Package 'GenRank'

October 16, 2019

Title Candidate gene prioritization based on convergent evidence

Version 1.12.0

Author Chakravarthi Kanduri

Maintainer Chakravarthi Kanduri <chakra.kanduri@gmail.com>

Description Methods for ranking genes based on convergent evidence obtained from multiple independent evidence layers. This package adapts three methods that are popular for meta-analysis.

Depends R (>= 3.2.3)

License Artistic-2.0

biocViews GeneExpression, SNP, CopyNumberVariation, Microarray, Sequencing, Software, Genetics

Suggests knitr, rmarkdown, testthat

Imports matrixStats, reshape2, survcomp

VignetteBuilder knitr

LazyData true

RoxygenNote 5.0.1

URL https://github.com/chakri9/GenRank

BugReports https://github.com/chakri9/GenRank/issues

NeedsCompilation no

git_url https://git.bioconductor.org/packages/GenRank

git_branch RELEASE_3_9

git_last_commit 621099f

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

R topics documented:

CombP *Convergent evidence based on combined p-values.*

Description

CombP returns ranks of the genes based on p-values combined using the famous 'fisher' or 'z-transform' methods.

Usage

```
CombP(file, weight, method = c("fisher", "z.transform", "logit"),
  na.remove = FALSE)
```

Arguments

file	A tab-delimited text file with a minimum of 3 columns. First column should contain gene names, second column should indicate the evidence type and third column should contain non-negative numeric values (p-values).
weight	A numeric vector containing weights of evidence types. For example, sample sizes of various evidence types. If not provided, equal weight is given to all evidence types.
method	A character string among 'fisher', 'z.transform' or 'logit'.
na.remove	An optional argument, defaults to FALSE. Set this argument to TRUE if all the genes were not detected across all evidence types.

Value

If all the inputs are in the correct format as suggested, then the output will be a dataframe containg genes, their combined p-values and corresponding ranks.

Examples

```
cus.weights <- c(100,50,200,300,150,400)
input_file_P <- system.file("extdata","CombP_toydata.txt",package="GenRank")
CP_ranking <- CombP(input_file_P, method = "fisher", na.remove = TRUE)
CP_ranking_z <- CombP(input_file_P, method = "z.transform", na.remove = TRUE, weight = cus.weights)
```

ComputeCE *Convergent Evidence (CE) scores of genes.*

Description

ComputeCE returns ranks of the genes based on CE scores.

Usage

```
ComputeCE(file, PC = c("equal", "ngene", "custom"), cust.weights = NULL)
```

Arguments

file	A tab-delimited text file with a minimum of 2 columns. First column should contain gene names and second column should indicate the evidence type.
PC	A character string among 'equal', 'ngene' or 'custom' indicating the prior credibility.
cust.weights	An optional argument required when the PC='custom'. A numeric vector containing weights reflecting prior credibility. Should contain as many weights as the number of evidence types.

Value

If all the inputs are in the correct format as suggested, then the output will be a dataframe containing genes and their ranks based on CE scores.

Examples

```
input_file <- system.file("extdata","CE_toydata.txt",package="GenRank")
CE_ranks <- ComputeCE(input_file,PC = "equal")
evid.weight <- c(1,1,0.8,0.8,0.5,1)
CE_ranks_cust <- ComputeCE(input_file,PC = "custom", cust.weights = evid.weight)
```

ComputeRP *Convergent evidence based on rank product method.*

Description

ComputeRP returns ranks of the genes based on rank product method.

Usage

```
ComputeRP(file, signif.type, n.perm = 100, setseed = NULL)
```

Arguments

file	A tab-delimited text file with a minimum of 3 columns. First column should contain gene names, second column should indicate the evidence type and third column should contain non-negative numeric values (e.g. p-values or effect size).
signif.type	A vector containing letters 'L' or 'H' or both. Length of the vector should be the same as the number of evidence types. 'L' or 'H' indicate whether the evidence type contains a low numeric value (e.g. p-value) or a high numeric value (e.g. effect size).
n.perm	A number indicating number of permutations used to calculate null density. Defaults to 100 permutations.
setseed	An optional argument. If provided a numeric value, sampling will be put in a reproducible state using the setseed value as seed.

Value

If all the inputs are in the correct format as suggested, then the output will be a dataframe containg genes, their ranks based on RP and corresponding pfp (equivalent to FDR).

Examples

```
input_file <- system.file("extdata","RP_toydata.txt",package="GenRank")
signif.val <- c('L','L','H','L','H','L')
RP_ranks <- ComputeRP(input_file, signif.type = signif.val)
RP_ranks_cust <- ComputeRP(input_file, signif.type = signif.val, n.perm=200, setseed=1234)
```

Index