

Package ‘QCpipeline’

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Type Package
Title Utilities for the QC pipeline
Description Configuration and plotting code
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Suggests MSBVAR
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boxplotMeanSD	<i>Boxplot with mean and SD</i>
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Description

Boxplot with mean and SD

Usage

```
boxplotMeanSD(x, y, data=NULL, xlab=NULL, ylab=NULL, nSD=1, ...)
```

Arguments

x	vector or character string denoting column in data
y	vector or character string denoting column in data
data	data.frame
xlab	title for x axis (defaults to x if data is not NULL)
ylab	title for y axis (defaults to y if data is not NULL)
nSD	number of standard deviations to plot
...	additional plotting arguments

Author(s)

Jess Shen

Examples

```
age <- sample(25:55, 100, replace=TRUE)
sex <- sample(c("M", "F"), 100, replace=TRUE)
boxplotMeanSD(sex, age)

data <- data.frame(age, sex)
boxplotMeanSD("sex", "age", data)
```

dbgapAnnotation

Write annotation files for dbGaP

Description

dbgapScanAnnotation and dbgapSnpAnnotation create text files appropriate for posting on db-GaP.

Usage

```
dbgapScanAnnotation(scanAnnot, dir=".",
  consentVar="consent", subjVar="subj.plink", dupVar="dup.post", omitVar="no.post",
  annotationCol="dbGaP.annot", analysisCol="dbGaP.anal")

dbgapSnpAnnotation(snpAnnot, dir=".",
  annotationCol="dbGaP.annot", analysisCol="dbGaP.anal")
```

Arguments

scanAnnot	A ScanAnnotationDataFrame .
snpAnnot	A SnpAnnotationDataFrame .
dir	A character string with the directory for file output.
consentVar	The variable in scanAnnot containing consent levels.
subjVar	The logical variable in scanAnnot indicating unique subjects to post.
dupVar	The logical variable in scanAnnot indicating duplicate scans to post.
omitVar	The logical variable in scanAnnot indicating scans to be omitted from posting.

annotationCol	The logical column in the metadata indicating which variables should be included in the annotation files.
analysisCol	The logical column in the metadata indicating which variables should be included in the analysis files.

Details

dbgapScanAnnotation writes the following files to dir:

- Sample_annotation.csv
- Sample_annotation_consent_*.csv
- Sample_annotation_duplicates.csv
- Sample_annotation_duplicates_consent_*.csv
- Sample_annotation_DD.txt
- Sample_analysis.csv
- Sample_analysis_duplicates.csv
- Sample_analysis_DD.txt

dbgapSnpAnnotation writes the following files to dir:

- SNP_annotation.csv
- SNP_annotation_DD.txt
- SNP_analysis.csv
- SNP_analysis_DD.txt

Which variables should be written to the annotation and analysis files are indicated in the metadata columns annotationCol and analysisCol.

The data dictionary files are populated from the metadata. The "type" column is automatically generated from the classes of the variables in scanAnnot and snpAnnot.

Author(s)

Stephanie Gogarten

plot2DwithHist	<i>Scatterplot with density</i>
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Description

plot2DwithHist produces a scatterplot of y vs x, along with histograms of the marginal distributions of x and y.

Usage

```
plot2DwithHist(x, y, xlab=NULL, ylab=NULL, xlim=NULL, ylim=NULL,
  sublab=NULL, mn=NULL, sd=NULL, ...)
```

Arguments

x	vector of x coordinates
y	vector of y coordinates
xlab	x-axis label (defaults to variable name)
ylab	y-axis label (defaults to variable name)
xlim	x-axis limits (defaults to [min,max] of X, plus a bit of space)
ylim	y-axis limits (defaults to [min,max] of Y, plus a bit of space)
sublab	sub-label (instead of main, since there's no room)
mn	2-element vector with mean of x and y
sd	2-element vector with sd of x and y
...	additional arguments to pass to points

Author(s)

Leila Zelnick

Examples

```
library(MSBVAR)
# generate some multivariate normal example data
n <- 5000
mu <- c(0, 2)
vmat <- matrix(c(1, 0.7, 0.7, 1), nrow=2)

dat <- rmultnorm(n, mu, vmat) # generates n multivariate normal obs.
x <- dat[,1]
y <- dat[,2]

plot2DwithHist(x, y, xlab="This is the X variable", ylab="This is the Y variable.",
  sub="Example Plot!")
# defining axis limits
plot2DwithHist(x, y, xlab="This is the X variable", ylab="This is the Y variable.",
  sub="Example Plot!", xlim=c(0,4), ylim=c(-2,2))
```

readConfig

Read a configuration file

Description

Read a configuration file

Usage

```
readConfig(file, ...)
```

Arguments

file	file where column 1 is parameter name and column 2 is value.
...	additional arguments to read.table

Value

Returns a named character vector of parameter values.

Author(s)

Stephanie Gogarten

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