

# Package ‘coMET’

May 25, 2022

**Type** Package

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

**Version** 1.29.0

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**Description** Visualisation of EWAS results in a genomic region. In addition to phenotype-association P-values, coMET also generates plots of co-methylation patterns and provides a series of annotation tracks. It can be used to other omic-wide association scans as long as the data can be translated to genomic level and for any species.

**Depends** R (>= 4.0.0), grid, utils, biomaRt, Gviz, psych

**Suggests** BiocStyle, knitr, RUnit, BiocGenerics, showtext

**Imports** colortools, hash,grDevices, gridExtra, rtracklayer, IRanges, S4Vectors, GenomicRanges, stats, corrplot

**License** GPL (>= 2)

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

**biocViews** Software, DifferentialMethylation, Visualization, Sequencing, Genetics, FunctionalGenomics, Microarray, MethylationArray, MethylSeq, ChIPSeq, DNASEq, RiboSeq, RNASeq, ExomeSeq, DNAMethylation, GenomeWideAssociation, MotifAnnotation

**VignetteBuilder** knitr

**NeedsCompilation** no

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

coMET is an R package for visualising EWAS results in a genomic region. Along with phenotype-association plots, coMET also generates plots of co-methylation patterns and provides a series of annotation tracks. The software is designed for epigenetic data, but can also be applied to genomic and functional genomic datasets (other omic-WAS results) in any species.

## Details

Package: coMET  
 Type: Package  
 Version: 1.11.5  
 Date: 2018-04-16  
 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, Thomas Hardiman, Idil Yet, Pei-Chien Tsai, Jordana T. Bell

Maintainer: Tiphaine Martin <[tiphaine.martin@mssm.edu](mailto:tiphaine.martin@mssm.edu)>

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

## References

Martin, T.C, Yet, I, Tsai, P-C, Bell, J.T., coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns, BMC bioinformatics, 2015.

**Examples**

```

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

chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg38"

if(interactive()){
  genetrack <- genes_ENSEMBL(gen, chrom, start, end, showId=TRUE)
  snptrack <- snpBiomart_ENSEMBL(gen, chrom, start, end,
    dataset="hsapiens_snp_som", showId=FALSE)
  strutrack <- structureBiomart_ENSEMBL(gen, chrom, start, end,
    strand, dataset="hsapiens_structvar_som")
  clinVariant <- ClinVarMain_UCSC(gen, chrom, start, end)
  clinCNV <- ClinVarCnv_UCSC(gen, chrom, start, end)
  gwastrack <- GWAScatalog_UCSC(gen, chrom, start, end)
  geneRtrack <- GeneReviews_UCSC(gen, chrom, start, end)
  listgviz <- list(genetrack, snptrack, strutrack, clinVariant,
    clinCNV, gwastrack, geneRtrack)
  comet(config.file=configfile, mydata.file=myinfofile, mydata.type="file",
    cormatrix.file=mycorrelation, cormatrix.type="listfile",
    mydata.large.file=myexpressfile, mydata.large.type="listfile",
    tracks.gviz=listgviz, verbose=FALSE, print.image=FALSE, disp.pvalueplot=FALSE)
} else {
  data(geneENSEMBLtrack)
  data(snpBiomarttrack)
  data(ISCATrack)
  data(strucBiomarttrack)
  data(ClinVarCnvTrack)
  data(clinVarMaintrack)
  data(GWASTrack)
  data(GeneReviewTrack)

  listgviz <- list(genetrack, snptrack, strutrack, clinVariant,
    clinCNV, gwastrack, geneRtrack)
  comet(config.file=configfile, mydata.file=myinfofile, mydata.type="listfile",
    cormatrix.file=mycorrelation, cormatrix.type="listfile",
    mydata.large.file=myexpressfile, mydata.large.type="listfile",
    tracks.gviz=listgviz,
    verbose=FALSE, print.image=FALSE, disp.pvalueplot=TRUE)
}

```

---

bindingMotifsBiomart\_ENSEMBL

*Creates a binding motif track from ENSEMBL*


---

**Description**

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

**Usage**

```
bindingMotifsBiomart_ENSEMBL(gen, chr, start, end, featureDisplay="all",
datasetEnsembl = NULL, title="Binding Motifs ENSEMBL")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

Tom Hardiman

**References**

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

Got to ENSEMBLregulation binding motif biomart

**Examples**

```

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

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

#####

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

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

#####

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

if(interactive()){
  bindMotifsBiomartTrackAll<-bindingMotifsBiomart_ENSEMBL(gen,chr,start,end,featureDisplay)
  plotTracks(bindMotifsBiomartTrackAll, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
} else {

```

```

data(bindMotifsBiomartTrackAll)
plotTracks(bindMotifsBiomartTrackAll, from = start, to = end,
fontfamily="sans",fontfamily.title="sans")
}

```

ChIPTF\_ENCODE

*Creates a TF motif track from ENCODE***Description**

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

**Usage**

```

ChIPTF_ENCODE(gen="hg19", chr, start, end, bedFilePath,
featureDisplay='all', motifColorFile, type_stacking='dense',
showId=FALSE,just_group="above", title="TF motifs ENCODE")

```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

Got to BindingMotifsBiomart binding motif biomart

**Examples**

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

if(interactive()){
  extdata <- system.file("extdata", package="coMET", mustWork=TRUE)
  bedFilePath <- file.path(extdata, "ENCODE/motifs1000_matches_ENCODE.txt")
  motif_color <- file.path(extdata, "ENCODE/TFmotifs_colors.csv")
  chipTFtrack <- ChIPTF_ENCODE(gen,chr,start, end, bedFilePath,
    featureDisplay=c("AHR::ARNT::HIF1A_1","AIRE_1","AIRE_2","AHR::ARNT_1"),
    motif_color,type_stacking="squish",showId=TRUE)
  plotTracks(chipTFtrack, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
} else {
  data(chipTFtrack)
  plotTracks(chipTFtrack, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
}
```

