# Package 'CoFRA'

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**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** CRAN

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`completeFunctionalRegulationAnalysis`
*This function performs complete functional regulation analysis*

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## 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 parelle 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","iN","iN","iN","iNT","iNT","iNT"))
dfComp=data.frame(Con=c("MCCT","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 ...

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`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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