Package 'cnvGSAdata'

October 13, 2022

Title Data used in the vignette of the cnvGSA package

Version 1.32.0

Author Joseph Lugo <joseph.r.lugo@gmail.com>

Description This package contains the data used in the vignette of the cnvGSA package.

Maintainer Joseph Lugo <joseph.r.lugo@gmail.com>

License LGPL

biocViews ExperimentData, Genome, CopyNumberVariationData

Depends R (>= 2.10), cnvGSA

git_url https://git.bioconductor.org/packages/cnvGSAdata

git_branch RELEASE_3_15

git_last_commit 78110e3

git_last_commit_date 2022-04-26

Date/Publication 2022-10-13

R topics documented:

cnvGSAdata-package *Data used in the examples and vignette of the cnvGSA package*

Description

This package contains data used in the examples and vignette of the cnvGSA package.

Details

Raw input files: cnv_AGP_demo.txt - CNV data enrGeneric_AGP_demo.txt - enrichment generic data enrGMT_AGP_demo.gmt - enrichment GMT data kl_gene_AGP_demo.txt - genes of interest data kl_loci_AGP_demo.txt - known loci data ph_AGP_demo.txt - phenotype/covariate data gene_ID_demo.txt - gene ID file

Pre-built input: cnvGSA_input_example.RData

Saved output: cnvGSA_output_example.RData

Pre-built Gene-set data: gs_data_example.RData

Author(s)

Joseph Lugo <joseph.r.lugo@gmail.com>

cnvGSA_input_example.RData *cnvGSA example input*

Description

Pre-built input used in the full workflow example in the cnvGSA vignette.

Usage

```
data("cnvGSA_input_example")
```

Details

The dataset contains cnvGSA.in, a single object of class CnvGSAInput as defined in the cnvGSA package. When processed by cnvGSAlogRegTest() – the main function in that package – it produces as its output an object of class CnvGSAOutput (such as the one stored in cnvGSA_output_example.RData).

cnvGSA_output_example.RData *cnvGSA example output*

Description

Saved output from the full workflow example in the cnvGSA vignette.

Usage

```
data("cnvGSA_output_example")
```

Details

The dataset contains cnvGSA.out, a single object of class CnvGSAOutput as defined in the cnvGSA package. CnvGSAOutput is a simple S4 class containing a slot for each data structure output by cnvGSAlogRegTest (the main function in the package):

res.ls

gsTables.ls

gsData.ls

phData.ls

config.df

res.ls contains the output from the regression tests, gsTables.ls contains the the gene-set tables, gsData.ls contains the gene-set data needed for other scripts, phData.ls contains the phenotype/covariate data and config.df contains the config data frame that allows the other scripts to read in the params.

See the cnvGSA vignette for complete details and discussion.

cnv_AGP_demo.txt *Rare CNV data from Pinto et al. 2014 ASD study*

Description

The file contains rare CNV data similar to that used in the Pinto et al. 2014 ASD study.

Details

The data is stored in a similar format as the Genome Variation Format http://www.sequenceontology.org/resources/gvf.html. See the user manual for more information.

Source

Pinto, D et al. Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. *Am J Hum Genet.* 2014 May 1; 94(5): 677–694.

Examples

```
cnvFile <- system.file( "extdata", "cnv_AGP_demo.txt", package="cnvGSAdata" )
cnv.df  <- read.table (cnvFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

---

enrGeneric_AGP_demo.txt

Generic file for Enrichment Map with data from Pinto et al. 2014 ASD study

---

Description

The file contains gene-sets with their FDR and p-values similar to that used in the Pinto et al. 2014 ASD study.

Details

The data is stored in a generic file format which can be seen here http://www.baderlab.org/Software/EnrichmentMap/UserManual#Generic_results_files

Source

Pinto, D et al. Functional impact of global rare copy number variation in autism spectrum disorders. *Nature.* 2010 Jul 15; 466(7304): 368–72.

Examples

```
enrFile      <- system.file( "extdata", "enrGeneric_AGP_demo.txt", package="cnvGSAdata" )
enrGeneric.df <- read.table (enrFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

---

enrGMT_AGP_demo.gmt *Gene-set data from Pinto et al. 2014 ASD study*

Description

The file contains gene-set data similar to that used in the Pinto et al. 2014 ASD study.

Details

The data is stored in the Gene Matrix Transposed format http://www.baderlab.org/Software/EnrichmentMap/UserManual#Gene_sets_file_.28GMT_file.29.

Source

Pinto, D et al. Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. *Am J Hum Genet.* 2014 May 1; 94(5): 677–694.

Examples

```
gmtFile <- system.file( "extdata", "enrGMT_AGP_demo.gmt", package="cnvGSAdata" )
no_col  <- max(count.fields(gmtFile, sep = "\t"))
gmt.df  <- read.table(gmtFile,sep="\t",fill=TRUE,col.names=1:no_col)
```

---

gene_ID_demo.txt *Gene System data*

Description

The file contains Entrez gene ID's

Details

The data is stored in a format that look like (geneID) -tab- (Symbol) -tab- (Name).

Examples

```
geneIDFile <- system.file( "extdata", "gene_ID_demo.txt", package="cnvGSAdata" )
geneID.df <- read.table (geneIDFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

---

gs_data_example.RData *gsData example output*

Description

Saved gsData described in the cnvGSA vignette.

Usage

```
data("gs_data_example")
```

Details

The dataset contains gsData. It contains the gene-sets analyzed in the cnvGSA vignette as well as the gene set names.

gs_all.ls

gsid2name.chv

gs_all.ls contains the gene-sets used in the analysis and gsid2name.chv contains the gene-set names.

See the cnvGSA vignette for complete details and discussion.

kl_gene_AGP_demo.txt *Genes of interest used in the Pinto et al. 2014 ASD study*

Description

Contains the genes of interest that were also used in the Pinto et al. 2014 ASD study.

Details

This file is used to provide the genes of interest that will be looked at in the testing.

Source

Pinto, D et al. Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. *Am J Hum Genet.* 2014 May 1; 94(5): 677–694.

Examples

```
klGeneFile <- system.file( "extdata", "kl_gene_AGP_demo.txt", package="cnvGSAdata" )
kl_gene.df <- read.table (klGeneFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

kl_loci_AGP_demo.txt *Known loci of genes in the Pinto et al. 2014 ASD study*

Description

Contains the known loci of genes as in the Pinto et al. 2014 ASD study.

Details

This file is used to provide the loci of certain genes and this will affect the results from the test.

Source

Pinto, D et al. Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. *Am J Hum Genet.* 2014 May 1; 94(5): 677–694.

Examples

```
klLociFile <- system.file( "extdata", "kl_loci_AGP_demo.txt", package="cnvGSAdata" )
kl_loci.df <- read.table (klLociFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

ph_AGP_demo.txt *Covariate/phenotype data from Pinto et al. 2014 ASD study*

Description

The file contains covariate/phenotype data similar to that used in the Pinto et al. 2014 ASD study.

Details

The data is stored in a format that is a subset of the the CNV data. It includes all the covariates and phenotypes that the user wants.

Source

Pinto, D et al. Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. *Am J Hum Genet.* 2014 May 1; 94(5): 677–694.

Examples

```
phFile <- system.file( "extdata", "ph_AGP_demo.txt", package="cnvGSAdata" )
ph.df  <- read.table (phFile, header = TRUE, sep = "\t", quote = "\"", stringsAsFactors = FALSE)
```

Index