Package 'coMET'

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Type Package

Title coMET: visualisation of regional epigenome-wide association scan (EWAS) results and DNA co-methylation patterns.

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Description Visualisation of EWAS results in a genomic region. In addition to phenotype-association P-values, coMET also generates plots of co-methylation patterns and provides a series of annotation tracks.

Depends R (>= 3.1.0), grid, biomaRt, Gviz, rtracklayer, GenomicRanges

Suggests knitr, RUnit, BiocGenerics, BiocStyle

Imports colortools, hash, grDevices, gridExtra, ggbio, ggplot2, trackViewer

License GPL (>= 2)

URL http://epigen.kcl.ac.uk/comet

biocViews
Software, DifferentialMethylation, Visualization, Sequencing, Genetics, FunctionalGenomics

VignetteBuilder knitr

NeedsCompilation no

Repository Bioconductor

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`coMET-package` *visualisation of regional epigenome-wide association scan (EWAS) results and DNA co-methylation patterns*

Description

coMET is an R package for visualising EWAS results in a genomic region. Along with phenotype-association plots, coMET also generates plots of co-methylation patterns and provides a series of annotation tracks.

Details

Package:	coMET
Type:	Package
Version:	0.99.4
Date:	2014-11-05
License:	GPL (>=2)

coMET is an R package that can generate regional plots of EWAS results, DNA co-methylation patterns, and genomic information. A coMET figure includes 3 panels with a plot of P-values from EWAS, customized annotation tracks, and a triangle heatmap plot which demonstrates the correlation structure of DNA methylation at the CpG sites in the genomic region. Plots are created as PDF or EPS files.

Author(s)

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Website: http://www.epigen.kcl.ac.uk/comet

References

Martin, T.C, Erte, I, Tsai, P-C, Bell, J.T., coMET: an R plotting package to visualize regional plots of epigenome-wide association scan results, QG14, 2014.

Examples

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4comet.txt")
myinfofile <- file.path(extdata, "cyp1b1_infofile.txt")
myexpressfile <- file.path(extdata, "cyp1b1_infofile_exprGene_region.txt")
mycorrelation <- file.path(extdata, "cyp1b1_res37_rawMatrix.txt")

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

if(interactive()){
  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, MYDATA.FILE=myinfofile, CORMATRIX.FILE=mycorrelation,
      MYDATA.LARGE.FILE=myexpressfile, TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)

} else {
  data(geneENSEMBLtrack)
  data(snpBiomarttrack)
  data(ISCAtrack)
  data(strucBiomarttrack)
  data(ClinVarCnvTrack)
  data(clinVarMaintrack)
  data(GWASTrack)
  data(GeneReviewTrack)

  listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile, MYDATA.FILE=myinfofile, CORMATRIX.FILE=mycorrelation,
      MYDATA.LARGE.FILE=myexpressfile, TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)
}
```

`chromatinHMMAll` *Creating multiple chromHMM tracks from the UCSC genome browser*

Description

Create multiple chromHMM Broad tracks by connecting to the UCSC genome browser using the GViz bioconductor package

Usage

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

Arguments

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

Value

list of AnnotationTrack objects of GViz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
  gen <- "hg19"
  chr <- "chr2"
  start <- 38290160
  end <- 38313219
if(interactive()){
  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]
  PATTERN.REGULATION<-"GM12878"

 chromhmmPattern<-chromatinHMMAll(gen,chr,start,end,mySession,track.name,PATTERN.REGULATION)
  plotTracks(chromhmmPattern, from = start, to =end)

  chromhmmNoPattern<-chromatinHMMAll(gen,chr,start,end,mySession,track.name)
  plotTracks(chromhmmNoPattern, from = start, to =end)
} else {

  data(chromhmmPattern)
  plotTracks(chromhmmPattern, from = start, to =end)

  data(chromhmmNoPattern)
  plotTracks(chromhmmNoPattern, from = start, to =end)
}
```

