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 (>= 3.3.0), grid, utils, biomaRt, Gviz, psych

Suggests knitr, RUnit, BiocGenerics, BiocStyle

Imports colortools, hash, grDevices, gridExtra, rtracklayer, IRanges, S4Vectors, GenomicRanges, ggbio, ggplot2, trackViewer, stats, corrplot

License GPL (>= 2)

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

biocViews Software, DifferentialMethylation, Visualization, Sequencing, Genetics, FunctionalGenomics, Microarray, MethylationArray, MethylSeq, ChIPSeq, DNASeq, RiboSeq, 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:	1.4.3
Date:	2016-05-29
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, Thomas Hardiman, 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, Yet, I, Tsai, P-C, Bell, J.T., coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns, BMC bioinformatics, 2015.

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 <- "hg38"

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)
}
```

---

bindingMotifsBiomart_ENSEMBL

Creates a binding motif track from ENSEMBL

Description

Creates a binding motif track from ENSEMBL using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
bindingMotifsBiomart_ENSEMBL(gen, chr, start, end, featureDisplay="all", datasetEnsembl = NULL)
```

Arguments

gen	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
featureDisplay	A vector of regulatory features to be displayed, such as Egr1. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "CTCF"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("Egr1","CTCF")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
datasetEnsembl	Allows the user to manually set which data set is used if required.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
```

```
end <- 50000
featureDisplay <- "CTCF"

if(interactive()){
 bindMotifsBiomartTrackSingle<-bindingMotifsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(bindMotifsBiomartTrackSingle, from = start, to = end)
} else {
  data(bindMotifsBiomartTrackSingle)
  plotTracks(bindMotifsBiomartTrackSingle, from = start, to = end)
}

######

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- c("CTCF","Egr1")

if(interactive()){
 bindMotifsBiomartTrackMultiple<-bindingMotifsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(bindMotifsBiomartTrackMultiple, from = start, to = end)
} else {
  data(bindMotifsBiomartTrackMultiple)
  plotTracks(bindMotifsBiomartTrackMultiple, from = start, to = end)
}

######

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "all"

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

ChIPTF_ENCODE *Creates a TF motif track from ENCODE*

Description

Creates a track of TF motifs from ENCODE using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
ChIPTF_ENCODE(gen="hg19", chr, start, end, bedFilePath, featureDisplay='all', motifColorFile, type_st
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.
featureDisplay	A vector of regulatory features to be displayed, such as Predicted heterochomatin. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Predicted heterochomatin"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("Predicted low activity","Predicted heterochomatin")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
motifColorFile	The path of the BED file with 2 columns (the first for motif name and the second for the color in hex format without \# in the beginning) with a header.
type_stacking	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz
showId	logical. say if we write the name of group
just_group	position. say where we write the name of group (choice in c("above","righ","left"))

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen <- "hg19"
chr<-"chr1"
start <- 1000
end <- 329000


if(interactive()){
    extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
    bedFilePath <- file.path(extdata, "ENCODE/motifs1000_matches_ENCODE.txt")
    motif_color <- file.path(extdata, "ENCODE/TFmotifs_colors.csv")
   chipTFtrack <- ChIPTF_ENCODE(gen,chr,start, end, bedFilePath, featureDisplay=c("AHR::ARNT::HIF1A_1","AIRE_1"
    plotTracks(chipTFtrack, from = start, to = end)
} else {
    data(chipTFtrack)
    plotTracks(chipTFtrack, from = start, to = end)
}
```

---

chromatinHMMAll_UCSC *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_UCSC(gen, chr, start, end, mySession, color='coMET',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
color	the colour scheme used for plots. By defult this is set to 'coMET' to allow easy indentifcation of differnent elements. The colour scheme set by UCSC can also be used. Consult userguide for table of colours.
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=wgI

See Also

chromatinHMMOne_UCSC

Examples

```
library("Gviz")
library(rtracklayer)
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_UCSC(gen,chr,start,end,mySession,color='coMET',PATTERN.REGULATION)
    plotTracks(chromhmmPattern, from = start, to =end)

  chromhmmNoPattern<-chromatinHMMAll_UCSC(gen,chr,start,end,mySession,color='coMET')
    plotTracks(chromhmmNoPattern, from = start, to =end)
} else {

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

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

---

chromatinHMMOne_UCSC *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_UCSC(gen, chr, start, end, mySession, color="coMET", table.name = NULL)
```

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
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
color	the color scheme used for plots. By defult this is set to 'coMET' to allow easy indentifcation of differnent elements. The color scheme set by UCSC can also be used. Consult userguide for table of colors.
table.name	the name of the table from the track

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

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

See Also

chromatinHMMAll_UCSC

Examples

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

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_UCSC(gen,chr,start,end,mySession,color="coMET",table.name)
    plotTracks(chromhmmtrackone, from = start, to =end)
}else {
    data(chromhmmtrackone)
    plotTracks(chromhmmtrackone, from = start, to =end)
}
```

---

chromHMM_RoadMap *Creates a ChromHMM track from a file of RoadMap*

Description

Creates a ChromHMM track from a file of RoadMap using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
chromHMM_RoadMap(gen="hg19",chr, start, end, bedFilePath, featureDisplay = 'all', colorcase='roadmap1
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The file path to the .BED file containing the data to be visualised
featureDisplay	A vector of features to be displayed, such as 1_TssA. Spelling and capitalisation of features must be identical to those in the user guide (in the 'State & Acronym' column). There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "1_TssA"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("1_TssA","2_TssAFlnk")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
colorcase	the type of colors used to visualise different elements contained in ROADmap data with 15-,18-,25- states. choice between roadmap15, roadmap18, comet18, roadmap25 and comet25.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to RoadMap Epigenome

