

# Package ‘coMET’

October 23, 2014

**Type** Package

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

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## **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, BiocStyle

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

**License** GPL (>= 2)

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

## **biocViews**

Software, DifferentialMethylation, Visualization, Sequencing, Genetics, FunctionalGenomics

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** Bioconductor

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coMET-package	<i>coMET: visualisation of regional epigenome-wide association scan (EWAS) results and DNA co-methylation patterns</i>
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## Description

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

## Details

Package: coMET  
Type: Package  
Version: 0.99.3  
Date: 2014-10-16  
License: GPL (>=2)

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

## Author(s)

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

Maintainer: Tiphaine Martin <[tiphaine.martin@kcl.ac.uk](mailto:tiphaine.martin@kcl.ac.uk)>

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

## References

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

## Examples

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

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

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

```

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

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

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

```

---

chromatinHMMall

---

*Creating multiple chromHMM tracks from the UCSC genome browser*


---

## Description

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

## Usage

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

## Arguments

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

**Value**

list of AnnotationTrack objects of GViz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

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

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

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

---

chromatinHMMOne

---

*Creating one chromHMM track from the UCSC genome browser*


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An `AnnotationTrack` object of `Gviz`

**Author(s)**

Tiphaine Martin

**Examples**

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

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

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

---

chrUCSC2ENSEMBL	<i>Removing "chr" to the chromosome number from UCSC to transform it to ENSEMBL chromosome format</i>
-----------------	---

---

**Description**

Removing "chr" at the beginning of the chromosome number

**Usage**

```
chrUCSC2ENSEMBL(chr)
```

**Arguments**

chr	the chromosome number in UCSC format
-----	--------------------------------------

**Value**

the number of chromosome at ENSEMBL format

**Author(s)**

Tiphaine Martin

**Examples**

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

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

**Description**

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

**Usage**

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



**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

comet

---

*Visualize EWAS results in a genomic region of interest*


---

**Description**

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

**Usage**

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

## Arguments

MYDATA.FILE	Name of the info file describing the coMET parameters
MYDATA.FORMAT	Format of the input data in MYDATA.FILE. There are 4 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files describing the coMET parameters. File names should be comma-separated.
MYDATA.LARGE.FORMAT	Format of additional data to be visualised in the p-value plot. File names should be comma-separated.
CORMATRIX.FILE	Name of the raw data file or the pre-computed correlation matrix file.
CORMATRIX.METHOD	Options for calculating the correlation matrix: spearman, pearson and kendall
CORMATRIX.FORMAT	Format of the input CORMATRIX.FILE. There are two options: raw file (RAW) and pre-computed correlation matrix (CORMATRIX)
CORMATRIX.COLOR.SCHEME	Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored
MYDATA.REF	The name of the reference CpG-site listed in MYDATA.FILE
START	The first nucleotide position to be visualised
END	the last nucleotide position to be visualised
ZOOM	Default=False
LAB.Y	Scale of the y-axis. Options: log or ln
PVAL.THRESHOLD	Significance threshold to be displayed as a red dashed line
DISP.PVAL.THRESHOLD	Display only the findings that pass the value put in DISP.PVAL.THRESHOLD
DISP.ASSOCIATION	This logical option works only if MYDATA.FILE contains the effect direction (MYDATA.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST. On the other hand, if the association is negative, the color is the opposed color.
DISP.ASSOCIATION.LARGE	This logical option works only if MYDATA.LARGE.FILE contains the effect direction (MYDATA.LARGE.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST.LARGE. On the other hand, if the association is negative, the color is the opposed color.

