

# Package: CoFRA (via r-universe)

September 10, 2024

**Title** Complete Functional Regulation Analysis

**Version** 0.1002

**Description** Calculates complete functional regulation analysis and visualize the results in a single heatmap. The provided example data is for biological data but the methodology can be used for large data sets to compare quantitative entities that can be grouped. For example, a store might divide entities into cloth, food, car products etc and want to see how sales changes in the groups after some event. The theoretical background for the calculations are provided in New insights into functional regulation in MS-based drug profiling, Ana Sofia Carvalho, Henrik Molina & Rune Matthiesen, Scientific Reports <doi:10.1038/srep18826>.

**Depends** R (>= 3.2.3)

**Imports** gplots, grid, methods, parallel, stats, stringr

**License** GPL-2 | file LICENSE

**LazyData** true

**RoxygenNote** 5.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** https://ruma1974.r-universe.dev

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completeFunctionalRegulationAnalysis

*This function performs complete functional regulation analysis*

---

### Description

This function performs complete functional regulation analysis

### Usage

```
completeFunctionalRegulationAnalysis(dfPro, func, Fac, dfComp,
  NbackGround = length(unique(unlist(func))), DataExtract = "FDR",
  minCounts = 10, Test = "t.test", no_cores = -1)
```

### Arguments

dfPro	data frame with quantitative values
func	data frame defining which gene ontology to use "BP","CC","MF"
Fac	factor describing the sample groups
dfComp	df containing the comparisons to perform
NbackGround	integer number of total proteins
DataExtract	string which P value correction to use
minCounts	integer minimum number of matching genes for functional category
Test	"t.test" or "wilcox.test"
no_cores	=-1 (no parallele execution) =0 (number of availble cores -1) >0 (use number of cores)

**Examples**

```
library(CoFRA)
data(iBAQ)
Fac=factor(c("MCCTT", "MCCTT", "MCCTT", "MCCT", "MCCT", "MCCT", "MC", "MC", "MC", "MCT", "MCT", "MCT",
"MTT", "MTT", "MTT", "MT", "MT", "MT", "sN", "sN", "sN", "sNT", "sNT", "sNT", "sNT", "iN", "iN", "iN", "iNT", "iNT", "iNT"))
dfComp=data.frame(Con=c("MCCTT", "MT", "MC", "iN", "sN", "AllC,MCCT,MT,MC,iN,sN"),Tre=c("MCCTT", "MTT",
"MCT", "iNT", "sNT", "AllT,MCCTT,MTT,MCT,iNT,sNT"))
Func=CoFRA::getFunctionalCategories("CC")
head(str(Func))
CC1=CoFRA::completeFunctionalRegulationAnalysis(iBAQ,Func[100:200],Fac,dfComp,NbackGround=142140)
```

---

filterData

*This function filter a data frame on column named "pro"*


---

**Description**

This function filter a data frame on column named "pro"

**Usage**

```
filterData(dfPro, filter)
```

**Arguments**

dfPro	data frame with iBAQ values
filter	character vector with items to remove

**Examples**

```
library(CoFRA)
data(iBAQ)
iBAQ2=filterData(iBAQ,">CON") # filter headers starting with >CON
```

---

getFunctionalCategories

*get named vector with functional categories*


---

**Description**

get named vector with functional categories

**Usage**

```
getFunctionalCategories(func = "CC")
```

**Arguments**

func                    string ("BP","CC","MF")

**Examples**

```
library(CoFRA)
Acc=getFunctionalCategories(func="CC")
```

---

HeatMapEnrichment        *This function plot a heatmap to summarize the results from complete functional enrichment analysis*

---

**Description**

This function plot a heatmap to summarize the results from complete functional enrichment analysis

**Usage**

```
HeatMapEnrichment(Eres, title = "")
```

**Arguments**

Eres                    object from complete functional enrichment analysis  
title                    string

---

iBAQ                    *data frame containing iBAQ values*

---

**Description**

A dataset containing iBAQ values for identified proteins

**Usage**

```
iBAQ
```

**Format**

A data frame with 18889 rows and 33 variables:

**MCCTT1** iBAQ values

**MCCTT2** iBAQ values

**MCCTT3** iBAQ values

**MCCT1** iBAQ values

**MCCT2** iBAQ values  
**MCCT3** iBAQ values  
**MC1** iBAQ values  
**MC2** iBAQ values  
**MC3** iBAQ values  
**MCT1** iBAQ values  
**MCT2** iBAQ values  
**MCT3** iBAQ values  
**MTT1** iBAQ values  
**MTT2** iBAQ values  
**MTT3** iBAQ values  
**MT1** iBAQ values  
**MT2** iBAQ values  
**MT3** iBAQ values  
**sN1** iBAQ values  
**sN2** iBAQ values  
**sN3** iBAQ values  
**sNT1** iBAQ values  
**sNT2** iBAQ values  
**sNT3** iBAQ values  
**iN1** iBAQ values  
**iN2** iBAQ values  
**iN3** iBAQ values  
**iNT1** iBAQ values  
**iNT2** iBAQ values  
**iNT3** iBAQ values  
**pro** FASTA header  
**E** Evidence groups  
**FDR** False Discovery Rate ...

---

plot.CompleteEnrichment

*This function plot a heatmap to summarize the results from complete functional enrichment analysis*

---

### Description

This function plot a heatmap to summarize the results from complete functional enrichment analysis

### Usage

```
## S3 method for class 'CompleteEnrichment'  
plot(x, ...)
```

### Arguments

x                    object from complete functional enrichment analysis  
...                   list of additional arguments

---

summary.CompleteEnrichment

*This function summarize and print the results from complete functional enrichment analysis*

---

### Description

This function summarize and print the results from complete functional enrichment analysis

### Usage

```
## S3 method for class 'CompleteEnrichment'  
summary(object, ...)
```

### Arguments

object                object from complete functional enrichment analysis  
...                    list of additional arguments

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