49]	"Ciliates"	"Crustaceans"
[51]	"Cucumber family"	"Daisy family"
[53]	"Diatoms"	"Dictyostelia"
[55]	"Dinoflagellates"	"Diplomonads"
[57]	"Dothideomycetes"	"Entamoeba"
[59]	"Eurotiomycetes"	"Eustigmatophytes"
[61]	"Fishes"	"Ginger family"
[63]	"Grape family"	"Grass family"
[65]	"Insects"	"Kinetoplasts"
[67]	"Leotiomycetes"	"Lopseed family"
[69]	"Lotus family"	"Mallow family"
[71]	"Mammals"	"Mint family"
[73]	"Morning-glory family"	"Mulberry family"
[75]	"Mustard family"	"Myrtle family"
[77]	"Nightshade family"	"Olive family"
[79]	"Oomycetes"	"Orchid family"
[81]	"Palm family"	"Papaya family"
[83]	"Parsley family"	"Pea family"
[85]	"Pelagophytes"	"Pezizomycetes"
[87]	"Poppy family"	"Protea family"
[89]	"Reptiles"	"Rose family"
[91]	"Rue family"	"Saccharomycetes"
[93]	"Schizosaccharomycetes"	"Sesame family"
[95]	"Sordariomycetes"	"Spurge family"
[97]	"Sumac family"	"Tea family"

[99]	"Tetramitia"	"Trichomonads"
[101]	"Walnut family"	"Water-lily family"
[103]	"Willow family"	"#MMB"
[105]	"0"	"0.0"
[107]	"0.0.0"	"0.0.0.0"
[109]	"0.0.1"	"0.0.1.0"
[111]	"0.0.1.1"	"0.0.1.2"
[113]	"0.0.1.3"	"0.0.1.4"
[115]	"0.0.1.4.0"	"0.0.1.4.1"
[117]	"0.0.1.4.2"	"0.0.1.4.3"
[119]	"0.0.1.4.4"	"0.0.1.4.5"
[121]	"0.0.1.5"	"0.0.1.5.0"
[123]	"0.0.2"	"0.0.3"
[125]	"0.0.3.0"	"0.0.4"
[127]	"0.0.4.0"	"0.0.4.0.0"
[129]	"0.0.4.0.0.0"	"0.0.4.1"
[131]	"0.0.5"	"0.0.6"
[133]	"0.0.7"	"0.0.8"
[135]	"0.0.9"	"0.0.9.0"
[137]	"0.0.10"	"0.0.11"
[139]	"0.0.11.0"	"0.0.11.1"
[141]	"0.0.11.2"	"0.0.11.3"
[143]	"0.0.11.4"	"0.0.11.5"
[145]	"0.0.11.6"	"0.0.11.7"
[147]	"0.0.11.8"	"0.0.11.9"
[149]	"0.0.11.10"	"0.0.11.11"
[151]	"0.0.12"	"0.0.13"
[153]	"0.0.14"	"0.0.14.0"
[155]	"0.0.14.0.0"	"0.0.14.0.1"
[157]	"0.0.14.0.1.0"	"0.0.14.0.1.1"
[159]	"0.0.14.1"	"0.0.15"
[161]	"0.0.17"	"0.0.17.0"
[163]	"0.0.19"	"0.0.20"
[165]	"0.0.21"	"0.0.21.0"
[167]	"0.0.21.0.0"	"0.0.21.1"
[169]	"0.0.21.2"	"0.0.21.2.0"
[171]	"0.0.21.2.1"	"0.0.21.2.2"
[173]	"0.0.21.2.3"	"0.0.21.2.3.0"
[175]	"0.0.21.2.3.0.0"	"0.0.21.2.4"
[177]	"0.0.21.2.5"	"0.0.22"
[179]	"0.0.22.0"	"0.0.23"
[181]	"0.0.24"	"0.0.25"
[183]	"0.0.25.0"	"0.0.25.0.0"

[185]	"0.0.25.0.1"	"0.0.25.1"
[187]	"0.0.25.2"	"0.0.25.3"
[189]	"0.0.25.4"	"0.0.25.4.0"
[191]	"0.0.31"	"0.0.32"
[193]	"0.0.32.0"	"0.0.32.1"
[195]	"0.0.35"	"0.0.35.0"
[197]	"0.0.35.0.0"	"0.0.35.1"
[199]	"0.0.36"	"0.0.37"
[201]	"0.0.38"	"0.0.40"
[203]	"0.0.41"	"0.0.42"
[205]	"0.0.43"	"0.0.43.0"
[207]	"0.0.47"	"0.0.47.0"
[209]	"0.0.48"	"0.0.48.0"
[211]	"0.0.49"	"0.0.50"
[213]	"0.0.51"	"0.0.51.0"
[215]	"0.0.51.0.0"	"0.0.51.0.0.0"
[217]	"0.0.51.0.0.1"	"0.0.51.1"
[219]	"0.0.51.2"	"0.0.51.2.0"
[221]	"0.0.51.2.0.0"	"0.0.51.2.0.1"
[223]	"0.0.51.2.1"	"0.0.51.2.1.0"
[225]	"0.0.51.2.1.0.0"	"0.0.51.2.1.0.0.0"
[227]	"0.0.52"	"0.0.52.0"
[229]	"0.0.52.0.0"	"0.0.53"
[231]	"0.0.53.0"	"0.0.53.0.0"
[233]	"0.0.54"	"0.0.54.0"
[235]	"0.0.54.1"	"0.0.54.2"
[237]	"0.0.54.2.0"	"0.0.55"
[239]	"0.0.57"	"0.0.57.0"
[241]	"0.0.57.1"	"0.0.58"
[243]	"0.0.58.0"	"0.0.58.0.0"
[245]	"0.0.58.0.0.0"	"0.0.58.0.0.1"
[247]	"0.0.58.0.0.2"	"0.0.58.0.0.2.0"
[249]	"0.0.58.0.0.3"	"0.0.58.0.0.4"
[251]	"0.0.58.0.0.5"	"0.0.58.0.0.5.0"
[253]	"0.0.58.0.0.5.1"	"0.0.58.0.0.5.2"
[255]	"0.0.58.0.0.6"	"0.0.58.0.0.7"
[257]	"0.0.58.0.0.7.0"	"0.0.58.0.0.7.1"
[259]	"0.0.58.0.0.7.2"	"0.0.58.0.0.7.3"
[261]	"0.0.58.0.1"	"0.0.58.0.1.0"
[263]	"0.0.58.0.1.0.0"	"0.0.58.0.1.0.1"
[265]	"0.0.58.0.2"	"0.0.62"
[267]	"0.0.62.0"	"0.0.62.1"
[269]	"0.0.62.1.0"	"0.0.62.1.1"

[271]	"0.0.62.1.2"	"0.0.62.2"
[273]	"0.0.62.3"	"0.0.62.3.0"
[275]	"0.0.63"	"0.0.63.0"
[277]	"0.0.63.1"	"0.0.63.2"
[279]	"0.0.63.3"	"0.0.63.4"
[281]	"0.0.63.5"	"0.0.63.6"
[283]	"0.0.64"	"0.0.65"
[285]	"0.0.67"	"0.0.70"
[287]	"0.0.71"	"0.0.71.0"
[289]	"0.0.71.1"	"0.0.75"
[291]	"0.0.75.0"	"0.0.75.0.0"
[293]	"0.0.75.1"	"0.0.76"
[295]	"0.0.76.0"	"0.0.76.0.0"
[297]	"0.0.76.0.0.0"	"0.0.76.0.0.1"
[299]	"0.0.76.0.0.1.0"	"0.0.76.0.0.1.0.0"
[301]	"0.0.76.0.0.1.0.1"	"0.0.76.0.0.1.1"
[303]	"0.0.76.0.1"	"0.0.76.0.1.0"
[305]	"0.0.76.0.1.1"	"0.0.76.0.2"
[307]	"0.0.76.1"	"0.0.76.1.0"
[309]	"0.0.76.1.0.0"	"0.0.76.1.0.0.0"
[311]	"0.0.76.1.1"	"0.0.76.2"
[313]	"0.0.76.3"	"0.0.76.3.0"
[315]	"0.0.76.3.0.0"	"0.0.76.3.0.0.0"
[317]	"0.0.76.3.0.1"	"0.0.77"
[319]	"0.0.78"	"0.0.78.0"
[321]	"0.0.78.0.0"	"0.0.78.1"
[323]	"0.0.78.2"	"0.0.78.3"
[325]	"0.0.78.4"	"0.0.78.5"
[327]	"0.0.79"	"0.0.80"
[329]	"0.0.80.0"	"0.0.80.0.0"
[331]	"0.0.80.0.0.0"	"0.0.80.1"
[333]	"0.0.80.2"	"0.0.81"
[335]	"0.0.81.0"	"0.0.81.1"
[337]	"0.0.83"	"0.0.83.0"
[339]	"0.0.85"	"0.0.85.0"
[341]	"0.0.85.0.0"	"0.0.85.1"
[343]	"0.0.85.2"	"0.0.85.3"
[345]	"0.0.87"	"0.0.87.0"
[347]	"0.0.87.1"	"0.0.89"
[349]	"0.0.89.0"	"0.0.89.0.0"
[351]	"0.0.90"	"0.0.90.0"
[353]	"0.0.90.0.0"	"0.0.91"
[355]	"0.0.91.0"	"0.0.94"

[357]	"0.0.94.0"	"0.0.94.0.0"
[359]	"0.0.94.1"	"0.0.94.2"
[361]	"0.0.94.2.0"	"0.0.94.2.0.0"
[363]	"0.0.94.2.0.0.0"	"0.0.94.2.0.0.0.0"
[365]	"0.0.94.2.0.0.0.1"	"0.0.94.2.0.0.0.2"
[367]	"0.0.94.2.0.0.1"	"0.0.94.2.0.0.1.0"
[369]	"0.0.94.2.0.1"	"0.0.94.2.0.1.0"
[371]	"0.0.94.2.0.1.1"	"0.0.94.2.0.1.2"
[373]	"0.0.94.2.0.2"	"0.0.94.2.1"
[375]	"0.0.97"	"0.0.97.0"
[377]	"0.0.97.1"	"0.0.98"
[379]	"0.0.99"	"0.0.99.0"
[381]	"0.0.100"	"0.0.100.0"
[383]	"0.0.100.0.0"	"0.0.101"
[385]	"0.0.101.0"	"0.0.101.0.0"
[387]	"0.0.101.0.0.0"	"0.0.101.0.0.1"
[389]	"0.0.101.0.1"	"0.0.101.0.1.0"
[391]	"0.0.101.0.1.0.0"	"0.0.101.0.1.0.0.0"
[393]	"0.0.101.0.1.0.0.1"	"0.0.101.0.1.0.0.1.0"
[395]	"0.0.101.0.1.0.0.2"	"0.0.101.0.1.0.0.3"
[397]	"0.0.101.0.1.0.0.4"	"0.0.101.0.1.0.1"
[399]	"0.0.101.0.1.0.1.0"	"0.0.101.0.1.0.1.0.0"
[401]	"0.0.101.0.1.0.1.0.1"	"0.0.101.0.1.0.1.0.2"
[403]	"0.0.101.0.1.0.1.0.2.0"	"0.0.101.0.1.0.1.1"
[405]	"0.0.102"	"0.0.102.0"
[407]	"0.0.102.0.0"	"0.0.102.0.0.0"
[409]	"0.0.102.0.0.0.0"	"0.0.102.0.0.1"
[411]	"0.0.102.0.0.1.0"	"0.0.102.0.1"
[413]	"0.0.102.0.1.0"	"0.0.102.0.1.0.0"
[415]	"0.0.102.1"	"0.0.102.1.0"
[417]	"0.0.102.1.0.0"	"0.0.102.1.1"
[419]	"0.0.102.2"	"0.0.102.2.0"
[421]	"0.0.102.3"	"0.0.102.3.0"
[423]	"0.0.102.4"	"0.0.103"
[425]	"0.0.103.0"	"0.0.103.0.0"
[427]	"0.0.104"	"0.0.104.0"
[429]	"0.0.104.0.0"	"0.0.104.0.0.0"
[431]	"0.0.104.0.0.1"	"0.0.104.0.1"
[433]	"0.0.104.0.2"	"0.0.104.0.2.0"
[435]	"0.0.105"	"0.0.105.0"
[437]	"0.0.105.0.0"	"0.0.105.1"
[439]	"0.0.105.1.0"	"0.0.107"
[441]	"0.0.107.0"	"0.0.108"

[443]	"0.0.109"	"0.0.109.0"
[445]	"0.0.109.1"	"0.0.110"
[447]	"0.0.111"	"0.0.111.0"
[449]	"0.0.111.1"	"0.0.111.2"
[451]	"0.0.112"	"0.0.115"
[453]	"0.0.116"	"0.0.117"
[455]	"0.0.117.0"	"0.0.117.0.0"
[457]	"0.0.119"	"0.0.119.0"
[459]	"0.0.121"	"0.0.121.0"
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[1703]	"0.1.18.9"	"0.1.18.9.0"
[1705]	"0.1.18.9.0.0"	"0.1.18.9.0.0.0"
[1707]	"0.1.18.9.1"	"0.1.18.10"
[1709]	"0.1.18.10.0"	"0.1.18.10.0.0"
[1711]	"0.1.18.10.0.0.6"	"0.1.18.10.0.0.8"
[1713]	"0.1.18.10.0.0.9"	"0.1.18.10.0.0.11"
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[1717]	"0.1.18.10.0.1.1"	"0.1.18.10.0.1.2"
[1719]	"0.1.18.10.0.1.3"	"0.1.18.10.0.2"
[1721]	"0.1.18.10.0.2.0"	"0.1.18.10.0.2.1"
[1723]	"0.1.18.10.0.2.2"	"0.1.18.10.0.2.3"
[1725]	"0.1.18.10.0.3"	"0.1.18.10.0.3.0"
[1727]	"0.1.18.10.0.3.0.0"	"0.1.18.10.0.3.1"
[1729]	"0.1.18.10.0.4"	"0.1.18.10.0.5"
[1731]	"0.1.18.10.0.6"	"0.1.18.10.0.7"

