Vignette lipidoscore R-package

August 2010 version 0.1.1

Package: lipidoscore

Type: Package

Title: query Pubmed to find lipidic citations in a gene list

Version: 0.1.1

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Description: lipidicscore is a package which allow to query pubmed with a gene list

  in order to find lipidic related citations

License: GNU

Encoding: UTF-8

lipidoquery: a function which allow to query pubmed lipidic citations for gene list

Description

lipidoquery allow to found in Pubmed lipidic citations for a gene list as input parameter

Usage

```
data<-lipidoquery(set$gene)
```

Arguments

x   vector in column of a gene list as input parameter "set$gene" a column of gene symbols in "set" as dataframe

Details

limited to a list containing less than 100 genes

Value

return a table of citations

lipidocompute a function which allow to compute a lipidoscore on each gene after having performed a lipidoquery before

Description

lipidocompute compute a lipidoscore after Pubmed query. This function used result "data" from lipidoquery function as input parameter

Usage

```
final<-lipidocompute(data)
```

Arguments

`data` take "data" result from lipidoquery function as input parameter

Details

remove also genes which have not been found citated in Pubmed

Value

return a compute table of results ranked by decreasing order based on lipidoscore

Author(s) Christophe Desterke

Examples

```
final<-lipidocompute(data)

## The function is currently defined as
function (data)
{
    data <- data.frame(data)
    attach(data)
    data$CitationsGeneInLipides <- with(data,
replace(CitationsGeneInLipides,
        CitationsGeneInLipides == -1, 0))
    subset = data[(data$CitationsGene != "-1"), ]
    lipidoscore = (((subset$CitationsGeneInLipides +
subset$CitationsGene)/subset$CitationsGene) *
        100) - 100
    result <- data.frame(subset, lipidoscore)
    order <- result[with(result, order(-lipidoscore)), ]
    final = order[(order$lipidoscore != "0"), ]
    final
  }
```

lipidoplot draw a scatterplot of lipidoscore versus gene citations in Pubmed and lipidic citations as size of the points

Description

lipidoplot is a function which summarized lipidoscore as a plot which is interactive to identify the gene symbols as labels. It draws a scatterplot (lipidoscore versus citations) with linear model in blue and lowess line in red. Size of the points is proportional to the lipidic citations. Date of the query is also input in the title of the plot.

Usage

```
lipidoplot(final)
```

Arguments

`final` final input parameter is the saved result of the function lipidocompute

Value

return an interactive scatterplot to identify gene symbols as labels

Author(s)

Christophe Desterke

Examples

```
lipidoplot(final)
## The function is currently defined as
function (final)
{
    plot(log(final$CitationsGene, 10), final$lipidoscore, cex =
log(final$CitationsGeneInLipides,
        2), main = paste("Lipidic Citations: ", Sys.time()))
    abline(lm(final$lipidoscore ~ log(final$CitationsGene, 10)),
        col = "blue")
    lines(lowess(log(final$CitationsGene, 10), final$lipidoscore),
        col = "red", lty = 2)
    identify(log(final$CitationsGene, 10), final$lipidoscore,
        labels = row.names(final))
  }
```