Package ‘goProfiles’

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goProfiles-package

Performs Gene Ontology based analysis using Functional Profiles.

Description

Performs Gene Ontology based analysis for gene sets or other type of biological identifiers which can be annotated in the Gene Ontology.

Details

Package: goProfiles
Type: Package
Version: 1.33.4
Date: 2016-03-29
License: GPL

Author(s)

Alex Sanchez and Jordi Ocana

References


See Also

goTools, GOstats, topGO, and other Bioconductor packages for GO based analysis
**basicProfile**

**Builds basic functional profile**

**Description**

Compute basic functional profile for a given list of genes/GO identifiers, a given ontology at a given level of the GO

**Usage**

```r
basicProfile(genelist, idType = "Entrez", onto = "ANY", level = 2, orgPackage=NULL, anotPackage=NULL, 
ord = TRUE, multilevels = NULL, empty.cats = TRUE, cat.names = TRUE, na.rm = TRUE)
```

**Arguments**

- **genelist**: List of genes on which the Profile has to be based
- **idType**: Type of identifiers for the genes. May be 'Entrez' (default), BiocProbes or GoTermsFrame (see details below).
- **onto**: Ontology on which the profile has to be built
- **level**: Level of the ontology at which the profile has to be built
- **orgPackage**: Name of a Bioconductor's organism annotations package ('org.Xx-eg-db'). This field must be provided if the gene list passed to the function is either a character vector of 'Entrez' (NCBI) identifiers or a character vector of probe names
- **anotPackage**: Name of Bioconductor's microarray annotations package. This field must be provided if the gene list passed to the function is a character vector of probe names
- **ord**: Set to 'TRUE' if the profile has to appear ordered by the category names
- **multilevels**: If it is not NULL it must be a vector of GO categories that defines the level at where the profile is built
- **empty.cats**: Set to 'TRUE' if empty categories should appear in the profile
- **cat.names**: Set to 'TRUE' if the profile has to contain the names of categories
- **na.rm**: Set to 'TRUE' if NAs should be removed

**Details**

The function admits three types of entries: Entrez ('Entrez'), Bioconductor probe set names ('BioCprobes') or a special type of data frames ('GOTermsFrames'). If the identifier type are 'BioCprobes' then an annotation package name must be provided too.

**Value**

An object of class GOProfile (one or more data frames in a list named by the ontologies)

**Author(s)**

Alex Sanchez
References


See Also

expandedProfile

Examples

data(CD4Ids)
CD4.MF.Profiles <-basicProfile(genelist=CD4LLids, onto='MF', level=2, orgPackage="org.Hs.eg.db")
print(CD4.MF.Profiles)

CD4Ids

Entrez identifiers for CD4-TCells example

Description

This dataset contains the entrez identifiers CD4EntrezIds and their associated GO Terms CD4GOTermsFrame and CD4GOTermsList corresponding to the list of differentially expressed genes in a study by Henkel et al.

Usage

data(CD4Ids)

Source


Examples

data(CD4Ids)
**compareGeneLists**

Compares two lists of genes by building (expanded) profiles and comparing them

**Description**

This function wraps all the needed steps to compare two lists of genes following the methodology developed by Sanchez, Salicru and Ocana (2007)

**Usage**

```r
compareGeneLists(genelist1, genelist2, idType = "Entrez", onto = "ANY", level = 2, orgPackage,
method = "lcombChisq", ab.approx = "asymptotic", confidence = 0.95, compareFunction="compareGOProfiles", ...)
```

**Arguments**

- **genelist1** First gene set to be compared
- **genelist2** Second gene set to be compared
- **idType** Type of identifiers for the genes. May be 'Entrez' (default), BiocProbes or GoTermsFrame. See the 'Details' section below
- **onto** Ontology on which the profile has to be built
- **level** Level of the ontology at which the profile has to be built
- **orgPackage** Name of a Bioconductor’s organism annotations package ('org.Xx-eg-db')
- **method** The approximation method to the sampling distribution under the null hypothesis specifying that the samples pn and qm come from the same population. See the 'Details' section below
- **confidence** The confidence level of the confidence interval in the result
- **ab.approx** The approximation used for computing 'a' and 'b' coefficients (see details)
- **compareFunction** Allows to use 'fitGOProfile' (sample vs population) or 'compareGOProfiles' (sample1 vs sample2)
- **...** Other arguments for the methods 'basicProfile' or 'compareGoProfiles'

**Value**

The result of the comparison is a list with a variable number of arguments, depending for which ontologies has been performed the comparison. Each list member is an object of class 'htest' corresponding to the output of the function `compareGOProfiles`

**Author(s)**

Alex Sanchez

**References**

compareGOProfiles

Comparison of lists of genes through their functional profiles

Description

Compare two samples of genes in terms of their GO profiles pn and qm. Both samples may share a common subsample of genes, with GO profile pqn0. 'compareGOProfiles' implements some inferential procedures based on asymptotic properties of the squared euclidean distance between the contracted versions of pn and qm.

Usage

compareGOProfiles(pn, qm = NULL, pqn0 = NULL, n = ngenes(pn), m = ngenes(qm), n0 = ngenes(pqn0), method = "lcombChisq", ab.approx = "asymptotic", confidence = 0.95, nsims = 10000, simplify = T, ...)

Arguments

- **pn**: an object of class ExpandedGOProfile representing one or more "sample" expanded GO profiles for a fixed ontology (see the 'Details' section)
- **qm**: an object of class ExpandedGOProfile representing one or more "sample" expanded GO profiles for a fixed ontology (see the 'Details' section)
- **pqn0**: an object of class ExpandedGOProfile representing one or more "sample" expanded GO profiles for a fixed ontology (see the 'Details' section)
- **n**: a numeric vector with the number of genes profiled in each column of pn. This parameter is included to allow the possibility of exploring the consequences of varying sample sizes, other than the true sample size in pn.
- **m**: a numeric vector with the number of genes profiled in each column of qm.
- **n0**: a numeric vector with the number of genes profiled in each column of pqn0.
- **method**: the approximation method to the sampling distribution under the null hypothesis specifying that the samples pn and qm come from the same population. See the 'Details' section below
- **confidence**: the confidence level of the confidence interval in the result
- **ab.approx**: the approximation used for computing 'a' and 'b' coefficients (see details)
- **nsims**: some inferential methods require a simulation step; the number of simulation replicates is specified with this parameter
- **simplify**: should the result be simplified, if possible? See the 'Details' section
- **...**: Other arguments needed

Examples

data(prostateIds)
prostateCompared <- compareGeneLists(welsh01EntrezIDs[1:500],
singh01EntrezIDs[1:500], level=2, orgPackage="org.Hs.eg.db")
print(prostateCompared)
# print(compSummary(prostateCompared))
Details

An object of S3 class 'ExpandedGOProfile' is, essentially, a 'data.frame' object with each column representing the relative frequencies in all observed node combinations, resulting from profiling a set of genes, for a given and fixed ontology. The row.names attribute codifies the node combinations and each data.frame column (say, each profile) has an attribute, 'ngenesis', indicating the number of profiled genes. The arguments 'pn', 'qm' and 'pqn0' are compared in a column by column wise, recycling columns, if necessary, in order to perform max(ncol(pn),ncol(qm),ncol(pqn0)) comparisons (each comparison resulting in an object of class 'GOProfileHtest', an specialization of 'htest'). In order to be properly compared, these arguments are expanded by row, according to their row names. That is, the data arguments can have unequal row numbers. Then, they are expanded adding rows with zero frequencies, in order to make them comparable.