---

chromatinHMMA11\_UCSC *Creating multiple chromHMM tracks from the UCSC genome browser*

---

**Description**

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

**Usage**

```
chromatinHMMA11_UCSC(gen, chr, start, end, mySession, color='coMET',
  pattern = NULL, table.name = NULL)
```



**Arguments**

gen	the name of the genome
chr	the chromosome of interest
start	the first position in region of interest (the smallest value)
end	the last position in region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
color	the colour scheme used for plots. By default this is set to 'coMET' to allow easy identification of different elements. The colour scheme set by UCSC can also be used. Consult userguide for table of colours.
pattern	the pattern of the track to visualise
table.name	the name of the table from the track

**Value**

list of AnnotationTrack objects of GViz

**Author(s)**

Tiphaine Martin

**References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg)

**See Also**

[chromatinHMMA11\\_UCSC](#)

**Examples**

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

  chromhmmPattern<-chromatinHMMA11_UCSC(gen,chr,start,end,mySession,
  color='coMET',PATTERN.REGULATION)
```

```

    plotTracks(chromhmmPattern, from = start, to =end,
fontfamily="sans",fontfamily.title="sans")

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

    data(chromhmmPattern)
    plotTracks(chromhmmPattern, from = start, to =end,
fontfamily="sans",fontfamily.title="sans")

    data(chromhmmNoPattern)
    plotTracks(chromhmmNoPattern, from = start, to =end,
fontfamily="sans",fontfamily.title="sans")
  }

```

---

chromatinHMMOne\_UCSC *Creating one chromHMM track from the UCSC genome browser*

---

## Description

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

## Usage

```
chromatinHMMOne_UCSC(gen, chr, start, end, mySession, color="coMET",
title="ENCODE/Broad chromHMM", table.name = NULL)
```

## Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in region of interest (the smallest value)
end	the last position in region of interest (the biggest value)
mySession	the object session from the function browserSession of rtracklayer
color	the color scheme used for plots. By default this is set to 'coMET' to allow easy indentification of differnent elements. The color scheme set by UCSC can also be used. Consult userguide for table of colors.
title	Name of tracks
table.name	the name of the table from the track

## Value

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**See Also**

[chromatinHMMAll\\_UCSC](#)

**Examples**

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

if(interactive()) {
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  track.name="Broad ChromHMM"
  tablestrack<-ucscTables(gen, track.name)
  table.name<-tablestrack[1]
  chromhmmtrackone<-chromatinHMMOne_UCSC(gen,chr,start,end
  ,mySession,color="coMET",table.name)
  plotTracks(chromhmmtrackone, from = start, to =end,
  fontfamily="sans",fontfamily.title="sans")
}else {
  data(chromhmmtrackone)
  plotTracks(chromhmmtrackone, from = start, to =end,
  fontfamily="sans",fontfamily.title="sans")
}
```

---

chromHMM\_RoadMap

*Creates a ChromHMM track from a file of RoadMap*

---

**Description**

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

**Usage**

```
chromHMM_RoadMap(gen="hg19",chr, start, end, bedFilePath,
featureDisplay = 'all', colorcase='roadmap15',
title=" chromHMM RoadMap")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>  
Got to RoadMap Epigenome

**Examples**

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

```

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

if(interactive()){
  chromHMM_RoadMapSingle <- chromHMM_RoadMap(gen="hg19",chr,start, end,
  bedFilePath, featureDisplay = featureDisplay, colorcase='roadmap15' )
  plotTracks(chromHMM_RoadMapSingle, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
} else {
  data(chromHMM_RoadMapSingle)
  plotTracks(chromHMM_RoadMapSingle, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
}

#####

library("Gviz")
chr <- "chr22"
start <- 38291000
end <- 38301200
featureDisplay <- c("7_Enh","13_ReprPC")

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

if(interactive()){
  chromHMM_RoadMapMultiple <- chromHMM_RoadMap(gen="hg19",chr,start, end,
  bedFilePath, featureDisplay = featureDisplay, colorcase='roadmap15' )
  plotTracks(chromHMM_RoadMapMultiple, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
} else {
  data(chromHMM_RoadMapMultiple)
  plotTracks(chromHMM_RoadMapMultiple, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
}

#####

library("Gviz")
chr <- "chr22"
start <- 38291000
end <- 38301200
featureDisplay <- "all"

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

if(interactive()){
  chromHMM_RoadMapAll <- chromHMM_RoadMap(gen="hg19",chr,start, end,
  bedFilePath, featureDisplay = featureDisplay, colorcase='roadmap15' )
  plotTracks(chromHMM_RoadMapAll, from = start, to = end,
  fontfamily="sans",fontfamily.title="sans")
}

```

```

} else {
  data(chromHMM_RoadMapAll)
  plotTracks(chromHMM_RoadMapAll, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
}

```

---

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)

```

---

ClinVarCnv_UCSC	<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

```
ClinVarCnv_UCSC(gen, chr, start, end, title="ClinVar Variants", 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)
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

**See Also**

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [snpBiomart\\_ENSEMBL](#), [CoreillCNV\\_UCSC](#), [COSMIC\\_UCSC](#), [ClinVarMain\\_UCSC](#)

**Examples**

```
library("Gviz")
chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg38"
if(interactive()){
  clinCNV<-ClinVarCnv_UCSC(gen,chrom,start,end)
  plotTracks(clinCNV, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
}else {
  data(ClinVarCnvTrack)
  plotTracks(clinCNV, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
}
```

---

ClinVarMain_UCSC	<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