---

chromatinHMMOne *Creating one chromHMM track from the UCSC genome browser*

Description

Create one track of only one type of chromHMM Broad element from the UCSC genome browser using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
  gen <- "hg19"
  chr <- "chr2"
  start <- 38290160
  end <- 38303219
if(interactive()) {

  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]
  chromhmmtrackone<-chromatinHMMOne(gen,chr,start,end,mySession,track.name,table.name)
  plotTracks(chromhmmtrackone, from = start, to =end)
}else {

  data(chromhmmtrackone)
  plotTracks(chromhmmtrackone, from = start, to =end)
}
```

chrUCSC2ENSEMBL *Removing "chr" to the chromosome number from UCSC to transform it to ENSEMBL chromosome format*

Description

Removing "chr" at the beginning of the chromosome number

Usage

```
chrUCSC2ENSEMBL(chr)
```

Arguments

chr	the chromosome number in UCSC format

Value

the number of chromosome at ENSEMBL format

Author(s)

Tiphaine Martin

Examples

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

ClinVarCnvTrack *Create one track of the genomic positions of variants from the ClinVar database (CNV only)*

Description

Create one track of the genomic positions of variants from the ClinVar database (CNV only, Variants excluded) using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"
if(interactive()){
  clinCNV<-ClinVarCnvTrack(gen,chrom,start,end)
  plotTracks(clinCNV, from = start, to =end)
}else {
  data(ClinVarCnvTrack)
  plotTracks(clinCNV, from = start, to =end)
}
```

ClinVarMainTrack *Create one track of the genomic positions of variants from the ClinVar database (variants only)*

Description

Create one track of the genomic positions of variants from the ClinVar database (Variants only, CNV excluded) using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()) {
  clinVariant<-ClinVarMainTrack(gen,chrom,start,end)
  plotTracks(clinVariant, from = start, to =end)
}else{
  data(clinVarMaintrack)
  plotTracks(clinVariant, from = start, to =end)
}
```

---

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

Description

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

Usage

