# Package 'coMET'

October 12, 2014

**Type** Package

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

**Version** 0.99.0

**Date** 2014-09-26

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

**Description**

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

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

**Suggests** knitr, RUnit, BiocGenerics

**Imports** colortools, hash, grDevices, ggbio, trackViewer

**License** GPL (>= 2)

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

**biocViews** Software, DifferentialMethylation, Visualization

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** Bioconductor

# R topics documented:



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

---

## Description

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

## Details

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

coMET package that can generate the regional plot capturing the features of co-methylation patterns, EWAS results, and genomic information. A coMET figure includes plot of p-value from the EWAS result, provides customized annotation tracks, and a triangle heatmap plot which demonstrates the correlation structure of CpG sites in a genomic region, calculated by the pairwise Spearman s rank correlation method.Plots are created as PDF,EPS files.

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

## Author(s)

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

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

## References

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

## See Also

<coMET>

## Examples

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

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

```
  geneRtrack <-GeneReviewsTrack(gen,chrom,start,end)

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

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

list of AnnotationTrack objects of GViz

## Author(s)

Tiphaine Martin

## Examples

```
library("Gviz")
  gen <- "hg19"
  chr <- "chr2"
  start <- 38290160
  end <- 38313219
if(interactive()){
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  track.name="Broad ChromHMM"
  tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
  table.name<-tablestrack[1]
  PATTERN.REGULATION<-"GM12878"

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

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

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

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

---

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

---

## Description

Creation of a track related to only one type of chromaHMM Broad from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  track.name="Broad ChromHMM"
  tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
  table.name<-tablestrack[1]
  chromhmmtrackone<-chromatinHMMOne(gen,chr,start,end,mySession,track.name,table.name)
  plotTracks(chromhmmtrackone, from = start, to =end)
}else {

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

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

## Description

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

## Usage

```
chrUCSC2ENSEMBL(chr)
```

## Arguments

| | |
|---|---|
| chr | the name of chromosome at UCSC format |

## Author(s)

Tiphaine Martin

## Examples

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

clinCNV *Data sets*

## Description

Some sample data sets used for the illustrative examples and the vignette.

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

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

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

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| MYDATA.FILE | Name of a info file for coMET parameters |
| MYDATA.FORMAT | Format of the input MYDATA.FILE. There are 6 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC |
| MYDATA.LARGE.FILE | Name of additional info files for coMET parameters. Multiple files are acceptable, files should be separated by comma |
| MYDATA.LARGE.FORMAT | Format of additional data visualised in p-value plot. Multiple files are acceptable, files should be separated by comma |
| CORMATRIX.FILE | Name of raw data or pre-computed correlation matrix |
| CORMATRIX.METHOD | Options for generating correlation matrix. There are three options: spearman, pearson and kendall |
| CORMATRIX.FORMAT | Format of the input CORMATRIX.FILE. TThere are two options: raw files (RAW) and and pre-computed correlation matrix (CORMATRIX) |
| CORMATRIX.COLOR.SCHEME | Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored |
| MYDATA.REF | The name of reference site listed in the MYDATA.FILE |
| START | The first nucleotide position visualised |
| END | the last nucleotide position visualised |
| ZOOM | Default=False |
| LAB.Y | Scale of y-axis. Options: log or ln |
| PVAL.THRESHOLD | Threshold of the significance. Displayed as a red dash line |
| DISP.PVAL.THRESHOLD | Display only the findings pass PVAL.THRESHOLD |

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

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

DISP.REGION
: Optional if MYDATA.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the region of genomic element will be shown by a continuous line with the color of element, in addition to a symbole in center of region

DISP.REGION.LARGE
: Optional if MYDATA.LARGE.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the region of genomic element will be shown by a continuous line with the color of element, in addition to a symbole in center of region

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

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

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

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

USE.COLORS
: Use the colors defined or grey color

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

TRACKS.GVIZ
: list of tracks created by Gviz.

TRACKS.GGBIO
: list of tracks created by ggbio.

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

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

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

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

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

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

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

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

DISP.TYPE
: Default: symbol

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

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

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

IMAGE.TITLE
: Title of the plot

IMAGE.NAME
: Name of the plot file

IMAGE.TYPE
: Options: pdf or eps

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

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

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

PRINT.IMAGE
: Print image in file or not.

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

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

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

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

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

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

## Value

Create a plot

## Author(s)

Tiphaine Martin

## Examples

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

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

```
gen <- "hg19"

if(interactive()){
  cat("interactive")
  genetrack <-genesENSEMBL(gen,chrom,start,end,showId=FALSE)
  snptrack <- snpBiomart(chrom, start, end,
                      dataset="hsapiens_snp_som",showId=FALSE)
  strutrack <- structureBiomart(chrom, start, end,
                              strand, dataset="hsapiens_structvar_som")
  clinVariant<-ClinVarMainTrack(gen,chrom,start,end)
  clinCNV<-ClinVarCnvTrack(gen,chrom,start,end)
  gwastrack <-GWASTrack(gen,chrom,start,end)
  geneRtrack <-GeneReviewsTrack(gen,chrom,start,end)
  listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile,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,TRACKS.GVIZ=listgviz,
      VERBOSE=FALSE, PRINT.IMAGE=FALSE,DISP.PVALUEPLOT=FALSE)
}
```

