Package 'coMET'

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Type Package

Title Visualization regional plots of (epigenome/transcritpome)genome-wide association scan results

Version 0.99.0

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Description
Creates plots of p-values of CpG DNA methylation. Main features of the package include options to display a linkage disequilibrium (LD) plot. Images are created as either PDF/EPS files.

Depends R (>= 3.0.0), grid, grDevices, biomaRt, Gviz, ggbio, trackViewer, rtracklayer, GenomicRanges, colortools, hash

Suggests knitr, RUnit, BiocGenerics

License GPL (>= 2)

URL http://comet.epigen.kcl.ac.uk:3838/coMET/ or http://epigen.kcl.ac.uk/comet

biocViews Software, Epigenetics, Genomics,Sequence, Visualization

VignetteBuilder knitr

NeedsCompilation no

Repository Bioconductor

R topics documented:

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`coMET-package` *coMET: Visualisation of pvalue and correlation between genomic data such as DNA methylation*

Description

The coMET is a R package to visualize the EWAS (epigenome-wide association scans) results in a genomic region. coMET package generates the plots of association, comethylation patterns and a series of annotation tracks at genomic scale.

Details

Package:	coMET
Type:	Package
Version:	0.99.0
Date:	2014-09-26
License:	GPL (>=2)

coMET package that can generate the regional plot capturing the features of co-methylation patterns, EWAS results, and genomic information. A coMET figure includes plot of p-value from the

EWAS result, provides customized annotation tracks, and a triangle heatmap plot which demonstrates the correlation structure of CpG sites in a genomic region, calculated by the pairwise Spearman s rank correlation method.Plots are created as PDF,EPS files.

A list containing two items: config.var and gbl.var, which includes the values of all significant variables used by coMET.

Author(s)

Tiphaine Martin, Idil Erte, Pei-Chien Tsai, Jordana T. Bell

Maintainer: Tiphaine Martin <tiphaine.martin@kcl.ac.uk> Website: http://www.epigen.kcl.ac.uk/comet

References

~~ Literature or other references for background information ~~

See Also

~~ Optionally other standard keywords, one per line, from file KEYWORDS in the R ~~ ~~ documentation directory ~~ ~~ Optional links to other man pages, e.g. ~~ ~~ <coMET> ~~

Examples

```
library(coMET)
library(Gviz)
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4comet.txt")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"

genetrack <-genesENSEMBL(gen,chrom,start,end,showId=FALSE)
snptrack <- snpBiomart(chrom, start, end,
                       dataset="hsapiens_snp_som",showId=FALSE)
strutrack <- structureBiomart(chrom, start, end,
                              strand, dataset="hsapiens_structvar_som")
clinVariant<-ClinVarMainTrack(gen,chrom,start,end)
clinCNV<-ClinVarCnvTrack(gen,chrom,start,end)
gwastrack <-GWASTrack(gen,chrom,start,end)
geneRtrack <-GeneReviewsTrack(gen,chrom,start,end)

listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                 clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile,TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)
```

chromatinHMMAll *Create multiple chromaHMM Broad tracks from UCSC's genome browser*

Description

Create multiple chromaHMM Broad tracks from a connection to UCSC genome browser in using the GViz bioconductor package

Usage

```
chromatinHMMAll(gen, chr, start, end, mySession, track.name = NULL, pattern = NULL,  table.name = NULL)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
track.name	the name of track, for example : Broad ChromHMM
pattern	the pattern of track to visualise
table.name	the name of table from the track

Value

An AnnotationTrack object of GViz

Author(s)

Tiphaine Martin

Examples

```
require("Gviz")
gen <- "hg19"
BROWSER.SESSION="UCSC"
mySession <- browserSession(BROWSER.SESSION)
genome(mySession) <- gen
track.name="Broad ChromHMM"
tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
table.name<-tablestrack[1]
chr <- "chr7"
start <- 38290160
end <- 38313219
PATTERN.REGULATION<-"GM12878"
tmp<-chromatinHMMAll(gen,chr,start,end,mySession,track.name,PATTERN.REGULATION)
```