```
ClinVarMain_UCSC(gen, chr, start, end, title="ClinVar Variants", 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)
title	The name of the annotation track
showId	Show the ID of the genetic elements

### Value

An UcsTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

### See Also

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [snpBiomart\\_ENSEMBL](#), [CoreilCNV\\_UCSC](#), [COSMIC\\_UCSC](#), [ClinVarCnv\\_UCSC](#)



**Examples**

```

library("Gviz")
gen <- "hg38"
chrom <- "chr2"
start <- 100000
end <- 1000000

if(interactive()) {
  clinVariant<-ClinVarMain_UCSC(gen,chrom,start,end)
  plotTracks(clinVariant, from = start, to =end,
    fontfamily="sans",fontfamily.title="sans")
}else{
  data(clinVarMaintrack)
  plotTracks(clinVariant, from = start, to =end,
    fontfamily="sans",fontfamily.title="sans")
}

```

comet

*Visualize EWAS results in a genomic region of interest***Description**

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

**Usage**

```

comet(mydata.file = NULL, mydata.format = "site", mydata.type = "file",
  mydata.large.file = NULL, mydata.large.format = "site",
  mydata.large.type = "listfile", cormatrix.file = NULL,
  cormatrix.method = "spearman", cormatrix.format = "raw",
  cormatrix.color.scheme = "bluewhitered",cormatrix.conf.level=0.05,
  cormatrix.sig.level= 1, cormatrix.adjust="none",
  cormatrix.type = "listfile", mydata.ref = NULL,
  start = NULL, end = NULL, zoom = FALSE, lab.Y = "log",
  pval.threshold = 1e-05,pval.threshold.2 = 0,disp.pval.threshold = 1,
  disp.association = FALSE, disp.association.large = FALSE,
  disp.region = FALSE, disp.region.large = FALSE,
  disp.beta.association = FALSE, disp.beta.association.large = FALSE, factor.beta = 0.3,
  symbols = "circle-fill",
  symbols.large = NA, sample.labels = NULL, sample.labels.large = NULL,
  use.colors = TRUE , disp.color.ref = TRUE, color.list = NULL, color.list.large = NULL,
  disp.mydata = TRUE, biofeat.user.file = NULL, biofeat.user.type = NULL,
  biofeat.user.type.plot = NULL,

```

```

genome = "hg19", dataset.gene = "hsapiens_gene_ensembl",
tracks.gviz = NULL,
disp.mydata.names = TRUE, disp.color.bar = TRUE, disp.phys.dist = TRUE,
disp.legend = TRUE, disp.marker.lines = TRUE, disp.cormatrixmap = TRUE,
disp.pvalueplot = TRUE, disp.type = "symbol", disp.mult.lab.X = FALSE,
disp.connecting.lines = TRUE, palette.file = NULL, image.title = NULL,
image.name = "coMET", image.type = NULL, image.size = 3.5,
fontsize.gviz=5, font.factor = 1,
symbol.factor = NULL, print.image = TRUE, connecting.lines.factor = 1.5,
connecting.lines.adj = 0.01, connecting.lines.vert.adj = -1,
connecting.lines.flex = 0, config.file = NULL, verbose = FALSE)

```

## Arguments

- `mydata.file` Name of the info file describing the coMET parameters
- `mydata.format` Format of the input data in `mydata.file`. There are 4 different options: `site`, `region`, `site_asso`, `region_asso`.
- `mydata.type` Format of `mydata.file`. There are 2 different options: `FILE` or `MATRIX`.
- `mydata.large.file`  
Name of additional info files describing the coMET parameters. File names should be comma-separated. It is optional, but if you add some, they need to be file(s) in tabular format with a header. Additional info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option `mydata.large.format`.
- `mydata.large.format`  
Format of additional data to be visualised in the p-value plot. Format should be comma-separated. There are 4 different options for each file: `site`, `region`, `site_asso`, `region_asso`.
- `mydata.large.type`  
Format of `mydata.large.file`. There are 2 different options: `listfile` or `listdataframe`.
- `cormatrix.file` Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.
- `cormatrix.method`  
Options for calculating the correlation matrix: `spearman`, `pearson` and `kendall`
- `cormatrix.format`  
Format of the input `cormatrix.file`. There are two options: `raw file` (raw if CpG sites are by column and samples by row or `raw_rev` if CpG site are by row and samples by column) and `pre-computed correlation matrix` (`cormatrix`)
- `cormatrix.color.scheme`  
Color scheme options: `heat`, `bluewhitered`, `cm`, `topo`, `gray`, `bluetored`
- `cormatrix.conf.level`  
Alpha level for the confidence interval. Default value= 0.05. CI will be the  $\alpha/2$  lower and upper values.