```
comet(MYDATA.FILE = NULL, MYDATA.FORMAT = "SITE", MYDATA.LARGE.FILE = NULL,
    MYDATA.LARGE.FORMAT = "SITE", CORMATRIX.FILE = NULL, CORMATRIX.METHOD = "spearman",
    CORMATRIX.FORMAT = "RAW", CORMATRIX.COLOR.SCHEME = "bluewhitered", MYDATA.REF = NULL,
     START = NULL, END = NULL, ZOOM = FALSE, LAB.Y = "log", PVAL.THRESHOLD = 1e-05,
    DISP.PVAL.THRESHOLD = 1, DISP.ASSOCIATION = FALSE, DISP.ASSOCIATION.LARGE = FALSE,
      DISP.REGION = FALSE, DISP.REGION.LARGE = FALSE, SYMBOLS = "circle-fill",
      SYMBOLS.LARGE = NA, SAMPLE.LABELS = NULL, SAMPLE.LABELS.LARGE = NULL,
    USE.COLORS = TRUE , DISP.COLOR.REF = TRUE, COLOR.LIST = NULL, COLOR.LIST.LARGE = NULL,
      DISP.MYDATA = TRUE, BIOFEAT.USER.FILE = NULL, BIOFEAT.USER.TYPE = NULL,
    BIOFEAT.USER.TYPE.PLOT = NULL, GENOME = "hg19", DATASET.GENE = "hsapiens_gene_ensembl",
      TRACKS.GVIZ = NULL, TRACKS.GGBIO = NULL, TRACKS.TRACKVIEWER = NULL,
      DISP.MYDATA.NAMES = TRUE, DISP.COLOR.BAR = TRUE, DISP.PHYS.DIST = TRUE,
      DISP.LEGEND = TRUE, DISP.MARKER.LINES = TRUE, DISP.CORMATRIXMAP = TRUE,
      DISP.PVALUEPLOT =TRUE, DISP.TYPE = "symbol", DISP.MULT.LAB.X = FALSE,
      DISP.CONNECTING.LINES = TRUE, PALETTE.FILE = NULL, IMAGE.TITLE = NULL,
     IMAGE.NAME = "coMET", IMAGE.TYPE = NULL, IMAGE.SIZE = 3.5, FONT.FACTOR = NULL,
      SYMBOL.FACTOR = NULL, PRINT.IMAGE = TRUE, CONNECTING.LINES.FACTOR = 1.5,
      CONNECTING.LINES.ADJ = 0.01, CONNECTING.LINES.VERT.ADJ = -1,
      CONNECTING.LINES.FLEX = 0, config.file = NULL, VERBOSE = FALSE)
```

Arguments

MYDATA.FILE	Name of the info file describing the coMET parameters
MYDATA.FORMAT	Format of the input data in MYDATA.FILE. There are 4 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files describing the coMET parameters. File names should be comma-separated.
MYDATA.LARGE.FORMAT	Format of additional data to be visualised in the p-value plot. File names should be comma-separated.
CORMATRIX.FILE	Name of the raw data file or the pre-computed correlation matrix file.
CORMATRIX.METHOD	Options for calculating the correlation matrix: spearman, pearson and kendall
CORMATRIX.FORMAT	Format of the input CORMATRIX.FILE. TThere are two options: raw file (RAW if CpG sites are by column and samples by row or RAW_REV if CpG site are by row and samples by column) and pre-computed correlation matrix (CORMATRIX)
CORMATRIX.COLOR.SCHEME	Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored
MYDATA.REF	The name of the reference CpG-site listed in MYDATA.FILE
START	The first nucleotide position to be visualised
END	the last nucleotide position to be visualised
ZOOM	Default=False

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

PVAL.THRESHOLD Significance threshold to be displayed as a red dashed line

DISP.PVAL.THRESHOLD
Display only the findings that pass the value put in DISP.PVAL.THRESHOLD

DISP.ASSOCIATION
This logical option works only if MYDATA.FILE contains the effect direction (MYDATA.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST. On the other hand, if the association is negative, the color is the opposed color.

DISP.ASSOCIATION.LARGE
This logical option works only if MYDATA.LARGE.FILE contains the effect direction (MYDATA.LARGE.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST.LARGE. On the other hand, if the association is negative, the color is the opposed color.

DISP.REGION This logical option works only if MYDATA.FILE contains regions (MYDATA.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.

