

Package ‘geuvPack’

April 13, 2017

Title summarized experiment with expression data from GEUVADIS

Version 1.6.0

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Description FPKM from GEUVADIS, annotated to gencode regions

Depends R (>= 2.10), SummarizedExperiment

License Artistic-2.0

LazyLoad yes

biocViews ExperimentData, Genome, SequencingData, MicroarrayData,
ArrayExpress

NeedsCompilation no

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geuvPack-package	<i>summarized experiment with expression data from GEUVADIS</i>
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Description

FPKM from GEUVADIS, annotated to gencode regions

could include more things like miRNA read counts

protco and hasout are convenience vectors enumerating protein coding features and features that appear to have outlying values. The outlier condition for gene g is $(sd(x)/mad(x)) > 2$.

Details

Package: geuvPack
Version: 0.0.0
Suggests:
Depends: GenomicRanges
License: Private
LazyLoad: yes
Built: R 3.1.1; ; 2014-08-22 17:12:50 UTC; unix

gtpath function will get 1000 genomes genotype VCF from Amazon S3; modify if you have local VCF

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geuFPKM

Expression data, gene level FPKM, from GEUVADIS

Description

see metadata(geuFPKM)

Usage

```
data("geuFPKM"); data(gs2p)
```

Format

geuFPKM: A [RangedSummarizedExperiment](#) object.
gsvs: A result from sva::sva
gs2p: a character vector with gene symbols as values and gencode identifiers as names
gencodeV12: a GRanges instance with metadata about V12 gencode genes

Details

FPKM as reported in EBI ArrayExpress E-GEUV-1. Other quantifications may be added in future versions of this package.

"500bffee8e0f770c157e0189e9e50ae" is the output of digest on the txt.gz file of quantifications from which the assay data in the geuFPKM [RangedSummarizedExperiment](#) instance is constructed. This was extracted at Channing Division of Network Medicine on 13 November 2013, and verified to be correct for the contents of the URL below on 11 December 2014.

The README file

http://www.ebi.ac.uk/arrayexpress/files/E-GEUV-1/GeuvadisRNASeqAnalysisFiles_README.txt

has the following remarks

Quantification file set:

- Sample set + sample size :

QC-passed: All QC-passed samples including replicates: 660 (mRNA) or 480 (miRNA)

QC-passed unique: Nonredundant set of unique samples used in most analyses: 462 (mRNA); 452 (miRNA)

- Normalization:

None: raw read counts

Library depth: Read counts scaled by total number of mapped reads (mRNA), or total number reads mapping to miRNAs (miRNA) per sample, then adjusted to the median of the sample set (45M for mRNA, 1.2M for miRNA)

Library depth and transcript length: RPKM

Library depth & expressed & PEER: Library depth scaling as above, removal of units with 0 counts in >50

- November 5, 2013 update: The file GD462.GeneQuantRPKM.50FN.samplename.resk10.norm.txt.gz that had the normalization as above PLUS an additional transformation of each gene's values to standard normal has been replaced by GD462.GeneQuantRPKM.50FN.samplename.resk10.txt.gz

Source

ftp://ftp.ebi.ac.uk/pub/databases/microarray/data/experiment/GEUV/E-GEUV-1/analysis_results/GD462.GeneQuantRPKM.50FN.samplename.resk10.txt.gz

References

PMID 24037378

Examples

```
data(geuFPKM)
geuFPKM
sd(assay(geuFPKM)[1,])
data(gs2p)
gs2p[1:10] # from rowRanges - use with extractBySymbols in gQTLBase
## Not run:
# this is how the gsvs surrogate variable structure
# was derived
library(sva)
library(geuvPack)
data(geuFPKM)
popm = model.matrix(~popcode, data=colData(geuFPKM))
int = popm[,1,drop=FALSE]
gsvs = sva(assay(geuFPKM), popm, int)
save(gsvs, file="gsvs.rda")

## End(Not run)

## maybe str(geuFPKM) ; plot(geuFPKM) ...
```

 gsvs

output of SVA on geuvadis FPKM

Description

output of SVA on geuvadis FPKM

Usage

```
data("gsvs")
```

Format

The format is: List of 4 \$ sv : num [1:462, 1:6] -0.01355 0.00506 0.5762 -0.00857 -0.01388 ... \$ pprob.gam: num [1:23722] 0.741 0.996 0.829 0.754 1 ... \$ pprob.b : num [1:23722] 0.0599 0.9921 0.3887 0.4483 0.8637 ... \$ n.sv : num 6

Details

see the example for information on generating the sv

Examples

```
data(geuFPKM)
geuFPKM
sd(assay(geuFPKM)[1,])
data(gs2p)
gs2p[1:10] # from rowRanges - use with extractBySymbols in gQTLBase
## Not run:
# this is how the gsvs surrogate variable structure
# was derived
library(sva)
library(geuvPack)
data(geuFPKM)
popm = model.matrix(~popcode, data=colData(geuFPKM))
int = popm[,1,drop=FALSE]
gsvs = sva(assay(geuFPKM), popm, int)
save(gsvs, file="gsvs.rda")

## End(Not run)
```

 gtpath

generate path for a VCF file for 1000 genomes genotypes

Description

generate path for a VCF file for 1000 genomes genotypes

Usage

```
gtpath(chrdigit, useS3=TRUE, tmlate)
```

Arguments

<code>chrdigit</code>	suffix to 'chr' to get the chromosome id
<code>useS3</code>	logical, if TRUE, returns URL of an Amazon S3 bucket-resident 1000 genomes VCF
<code>tmplate</code>	character string, used only if useS3 is FALSE. The substring "%N%" will be replaced by value of <code>chrdigit</code>

Details

A subset of samples in GEUVADIS have genotypes recorded in 1000 genomes. This function creates the URL for the VCF corresponding to a chromosome. [cisAssoc](#) can operate on these genotypes.

Value

character string

Examples

```
gtpath(1)
gtpath(1, FALSE, "/tmp/my%%N%.vcf.gz")
```

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