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)

<table>
<thead>
<tr>
<th>CD4Ids</th>
<th>Entrez identifiers for CD4-TCells example</th>
</tr>
</thead>
</table>

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

**Usage**

```r
cmpareGeneLists(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

```r
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

```r
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, 'ngen', 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 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 (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 (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

compares two of expanded profiles

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, ...)

estimate  squared euclidean distance between the contracted 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 (always 'true squared Euclidean distance between the contracted profiles is greater than zero'

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 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)
- `...`: 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**


**See Also**

`compareGeneLists`, `expandedProfile`

**Examples**

```r
# [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))
```
compSummary

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.intLower value for the desired confidence interval, up conf.intUpper 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,
#     pqn0= commonExpanded)
# print(comparedMF)
# print(compSummary(comparedMF))
#
contractedProfile

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 \( X, Y, Z, \ldots \) 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 \( X, Y, Z, \ldots \), jointly with all hits simultaneously in nodes \( X \) and \( Y \) (and only in \( X \) and \( Y \)), simultaneously in \( X \) and \( Z \), in \( Y \) and \( Z \), \ldots, 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 `nams` 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
Examples

```r
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)
genenes(reContractedWelsh)
```

Description

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

Usage

```r
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
**drosophila**

**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.

**drosophilaIds** 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, typically 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 combinations 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 $d0 < -s \cdot equivEpsilon^2$, 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, $\frac{(\text{distance} - d0)}{\text{se}}$

- **parameter**
  $d0$ 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 $d0$')

**Author(s)**

Jordi Ocana

**See Also**

'compareGOProfiles'

**Examples**

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:
equivMF <- 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]])
  })

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])
#commonExpanded <- expandedProfile(commonGenes, onto="MF", level=2, orgPackage="org.Hs.eg.db")

# equivMF <- equivalentGOProfiles (pn=expandedWelsh,
# qm = expandedSingh,
# pqn0= commonExpanded)
# print(equivSummary(equivMF, decs=5))

## expandedLevel

### 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 ))))
mixedLevel2<-c(MFLevel2[-2],bindingLevel3)
print(mixedLevel2<-as.matrix(sapply(mixedLevel2,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

genelist
Type of identifiers for the genes. Use 'Entrez' preferably

idType
List of genes on which the Profile has to be based

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 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

na.rm
Set to 'TRUE' if NAs should be removed

percentage
Set to 'TRUE' if the profile must be built using percentages

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 relevant 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", golds=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, ..., 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

<table>
<thead>
<tr>
<th>GO node 1</th>
<th>N[1,1]</th>
<th>N[1,2]</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO node 2</td>
<td>N[2,1]</td>
<td>N[2,2]</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>GO node s</td>
<td>N[s,1]</td>
<td>N[s,2]</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>GO node i</th>
<th>N[i,1]</th>
<th>N[i,2]</th>
</tr>
</thead>
<tbody>
<tr>
<td>All nodes except i</td>
<td>N1 - N[i,1]</td>
<td>N2 - N[i,2]</td>
</tr>
</tbody>
</table>

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 over-expressed 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 analysed.

If both qm and pqn0 are NULL, pn should correspond to an absolute frequencies matrix with s rows
The arguments \( n, m \) or \( n_0 \) are only required in case of numeric vectors or matrices specifying profiles but lacking the 'ngenesis' 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")
```

---

**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 \( p_0 \).

**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. See the 'Details' section below

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))

GOTermsList  Functions to create and manage lists of GO terms associated with a vector of 'Entrez' identifiers

Description
These functions prepare data to be processed by the 'basicProfile' function. To create a profile a set of GOterms belonging to one or more ontologies is needed. The terms belonging to each gene must be given separately so that they can be counted. This function queries the environment 'GOENTREZID2GO' with the vector of Entrez terms and formats the output into a list whose components -one per Entrez term- contain the most specific GO identifiers associated with this term.
Usage

GOTermsList(LLids, onto = "any", evid = "any", na.rm = TRUE, orgPkg )
getAncestorsList(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

getAncestorsList

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

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"))
```

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

```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]
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 belongs 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

aProf 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)
HORIZVERT Plot horizontal or vertical bars
legendText Text of the legend for the plot
colores Colors to be used
multiplePlots Plot all profiles for a given dataset in one figure
multipleWindows Open a new window after each plot
labelWidth Width of Y axis labels (Names of GO categories) in the plot
...
Other graphical parameters that should be passed for plotting

Value

The plot

Author(s)

Alex Sanchez

Examples

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

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

aProf  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)

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")
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)
```

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.
Source


Examples

```r
data(prostateIds)
```
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