Package 'MiRaGE'

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Title MiRNA Ranking by Gene Expression

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Imports BiocGenerics, S4Vectors, AnnotationDbi, BiocManager

Description The package contains functions for inferece of target gene regulation by miRNA, based on only target gene expression profile.

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Collate MiRaGE_r.R HS_conv_id.R MM_conv_id.R id_conv_gen.R TBL2_HS_gen.R TBL2_MM_gen.R MiRaGEAnalysis.R MiRaGEMean.R MiRaGEMixed.R MiRaGEOneByOne.R getMiRaGEData.R

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`gene_exp` *This ExpressionSet represents gene expression of lung cancer cell line one day after let-7a transfection.*

Description

Gene expression of lung cancer cell line one day after let-7a transfection and negative control. Each of them consists of two biological replicates.

Usage

```
data(gene_exp)
```

Format

gene_id in featureData is mainly, RefSeq mRNA, which is supplemented by GenBank ID if RefSeq mRNA is not available. The expressions are two biological replicates: one day after transfection of let-7a and two biological replicates one day after transfection of mock (negative control), respectively. Sample_name in phenoData represents these characteristic features of samples.

Source

This comes from experiments described in Takahashi et al. (2009).

References

Takahashi, Y., Forrest, A.A.R., Maeno, E., Hashimoto, T., Daub, C.O., Yasuda, J.: MiR-107 and MiR-185 Can Induce Cell cycle Arrest in Human Non Small Cell Lung Cancer Cell Lines? PLoS One 4, e6677 (2009)

getMiRaGEData *Data retrieval function for MiRaGE*

Description

This function retrieves target gene tables of miRNAs, gene id conversion table and miRNA consevation tables

Usage

```
getMiRaGEData(location="local", species="MM", ID="refseq",method="mean",test="ks",
conv="conserved",species_force=T,ID_force=T,conv_force=T)
```

Arguments

location	Specify from where tables are retrieved. If location="local", then tables are retrieved from experimental package, "miRNATarget". If location="web", tables are downloaded from MiRaGE Server web site, "http://www.granular.com/DATA/". Default is "local"
species	a string specifies target species. This should be either "MM" (mouse) or "HS" (human). Default is "MM".
ID	a string specifies gene ID. Default is "refseq".
method	a string specifies the treatment of samples. This should be one of "mean", "mixed", or "one_by_one". Default is "mean".
test	a string specifies statistical test for P-value computation. This should be one of "ks" (Kolmogorov-Smirnov test), "t" (t-test), or "wilcox" (Wilcoxon test). Default is "ks".
conv	a string specifies conservation of miRNA. This should be one of "conserved", "weak_conserve", and "all". Default is "conserved".
species_force	a boolean indicating whether target gene table is downloaded (TRUE) or not (FALSE). Default is TRUE.
ID_force	a boolean indicating whether gene ID conversion table is downloaded (TRUE) or not (FALSE). Default is TRUE.
conv_force	a boolean indicating whether miRNA conservation table is downloaded (TRUE) or not (FALSE). Default is TRUE.

Details

This function retrieves various tables necessary for inference of target gene regulation by miRNAs, based upon the algorithm implemented in the MiRaGE server described in Yoshizawa et al (2011).

Value

tb1	target gene tables of miRNAs. Rownames are miRNA named and colnames are gene ids
TBL2	Transposed matrix of tb1. This object is loaded after this function is called.
conv_id	Conservation table of miRNAs. It is retrieved only when "conv" is not equal to "all". This object is loaded after this function is called.
id_conv	Gene id conversion table between "refseq" ad specified gene id or probe id. This object is loaded after this function is called.

Note

It is usually called inside the function of "MiRaGE". After the execution of getMiRaGEData, objects listed in value are automatically loaded

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
tb1 <- getMiRaGEData(species="HS")
```

HS_conv_id *miRNA conservation table generation function*

Description

This function generates conv_id, which describes conservation information of each human miRNA, from the scratch

Usage

```
HS_conv_id(taxid=9606,species="hsa",destdir="./")
```

Arguments

taxid	taxon id for human. Default is 9606
species	Three characters string which describe human. Default is "hsa".
destdir	Directory where "HS_conv_id" is saved. Default is "./".

Details

This function computes conv_id, which describes conservation information of each human miRNA, used in the MiRaGE server described in Yoshizawa et al (2011). It saves data frame conv_id as the name of "HS_conv_id" in the destination directory.

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
## Not run: HS_conv_id()
```

`id_conv_gen` *Conversion table between refseq id vs various gene id/probe id generation function*

Description

This function generate id_conv, which describes conversion between refseq gene id vs various gene id/prob id, from the scratch

Usage

```
id_conv_gen(SP="MM",gene_id="all",destdir="./")
```

Arguments

`SP`	Species for which gene id conversion table is generated. "MM" for mouse, "HS" for human. Default is "MM"
`gene_id`	gene id for which conversion table toward refseq gene is generated. If "all" is specified, tables for all of available gene ids are generated. Default is "all".
`destdir`	Directory where data sets are saved. Default is "./".