<code>cormatrix.sig.level</code>	Significant level to visualise the correlation. If the correlation has a pvalue under the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme choosen.Default value =1.
<code>cormatrix.adjust</code>	indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".Default value="none"
<code>cormatrix.type</code>	Format of <code>cormatrix.file</code> . There are 2 different options: listfile or listdataframe.
<code>mydata.ref</code>	The name of the referenceomic feature (e.g. CpG-site) listed in <code>mydata.file</code>
<code>start</code>	The first nucleotide position to be visualised. It could be bigger or smaller than the first position of our list of omic features.
<code>end</code>	the last nucleotide position to be visualised. It has to be bigger than the value in the option start, but it could be smaller or bigger than the last position of our list of omic features.
<code>zoom</code>	Default=False
<code>lab.Y</code>	Scale of the y-axis. Options: log or ln
<code>pval.threshold</code>	Significance threshold to be displayed as a red dashed line
<code>pval.threshold.2</code>	the second significance threshold to be displayed as a orange dashed line
<code>disp.pval.threshold</code>	Display only the findings that pass the value put in <code>disp.pval.threshold</code>
<code>disp.association</code>	This logical option works only if <code>mydata.file</code> contains the effect direction ( <code>mydata.format=site_asso</code> or <code>region_asso</code> ). 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</code> . On the other hand, if the association is negative, the color is the opposed color.
<code>disp.association.large</code>	This logical option works only if <code>mydata.large.file</code> contains the effect direction ( <code>mydata.large.format=site_asso</code> or <code>region_asso</code> ). 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_asso</code> ). 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.
<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_asso</code> ). 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.
<code>disp.beta.association</code>	This logical option works only if <code>mydata.file</code> contains the effect direction ( <code>mydata.format=site_asso</code> or <code>region_asso</code> ). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the size of symbol is the default size of symbole; if TRUE, the effect direction is shown.
<code>disp.beta.association.large</code>	This logical option works only if <code>mydata.large.file</code> contains the effect direction ( <code>mydata.large.format=site_asso</code> or <code>region_asso</code> ). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the size of symbol is ththe default size of symbole; if TRUE, the effect direction is shown.
<code>factor.beta</code>	Factor to visualise the size of beta. Default value = 0.3.
<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 TRUE or FALSE (TRUE default). if TRUE, the connection line related to the reference probe is in purple, if FALSE if the connection line related to the reference probe stay black.
<code>color.list</code>	List of colors for displaying the P-value symbols related to the data in <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 TRUE or FALSE. TRUE (default). If TRUE, the P-value plot is shown; if FALSE the plot will be defined by GViz
<code>biofeat.user.file</code>	Name of data file to visualise in the tracks. File names should be comma-separated.
<code>biofeat.user.type</code>	Track type, where multiple tracks can be shown (comma-separated): <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 Gviz's function called <code>DataTrack</code> (comma-separated)
<code>genome</code>	The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37), "grch38" (GRCh38)

<code>dataset.gene</code>	The gene names from ENSEMBL. e.g. <code>hsapiens_gene</code>
<code>tracks.gviz</code>	list of tracks created by Gviz.
<code>disp.mydata.names</code>	logical option TRUE or FALSE. If True (default), the names of the CpG sites are displayed.
<code>disp.color.bar</code>	Color legend for the correlation matrix (range -1 to 1). Default: blue-white-red
<code>disp.phys.dist</code>	logical option (TRUE or FALSE). TRUE (default).Display the bp distance on the plots
<code>disp.legend</code>	logical option TRUE or FALSE. TRUE (default) Display the sample labels and corresponding symbols on the lower right side
<code>disp.marker.lines</code>	logical option TRUE or FALSE. TRUE (default), if FALSE the red line for <code>pval.threshold</code> is not shown
<code>disp.cormatrixmap</code>	logical option TRUE or FALSE. TRUE (default), if FALSE correlation matrix is not shown
<code>disp.pvalueplot</code>	logical option (TRUE or FALSE). TRUE (default), if FALSE the pvalue plot is not shown
<code>disp.type</code>	Default: symbol
<code>disp.mult.lab.X</code>	logical option TRUE or FALSE. FALSE (default).Display evenly spaced X-axis labels; up to 5 labels are shown.
<code>disp.connecting.lines</code>	logical option TRUE or FALSE. TRUE (default) displays connecting lines between p-value plot and correlation matrix
<code>palette.file</code>	File that contains color scheme for the heatmap. Colors are hexadecimal HTML color codes; one color per line; if you do not want to use this option, use the color defined by the option <code>cormatrix.color.scheme</code>
<code>image.title</code>	Title of the plot
<code>image.name</code>	The path and the name of the plot file without extension. The extension will be added by coMET depending on the option <code>image.type</code> .
<code>image.type</code>	Options: pdf or eps
<code>image.size</code>	Default: 3.5 inches. Possible sizes : 3.5 or 7
<code>fontsize.gviz</code>	Font size of writing in annotation track. Default value =5
<code>font.factor</code>	Font size of the sample labels. Range: 0-1
<code>symbol.factor</code>	Size of the symbols. Range: 0-1
<code>print.image</code>	Print image in file or not.
<code>connecting.lines.factor</code>	Length of the connecting lines. Range: 0-2
<code>connecting.lines.adj</code>	Position of the connecting lines horizontally. Negative values shift the connecting lines to the left and positive values shift the lines to the right. Range: (-1;1) option -1 means no connecting lines.

<code>connecting.lines.vert.adj</code>	Position of the connecting lines vertically. Can be used to vertically adjust the position of the connecting lines in relation to the CpG-site names. Negative value shift the connecting lines down. Range: (-0.5 - 0), option -1 mean the default value related to the plot size (-0.5 for 3.5 plot size; -0.7 for 7.5 plot size)
<code>connecting.lines.flex</code>	Adjusts the spread of the connecting lines. Range: 0-2
<code>config.file</code>	Configuration file contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=". If there are multiple values such as for the option <code>list.tracks</code> or the options for additional data, you need to separated them by a "comma" and not extra space. (i.e. <code>list.tracks=geneENSEMBL,CGI,ChromHMM,DNAse,RegENSEMBL</code> )
<code>verbose</code>	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

### Details

The function is limited to visualize 120 omic features.