---

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

---

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| MYDATA.FILE | Name of a info file for coMET parameters |
| MYDATA.FORMAT | Format of the input MYDATA.FILE. There are 6 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC |
| MYDATA.LARGE.FILE | Name of additional info files for coMET parameters. Multiple files are acceptable, files should be separated by comma |
| MYDATA.LARGE.FORMAT | Format of additional data visualised in p-value plot. Multiple files are acceptable, files should be separated by comma |
| CORMATRIX.FILE | File with correlation matrix or raw data to create the correlation |
| CORMATRIX.METHOD | Options for generating correlation matrix. There are three options: spearman, pearson and kendall |
| CORMATRIX.FORMAT | Format of the input CORMATRIX.FILE. There are two options: raw files (RAW) and and pre-computed correlation matrix (CORMATRIX) |
| CORMATRIX.COLOR.SCHEME | Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored |
| MYDATA.REF | The name of reference site listed in the MYDATA.FILE |
| START | The first nucleotide position visualised |
| END | the last nucleotide position visualised |
| ZOOM | Default=False |
| LAB.Y | Scale of y-axis. Options: log or ln |
| PVAL.THRESHOLD | Threshold of the significance. Displayed as a red dash line |
| DISP.PVAL.THRESHOLD | Display only the findings pass PVAL.THRESHOLD |
| DISP.ASSOCIATION | Optional if MYDATA.FILE= SITE_ASSOC or REGION_ASSOC and contains the effect directions. A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot |
| DISP.ASSOCIATION.LARGE | Optinal if MYDATA.LARGE.FILE contains the effect directions (SITE_ASSOC, REGION_ASSOC). A value which can be TRUE or False. If it is False (the default), the comethylation pattern is shown in p-value plot; if it is True, the effect directions is shown on the plot |
| DISP.REGION | Optional if MYDATA.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the region of genomic element will be shown by a continuous line with the color of element, in addition to a symbole in center of region |

DISP.REGION.LARGE
: Optional if MYDATA.LARGE.FILE= REGION or REGION_ASSOC. A value which can be TRUE or False (the default). If it is TRUE, the region of genomic element will be shown by a continuous line with the color of element, in addition to a symbole in center of region

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

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

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

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

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

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

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

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

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

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

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

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

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

IMAGE.TITLE
: Title of the plot

IMAGE.NAME
: Name of the plot file

IMAGE.TYPE
: Options: pdf or eps

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

| | |
|---|---|
| PRINT.IMAGE | DEFAULT=FALSE. if the value is false, it does not produce the plot in a file. If the value is true, it print the plot in a file |
| config.file | Configuration file that contains the values of options instead of defining by command line |
| VERBOSE | Visualisation of comment to understand what happens |

## Author(s)

Tiphaine Martin

## Examples

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

---

# CoreillCNVTrack

*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*

---

## 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 in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

---

`cpgIslandsUCSC` *create track CpG Island from UCSC*

---

## Description

create track CpG Island from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

```
library("Gviz")
gen <- "hg19"
chr <- "chr7"
start <- 38290160
end <- 38303219
if(interactive()){
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  track.name="Broad ChromHMM"
  tablestrack<-tableNames(ucscTableQuery(mySession, track=track.name))
  table.name<-tablestrack[1]
  dnasetrack<-DNAseUCSC(gen,chr,start,end,mySession)
  plotTracks(dnasetrack, from = start, to =end)
}else {
    data(dnasetrack)
   plotTracks(dnasetrack, from = start, to =end)
}
```

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

`gcContent` *Create track GC content from UCSC*

---

## Description

Create track GC content from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

A BiomartGeneRegionTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

---

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

---

## Description

Get the name of genes in the genomic regions of interest from ENSEMBL

## Usage

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

## Arguments

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

## Author(s)

Tiphaine Martin

## Examples

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

if(interactive()) {
```

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

---

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

---

## Description

Create multiple tracks of Histone from UCSC's genome browser (ENCODE/Broad) in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

A list of AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

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

---

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

---

## Description

Create track one type of Histone density from UCSC (ENCODE/Broad) in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

# knownGenesUCSC *create track Known genes from UCSC*

---

## Description

create track Known genes from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

### Author(s)

Tiphaine Martin

### Examples

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

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

---

## regulationBiomart *create track Regulation from ENSEMBL*

---

### Description

create track Regulation from ENSEMBL in using the Gviz bioconductor package

### Usage

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

### Arguments

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

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

## Examples

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

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

---

`snpBiomart` *Create track Short Variation from ENSEMBL*

---

## Description

Create track Short Variation from ENSEMBL in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

`snpLocationsUCSC` *Create track SNPs from UCSC*

---

## Description

Create track SNPs from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

`structureBiomart` *Create track Structural Variation from ENSEMBL*

---

## Description

Create track Structural Variation from ENSEMBL in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

`transcriptENSEMBL` *Creation track for transcription sites*

---

## Description

Creation track for transcription sites in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

A BiomartGeneRegionTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

---

`xenorefGenesUCSC` *Create track xeno-reference Genes from UCSC*

---

## Description

Create track xeno-reference Genes from UCSC in using the Gviz bioconductor package

## Usage

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

## Arguments

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

## Value

An UcscTrack object of Gviz

## Author(s)

Tiphaine Martin

## Examples

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

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

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