[1733]	"0.1.18.10.0.8"	"0.1.18.10.0.9"
[1735]	"0.1.18.10.0.10"	"0.1.18.10.0.10.0"
[1737]	"0.1.18.10.0.10.0.0"	"0.1.18.10.0.10.1"
[1739]	"0.1.18.10.0.10.2"	"0.1.18.10.1"
[1741]	"0.1.18.10.1.0"	"0.1.18.10.1.0.0"
[1743]	"0.1.18.10.1.0.0.0"	"0.1.18.10.1.0.0.0.0"
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[1747]	"0.1.18.10.1.0.0.0.0.1.0"	"0.1.18.10.1.0.0.0.0.1.0.0"
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[1757]	"0.1.18.10.1.0.0.2.0"	"0.1.18.10.1.0.0.2.0.1"
[1759]	"0.1.18.10.1.0.0.2.0.3"	"0.1.18.10.1.0.0.2.0.8"
[1761]	"0.1.18.10.1.0.0.2.0.20"	"0.1.18.10.1.0.0.2.0.21"
[1763]	"0.1.18.10.1.0.0.2.0.22"	"0.1.18.10.1.0.0.2.0.23"
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[1767]	"0.1.18.10.1.0.0.2.0.41"	"0.1.18.10.1.0.0.2.0.42"
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[1779]	"0.1.18.10.1.0.0.5"	"0.1.18.10.1.0.0.6"
[1781]	"0.1.18.10.1.0.0.7"	"0.1.18.10.1.0.1"
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[1823]	"0.1.20.0.0.1.0"	"0.1.20.0.0.1.0.0"
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[1827]	"0.1.20.0.0.1.1"	"0.1.20.0.0.1.2"
[1829]	"0.1.20.0.0.1.2.0"	"0.1.20.0.1"
[1831]	"0.1.20.0.0.1.0"	"0.1.20.0.1.0.0"
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[1899]	"0.2.33.34"	"0.2.33.34.0"
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[1911]	"0.2.33.34.9"	"0.2.33.34.10"
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[1921]	"0.2.33.34.10.18.0.0"	"0.2.33.34.10.18.1"
[1923]	"0.2.33.34.10.18.1.0"	"0.2.33.34.10.18.2"
[1925]	"0.2.33.34.10.18.3"	"0.2.33.34.10.19"
[1927]	"0.2.33.34.10.20"	"0.2.33.34.10.20.0"
[1929]	"0.2.33.34.10.20.1"	"0.2.33.34.10.20.1.0"
[1931]	"0.2.33.34.10.20.2"	"0.2.33.34.10.21"
[1933]	"0.2.33.34.10.21.0"	"0.2.33.34.10.21.0.0"
[1935]	"0.2.33.34.10.21.0.1"	"0.2.33.34.10.21.0.1.0"
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[1953]	"0.2.33.34.10.27.12"	"0.2.33.34.10.27.12.0"
[1955]	"0.2.33.34.10.27.13"	"0.2.33.34.10.27.14"
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[1961]	"0.2.33.34.10.27.18.0"	"0.2.33.34.10.27.18.0.0"
[1963]	"0.2.33.34.10.27.19"	"0.2.33.34.10.27.20"
[1965]	"0.2.33.34.10.27.21"	"0.2.33.34.10.28"
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[1969]	"0.2.33.34.10.28.1.0"	"0.2.33.34.10.28.1.0.0"
[1971]	"0.2.33.34.10.28.1.1"	"0.2.33.34.10.28.2"
[1973]	"0.2.33.34.10.28.3"	"0.2.33.34.10.29"
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[1987]	"0.2.33.34.10.40"	"0.2.33.34.10.41"
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[2019]	"0.2.33.34.165"	"0.2.33.34.165.0"
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[2189]	"0.2.33.36.82"	"0.2.33.36.83"
[2191]	"0.2.33.36.84"	"0.2.33.36.85"
[2193]	"0.2.33.36.86"	"0.2.33.36.88"
[2195]	"0.2.33.36.89"	"0.2.33.36.92"
[2197]	"0.2.33.36.94"	"0.2.33.36.94.0"
[2199]	"0.2.33.36.94.0.0"	"0.2.33.36.97"
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[2203]	"0.2.33.36.107"	"0.2.33.36.107.0"
[2205]	"0.2.33.36.108"	"0.2.33.36.111"
[2207]	"0.2.33.36.114"	"0.2.33.36.115"
[2209]	"0.2.33.36.132"	"0.2.33.36.135"
[2211]	"0.2.34"	"0.2.34.0"
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[2215]	"0.2.34.3.0.3"	"0.2.34.3.1"
[2217]	"0.2.34.4"	"0.2.34.5"
[2219]	"0.2.34.5.0"	"0.2.34.10"
[2221]	"0.2.34.10.0"	"0.2.34.11"
[2223]	"0.2.34.11.0"	"0.2.35"
[2225]	"0.2.35.0"	"0.2.35.1"
[2227]	"0.2.35.6"	"0.2.35.7"
[2229]	"0.2.35.7.0"	"0.2.35.7.1"
[2231]	"0.2.35.7.1.0"	"0.2.35.7.1.0.0"
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[2239]	"0.2.35.7.1.1"	"0.2.35.7.2"
[2241]	"0.2.35.7.2.0"	"0.2.35.7.2.0.0"
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[2247]	"0.2.35.7.5.0"	"0.2.35.7.5.0.0"

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[2257]	"0.2.36.2"	"0.2.36.3"
[2259]	"0.2.36.4"	"0.2.36.4.22"
[2261]	"0.2.36.4.23"	"0.2.36.4.24"
[2263]	"0.2.36.4.24.5"	"0.2.36.4.24.5.0"
[2265]	"0.2.36.4.24.6"	"0.2.36.4.24.7"
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[2271]	"0.2.36.4.26"	"0.2.36.4.27"
[2273]	"0.2.36.4.28"	"0.2.36.4.28.0"
[2275]	"0.2.36.4.29"	"0.2.36.4.29.0"
[2277]	"0.2.36.5"	"0.2.36.6"
[2279]	"0.2.36.7"	"0.2.36.8"
[2281]	"0.2.36.9"	"0.2.37"
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[2285]	"0.2.37.2"	"0.2.37.2.0"
[2287]	"0.2.37.2.1"	"0.2.37.3"
[2289]	"0.2.37.4"	"0.2.38"
[2291]	"0.2.38.0"	"0.2.38.1"
[2293]	"0.2.38.2"	"0.2.38.2.11"
[2295]	"0.2.38.2.12"	"0.2.38.2.13"
[2297]	"0.2.38.2.14"	"0.2.38.2.15"
[2299]	"0.2.38.3"	"0.2.38.4"
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[2307]	"0.2.38.10.0"	"0.2.38.11"
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[2319]	"0.2.40"	"0.2.40.15"
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[2329]	"0.2.40.15.1.1"	"0.2.40.15.1.1.0"
[2331]	"0.2.40.15.1.1.0.0"	"0.2.40.15.1.1.1"
[2333]	"0.2.40.15.1.2"	"0.2.40.15.1.3"

[2335]	"0.2.40.15.1.4"	"0.2.40.15.1.5"
[2337]	"0.2.40.15.1.6"	"0.2.40.15.1.7"
[2339]	"0.2.40.15.1.8"	"0.2.40.15.1.9"
[2341]	"0.2.40.15.1.10"	"0.2.40.15.2"
[2343]	"0.2.40.15.2.0"	"0.2.40.15.2.0.0"
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[2349]	"0.2.40.15.2.0.0.2"	"0.2.40.15.2.0.0.3"
[2351]	"0.2.40.15.2.0.0.4"	"0.2.40.15.2.0.0.5"
[2353]	"0.2.40.15.2.0.0.6"	"0.2.40.15.2.0.1"
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[2361]	"0.2.40.15.2.0.7"	"0.2.40.15.2.0.7.0"
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[2413]	"0.2.40.17.0.3.0.0"	"0.2.40.17.0.3.0.1"
[2415]	"0.2.40.17.0.3.0.1.0"	"0.2.40.17.0.3.0.2"
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[2423]	"0.2.40.17.0.3.0.2.0.2.0"	"0.2.40.17.0.3.0.2.0.3"
[2425]	"0.2.40.17.0.3.0.2.0.4"	"0.2.40.17.0.3.0.2.0.5"
[2427]	"0.2.40.17.0.3.0.2.0.5.0"	"0.2.40.17.0.3.0.2.0.6"
[2429]	"0.2.40.17.0.3.0.2.0.7"	"0.2.40.17.0.3.0.2.0.8"
[2431]	"0.2.40.17.0.3.0.2.0.9"	"0.2.40.17.0.3.0.2.0.9.0"
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[2441]	"0.2.40.17.0.3.0.2.1.3"	"0.2.40.17.0.3.0.2.1.4"
[2443]	"0.2.40.17.0.3.0.2.2"	"0.2.40.17.0.3.0.2.2.0"
[2445]	"0.2.40.17.0.3.0.2.2.1"	"0.2.40.17.0.3.0.2.3"
[2447]	"0.2.40.17.0.3.0.2.4"	"0.2.40.17.0.3.0.2.5"
[2449]	"0.2.40.17.0.3.0.2.5.0"	"0.2.40.17.0.3.0.2.6"
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[2457]	"0.2.40.17.0.3.0.2.10.1"	"0.2.40.17.0.3.0.2.11"
[2459]	"0.2.40.17.0.3.0.2.12"	"0.2.40.17.0.3.0.2.12.0"
[2461]	"0.2.40.17.0.3.0.2.13"	"0.2.40.17.0.3.0.2.13.0"
[2463]	"0.2.40.17.0.3.0.2.13.0.0"	"0.2.40.17.0.3.0.2.13.1"
[2465]	"0.2.40.17.0.3.0.2.13.2"	"0.2.40.17.0.3.0.2.13.3"
[2467]	"0.2.40.17.0.3.0.3"	"0.2.40.17.0.3.0.3.0"
[2469]	"0.2.40.17.0.3.0.3.1"	"0.2.40.17.0.3.0.4"
[2471]	"0.2.40.17.0.3.0.4.0"	"0.2.40.17.0.3.0.5"
[2473]	"0.2.40.17.0.3.0.6"	"0.2.40.17.0.3.0.7"
[2475]	"0.2.40.17.0.3.0.8"	"0.2.40.17.0.3.0.8.0"
[2477]	"0.2.40.17.0.3.0.8.1"	"0.2.40.17.0.4"
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[2489]	"0.2.40.17.42.1.2"	"0.2.40.17.42.1.3"
[2491]	"0.2.40.17.42.1.4"	"0.2.40.17.42.2"
[2493]	"0.2.40.17.42.3"	"0.2.40.17.42.5"
[2495]	"0.2.40.17.42.5.0"	"0.2.40.17.42.27"
[2497]	"0.2.40.17.42.28"	"0.2.40.17.42.33"
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[2501]	"0.2.40.17.42.50"	"0.2.40.17.42.52"
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[2505]	"0.2.40.17.42.61"	"0.2.40.18"

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[2515]	"0.2.40.18.2.0.0"	"0.2.40.18.2.0.1"
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[2567]	"0.2.40.18.2.0.2.12.1.0"	"0.2.40.18.2.0.2.13"
[2569]	"0.2.40.18.2.0.2.14"	"0.2.40.18.2.0.2.15"
[2571]	"0.2.40.18.2.0.2.15.0"	"0.2.40.18.2.0.2.15.1"
[2573]	"0.2.40.18.2.0.2.16"	"0.2.40.18.2.0.2.16.0"
[2575]	"0.2.40.18.2.0.3"	"0.2.40.18.2.0.4"
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[2579]	"0.2.40.18.2.0.7"	"0.2.40.18.2.0.8"
[2581]	"0.2.40.18.2.0.9"	"0.2.40.18.2.0.10"
[2583]	"0.2.40.18.2.0.11"	"0.2.40.18.2.0.12"
[2585]	"0.2.40.18.2.0.13"	"0.2.40.18.2.0.13.0"
[2587]	"0.2.40.18.2.0.13.1"	"0.2.40.18.2.1"
[2589]	"0.2.40.18.2.2"	"0.2.40.18.2.2.0"
[2591]	"0.2.40.18.2.2.1"	"0.2.40.18.2.3"

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[2595]	"0.2.40.18.2.6"	"0.2.40.18.2.6.0"
[2597]	"0.2.40.18.2.6.1"	"0.2.40.18.2.6.2"
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[2605]	"0.2.40.18.2.6.6.0"	"0.2.40.18.2.6.7"
[2607]	"0.2.40.18.2.6.8"	"0.2.40.18.2.6.9"
[2609]	"0.2.40.18.2.7"	"0.2.40.18.2.8"
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[2613]	"0.2.40.18.2.10"	"0.2.40.18.2.11"
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[2623]	"0.2.40.18.169.0"	"0.2.40.18.169.0.1"
[2625]	"0.2.40.18.169.0.3"	"0.2.40.18.169.0.3.0"
[2627]	"0.2.40.18.169.0.4"	"0.2.40.18.169.0.4.1"
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1.3 Results