DISP.REGION.LARGE
This logical option works only if MYDATA.LARGE.FILE contains regions (MYDATA.LARGE.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.

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. Example: circle,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. Example: circle,diamond-fill,triangle

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

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

USE.COLORS Use the colors defined or use the grey color scheme

DISP.COLOR.REF Logical option TRUE or FALSE (TRUE default). if TRUE, the connection line related to the reference probe is in purple, if FALSE if the connection line related to the reference probe stay black.

COLOR.LIST List of colors for displaying the P-value symbols related to the data in MYDATA.FILE

COLOR.LIST.LARGE
List of colors for displaying the P-value symbols related to the data in MYDATA.LARGE.FILE

DISP.MYDATA logical option TRUE or FALSE. TRUE (default). If TRUE, the P-value plot is shown; if FALSE the plot will be defined by GViz

BIOFEAT.USER.FILE
Name of data file to visualise in the tracks. File names should be comma-separated.

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

BIOFEAT.USER.TYPE.PLOT
Format of the plot if the data are shown with the Gviz's function called DataTrack (comma-separated)

GENOME The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37),"grch38" (GRCh38)

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

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 option TRUE or FALSE. If True (default), the names of the CpG sites are displayed.

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

DISP.PHYS.DIST logical option (TRUE or FALSE). TRUE (default).Display the bp distance on the plots

DISP.LEGEND logical option TRUE or FALSE. TRUE (default) Display the sample labels and corresponding symbols on the lower right side

DISP.MARKER.LINES
logical option TRUE or FALSE. TRUE (default), if FALSE the red line for PVAL.THRESHOLD is not shown

DISP.CORMATRIXMAP
logical option TRUE or FALSE. TRUE (default), if FALSE correlation matrix is not shown

DISP.PVALUEPLOT
logical option (TRUE or FALSE). TRUE (default), if FALSE the pvalue plot is not shown

DISP.TYPE Default: symbol

DISP.MULT.LAB.X
logical option TRUE or FALSE. FALSE (default).Display evenly spaced X-axis labels; up to 5 labels are shown.

DISP.CONNECTING.LINES
: logical option TRUE or FALSE. TRUE (default) displays connecting lines between p-value plot and correlation matrix

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

IMAGE.TITLE
: Title of the plot

IMAGE.NAME
: Path and Name of the plot file without extension

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.

CONNECTING.LINES.VERT.ADJ
: Position of the connecting lines vertically. Can be used to vertically adjust the position of the connecting lines in relation to the CpG-site names. Negative value shift the connecting lines down. Range: (-0.5 - 0), option -1 mean 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 these options instead of defining these by command line

VERBOSE
: logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

Value

Create a plot

Author(s)

Tiphaine Martin

Examples

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4comet.txt")
myinfofile <- file.path(extdata, "cyp1b1_infofile.txt")
myexpressfile <- file.path(extdata, "cyp1b1_infofile_exprGene_region.txt")
mycorrelation <- file.path(extdata, "cyp1b1_res37_rawMatrix.txt")
```