Examples

```
library("Gviz")
chr <- "chr1"
start <- 4500000
end <- 4600000
featureDisplay <- "7_Enh"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/E063_15_coreMarks_mnemonics.bed")

if(interactive()){
  chromHMM_RoadMapSingle <- chromHMM_RoadMap(gen="hg19",chr,start, end, bedFilePath, featureDisplay = featureDis
  plotTracks(chromHMM_RoadMapSingle, from = start, to = end)
} else {
  data(chromHMM_RoadMapSingle)
  plotTracks(chromHMM_RoadMapSingle, from = start, to = end)
}

######

library("Gviz")
chr <- "chr1"
start <- 4500000
end <- 4600000
featureDisplay <- c("7_Enh","13_ReprPC")

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/E063_15_coreMarks_mnemonics.bed")

if(interactive()){
  chromHMM_RoadMapMultiple <- chromHMM_RoadMap(gen="hg19",chr,start, end, bedFilePath, featureDisplay = featureD
  plotTracks(chromHMM_RoadMapMultiple, from = start, to = end)
} else {
  data(chromHMM_RoadMapMultiple)
  plotTracks(chromHMM_RoadMapMultiple, from = start, to = end)
}

#####

library("Gviz")
chr <- "chr1"
```

```
start <- 4500000
end <- 4600000
featureDisplay <- "all"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/E063_15_coreMarks_mnemonics.bed")

if(interactive()){
  chromHMM_RoadMapAll <- chromHMM_RoadMap(gen="hg19",chr,start, end, bedFilePath, featureDisplay = featureDispla
  plotTracks(chromHMM_RoadMapAll, from = start, to = end)
} else {
  data(chromHMM_RoadMapAll)
  plotTracks(chromHMM_RoadMapAll, 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)
```

`ClinVarCnv_UCSC` *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

```
ClinVarCnv_UCSC(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

`snpLocations_UCSC`, `structureBiomart_ENSEMBL`, `snpBiomart_ENSEMBL`, `CoreillCNV_UCSC`, `COSMIC_UCSC`, `ClinVarMain_UCSC`

Examples

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg38"
if(interactive()){
```

```
    clinCNV<-ClinVarCnv_UCSC(gen,chrom,start,end)
    plotTracks(clinCNV, from = start, to =end)
}else {
    data(ClinVarCnvTrack)
    plotTracks(clinCNV, from = start, to =end)
}
```

`ClinVarMain_UCSC` *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

```
ClinVarMain_UCSC(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

`snpLocations_UCSC`, `structureBiomart_ENSEMBL`, `snpBiomart_ENSEMBL`, `CoreillCNV_UCSC`, `COSMIC_UCSC`, `ClinVarCnv_UCSC`

Examples

```
library("Gviz")
gen <- "hg38"
chrom <- "chr2"
start <- 100000
end <- 10000000

if(interactive()) {
    clinVariant<-ClinVarMain_UCSC(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,pval.threshold.2 = 0,disp.pval.threshold = 1,
    disp.association = FALSE, disp.association.large = FALSE,
    disp.region = FALSE, disp.region.large = FALSE,
   disp.beta.association = FALSE, disp.beta.association.large = FALSE, factor.beta = 0.3,
   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, fontsize.gviz=5, font.factor = 1,
    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

`pval.threshold.2`
: the second significance threshold to be displayed as a orange 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.

`disp.beta.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 size of symbol is the default size of symbole; if TRUE, the effect direction is shown.

`disp.beta.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 size of symbol is ththe default size of symbole; if TRUE, the effect direction is shown.

`factor.beta`
: Factor to visualise the size of beta. Default value = 0.3.

`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

`fontsize.gviz` Font size of writing in annotation track. Default value =5

`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 <- "hg38"
```

```
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, pval.threshold.2 = 0,  disp.pval.threshold = 1,
        disp.association= FALSE, disp.association.large = FALSE,
      disp.beta.association = "FALSE",disp.beta.association.large = "FALSE", factor.beta = 0.3,
       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, fontsize.gviz=5, font.factor = 1,
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. Default value = 1e-7

`pval.threshold.2`
: the second significance threshold to be displayed as a orange dashed line. Default value= 0 (no printed)

`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.beta.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 size of symbol is the default size of symbole; if TRUE, the effect direction is shown.

`disp.beta.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 size of symbol is ththe default size of symbole; if TRUE, the effect direction is shown.

`factor.beta`
: Factor to visualise the size of beta. Default value = 0.3.