Tabular data `Results` for this experiment

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kable(Results[1:20,1:10])%>%  
  row_spec(0, angle = -90) %>%  
  scroll_box(width = "300%", height = "1000px")
```

organism	Categories	mDAG Id	Full Name
aaf	Protists Stramenopiles Pelagophytes	0036	Aureococcus anophagefferens
aag	Animals Arthropods Insects	0035	Aedes aegypti (yellow fever mosquito)
aalb	Animals Arthropods Insects	0276	Aedes albopictus (Asian tiger mosquito)
aali	Animals Arthropods Insects	0267	Anopheles albimanus
aalt	Fungi Ascomycetes Dothideomycetes	0240	Alternaria alternata
aam	Animals Vertebrates Birds	0040	Apteryx mantelli mantelli (North Island brown kiwi)
aamp	Animals Vertebrates Mammals	0313	Arvicola amphibius (Eurasian water vole)
aang	Animals Vertebrates Fishes	0317	Anguilla anguilla (European eel)
aara	Animals Arthropods Insects	0362	Anopheles arabiensis
abe	Fungi Ascomycetes Eurotiomycetes	0060	Trichophyton benhamiae
abp	Fungi Basidiomycetes	0068	Agaricus bisporus var. burnettii JB137-S8
abv	Fungi Basidiomycetes	0073	Agaricus bisporus var. bisporus H97
acan	Protists Amoebozoa Acanthamoeba	0873	Acanthamoeba castellanii
acar	Animals Vertebrates Birds	0884	Antrostomus carolinensis (chuck-will's-widow)
acep	Animals Arthropods Insects	0054	Atta cephalotes (leaf cutting ant)
acer	Animals Arthropods Insects	0057	Apis cerana (Asiatic honeybee)
achc	Animals Vertebrates Birds	0103	Aquila chrysaetos chrysaetos (golden eagle)
ache	Fungi Ascomycetes Eurotiomycetes	0106	Aspergillus chevalieri
achl	Animals Vertebrates Birds	0081	Acanthisitta chloris (rifleman)
acoz	Animals Arthropods Insects	0255	Anopheles coluzzii

```
dim(Results)
```

```
[1] 884 3997
```

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

```
[1] "organism"
```

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

```

[1] "Categories"

names(Results) [3]# mDAG_Id

[1] "mDAG_Id"

names(Results) [4]# Full name representant

[1] "Full Name"

names(Results) [6:36]# 6 to 2726 Variable Reactions name id: This reaction belongs to this

[1] "R00710_rev(1.2.1.3)"  "R00711(1.2.1.5)"      "R00711_rev(1.2.1.5)"
[4] "R00755(4.1.1.1)"     "R00746(1.1.1.2)"      "R00746_rev(1.1.1.2)"
[7] "R00754(1.1.1.1)"     "R00754_rev(1.1.1.1)"  "R00014(4.1.1.1)"
[10] "R00014(1.2.4.1)"    "R03270(1.2.4.1)"      "R02569(2.3.1.12)"
[13] "R02569_rev(2.3.1.12)" "R00703(1.1.1.27)"   "R00703_rev(1.1.1.27)"
[16] "R00200(2.7.1.40)"    "R00658(4.2.1.11)"    "R00658_rev(4.2.1.11)"
[19] "R01518(5.4.2.11)"    "R01518_rev(5.4.2.11)" "R01061(1.2.1.12)"
[22] "R01061_rev(1.2.1.12)" "R01015(5.3.1.1)"    "R01015_rev(5.3.1.1)"
[25] "R01070(4.1.2.13)"    "R01070_rev(4.1.2.13)" "R04779(2.7.1.11)"
[28] "R04780(3.1.3.11)"    "R02740(5.3.1.9)"     "R02740_rev(5.3.1.9)"
[31] "R00959(5.4.2.2)"

library(stringr)
reactions=names(Results)[-c(1:5)]
reverse_reactions=stringr::str_detect(reactions,"rev")
table(reverse_reactions)

reverse_reactions
FALSE  TRUE
3398  594

```

2 Read graph

```
library(igraph)

Attaching package: 'igraph'

The following objects are masked from 'package:lubridate':
    %--%, union

The following objects are masked from 'package:dplyr':
    as_data_frame, groups, union

The following objects are masked from 'package:purrr':
    compose, simplify

The following object is masked from 'package:tidyverse':
    crossing

The following object is masked from 'package:tibble':
    as_data_frame

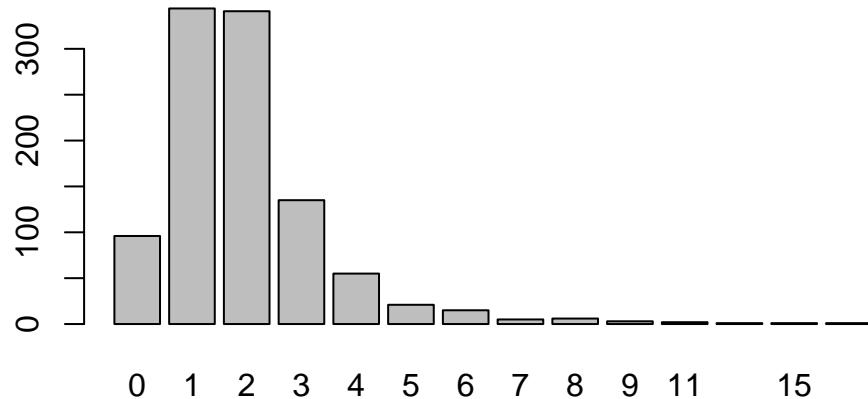
The following objects are masked from 'package:stats':
    decompose, spectrum

The following object is masked from 'package:base':
    union
```

```
gg1_mDAG=read.graph(paste0(path_exp,"Individuals/hsa/hsa_mDAG.graphml"),format = "graphml")
summary(gg1_mDAG)
```

```
IGRAPH 6b5d3a5 D--- 1026 1086 --
+ attr: color (v/c), label (v/c), id (v/c), id (e/c)
```

```
barplot(table(degree(gg1_mDAG)))
```



```
gg1_core_mDAG=read.graph(
  paste0(path_exp,"Global/core/core_mDAG.graphml"), format = "graphml")
```

```
gg1_core_RC=read.graph(
  paste0(path_exp, "Global/core/core_RC.graphml"), format = "graphml")
```

```
compo=components(gg1_mDAG,mode = "weak")
str(compo)
```

```
List of 3
$ membership: num [1:1026] 1 1 1 1 1 1 1 1 1 1 ...
$ csizes      : num [1:167] 589 1 1 1 1 4 3 4 3 ...
$ no          : int 167
```

```
compo$csizes
```

```
[1] 589 1 1 1 1 1 4 3 4 3 2 3 3 1 1 2 6
```

```

[19] 3 1 3 6 1 1 1 1 3 1 6 2 1 1 1 1 2 1
[37] 1 14 1 16 1 6 2 2 4 1 1 1 1 1 1 1 1 1
[55] 13 1 1 1 1 2 6 5 5 2 2 10 1 1 1 2 2 1
[73] 1 1 62 6 2 1 2 1 1 1 2 1 2 14 3 1 1 1
[91] 1 1 1 1 1 3 6 1 3 1 3 2 1 1 2 3 4 1 1 2
[109] 3 1 1 2 5 1 1 2 3 2 1 1 2 3 4 1 1 1 2
[127] 1 1 2 1 1 1 1 3 1 2 2 1 6 1 1 1 1 2
[145] 1 1 1 1 1 2 7 1 15 3 1 1 1 1 2 1 3 1
[163] 1 1 1 1 2

```

```

k=which.max(compo$csize==max(compo$csize))
k

```

```
[1] 1
```

```
table(compo$membership)
```

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
589	1	1	1	1	1	4	3	4	3	2	3	3	1	1	1	2	6	3	1	
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
3	6	1	1	1	1	1	3	1	6	2	1	1	1	2	1	1	14	1	16	
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
1	6	2	2	4	1	1	1	1	1	1	1	1	1	13	1	1	1	1	2	
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
6	5	5	2	2	10	1	1	1	2	2	1	1	1	62	6	2	1	2	1	
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	1	2	1	2	14	3	1	1	1	1	1	1	1	1	1	3	6	1	3	
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
1	3	2	1	1	1	2	2	3	1	1	2	5	1	1	2	3	2	1	1	
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	
2	3	4	1	1	2	1	1	2	1	1	1	1	1	1	3	1	2	2	1	6
141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	
1	1	1	2	1	1	1	1	1	2	7	1	15	3	1	1	1	1	2	1	
161	162	163	164	165	166	167														
3	1	1	1	1	1	2														

```

vertex=which(compo$membership==k)
length(vertex)

```

[1] 589

vertex

[1]	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
[16]	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
[31]	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
[46]	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
[61]	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
[76]	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
[91]	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
[106]	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
[121]	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
[136]	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
[151]	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
[166]	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
[181]	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
[196]	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
[211]	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
[226]	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
[241]	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255
[256]	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270
[271]	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285
[286]	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
[301]	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315
[316]	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330
[331]	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345
[346]	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
[361]	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375
[376]	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390
[391]	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405
[406]	406	408	409	411	412	413	414	415	417	418	420	422	423	444	445
[421]	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460
[436]	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475
[451]	476	477	478	479	486	488	489	490	491	492	493	495	496	497	498
[466]	502	515	517	518	519	520	521	522	523	524	525	526	527	528	529
[481]	530	531	532	533	534	535	536	537	540	541	542	543	544	545	546
[496]	547	548	549	550	551	565	566	569	570	571	574	577	578	579	580
[511]	581	582	621	622	627	628	629	630	644	645	646	647	648	649	650
[526]	651	668	669	670	671	672	707	709	710	711	712	714	715	716	717
[541]	718	719	720	721	722	723	724	732	733	808	809	812	813	819	820
[556]	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835

[571] 836 837 838 839 840 841 979 980 981 982 983 1003 1004 1008 1009
[586] 1010 1014 1018 1026

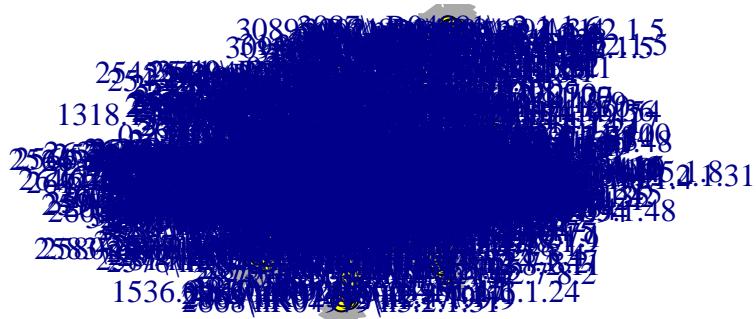
V(gg1_mDAG)

+ 1026/1026 vertices, from 6b5d3a5:

[1]	1	2	3	4	5	6	7	8	9	10	11	12	13	14
[15]	15	16	17	18	19	20	21	22	23	24	25	26	27	28
[29]	29	30	31	32	33	34	35	36	37	38	39	40	41	42
[43]	43	44	45	46	47	48	49	50	51	52	53	54	55	56
[57]	57	58	59	60	61	62	63	64	65	66	67	68	69	70
[71]	71	72	73	74	75	76	77	78	79	80	81	82	83	84
[85]	85	86	87	88	89	90	91	92	93	94	95	96	97	98
[99]	99	100	101	102	103	104	105	106	107	108	109	110	111	112
[113]	113	114	115	116	117	118	119	120	121	122	123	124	125	126
[127]	127	128	129	130	131	132	133	134	135	136	137	138	139	140

+ ... omitted several vertices

```
CC1=induced_subgraph(gg1_mDAG, vids=vertex)
plot(CC1)
```



summary(CC1)

```
IGRAPH 6c37d99 D--- 589 774 --
+ attr: color (v/c), label (v/c), id (v/c), id (e/c)
```

3 Load several similarities and metadata for an experiment

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr     1.1.2     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.2     v tibble    3.2.1
v lubridate 1.9.2     v tidyr    1.3.0
v purrr     1.0.1
-- Conflicts -----
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become non-conflicting
```

```
library(ComplexHeatmap)
```

```
Loading required package: grid
=====
ComplexHeatmap version 2.16.0
Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
Github page: https://github.com/jokergoo/ComplexHeatmap
Documentation: http://jokergoo.github.io/ComplexHeatmap-reference
```

If you use it in published research, please cite either one:

- Gu, Z. Complex Heatmap Visualization. iMeta 2022.
- Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics 2016.