In the i-th comparison (i from 1 to max(ncol(pn),ncol(qm),ncol(pqn0))), the parameters n, m and n0 are included to allow the possibility of exploring the consequences of varying sample sizes, other than the true sample sizes included as an attribute in pn, qm and pqn0.

When qm = NULL, the genes profiled in pn are compared with a subsample of them, those profiled in pqn0 (compare a set of genes with a restricted subset, e.g. those overexpressed under a disease). In this case we take qm=pqn0. When pqn0 = NULL, two profiles with no genes in common are compared.

Let Pn and Qm correspond to the contracted functional profiles (the total counts or relative frequencies of hits in each one of the s GO categories being compared) obtained from pn and qm. If P stands for the "population" profile originating the sample profile Pn[,j], Q for the profile originating Qm[,j] and d(,) for the squared euclidean distance, if P != Q, the distribution of \( \frac{\sqrt{nm/(n+m)}(d(Pn[,j],Qm[,j]) - d(P,Q))}{se(d)} \) is approximately standard normal, N(0,1). This provides the basis for the confidence interval in the result field icDistance. When P=Q, the asymptotic distribution of \( \frac{nm/(n+m)}{d(Pn[,j],Qm[,j])} \) corresponds to the distribution of a mixture of independent chi-square random variables, each one with one degree of freedom. The sampling distribution under H0 P=Q may be directly computed from this distribution (approximating it by simulation) (method="lcombChisq") or by a chi-square approximation to it, based on two correcting constants a and b (method="chi-square"). These constants are chosen to equate the first two moments of both distributions (the linear combination of chi-square random variables distribution and the approximating chi-square distribution). When method="chi-square", the returned test statistic value is the chi-square approximation (n d(pn[,j],qm[,j]) - b) / a. Then, the result field 'parameter' is a vector containing the 'a' and 'b' values and the number of degrees of freedom, 'df'. Otherwise, the returned test statistic value is \( \frac{nm/(n+m)}{d(Pn[,j],Qm[,j])} \) and 'parameter' contains the coefficients of the linear combination of chi-squares.

Value

A list containing max(ncol(pn),ncol(qm),ncol(pqn0)) objects of class 'GOProfileHtest', directly inheriting from 'htest' or a single 'GOProfileHtest' object if max(ncol(pn),ncol(qm),ncol(pqn0))==1 and simplify == T. Each object of class 'GOProfileHtest' has the following fields:

- **profilePn**: the first contracted profile to compute the squared Euclidean distance
- **profileQm**: the second contracted profile to compute the squared Euclidean distance
- **statistic**: test statistic; its meaning depends on the value of "method", see the 'Details' section.
- **parameter**: parameters of the sample distribution of the test statistic, see the 'Details' section.
- **p.value**: associated p-value to test the null hypothesis of profiles equality.
- **conf.int**: asymptotic confidence interval for the squared euclidean distance. Its attribute "conf.level" contains its nominal confidence level.
compareProfilesLists

Description

This function compares two lists ("sensu R lists") of expanded profiles by successive calls to function compareGOProfiles following the methodology developed by Sanchez, Salicru and Ocana (2007).

Usage

compareProfilesLists(expanded1, expanded2, common.expanded=NULL, relationType, method = "lcombChisq", ab.approx = "asymptotic", confidence = 0.95, ...)

Author(s)

Jordi Ocana

References


See Also

fitGOProfile, equivalentGOProfiles

Examples

# [NOT RUN COMPLETELY]
data(prostateIds)
expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
expandedSingh <- expandedProfile(singh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
commonGenes <- intersect(welsh01EntrezIDs[1:100], singh01EntrezIDs[1:100])
commonExpanded <- expandedProfile(commonGenes, onto="MF", level=2, orgPackage="org.Hs.eg.db")
# comparedMF <- compareGOProfiles (pn=expandedWelsh,
# qm = expandedSingh,
# pqn0= commonExpanded)
# print(comparedMF)
# print(compSummary(comparedMF))
#
**compareProfilesLists**

**Arguments**

- `expanded1`: First expanded profile to be compared
- `expanded2`: Second expanded profile to be compared
- `common.expanded`: Expanded profile made from the genes appearing in both lists of genes
- `relationType`: Type of relation between gene lists compared through the expanded profiles. It can be INCLUSION, INTERSECTION or DISJOINT
- `method`: The approximation method to the sampling distribution under the null hypothesis specifying that the samples $p_n$ and $q_m$ come from the same population. See the 'Details' section below
- `confidence`: The confidence level of the confidence interval in the result
- `ab.approx`: The approximation used for computing ‘a’ and ‘b’ coefficients (see details)
- `...`: Other arguments for the methods ’basicProfile’ or ’compareGoProfiles’

**Value**

The result of the comparison is a list with a variable number of arguments, depending on for which ontologies has been performed the comparison. Each list member is an object of class 'htest' corresponding to the output of the function compareGOProfiles

**Author(s)**

Alex Sanchez

**References**


**See Also**

`compareGeneLists`, `expandedProfile`

**Examples**

```
# NOT RUN
#data(ProstateIds)
#expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="MF", 
#   level=2, orgPackage="org.Hs.eg.db")
#expandedSingh <- expandedProfile(singh01EntrezIDs[1:100], onto="MF", 
#   level=2, orgPackage="org.Hs.eg.db")
#commonGenes <- intersect(welsh01EntrezIDs[1:100], singh01EntrezIDs[1:100])
#commonExpanded <- expandedProfile(commonGenes, onto="MF", level=2, orgPackage="org.Hs.eg.db")
#comparedMF<- compareProfilesLists (expandedWelsh, expandedSingh, commonExpanded, relationType="COMMON")
#print(comparedMF)
#print(compSummary(comparedMF))
```
This function returns a brief summary of the comparison between two (expanded) profiles.

Description

Function to return a brief summary of the comparison between two (expanded) profiles.

Usage

```
compSummary(l, decs = 6)
```

Arguments

- `l`: A list of comparison results as returned by a call to `compareGenelists`.
- `decs`: Number of decimal places to use in the output.

Value

A data frame with the summarized results of each comparison. The values contained are:
- `Sqr.Eucl.Dist`: The squared euclidean distance,
- `Standard Err`: The standard error estimate,
- `pValue`: p value of the test,
- `low conf.int`: Lower value for the desired confidence interval,
- `up conf.int`: Upper value for the desired confidence interval.