`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, BindingMotifENSEMBL, otherRegulatoryENSEMBL, regulatoryEvidenceENSEMBL, regulatoryFeaturesENSEMBL, regulatorySegmeENSEMBL, miRNAENSEMBL, ImprintedtissuesGenes, COSMIC, GAD, ClinVar, GeneReviews, GWAS, ClinVarCNV, GCcontent, genesUCSC, xenogenesUCSC, SegDuplication,RepeatElt.
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
fontsize.gviz	Font size of writing in annotation track. Default value =5
font.factor	Font size of the sample labels. Range: 0-1
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)
```

`CoreillCNV_UCSC` *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

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

Arguments

`gen`	the name of the genome. Data is not currently available for GRCh38 (hg38).
`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

snpLocations_UCSC, structureBiomart_ENSEMBL, snpBiomart_ENSEMBL, COSMIC_UCSC, ClinVarMain_UCSC, ClinVarCnv_UCSC

Examples

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

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

COSMIC_UCSC *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

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

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38)
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

snpLocations_UCSC, structureBiomart_ENSEMBL, snpBiomart_ENSEMBL, CoreillCNV_UCSC, ClinVarMain_UCSC, ClinVarCnv_UCSC,

Examples

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

---

cpgIslands_UCSC *create track CpG Island from UCSC*

Description

create track CpG Island from UCSC using the Gviz bioconductor package

Usage

```
cpgIslands_UCSC(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 <- 100000
end <- 1000000
gen <- "hg38"

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

---

dgfootprints_RoadMap *Creates a track of DNA motif positional bias in digital genomic Footprinting Sites (DGFP) from a file of RoadMap*

Description

Creates a DGFP track from a file of RoadMap using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
dgfootprints_RoadMap(gen="hg19", chr, start, end, bedFilePath, tissueGroupDisplay='Blood & T-cell',sh
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The file path to the .BED file containing the data to be visualised

`tissueGroupDisplay` the group of tissue visualised among list("Neurosph","Epithelial","IMR90","Thymus","Heart","Brain","D & B-cell","Blood & T-cell"="ES-deriv")

`showId` logical. say if we write the name of group

`type_stacking` Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to RoadMap Epigenome

Examples

```
library("Gviz")
chr <- "chr1"
start <- 236728
end <- 238778
gen="hg19"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/CD3-DS17198.hg19.bed")

if(interactive()){
  dgfootprints_RoadMapSingle <- dgfootprints_RoadMap(gen,chr,start, end, bedFilePath, tissueGroupDisplay='Blood
  plotTracks(dgfootprints_RoadMapSingle, from = start, to = end)
} else {
  data(dgfootprints_RoadMapSingle)
  plotTracks(dgfootprints_RoadMapSingle, from = start, to = end)
}
```

DNaseI_FANTOM *Creates a enhancer/promoter track from FANTOM*

Description

Creates a track of promoters/enhancers from FANTOM using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
DNaseI_FANTOM(gen="hg19", chr, start, end, bedFilePath, featureDisplay='enhancer', stacking_type="de
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.
featureDisplay	A vector of regulatory features to be displayed, such as enhancer. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Predicted heterochomatin"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("enhancer","promoter")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
stacking_type	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen <- "hg19"
chr<- "chr1"
start <- 6000000
end <- 6500000

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
enhFantomFile <- file.path(extdata, "/FANTOM/human_permissive_enhancers_phase_1_and_2.bed")

if(interactive()){
 enhFANTOMtrack <- DNaseI_FANTOM(gen,chr,start, end, enhFantomFile, featureDisplay='enhancer')
  plotTracks(enhFANTOMtrack, from = start, to = end)
} else {
  data(enhFANTOMtrack)
  plotTracks(enhFANTOMtrack, from = start, to = end)
}
```

DNaseI_RoadMap *Creates a promoter/enhancer regions track from a file of RoadMap*

Description

Creates a track of promoter/enhancer regions from a file of RoadMap using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
DNaseI_RoadMap(gen="hg19", chr, start, end, bedFilePath, featureDisplay='promotor',showId=TRUE, type
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The file path to the .BED file containing the data to be visualised
featureDisplay	A vector of features to be displayed, such as 1_TssA. Spelling and capitalisation of features must be identical to those in the user guide (in the 'State & Acronym' column). There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "1_TssA"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("1_TssA","2_TssAFlnk")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.

showId	Allows to visualise the Id of DNAse group.
type_stacking	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to RoadMap Epigenome

Examples

```
library("Gviz")
chr <- "chr1"
start <- 707612
end <- 722151
gen="hg19"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/regions_prom_E063.bed")

if(interactive()){
  DNaseI_RoadMapSingle <- DNaseI_RoadMap(gen,chr,start, end, bedFilePath, featureDisplay='promotor'  )
  plotTracks(DNaseI_RoadMapSingle, from = start, to = end)
} else {
  data(DNaseI_RoadMapSingle)
  plotTracks(DNaseI_RoadMapSingle, from = start, to = end)
}
```

DNAse_UCSC *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

```
DNAse_UCSC(gen, chr, start, end, mySession, track.name = "DNase Clusters", table.name = NULL)
```

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
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 DNAse_UCSC. "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=wgl

Examples

```
library("Gviz")
library("rtracklayer")

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<-DNAse_UCSC(gen,chr,start,end,mySession)
  plotTracks(dnasetrack, from = start, to =end)
}else {
    data(dnasetrack)
   plotTracks(dnasetrack, from = start, to =end)
}
```

eQTL *Creates a track from a file for eQTL data*

Description

Creates a track from a BED file for eQTL data using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
eQTL(gen,chr, start, end, bedFilePath, featureDisplay, showId=FALSE,type_stacking="squish",just_grou
```

Arguments

gen	the name of the genome.
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The file path to the .BED file containing the data to be visualised
featureDisplay	A vector of eQTL features to be displayed, such as SNP. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "CpG"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("SNP","CpG")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
showId	Allows to visualise the Id of eQTL group.
type_stacking	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz
just_group	position. say where we write the name of group (choice in c("above","righ","left"))

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
chr <- "chr15"
start <- 74889136
end <-   75018200
featureDisplay <- "SNP"
gen="hg19"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "eQTL.bed")

if(interactive()){
  eQTLTrackSingle <- eQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
  plotTracks(eQTLTrackSingle, from = start, to = end)
} else {
  data(eQTLTrackSingle)
  plotTracks(eQTLTrackSingle, from = start, to = end)
}