The new `InteractiveComplexHeatmap` package can directly export static complex heatmaps into an interactive Shiny app with zero effort. Have a try!

```
This message can be suppressed by:  
  suppressPackageStartupMessages(library(ComplexHeatmap))  
=====
```

```
library(viridis)
```

```
Loading required package: viridisLite
```

```
library(circlize)
```

```
=====  
circlize version 0.4.15  
CRAN page: https://cran.r-project.org/package=circlize  
Github page: https://github.com/jokergoo/circlize  
Documentation: https://jokergoo.github.io/circlize\_book/book/
```

```
If you use it in published research, please cite:  
Gu, Z. circlize implements and enhances circular visualization  
in R. Bioinformatics 2014.
```

```
This message can be suppressed by:  
  suppressPackageStartupMessages(library(circlize))  
=====
```

```
library(plotly)
```

```
Attaching package: 'plotly'
```

```
The following object is masked from 'package:ComplexHeatmap':
```

```
add_heatmap
```

```
The following object is masked from 'package:ggplot2':
```

```
last_plot
```

```
The following object is masked from 'package:stats':
```

```
filter
```

```
The following object is masked from 'package:graphics':
```

```
layout
```

```
library(randomcoloR)
#library(knitr)
#library(kableExtra)
library(factoextra)
```

```
Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
library(RColorBrewer)
library(kableExtra)
```

```
Attaching package: 'kableExtra'
```

```
The following object is masked from 'package:dplyr':
```

```
group_rows
```

```
path_exp="data/results_ff15c187-62e7-37c2-96a7-c824f7eab671/data/"
```

3.1 Data analysis whit 4 methods distance Direct, Munkrest, Direct_Munkrest and Munkrest_Direct

3.2 Load several similarities for mDag

4 Load meta data from experiment all eukariotes

Meta data mDa_Id and taxonomy sort by Kingdom,Filum,Class,mDAG_Id

```
path_exp
```

```
[1] "data/results_ff15c187-62e7-37c2-96a7-c824f7eab671/data/"
```

```
Results=read_csv(paste0(path_exp,"Results.csv"))
```

```
Rows: 884 Columns: 3997
-- Column specification -----
Delimiter: ","
chr (1924): organism, Categories, mDAG_Id, Full_Name, R00710(1.2.1.3), R0071...
dbl (2073): R01982(3.2.1.15), R02439(2.7.1.16), R02439_rev(2.7.1.16), R02429...
```

```
i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
names(Results)[c(1,3,4)]=c("Organism","mDAG_Id","Full_Name")
#code=Results %>% select(Organism:mDAG_Id)
taxo=Results %>% select(Organism:Full_Name)
index=is.na(taxo$Categories)
taxo=taxo %>% separate(Categories,into=c("Kingdom","Phylum","Class"))
```

```
Warning: Expected 3 pieces. Additional pieces discarded in 126 rows [27, 41, 42, 51, 62,
64, 69, 79, 80, 81, 95, 102, 109, 112, 119, 127, 132, 134, 143, 148, ...].
```

```
Warning: Expected 3 pieces. Missing pieces filled with `NA` in 93 rows [11, 12, 25, 26,
43, 55, 67, 72, 78, 85, 97, 101, 108, 139, 149, 158, 165, 179, 198, 199, ...].
```

```

taxo$Class[index]=paste(taxo$Kingdom[index],taxo$Phylum[index])
meta_taxo=taxo %>% arrange(Kingdom,Phylum,Class)
#order_class=order(table(taxo$Class),decreasing = TRUE)
#table(is.na(taxo$Class))
#meta_taxo= taxo %>%
# right_join(code,by="Organism") %>%
#arrange(Kingdom,Phylum,Class,mDAG_Id)
index=which(is.na(meta_taxo$Class))
meta_taxo$Class[index]=meta_taxo$Phylum[index]

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
Brachiopoda	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

5 Similarities for method Direct

In this section we will show the similarities between mDAG's using different methods.

The experiment data set consists of 884 eukaryotes from the animal, plant, fungus, and protist kingdoms.

Kingdom	Abs. Freq.
Animals	535
Fungi	154
Plants	139
Protists	56

```
list_Sim=dir(path_exp,pattern="^Similarities")
list_Sim

[1] "Similarities_MBB_MSAMethod.csv"
[2] "Similarities_MBB_MunkresMethod.csv"
[3] "Similarities_mDAG_MSAMethod.csv"
[4] "Similarities_mDAG_MSAMethod_MunkresMethod.csv"
[5] "Similarities_mDAG_MunkresMethod.csv"
[6] "Similarities_mDAG_MunkresMethod_MSAMethod.csv"
[7] "Similarities_mDAGOnReaction.csv"

list_Sim_mDAG=dir(path_exp,pattern="^Similarities_mDAG")
list_Sim_mDAG

[1] "Similarities_mDAG_MSAMethod.csv"
[2] "Similarities_mDAG_MSAMethod_MunkresMethod.csv"
[3] "Similarities_mDAG_MunkresMethod.csv"
[4] "Similarities_mDAG_MunkresMethod_MSAMethod.csv"
[5] "Similarities_mDAGOnReaction.csv"

Sim_MSA_mDAG=read_csv(paste0(path_exp,list_Sim_mDAG[1]))
```

```
New names:  
Rows: 884 Columns: 885  
-- Column specification  
----- Delimiter: "," chr  
(1): ...1 dbl (884): 0001, 0002, 0003, 0004, 0005, 0006, 0007, 0008, 0009,  
0010, 0011,...  
i Use `spec()` to retrieve the full column specification for this data. i  
Specify the column types or set `show_col_types = FALSE` to quiet this message.  
* `` -> `...1`
```

```
Sim_MSA_mDAG=as.matrix(Sim_MSA_mDAG[,-1])  
rownames(Sim_MSA_mDAG)=colnames(Sim_MSA_mDAG)  
Sim_MSA_mDAG=Sim_MSA_mDAG[meta_taxo$mDAG_Id,meta_taxo$mDAG_Id]
```

```
Sim_MSA_Mun_mDAG=read_csv(paste0(path_exp,list_Sim_mDAG[2]))
```

```
New names:  
Rows: 884 Columns: 885  
-- Column specification  
----- Delimiter: "," chr  
(1): ...1 dbl (884): 0001, 0002, 0003, 0004, 0005, 0006, 0007, 0008, 0009,  
0010, 0011,...  
i Use `spec()` to retrieve the full column specification for this data. i  
Specify the column types or set `show_col_types = FALSE` to quiet this message.  
* `` -> `...1`
```

```
Sim_MSA_Mun_mDAG=as.matrix(Sim_MSA_Mun_mDAG[,-1])  
rownames(Sim_MSA_Mun_mDAG)=colnames(Sim_MSA_Mun_mDAG)  
Sim_MSA_Mun_mDAG=Sim_MSA_Mun_mDAG[meta_taxo$mDAG_Id,meta_taxo$mDAG_Id]
```

```
Sim_Mun_mDAG=read_csv(paste0(path_exp,list_Sim_mDAG[3]))
```

```
New names:  
Rows: 884 Columns: 885  
-- Column specification  
----- Delimiter: "," chr  
(1): ...1 dbl (884): 0001, 0002, 0003, 0004, 0005, 0006, 0007, 0008, 0009,  
0010, 0011,...  
i Use `spec()` to retrieve the full column specification for this data. i
```

```

Specify the column types or set `show_col_types = FALSE` to quiet this message.
* `` -> `...1`


Sim_Mun_mDAG=as.matrix(Sim_Mun_mDAG[,-1])
rownames(Sim_Mun_mDAG)=colnames(Sim_Mun_mDAG)
Sim_MSA_mDAG=Sim_MSA_mDAG[meta_taxo$mDAG_Id,meta_taxo$mDAG_Id]

Sim_Mun_MSA_mDAG=read_csv(paste0(path_exp,list_Sim_mDAG[4]))


New names:
Rows: 884 Columns: 885
-- Column specification
----- Delimiter: ","
(1): ...1 dbl (884): 0001, 0002, 0003, 0004, 0005, 0006, 0007, 0008, 0009,
0010, 0011, ...
i Use `spec()` to retrieve the full column specification for this data. i
Specify the column types or set `show_col_types = FALSE` to quiet this message.
* `` -> `...1`
```

```

Sim_Mun_MSA_mDAG=as.matrix(Sim_Mun_MSA_mDAG[,-1])
rownames(Sim_Mun_MSA_mDAG)=colnames(Sim_Mun_MSA_mDAG)
Sim_Mun_MSA_mDAG=Sim_Mun_MSA_mDAG[meta_taxo$mDAG_Id,meta_taxo$mDAG_Id]
```

5.1 Heatmaps

```

dis_DirectedMethod<-read_csv(paste0(path_exp,
                                      "Similarities_MBB_MSAMethod.csv"))
names(dis_DirectedMethod)[1]="mDAG_Id"
dis_DirectedMethod[,-1]=sqrt(1-dis_DirectedMethod[,-1])
dis_DirectedMethod_meta =dis_DirectedMethod %>% right_join(select(meta_taxo,mDAG_Id,Kingdom,Filum,Class)
  arrange(Kingdom,Filum,Class)

ID=dis_DirectedMethod_meta$mDAG_Id
dis_DirectedMethod= dis_DirectedMethod_meta %>%
  select(-Kingdom) %>%
  relocate(mDAG_Id,ID) %>%
  select(2:570) %>%
  as.matrix()
```

```
#dis_dir=as.matrix(sqrt(2*(1-sim0[,c(2:570)]^2)))
dimnames(dis_DirectedMethod) = list(ID, ID)
```

5.2 Heatmap Similarity MSA method

```
dff<-meta_taxo %>% select(Kingdom) %>% as.data.frame()
#str(dff)

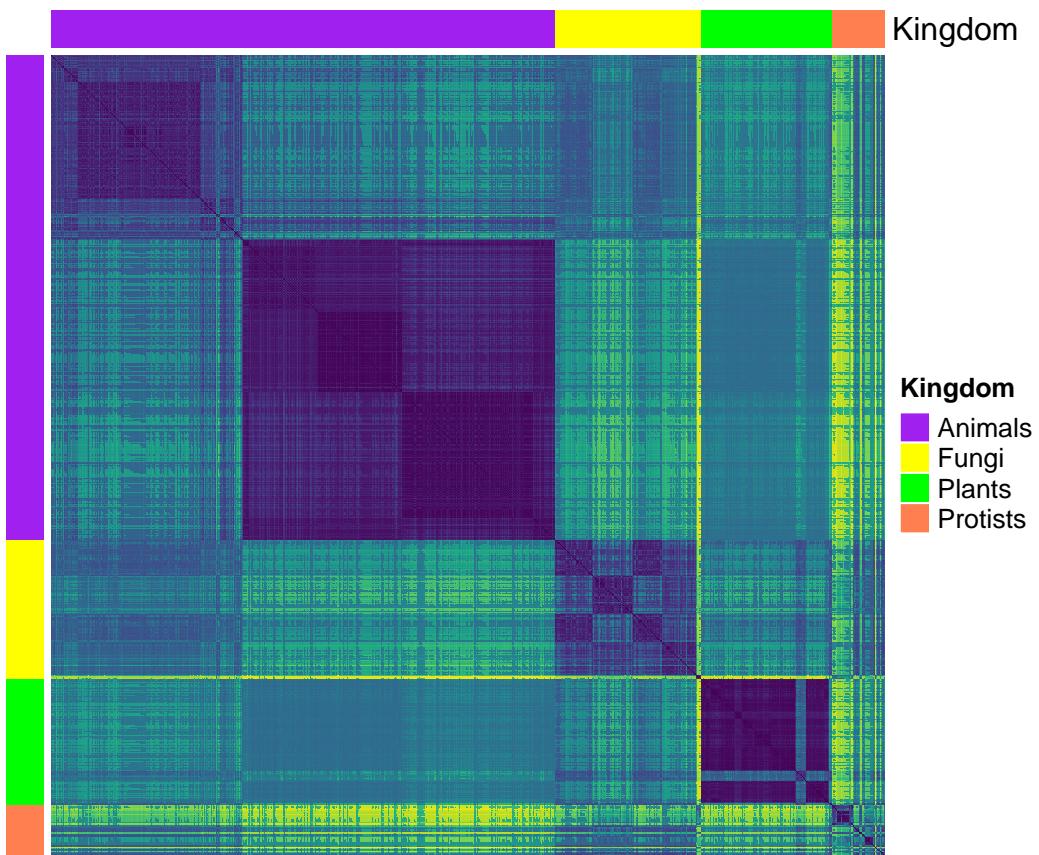
colores <- list(Kingdom= c("Animals"="purple","Plants"="green","Fungi"="yellow","Protists"="blue"))

anotacion <- HeatmapAnnotation(df=dff, col = colores)

S=Sim_MSA_mDAG
a<- Heatmap(matrix = Sim_MSA_mDAG,
             column_title="Similarity mDag MSA Method\n Eukariotas by Kingdom",
             name = "Kingdom",
             heatmap_legend_param = list(
               at = c(0.4,0.5,0.6,0.7,0.8,0.9,1)),
             col=rev(viridis(256)),
             cluster_rows = FALSE,
             cluster_columns = FALSE,
             top_annotation = anotacion,
             show_column_names = FALSE,
             show_row_names = FALSE,
             left_annotation = rowAnnotation(df = dff, col = colores,show_annotation_name=FALSE))

draw(a, merge_legend = TRUE)
```

Similarity mDag MSA Method Eukariotas by Kingdom



```

meta_animals= meta_taxo %>% filter(Kingdom=="Animals")
nombres=unique(meta_animals$Phylum)
aux_order=table(meta_animals$Phylum)
dff<-meta_taxo %>% filter(Kingdom=="Animals") %>% select(Class) %>% as.data.frame()
#str(dff)
nombres=unique(dff$Class)
col=rainbow(length(nombres))
colores=list(Class=col)
names(colores$Class)=nombres
#paste0(paste0('"' ,nombres,''"= "' ,col,''" ),collapse="," )
# colores <- list(Class=c(
# "Amphibians"="#FF0000", "Annelids"="#FF4900",
# "Cartilaginous"="#FF9200", "Cephalochordates"="#FFDB00",
# "Chelicerates"="#DBFF00", "Cnidarians"="#92FF00",

```