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

if(interactive()){
  cat("interactive")
  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, MYDATA.FILE=myinfofile, CORMATRIX.FILE=mycorrelation,
      MYDATA.LARGE.FILE=myexpressfile, TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)

} else {
  cat("Non interactive")
  data(geneENSEMBLtrack)
  data(snpBiomarttrack)
  data(ISCAtrack)
  data(strucBiomarttrack)
  data(ClinVarCnvTrack)
  data(clinVarMaintrack)
  data(GWASTrack)
  data(GeneReviewTrack)
  listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile, MYDATA.FILE=myinfofile, CORMATRIX.FILE=mycorrelation,
      MYDATA.LARGE.FILE=myexpressfile, TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)
}
```

`comet.web` *Visualize EWAS results in a genomic region of interest with predefined annotation tracks*

Description

coMET is an R-based package to visualize EWAS (epigenome-wide association scans) results in a genomic region of interest. The main feature of coMET is to plot the the significance level of EWAS

results in the selected region, along with correlation in DNA methylation values between CpG sites in the region. The coMET package generates plots of phenotype-association, co-methylation patterns, and a series of annotation tracks.

Usage

```
comet.web(MYDATA.FILE = NULL, MYDATA.FORMAT = c("SITE", "REGION", "SITE_ASSO", "REGION_ASSO"),
          MYDATA.LARGE.FILE = NULL,
         MYDATA.LARGE.FORMAT = c("SITE", "REGION", "SITE_ASSO", "REGION_ASSO"),
       CORMATRIX.FILE = NULL, CORMATRIX.METHOD = c("spearman", "pearson", "kendall"),
          CORMATRIX.FORMAT = c("CORMATRIX", "RAW","RAW_REV"),
          CORMATRIX.COLOR.SCHEME = "heat", MYDATA.REF = NULL,
          GENOME="hg19", START = NULL, END = NULL, ZOOM = FALSE, LAB.Y = "log",
          PVAL.THRESHOLD = 1e-07, DISP.PVAL.THRESHOLD = 1,
          DISP.ASSOCIATION = FALSE, DISP.ASSOCIATION.LARGE = FALSE,
        DISP.REGION = FALSE, DISP.REGION.LARGE = FALSE, SYMBOLS = "circle-fill",
          SYMBOLS.LARGE = NA, SAMPLE.LABELS = NULL, SAMPLE.LABELS.LARGE = NULL,
          USE.COLORS = TRUE, DISP.COLOR.REF = TRUE, COLOR.LIST = NULL,
          COLOR.LIST.LARGE = NULL, BIOFEAT.USER.FILE = NULL,
          BIOFEAT.USER.TYPE = c("GeneRegion", "Annotation", "Data"),
          BIOFEAT.USER.TYPE.PLOT = NULL,
          LIST.TRACKS = "geneENSEMBL,CGI,ChromHMM,DNAse,RegENSEMBL,SNP",
          PATTERN.REGULATION = "GM12878",
         IMAGE.TITLE = NULL, IMAGE.NAME = "coMET", IMAGE.TYPE = c("pdf", "eps"),
       IMAGE.SIZE = 3.5, PRINT.IMAGE = FALSE, config.file = NULL, VERBOSE = FALSE)
```

Arguments

MYDATA.FILE	Name of the info file describing the coMET parameters
MYDATA.FORMAT	Format of the input data in MYDATA.FILE. There are 4 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files describing the coMET parameters. File names should be comma-separated.
MYDATA.LARGE.FORMAT	Format of additional data to be visualised in the p-value plot. File names should be comma-separated.
CORMATRIX.FILE	Name of the raw data file or the pre-computed correlation matrix file.
CORMATRIX.METHOD	Options for calculating the correlation matrix: spearman, pearson and kendall
CORMATRIX.FORMAT	Format of the input CORMATRIX.FILE. There are three options: raw file (RAW if CpG sites are by column and samples by row or RAW_REV if CpG site are by row and samples by column) and pre-computed correlation matrix (CORMATRIX)
CORMATRIX.COLOR.SCHEME	Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored

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

GENOME The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37),"grch38" (GRCh38)

START The first nucleotide position to be visualised

END the last nucleotide position to be visualised

ZOOM logical option TRUE or FALSE. FALSE (default)

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

PVAL.THRESHOLD Significance threshold to be displayed as a red dashed line

DISP.PVAL.THRESHOLD
Display only the findings that pass the value put in DISP.PVAL.THRESHOLD

DISP.ASSOCIATION
This logical option works only if MYDATA.FILE contains the effect direction (MYDATA.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST. On the other hand, if the association is negative, the color is the opposed color.

DISP.ASSOCIATION.LARGE
This logical option works only if MYDATA.LARGE.FILE contains the effect direction (MYDATA.LARGE.FORMA=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST.LARGE. On the other hand, if the association is negative, the color is the opposed color.

DISP.REGION This logical option works only if MYDATA.FILE contains regions (MYDATA.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.

DISP.REGION.LARGE
This logical option works only if MYDATA.LARGE.FILE contains regions (MYDATA.LARGE.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.

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. Example: circle,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. Example: circle,diamond-fill,triangle

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

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

USE.COLORS
: Use the colors defined or use the grey color scheme

DISP.COLOR.REF
: Logical option TRUE or FALSE (TRUE default). if TRUE, the connection line related to the reference probe is in purple, if FALSE if the connection line related to the reference probe stay black.

COLOR.LIST
: List of colors for displaying the P-value symbols related to the data in MYDATA.FILE

COLOR.LIST.LARGE
: List of colors for displaying the P-value symbols related to the data in MYDATA.LARGE.FILE

BIOFEAT.USER.FILE
: Name of data file to visualise in the tracks. File names should be comma-separated.

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

BIOFEAT.USER.TYPE.PLOT
: Format of the plot if the data are shown with the Gviz's function called DataTrack (comma-separated)

LIST.TRACKS
: List of annotation tracks to visualise. Options include geneENSEMBL, CGI, ChromHMM, DNAse, RegENSEMBL, SNP, transcriptENSEMBL, SNPstoma, SNPstru, SNPstrustoma, ISCA, COSMIC, GAD, ClinVar, GeneReviews, GWAS, ClinVarCNV, GCcontent, genesUCSC, xenogenesUCSC.

PATTERN.REGULATION
: The cell/tissue or the list of cells/tissues to visualise in the regulation region defined by Broad ChromHMM

IMAGE.TITLE
: Title of the plot

IMAGE.NAME
: path and Name of the plot file without extension

IMAGE.TYPE
: Options: pdf or eps

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

PRINT.IMAGE
: Print image in file or not.

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

VERBOSE
: logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

Author(s)

Tiphaine Martin

Examples

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4webserver.txt")
```

```
myinfofile <- file.path(extdata, "cyp1b1_infofile.txt")
myexpressfile <- file.path(extdata, "cyp1b1_infofile_exprGene_region.txt")
mycorrelation <- file.path(extdata, "cyp1b1_res37_rawMatrix.txt")

comet.web(config.file=configfile,  MYDATA.FILE=myinfofile, CORMATRIX.FILE=mycorrelation,
      MYDATA.LARGE.FILE=myexpressfile, PRINT.IMAGE=FALSE,VERBOSE=FALSE)
```