############

library("Gviz")
chr <- "chr15"
start <- 74889136
end <-   75018200
featureDisplay <- c("SNP","mRNA_pheno")
gen="hg19"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "eQTL.bed")

if(interactive()){
  eQTLTrackMultiple <- eQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
  plotTracks(eQTLTrackMultiple, from = start, to = end)
} else {
  data(eQTLTrackMultiple)
  plotTracks(eQTLTrackMultiple, from = start, to = end)
}

######

library("Gviz")
chr <- "chr15"
start <- 74889136
end <-   75018200
featureDisplay <- "all"
gen="hg19"
```

```
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "eQTL.bed")

if(interactive()){
  eQTLTrackAll <- eQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
  plotTracks(eQTLTrackAll, from = start, to = end)
} else {
  data(eQTLTrackAll)
  plotTracks(eQTLTrackAll, from = start, to = end)
}
```

---

eQTL_GTEx *Creates a eQTL track from GTEx*

Description

Creates a track of eQTL from GTEx using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
eQTL_GTEx(gen="hg19",chr,start, end, bedFilePath, featureDisplay = 'all', showId=FALSE, type_stacking
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.
featureDisplay	A vector of regulatory features to be displayed, such as Predicted heterochomatin. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Predicted heterochomatin"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("Predicted low activity","Predicted heterochomatin")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
showId	logical. say if we write the name of group
type_stacking	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz
just_group	position. say where we write the name of group (choice in c("above","righ","left"))

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen <- "hg19"
chr<-"chr3"
start <- 132423172
end <- 132442807
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "/GTEX/eQTL_Uterus_Analysis_extract100.snpgenes")


if(interactive()){
 eGTexTrackall <- eQTL_GTEx(gen,chr,start, end, bedFilePath, featureDisplay="all", showId=TRUE,just_group="left'
  plotTracks(eGTexTrackall, from = start, to = end)
} else {
  data(eGTexTrackall)
  plotTracks(eGTexTrackall, from = start, to = end)
}


if(interactive()){
 eGTexTrackSNP <- eQTL_GTEx(gen,chr,start, end, bedFilePath, featureDisplay="SNP", showId=TRUE,just_group="left'
  plotTracks(eGTexTrackSNP, from = start, to = end)
} else {
  data(eGTexTrackSNP)
  plotTracks(eGTexTrackSNP, from = start, to = end)
}
```

GAD_UCSC *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

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

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

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

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

gcContent_UCSC *Create one track of GC content from UCSC*

Description

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

Usage

```
gcContent_UCSC(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 <- "hg38"
chr <- "chr7"
start <- 38290160
end <- 38303219

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

GeneReviews_UCSC *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

```
GeneReviews_UCSC(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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
library("Gviz")
gen <- "hg38"
chrom <- "chr2"
start <- 10000000
end <- 100000000
if(interactive()){
```

```
  geneRtrack <-GeneReviews_UCSC(gen,chrom,start,end,showId=TRUE)
  plotTracks(geneRtrack, from = start, to = end)
} else {
  data(GeneReviewTrack)
  plotTracks(geneRtrack, from = start, to = end)
}
```

---

genesName_ENSEMBL *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

```
genesName_ENSEMBL(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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr7"
start <- 38290160
end <- 38303219

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

---

genes_ENSEMBL *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

```
genes_ENSEMBL(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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

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

GWAScatalog_UCSC *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

```
GWAScatalog_UCSC(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

ISCA_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
library("Gviz")
gen <- "hg38"
chrom <- "chr2"
start <- 10000
end <- 100000

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

HiCdata2matrix *Creates a HiC matrix from a file (Rao et al., 2014)*

Description

Creates a HiC matrix from Rao et al.,2014.

Usage

```
HiCdata2matrix( chr, start, end, bedFilePath)
```

Arguments

chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("corrplot")
gen <- "hg19"
chr<-"chr1"
start <- 5000000
end <- 9000000

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "HiC/chr1_1mb.RAWobserved")

if(interactive()){
  matrix_HiC_Rao <- HiCdata2matrix(chr,start, end, bedFilePath)
cor_matrix_HiC <- cor(matrix_HiC_Rao)
diag(cor_matrix_HiC)<-1
corrplot(cor_matrix_HiC, method = "circle")
} else {
```

```
  data(matrix_HiC_Rao)
  cor_matrix_HiC <- cor(matrix_HiC_Rao)
diag(cor_matrix_HiC)<-1
corrplot(cor_matrix_HiC, method = "circle")
}
```

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

Arguments

`gen`	the name of the genome. Data is not currently available for GRCh38 (hg38).
`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_UCSC,

Examples

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

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

  histonalltrack<-HistoneAll_UCSC(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_UCSC *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_UCSC(gen, chr, start, end, mySession, track.name = "Broad Histone", table.name = NULL)
```

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
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=wgI