```
plotTracks(tmp)

tmp<-chromatinHMMAll(gen,chr,start,end,mySession,track.name)
plotTracks(tmp)
```

---

chromatinHMMOne *Create one track of chromaHMM Broad from UCSC's genome browser*

Description

Creation of a track related to only one type of chromaHMM Broad from UCSC

Usage

```
chromatinHMMOne(gen, chr, start, end, mySession, track.name = NULL, table.name = NULL)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
track.name	the name of track, for example : Broad ChromHMM
table.name	the name of table from the track

Value

An AnnotationTrack object of GViz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
BROWSER.SESSION="UCSC"
mySession <- browserSession(BROWSER.SESSION)
genome(mySession) <- gen
track.name="Broad ChromHMM"
tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
table.name<-tablestrack[1]
chr <- "chr7"
start <- 38290160
```

```
end <- 38303219
tmp<-chromatinHMMOne(gen,chr,start,end,mySession,track.name,table.name)
plotTracks(tmp)
```

`chrUCSC2ENSEMBL` *Adding "chr" from the chromsome of UCSC to become ENSEMBL's chromosome*

Description

Adding the letter chr in the beginning of the name of chromosome from UCSC

Usage

```
chrUCSC2ENSEMBL(chr)
```

Arguments

`chr`	the name of chromosome at UCSC format

Author(s)

Tiphaine Martin

Examples

```
chr<-"chr7"
chrUCSC2ENSEMBL(chr)
```

`ClinVarCnvTrack` *Get the genomic positions of variants in the ClinVar database (CNV only)*

Description

Get the genomic positions of variants in the ClinVar database (CNV only, Variants excluded)

Usage

```
ClinVarCnvTrack(gen, chr, start, end, showId = FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"
clinCNV<-ClinVarCnvTrack(gen,chrom,start,end)
plotTracks(clinCNV)
```

ClinVarMainTrack *Get the genomic positions of variants in the ClinVar database (variants only)*

Description

Get the genomic positions of variants in the ClinVar database (Variants only, CNV excluded)

Usage

```
ClinVarMainTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chrom <- "chr2"
start <- 38290160
end <- 38303219

clinVariant<-ClinVarMainTrack(gen,chrom,start,end)
plotTracks(clinVariant)
```

---

comet *Visualize the EWAS results in a genomic region of interest*

Description

The coMET is a R-based package to visualize the EWAS (epigenome-wide association scans) results in a genomic region of interest. The main feature of coMET is to plot the methylation correlation between CpG sites and demonstrate the significance level of EWAS results in the selected region. coMET package generates the plots of association, co-methylation patterns and a series of annotation tracks at genomic scale.

Usage