Author(s)

Alex Sanchez

Examples

```
# (NOT RUN)
# data(prostateIds)
# expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
# expandedSingh <- expandedProfile(singh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
# commonGenes <- intersect(welsh01EntrezIDs[1:100], singh01EntrezIDs[1:100])
# commonExpanded <- expandedProfile(commonGenes, onto="MF", level=2, orgPackage="org.Hs.eg.db")
# comparedMF <- compareGOProfiles (pn=expandedWelsh, qm = expandedSingh, pqn= commonExpanded)
# print(comparedMF)
# print(compSummary(comparedMF))
```
**contractedProfile**

Converts an expanded GO profile into a basic (contracted) GO profile

**Description**

Converts an object of class 'ExpandedGOProfile', or assimilable to it, in an object of class 'BasicGOProfile'

**Usage**

```r
contractedProfile(prof, nams = NULL)
## S3 method for class 'ExpandedGOProfile'
contractedProfile(prof, nams = NULL)
## Default S3 method:
contractedProfile(prof, nams = NULL)
```

**Arguments**

- `prof`: an expanded GO profile, i.e. and object of class 'ExpandedGOProfile', or a numeric vector assimilable to an expanded profile, see the "details" section
- `nams`: optionally, the names of the annotated combinations of GO nodes whose frequency is represented in the expanded profile, see the "details" section

**Details**

Given a list of n genes, and a set of s GO nodes X, Y, Z, ... in a given ontology (BP, MF or CC), its associated (contracted) "profile" is the frequencies vector (either absolute or relative frequencies) of annotations or hits of the n genes in each node. For a given node, say X, this frequency includes all annotations for X alone, for X and Y, for X and Z and so on. Thus, as relative frequencies, its sum is not necessarily one, or as absolute frequencies their sum is not necessarily n. Basic contracted profiles are represented by objects of S3 class 'BasicGOProfile'. On the other hand, an "expanded profile" corresponds to the frequencies in ALL OBSERVED NODE COMBINATIONS. That is, if n genes have been profiled, the expanded profile stands for the frequency of all hits EXCLUSIVELY in nodes X, Y, Z, ..., jointly with all hits simultaneously in nodes X and Y (and only in X and Y), simultaneously in X and Z, in Y and Z, ... , in X and Y and Z (and only in X,Y,Z), and so on. Thus, their sum is one. Expanded profiles are represented by objects of S3 class 'ExpandedGOProfile'. The generic function 'contractedProfile' "contracts" an expanded profile, either represented by a 'ExpandedGOProfile' object or a numeric vector interpretable as an expanded profile, in order to obtain its contracted profile representation.

The rownames attribute of an 'ExpandedGOProfile' or, equivalently, the names attribute of a vector representing an expanded profile, or the names argument, must represent the GO nodes combinations separating the node names with dots, ".", for example: "X", "Y", "Z", "X.Y", "X.Z", "Y.Z", "X.Y.Z" and so on.

**Value**

An object of class 'BasicGOProfile' the contracted profile representation of the expanded profile

**Author(s)**

Jordi Ocana
conversionFunctions

Examples

data(prostateIds)
expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="MF",
  level=2, orgPackage="org.Hs.eg.db")
reContractedWelsh <- contractedProfile(expandedWelsh["MF"])
print(expandedWelsh)
print(reContractedWelsh)
class(reContractedWelsh)
ngenes(reContractedWelsh)

conversionFunctions  Functions to transform convert objects between different types

Description

These functions transform data from one class type into another, or pack simple processes such as compute the profiles needed for one annotations package.

Usage

as.GOTerms.frame(myGOTermsList, na.rm=TRUE)
as.GOTerms.list(genelist, probeType, orgPackage=NULL, anotPkg=NULL, onto="any", na.rm=TRUE)
BioCpack2EntrezIDS(anotPkg, na.rm=TRUE)
BioCpack2Profiles(anotPkg, orgPackage, level=2, na.rm=TRUE, expanded=FALSE)
BioCprobes2Entrez(probeslist, anotPkg, na.rm=TRUE)
GOTermsFrame2GOTermsList(myGOTermsFrame, evid=FALSE)

Arguments

myGOTermsList  GOTermsList object to transform
myGOTermsFrame  GOTermsFrame object to transform
genelist  List of genes (Entrez Ids) to transform
evid  Type of evidence supporting the selected GO Terms
na.rm  Flag indicating if those ids returning NA must be removed from the output
probeType  Type of probes to transform into Entrez Ids
probeslist  List of probes to transform into Entrez Ids
orgPackage  Name of the organism ("org.Xx.eg.db") annotation package
anotPkg  Name of the chip annotation package
level  GO level at which the profile is built
onto  ontology
expanded  Flag to decide if an expanded profile has to be computed

Details

Not yet available

Value

Every function returns a transformed object or a list of computed profiles
Author(s)
Alex Sanchez

Examples
data(CD4Ids)
myGOTermsList <- GOTermsList(CD4LLids[1:5], orgPkg="org.Hs.eg.db")
myGOTermsFrame<- as.GOTerms.frame(myGOTermsList, na.rm=TRUE)
GOTermsFrame2GOTermsList(myGOTermsFrame, evid=FALSE)

drosophila
Entrez identifiers for genes related with an eye mutation in drosophila

Description
Entrez identifiers for genes related with an eye mutation in drosophila.
ostrinIds List of genes in Entrez, generated by Ostrin et al.
michaudIds List of genes in Entrez, generated by Michaud et al.
drosophilasIds List of Drosophila genes in Entrez.

Usage
data(drosophila)

Format
Each dataset is a character vector with a different number of elements which (should) correspond to valid Entrez identifiers

Examples
data(drosophila)

equivalentGOProfiles Are two lists of genes equivalent in terms of their Gene Ontology profiles?

Description
Performs an equivalence test based on the squared Euclidean distance between the Gene Ontology profiles of two lists of genes. Equivalence is declared if the upper limit d.sup of a one-sided confidence interval [0, d.sup] for the distance is lesser than the equivalence limit d0.
equivalentGOProfiles

Usage

equivalentGOProfiles(goObject, ...)
## S3 method for class 'GOProfileHtest'
equivalentGOProfiles(goObject, equivEpsilon = 0.05, d0 = NULL, confidence = NULL, ...)
## S3 method for class 'ExpandedGOProfile'
equivalentGOProfiles(goObject, qm=NULL, pqn0=NULL, 
  n = ngenes(goObject), m = ngenes(qm), n0 = ngenes(pqn0),
  confidence = 0.95,
  equivEpsilon = 0.05, d0 = NULL,
  simplify = FALSE, ...)
## Default S3 method:
equivalentGOProfiles(goObject, ...)