`CoreillCNVTrack` *Create one track of the genomic positions of CNV in chromosomal aberration and inherited disorders from the NIGMS Human Genetic Cell Repository data*

Description

Create one track of the genomic positions of copy-number variants (CNVs) in chromosomal aberration and inherited disorder cell lines from the NIGMS Human Genetic Cell Repository using the Gviz bioconductor package

Usage

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

Arguments

`gen`	the name of the genome
`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`showId`	Show the ID of the genetic elements

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
```

```
  coreilVariant<-CoreillCNVTrack(gen,chrom,start,end)
  plotTracks(coreilVariant, from = start, to =end)
} else {
   data(coreilVarianttrack)
  plotTracks(coreilVariant, from = start, to =end)
}
```

COSMICTrack *Create one track of the genomic positions of variants from COSMIC*

Description

Create one track of the genomic positions of variants from COSMIC, the "Catalogue Of Somatic Mutations In Cancer" using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg19"
if(interactive()){
  cosmicVariant<-COSMICTrack(gen,chrom,start,end)
  plotTracks(cosmicVariant, from = start, to =end)
}else {
```

```
  data(cosmicVarianttrack)
  plotTracks(cosmicVariant, from = start, to =end)
}
```

---

cpgIslandsUCSC *create track CpG Island from UCSC*

Description

create track CpG Island from UCSC using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()) {
  cpgIstrack<-cpgIslandsUCSC(gen, chrom, start, end)
  plotTracks(cpgIstrack, from = start, to =end)
}else {
  data(cpgIslandtrack)
  plotTracks(cpgIstrack, from = start, to =end)
}
```

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 = "DNase Clusters", table.name = NULL)
```

Arguments

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

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
if(interactive()){
  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]
  dnasetrack<-DNAseUCSC(gen,chr,start,end,mySession)
  plotTracks(dnasetrack, from = start, to =end)
}else {
```

```
    data(dnasetrack)
   plotTracks(dnasetrack, from = start, to =end)
}
```

GADTrack *Create one track of the genomic positions of variants from the Genetic Association Database (GAD)*

Description

Create one track of the genomic positions of variants from the Genetic Association Database (GAD) (archive of human genetic association studies of complex diseases and disorders) using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen2 <- "hg19"
chrom2 <- "chr2"
start2 <- 38290160
end2 <- 38303219

if(interactive()) {
  gadtrack<-GADTrack(gen=gen2 ,chr=chrom2 ,start=start2 ,end=end2)
  plotTracks(gadtrack, from = start2, to =end2)
} else {
  data(gadtrack)
```

```
   plotTracks(gadtrack, from = start2, to =end2)
}
```

---

gcContent *Create one track of GC content from UCSC*

Description

Create a track of GC content from UCSC using the Gviz bioconductor package

Usage

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

Arguments

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

Value

A UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
  gctrack<-gcContent(gen,chr,start,end)
  plotTracks(gctrack,from= start, to=end)
} else {
  data(gctrack)
  plotTracks(gctrack,from= start, to=end)
}
```

GeneReviewsTrack *Create one track of the genomic positions of variants from GeneReviews*

Description

Create one track of the genomic positions of variants from GeneReviews using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 38290160
end <- 38303219
if(interactive()){
  geneRtrack <-GeneReviewsTrack(gen,chrom,start,end,showId=TRUE)
  plotTracks(geneRtrack, from = start, to = end)
} else {
  data(GeneReviewTrack)
  plotTracks(geneRtrack, from = start, to = end)
}
```

genesENSEMBL *Create one track of the genes in the genomic regions of interest from EMSEMBL*

