

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. It can be used to other omic-wide association scans as long as the data can be translated to genomic level and for any species.

Depends R (>= 3.1.0), grid, biomaRt, Gviz (>= 1.10.9), psych

Suggests knitr, RUnit, BiocGenerics, BiocStyle

Imports colortools, hash, grDevices, gridExtra, rtracklayer, IRanges, S4Vectors, GenomicRanges, gg-bio, ggplot2, trackViewer

License GPL (>= 2)

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

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

VignetteBuilder knitr

NeedsCompilation no

Repository Bioconductor

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coMET-package	<i>visualisation of regional epigenome-wide association scan (EWAS) results and DNA co-methylation patterns (and also for other omic-WAS)</i>
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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. The software is designed for epigenetic data, but can also be applied to genomic and functional genomic datasets (other omic-WAS results) in any species.

Details

Package: coMET
Type: Package
Version: 0.99.9
Date: 2015-02-27
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=TRUE)
  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, mydata.type="listfile",
    cormatrix.file=mycorrelation, cormatrix.type="listfile",
    mydata.file=myexpressfile, mydata.large.type="listfile",
    tracks.gviz=listgviz,
    verbose=FALSE, print.image=FALSE, disp.pvalueplot=TRUE)
} 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, mydata.type="listfile",
      cormatrix.file=mycorrelation, cormatrix.type="listfile",
      mydata.large.file=myexpressfile, mydata.large.type="listfile",
      tracks.gviz=listgviz,
      verbose=FALSE, print.image=FALSE,disp.pvalueplot=TRUE)
}

```

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

References<http://bioconductor.org/packages/release/bioc/html/Gviz.html>http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg**See Also**[chromatinHMMOne](#)**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"
  tabletrack<-tableNames(ucscTableQuery(mySession, track=track.name))
  table.name<-tabletrack[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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=wgl

See Also

[chromatinHMMAll](#)

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"
  tabletrack<-tableNames(ucscTableQuery(mySession, track=track.name))
  table.name<-tabletrack[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	<i>Removing "chr" to the chromosome number from UCSC to transform it to ENSEMBL chromosome format</i>
-----------------	---

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	<i>Create one track of the genomic positions of variants from the ClinVar database (CNV only)</i>
-----------------	---

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 UcsTrack object of Gviz

Author(s)

Tiphaine Martin

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=clin
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [snpBiomart](#), [CoreillCNVTrack](#), [COSMICTrack](#), [ClinVarMainTrack](#)

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	<i>Create one track of the genomic positions of variants from the ClinVar database (variants only)</i>
------------------	--

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 UcsTrack object of Gviz

Author(s)

Tiphaine Martin

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=clin
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [snpBiomart](#), [CoreillCNVTrack](#), [COSMICTrack](#), [ClinVarCnvTrack](#),

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.type = "file",
      mydata.large.file = NULL, mydata.large.format = "site",
      mydata.large.type = "listfile", cormatrix.file = NULL,
      cormatrix.method = "spearman", cormatrix.format = "raw",
      cormatrix.color.scheme = "bluewhitered", cormatrix.conf.level=0.05,
      cormatrix.sig.level= 1, cormatrix.adjust="none",
      cormatrix.type = "listfile", 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

<code>mydata.file</code>	Name of the info file describing the coMET parameters
<code>mydata.format</code>	Format of the input data in <code>mydata.file</code> . There are 4 different options: <code>site</code> , <code>region</code> , <code>site_asso</code> , <code>region_asso</code> .
<code>mydata.type</code>	Format of <code>mydata.file</code> . There are 2 different options: <code>FILE</code> or <code>MATRIX</code> .
<code>mydata.large.file</code>	Name of additional info files describing the coMET parameters. File names should be comma-separated. It is optional, but if you add some, they need to be file(s) in tabular format with a header. Additional info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option <code>mydata.large.format</code> .
<code>mydata.large.format</code>	Format of additional data to be visualised in the p-value plot. Format should be comma-separated. There are 4 different options for each file: <code>site</code> , <code>region</code> , <code>site_asso</code> , <code>region_asso</code> .
<code>mydata.large.type</code>	Format of <code>mydata.large.file</code> . There are 2 different options: <code>listfile</code> or <code>listdataframe</code> .
<code>cormatrix.file</code>	Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.
<code>cormatrix.method</code>	Options for calculating the correlation matrix: <code>spearman</code> , <code>pearson</code> and <code>kendall</code>
<code>cormatrix.format</code>	Format of the input <code>cormatrix.file</code> . There are two options: <code>raw</code> file (raw if CpG sites are by column and samples by row or <code>raw_rev</code> if CpG site are by row and samples by column) and pre-computed correlation matrix (<code>cormatrix</code>)
<code>cormatrix.color.scheme</code>	Color scheme options: <code>heat</code> , <code>bluewhitered</code> , <code>cm</code> , <code>topo</code> , <code>gray</code> , <code>bluetored</code>
<code>cormatrix.conf.level</code>	Alpha level for the confidence interval. Default value= 0.05. CI will be the $\alpha/2$ lower and upper values.