```
comet(MYDATA.FILE = NULL, MYDATA.FORMAT = "SITE", MYDATA.LARGE.FILE = NULL, MYDATA.LARGE.FORMAT = "SITE
```

Arguments

MYDATA.FILE	Name of a info file for coMET parameters
MYDATA.FORMAT	Format of the input MYDATA.FILE. There are 6 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files for coMET parameters. Multiple files are acceptable, files should be separated by comma
MYDATA.LARGE.FORMAT	Format of additional data visualised in p-value plot. Multiple files are acceptable, files should be separated by comma
CORMATRIX.FILE	Name of raw data or pre-computed correlation matrix
CORMATRIX.METHOD	Options for generating correlation matrix. There are three options: spearman, pearson and kendall
CORMATRIX.FORMAT	Format of the input CORMATRIX.FILE. Two options for raw files (RAW or DTR_RAW) and and pre-computed correlation matrix (CORMATRIX)
CORMATRIX.COLOR.SCHEME	Color scheme options: heat, ETC

MYDATA.REF The name of reference site listed in the MYDATA.FILE

START The first nucleotide position visualised

END the last nucleotide position visualised

ZOOM Default=False

LAB.Y Scale of y-axis. Options: log or ln

PVAL.THRESHOLD Threshold of the significance. Displayed as a red dash line

DISP.PVAL.THRESHOLD
Display only the findings pass PVAL.THRESHOLD

DISP.ASSOCIATION
Optional if MYDATA.FILE= SITE_ASSOC or REGION_ASSOC and contains the effect directions. A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot

DISP.ASSOCIATION.LARGE
Optinal if MYDATA.LARGE.FILE contains the effect directions (SITE_ASSOC, REGION_ASSOC). A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot

DISP.REGION Optional if MYDATA.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the plot will shown in the newly defined x-scale limits

DISP.REGION.LARGE
Optional if MYDATA.LARGE.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the plot will shown in the newly defined x-scale limits

SYMBOLS The symbol shown in the p-value plot. Options: circle, square, diamond, triangle. Symbols can be filled by appending -fill, e.g. square-fill. In this case, the SNP.FILE ASSOC column is read and an up-triangle and down-triangle are used to indicate positive and negative association (indicating susceptibility or protective alleles), respectively. Example: circle,NA,diamond-fill,triangle

SYMBOLS.LARGE The symbol to visualise the data defined in MYDATA.LARGE.FILE. Options: circle, square, diamond, triangle; Symbols can either be filled or not filled by appending -fill e.s., square-fill. NA may be specified. In this case, the SNP.FILE ASSOC column is read and an up-triangle and down-triangle are used to indicate positive and negative association (indicating susceptibility or protective alleles), respectively. Example: circle,NA,diamond-fill,triangle

SAMPLE.LABELS Labels for sample described in MYDATA.FILE to put in the legend

SAMPLE.LABELS.LARGE
Labels for sample described in MYDATA.LARGE.FILE to put in the legend

USE.COLORS Use the colors defined or grey color

DISP.COLOR.REF True if you want to color connection line related to the reference probe in purple, FALSE if you do not want to color connection line related to the reference probe

COLOR.LIST List of colors for displaying p-value symbols related to data coming from MYDATA.FILE

COLOR.LIST.LARGE
: List of colors for displaying p-value symbols related to data coming from MYDATA.LARGE.FILE

DISP.MYDATA
: Logical True or False. The p-value plot is shown if it is TRUE; else the plot will be defined by GViz

BIOFEAT.USER.FILE
: Name of data file to visualise in tracks. They are separated by comma.

BIOFEAT.USER.TYPE