```

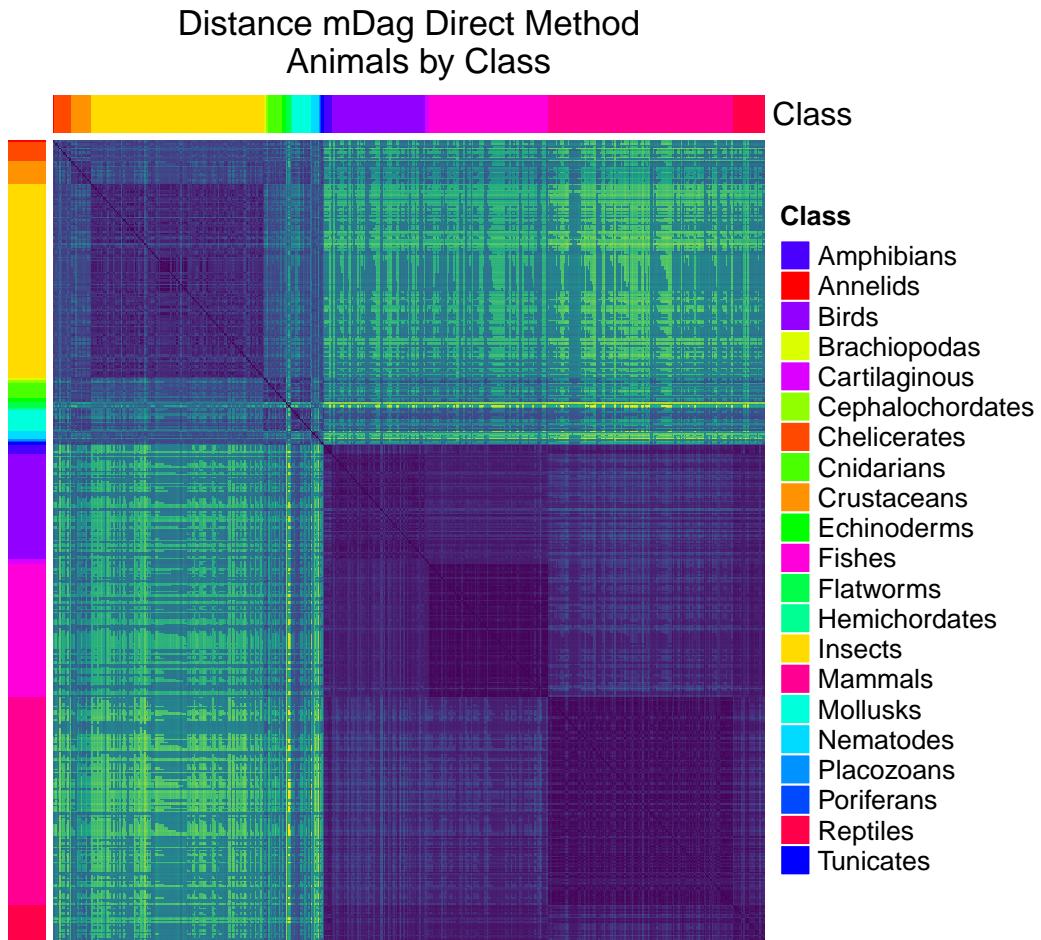
# "Crustaceans"="#49FF00", "Echinoderms"="#00FF00",
# "Fishes"="#00FF49", "Flatworms"="#00FF92",
# "Hemichordates"="#00FFDB", "Insects"="#00DBFF",
# "Mammals"="#0092FF", "Mollusks"="#0049FF",
# "Nematodes"="#0000FF", "Placozoans"="#4900FF",
# "Poriferans"="#9200FF",
# "Reptiles"="#DB00FF",
# "Tunicates"="#FF00DB",
# "Mammals"="#FF0092",
# "Reptiles"="#FF0049"))
# aux=names(colores$Class)
# colores$Class=as.character(palette.colors(n=21,palette="Polychrome 36"))
# attr(colores$Class,"names")=aux

anotacion <- HeatmapAnnotation(df=dff, col = colores)

a2<- Heatmap(matrix = S[1:535,1:535],
              column_title="Distance mDag Direct Method\n Animals by Class",
              name = "Class",
              heatmap_legend_param = list(
at = seq(0,1.5,by=0.1)),
              col=rev(viridis(256)),
              cluster_rows = FALSE,
              cluster_columns = FALSE,
              top_annotation = anotacion,
              show_column_names = FALSE,
              show_row_names = FALSE,
              left_annotation = rowAnnotation(df = dff, col = colores,show_annotation_name=FALSE)

draw(a2, merge_legend = TRUE)

```



5.3 MDS (Multidimensional Scaling)

```
## Metric multidimensional scaling (mMDS)
mds7 <- cmdscale(sqrt(1-Sim_MSA_mDAG^2), k=7, eig=TRUE)
#pairs(mds7$points[,1:4])
mds7$GOF
```

```
[1] 0.4406568 0.5541042
```

```
mds <- mds7$points %>% as_tibble()
```

```
Warning: The `x` argument of `as_tibble.matrix()` must have unique column names if
`.name_repair` is omitted as of tibble 2.0.0.
  i Using compatibility `$.name_repair`.
```

```
colnames(mds) <- paste0("Dim.", 1:dim(mds7$points)[2])
```

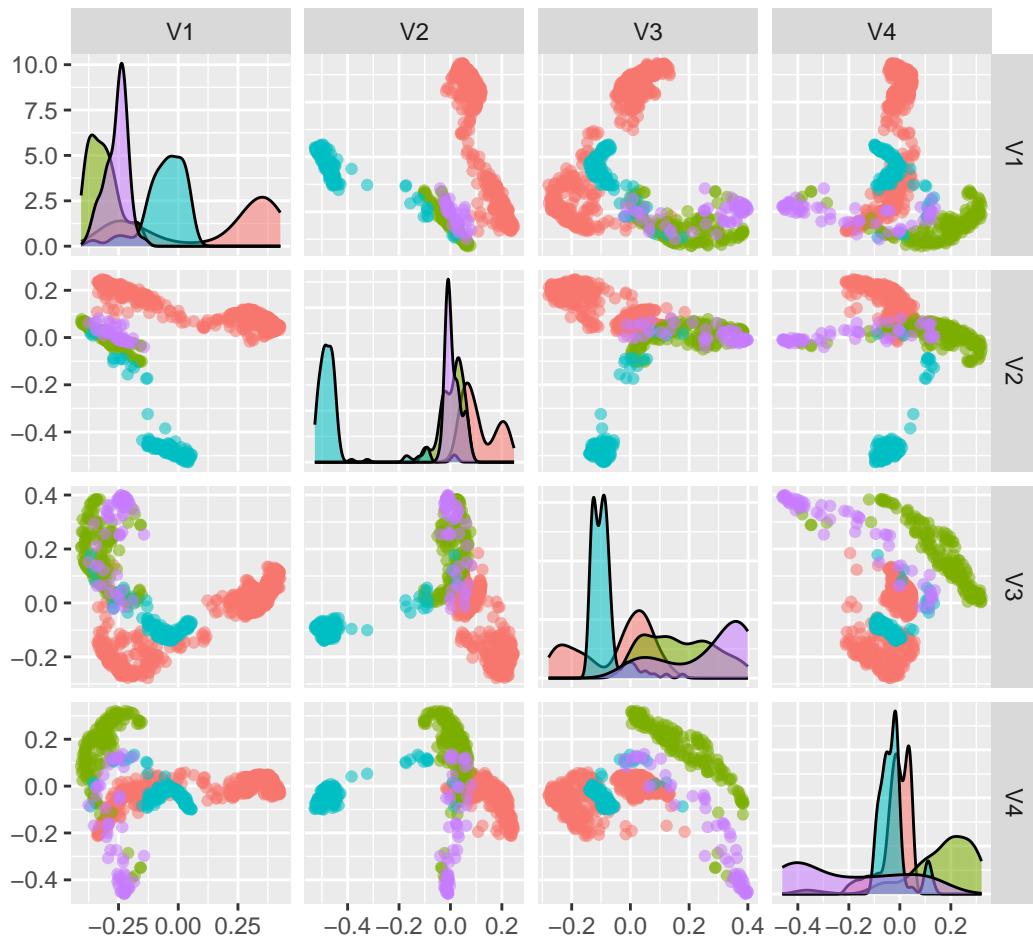
```
library(GGally)
```

```
Registered S3 method overwritten by 'GGally':
```

```
method from
```

```
+.gg ggplot2
```

```
ggpairs(as_tibble(mds7$points), columns=1:4, aes(color=meta_taxo$Kingdom, alpha=0.5), upper=li
```



```

mds <- mds %>%
  mutate(groups = as.factor(meta_taxo$Kingdom))

#,text= ~paste("Age:", groups, '<br>Name:')
length(unique(meta_taxo$Phylum))

[1] 33

#col_mds=c("purple","green","yellow","coral")
col_mds=rainbow(33)
#mcol_mds=bremer.pal(7,"Greens")

fig <-
plot_ly(
  mds, x = ~Dim.1, y = ~Dim.2,
  color = ~groups,
  colors= col_mds,
  type="scatter",
  mode="markers") %>%
  layout(
    xaxis = list(autorange=2,
      range=c(-0.8,0.8)), yaxis = list(autorange=2,
      range=c(-0.8,0.8)))

#fig

```

6 Hierarchical cluster

```
library(dendextend)
```

```
-----  
Welcome to dendextend version 1.17.1  
Type citation('dendextend') for how to cite the package.
```

```
Type browseVignettes(package = 'dendextend') for the package vignette.  
The github page is: https://github.com/talgalili/dendextend/
```

```
Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues  
You may ask questions at stackoverflow, use the r and dendextend tags:  
https://stackoverflow.com/questions/tagged/dendextend
```

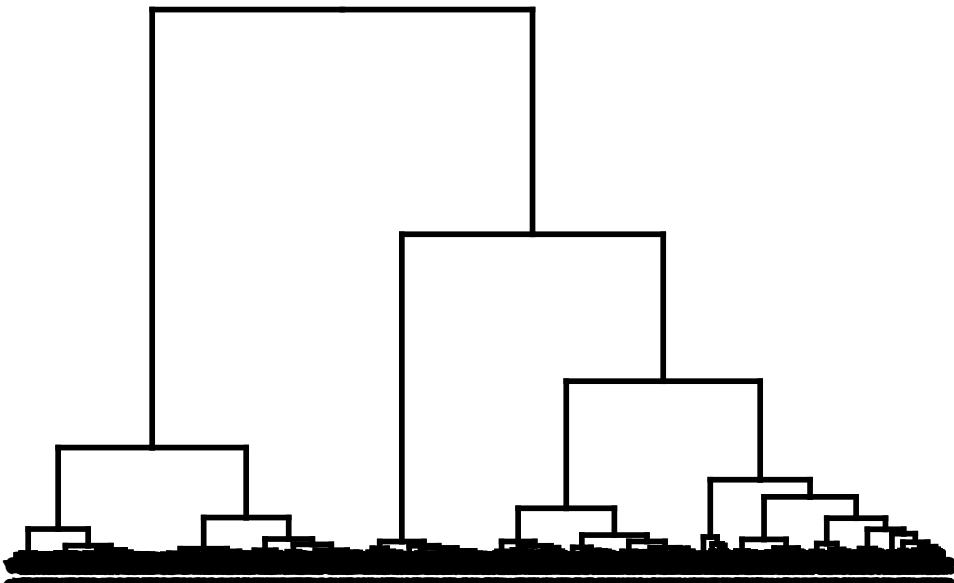
```
To suppress this message use: suppressPackageStartupMessages(library(dendextend))  
-----
```

```
Attaching package: 'dendextend'
```

```
The following object is masked from 'package:stats':
```

```
cutree
```

```
D=as.dist(sqrt(1-Sim_MSA_mDAG^2))  
hc=hclust(as.dist(D),method ="ward.D")  
ggplot(as.ggdend(as.dendrogram(hc)))
```



```
clust4=cutree(hc,4)
table(clust4,meta_taxo$Kingdom)
```

	Animals	Fungi	Plants	Protists
1	195	0	0	0
2	9	154	14	56
3	331	0	0	0
4	0	0	125	0

6.1 Heatmap Similarity Mun_MSA method

```
dff<-meta_taxo %>% select(Kingdom) %>% as.data.frame()
#str(dff)

colores <- list(Kingdom= c("Animals"="purple","Plants"="green","Fungi"="yellow","Protists"="blue"))

anotacion <- HeatmapAnnotation(df=dff, col = colores)

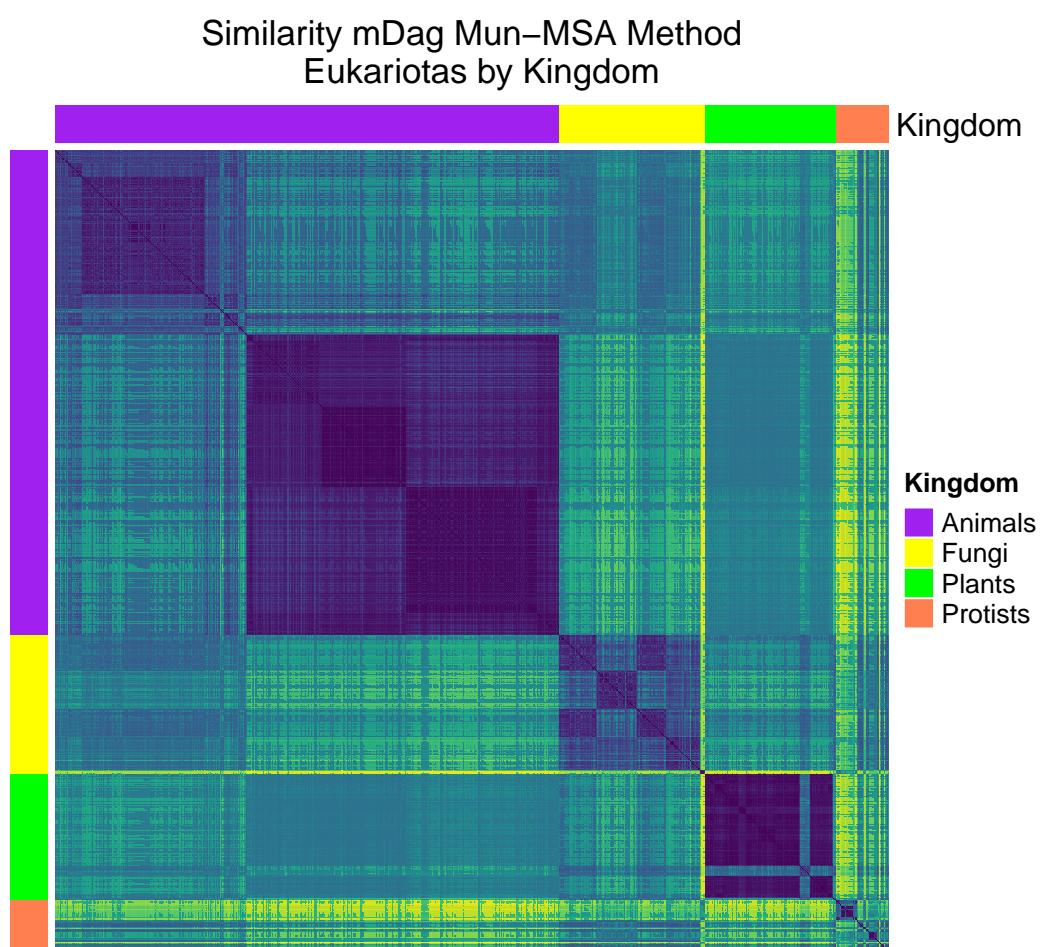
S=Sim_Mun_MSA_mDAG
a<- Heatmap(matrix = Sim_Mun_MSA_mDAG,
            column_title="Similarity mDag Mun-MSA Method\n Eukariotas by Kingdom")
```