Description

Create one track of the genes in the genomic regions of interest from EMSEMBL using the Gviz bioconductor package

Usage

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

Arguments

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

Value

A BiomartGeneRegionTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chrom <- "chr2"
start <- 38290160
end <- 38303219
if(interactive()) {
  genetrack <-genesENSEMBL(gen,chrom,start,end,showId=FALSE)
  plotTracks(genetrack, from = start, to =end)
} else {
  data(geneENSEMBLtrack)
  plotTracks(genetrack, from = start, to =end)
}
```

genesNameENSEMBL *Obtain the genes names in the genomic regions of interest from ENSEMBL*

Description

Obtain the genes names in the genomic regions of interest from ENSEMBL

Usage

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

Arguments

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

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
  dataset<- "hsapiens_gene_ensembl"
  geneNameEnsembl<- genesNameENSEMBL(gen,chr,start,end,dataset)
  geneNameEnsembl
} else {
  data(geneNameEnsembl)
  geneNameEnsembl
}
```

GWASTrack *Create one track of the genomic positions of variants from the GWAS catalog*

Description

Create one track of the genomic positions of variants from the NHGRI Catalog of Published Genome-Wide Association Studies using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 37949607
end <- 37965207

if(interactive()) {
  gwastrack <-GWASTrack(gen,chrom,start,end)
  plotTracks(gwastrack, from = start, to =end)
} else {
  data(GWASTrack)
  plotTracks(gwastrack, from = start, to =end)
}
```

HistoneAll *Create multiple tracks of histone modifications from the UCSC genome browser*

Description

Create multiple tracks of histone modifications from the UCSC genome browser (ENCODE/Broad) using the Gviz bioconductor package

Usage

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

Arguments

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

Value

A list of AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 38290160
end <- 38313219

if(interactive()){
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  pattern1 <- "GM12878"
```

```
 histonalltrack<-HistoneAll(gen,chr,start,end,mySession, pattern=pattern1,track.name="Broad Histone")
  plotTracks(histonalltrack, from = start, to =end)
} else {
  data(histonalltrack)
  plotTracks(histonalltrack, from = start, to =end)
}
```

HistoneOne *Create one track of one histone modification profile from the UCSC genome browser*

Description

Create one track of one histone modification profile from the UCSC genome browser (ENCODE/Broad) using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()) {
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  histoneonetrack<-HistoneOne(gen,chr,start,end,mySession)
  plotTracks(histoneonetrack, from = start, to =end)
} else {
  data(histoneonetrack)
  plotTracks(histoneonetrack, from = start, to =end)
}
```

ISCATrack *Create one track of the genomic positions of variants from ISCA*

Description

Create one track of the genomic positions of variants from International Standards for Cytogenomic Arrays (ISCA) Consortium using the Gviz bioconductor package

Usage

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

Arguments

gen	the name of the genome
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
mySession	the object session from the function browserSession of rtracklayer
table.name	A table of ISCAT classifications: iscaBenign, iscaCuratedBenign, iscaCuratedPathogenic, iscaLikelyBenign, iscaLikelyPathogenic, iscaPathGainCum, iscaPathLossCum, iscaPathogenic, iscaUncertain
showId	Show the ID of the genetic elements

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 38292433
end <- 38305492

if(interactive()){
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  iscatrack <-ISCATrack(gen,chrom,start,end,mySession, table="iscaPathogenic")
  plotTracks(iscatrack, from = start, to =end)
} else {
  data(ISCAtrack)
  plotTracks(iscatrack, from = start, to =end)
}
```