<code>cormatrix.sig.level</code>	Significant level to visualise the correlation. If the correlation has a pvalue under the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme choosen.Default value =1.
<code>cormatrix.adjust</code>	indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".Default value="none"
<code>cormatrix.type</code>	Format of <code>cormatrix.file</code> . There are 2 different options: <code>listfile</code> or <code>listdataframe</code> .
<code>mydata.ref</code>	The name of the referenceomic feature (e.g. CpG-site) listed in <code>mydata.file</code>
<code>start</code>	The first nucleotide position to be visualised. It could be bigger or smaller than the first position of our list of omic features.

end	the last nucleotide position to be visualised. It has to be bigger than the value in the option start, but it could be smaller or bigger than the last position of our list of omic features.
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_asso or region_asso). 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_asso or region_asso). 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_asso). 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_asso). 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

<code>disp.color.ref</code>	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.
<code>color.list</code>	List of colors for displaying the P-value symbols related to the data in my-data.file
<code>color.list.large</code>	List of colors for displaying the P-value symbols related to the data in my-data.large.file
<code>disp.mydata</code>	logical option TRUE or FALSE. TRUE (default). If TRUE, the P-value plot is shown; if FALSE the plot will be defined by GViz
<code>biofeat.user.file</code>	Name of data file to visualise in the tracks. File names should be comma-separated.
<code>biofeat.user.type</code>	Track type, where multiple tracks can be shown (comma-separated): DataTrack, AnnotationTrack, GeneregionTrack.
<code>biofeat.user.type.plot</code>	Format of the plot if the data are shown with the Gviz's function called DataTrack (comma-separated)
<code>genome</code>	The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37), "grch38" (GRCh38)
<code>dataset.gene</code>	The gene names from ENSEMBL. e.g. hsapiens_gene
<code>tracks.gviz</code>	list of tracks created by Gviz.
<code>tracks.ggbio</code>	list of tracks created by ggbio.
<code>tracks.trackviewer</code>	list of tracks created by track viewer.
<code>disp.mydata.names</code>	logical option TRUE or FALSE. If True (default), the names of the CpG sites are displayed.
<code>disp.color.bar</code>	Color legend for the correlation matrix (range -1 to 1). Default: blue-white-red
<code>disp.phys.dist</code>	logical option (TRUE or FALSE). TRUE (default). Display the bp distance on the plots
<code>disp.legend</code>	logical option TRUE or FALSE. TRUE (default) Display the sample labels and corresponding symbols on the lower right side
<code>disp.marker.lines</code>	logical option TRUE or FALSE. TRUE (default), if FALSE the red line for pval.threshold is not shown
<code>disp.cormatrixmap</code>	logical option TRUE or FALSE. TRUE (default), if FALSE correlation matrix is not shown
<code>disp.pvalueplot</code>	logical option (TRUE or FALSE). TRUE (default), if FALSE the pvalue plot is not shown
<code>disp.type</code>	Default: symbol

<code>disp.mult.lab.X</code>	logical option TRUE or FALSE. FALSE (default). Display evenly spaced X-axis labels; up to 5 labels are shown.
<code>disp.connecting.lines</code>	logical option TRUE or FALSE. TRUE (default) displays connecting lines between p-value plot and correlation matrix
<code>palette.file</code>	File that contains color scheme for the heatmap. Colors are hexadecimal HTML color codes; one color per line; if you do not want to use this option, use the color defined by the option <code>cormatrix.color.scheme</code>
<code>image.title</code>	Title of the plot
<code>image.name</code>	The path and the name of the plot file without extension. The extension will be added by coMET depending on the option <code>image.type</code> .
<code>image.type</code>	Options: pdf or eps
<code>image.size</code>	Default: 3.5 inches. Possible sizes : 3.5 or 7
<code>font.factor</code>	Font size of the sample labels. Range: 0-1
<code>symbol.factor</code>	Size of the symbols. Range: 0-1
<code>print.image</code>	Print image in file or not.
<code>connecting.lines.factor</code>	Length of the connecting lines. Range: 0-2
<code>connecting.lines.adj</code>	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.
<code>connecting.lines.vert.adj</code>	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)
<code>connecting.lines.flex</code>	Adjusts the spread of the connecting lines. Range: 0-2
<code>config.file</code>	Configuration file contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=". If there are multiple values such as for the option <code>list.tracks</code> or the options for additional data, you need to separated them by a "comma" and not extra space. (i.e. <code>list.tracks=geneENSEMBL,CGI,ChromHMM,DNAse,RegENSEMBL</code>)
<code>verbose</code>	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

Details

The function is limited to visualize 120 omic features.

Value

Create a plot in pdf or eps format depending to some options

Author(s)

Tiphaine Martin

References

<http://epigen.kcl.ac.uk/comet/>

See Also

[comet.web](#), [comet.list](#)

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=TRUE)
  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, mydata.type="file",
    cormatrix.file=mycorrelation, cormatrix.type="listfile",
    mydata.large.file=myexpressfile, mydata.large.type="listfile",
    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, mydata.type="file",
      cormatrix.file=mycorrelation, cormatrix.type="listfile",
      mydata.large.file=myexpressfile, mydata.large.type="listfile",
      tracks.gviz=listgviz, verbose=FALSE, print.image=FALSE,disp.pvalueplot=FALSE)
}