Arguments

goObject an object related to GO profiles or comparisons between them
qm an expanded GO profile, i.e. and object of class 'ExpandedGOProfile'
pqn0 an expanded GO profile, i.e. and object of class 'ExpandedGOProfile'
 n a numeric vector with the number of genes profiled in each column of goObject.
  This parameter is included to allow the possibility of exploring the consequences
  of varying sample sizes, other than the true sample size in goObject.
m a numeric vector with the number of genes profiled in each column of qm.
n0 a numeric vector with the number of genes profiled in each column of pqn0.
confidence the nominal confidence level of the one-sided confidence interval on the distance
d0 a positive value specifying the equivalence limit
equivEpsilon a positive value used to compute 'd0' if it is not directly available
simplify should the result be simplified, if possible? See the 'Details' section
... further arguments, tipically the same than to `compareGOProfiles`

Details

An object of S3 class "ExpandedGOProfile" is, essentially, a "data.frame" object with each column
representing the relative frequencies in all observed node combinations, resulting from profiling a
set of genes, for a given and fixed ontology. The 'row.names' attribute codifies the node combi-
nations and each "data.frame" column (say, each profile) has an attribute, 'ngenes', indicating the
number of profiled genes.

In the 'ExpandedGOProfile' interface, the arguments 'goObject', 'qm' and 'pqn0' are compared in a
column by column wise, recycling columns, if necessary, in order to perform max(ncol(goObject),ncol(qm),ncol(pqn0))
equivalence tests (each test resulting in an object of class 'htest'). In order to be properly tested,
these arguments are expanded by row, according to their row names. That is, the data arguments can
have unequal row numbers. Then, they are expanded adding rows with zero frequencies, in order to
make them comparable. In the i-th comparison (i from 1 to max(ncol(goObject),ncol(qm),ncol(pqn0))),
the parameters n, m and n0 are included to allow the possibility of exploring the consequences of
varying sample sizes, other than the true sample sizes included as an attribute in goObject, qm and
pqn0. When qm = NULL, the genes profiled in goObject are compared with a subsample of them,
those profiled in pqn0 (is there equivalence between a set of genes and a restricted subset, e.g. those
overexpressed under a disease, in terms of their profiles?). When pqn0 = NULL, an equivalence
test between two profiles with no genes in common is performed.
In the 'GOProfileHtest' interface, the one-sided confidence interval for the squared Euclidean distance is computed from the distance and its standard error stored in the corresponding fields of the argument goObject, itself typically an object of class 'GOProfileHtest' resulting from a call to 'compareGOProfiles' with simplify=T.

In the default interface, the 'goObject' argument is previously converted into an object of class 'ExpandedGOProfile' and then this interface is used.

If the argument 'd0' is not provided it is computed as \[ d_0 = -s \times \text{equivEpsilon}^2 \], where 's' stands for the number of non empty GO nodes in any of the GO profiles being compared.

### Value

In the 'ExpandedGOProfile' interface, the result is an object of class "list" containing one or more "htest" objects, each of which may come from previous profiles comparisons. In the other interfaces, the result is a single "htest" object. Each one of these "htest" objects has the following fields:

- **statistic**: test statistic, \( (\text{distance} - d_0) / \text{se} \)
- **parameter**: \( d_0 \) and the sample sizes (number of genes) \( n \) and \( m \)
- **p.value**: associated p-value to test the null hypothesis of profiles inequivalence
- **conf.int**: asymptotic one-sided confidence interval for the squared euclidean distance. Its attribute "conf.level" contains its nominal confidence level.
- **estimate**: squared euclidean distance between the contracted profiles. Its attribute "se" contains its standard error estimate
- **data.name**: a character string giving the names of the data
- **alternative**: a character string describing the alternative hypothesis (always 'Equivalence or similarity, true squared Euclidean distance between the contracted profiles is less than \( d_0 \)')

### Author(s)

Jordi Ocana

### See Also

'compareGOProfiles'