: Track type, multiple tracks can be shown (comma-separated): DataTrack, AnnotationTrack, GeneRegionTrack.

BIOFEAT.USER.TYPE.PLOT
: Format of plot if the data are DataTrack. They are separated by comma.

GENOME
: The human genome reference file. e.g. hg19 for Human genome 19 (NCBI 37)

DATASET.GENE
: The gene names from ENSEMBL. e.g. hsapiens_gene

DATASET.SNP
: Name of SNP database from ENSEMBL; Default: hsapiens_snp

VERSION.DBSNP
: Name of dbSNP used; Default : snp138 version from DBSNP

DATASET.SNP.STOMA
: Optional. Name of somatic SNP database from ENSEMBL. Default : hsapiens_snp_som

DATASET.REGULATION
: Optional. Name of regulation database from ENSEMBL. Default: hsapiens_feature_set

DATASET.STRU
: Optional. Name of structural variation database from ENSEMBL. Default: hsapiens_structvar

DATASET.STRU.STOMA
: Optional. Name of somatic structural variation database from ENSEMBL. Default: hsapiens_structvar_som

PATTERN.REGULATION
: Name of cell type of DATASET.REGULATION. Default: GM12878

BROWSER.SESSION
: Name of database for BioMART connection. Default: UCSC

TRACKS.GVIZ
: list of tracks created by Gviz.

TRACKS.GGBIO
: list of tracks created by ggbio.

TRACKS.TRACKVIEWER
: list of tracks created by track viewer.

DISP.MYDATA.NAMES
: Logical. If it is True (default), it displays the name of CpG sites.

DISP.COLOR.BAR
: color legend for the correlation matrix (range -1 to 1). Default: blue-white-red

DISP.PHYS.DIST
: display the distance of DNA sequence on plots instead of correlation matrix

DISP.LEGEND
: Logical. Display the sample labels and corresponding symbols on the lower right side

DISP.MARKER.LINES
: Logical: True (default) or False. If it is False the red line for PVAL.THRESHOLD is not shown

DISP.CORMATRIXMAP
: Logical: True (default) or False. If it is False, correlation matrix is not shown

DISP.PVALUEPLOT
: Logical: True (default) or False. If it is False, pvalue plot is not shown

DISP.TYPE
: Default: symbol

DISP.MULT.LAB.X
: Logical. Display evenly spaced X-axis thick-labels; up to 5 labels are shown

DISP.CONNECTING.LINES
: Logical: True (default) or False. Display connecting lines between p-value plot and correlation matrix

PALETTE.FILE
: The path of file that contains color codes for heatmap. Colors are hexidecimal HTML color codes; one color per line; if do not want use this option, use the color defined by the option CORMATRIX.COLOR.SCHEME

IMAGE.TITLE
: Title of the plot

IMAGE.NAME
: Name of the plot file

IMAGE.TYPE
: Options: pdf or eps

IMAGE.SIZE
: Default:3.5 inches. Possible sizes : 3.5 or 7

FONT.FACTOR
: Font size of the sample labels. Range: 0-1

SYMBOL.FACTOR
: Size of the symbols. Range: 0-1

PRINT.IMAGE
: Print image in file or not.

CONNECTING.LINES.FACTOR
: Length of the connecting lines. Range: 0-2

CONNECTING.LINES.ADJ
: Position of the connecting lines horizontally. Negative values shift the connecting lines to the left and positive values shift the lines to the right. Range: (-1;1) option -1 means; no connecting lines adj

CONNECTING.LINES.VERT.ADJ
: Position of the connecting lines vertically. Can be used to vertically adjust the position of connecting lines in relation to cpg names. More negative value shift the connecting lines down. Range: -0.5 - 0, if -1,, use the default value related to the plot size (-0.5 for 3.5 plot size; -0.7 for 7.5 plot size)

CONNECTING.LINES.FLEX
: Adjusts the spread of the connecting lines. Range: 0-2

config.file
: Configuration file that contains the values of options instead of defining by command line

VERBOSE
: DEFAULT=FALSE. If it is TRUE, it shows the comments.

Value

Create a plot

Author(s)

Tiphaine Martin

Examples