```

comet.list

List the correlations between omic features

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. In addition, the function comet.list gives the list of correlations between omic features

Usage

```

comet.list(cormatrix.file = NULL, cormatrix.method = "spearman", cormatrix.format = "raw",
  cormatrix.conf.level=0.05, cormatrix.sig.level= 1, cormatrix.adjust="none",
  cormatrix.type = "listdataframe", cormatrix.output="cormatrix_list",
  config.file = NULL, verbose = FALSE)

```

Arguments

cormatrix.file Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.

cormatrix.method
Options for calculating the correlation matrix: spearman, pearson and kendall.
Default value= spearman

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.conf.level
Alpha level for the confidence interval. Default value= 0.05. CI will be the alpha/2 lower and upper values.

cormatrix.sig.level
Significant level to visualise the correlation. If the correlation has a pvalue below the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme choosen.Default value =1.

cormatrix.adjust	indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".Default value="none"
cormatrix.type	Format of cormatrix.file. There are 2 different options: listfile or listdataframe.
cormatrix.output	The path and the name of the output file without the extension
config.file	Configuration file contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=".
verbose	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

Value

Create a list of correlation between omic features

Author(s)

Tiphaine Martin

References

<http://epigen.kcl.ac.uk/comet/>

See Also

[comet.web,comet](#)