### Examples

```r
data(prostateIds)

expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="ANY", level=2, orgPackage="org.Hs.eg.db")
expandedSingh <- expandedProfile(singh01EntrezIDs[1:100], onto="ANY", level=2, orgPackage="org.Hs.eg.db")
commonGenes <- intersect(welsh01EntrezIDs[1:100], singh01EntrezIDs[1:100])
commonExpanded <- expandedProfile(commonGenes, onto="ANY", level=2, orgPackage="org.Hs.eg.db")

### Funciona si fem:
equivWF <- equivalentGOProfiles (expandedWelsh["MF"], qm = expandedSingh["MF"], pqn0= commonExpanded["MF"])```

equivSummary <- lapply(1:length(expandedWelsh),
  function (onto){
    equivalentGOProfiles (expandedWelsh[[onto]],
    qm = expandedSingh[[onto]],
    pqn0= commonExpanded[[onto]])
  })

equivSummary This function returns a brief summary of the equivalence test between two profiles.

Description
Function to return a brief summary of the equivalence test between two profiles. If in its current version it is better that equivalentGOProfiles is called with option simplify set to FALSE before equivSummary can be used.

Usage
equivSummary(l, decs = 6)

Arguments
l A list of comparison results as returned by a call to compareGenelists
decs Number of decimal places to use in the output

Value
A data frame with the summarized results of each comparison. The values contained are: Sqr.Eucl.Dist: The squared euclidean distance, Standard Err: The standard error estimate, pValue p value of the equivalence test, up conf.int Upper value for the desired confidence interval. d0 Threshold value for equivalence test. Equivalent? Numerical value set to 1 if profiles can be considered equivalent and to zero if they cannot.

Author(s)
Alex Sanchez

See Also
'equivalentGOProfiles'

Examples
# data(prostateIds)
# expandedWelsh <- expandedProfile(welsh01EntrezIDs[1:100], onto="MF",
# level=2, orgPackage="org.Hs.eg.db")
# expandedSingh <- expandedProfile(singh01EntrezIDs[1:100], onto="MF",
# level=2, orgPackage="org.Hs.eg.db")
#commonGenes <- intersect(welsh01EntrezIDs[1:100], singh01EntrezIDs[1:100])
expandedLevel

Function to create expanded levels which can contain GO Terms at different GO levels

Description
This function, combined with function expandTerm, allows to create mixed levels which can contain terms belonging to different GO levels. Specifically one can take one (or several, but one by one) term at a given GO level and expand it into its children terms using function expandTerm and then combine them into a new level using this function.

Usage
expandedLevel(LevelTerms, Term2Expand, onto)
expandTerm(GOTerm, onto)

Arguments
LevelTerms Other terms which have not been expanded, and will be combined with the expanded ones
Term2Expand The GO term which will be substituted by its children terms
GOTerm The GO term which will be substituted by its children terms
onto The ontology ("MF", "BP", "CC")

Value
The value returned is the vector combining the original terms with the children of the term that had to be expanded.

Author(s)
Alex Sanchez

Examples
got<-toTable(GOTERM)[,2:3]
desc<-function(s) got[got[,1]==s,2]
MFLevel2<-getGOLevel("MF",2)
bindingLevel2<-MFLevel2[2]
bindingLevel3 <- expandTerm(bindingLevel2,"MF")
print(desc(bindingLevel3<-as.matrix(sapply(bindingLevel3,desc ))))
mixedLevel<-c(MFLevel2[-2],bindingLevel3)
print(mixedLevel<-as.matrix(sapply(mixedLevel,desc )))
expandedProfile

Builds expanded profiles

Description
Expanded profiles are used mainly for comparison of profiles based on the theory developed by Sanchez et al (2007) (see references)

Usage
expandedProfile(genelist, idType = "Entrez", onto = "ANY", level = 2, orgPackage=NULL, anotPackage=NULL, multilevels = NULL, ord = TRUE, na.rm = TRUE, percentage = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>genelist</td>
<td>List of genes on which the Profile has to be based</td>
</tr>
<tr>
<td>idType</td>
<td>Type of identifiers for the genes. Use 'Entrez' preferably</td>
</tr>
<tr>
<td>onto</td>
<td>Ontology on which the profile has to be built</td>
</tr>
<tr>
<td>level</td>
<td>Level of the ontology at which the profile has to be built</td>
</tr>
<tr>
<td>orgPackage</td>
<td>Name of a Bioconductor’s organism annotations package (‘org.Xx-eg-db’). This field must be provided if the gene list passed to the function is either a character vector of 'Entrez' (NCBI) identifiers or a character vector of probe names</td>
</tr>
<tr>
<td>anotPackage</td>
<td>Name of Bioconductor annotations package. This field must be provided if the gene list passed to the function is a character vector of probe names</td>
</tr>
<tr>
<td>ord</td>
<td>Set to 'TRUE' if the profile has to appear ordered by the category names</td>
</tr>
<tr>
<td>multilevels</td>
<td>If it is not NULL it must be a vector of GO categories that defines the level at where the profile is built</td>
</tr>
<tr>
<td>na.rm</td>
<td>Set to 'TRUE' if NAs should be removed</td>
</tr>
<tr>
<td>percentage</td>
<td>Set to 'TRUE' if the profile must be built using percentages</td>
</tr>
</tbody>
</table>

Details
The function admits three types of entries: Entrez (‘Entrez’), Bioconductor probe set names (‘BioCprobes’) or a special type of data frames (‘GOTermsFrames’). If the identifier type are 'BioCprobes' then an annotation package name must be provided too.

Value
An object of class GOProfile containing an expanded profile

Author(s)
Alex Sanchez

References
fisherGOProfiles

See Also

basicProfile

Examples

data(CD4Ids)
CD4.Expanded <- expandedProfile(genelist=CD4LLids[1:50], onto='MF', level=2, orgPackage="org.Hs.eg.db")

fisherGOProfiles

GO Class-by-class Fisher tests in lists of genes characterized by their functional profiles

Description