DISP.REGION	This logical option works only if MYDATA.FILE contains regions (MYDATA.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.
DISP.REGION.LARGE	This logical option works only if MYDATA.LARGE.FILE contains regions (MYDATA.LARGE.FORMAT=REGION or REGION_ASSOC). The value can be TRUE or FALSE (default). If TRUE, the genomic element will be shown by a continuous line with the color of the element, in addition to the symbol at the center of the region. If FALSE, only the symbol is shown.
SYMBOLS	The symbol shown in the p-value plot. Options: circle, square, diamond, triangle. Symbols can be filled by appending -fill, e.g. square-fill. Example: circle,diamond-fill,triangle
SYMBOLS.LARGE	The symbol to visualise the data defined in MYDATA.LARGE.FILE. Options: circle, square, diamond, triangle; Symbols can either be filled or not filled by appending -fill e.s., square-fill. Example: circle,diamond-fill,triangle
SAMPLE.LABELS	Labels for the sample described in MYDATA.FILE to include in the legend
SAMPLE.LABELS.LARGE	Labels for the sample described in MYDATA.LARGE.FILE to include in the legend
USE.COLORS	Use the colors defined or use the grey color scheme
DISP.COLOR.REF	Logical option TRUE or FALSE (TRUE default). if TRUE, the connection line related to the reference probe is in purple, if FALSE if the connection line related to the reference probe stay black.
COLOR.LIST	List of colors for displaying the P-value symbols related to the data in MYDATA.FILE
COLOR.LIST.LARGE	List of colors for displaying the P-value symbols related to the data in MYDATA.LARGE.FILE
DISP.MYDATA	logical option TRUE or FALSE. TRUE (default). If TRUE, the P-value plot is shown; if FALSE the plot will be defined by GViz
BIOFEAT.USER.FILE	Name of data file to visualise in the tracks. File names should be comma-separated.
BIOFEAT.USER.TYPE	Track type, where multiple tracks can be shown (comma-separated): DataTrack, AnnotationTrack, GeneRegionTrack.
BIOFEAT.USER.TYPE.PLOT	Format of the plot if the data are shown with the Gviz's function called DataTrack (comma-separated)
GENOME	The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), gr
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 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 hexadecimal HTML color codes; one color per line; if you do not want to use this option, use the color defined by the option CORMATRIX.COLOR.SCHEME
IMAGE.TITLE	Title of the plot
IMAGE.NAME	Path and Name of the plot file without extension
IMAGE.TYPE	Options: pdf or eps
IMAGE.SIZE	Default: 3.5 inches. Possible sizes : 3.5 or 7
FONT.FACTOR	Font size of the sample labels. Range: 0-1
SYMBOL.FACTOR	Size of the symbols. Range: 0-1
PRINT.IMAGE	Print image in file or not.
CONNECTING.LINES.FACTOR	Length of the connecting lines. Range: 0-2
CONNECTING.LINES.ADJ	Position of the connecting lines horizontally. Negative values shift the connecting lines to the left and positive values shift the lines to the right. Range: (-1;1) option -1 means no connecting lines.
CONNECTING.LINES.VERT.ADJ	Position of the connecting lines vertically. Can be used to vertically adjust the position of the connecting lines in relation to the CpG-site names. Negative value shift the connecting lines down. Range: (-0.5 - 0), option -1 mean the default value related to the plot size (-0.5 for 3.5 plot size; -0.7 for 7.5 plot size)
CONNECTING.LINES.FLEX	Adjusts the spread of the connecting lines. Range: 0-2
config.file	Configuration file that contains the values of these options instead of defining these by command line
VERBOSE	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

**Value**

Create a plot

**Author(s)**

Tiphaine Martin

**Examples**

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

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

```

gen <- "hg19"

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

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

```

---

comet.web

---

*Visualize EWAS results in a genomic region of interest with predefined  
annotation tracks*