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

See Also

HistoneAll_UCSC

Examples

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

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

---

imprintedGenes_GTEx *Creates a imprinted genes track from GTEx*

Description

Creates a track of imprinted genes from GTEx using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
imprintedGenes_GTEx(gen="hg19", chr,start, end, tissues="all", classification="all",showId=FALSE)
```

Arguments

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
tissues	list of tissues among 33 tissues in GTEx
classification	list of classification from 5 types (biallelic, consistent with biallelic, consistent with imprinting, imprinted, NC)
showId	logical. say if we write the name of group

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen<-"hg19"
chr<- "chr6"
start <- 144251437
end <- 144330541


if(interactive()){
   allIGtrack <- imprintedGenes_GTEx(gen,chr,start, end, tissues="all", classification="imprinted",showId=TRUE)
   allimprintedIGtrack <- imprintedGenes_GTEx(chr,start, end, tissues="all", classification="imprinted",showId=T
   StomachIGtrack <-imprintedGenes_GTEx(chr,start, end, tissues="Stomach", classification="all",showId=TRUE)
   PancreasIGtrack <- imprintedGenes_GTEx(chr,start, end, tissues="Pancreas", classification="all",showId=TRUE)
   PancreasimprintedIGtrack <- imprintedGenes_GTEx(chr,start, end, tissues="Pancreas", classification="biallelic

   imprintinglist <- list(allIGtrack,allimprintedIGtrack,StomachIGtrack,PancreasIGtrack,PancreasimprintedIGtrac

  plotTracks(,imprintinglist, from = start, to = end)

} else {

  data(allIGtrack)
  data(allimprintedIGtrack)
  data(StomachIGtrack)
  data(PancreasIGtrack)
```

```
  data(PancreasimprintedIGtrack)

  imprintinglist <- list(allIGtrack,allimprintedIGtrack,StomachIGtrack,PancreasIGtrack,PancreasimprintedIGtrac

  plotTracks(imprintinglist, from = start, to = end)
}
```

`interestGenes_ENSEMBL` *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

```
interestGenes_ENSEMBL(gen, chr, start, end, interestfeatures,interestcolor, 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)
`interestfeatures`	A data frame with 3 columns: start of features, end of features, and type of features
`interestcolor`	A list with the color for each new features defined
`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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr15"
start <- 75011669
end <- 75019876
interestfeatures <- rbind(c("75011883","75013394","bad"),c("75013932","75014410","good"))
interestcolor <- list("bad"="red", "good"="green")

if(interactive()) {
  interestgenesENSMBLtrack<-interestGenes_ENSEMBL(gen,chr,start,end,interestfeatures,interestcolor,showId=TRUE)
  plotTracks(interestgenesENSMBLtrack, from = start, to =end)
} else {
  data(interestgenesENSMBLtrack)
  plotTracks(interestgenesENSMBLtrack, from = start, to =end)
}
```

---

interestTranscript_ENSEMBL

Create a track of transcripts from ENSEMBL

Description

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

Usage

```
interestTranscript_ENSEMBL(gen, chr, start, end,interestfeatures,interestcolor,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)
interestfeatures	A data frame with 3 columns: start of features, end of features, and type of features
interestcolor	A list with the color for each new features defined
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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC,

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr15"
start <- 75011669
end <- 75019876
interestfeatures <- rbind(c("75017782","75017835","bad"),c("75013755","75013844","good"))
interestcolor <- list("bad"="red", "good"="green")

if(interactive()){
  interesttransENSMBLtrack<-interestTranscript_ENSEMBL(gen,chr,start,end,interestfeatures,interestcolor,showId=
  plotTracks(interesttransENSMBLtrack, from=start, to=end)
} else {
  data(interesttransENSMBLtrack)
  plotTracks(interesttransENSMBLtrack, from=start, to=end)
}
```

ISCA_UCSC *Create one track of the genomic positions of variants from ISCA (obselete database)*

Description

Create one track of the genomic positions of variants from International Standards for Cytogenomic Arrays (ISCA) Consortium using the Gviz bioconductor package (obselete datbase, Impossible to access to data from UCSC from September 2015)

Usage

```
ISCA_UCSC(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

GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
# Oboselet function

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

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

```
#  data(ISCAtrack_Grch38)
#  plotTracks(iscatrack, from = start, to =end)
#}
```

---

knownGenes_UCSC *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

```
knownGenes_UCSC(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

ISCA_UCSC, GWAScatalog_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL,

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr7"
start <- 38290160
end <- 38303219

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

`metQTL` *Creates a track from a file for metQTL data*

Description

Creates a track from a BED file for metQTL data using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
metQTL(gen, chr, start, end, bedFilePath, featureDisplay, showId=FALSE,type_stacking="squish",just_gr
```

Arguments

`gen`	the name of the genome. Default value=hg19
`chr`	The chromosome of interest
`start`	The starting position in the region of interest (the smallest value)
`end`	The end position in the region of interest (the largest value)
`bedFilePath`	The file path to the .BED file containing the data to be visualised
`featureDisplay`	A vector of metQTL features to be displayed, such as SNP. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "CpG"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("SNP","CpG")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
`showId`	Allows the visualization of the Id of metQTL group.
`type_stacking`	Sets the type of stacking used by Gviz for plots. By default this is set to 'squish'. For more information see Gviz user guide.
`just_group`	position. say where we write the name of group (choice in c("above","righ","left"))

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")

gen <- 'hg19'
chr <- "chr15"
start <- 74889136
end <-   75018200
featureDisplay <- "trans_local_metQTL"
type_stacking <- "squish"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
mqtlbedFilePath <- file.path(extdata, "metQTL.bed")

if(interactive()){
  metQTLTrackSingle <- metQTL(gen,chr,start, end,mqtlbedFilePath, featureDisplay = featureDisplay )
  plotTracks(metQTLTrackSingle, from = start, to = end)
} else {
  data(metQTLTrackSingle)
  plotTracks(metQTLTrackSingle, from = start, to = end)
}

###

library("Gviz")

gen <- 'hg19'
chr <- "chr15"
start <- 74889136
end <-   75018200

featureDisplay <- c("trans_local_metQTL","CpG")

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "metQTL.bed")

if(interactive()){
  metQTLTrackMultiple <- metQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
```

```
  plotTracks(metQTLTrackMultiple, from = start, to = end)
} else {
  data(metQTLTrackMultiple)
  plotTracks(metQTLTrackMultiple, from = start, to = end)
}

#####

library("Gviz")

gen <- 'hg19'
chr <- "chr15"
start <- 74889136
end <-   75018200

featureDisplay <- "all"

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
bedFilePath <- file.path(extdata, "metQTL.bed")

if(interactive()){
  metQTLTrackAll <- metQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
  plotTracks(metQTLTrackAll, from = start, to = end)
} else {
  data(metQTLTrackAll)
  plotTracks(metQTLTrackAll, from = start, to = end)
}
```

