Description

Signal-to-Noise Applied to Gene Expression Experiments

Details
### qualSample

**Quality of samples in a study**

#### Description

Calculate the relative quality of all samples from a study.

#### Usage

```r
qualSample(data, mode="complete", cc=NULL, multicore=FALSE)
```

#### Arguments

- **data**
  
  The study data. If an Eset, `toSnageeFormat` is called on it. Otherwise, must be a list with fields `genes` containing the vector of gene IDs (from Entrez) and `data` containing the gene expression data.

- **mode**
  
  Which gene-gene correlation matrix should be used. Can be `complete` (using all platforms) or `woAffy` (without the Affy platforms).
qualStudy

cc Can be used if wishing to use a custom gene-gene correlation matrix. Must be a list with fields 'g' containing the gene IDs and 'cc' containing the (upper triangular part of the) correlations.

multicore Should the parallel version be used? This is based on the parallel package, if that package cannot be loaded it will fall back on single core, with a warning.

Details

The function calculates the quality of all samples in a study. Lower values are of lower quality. The numerical values of the study (the 'data' field) should be in log-scale, and normalized. It is recommended to used medpolish on the data.

Each gene should only appear once in the gene list. Duplicated genes must be merged before using the function. Non-finite values should also be removed first (using the impute package for instance).

See Also

SNAGEE, qualStudy, toSnageeFormat

Examples

```r
# Get the list of genes
geneList = getCC()$g;
# Create a random data set
d=list(genes=geneList, data=matrix(rnorm(length(geneList)*50),ncol=50));
# And calculate the quality of the samples (they are all about the same)
qualSample(d);
```

qualStudy

Quality of a study

Description

Calculate the quality of a study.

Usage

```r
qualStudy(d,mode="complete",cc=NULL,disattenuate=TRUE)
```

Arguments

d The study data. If an Eset, toSnageeFormat is called on it. Otherwise, must be a list with fields 'genes' containing the vector of gene IDs (from NCBI’s Gene DB) and 'data' containing the actual data.

mode Which gene-gene correlation matrix should be used. Can be 'complete' (using all platforms) or 'woAffy' (without the Affy platforms).

cc Can be used if wishing to use a custom gene-gene correlation matrix. Must be a list with fields 'g' containing the gene IDs and 'cc' containing the (upper triangular part of the) correlations.

disattenuate Should the qualities be disattenuated?
Details

The function calculates the quality of a study. The numerical values of the study (the `data` field) should be in log-scale, and normalized. It is recommended to used medpolish on the data.

Each gene should only appear once in the gene list. Duplicated genes must be merged before using the function.

The mode 'woAffy' may be useful to compare Affymetrix to not Affymetrix studies. As the median gene correlation matrix was calculated with a majority of Affymetrix platforms, those platforms tend to be given higher quality than the others with the 'complete' mode, which may be misleading.

See Also

   SNAGEE, qualSample, linktoSnageeFormat

Examples

# Get the list of genes
geneList = getCC()$g;
# Create a random data set
d=list(genes=geneList, data=matrix(rnorm(length(geneList)*50),ncol=50));
# And calculate its quality (it's going to be close to 0)
qualStudy(d, disattenuate=FALSE);

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toSnageeFormat  

**Turns an Eset into a list**

Description

Turns an Eset into a list usable by SNAGEE.

Usage

toSnageeFormat(data)

Arguments

data  

An Eset. If already a list, leaves it as it is.

Details

The function turns an Eset into a list usable by SNAGEE. Gene ID annotations are found using the annotation slot of the Eset, and the related annotation DB. If no annotation DB can be found, gives an error.

In addition, features with identical gene IDs are averaged, and the data are medpolished.

See Also

   SNAGEE, qualStudy, qualSample
Examples

# Get the list of genes
geneList = getCC()$g;

# Create a random data set
d = list(genes = geneList, data = matrix(rnorm(length(geneList) * 50), ncol = 50));

# And calculate its quality (it's going to be close to 0)
qualStudy(d, disattenuate = FALSE);
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