Examples

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
mycorrelation <- file.path(extdata, "cyp1b1_res37_rawMatrix.txt")
myoutput <- file.path(extdata, "cyp1b1_res37_cormatrix_list_BH05.txt")

comet.list(cormatrix.file=mycorrelation,cormatrix.method = "spearman",
           cormatrix.format= "raw", cormatrix.conf.level=0.05,
           cormatrix.sig.level= 0.05, cormatrix.adjust="BH",
           cormatrix.type = "listfile", cormatrix.output=myoutput,
           verbose=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", cormatrix.conf.level=0.05,
  cormatrix.sig.level= 1, cormatrix.adjust="none", 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

<code>mydata.file</code>	Name of the info file describing the coMET parameters. It is mandatory and has to be a file in tabular format with a header. Info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option mydata.format.
<code>mydata.format</code>	Format of the input data in mydata.file. There are 4 different options: site, region, site_asso, region_asso.

<code>mydata.large.file</code>	Name of additional info files describing the coMET parameters. File names should be comma-separated. It is optional, but if you add some, they need to be file(s) in tabular format with a header. Additional info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option <code>mydata.large.format</code> .
<code>mydata.large.format</code>	Format of additional data to be visualised in the p-value plot. Format should be comma-separated. There are 4 different options for each file: <code>site</code> , <code>region</code> , <code>site_asso</code> , <code>region_asso</code> .
<code>cormatrix.file</code>	Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.
<code>cormatrix.method</code>	A character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.
<code>cormatrix.format</code>	A character string indicating which format of the input <code>cormatrix.file</code> is to be used. There are three options: raw file (raw if CpG sites are by column and samples by row or <code>row_rev</code> if CpG site are by row and samples by column) and pre-computed correlation matrix (<code>cormatrix</code>)
<code>cormatrix.color.scheme</code>	A character string indicating which Color scheme options is to be used: <code>heat</code> , <code>bluewhitered</code> , <code>cm</code> , <code>topo</code> , <code>gray</code> , <code>bluetored</code>
<code>cormatrix.conf.level</code>	Alpha level for the confidence interval. Default value= 0.05. CI will be the $\alpha/2$ lower and upper values.
<code>cormatrix.sig.level</code>	Significant level to visualise the correlation. If the correlation has a pvalue under the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme choosen. Default value =1.
<code>cormatrix.adjust</code>	indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". Default value="none"
<code>mydata.ref</code>	The name of the reference omic feature (e.g. CpG-site) listed in <code>mydata.file</code>
<code>genome</code>	The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37), "grch38" (GRCh38)
<code>start</code>	The first nucleotide position to be visualised. It could be bigger or smaller than the first position of our list of omic features.
<code>end</code>	the last nucleotide position to be visualised. It has to be bigger than the value in the option <code>start</code> , but it could be smaller or bigger than the last position of our list of omic features.
<code>zoom</code>	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_asso or region_asso). 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_asso or region_asso). 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_asso). 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_asso). 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 my-data.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	The path and the name of the plot file without extension. The extension will be added by coMET depending on the option image.type.
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 contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=". If there are multiple values such as for the option list.tracks or the options for additional data, you need to separated them by a "comma" and not extra space. (i.e. list.tracks=geneENSEMBL,CGI,ChromHMM,DNase,RegENSEMBL
verbose	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

Details

The function is limited to visualize 120 omic features.

Value

Create a plot in pdf or eps format depending to some options

Author(s)

Tiphaine Martin

References

<http://epigen.kcl.ac.uk/comet/>

See Also

[comet.comet.list](#)

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 UcsbTrack object of Gviz

Author(s)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>
http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=cor

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [snpBiomart](#), [CoreillCNVTrack](#), [ClinVarMainTrack](#), [ClinVarCnvTrack](#),

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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=cos

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [snpBiomart](#), [CoreillCNVTrack](#), [ClinVarMainTrack](#), [ClinVarCnvTrack](#),

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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=cpg

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)