Details

This function generates gene id conversion table, id_conv, used in the MiRaGE server described in Yoshizawa et al (2011). It saves data frames in the destination directory. The name of data set including each id_conv is the form, "SP_refseq_to_gene_id_id", where SP is either MM or HS and gene_id is gene id defined in biomaRt attributes.

Note

If the number of empty rows of each id_conv is less than 20000, its usage is strongly discouraged because the resulting P-values are not trusted.

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
## Not run: id_conv_gen(gene_id="ensembl_transcript_id")
```

MiRaGE *Inference of Target Gene Regulation via MicroRNA*

Description

Wrapper function computes P-values for target gene regulation via miRNAs.

Usage

```
MiRaGE(gene_exp,location="local",species="MM",ID="refseq",method="mean",test="ks",
conv="conserved",species_force=T,ID_force=T,conv_force=T)
```

Arguments

gene_exp	ExpressionSet object which stores target gene expression. featureData must include "gene_id" and phenoData must include "sample_name". The number of columns of expression data MUST be the length of "sample_name". If not, subsetting is required.
location	Specify from where tables are retrieved. If location="local", then tables are retrieved from experimental package, "miRNATarget". If location="web", tables are downloaded from MiRaGE Server web site, "http://www.granular.com/DATA/". Default is "local"
species	a string specifies target species. This should be either "MM" (mouse) or "HS" (human).Default is "MM".
ID	a string specifies gene ID. Default is "refseq".
method	a string specifies the treatment of samples. This should be one of "mean", "mixed", or "one_by_one". Default is "mean".
test	a string specifies statistical test for P-value computation. This should be one of "ks" (Kolmogorov-Smirnov test), "t" (t-test), or "wilcox" (Wilcoxon test). Default is "ks".
conv	a string specifies conservation of miRNA. This should be one of "conserved", "weak_conserve", and "all". Default is "conserved".
species_force	a boolean indicating whether target gene table is downloaded (TRUE) or not (FALSE). Default is TRUE.
ID_force	a boolean indicating whether gene ID conversion table is downloaded (TRUE) or not (FALSE). Default is TRUE.
conv_force	a boolean indicating whether miRNA conservation table is downloaded (TRUE) or not (FALSE). Default is TRUE.

Details

This wrapper function computes P-values for target gene regulation via miRNAs using the algorithm employed for the MiRaGE server described in Yoshizawa et al (2011). P-values are computed based upon the target gene expression change between two experimental conditions.

Value

P0	data frame. The first column of "P0" contains miRNA names. From the second column to last column includes P-values. Smaller P-values mean that target genes are more likely upregulated in the later sample groups than in the former sample groups
P1	data frame. The first column of "P1" contains miRNA names. From the second column to last column includes P-values. Smaller P-values mean that target genes are more likely downregulated in the later sample groups than in the former sample groups

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
data(gene_exp)
result <- MiRaGE(gene_exp,species="HS")
result$P1[1:3,]
```

MM_conv_id *miRNA conservation table generation function*

Description

This function generates conv_id, which describes conservation information of each mouse miRNA, from the scratch

Usage

```
MM_conv_id(taxid=10090,species="mmu",destdir="./")
```

Arguments

taxid	taxon id for human. Default is 11090
species	Three characters string which describe human. Default is "mmu".
destdir	Directory where "MM_conv_id" is saved. Default is "./".

Details

This function computes conv_id, which describes conservation information of each mouse miRNA, used in the MiRaGE server described in Yoshizawa et al (2011). It saves data frame conv_id as the name of "MM_conv_id" in the destination directory.

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
## Not run: MM_conv_id()
```

TBL2_HS_gen *The target genes table for human miRNAs*

Description

This function generates target gene tables for human miRNAs base upon simple seed match toward 3' UTR of target genes

Usage

```
TBL2_HS_gen(SP="hsa",destdir="./")
```

Arguments

SP	Three characters string which describe human. Default is "hsa".
destdir	Directory where "TBL2_HS" is saved. Default is "./".

Details

This function generates target gene tables for human miRNAs, used in the MiRaGE server described in Yoshizawa et al (2011). It saves data frame "TBL2" as the name of "TBL2_HS" in the destination directory.

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
## Not run: TBL2_HS_gen()
```

TBL2_MM_gen *The target genes table for mouse miRNAs*

Description

This function generates target gene tables for human miRNAs base upon simple seed match toward 3' UTR of target genes

Usage

```
TBL2_MM_gen(SP="mmu",destdir="./")
```

Arguments

SP	Three characters string which describe mouse. Default is "mmu".
destdir	Directory where "id_conv" is saved. Default is "./".

Details

This function generates target gene tables for mouse miRNAs, used in the MiRaGE server described in Yoshizawa et al (2011). It saves data frame "TBL2" as the name of "TBL2_MM" in the destination directory.

References

Yoshizawa, M., Taguchi, Y-h., and Yasuda, J. (2011), Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method. Int J Mol Sci 12(12):9265-9276

Examples

```
## Not run: TBL2_MM_gen()
```

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