```

        name = "Kingdom",
        heatmap_legend_param = list(
at = c(0.4,0.5,0.6,0.7,0.8,0.9,1)),
        col=rev(viridis(256)),
        cluster_rows = FALSE,
        cluster_columns = FALSE,
        top_annotation = anotacion,
        show_column_names = FALSE,
        show_row_names = FALSE,
        left_annotation = rowAnnotation(df = dff, col = colores,show_annotation_name=FALSE)

draw(a, merge_legend = TRUE)

```



```

meta_animals= meta_taxo %>% filter(Kingdom=="Animals")
nombres=unique(meta_animals$Phylum)
aux_order=table(meta_animals$Phylum)
dff<-meta_taxo %>% filter(Kingdom=="Animals") %>% select(Class) %>% as.data.frame()
#str(dff)
nombres=unique(dff$Class)
col=rainbow(length(nombres))
colores=list(Class=col)
names(colores$Class)=nombres
#paste0(paste0('"' ,nombres,''" ,col,'"' ),collapse=",")
# colores <- list(Class=c(
# "Amphibians"="#FF0000", "Annelids"="#FF4900",
# "Cartilaginous"="#FF9200", "Cephalochordates"="#FFDB00",
# "Chelicerates"="#DBFF00", "Cnidarians"="#92FF00",
# "Crustaceans"="#49FF00", "Echinoderms"="#00FF00",
# "Fishes"="#00FF49", "Flatworms"="#00FF92",
# "Hemichordates"="#00FFDB", "Insects"="#00DBFF",
# "Mammals"="#0092FF", "Mollusks"="#0049FF",
# "Nematodes"="#0000FF", "Placozoans"="#4900FF",
# "Poriferans"="#9200FF",
# "Reptiles"="#DB00FF",
# "Tunicates"="#FF00DB",
# "Mammals"="#FF0092",
# "Reptiles"="#FF0049"))
# aux=names(colores$Class)
# colores$Class=as.character(palette.colors(n=21,palette="Polychrome 36"))
# attr(colores$Class,"names")=aux

anotacion <- HeatmapAnnotation(df=dff, col = colores)

a2<- Heatmap(matrix = S[1:535,1:535],
             column_title="Distance mDag Mun_MSA Method\n Animals by Class",
             name = "Class",
             heatmap_legend_param = list(
at = seq(0,1.5,by=0.1)),
col=rev(viridis(256)),
cluster_rows = FALSE,
cluster_columns = FALSE,
top_annotation = anotacion,

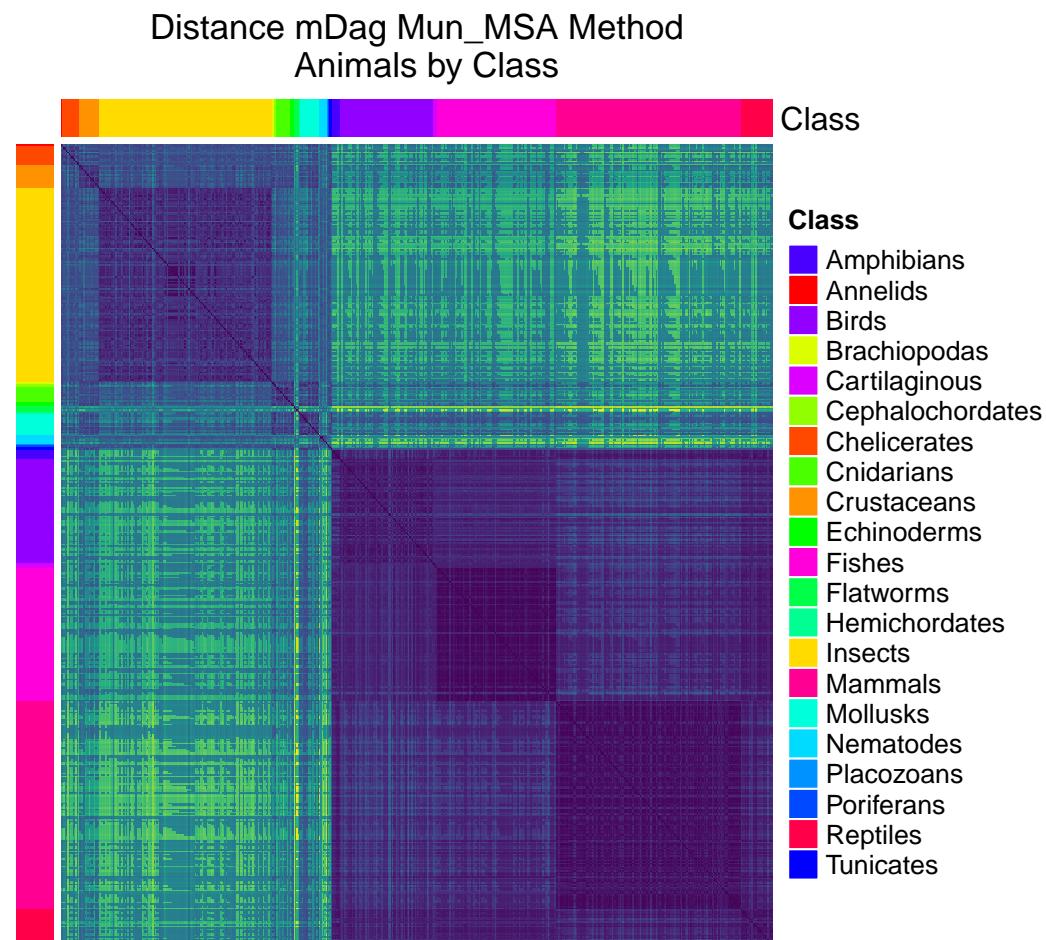
```

```

show_column_names = FALSE,
show_row_names = FALSE,
left_annotation = rowAnnotation(df = df, col = colores, show_annotation_name=FALSE)

draw(a2, merge_legend = TRUE)

```



6.2 MDS (Multidimensional Scaling)

```

## Metric multidimensional scaling (mMDS)
mds7 <- cmdscale(sqrt(1-Sim_Mun_MSA_mDAG^2), k=7, eig=TRUE)
#pairs(mds7$points[,1:4])
mds7$GOF

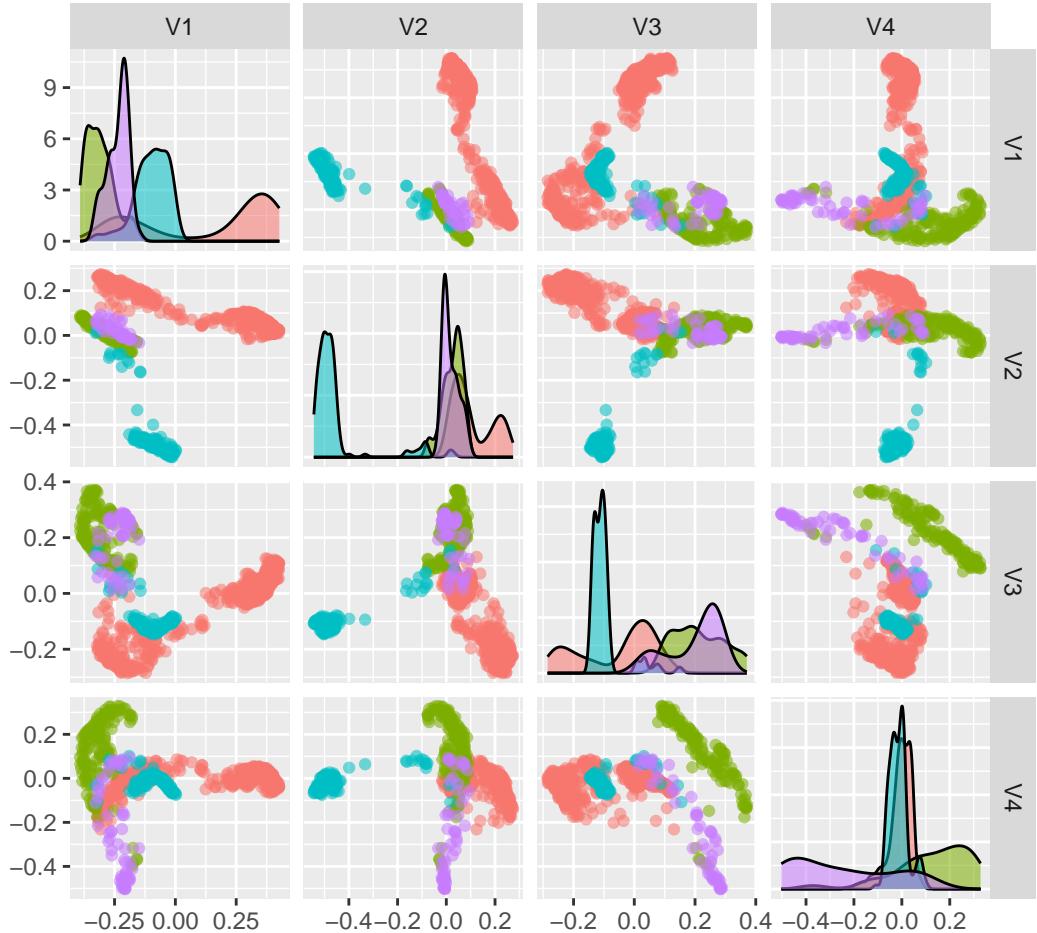
```

```
[1] 0.4464797 0.5474100
```

```
mds <- mds7$points %>% as_tibble()  
colnames(mds) <- paste0("Dim.", 1:dim(mds7$points)[2])
```

```
library(GGally)
```

```
ggpairs(as_tibble(mds7$points), columns=1:4, aes(color=meta_taxo$Kingdom, alpha=0.5), upper=li
```



```
#cmdscale(D, 2, eig=TRUE)$GOF
```

```
# Plot MDS
```

```
#mds <- mds %>%
```

```

# mutate(groups =as.factor(sim0_meta$Kingdom))

mds <- mds %>%
  mutate(groups =as.factor(meta_taxo$Kingdom))

#,text= ~paste("Age:", groups, '<br>Name:')
length(unique(meta_taxo$Phylum))

[1] 33

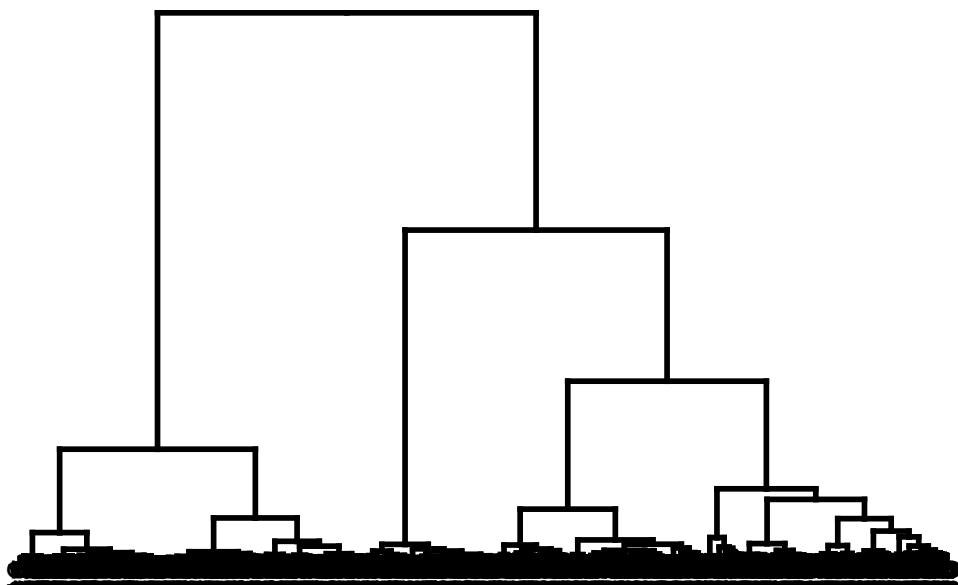
#col_mds=c("purple","green","yellow","coral")
col_mds=rainbow(33)
#mcol_mds=bremer.pal(7,"Greens")

fig <-
plot_ly(
  mds, x = ~Dim.1, y = ~Dim.2,
  color = ~groups,
  colors= col_mds
) %>%
  layout(
    xaxis = list(autorange=2,
      range=c(-0.8,0.8)), yaxis = list(autorange=2,
      range=c(-0.8,0.8)))
#fig

```

7 Hierarchical cluster

```
library(dendextend)
D=as.dist(sqrt(1-Sim_Mun_MSA_mDAG^2))
hc=hclust(as.dist(D),method ="ward.D")
ggplot(as.ggdend(as.dendrogram(hc)))
```