```
library(Gviz)
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4comet.txt")

chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"

genetrack <-genesENSEMBL(gen,chrom,start,end,showId=FALSE)
snptrack <- snpBiomart(chrom, start, end,
                       dataset="hsapiens_snp_som",showId=FALSE)
strutrack <- structureBiomart(chrom, start, end,
                              strand, dataset="hsapiens_structvar_som")
clinVariant<-ClinVarMainTrack(gen,chrom,start,end)
clinCNV<-ClinVarCnvTrack(gen,chrom,start,end)
gwastrack <-GWASTrack(gen,chrom,start,end)
geneRtrack <-GeneReviewsTrack(gen,chrom,start,end)

listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                 clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile,TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)
```

---

comet.web *Visualize the EWAS results in a genomic region of interest with a pre-defined annotation tracks*

Description

The coMET is a R-based package to visualize the EWAS (epigenome-wide association scans) results in a genomic region of interest. The main feature of coMET is to plot the methylation correlation between CpG sites and demonstrate the significance level of EWAS results in the selected region. coMET package generates the plots of association, co-methylation patterns and a series of annotation tracks at genomic scale.

Usage

```
comet.web(MYDATA.FILE = NULL, MYDATA.FORMAT = c("SITE", "REGION", "SITE_ASSO", "REGION_ASSO"), MYDATA.
```

Arguments

MYDATA.FILE	Name of a info file for coMET parameters
MYDATA.FORMAT	Format of the input MYDATA.FILE. There are 6 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files for coMET parameters. Multiple files are acceptable, files should be separated by comma

MYDATA.LARGE.FORMAT
: Format of additional data visualised in p-value plot. Multiple files are acceptable, files should be separated by comma

CORMATRIX.FILE
: File with correlation matrix or raw data to create the correlation

CORMATRIX.METHOD
: Options for generating correlation matrix. There are three options: spearman, pearson and kendall

CORMATRIX.FORMAT
: Format of the input CORMATRIX.FILE. Two options for raw files (RAW or DTR_RAW) and and pre-computed correlation matrix (CORMATRIX)

CORMATRIX.COLOR.SCHEME
: Color scheme options: heat, ETC

MYDATA.REF
: The name of reference site listed in the MYDATA.FILE

START
: The first nucleotide position visualised

END
: the last nucleotide position visualised

ZOOM
: Default=False

LAB.Y
: Scale of y-axis. Options: log or ln

PVAL.THRESHOLD
: Threshold of the significance. Displayed as a red dash line

DISP.PVAL.THRESHOLD
: Display only the findings pass PVAL.THRESHOLD

DISP.ASSOCIATION
: Optional if MYDATA.FILE= SITE_ASSOC or REGION_ASSOC and contains the effect directions. A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot

DISP.ASSOCIATION.LARGE
: Optinal if MYDATA.LARGE.FILE contains the effect directions (SITE_ASSOC, REGION_ASSOC). A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot

DISP.REGION
: Optional if MYDATA.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the plot will shown in the newly defined x-scale limits

DISP.REGION.LARGE
: Optional if MYDATA.LARGE.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the plot will shown in the newly defined x-scale limits

SYMBOLS
: The symbol shown in the p-value plot. Options: circle, square, diamond, triangle. Symbols can be filled by appending -fill, e.g. square-fill. In this case, the SNP.FILE ASSOC column is read and an up-triangle and down-triangle are used to indicate positive and negative association (indicating susceptibility or protective alleles), respectively. Example: circle,NA,diamond-fill,triangle

SYMBOLS.LARGE
: The symbol to visualise the data defined in MYDATA.LARGE.FILE. Options: circle, square, diamond, triangle; Symbols can either be filled or not filled by

appending -fill e.s., square-fill. NA may be specified. In this case, the SNP.FILE ASSOC column is read and an up-triangle and down-triangle are used to indicate positive and negative association (indicating susceptibility or protective alleles), respectively. Example: circle,NA,diamond-fill,triangle

`SAMPLE.LABELS` Labels for sample described in MYDATA.FILE to put in the legend

`SAMPLE.LABELS.LARGE`
Labels for sample described in MYDATA.LARGE.FILE to put in the legend

`USE.COLORS` DEFAULT= TRUE; it is FALSE, no color

`DISP.COLOR.REF` True if you want to color connection line related to the reference probe in purple, FALSE if you do not want to color connection line related to the reference probe

`COLOR.LIST` List of colors for displaying p-value symbols related to data coming from MYDATA.FILE

`COLOR.LIST.LARGE`
List of colors for displaying p-value symbols related to data coming from MYDATA.LARGE.FILE

`BIOFEAT.USER.FILE`
Name of data file to visualise in tracks. They are separated by comma.

`BIOFEAT.USER.TYPE`
Track type, multiple tracks can be shown (comma-separated): DataTrack, AnnotationTrack, GeneRegionTrack.

`BIOFEAT.USER.TYPE.PLOT`
Format of plot if the data are DataTrack. They are separated by comma.

`LIST.TRACKS` Options from geneENSEMBL,CGI,ChromHMM,DNAse,RegENSEMBL,SNP

`PATTERN.REGULATION`
The tissue or the list of tissues to visualise the regulation region defined by Broad ChromHMM

`IMAGE.TITLE` Title of the plot

`IMAGE.NAME` Name of the plot file

`IMAGE.TYPE` Options: pdf or eps

`IMAGE.SIZE` Default:3.5 inches. Possible sizes : 3.5 or 7

`PRINT.IMAGE` DEFAULT=FALSE. if the value is false, it does not produce the plot in a file. If the value is true, it print the plot in a file

`config.file` Configuration file that contains the values of options instead of defining by command line

`VERBOSE` Visualisation of comment to understand what happens

Author(s)

Tiphaine Martin

Examples

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom.txt")
comet.web(config.file=configfile,PRINT.IMAGE=FALSE,VERBOSE=FALSE)
```