`miRNATargetRegionsBiomart_ENSEMBL`

Creates a track of miRNA target regions from ENSEMBL

Description

Creates a track of miRNA target regions from ENSEMBL using the Gviz bioconductor package.

Usage

```
miRNATargetRegionsBiomart_ENSEMBL(gen, chr, start, end, showId=FALSE, datasetEnsembl = "hsapiens_mirn
```

Arguments

gen	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
showId	Show the ID of the genetic elements
datasetEnsembl	Allows the user to manually set which data set is used if required.Default=hsapiens_mirna_target_feature

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 1000000
end <- 20000000


if(interactive()){
 miRNATargetRegionsBiomartTrack<-miRNATargetRegionsBiomart_ENSEMBL(gen,chr,start,end,
                                      datasetEnsembl = "hsapiens_mirna_target_feature")
  plotTracks(miRNATargetRegionsBiomartTrack, from = start, to = end)
} else {
  data(miRNATargetRegionsBiomartTrack)
  plotTracks(miRNATargetRegionsBiomartTrack, from = start, to = end)
}
```

---

otherRegulatoryRegions_ENSEMBL

Creates a track of other regulatory regions from ENSEMBL

Description

Creates a track from ENSEMBL of other regulatory regions using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
otherRegulatoryRegions_ENSEMBL(gen, chr, start, end, featureDisplay = "all",datasetEnsembl = "hsapier
```

Arguments

gen	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
featureDisplay	A vector of regulatory features to be displayed, such as Enhancer. Spelling and capitalisation of features must be identical to those in the user guide. There are two possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Enhancer"), only the name of the specific feature is required. Second, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
datasetEnsembl	Allows the user to manually set which data set is used if required.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 100000
end <- 5000000
featureDisplay <- "Enhancer"

if(interactive()){
 otherRegulatoryRegionsTrackSingle<-otherRegulatoryRegions_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(otherRegulatoryRegionsTrackSingle, from = start, to = end)
} else {
  data(otherRegulatoryRegionsTrackSingle)
  plotTracks(otherRegulatoryRegionsTrackSingle, from = start, to = end)
}

########
```

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 100000
end <- 5000000
featureDisplay <- "all"
if(interactive()){
 otherRegulatoryRegionsTrackAll<-otherRegulatoryRegions_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(otherRegulatoryRegionsTrackAll, from = start, to = end)
} else {
  data(otherRegulatoryRegionsTrackAll)
  plotTracks(otherRegulatoryRegionsTrackAll, from = start, to = end)

}
```

---

psiQTL_GTEx *Creates a psiQTL track from GTEx*

Description

Creates a track of psiQTL from GTEx using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
psiQTL_GTEx(gen,chr,start, end, bedFilePath, featureDisplay = 'all', showId=FALSE, type_stacking="squ
```

Arguments

gen	the name of the genome.
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.
featureDisplay	A vector of regulatory features to be displayed, such as Predicted heterochomatin. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Predicted heterochomatin"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("Predicted low activity","Predicted heterochomatin")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
showId	logical. say if we write the name of group

type_stacking	Object of class"character", the stacking type of overlapping items on the final plot.One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz
just_group	position. say where we write the name of group (choice in c("above","righ","left"))

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen <- "hg19"
chr<-"chr13"
start <- 52713837
end <- 52715894
extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
psiQTLFilePath <- file.path(extdata, "/GTEX/psiQTL_Assoc-total.AdiposeTissue.txt")



if(interactive()){
  psiGTexTrackall<- psiQTL_GTEx(gen,chr,start, end, psiQTLFilePath, featureDisplay = 'all', showId=TRUE, type_st
  plotTracks(psiGTexTrackall, from = start, to = end)
} else {
  data(psiGTexTrackall)
  plotTracks(psiGTexTrackall, from = start, to = end)
}


if(interactive()){
 psiGTexTrackSNP<- psiQTL_GTEx(gen,chr,start, end, psiQTLFilePath, featureDisplay = 'SNP', showId=TRUE, type_sta
  plotTracks(psiGTexTrackSNP, from = start, to = end)
} else {
  data(psiGTexTrackSNP)
  plotTracks(psiGTexTrackSNP, from = start, to = end)
}
```

refGenes_UCSC *Create a track of RefSeq genes from the UCSC genome browser*

Description

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

Usage

```
refGenes_UCSC(gen, chr, start, end, IdType="Ref", 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)
IdType	When set to 'ref' shows the gene reference, when set to "name" shows the gene name
showId	Shows the ID or name of the genetic elements

Value

An UcscTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

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

ISCA_UCSC, GWAScatalog_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC, transcript_ENSEMBL, knownGenes_UCSC

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr7"
start <- 38203219
end <- 38303219
IdType <- "name"

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

`regulationBiomart_ENSEMBL`

Create a regulation track from ENSEMBL

Description

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

Usage