Given two lists of genes, both characterized by their frequencies of annotations (or "hits") in the same set of GO nodes (also designated as GO terms or GO classes), for each node determine if the annotation frequencies depart from what is expected by chance. The annotation frequencies are specified in the "GO profiles" arguments pn, qn and pn. Both samples may share a common subsample of genes, with GO profile pqn0. The analysis is based on the Fisher's exact test, as is implemented by fisher.test R function, followed by p-value adjustment for multitesting based on function p.adjust. Usually, this function will be called after a significant result on compareGOProfiles which performs global (all GO nodes simultaneously) profile comparisons (with better type I and type II error control), to identify the more rellevant nodes.

Usage

fisherGOProfiles(pn, ...)
## S3 method for class 'numeric'
fisherGOProfiles(pn, qm=NULL, pqn0=NULL, 
                 n = ngenes(pn), m = ngenes(qm), n0 = ngenes(pqn0),
                 method = "BH", simplify=T, expanded=F, ...)
## S3 method for class 'matrix'
fisherGOProfiles(pn, n, m, method = "BH", ...)
## S3 method for class 'BasicGOProfile'
fisherGOProfiles(pn, qm=NULL, pqn0=NULL, 
                 method = "BH", goIds=T, ...)
## S3 method for class 'ExpandedGOProfile'
fisherGOProfiles(pn, qm=NULL, pqn0=NULL, 
                 method = "BH", simplify=T, ...)

Arguments

pn
  an object of class BasicGOProfile or ExpandedGOProfile representing a "sample" GO profile for a fixed ontology, or a numeric vector interpretable as a GO profile (expanded or not), or a two-dimensional frequency matrix (see the 'Details' section). This is a required argument
qm
  similarly, an object representing a "sample" GO profiles for a fixed ontology
pqn0
  an object representing a "sample" GO profile for a fixed ontology
n
  the number of genes profiled in pn
m
  the number of genes profiled in qm
fisherGOProfiles

- **n0**: the number of genes profiled in pqn0
- **method**: the p-values adjusting method for multiple comparisons; the same possibilities as in standard R function `p.adjust`
- **expanded**: boolean; are these numeric vectors representing expanded profiles?
- **simplify**: should the result be simplified, if possible? See the 'Details' section
- **goIds**: if TRUE, each node is represented by its GO identifier
- **...**: other arguments (to be passed to `p.adjust` or `fisher.test` functions)

### Details

Given a list of \( n \) genes, and a set of \( s \) GO classes or nodes X, Y, Z, ... in a given ontology (BP, MF or CC), its associated ("contracted" or "basic") "profile" is the absolute frequencies vector of annotations or hits of the \( n \) genes in each one of the \( s \) GO nodes. For a given node, say X, this frequency includes all annotations for X alone, for X and Y, for X and Z and so on. Thus, as relative frequencies, its sum is not necessarily one, or as absolute frequencies their sum is not necessarily \( n \). On the other hand, an "expanded profile" corresponds to the relative frequencies in ALL NODE COMBINATIONS. That is, if \( n \) genes have been profiled, the expanded profile stands for the frequency of all hits EXCLUSIVELY in node X, exclusively in node Y, exclusively in Z, ..., jointly with all hits simultaneously in nodes X and Y (and only in X and Y), simultaneously in X and Z, in Y and Z, ..., in X and Y and Z (and only in X,Y,Z), and so on. Thus, their sum is one.

Let \( n, m \) and \( n0 \) designate the total number of genes profiled in \( pn, qm \) and \( pqn0 \) respectively. According to these profiles, \( n[i], m[i] \) and \( n0[i] \) genes are annotated for node 'i', \( i = 1, \ldots, s \). Note that the sum of all the \( n[i] \) not necessarily equals \( n \) and so on. If not NULL, \( pqn0 \) stands for the profile of the \( n0 \) genes common to the gene lists that gave rise to \( pn \) and \( qm \). `fisherGOProfiles` builds a \( sx2 \) absolute frequencies matrix

\[
\begin{array}{ccc}
go \text{ node 1} & N[1,1] & N[1,2] \\
goose \text{ node 2} & N[2,1] & N[2,2] \\
\cdots & \cdots & \cdots \\
\text{go \node s} & N[s,1] & N[s,2] \\
\end{array}
\]

with column totals \( N1 \) and \( N2 \) (not necessarily equal to the column sums) and performs a Fisher’s exact test over each one of the 2x2 tables

\[
\begin{array}{ccc}
go \text{ node i} & N[i,1] & N[i,2] \\
\text{All nodes except i} & N1 - N[i,1] & N2 - N[i,2] \\
\end{array}
\]

followed by a p-value correction for multiplicity in testing. If \( pqn0 \) is NULL, then both gene lists do not have any genes in common, \( N[i,1] = n[i] \) and \( N[i,2] = m[i] \), and \( N1 = n, N2 = m, n0 = 0 \). Otherwise, (if \( pqn0 \) is not NULL) \( N[i,1] = n[i] - n0[i], N1 = n - n0 \) and \( N[i,2] = n0[i], N2 = n0 \) if \(qm\) is NULL, or \( N[i,2] = m[i], N2 = m \) if \(qm\) is not NULL.

In other words, this function provides a general setting for diverse, common in practice, situations where a node-by-node analysis is required. When \( pqn0 = NULL \), two lists with no genes in common are compared. Otherwise, when \(qm = NULL \), the genes profiled in \( pn \) are compared with a subsample of them, those profiled in \( pqn0 \)(a set of genes vs a restricted subset, e.g. those overexpressed under a disease). Finally, if both arguments \(qm\) and \(pqn0\) are not NULL (\( pn \) is always required) two gene lists with some genes in common are analised.

If both \( qm \) and \( pqn0 \) are NULL, \( pn \) should correspond to an absolute frequencies matrix with \( s \) rows
and 2 columns.

The arguments n, m or n0 are only required in case of numeric vectors or matrices specifying profiles but lacking the 'ngen' attribute.

Value

A list containing \( \max(ncol(pn), ncol(qm), ncol(pqn0)) \) p-values numeric vectors, or a single p-values vector if \( \max(ncol(pn), ncol(qm), ncol(pqn0)) = 1 \) and simplify == T.

Author(s)

Jordi Ocana

References


See Also

fitGOProfile, compareGOProfiles, equivalentGOProfiles

Examples