### Value

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

### Author(s)

Tiphaine Martin

### References

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

### See Also

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

### Examples

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

chrom <- "chr2"
start <- 38290160
end <- 38303219
gen <- "hg38"

if(interactive()){
  cat("interactive")
  genetrack <- genes_ENSEMBL(gen, chrom, start, end, showId=TRUE)
```

```

snptrack <- snpBiomart_ENSEMBL(gen, chrom, start, end,
                             dataset="hsapiens_snp_som", showId=FALSE)
strutrack <- structureBiomart_ENSEMBL(gen, chrom, start, end,
                                     strand, dataset="hsapiens_structvar_som")
clinVariant<-ClinVarMain_UCSC(gen,chrom,start,end)
clinCNV<-ClinVarCnv_UCSC(gen,chrom,start,end)
gwastrack <-GWAScatalog_UCSC(gen,chrom,start,end)
geneRtrack <-GeneReviews_UCSC(gen,chrom,start,end)
listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                clinCNV,gwastrack,geneRtrack)
comet(config.file=configfile, mydata.file=myinfofile, mydata.type="file",
      cormatrix.file=mycorrelation, cormatrix.type="listfile",
      mydata.large.file=myexpressfile, mydata.large.type="listfile",
      tracks.gviz=listgviz, verbose=FALSE, print.image=FALSE, disp.pvalueplot=FALSE)
} else {
  cat("Non interactive")
  data(geneENSEMBLtrack)
  data(snpBiomarttrack)
  data(ISCATrack)
  data(strucBiomarttrack)
  data(ClinVarCnvTrack)
  data(clinVarMaintrack)
  data(GWASTrack)
  data(GeneReviewTrack)
  listgviz <- list(genetrack,snptrack,strutrack,clinVariant,
                  clinCNV,gwastrack,geneRtrack)
  comet(config.file=configfile, mydata.file=myinfofile, mydata.type="file",
        cormatrix.file=mycorrelation, cormatrix.type="listfile",
        mydata.large.file=myexpressfile, mydata.large.type="listfile",
        tracks.gviz=listgviz, verbose=FALSE, print.image=FALSE, disp.pvalueplot=FALSE)
}

```

---

comet.list

*List the correlations between omic features*


---

## Description

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

## Usage

```

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

```

**Arguments**

- `cormatrix.file` Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.
- `cormatrix.method`  
Options for calculating the correlation matrix: spearman, pearson and kendall. Default value= spearman
- `cormatrix.format`  
Format of the input `cormatrix.file`. There are two options: raw file (raw if CpG sites are by column and samples by row or `raw_rev` if CpG site are by row and samples by column) and pre-computed correlation matrix (`cormatrix`)
- `cormatrix.conf.level`  
Alpha level for the confidence interval. Default value= 0.05. CI will be the  $\alpha/2$  lower and upper values.
- `cormatrix.sig.level`  
Significant level to visualise the correlation. If the correlation has a pvalue below the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme chosen. Default value =1.
- `cormatrix.adjust`  
indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". Default value="none"
- `cormatrix.type` Format of `cormatrix.file`. There are 2 different options: listfile or listdataframe.
- `cormatrix.output`  
The path and the name of the output file without the extension
- `config.file` Configuration file contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=".
- `verbose` logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

**Value**

Create a list of correlation between omic features

**Author(s)**

Tiphaine Martin

**References**

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

**See Also**

[comet.web,comet](#)



## Examples

```

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

comet.list(cormatrix.file=mycorrelation, cormatrix.method = "spearman",
           cormatrix.format= "raw", cormatrix.conf.level=0.05,
           cormatrix.sig.level= 0.05, cormatrix.adjust="BH",
           cormatrix.type = "listfile", cormatrix.output=myoutput,
           verbose=FALSE)

```

---

comet.web	<i>Visualize EWAS results in a genomic region of interest with predefined annotation tracks</i>
-----------	---

---

## Description

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

## Usage

```

comet.web(mydata.file = NULL, mydata.format = c("site", "region",
"site_asso", "region_asso"),
         mydata.large.file = NULL,
         mydata.large.format = c("site", "region", "site_asso", "region_asso"),
         cormatrix.file = NULL, cormatrix.method = c("spearman", "pearson", "kendall"),
         cormatrix.format = c("cormatrix", "raw", "raw_rev"),
         cormatrix.color.scheme = "heat", cormatrix.conf.level=0.05,
         cormatrix.sig.level= 1, cormatrix.adjust="none", mydata.ref = NULL,
         genome="hg19", start = NULL, end = NULL, zoom = FALSE, lab.Y = "log",
         pval.threshold = 1e-07, pval.threshold.2 = 0, disp.pval.threshold = 1,
         disp.association= FALSE, disp.association.large = FALSE,
         disp.beta.association = "FALSE", disp.beta.association.large = "FALSE",
         factor.beta = 0.3,
         disp.region = FALSE, disp.region.large = FALSE, symbols = "circle-fill",
         symbols.large = NA, sample.labels = NULL, sample.labels.large = NULL,
         use.colors = TRUE, disp.color.ref = TRUE, color.list = NULL,
         color.list.large = NULL, biofeat.user.file = NULL,
         biofeat.user.type = c("GeneRegion", "Annotation", "Data"),
         biofeat.user.type.plot = NULL,
         list.tracks = "geneENSEMBL,CGI,ChromHMM,DNAse,RegENSEMBL,SNP",

```