---

## Description

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

**Usage**

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

**Arguments**

MYDATA.FILE	Name of the info file describing the coMET parameters
MYDATA.FORMAT	Format of the input data in MYDATA.FILE. There are 4 different options: SITE, REGION, SITE_ASSOC, REGION_ASSOC
MYDATA.LARGE.FILE	Name of additional info files describing the coMET parameters. File names should be comma-separated.
MYDATA.LARGE.FORMAT	Format of additional data to be visualised in the p-value plot. File names should be comma-separated.
CORMATRIX.FILE	Name of the raw data file or the pre-computed correlation matrix file.
CORMATRIX.METHOD	Options for calculating the correlation matrix: spearman, pearson and kendall
CORMATRIX.FORMAT	Format of the input CORMATRIX.FILE. There are two options: raw file (RAW) and pre-computed correlation matrix (CORMATRIX)
CORMATRIX.COLOR.SCHEME	Color scheme options: heat, bluewhitered, cm, topo, gray, bluetored
MYDATA.REF	The name of the reference CpG-site listed in MYDATA.FILE
START	The first nucleotide position to be visualised
END	the last nucleotide position to be visualised
ZOOM	logical option TRUE or FALSE. FALSE (default)
LAB.Y	Scale of the y-axis. Options: log or ln
PVAL.THRESHOLD	Significance threshold to be displayed as a red dashed line
DISP.PVAL.THRESHOLD	Display only the findings that pass the value put in DISP.PVAL.THRESHOLD
DISP.ASSOCIATION	This logical option works only if MYDATA.FILE contains the effect direction (MYDATA.FORMAT=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option COLOR.LIST. On the other hand, if the association is negative, the color is the opposed color.
DISP.ASSOCIATION.LARGE	This logical option works only if MYDATA.LARGE.FILE contains the effect direction (MYDATA.LARGE.FORMA=SITE_ASSOC or REGION_ASSOC). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is

	shown. If the association is positive, the color is the one defined with the option <code>COLOR.LIST.LARGE</code> . On the other hand, if the association is negative, the color is the opposed color.
<code>DISP.REGION</code>	This logical option works only if <code>MYDATA.FILE</code> contains regions ( <code>MYDATA.FORMAT=REGION</code> or <code>REGION_ASSOC</code> ). The value can be <code>TRUE</code> or <code>FALSE</code> (default). If <code>TRUE</code> , 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 <code>FALSE</code> , only the symbol is shown.
<code>DISP.REGION.LARGE</code>	This logical option works only if <code>MYDATA.LARGE.FILE</code> contains regions ( <code>MYDATA.LARGE.FORMAT=REGION</code> or <code>REGION_ASSOC</code> ). The value can be <code>TRUE</code> or <code>FALSE</code> (default). If <code>TRUE</code> , 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 <code>FALSE</code> , only the symbol is shown.
<code>SYMBOLS</code>	The symbol shown in the p-value plot. Options: circle, square, diamond, triangle. Symbols can be filled by appending <code>-fill</code> , e.g. <code>square-fill</code> . Example: <code>circle,diamond-fill,triangle</code>
<code>SYMBOLS.LARGE</code>	The symbol to visualise the data defined in <code>MYDATA.LARGE.FILE</code> . Options: circle, square, diamond, triangle; Symbols can either be filled or not filled by appending <code>-fill</code> e.s., <code>square-fill</code> . Example: <code>circle,diamond-fill,triangle</code>
<code>SAMPLE.LABELS</code>	Labels for the sample described in <code>MYDATA.FILE</code> to include in the legend
<code>SAMPLE.LABELS.LARGE</code>	Labels for the sample described in <code>MYDATA.LARGE.FILE</code> to include in the legend
<code>USE.COLORS</code>	Use the colors defined or use the grey color scheme
<code>DISP.COLOR.REF</code>	Logical option <code>TRUE</code> or <code>FALSE</code> ( <code>TRUE</code> default). if <code>TRUE</code> , the connection line related to the reference probe is in purple, if <code>FALSE</code> if the connection line related to the reference probe stay black.
<code>COLOR.LIST</code>	List of colors for displaying the P-value symbols related to the data in <code>MYDATA.FILE</code>
<code>COLOR.LIST.LARGE</code>	List of colors for displaying the P-value symbols related to the data in <code>MYDATA.LARGE.FILE</code>
<code>DISP.MYDATA</code>	logical option <code>TRUE</code> or <code>FALSE</code> . <code>TRUE</code> (default).If <code>TRUE</code> , the P-value plot is shown; if <code>FALSE</code> the plot will be defined by <code>GViz</code>
<code>BIOFEAT.USER.FILE</code>	Name of data file to visualise in the tracks. File names should be comma-separated.
<code>BIOFEAT.USER.TYPE</code>	Track type, where multiple tracks can be shown (comma-separated): <code>DataTrack</code> , <code>AnnotationTrack</code> , <code>GeneRegionTrack</code> .
<code>BIOFEAT.USER.TYPE.PLOT</code>	Format of the plot if the data are shown with the <code>Gviz</code> 's function called <code>DataTrack</code> (comma-separated)