```r
require("org.Hs.eg.db")
data(prostateIds)  # "singh01EntrezIDs", "singh05EntrezIDs", "welsh01EntrezIDs", "welsh05EntrezIDs"
# To improve speed, use only the first 100 genes:
list1 <- welsh01EntrezIDs[1:100]
list2 <- singh01EntrezIDs[1:100]
prof1 <- basicProfile(list1, onto="MF", level=2, orgPackage="org.Hs.eg.db")$MF
prof2 <- basicProfile(list2, onto="MF", level=2, orgPackage="org.Hs.eg.db")$MF
commProf <- basicProfile(intersect(list1, list2), onto="MF", level=2, orgPackage="org.Hs.eg.db")$MF
fisherGOProfiles(prof1, prof2, commProf, method="holm")
```

---

**fitGOProfile**

Does a "sample" GO profile 'pn', observed in a sample of 'n' genes, fit a "population" or "model" p0?

**Description**

'fitGOProfile' implements some inferential procedures to solve the preceding question. These procedures are based on asymptotic properties of the squared euclidean distance between the contracted versions of pn and p0.

**Usage**

```r
fitGOProfile(pn, p0, n = ngenes(pn), method = "lcombChisq", ab.approx = "asymptotic", confidence =
```
Arguments

- **pn**: an object of class ExpandedGOProfile representing one or more "sample" expanded GO profiles for a fixed ontology (see the 'Details' section)
- **p0**: an object of class ExpandedGOProfile representing one or more "population" or "theoretical" expanded GO profiles (see also the 'Details' section)
- **n**: a numeric vector with the number of genes profiled in each column of pn. This parameter is included to allow the possibility of exploring the consequences of varying sample sizes, other than the true sample size in pn
- **method**: the approximation method to the sampling distribution under the null hypothesis "p = p0", where p is the 'true' population profile originating each column of pn.
- **ab.approx**: the method used to compute the constants 'a' and 'b' described in the paper. See the 'Details' section
- **confidence**: the confidence level of the confidence interval in the result
- **nsims**: some inferential methods require a simulation step; the number of simulation replicates is specified with this parameter
- **simplify**: should the result be simplified, if possible? See the 'Details' section

Details

An object of class 'ExpandedGOProfile' is, essentially, a 'data.frame' object with each column representing the relative frequencies in all observed node combinations, resulting from profiling a set of genes, for a given and fixed ontology. The row.names attribute codifies the node combinations and each data.frame column (say, each profile) has an attribute, 'ngenes', indicating the number of profiled genes. (Actually, the 'ngenes' attribute of each 'p0' column is ignored and is taken as if it were infinite, 'Inf'.) The arguments 'pn' and 'p0' are compared in a column by column wise, recycling columns, if necessary, in order to perform max(ncol(pn),ncol(p0)) comparisons (each comparison resulting in an object of class 'htest'). In order to be properly compared, 'pn' and 'p0' are expanded by row, according to their row names. That is, both arguments can have unequal row numbers. Then, they are expanded adding rows with zero frequencies, in order to make them comparable.

In the i-th comparison (i from 1 to max(ncol(pn),ncol(p0))), if p stands for the profile originating the sample profile pn[,i] and d(,) for the squared euclidean distance, if p /= p0[,i], the distribution of sqrt(n)(d(pn[,i],p0[,i]) - d(p,p0[,i]))/se is approximately standard normal, N(0,1). This provides the basis for the confidence interval in the result field conf.int. When p==p0[,i], the asymptotic distribution of n d(pn[,i],p0[,i]) is the distribution of a linear combination of independent chi-square random variables, each one with one degree of freedom. This sampling distribution may be directly computed (approximating it by simulation, method="lcombChisq") or approximated by a chi-square distribution, based on two correcting constants a and b (method="chi-square"). These constants are chosen to equate the first two moments of both distributions (the distribution of a linear combination of chi square variables and the approximating chi-square distribution). When method="chi-square", the returned test statistic value is the chi-square approximation (n d(pn,p0) - b) / a. Then, the result field 'parameter' is a vector containing the 'a' and 'b' values and the number of degrees of freedom, 'df'. Otherwise, the returned test statistic value is n d(pn,p0) and 'parameter' contains the coefficients of the linear combination of chi-squares

Value

A list containing max(ncol(pn),ncol(p0)) objects of class 'htest', or a single 'htest' object if ncol(pn)==1 and ncol(p0)==1 and simplify == T. Each 'htest' object has the following fields:
GOTermsList

statistic  test statistic; its meaning depends on the value of "method", see the 'Details' section
parameter  parameters of the sample distribution of the test statistic, see the 'Details' section
p.value   associated p-value to test the null hypothesis "pn[,i] is a random sample taken from p0[,i]"
conf.int  asymptotic confidence interval for the squared euclidean distance. Its attribute "conf.level" contains its nominal confidence level
estimate  squared euclidean distance between the contracted pn and p0 profiles. Its attribute "se" contains its standard error estimate
method    a character string indicating the method used to perform the test
data.name  a character string giving the names of the data
alternative a character string describing the alternative hypothesis

Author(s)
Jordi Ocana

References

See Also
compareGOProfiles

Examples
#data(sampleProfiles)
#comparedMF <- fitGOProfile(pn=expandedWelsh01[['MF']],
#                          p0 = expandedSingh01[['MF']])
#print(comparedMF)
#print(compSummary(comparedMF))
Usage

GOTermsList(LLids, onto = "any", evid = "any", na.rm = TRUE, orgPkg )
getAncestorsLst(GOTermslist, onto, unique.ancestor=TRUE, na.rm=TRUE, combine=TRUE)
getGOLevel(onto, level)

Arguments

LLids  Character vector of Entrez (formerly Locuslink identifiers)
onto  ontology to be queried using the genes list
evid  type of evidence supporting the selected GO Terms
na.rm  flag indicating if those ids returning NA must be removed from the output
orgPkg  Organism annotation package ('org.Xx.eg.db') required to obtain the GO terms associated with the Entrez identifiers
GOTermslist  List produced by a call to function GOTermsList
unique.ancestor  Flag to remove repeated ancestor identifiers
combine  Flag to combine ancestors
level  GO level at which the profile is built

Details

During the call to this function there may appear two types of NAs.

By one side if a name is not mapped in LocusLink this yields an NA that must be eliminated because nothing can be found through LL about this name

By another side if a gene is identified in LL but yields NA it seems to mean that it is not mapped in the GO

This may be eliminated but it may be worth the pity to keep track of them and to put these terms in an 'Seemingly unnanotated' category. In the case that its number was very high it migt suggest reviewing the list or reconsidering the results.

Value

A list whose components -one per Entrez term- are character vectors with the most specific GO identifiers associated with this term

Author(s)

Alex Sanchez

See Also

getAncestorsLst

Examples

#data(CD4Ids)
#simpleLLids<- as.character(c(2189,5575,5569,11)) #1 is not a Locuslink identifier
#simpleGOlist<- GOTermsList (simpleLLids, orgPkg="org.Hs.eg.db")
#print(simpleGOlist.CC<-GOTermsList (simpleLLids,"CC", orgPkg="org.Hs.eg.db"))
#print(simpleGOlist.IEA<-GOTermsList (simpleLLids,evid="IEA",na.rm=TRUE, orgPkg="org.Hs.eg.db"))
**hugoIds**

| hugoIds | Entrez Identifiers obtained from the Human Genome Organization |

**Description**

Entrez identifiers obtained from the Human Genome Organization. They correspond to the column named 'Entrez Gene Id (mapped)' in the 'All data' table in the Hugo Genome Nomenclature website (http://www.genenames.org/index.html)

**Usage**

data(hugoIds)

**References**

http://www.genenames.org/cgi-bin/hgnc_downloads.cgi

**Examples**

data(hugoIds)

---

**mergeProfilesLists**

Combines two lists of profiles into one

**Description**

Combines two lists of profiles, that is two lists with three components, 'MF', 'BP', 'CC' into a single one.

**Usage**

mergeProfilesLists(profilesList1, profilesList2, emptyCats = F, profNames = NULL)

**Arguments**

- **profilesList1**: First list to combine
- **profilesList2**: Second list to combine
- **emptyCats**: Boolean. Set to TRUE if there are empty categories that should be accounted for in any of the profiles
- **profNames**: Names for the profiles (optional). If missing they are set to 'Frequency-1', 'Frequency-2', etc.

**Value**

A list of profiles with more than one column each.

**Author(s)**

Alex Sanchez
Examples