```

pattern.regulation = "GM12878",
image.title = NULL, image.name = "coMET", image.type = c("pdf", "eps"),
image.size = 3.5, fontsize.gviz=5, font.factor = 1,
print.image = FALSE, config.file = NULL, verbose = FALSE)

```

## Arguments

- `info.file` Name of the info file describing the coMET parameters. It is mandatory and has to be a file in tabular format with a header. Info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option `mydata.format`.
- `mydata.format` Format of the input data in `mydata.file`. There are 4 different options: `site`, `region`, `site_asso`, `region_asso`.
- `mydata.large.file` Name of additional info files describing the coMET parameters. File names should be comma-separated. It is optional, but if you add some, they need to be file(s) in tabular format with a header. Additional info file can be a list of CpG sites with/without Beta value (DNA methylation level) or direction sign. If it is a site file then it is mandatory to have the 4 columns as shown below with headers in the same order. Beta can be the 5th column(optional) and it can be either a numeric value (positive or negative values) or only direction sign ("+", "-"). The number of columns and their types are defined but the option `mydata.large.format`.
- `mydata.large.format` Format of additional data to be visualised in the p-value plot. Format should be comma-separated. There are 4 different options for each file: `site`, `region`, `site_asso`, `region_asso`.
- `cormatrix.file` Name of the raw data file or the pre-computed correlation matrix file. It is mandatory and has to be a file in tabular format with an header.
- `cormatrix.method` A character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.
- `cormatrix.format` A character string indicating which format of the input `cormatrix.file` is to be used. There are three options: `raw` file (raw if CpG sites are by column and samples by row or `row_rev` if CpG site are by row and samples by column) and pre-computed correlation matrix (`cormatrix`)
- `cormatrix.color.scheme` A character string indicating which Color scheme options is to be used: `heat`, `bluwhitered`, `cm`, `topo`, `gray`, `bluetored`
- `cormatrix.conf.level` Alpha level for the confidence interval. Default value= 0.05. CI will be the  $\alpha/2$  lower and upper values.

<code>cormatrix.sig.level</code>	Significant level to visualise the correlation. If the correlation has a pvalue under the significant level, the correlation will be colored in "goshwhite", else the color is related to the correlation level and the color scheme choosen.Default value =1.
<code>cormatrix.adjust</code>	indicates which adjustment for multiple tests should be used. "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".Default value="none"
<code>mydata.ref</code>	The name of the reference omic feature (e.g. CpG-site) listed in mydata.file
<code>genome</code>	The human genome reference file. e.g. "hg19" for Human genome 19 (NCBI 37), "grch37" (GRCh37),"grch38" (GRCh38)
<code>start</code>	The first nucleotide position to be visualised. It could be bigger or smaller than the first position of our list of omic features.
<code>end</code>	the last nucleotide position to be visualised. It has to be bigger than the value in the option start, but it could be smaller or bigger than the last position of our list of omic features.
<code>zoom</code>	logical option TRUE or FALSE. FALSE (default)
<code>lab.Y</code>	Scale of the y-axis. Options: log or ln
<code>pval.threshold</code>	Significance threshold to be displayed as a red dashed line. Default value = 1e-7
<code>pval.threshold.2</code>	the second significance threshold to be displayed as a orange dashed line. Default value= 0 (no printed)
<code>disp.pval.threshold</code>	Display only the findings that pass the value put in <code>disp.pval.threshold</code>
<code>disp.association</code>	This logical option works only if mydata.file contains the effect direction (mydata.format=site_asso or region_asso). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option color.list. On the other hand, if the association is negative, the color is the opposed color.
<code>disp.association.large</code>	This logical option works only if mydata.large.file contains the effect direction (MYDATA.large.FORMA=site_asso or region_asso). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the color of symbol is the color of co-methylation pattern between the point and the reference site; if TRUE, the effect direction is shown. If the association is positive, the color is the one defined with the option color.list.large. On the other hand, if the association is negative, the color is the opposed color.
<code>disp.beta.association</code>	This logical option works only if mydata.file contains the effect direction (mydata.format=site_asso or region_asso). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the size of symbol is the default size of symbole; if TRUE, the effect direction is shown.

<code>disp.beta.association.large</code>	This logical option works only if <code>mydata.large.file</code> contains the effect direction ( <code>mydata.large.format=site_asso</code> or <code>region_asso</code> ). The value can be TRUE or FALSE: if FALSE (default), for each point of data in the p-value plot, the size of symbol is the default size of symbol; if TRUE, the effect direction is shown.
<code>factor.beta</code>	Factor to visualise the size of beta. Default value = 0.3.
<code>disp.region</code>	This logical option works only if <code>mydata.file</code> contains regions ( <code>mydata.format=region</code> or <code>region_asso</code> ). 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.
<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_asso</code> ). 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.
<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 TRUE or FALSE (TRUE default). if TRUE, the connection line related to the reference probe is in purple, if FALSE if the connection line related to the reference probe stay black.
<code>color.list</code>	List of colors for displaying the P-value symbols related to the data in <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>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 Gviz's function called <code>DataTrack</code> (comma-separated)

<code>list.tracks</code>	List of annotation tracks to visualise. Options include geneENSEMBL, CGI, ChromHMM, DNase, RegENSEMBL, SNP, transcriptENSEMBL, SNPstoma, SNPstru, SNPstrustoma, BindingMotifENSEMBL, otherRegulatoryENSEMBL, regulatoryEvidenceENSEMBL, regulatoryFeaturesENSEMBL, regulatorySegmeENSEMBL, miRNAENSEMBL, ImprintedtissuesGenes, COSMIC, GAD, ClinVar, GeneReviews, GWAS, ClinVarCNV, GCcontent, genesUCSC, xenogenesUCSC, SegDuplication,RepeatElt.
<code>pattern.regulation</code>	The cell/tissue or the list of cells/tissues to visualise in the regulation region defined by Broad ChromHMM
<code>image.title</code>	Title of the plot
<code>image.name</code>	The path and the name of the plot file without extension. The extension will be added by coMET depending on the option <code>image.type</code> .
<code>image.type</code>	Options: pdf or eps
<code>image.size</code>	Default: 3.5 inches. Possible sizes : 3.5 or 7
<code>fontsize.gviz</code>	Font size of writing in annotation track. Default value =5
<code>font.factor</code>	Font size of the sample labels. Range: 0-1
<code>print.image</code>	Print image in file or not.
<code>config.file</code>	Configuration file contains the values of these options instead of defining these by command line. It is a file where each line is one option. The name of option and its value are separated by "=". If there are multiple values such as for the option <code>list.tracks</code> or the options for additional data, you need to separated them by a "comma" and not extra space. (i.e. <code>list.tracks=geneENSEMBL,CGI,ChromHMM,DNase,RegENSEMBL</code> )
<code>verbose</code>	logical option TRUE or FALSE. TRUE (default). If TRUE, shows comments.

### Details

The function is limited to visualize 120 omic features.

### Value

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

### Author(s)

Tiphaine Martin

### References

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

### See Also

[comet,comet.list](#)

**Examples**