LIST.TRACKS	List of annotation tracks to visualise. Options include geneENSEMBL, CGI, ChromHMM, DNase, RegENSEMBL, SNP, transcriptENSEMBL, SNPstoma, SNPstru, SNPstrustoma, ISCA, COSMIC, GAD, ClinVar, GeneReviews, GWAS, ClinVarCNV, GCcontent, genesUCSC, xenogenesUCSC.
PATTERN.REGULATION	The cell/tissue or the list of cells/tissues to visualise in the regulation region defined by Broad ChromHMM
IMAGE.TITLE	Title of the plot
IMAGE.NAME	path and Name of the plot file without extension
IMAGE.TYPE	Options: pdf or eps
IMAGE.SIZE	Default: 3.5 inches. Possible sizes : 3.5 or 7
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.
config.file	Configuration file that contains the values of these options instead of defining these by command line
VERBOSE	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

**Author(s)**

Tiphaine Martin

**Examples**

```
extdata <- system.file("extdata", package="coMET", mustWork=TRUE)
configfile <- file.path(extdata, "config_cyp1b1_zoom_4webserver.txt")
myinfofile <- file.path(extdata, "cyp1b1_infofile.txt")
myexpressfile <- file.path(extdata, "cyp1b1_infofile_exprGene_region.txt")
mycorrelation <- file.path(extdata, "cyp1b1_res37_rawMatrix.txt")

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

---

CoreillCNVTrack	<i>Create one track of the genomic positions of CNV in chromosomal aberration and inherited disorders from the NIGMS Human Genetic Cell Repository data</i>
-----------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

COSMICTrack

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

---

cpgIslandsUCSC

*create track CpG Island from UCSC*


---

**Description**

create track CpG Island from UCSC using the Gviz bioconductor package

**Usage**

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

**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

DNaseUCSC

---

*Creation of an UCSC's DNase clusters track*


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

---

GADTrack

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

---

**Description**

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

**Usage**

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

**Arguments**

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

end                    the last position in the region of interest (the largest value)  
 showId                Show the ID of the genetic elements

### Value

An UcscTrack object of Gviz

### Author(s)

Tiphaine Martin

### Examples

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

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

---

gcContent

*Create one track of GC content from UCSC*

---

### Description

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

### Usage

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

### Arguments

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

**Value**

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A BiomartGeneRegionTrack object of Gviz



**Author(s)**

Tiphaine Martin

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

GWASTrack

---

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


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

HistoneAll	<i>Create multiple tracks of histone modifications from the UCSC genome browser</i>
------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A list of AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

```

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

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

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

```

---

HistoneOne

---

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


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

ISCATrack

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

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

**Usage**

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

**Arguments**

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

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

knownGenesUCSC

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

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

---

**Description**

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

**Usage**

```
regulationBiomart(chr, start, end, dataset="hsapiens_feature_set")
```

**Arguments**

chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
dataset	The name of the database."hsapiens_feature_set"(default)

**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 a short variation track from ENSEMBL***Description**

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

**Usage**

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

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin



**Examples**

```

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

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

```

---

snpLocationsUCSC

---

*Create a SNP track from UCSC*


---

**Description**

Create a SNP track from UCSC using the Gviz bioconductor package

**Usage**

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

**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

```

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

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

```

---

structureBiomart

---

*Create a structural variation track from ENSEMBL*


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**Examples**

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

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

---

transcriptENSEMBL	<i>Create a track of transcripts from ENSEMBL</i>
-------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A BiomartGeneRegionTrack object of Gviz

**Author(s)**

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**Examples**

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

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

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