CoreillCNVTrack *Get the genomic positions of copy-number variants (CNVs) in chromosomal aberration and inherited disorder cell lines in the NIGMS Human Genetic Cell Repository*

Description

Get the genomic positions of copy-number variants (CNVs) in chromosomal aberration and inherited disorder cell lines in the NIGMS Human Genetic Cell Repository

Usage

```
CoreillCNVTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chrom <- "chr2"
start <- 38290160
end <- 38303219

coreilVariant<-CoreillCNVTrack(gen,chrom,start,end)
plotTracks(coreilVariant)
```

COSMICTrack *Get the genomic positions of variants of COSMIC*

Description

Get the genomic positions of variants of COSMIC, the "Catalogue Of Somatic Mutations In Cancer"

Usage

```
COSMICTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"
cosmicVariant<-COSMICTrack(gen,chrom,start,end)
plotTracks(cosmicVariant)
```

cpgIslandsUCSC *Compute the correlation matrix between CpG sites*

Description

Compute the correlation matrix between CpG sites

Usage

```
cpgIslandsUCSC(gen, chr, start, end)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"

tmp<-cpgIslandsUCSC(gen, chr, start, end)
plotTracks(tmp)
```

DNAseUCSC *Creation of an UCSC's DNase clusters track*

Description

Creation of DNase cluster track from a connection to UCSC genome browser in using the GViz bioconductor package

Usage

```
DNAseUCSC(gen, chr, start, end, mySession, track.name = NULL, table.name = NULL)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
track.name	the name of track DNAseUCSC
table.name	the name of table from the track

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
BROWSER.SESSION="UCSC"
mySession <- browserSession(BROWSER.SESSION)
genome(mySession) <- gen
track.name="Broad ChromHMM"
tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
table.name<-tablestrack[1]
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-DNAseUCSC(gen,chr,start,end,mySession)
plotTracks(tmp)
```

GADTrack *Get the genomic positions of variants of Genetic Association Database (GAD)*

Description

Get the genomic positions of variants of Genetic Association Database (GAD) (archive of human genetic association studies of complex diseases and disorders)

Usage

```
GADTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-GADTrack(gen,chr,start,end)
plotTracks(tmp)
```

gcContent *create track GC content from UCSC*

Description

create track GC content from UCSC

Usage

```
gcContent(gen, chr, start, end)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-gcContent(gen,chr,start,end)
plotTracks(tmp)
```

GeneReviewsTrack *Get the genomic positions of variants in GeneReviews*

Description

Get the genomic positions of variants in GeneReviews

Usage

```
GeneReviewsTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"

chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-GeneReviewsTrack(gen,chr,start,end)
plotTracks(tmp)
```

---

genesENSEMBL *Get the genes in the genomic regions of interest*

Description

Get the genes in the genomic regions of interest

Usage

```
genesENSEMBL(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-genesENSEMBL(gen,chr,start,end)
plotTracks(tmp)
```

---

genesNameENSEMBL *Get the name of genes in the genomic regions of interest*

Description

Get the name of genes in the genomic regions of interest

Usage

```
genesNameENSEMBL(gen, chr, start, end, dataset)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
dataset	Name of database to select genes

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
dataset<- "hsapiens_gene_ensembl"
genesNameENSEMBL(gen,chr,start,end,dataset)
```

GWASTrack *Get the genomic positions of variants in GWAS catalog*

Description

Get the genomic positions of variants in NHGRI Catalog of Published Genome-Wide Association Studies

Usage

```
GWASTrack(gen, chr, start, end, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-GWASTrack(gen,chr,start,end)
plotTracks(tmp)
```

HistoneAll *Create multiple tracks of Histone from UCSC's genome browser*

Description

Create multiple tracks of Histone from UCSC's genome browser (ENCODE/Broad)

Usage

```
HistoneAll(gen, chr, start, end, mySession, pattern = NULL, track.name = NULL, table.name = NULL)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
pattern	The pattern of cell type
track.name	the name of track, for example : Histone
table.name	the name of table from the track

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
BROWSER.SESSION="UCSC"
mySession <- browserSession(BROWSER.SESSION)
genome(mySession) <- gen
chr <- "chr7"
start <- 38290160
end <- 38313219

tmp<-HistoneAll(gen,chr,start,end,mySession)
plotTracks(tmp)
```