```

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

comet.web(config.file=configfile, mydata.file=myinfofile, cormatrix.file=mycorrelation,
          mydata.large.file=myexpressfile, print.image=FALSE, verbose=FALSE)

```

---

CoreillCNV_UCSC	<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**

```
CoreillCNV_UCSC(gen, chr, start, end, title="Coriell CNVs", showId=FALSE)
```

**Arguments**

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An Ucsctrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=cori](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=cori)

**See Also**

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [snpBiomart\\_ENSEMBL](#), [COSMIC\\_UCSC](#), [ClinVarMain\\_UCSC](#), [ClinVarCnv\\_UCSC](#)

**Examples**

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

if(interactive()){
  coreilVariant<-CoreilCNV_UCSC(gen,chrom,start,end)
  plotTracks(coreilVariant, from = start, to =end,
    fontfamily="sans",fontfamily.title="sans")
} else {
  data(coreilVarianttrack)
  plotTracks(coreilVariant, from = start, to =end,
    fontfamily="sans",fontfamily.title="sans")
}
```

---

COSMIC\_UCSC

*Create one track of the genomic positions of variants from COSMIC  
[obselete]*

---

**Description**

[obselete] No more possible to extract COSMIC data from UCSC.

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

**Usage**

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

**Arguments**

gen	the name of the genome. Data is not currently available for GRCh38 (hg38)
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

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

**See Also**

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [snpBiomart\\_ENSEMBL](#), [CoreillCNV\\_UCSC](#), [ClinVarMain\\_UCSC](#), [ClinVarCnv\\_UCSC](#),

**Examples**

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

---

cpgIslands\_UCSC

*create track CpG Island from UCSC*

---

**Description**

create track CpG Island from UCSC using the Gviz bioconductor package

**Usage**

```
cpgIslands_UCSC(gen, chr, start, end, title="CpG Islands UCSC")
```



**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)
title	Name of tracks

**Value**

An Ucsctrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

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

**Examples**

```
library("Gviz")
chrom <- "chr2"
start <- 100000
end <- 1000000
gen <- "hg38"

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

---

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

---

**Description**

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

**Usage**

```
dgfootprints_RoadMap(gen="hg19", chr, start, end, bedFilePath,
  tissueGroupDisplay='Blood & T-cell',showId=FALSE, type_stacking="dense",
  title= "DGFP RoadMap")
```

**Arguments**

gen	the name of the genome. Default value=hg19
chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
bedFilePath	The file path to the .BED file containing the data to be visualised
tissueGroupDisplay	the group of tissue visualised among list("Neurosp", "Epithelial", "IMR90", "Thymus", "Heart", "Brain", "D & B-cell", "Blood & T-cell"="ES-deriv")
showId	logical. say if we write the name of group
type_stacking	Object of class"character", the stacking type of overlapping items on the final plot. One in c(hide, dense, squish, pack,full). More information cf the option "stacking" in Gviz
title	The name of the annotation track

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>  
Got to RoadMap Epigenome

**Examples**

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

extdata <- system.file("extdata", package="coMET", mustWork=TRUE)
bedFilePath <- file.path(extdata, "RoadMap/CD3-DS17198.hg19_subset.bed")

if(interactive()){
```

```

dgfootprints_RoadMapSingle <- dgfootprints_RoadMap(gen,chr,start, end,
bedFilePath, tissueGroupDisplay='Blood & T-cell' )
plotTracks(dgfootprints_RoadMapSingle, from = start, to = end,
fontfamily="sans",fontfamily.title="sans")
} else {
data(dgfootprints_RoadMapSingle)
plotTracks(dgfootprints_RoadMapSingle, from = start, to = end,
fontfamily="sans",fontfamily.title="sans")
}

```

---

DNaseI\_FANTOM

*Creates a enhancer/promoter track from FANTOM*


---

### Description

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

### Usage

```

DNaseI_FANTOM(gen="hg19", chr, start, end, bedFilePath,
featureDisplay='enhancer', stacking_type="dense",
title=" DNaseI Fantom")

```

### Arguments

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

Got to BindingMotifsBiomart binding motif biomart

**Examples**

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

extdata <- system.file("extdata", package="coMET", mustWork=TRUE)
enhFantomFile <- file.path(extdata,
"/FANTOM/human_permissive_enhancers_phase_1_and_2_example970.bed")

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

---

DNaseI\_RoadMap

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

---

**Description**

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

**Usage**

```
DNaseI_RoadMap(gen="hg19", chr, start, end, bedFilePath,
featureDisplay='promotor', showId=TRUE, type_stacking="dense",
title = "DNaseI RoadMap")
```

**Arguments**

<code>gen</code>	the name of the genome. Default value=hg19
<code>chr</code>	The chromosome of interest
<code>start</code>	The starting position in the region of interest (the smallest value)
<code>end</code>	The end position in the region of interest (the largest value)
<code>bedFilePath</code>	The file path to the .BED file containing the data to be visualised
<code>featureDisplay</code>	A vector of features to be displayed, such as 1_TssA. Spelling and capitalisation of features must be identical to those in the user guide (in the 'State & Acronym' column). There are three possibilities. First, the visualisation of only one feature (e.g. <code>featureDisplay &lt;- "1_TssA"</code> ), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. <code>featureDisplay &lt;- c("1_TssA","2_TssAFlnk")</code> ). Finally, visualise all features in the genomic region, achieved by using the word "all" (e.g. <code>featureDisplay &lt;- "all"</code> ), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
<code>showId</code>	Allows to visualise the Id of DNase group.
<code>type_stacking</code>	Object of class "character", the stacking type of overlapping items on the final plot. One in <code>c(hide, dense, squish, pack, full)</code> . More information of the option "stacking" in Gviz
<code>title</code>	The name of the annotation track