```
clust4=cutree(hc,4)
table(clust4,meta_taxo$Kingdom)
```

clust4	Animals	Fungi	Plants	Protists
1	197	0	0	0
2	7	154	14	56
3	331	0	0	0
4	0	0	125	0

8 Load data graphs

8.1 Read all graphs from a level of the experiment

Read all graphs from a level from experiment; for example individuals. We read only first (alphabetic) two graph

```
path_exp="data/results_ff15c187-62e7-37c2-96a7-c824f7eab671/data/"
list_names=dir(paste0(path_exp,"Individuals/"))
list_names

[1] "0000_RefPw" "aaf"      "aag"      "aalb"     "aali"
[6] "aalt"       "aam"      "aamp"     "aang"     "aara"
[11] "abe"        "abp"      "abv"      "acan"     "acar"
[16] "acep"       "acer"     "achc"     "ache"     "achl"
[21] "acoz"       "acs"      "act"      "acun"     "acyg"
[26] "adf"        "adl"      "adu"      "aec"      "afm"
[31] "afor"       "aful"     "afv"      "afz"      "aga"
[36] "agb"        "agen"     "agif"     "ago"      "agrg"
[41] "ags"        "ahf"      "aip"      "ajc"      "aje"
[46] "ajm"        "aju"      "alab"     "alat"     "alim"
[51] "aluc"       "aly"      "ame"      "amer"    "amex"
[56] "amil"       "amj"      "aml"      "ang"      "ani"
[61] "anu"        "aoce"     "aof"      "aor"      "apan"
[66] "api"        "apla"     "aplcl"    "apln"     "aprc"
[71] "apro"       "apuu"     "aqu"      "arow"     "arut"
[76] "asn"        "aste"     "atd"      "aten"     "ath"
[81] "atr"        "ats"      "avit"     "bacu"     "bany"
[86] "bbel"       "bbif"     "bbig"     "bbis"     "bbo"
[91] "bbrx"       "bbub"     "bbuf"     "bcom"     "bcoo"
[96] "bdi"        "beq"      "bfo"      "bfu"      "bgar"
[101] "bgh"       "bgt"      "bhj"      "bim"      "biu"
[106] "bman"      "bmic"     "bmor"     "bmy"      "bna"
[111] "bnn"        "bod"      "boe"      "bom"      "bor"
[116] "bpec"      "bpge"     "bpyo"     "brhi"     "brp"
```

[121]	"bsc"	"bspl"	"bta"	"btab"	"btax"
[126]	"bter"	"bvan"	"bvg"	"bvk"	"bze"
[131]	"cabi"	"cal"	"cam"	"cang"	"cann"
[136]	"caty"	"caua"	"caur"	"cbai"	"cbr"
[141]	"cbrc"	"ccad"	"ccae"	"ccaj"	"ccal"
[146]	"ccan"	"ccar"	"ccat"	"ccav"	"cci"
[151]	"ccin"	"cclu"	"ccp"	"ccrc"	"ccri"
[156]	"ccw"	"cdk"	"cdv"	"cel"	"cfa"
[161]	"cfel"	"cfj"	"cfo"	"cfr"	"cge"
[166]	"cgi"	"cgib"	"cgig"	"cglo"	"cgob"
[171]	"cgr"	"chig"	"cho"	"chx"	"cic"
[176]	"cide"	"cill"	"cim"	"cimi"	"cin"
[181]	"cins"	"cit"	"cjc"	"cjo"	"clec"
[186]	"clu"	"clud"	"clup"	"clus"	"clv"
[191]	"cmac"	"cmax"	"cme"	"cmk"	"cmo"
[196]	"cmos"	"cmt"	"cmy"	"cnb"	"cne"
[201]	"cng"	"cns"	"cot"	"cpap"	"cpea"
[206]	"cpep"	"cpic"	"cpii"	"cpla"	"cpoc"
[211]	"cpoo"	"cpuf"	"cpv"	"cpw"	"cqi"
[216]	"cqu"	"crb"	"cre"	"crg"	"csab"
[221]	"csat"	"cscu"	"csec"	"csem"	"cset"
[226]	"csin"	"csl"	"csol"	"csti"	"csv"
[231]	"csyr"	"cten"	"cthr"	"ctig"	"ctp"
[236]	"ctul"	"cuca"	"cud"	"cvf"	"cvg"
[241]	"cvr"	"dam"	"dan"	"daz"	"dci"
[246]	"dcr"	"dct"	"ddi"	"der"	"dfa"
[251]	"dfr"	"dgr"	"dgt"	"dha"	"dhe"
[256]	"dle"	"dme"	"dmk"	"dmn"	"dmo"
[261]	"dne"	"dnm"	"dnv"	"dnx"	"dord"
[266]	"dosa"	"dpa"	"dpe"	"dpl"	"dpo"
[271]	"dpol"	"dpp"	"dpte"	"dpub"	"dpox"
[276]	"dpz"	"dqu"	"dre"	"dro"	"dse"
[281]	"dsi"	"dsm"	"dsp"	"dsq"	"dsr"
[286]	"dsv"	"dvi"	"dwi"	"dya"	"dzi"
[291]	"eaf"	"eai"	"ecad"	"ecb"	"ecra"
[296]	"ecu"	"edi"	"eee"	"efo"	"egl"
[301]	"egr"	"egt"	"egu"	"egz"	"ehe"
[306]	"ehi"	"ehs"	"ehx"	"ein"	"eiv"
[311]	"eju"	"ela"	"elk"	"els"	"ely"
[316]	"epa"	"epz"	"erc"	"ero"	"esn"
[321]	"esp"	"etf"	"etl"	"eus"	"fab"
[326]	"fas"	"fca"	"fcd"	"fch"	"fcy"
[331]	"fex"	"ffu"	"fga"	"fgr"	"fme"

[336]	"foc"	"fox"	"fpg"	"fpu"	"fve"
[341]	"fvr"	"gab"	"gae"	"gaf"	"gas"
[346]	"gat"	"gcl"	"gfr"	"gga"	"ggn"
[351]	"ggo"	"ghi"	"gja"	"gla"	"glz"
[356]	"gmu"	"gmx"	"gra"	"gsj"	"gsl"
[361]	"gste"	"gtr"	"gtt"	"gvr"	"hai"
[366]	"hald"	"hame"	"han"	"haw"	"hazt"
[371]	"hbr"	"hcg"	"hcq"	"hgl"	"hhal"
[376]	"hhip"	"hhv"	"hir"	"his"	"hle"
[381]	"hmg"	"hmh"	"hrf"	"hrj"	"hro"
[386]	"hsa"	"hsp"	"hst"	"hze"	"ini"
[391]	"ipu"	"isc"	"itr"	"jcu"	"jre"
[396]	"kaf"	"kla"	"kmr"	"kmx"	"kng"
[401]	"lak"	"lang"	"lav"	"lbc"	"lbd"
[406]	"lbz"	"lcat"	"lcf"	"lcm"	"lco"
[411]	"lcq"	"ldc"	"ldi"	"ldo"	"lel"
[416]	"lgi"	"lht"	"lhu"	"lif"	"lja"
[421]	"llv"	"lma"	"lmi"	"loa"	"loc"
[426]	"lpan"	"lper"	"lpol"	"lruf"	"lsm"
[431]	"lsq"	"lsr"	"lsv"	"lth"	"lve"
[436]	"lww"	"maj"	"malb"	"mamb"	"masi"
[441]	"maua"	"maw"	"mbe"	"mbr"	"mcaf"
[446]	"mcal"	"mcc"	"mcep"	"mcf"	"mcha"
[451]	"mcoc"	"mde"	"mdl"	"mdm"	"mdo"
[456]	"mesc"	"mfot"	"mgen"	"mgl"	"mgp"
[461]	"mgr"	"minc"	"ming"	"mis"	"mjv"
[466]	"mleu"	"mlf"	"mlr"	"mlx"	"mmer"
[471]	"mmf"	"mmu"	"mmur"	"mmyo"	"mna"
[476]	"mnb"	"mng"	"mni"	"mnt"	"more"
[481]	"morg"	"mpah"	"mpah"	"mpp"	"mpr"
[486]	"mpuf"	"mrr"	"mrt"	"mrw"	"msam"
[491]	"msex"	"msym"	"mthb"	"mtm"	"mtr"
[496]	"mui"	"mun"	"mus"	"myb"	"myd"
[501]	"myi"	"mze"	"nai"	"nasi"	"nau"
[506]	"ncar"	"ncc"	"nce"	"ncol"	"ncr"
[511]	"ncs"	"ndi"	"nfi"	"nfu"	"ngd"
[516]	"ngi"	"ngr"	"nhe"	"niq"	"nle"
[521]	"nlu"	"nmea"	"nmel"	"nni"	"nnt"
[526]	"nnu"	"npa"	"npd"	"npr"	"npt"
[531]	"nsu"	"nsy"	"nta"	"nte"	"nto"
[536]	"nve"	"nvi"	"nvl"	"nvs"	"nwh"
[541]	"oaa"	"oas"	"oau"	"obb"	"obi"
[546]	"obo"	"obr"	"oci"	"oda"	"oeu"

[551]	"ofu"	"oga"	"ogl"	"ogo"	"oha"
[556]	"ola"	"olu"	"oml"	"omy"	"one"
[561]	"onl"	"oor"	"opa"	"opi"	"oro"
[566]	"osa"	"osn"	"ota"	"otc"	"otu"
[571]	"otw"	"ovi"	"padl"	"pale"	"palz"
[576]	"pan"	"panu"	"pavi"	"pbar"	"pbe"
[581]	"pbg"	"pbi"	"pbl"	"pbn"	"pbx"
[586]	"pcad"	"pcan"	"pcao"	"pcb"	"pcf"
[591]	"pchn"	"pcln"	"pco"	"pcoc"	"pcoo"
[596]	"pcoq"	"pcri"	"pcs"	"pcub"	"pcw"
[601]	"pcy"	"pda"	"pdam"	"pdic"	"pdp"
[606]	"pdul"	"peq"	"peu"	"pfa"	"pdf"
[611]	"pfh"	"pfj"	"pflv"	"pfor"	"pfp"
[616]	"pfuc"	"pfy"	"pgab"	"pgc"	"pgig"
[621]	"pgr"	"pgu"	"pgut"	"pguu"	"phai"
[626]	"phas"	"phi"	"phu"	"phyp"	"pic"
[631]	"pif"	"pja"	"pki"	"pkl"	"pkn"
[636]	"pkz"	"plai"	"plep"	"plet"	"pleu"
[641]	"plj"	"plop"	"pmac"	"pmaj"	"pmax"
[646]	"pmei"	"pmoa"	"pmoo"	"pmua"	"pmum"
[651]	"pmur"	"pnap"	"pno"	"pon"	"pop"
[656]	"pov"	"ppa"	"ppad"	"ppei"	"pper"
[661]	"ppl"	"ppoi"	"ppot"	"ppp"	"pprm"
[666]	"pps"	"ppug"	"ppyr"	"prap"	"prei"
[671]	"pret"	"prob"	"pruf"	"psat"	"psco"
[676]	"psex"	"psiu"	"psoj"	"psom"	"pspa"
[681]	"psq"	"pss"	"pte"	"pteh"	"ptep"
[686]	"ptg"	"pti"	"ptkz"	"ptm"	"ptr"
[691]	"ptru"	"puc"	"pvir"	"pvm"	"pvp"
[696]	"pvt"	"pvu"	"pvv"	"pxv"	"pvy"
[701]	"pxb"	"pxu"	"pxy"	"pyo"	"pyu"
[706]	"qlo"	"qsu"	"ray"	"rbb"	"rcn"
[711]	"rcu"	"rfq"	"rmd"	"rmp"	"rno"
[716]	"rro"	"rsan"	"rsz"	"rtem"	"rtp"
[721]	"rze"	"salp"	"sanh"	"sapo"	"sara"
[726]	"sasa"	"sbi"	"sbq"	"scac"	"scam"
[731]	"scan"	"sce"	"schu"	"sclv"	"scm"
[736]	"sdm"	"sdu"	"seub"	"sfm"	"sgf"
[741]	"sgre"	"shab"	"shon"	"shr"	"shs"
[746]	"shx"	"sind"	"sita"	"sko"	"sla"
[751]	"slal"	"slb"	"sliu"	"sluc"	"slud"
[756]	"sly"	"smeo"	"smin"	"smm"	"smo"
[761]	"smp"	"snh"	"soc"	"soe"	"sot"

```

[766] "soy"      "spaa"      "spao"      "spar"      "spen"
[771] "spis"      "spo"       "spu"       "sre"       "srx"
[776] "ssc"       "ssck"      "sscv"      "ssen"      "ssl"
[781] "sspl"      "sstn"      "stow"      "stru"      "sund"
[786] "svg"       "svs"       "tad"       "taes"      "tala"
[791] "tan"       "tasa"      "tbg"       "tbl"       "tbr"
[796] "tca"       "tcc"       "tcr"       "tdc"       "tdl"
[801] "teo"       "tet"       "tfd"       "tfn"       "tgb"
[806] "tge"       "tgo"       "tgt"       "tgu"       "thj"
[811] "tmf"       "tml"       "tmn"       "tms"       "tmu"
[816] "tng"       "tnl"       "tod"       "tot"       "tpai"
[821] "tpal"      "tpf"       "tpra"      "tpre"      "tps"
[826] "tpv"       "tre"       "trg"       "trr"       "tru"
[831] "tsp"       "tsr"       "tss"       "tst"       "ttt"
[836] "tua"       "tup"       "tut"       "tva"       "tve"
[841] "tvs"       "twl"       "uah"       "uar"       "uma"
[846] "umr"       "ure"       "val"       "var"       "vcn"
[851] "vda"       "vde"       "vem"       "vja"       "vko"
[856] "vlg"       "vpc"       "vpo"       "vps"       "vra"
[861] "vri"       "vun"       "vvi"       "vvp"       "wic"
[866] "wse"       "xco"       "xen"       "xgl"       "xhe"
[871] "xla"       "xma"       "xtr"       "yli"       "zab"
[876] "zca"       "zce"       "zju"       "zma"       "zmk"
[881] "zne"       "zof"       "zro"       "ztr"       "zvi"

```

