Package 'coMET'

October 9, 2015

Type Package

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

Version 1.0.0

Date 2015-04-10

Author Tiphaine C. Martin, Idil Yet, Pei-Chien Tsai, Jordana T. Bell

Maintainer Tiphaine Martin <tiphaine.martin@kcl.ac.uk>

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, ggbio, ggplot2, trackViewer

License GPL (>= 2)

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

biocViews Software, DifferentialMethylation, Visualization, Sequencing, Genetics, FunctionalGenomics, Microarray, MethylationArray, MethylSeq, ChIPSeq, DNASeq, RIPSeq, RNASeq, ExomeSeq, DNAMethylation, GenomeWideAssociation

VignetteBuilder knitr

NeedsCompilation no

Repository Bioconductor

R topics documented:

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

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:	0.99.10
Date:	2015-04-10
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)

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

Maintainer: Tiphaine Martin <tiphaine.martin@kcl.ac.uk>

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=wgl

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"
    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

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"
    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

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 *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

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

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_asso, region_asso.
mydata.type	Format of mydata.file. There are 2 different options: FILE or MATRIX.
mydata.large.file	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 mydata.large.format.
mydata.large.format	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: site, region, site_asso, region_asso.
mydata.large.type	Format of mydata.large.file. There are 2 different options: listfile or listdataframe.
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
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
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 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.
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.
mydata.ref	The name of the referenceomic feature (e.g. CpG-site) listed in mydata.file
start	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

`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`
: 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

`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 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.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

	.
	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.
mydata.format	Format of the input data in mydata.file. There are 4 different options: site, region, site_asso, region_asso.

`mydata.large.file`
: 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 mydata.large.format.

`mydata.large.format`
: 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: site, region, site_asso, region_asso.

`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`
: A character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.

`cormatrix.format`
: A character string indicating which format of the input cormatrix.file is to be used. There are three options: raw file (raw if CpG sites are by column and samples by row or row_rev if CpG site are by row and samples by column) and pre-computed correlation matrix (cormatrix)

`cormatrix.color.scheme`
: A character string indicating which Color scheme options is to be used: heat, bluewhitered, cm, topo, gray, bluetored

`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 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.

`cormatrix.adjust`
: indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".Default value="none"

`mydata.ref`
: The name of the reference omic feature (e.g. 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. 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`
: 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 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`
: 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 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=cori

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)

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

References

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

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

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

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

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

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 *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

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 *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

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` *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

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 *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

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

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

References

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

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 *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

References

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

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, 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

References

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

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=kno

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 *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

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 *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

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` *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

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

Index