```r
require(goProfiles)
data(prostateIds)
welsh.MF <- basicProfile(welsh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
singh.MF <- basicProfile(singh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
plotProfiles(welsh.MF, 'Functional profiles for Welsh dataset',percentage=TRUE)
welsh.singh.MF <-mergeProfilesLists(welsh.MF, singh.MF, profNames=c("Welsh", "Singh"))
```

ngenesis

Returns the number of genes that lead to this GO profile (an object of class ExpandedGOProfile, BasicGOProfile or assimilable to them)

Description

The information contained in one or more lists of genes may be summarized by their GO profiles, that is to say, the absolute or relative frequencies of annotations or hits in all the classes or nodes of a given leven in a given GO ontology, or by the corresponding frequencies in a selected set of nodes (possibly belonging to more than one GO level but not hierarchically related). This function returns the number of genes in each list that were annotated to compute the profiles.

Usage

```r
ngenesis(pn, i=NULL)
## Default S3 method:
ngenesis(pn, i=NULL)
## S3 method for class numeric
ngenesis(pn, i=NULL)
## S3 method for class matrix
ngenesis(pn, i=NULL)
## S3 method for class ExpandedGOProfile
ngenesis(pn, i=NULL)
## S3 method for class BasicGOProfile
ngenesis(pn, i=NULL)
```

Arguments

- `pn` an object of class ExpandedGOProfile or BasicGOProfile representing one or more "sample" expanded GO profiles for a fixed ontology, or a numeric vector interpretable as a GO profile (expanded or not), or a frequency matrix (see the 'Details' section)
- `i` i-th profile in the case of more than one profiles. A vector with the number of genes of all profiles is returned if this argument is absent

Details

Given a list of n genes, and a set of s GO nodes X, Y, Z, ... in a given ontology (BP, MF or CC), its associated (contracted) "basic profile" is the frequencies vector (either absolute or relative frequencies) of annotations or hits of the n genes in each node. For a given node, say X, this frequency includes all annotations for X alone, for X and Y, for X and Z and so on. Thus, as relative frequencies, its sum is not necessarily one, or as absolute frequencies their sum is not necessarily n. On the other hand, an "expanded profile" corresponds to the frequencies in ALL OBSERVED
NODE COMBINATIONS. That is, if n genes have been profiled, the expanded profile stands for the frequency of all hits EXCLUSIVELY in nodes X, Y, Z, ..., jointly with all hits simultaneously in nodes X and Y (and only in X and Y), simultaneously in X and Z, in Y and Z, ... , in X and Y and Z (and only in X,Y,Z), and so on. Thus, their sum is one.

An object of S3 class 'ExpandedGOProfile' is, essentially, a 'data.frame' object with each column representing an expanded profile. The row.names attribute codifies the node combinations and each data.frame column (say, each profile) has an attribute, 'ngenes', indicating the number of profiled genes.

Value

A vector with the number of genes annotated in one or more GO profiles

Author(s)

Jordi Ocana

See Also

BasicGOProfile object, ExpandedGOProfile object

Examples

require("org.Hs.eg.db")
data(prostateIds)  # "singh01EntrezIDs", "singh05EntrezIDs", "welsh01EntrezIDs", "welsh05EntrezIDs"
# To improve speed, use only the first 100 genes:
list1 <- welsh01EntrezIDs[1:100]
prof1 <- expandedProfile(list1, onto="MF", level=2, orgPackage="org.Hs.eg.db", na.rm=TRUE)$MF
length(list1)
# Only a subset of the initial gene list are annotated in the profile
ngenes(prof1)

omimIds

Entrez identifiers for disease-related genes in the OMIM database

Description

Entrez identifiers for several lists of genes related with human disease.

diseaseIds contains the Entrez identifiers corresponding to disease-related genes found in the OMIM database. This list has been manually curated by Nuria Lopez-Bigas et al. who kindly provided it to us.
morbidmapIds contains the Entrez identifiers for all the genes in the morbidmap table. This list would correspond to disease-related genes if there had been no manual curation, as in the previous list (‘diseaseIds’).
dominantIds contains the Entrez identifiers for dominant genes after manual curation by Nuria Lopez-Bigas who has kindly allowed us to include them in the package.
recessiveIds contains the Entrez identifiers for recessive genes after manual curation by Nuria Lopez-Bigas who has kindly allowed us to include them in the package.
dominantIdsEBI contains the Entrez identifiers for dominant genes in the EBI version of the OMIM database recovered using SRS with the term 'dominant' in the KEYWORDS field.
recessiveIdsEBI contains the Entrez identifiers for recessive genes in the EBI version of the OMIM database recovered using SRS with the term 'recessive' in the KEYWORDS field.
dominantIdsNCBI contains the Entrez identifiers for dominant genes in the NCBI version of the OMIM database recovered using ENTREZ with the term 'dominant' in the CLINICAL field.
recessiveIdsNCBI contains the Entrez identifiers for recessive genes in the NCBI version of the OMIM database recovered using ENTREZ with the term 'recessive' in the CLINICAL field.

Usage
data(omimIds)

Format
Each dataset is a character vector with a different number of elements which (should) correspond to valid Entrez identifiers

Details
Lopez-Bigas et al. analyzed the distribution of functional categories in genes causing disease in human. They did several comparisons which can also be done using goProfiles. In order to perform these comparisons we first tried to obtain the same lists of genes using standard database browsers, such as 'SRS', at the European Bioinformatics Institute, or 'Entrez', at the National Center for Biotechnological Information. Curiously both approaches provided very different lists so we asked the authors for their data and they kindly provided them to us. In order to facilitate the use of functions included in goProfiles we have trimmed the list of recessive and dominant genes so that (i) They become exclusive (no gene belows to both lists) (2) They are both included in the diseaseIds list. This eliminated 39 genes (out of 639) from the list of recessive genes and 52 genes (out of 414) from the list of dominant genes

References

Examples
data(omimIds)

plotProfiles
Plot functional profiles

Description
Plots basic functional profiles created with the 'basicProfile' instruction. If several profiles have to be plot together they must be first merged using the 'mergeProfiles' function. The labels of the Y-axis of the plots are the descriptions of the GO Terms. If the label is longer than 20 characters it is truncated and ended by three dots.

Usage
plotProfiles(aProf, aTitle = "Functional Profile", anOnto = NULL, percentage = FALSE, HORIZVERT = TRUE, legendText = NULL, colores = c("white", "red"), multiplePlots = F, multipleWindows = T, labelWidth=25,...)
printProfiles

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>aProf</td>
<td>Functional profile to plot</td>
</tr>
<tr>
<td>aTitle</td>
<td>Title for the figures</td>
</tr>
<tr>
<td>anOnto</td>
<td>Ontology (to appear in the title)</td>
</tr>
<tr>
<td>percentage</td>
<td>Plot absolute or relative frequencies (not summing to 100)</td>
</tr>
<tr>
<td>HORIZVERT</td>
<td>Plot horizontal or vertical bars</td>
</tr>
<tr>
<td>legendText</td>
<td>Text of the legend for the plot</td>
</tr>
<tr>
<td>colores</td>
<td>Colors to be used</td>
</tr>
<tr>
<td>multiplePlots</td>
<td>Plot all profiles for a given dataset in one figure</td>
</tr>
<tr>
<td>multipleWindows</td>
<td>Open a new window after each plot</td>
</tr>
<tr>
<td>labelWidth</td>
<td>Width of Y axis labels (Names of GO categories) in the plot</td>
</tr>
<tr>
<td>...</td>
<td>Other graphical parameters that should be passed for plotting</td>
</tr>
</tbody>
</table>

Value

The plot

Author(s)

Alex Sanchez

Examples

```r
require(goProfiles)
data(prostateIds)
welsh.MF <- basicProfile (welsh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
singh.MF <- basicProfile (singh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
plotProfiles(welsh.MF, 'Functional profiles for Welsh dataset',percentage=TRUE)
welsh.singh.MF <-mergeProfilesLists(welsh.MF, singh.MF, profNames=c("Welsh", "Singh"))
plotProfiles(welsh.singh.MF , percentage=TRUE, multiplePlots=TRUE, labelWidth=30)
```

printProfiles  Print functional profiles

Description

Prints basic functional profiles created with the 'basicProfile' instruction. Allows for several formatting operations such as truncating long labels, removing empty categories or choosing between absolute or relative frequencies. If several profiles have to be printed together they must be first merged using the 'mergeProfiles' function.

Usage

```r
printProfiles(aProf, aTitle = "Functional Profile", anOnto = NULL, percentage = FALSE, Width=25, emptyCats=FALSE)
```
Arguments

- **prof**
  Functional profile to plot
- **aTitle**
  Title for the figures
- **anOnto**
  Ontology (to appear in the title)
- **percentage**
  Plot absolute or relative frequencies (not summing to 100)
- **Width**
  Maximum width for the description of GO categories
- **emptyCats**
  Set to 'TRUE' if empty categories should appear in the profile

Value

The printout

Author(s)

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Examples

```r
require(goProfiles)
data(prostateIds)
welsh.MF <- basicProfile (welsh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
singh.MF <- basicProfile (singh01EntrezIDs[1:100], onto="MF", level=2, orgPackage="org.Hs.eg.db")
printProfiles(welsh.MF, 'Functional profiles for Welsh dataset', percentage=TRUE, anOnto='MF')
welsh.singh.MF <-mergeProfilesLists(welsh.MF, singh.MF, profNames=c("Welsh", "Singh"))
printProfiles(welsh.singh.MF, percentage=TRUE, emptyCats=TRUE)
```

prostateIds

Prostate cancer-related genes

Description

Entrez identifiers for genes related with Prostate Cancer selected from two datasets analyzed by Welsh et al. (2001) and Singh et al. (2002) respectively. The genes have been selected from freely available datasets in the internet using a standard workflow for selecting differentially expressed genes. The dataset contains 4 character vectors, each corresponding to the entrez identifiers of the genes selected at a 5% and 1% significance level from the Welsh and Singh dataset respectively.

- **welsh05EntrezIDs** List of genes selected from Welsh et al. study at a 0.05 significance level.
- **welsh01EntrezIDs** List of genes selected from Welsh et al. study at a 0.01 significance level.
- **singh05EntrezIDs** List of genes selected from Singh et al. study at a 0.05 significance level.
- **singh01EntrezIDs** List of genes selected from Singh et al. study at a 0.01 significance level.

Usage

```r
data(prostateIds)
```

Format

Each dataset is a character vector with a different number of elements which (should) correspond to valid Entrez identifiers.
**prostateIds**

**Source**


**Examples**

```r
data(prostateIds)
```
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