```
regulationBiomart_ENSEMBL(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_ENSEMBL(gen,chr,start,end)
  plotTracks(regulationENSEMBLtrack, from = start, to =end)
} else {
  data(regulationENSEMBLtrack)
  plotTracks(regulationENSEMBLtrack, from = start, to =end)
}
```

---

regulatoryEvidenceBiomart_ENSEMBL

Creates a regulatory feature track from ENSEMBL

Description

Creates a regulatory feature track from ENSEMBL using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
regulatoryEvidenceBiomart_ENSEMBL (gen, chr, start, end, featureDisplay = "all", datasetEnsembl = "hs
```

Arguments

gen	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
featureDisplay	A vector of regulatory features to be displayed, such as DNase1. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "DNase1"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("CTCF","DNase1")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
datasetEnsembl	Allows the user to manually set which data set is used if required.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 40000
end <- 50000
featureDisplay <- "H3K27me3"

if(interactive()){
 regulatoryEvidenceBiomartTrackSingle <- regulatoryEvidenceBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryEvidenceBiomartTrackSingle, from = start, to = end)
} else {
  data(regulatoryEvidenceBiomartTrackSingle)
  plotTracks(regulatoryEvidenceBiomartTrackSingle, from = start, to = end)
}

#####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 40000
end <- 100000
featureDisplay <- c("H3K27me3","H3K36me3")

if(interactive()){
 regulatoryEvidenceBiomartTrackMultiple<-regulatoryEvidenceBiomart_ENSEMBL (gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryEvidenceBiomartTrackMultiple, from = start, to = end)
} else {
  data(regulatoryEvidenceBiomartTrackMultiple)
  plotTracks(regulatoryEvidenceBiomartTrackMultiple, from = start, to = end)
}

#####

library("Gviz")
gen <- "hg38"
```

```
chr <- "chr1"
start <- 50000
end <- 100000
featureDisplay <- "all"
if(interactive()){
 regulatoryEvidenceBiomartTrackAll<-regulatoryEvidenceBiomart_ENSEMBL (gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryEvidenceBiomartTrackAll, from = start, to = end)
} else {
  data(regulatoryEvidenceBiomartTrackAll)
  plotTracks(regulatoryEvidenceBiomartTrackAll, from = start, to = end)

}
```

`regulatoryFeaturesBiomart_ENSEMBL`
Creates a regulatory feature track from ENSEMBL

Description

Creates a regulatory feature track from ENSEMBL using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
regulatoryFeaturesBiomart_ENSEMBL(gen, chr, start, end, featureDisplay = "all",datasetEnsembl = "hsap
```

Arguments

`gen`	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
`chr`	The chromosome of interest
`start`	The starting position in the region of interest (the smallest value)
`end`	The end position in the region of interest (the largest value)
`featureDisplay`	A vector of regulatory features to be displayed, such as Promoter. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Promoter"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("TF binding site","Promoter")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
`datasetEnsembl`	Allows the user to manually set which data set is used if required.Default=hsapiens_regulatory_feature

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 500000
featureDisplay <- "Enhancer"

if(interactive()){
 regulatoryFeaturesBiomartTrackSingle<-regulatoryFeaturesBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryFeaturesBiomartTrackSingle, from = start, to = end)
} else {
  data(regulatoryFeaturesBiomartTrackSingle)
  plotTracks(regulatoryFeaturesBiomartTrackSingle, from = start, to = end)
}

#####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 100000
featureDisplay <- c("CTCF Binding Site","Enhancer")

if(interactive()){
 regulatoryFeaturesBiomartTrackMultiple<-regulatoryFeaturesBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryFeaturesBiomartTrackMultiple, from = start, to = end)
} else {
  data(regulatoryFeaturesBiomartTrackMultiple)
  plotTracks(regulatoryFeaturesBiomartTrackMultiple, from = start, to = end)
}

#####

library("Gviz")
gen <- "hg38"
```

```
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "all"
if(interactive()){
 regulatoryFeaturesBiomartTrackAll<-regulatoryFeaturesBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatoryFeaturesBiomartTrackAll, from = start, to = end)
} else {
  data(regulatoryFeaturesBiomartTrackAll)
  plotTracks(regulatoryFeaturesBiomartTrackAll, from = start, to = end)

}
```

`regulatorySegmentsBiomart_ENSEMBL`

Creates a binding motif track from ENSEMBL

Description

Creates a track of regulatory segments from ENSEMBL using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
regulatorySegmentsBiomart_ENSEMBL(gen, chr, start, end, featureDisplay = 'all', datasetEnsembl = "hsa
```

Arguments

`gen`	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
`chr`	The chromosome of interest
`start`	The starting position in the region of interest (the smallest value)
`end`	The end position in the region of interest (the largest value)
`featureDisplay`	A vector of regulatory features to be displayed, such as Predicted heterochomatin. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Predicted heterochomatin"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("Predicted low activity","Predicted heterochomatin")). Finally, visualison all features in the genomic region, achived by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
`datasetEnsembl`	Allows the user to manually set which data set is used if required.Default=hsapiens_segmentation_feature