HistoneOne *Create track one type of Histone density from UCSC*

Description

Create track one type of Histone density from UCSC (ENCODE/Broad)

Usage

```
HistoneOne(gen, chr, start, end, mySession, track.name = NULL, table.name = NULL)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
track.name	the name of track, for example : Histone
table.name	the name of table from the track

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
BROWSER.SESSION="UCSC"
mySession <- browserSession(BROWSER.SESSION)
genome(mySession) <- gen

chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-HistoneOne(gen,chr,start,end,mySession)
plotTracks(tmp)
```

ISCATrack *Get the genomic positions of variants in ISCA*

Description

Get the genomic positions of variants from International Standards for Cytogenomic Arrays (ISCA) Consortium

Usage

```
ISCATrack(gen, chr, start, end, table, showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)

table	A table of ISCAT : iscaBenign, iscaCuratedBenign, iscaCuratedPathogenic, iscaLikelyBenign, iscaLikelyPathogenic, iscaPathGainCum, iscaPathLossCum, iscaPathogenic, iscaUncertain
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-ISCATrack(gen,chr,start,end,"iscaPathGainCum")
plotTracks(tmp)
```

---

knownGenesUCSC *create track Known genes from UCSC*

Description

create track Known genes from UCSC

Usage

```
knownGenesUCSC(gen, chr, start, end)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-knownGenesUCSC(gen,chr,start,end)
plotTracks(tmp)
```

regulationBiomart *create track Regulation from ENSEMBL*

Description

create track Regulation from ENSEMBL

Usage

```
regulationBiomart(chr, start, end, dataset)
```

Arguments

chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
dataset	The name of database

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-regulationBiomart(gen,chr,start,end,"hsapiens_feature_set")
plotTracks(tmp)
```

snpBiomart *Create track Short Variation from ENSEMBL*

Description

Create track Short Variation from ENSEMBL

Usage

```
snpBiomart(chr, start, end, dataset, showId=FALSE, title = NULL)
```

Arguments

chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
dataset	The name of SNP database
showId	Show the id of element or not
title	The name of annotation track

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-snpBiomart(gen,chr,start,end,"hsapiens_snp_som")
plotTracks(tmp)
```

---

snpLocationsUCSC *Create track SNPs from UCSC*

Description

Create track SNPs from UCSC

Usage

```
snpLocationsUCSC(gen, chr, start, end, track)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
track	The name of database

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-snpLocationsUCSC(gen,chr,start,end,"snp138")
plotTracks(tmp)
```

`structureBiomart` *Create track Structural Variation from ENSEMBL*

Description

Create track Structural Variation from ENSEMBL

Usage

```
structureBiomart(chr, start, end, strand, dataset, showId=FALSE, title = NULL)
```

Arguments

`chr`	the chromosome of interest
`start`	the first position of region of interest (the smallest value)
`end`	the last position of region of interest (the biggest value)
`strand`	the strand of genome to extract structure
`dataset`	The name of database
`showId`	Show the id of element or not
`title`	The name of annotation track

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-structureBiomart(gen,chr,start,end,"hsapiens_structvar")
plotTracks(tmp)
```

transcriptENSEMBL *Creation track for transcription sites*

Description

Creation track for transcription sites

Usage

```
transcriptENSEMBL(gen, chr, start, end,showId = FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-transcriptENSEMBL(gen,chr,start,end)
plotTracks(tmp)
```

xenorefGenesUCSC *Create track reference Genes from UCSC*

Description

Create track reference Genes from UCSC

Usage

```
xenorefGenesUCSC(gen, chr, start, end,showId=FALSE)
```

Arguments

gen	the name of genome
chr	the chromosome of interest
start	the first position of region of interest (the smallest value)
end	the last position of region of interest (the biggest value)
showId	Show Id of genetic elements

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
tmp<-xenorefGenesUCSC(gen,chr,start,end)
plotTracks(tmp)
```

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