<code>mySession</code>	the object session from the function <code>browserSession</code> of <code>rtracklayer</code>
<code>track.name</code>	the name of the track DNaseUCSC. "DNase Clusters"(default)
<code>table.name</code>	the name of the table from the track

Value

An `AnnotationTrack` object of `Gviz`

Author(s)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wgl

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 UcsTrack object of Gviz

Author(s)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=gad

See Also

[ISCATrack](#), [GWASTrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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

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

Value

A `UcscTrack` object of Gviz

Author(s)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=gc5

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	<i>Create one track of the genomic positions of variants from GeneReviews</i>
------------------	---

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 UcsTrack object of Gviz

Author(s)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=gen

See Also

[ISCATrack](#), [GWASTrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GADTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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	<i>Create one track of the genes in the genomic regions of interest from EMSEMBL</i>
--------------	--

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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>
http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=ens

See Also

[ISCATrack](#), [GWASTrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [GADTrack](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

Examples

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

genesNameENSEMBL	<i>Obtain the genes names in the genomic regions of interest from ENSEMBL</i>
------------------	---

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

Details

Can be null

Value

List of name of genes found in this region of interest.

Author(s)

Tiphaine Martin

References

go to ENSEMBL
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[ISCATrack](#), [GWASTrack](#), [knownGenesUCSC](#), [GeneReviewsTrack](#), [GADTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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	<i>Create one track of the genomic positions of variants from the GWAS catalog</i>
-----------	--

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

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=gwa
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[ISCATrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [GADTrack](#), [genesENSEMBL](#),
[xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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

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

Value

A list of `AnnotationTrack` object of `Gviz`

Author(s)

Tiphaine Martin

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[HistoneOne](#),

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	<i>Create one track of one histone modification profile from the UCSC genome browser</i>
------------	--

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

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[HistoneAll](#)

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, iscaCurated-Pathogenic, iscaLikelyBenign, iscaLikelyPathogenic, iscaPathGainCum, iscaPathLossCum, iscaPathogenic, iscaUncertain
showId	Show the ID of the genetic elements

Value

An UcsTrack object of Gviz

Author(s)

Tiphaine Martin

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=iscat
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[GWASTrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [GADTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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, showId=TRUE)
```

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

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=knownGenesUCSC
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[ISCATrack](#), [GWASTrack](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [GADTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#), [transcriptENSEMBL](#),

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	<i>Create a regulation track from ENSEMBL</i>
-------------------	---

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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>
Got to ENSEMBLregulation biomart

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	<i>Create one track of the genomic positions of regions from RepeatMaskerTrack</i>
-------------------	--

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

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=rms

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 38290160
end <- 38303219
if(interactive()){
  rmtrack <- RepeatMaskerTrack(gen, chr, start, end, showId=TRUE)
  plotTracks(rmtrack, 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

References

Go to ENSEMBL Biomart
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [COSMICTrack](#), [CoreillCNVTrack](#), [ClinVarMainTrack](#),
[ClinVarCnvTrack](#),

Examples

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

if(interactive()){
```

```

    snptrack <- snpBiomart(chr, 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

References

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=snp
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[snpLocationsUCSC](#), [structureBiomart](#), [COSMICTrack](#), [CoreillCNVTrack](#), [ClinVarMainTrack](#), [ClinVarCnvTrack](#),

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	<i>Create a structural variation track from ENSEMBL</i>
------------------	---

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

References

Go to ENSEMBL Biomart

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

See Also

[snpLocationsUCSC](#), [snpBiomart](#), [COSMICTrack](#), [CoreillCNVTrack](#), [ClinVarMainTrack](#), [ClinVarCnvTrack](#),

Examples

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

if(interactive()){
  strutrack <- structureBiomart(chr, 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)

Tiphaine Martin

References

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=ens

See Also

[ISCATrack](#), [GWASTrack](#), [knownGenesUCSC](#), [genesNameENSEMBL](#), [GeneReviewsTrack](#), [GADTrack](#), [genesENSEMBL](#), [xenorefGenesUCSC](#),

Examples

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

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

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