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

Tom Hardiman

References

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

Got to ENSEMBLregulation binding motif biomart

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "CTCF enriched"

if(interactive()){
 regulatorySegmentsBiomartTrackSingle<-regulatorySegmentsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatorySegmentsBiomartTrackSingle, from = start, to = end)
} else {
  data(regulatorySegmentsBiomartTrackSingle)
  plotTracks(regulatorySegmentsBiomartTrackSingle, from = start, to = end)
}

####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- c("CTCF enriched","Predicted Promoter Flank")

if(interactive()){
 regulatorySegmentsBiomartTrackMultiple<-regulatorySegmentsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatorySegmentsBiomartTrackMultiple, from = start, to = end)
} else {
  data(regulatorySegmentsBiomartTrackMultiple)
  plotTracks(regulatorySegmentsBiomartTrackMultiple, from = start, to = end)
}

####

library("Gviz")
gen <- "hg38"
```

```
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "all"
if(interactive()){
 regulatorySegmentsBiomartTrackAll<-regulatorySegmentsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(regulatorySegmentsBiomartTrackAll, from = start, to = end)
} else {
  data(regulatorySegmentsBiomartTrackAll)
  plotTracks(regulatorySegmentsBiomartTrackAll, from = start, to = end)

}
```

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

Description

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

Usage

```
repeatMasker_UCSC(gen, chr, start, end, showId=FALSE,type_stacking="full")
```

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
`type_stacking`	the type of stacking data for this track. More information go to Gviz (the option "stacking")

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 <- "hg38"
chr <- "chr2"
start <- 38290160
end <- 38303219

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

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

Description

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

Usage

```
segmentalDups_UCSC(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

Tom Hardiman

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 <- "hg38"
chr <- "chr2"
start <- 100000
end <- 200000

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

---

snpBiomart_ENSEMBL *Create a short variation track from ENSEMBL*

Description

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

Usage

```
snpBiomart_ENSEMBL(gen,chr, start, end, dataset, showId=FALSE, title_track = 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)
dataset	The name of the database. Example "hsapiens_snp_som"
showId	Show the the ID of element or not
title_track	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

snpLocations_UCSC, structureBiomart_ENSEMBL, COSMIC_UCSC, CoreillCNV_UCSC, ClinVarMain_UCSC, ClinVarCnv_UCSC,

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr2"
start <- 38290160
end <- 38303219

if(interactive()){
  snptrack <- snpBiomart_ENSEMBL(gen,chr, start, end,
                       dataset="hsapiens_snp",showId=FALSE)
  plotTracks(snptrack, from=start, to=end)
} else {
  data(snpBiomarttrack)
  plotTracks(snptrack, from=start, to=end)
}
```

---

snpLocations_UCSC *Create a SNP track from UCSC*

Description

Create a SNP track from UCSC using the Gviz bioconductor package

Usage

```
snpLocations_UCSC(gen, chr, start, end, track="All SNPs(142)")
```

Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
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. Default "All SNPs(142)"

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

snpLocations_UCSC, structureBiomart_ENSEMBL, COSMIC_UCSC, CoreillCNV_UCSC, ClinVarMain_UCSC, ClinVarCnv_UCSC,

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr7"
start <- 38290160
end <- 38303219

if(interactive()) {
  snpUCSCtrack<-snpLocations_UCSC(gen,chr,start,end,"All SNPs(142)")
  plotTracks(snpUCSCtrack, from = start, to =end)
} else {
  data(snpUCSCtrack)
  plotTracks(snpUCSCtrack, from = start, to =end)
}
```

---

structureBiomart_ENSEMBL

Create a structural variation track from ENSEMBL

Description

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

Usage

```
structureBiomart_ENSEMBL(gen, chr, start, end, strand, dataset, showId=FALSE, title_track = 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)
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_track	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

snpLocations_UCSC, snpBiomart_ENSEMBL, COSMIC_UCSC, CoreillCNV_UCSC, ClinVarMain_UCSC, ClinVarCnv_UCSC,

Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr2"
start <- 38290160
end <- 38303219

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

TFBS_FANTOM *Creates a TFBS motif track from FANTOM*

Description

Creates a track of TFBS motifs from FANTOM using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

Usage

```
TFBS_FANTOM(gen, chr, start, end, bedFilePath)
```

Arguments

gen	the name of the genome.
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The path of the BED file from Kheradpour and Kellis, 2014.

Value

An AnnotationTrack object of Gviz

Author(s)

Tiphaine Martin

References

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

Got to BindingMotifsBiomart binding motif biomart

Examples

```
library("Gviz")
gen <- "hg19"
chr<- "chr1"
start <- 6000000
end <- 6500000

extdata <- system.file("extdata", package="coMET",mustWork=TRUE)
AP1FantomFile <- file.path(extdata, "/FANTOM/Fantom_hg19.AP1_MA0099.2.sites.txt")

if(interactive()){
  tfbsFANTOMtrack <- TFBS_FANTOM(gen,chr,start, end, AP1FantomFile)
  plotTracks(tfbsFANTOMtrack, from = start, to = end)
```

```
} else {
  data(tfbsFANTOMtrack)
  plotTracks(tfbsFANTOMtrack, from = start, to = end)
}
```

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

Description

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

Usage

```
transcript_ENSEMBL(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

ISCA_UCSC, GWAScatalog_UCSC, knownGenes_UCSC, genesName_ENSEMBL, GeneReviews_UCSC, GAD_UCSC, genes_ENSEMBL, xenorefGenes_UCSC,

Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr2"
start <- 32290160
end <- 33303219

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

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