---

knownGenesUCSC *Create a track of known genes from the UCSC genome browser*

Description

Create a track of known genes from the UCSC genome browser using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()) {
  genesUcsctrack<-knownGenesUCSC(gen,chr,start,end)
  plotTracks(genesUcsctrack, from = start, to =end)
}else {
  data(genesUcsctrack)
  plotTracks(genesUcsctrack, from = start, to =end)
}
```

`regulationBiomart` *Create a regulation track from ENSEMBL*

Description

Create a 'Regulation' track from ENSEMBL using the Gviz bioconductor package

Usage

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

Arguments

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

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
  regulationENSEMBLtrack<-regulationBiomart(gen,chr,start,end)
  plotTracks(regulationENSEMBLtrack, from = start, to =end)
} else {
  data(regulationENSEMBLtrack)
  plotTracks(regulationENSEMBLtrack, from = start, to =end)
}
```

`RepeatMaskerTrack` *Create one track of the genomic positions of regions from RepeatMaskerTrack*

Description

Create one track of the genomic positions of regions from RepeatMaskerTrack using the Gviz bioconductor package

Usage

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

Arguments

`gen`	the name of the genome
`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`showId`	Show the ID of the genetic elements

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 38290160
end <- 38303219
if(interactive()){
  rmtrack <-RepeatMaskerTrack(gen,chrom,start,end)
  plotTracks(geneRtrack, from = start, to = end)
} else {
  data(RepeatMaskerTrack)
  plotTracks(rmtrack, from = start, to = end)
}
```

`snpBiomart` *Create a short variation track from ENSEMBL*

Description

Create a 'Short Variation' track from ENSEMBL using the Gviz bioconductor package

Usage

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

Arguments

`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`dataset`	The name of the database. Example "hsapiens_snp_som"
`showId`	Show the the ID of element or not
`title`	The name of the annotation track

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
  snptrack <- snpBiomart(chrom, start, end,
                         dataset="hsapiens_snp_som",showId=FALSE)
  plotTracks(snptrack, from = start, to =end)
} else {
  data(snpBiomarttrack)
  plotTracks(snptrack, from = start, to =end)
}
```

`snpLocationsUCSC` *Create a SNP track from UCSC*

Description

Create a SNP track from UCSC using the Gviz bioconductor package

Usage

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

Arguments

`gen`	the name of the genome
`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`track`	The name of the database. Example "snp138"

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()) {
  snpUCSCtrack<-snpLocationsUCSC(gen,chr,start,end,"snp138")
  plotTracks(snpUCSCtrack, from = start, to =end)
} else {
  data(snpUCSCtrack)
  plotTracks(snpUCSCtrack, from = start, to =end)
}
```

`structureBiomart` *Create a structural variation track from ENSEMBL*

Description

Create a 'Structural Variation' track from ENSEMBL using the Gviz bioconductor package

Usage

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

Arguments

`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`strand`	the strand to extract structure data for
`dataset`	The name of the database. Example "hsapiens_structvar_som"
`showId`	Show the the ID of the element
`title`	The name of the annotation track

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Examples

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

if(interactive()){
  strutrack <- structureBiomart(chrom, start, end,
                                strand, dataset="hsapiens_structvar_som")
  plotTracks(strutrack, from = start, to =end)
}else {
  data(strucBiomarttrack)
  plotTracks(strutrack, from = start, to =end)
}
```

`transcriptENSEMBL` *Create a track of transcripts from ENSEMBL*

Description

Create a track to visualize different transcripts from ENSEMBL using the Gviz bioconductor package

Usage

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

Arguments

`gen`	the name of the genome
`chr`	the chromosome of interest
`start`	the first position in the region of interest (the smallest value)
`end`	the last position in the region of interest (the largest value)
`showId`	Show the ID of the genetic elements

Value

A BiomartGeneRegionTrack object of Gviz

Author(s)

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Examples

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

if(interactive()){
  transENSMBLtrack<-transcriptENSEMBL(gen,chr,start,end)
  plotTracks(transENSMBLtrack, from = start, to =end)
} else {
  data(transENSMBLtrack)
  plotTracks(transENSMBLtrack, from = start, to =end)
}
```

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