```

list_names= list_names[-1] # filter 0000_RefPw
length(list_names)

```

```
[1] 884
```

```

k=length(list_names)
list_names= list_names[1:k] # select ONLY 5 individuals
list_names

```

```

[1] "aaf"   "aag"   "aalb"  "aali"  "aalt"  "aam"   "aamp"  "aang"  "aara"  "abe"
[11] "abp"   "abv"   "acan"  "acar"  "acep"  "acer"  "achc"  "ache"  "achl"  "acozi"
[21] "acs"   "act"   "acun"  "acyg"  "adf"   "adl"   "adu"   "aec"   "afm"   "afor"
[31] "aful"  "afv"   "afz"   "aga"   "agb"   "agen"  "agif"  "ago"   "agrg"  "ags"
[41] "ahf"   "aip"   "ajc"   "aje"   "ajm"   "aju"   "alab"  "alat"  "alim"  "aluc"
[51] "aly"   "ame"   "amer"  "amex"  "amil"  "amj"   "aml"   "ang"   "ani"   "anu"

```

```

[61] "aoce" "aof" "aor" "apan" "api" "apla" "aplcl" "apln" "aprc" "apro"
[71] "apuu" "aqu" "arow" "arut" "asn" "aste" "atd" "aten" "ath" "atr"
[81] "ats" "avit" "bacu" "bany" "bbel" "bbif" "bbig" "bbis" "bbo" "bbrx"
[91] "bbub" "bbuf" "bcom" "bcoo" "bdi" "beq" "bfo" "bfu" "bgar" "bgh"
[101] "bgt" "bhj" "bim" "biu" "bman" "bmic" "bmor" "bmy" "bna" "bnn"
[111] "bod" "boe" "bom" "bor" "bpec" "bpg" "bpyo" "brhi" "brp" "bsc"
[121] "bspl" "bta" "btab" "btax" "bter" "bvan" "bvg" "bvk" "bze" "cabi"
[131] "cal" "cam" "cang" "cann" "caty" "caua" "caur" "cbai" "cbr" "cbrc"
[141] "ccad" "ccae" "ccaj" "ccal" "ccan" "ccar" "ccat" "ccav" "cci" "ccin"
[151] "cclu" "ccp" "ccrc" "ccri" "ccw" "cdk" "cdu" "cel" "cfa" "cfel"
[161] "cfj" "cfo" "cfr" "cge" "cgi" "cgib" "cgig" "cglo" "cgob" "cgr"
[171] "chig" "cho" "chx" "cic" "cide" "cill" "cim" "cimi" "cin" "cins"
[181] "cit" "cjc" "cjo" "clec" "clu" "clud" "clup" "clus" "clv" "cmac"
[191] "cmax" "cme" "cmk" "cmo" "cmos" "cmt" "cmy" "cnb" "cne" "cng"
[201] "cns" "cot" "cpap" "cpea" "cpep" "cpic" "cipi" "cpla" "cpoc" "cpoo"
[211] "cput" "cpv" "cpw" "cqj" "cqu" "crb" "cre" "crg" "csab" "csat"
[221] "cscu" "csec" "csem" "cset" "csin" "csil" "csol" "csti" "csv" "csyr"
[231] "cten" "cthr" "ctig" "ctp" "ctul" "cuca" "cud" "cvf" "cvg" "cvr"
[241] "dam" "dan" "daz" "dci" "dcr" "dct" "ddi" "der" "dfa" "dfr"
[251] "dgr" "dgt" "dha" "dhe" "dle" "dme" "dmk" "dmn" "dmo" "dne"
[261] "dnm" "dnv" "dnx" "dord" "dosa" "dpa" "dpe" "dpl" "dpo" "dpol"
[271] "dpp" "dpte" "dpub" "dpx" "dpz" "dqu" "dre" "dro" "dse" "dsi"
[281] "dsm" "dsp" "dsq" "dsr" "dsv" "dvi" "dwi" "dya" "dzi" "eaf"
[291] "eai" "ecad" "ecb" "ecra" "ecu" "edi" "eee" "efo" "egl" "egr"
[301] "egt" "egu" "egz" "ehe" "ehi" "ehs" "ehx" "ein" "eiv" "eju"
[311] "ela" "elk" "els" "ely" "epa" "epz" "erc" "ero" "esn" "esp"
[321] "etf" "etl" "eus" "fab" "fas" "fca" "fcd" "fch" "fcy" "fex"
[331] "ffu" "fga" "fgr" "fme" "foc" "fox" "fpg" "fpu" "fve" "fvr"
[341] "gab" "gae" "gaf" "gas" "gat" "gcl" "gfr" "gga" "ggn" "ggo"
[351] "ghi" "gja" "gla" "glz" "gmu" "gmx" "gra" "gsj" "gsl" "gste"
[361] "gtr" "gtt" "gvr" "hai" "hald" "hame" "han" "haw" "hazt" "hbr"
[371] "hcg" "hcq" "hgl" "hhal" "hhip" "hhv" "hir" "his" "hle" "hmg"
[381] "hmh" "hrf" "hrj" "hro" "hsa" "hsp" "hst" "hze" "ini" "ipu"
[391] "isc" "itr" "jcu" "jre" "kaf" "kla" "kmr" "kmx" "kng" "lak"
[401] "lang" "lav" "lbc" "lbd" "lbz" "lcat" "lcf" "lcm" "lco" "lcq"
[411] "ldc" "ldi" "ldo" "lel" "lgj" "lht" "lhu" "lif" "lja" "llv"
[421] "lma" "lmi" "loa" "loc" "lpan" "lper" "lpol" "lruf" "lsm" "lsq"
[431] "lsr" "lsv" "lth" "lve" "lw" "maj" "malb" "mamb" "masi" "maua"
[441] "maw" "mbe" "mbr" "mcraf" "mcal" "mcc" "mcep" "mcf" "mcha" "mcoc"
[451] "mde" "mdl" "mdm" "mdo" "mesc" "mfot" "mgen" "mgl" "mpg" "mgr"
[461] "minc" "ming" "mis" "mjv" "mleu" "mlf" "mlr" "mlx" "mmer" "mmf"
[471] "mmu" "mmur" "mmyo" "mna" "mnb" "mng" "mni" "mnt" "more" "morg"
[481] "mpah" "mpah" "mpp" "mpr" "mpuf" "mrr" "mrt" "mrw" "msam" "msex"

```

```

[491] "msym"  "mthb"  "mtm"   "mtr"   "mui"   "mun"   "mus"    "myb"   "myd"   "myi"
[501] "mze"   "nai"   "nasi"  "nau"   "ncar"  "ncc"   "nce"    "ncol"  "ncr"   "ncs"
[511] "ndi"   "nfi"   "nfu"   "ngd"   "ngi"   "ngr"   "nhe"    "niq"   "nle"   "nlu"
[521] "nmea"  "nmel"  "nni"   "nnt"   "nnu"   "npa"   "npd"    "npr"   "npt"   "nsu"
[531] "nsy"   "nta"   "nte"   "nto"   "nve"   "nvi"   "nvl"    "nvs"   "nwh"   "oaa"
[541] "oas"   "oau"   "obb"   "obi"   "obo"   "obr"   "ocu"    "oda"   "oeu"   "ofu"
[551] "oga"   "ogl"   "ogo"   "oha"   "ola"   "olu"   "oml"    "omy"   "one"   "onl"
[561] "oor"   "opa"   "opi"   "oro"   "osa"   "osn"   "ota"    "otc"   "otu"   "otw"
[571] "ovi"   "padl"  "pale"  "palz"  "pan"   "panu"  "pavi"   "pbar"  "pbe"   "pbg"
[581] "pbi"   "pbl"   "pbn"   "pbx"   "pcad"  "pcan"  "pcao"   "pcb"   "pcf"   "pchn"
[591] "pcl"   "pco"   "pcoc"  "pcoo"  "pcq"   "pcri"  "pcs"    "pcub"  "pcw"   "pcy"
[601] "pda"   "pdam"  "pdic"  "pdp"   "pdul"  "peq"   "peu"    "pfa"   "pdf"   "pfh"
[611] "pfj"   "pflv"  "pfor"  "pfp"   "pfuc"  "pfy"   "pgab"   "pgc"   "pgig"  "pgr"
[621] "pgu"   "pgut"  "pguu"  "phai"  "phas"  "phi"   "phu"    "phyp"  "pic"   "pif"
[631] "pja"   "pki"   "pkl"   "pkn"   "pkz"   "plai"  "plep"   "plet"   "pleu"  "plj"
[641] "plop"  "pmac"  "pmaj"  "pmax"  "pmei"  "pmoa"  "pmoo"   "pmua"  "pmum"  "pmur"
[651] "pnap"  "pno"   "pon"   "pop"   "pov"   "ppa"   "ppad"   "ppei"  "pper"  "ppl"
[661] "ppoi"  "ppot"  "ppp"   "pprm"  "pps"   "ppug"  "ppyr"   "prap"  "prei"  "pret"
[671] "prob"  "pruf"  "psat"  "psco"  "psex"  "psiu"  "psoj"   "psom"  "pspa"  "psq"
[681] "pss"   "pte"   "pteh"  "ptep"  "ptg"   "pti"   "ptkz"   "ptm"   "ptr"   "ptru"
[691] "puc"   "pvir"  "pvm"   "pvp"   "pvt"   "pvu"   "pvv"    "pxv"   "pvy"   "pxb"
[701] "pxu"   "pxy"   "pyo"   "pyu"   "qlo"   "qsu"   "ray"    "rbb"   "rcn"   "rcu"
[711] "rfq"   "rmd"   "rmp"   "rno"   "rro"   "rsan"  "rsz"    "rtem"  "rtp"   "rze"
[721] "salp"  "sanh"  "sapo"  "sara"  "sasa"  "sbi"   "sbq"    "scac"  "scam"  "scan"
[731] "sce"   "schu"  "sclv"  "scm"   "sdm"   "sdu"   "seub"   "sfm"   "sgh"   "sgre"
[741] "shab"  "shon"  "shr"   "shs"   "shx"   "sind"  "sita"   "sko"   "sla"   "slal"
[751] "slb"   "sliu"  "sluc"  "slud"  "sly"   "smeo"  "smin"   "smm"   "smo"   "smp"
[761] "snh"   "soc"   "soe"   "sot"   "soy"   "spaa"  "spao"   "spar"   "spen"  "spis"
[771] "spo"   "spu"   "sre"   "srx"   "ssc"   "ssck"  "sscv"   "ssen"  "ssl"   "sspl"
[781] "sstn"  "stow"  "stru"  "sund"  "svg"   "svs"   "tad"    "taes"  "tala"  "tan"
[791] "tasa"  "tbг"   "tbl"   "tbr"   "tca"   "tcc"   "tcr"    "tdc"   "tdl"   "teo"
[801] "tet"   "tfд"   "tfн"   "tgb"   "tge"   "tgo"   "tgt"    "tgu"   "thj"   "tmf"
[811] "tml"   "tmн"  "tms"   "tmу"   "tng"   "tnл"   "tod"    "tot"   "tpai" "tpal"
[821] "tpf"   "tpra"  "tpre"  "tps"   "tpv"   "tre"   "trg"    "trr"   "tru"   "tsp"
[831] "tsr"   "tss"   "tst"   "ttt"   "tua"   "tup"   "tut"    "tva"   "tve"   "tvs"
[841] "twl"   "uah"   "uar"   "uma"   "umr"   "ure"   "val"    "var"   "vcn"   "vda"
[851] "vde"   "vem"   "vja"   "vko"   "vlg"   "vpc"   "vpo"    "vps"   "vra"   "vri"
[861] "vun"   "vvi"   "vvp"   "wic"   "wse"   "xco"   "xen"    "xgl"   "xhe"   "xla"
[871] "xma"   "xtr"   "yli"   "zab"   "zca"   "zce"   "zju"    "zma"   "zmк"   "zne"
[881] "zof"   "zro"   "ztr"   "zvi"

```

```
dir(paste0("Individuals/",list_names[1],"/"))
```

```
character(0)
```

```
library(igraph)
```

```
Attaching package: 'igraph'
```

```
The following objects are masked from 'package:stats':
```

```
decompose, spectrum
```

```
The following object is masked from 'package:base':
```

```
union
```

```
graphs_list=paste0(path_exp,"Individuals/",list_names,"/",list_names,"_MDAG.graphml")
g_MDAG_list=
lapply(graphs_list,FUN=function(x) read.graph(file=x,
format="graphml"))
names(g_MDAG_list)=list_names
summary(g_MDAG_list[[1]])
```

```
IGRAPH bd45686 D--- 534 477 --
+ attr: color (v/c), label (v/c), id (v/c), id (e/c)
```

```
head(as_long_data_frame(g_MDAG_list[[1]]))
```

	from	to	id	from_color	from_label	from_id
1	2	1	2431x1532	yellow	2431\\nR07762\\n2.3.1.179	2431
2	3	2	0.0.237x2431	gray	MBB\\n0.0.237	0.0.237
3	4	3	0.0.752x0.0.237	yellow	0.0.752\\nR04968\\n2.3.1.179	0.0.752
4	5	4	0.0.238x0.0.752	gray	MBB\\n0.0.238	0.0.238
5	6	5	0.0.753x0.0.238	yellow	0.0.753\\nR04726\\n2.3.1.179	0.0.753
6	7	6	0.0.239x0.0.753	gray	MBB\\n0.0.239	0.0.239

	to_color	to_label	to_id