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

<http://bioconductor.org/packages/release/bioc/html/Gviz.html>  
Got to RoadMap Epigenome

**Examples**

```
library("Gviz")
chr <- "chr2"
start <- 38300049
end <- 38302592
gen="hg19"

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

```

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

```

---

DNase\_UCSC

*Creation of an UCSC's DNase clusters track - obsolete function*


---

### Description

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

### Usage

```

DNase_UCSC(gen, chr, start, end, mySession, title="DNA cluster",
  track.name = "DNase Clusters", table.name = NULL)

```

### Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
mySession	the object session from the function browserSession of rtracklayer
title	Name of tracks
track.name	the name of the track DNase_UCSC. "DNase Clusters"(default)
table.name	the name of the table from the track

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=wg)

**Examples**

```

# library("Gviz")
# library("rtracklayer")

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

```

---

eQTL

*Creates a track from a file for eQTL data*


---

**Description**

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

**Usage**

```
eQTL(gen,chr, start, end, bedFilePath, featureDisplay, showId=FALSE,
type_stacking="squish",just_group="above", title="eQTL" )
```

**Arguments**

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

<code>featureDisplay</code>	A vector of eQTL features to be displayed, such as SNP. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. <code>featureDisplay &lt;- "CpG"</code> ), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. <code>featureDisplay &lt;- c("SNP","CpG")</code> ). Finally, visualise all features in the genomic region, achieved by using the word "all" (e.g. <code>featureDisplay &lt;- "all"</code> ), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
<code>showId</code>	Allows to visualise the Id of eQTL group.
<code>type_stacking</code>	Object of class "character", the stacking type of overlapping items on the final plot. One in <code>c(hide, dense, squish, pack, full)</code> . More information of the option "stacking" in Gviz
<code>just_group</code>	position. say where we write the name of group (choice in <code>c("above", "right", "left")</code> )
<code>title</code>	The name of the annotation track

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

Tom Hardiman

**References**

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

Got to ENSEMBL regulation binding motif biomart

**Examples**

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

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

if(interactive()){
  eQTLTrackSingle <- eQTL(gen,chr,start, end, bedFilePath,
    featureDisplay = featureDisplay )
  plotTracks(eQTLTrackSingle, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
} else {
  data(eQTLTrackSingle)
```



```

    plotTracks(eQTLTrackSingle, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
  }

#####

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

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

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

#####

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

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

if(interactive()){
  eQTLTrackAll <- eQTL(gen,chr,start, end, bedFilePath, featureDisplay = featureDisplay )
  plotTracks(eQTLTrackAll, from = start, to = end,
            fontfamily="sans",fontfamily.title="sans")
} else {
  data(eQTLTrackAll)
  plotTracks(eQTLTrackAll, from = start, to = end,
            fontfamily="sans",fontfamily.title="sans")
}

```

**Description**

Creates a track of eQTL from GTE<sub>x</sub> using the Gviz bioconductor package. A complete list of features and their associated colours can be found in the user guide.

**Usage**

```
eQTL_GTEx(gen="hg19",chr,start, end, bedFilePath, featureDisplay = 'all',
showId=FALSE, type_stacking="squish",just_group="above",title="eQTL GTEx")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

Got to BindingMotifsBiomart binding motif biomart

**Examples**

```

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

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

if(interactive()){
  eGTexTrackSNP <- eQTL_GTEEx(gen,chr,start, end, bedFilePath,
    featureDisplay="SNP", showId=TRUE,just_group="left")
  plotTracks(eGTexTrackSNP, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
} else {
  data(eGTexTrackSNP)
  plotTracks(eGTexTrackSNP, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
}

```

GAD\_UCSC

---

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

---

**Description**

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

**Usage**

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

**Arguments**

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=gad](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=gad)

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

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

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

---

gcContent_UCSC	<i>Create one track of GC content from UCSC</i>
----------------	---

---

**Description**

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

**Usage**

```
gcContent_UCSC(gen, chr, start, end, title="GC Percent")
```

**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)
title	Name of tracks

**Value**

A UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=gc5](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=gc5)

**Examples**

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

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

```
fontfamily="sans",fontfamily.title="sans")
}
```

---

GeneReviews\_UCSC      *Create one track of the genomic positions of variants from GeneReviews*

---

### Description

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

### Usage

```
GeneReviews_UCSC(gen, chr, start, end,title="GeneReviews", 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)
title	The name of the annotation track
showId	Show the ID of the genetic elements

### Value

An UcsTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

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

### See Also

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

### Examples

```
library("Gviz")
gen <- "hg38"
chrom <- "chr2"
start <- 100000000
end <- 1000000000
if(interactive()){
  geneRtrack <-GeneReviews_UCSC(gen,chrom,start,end,showId=TRUE)
  plotTracks(geneRtrack, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(GeneReviewTrack)
  plotTracks(geneRtrack, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}
```

---

genesName_ENSEMBL	<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

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

### Arguments

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

### Details

Can be null

### Value

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

### Author(s)

Tiphaine Martin

**References**

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

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

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

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

---

genes_ENSEMBL	<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**

```
genes_ENSEMBL(gen, chr, start, end, showId=FALSE,title="genes (ENSEMBL)")
```

**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
title	Name of tracks



**Value**

A BiomartGeneRegionTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=ens](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=ens)

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

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

---

GWAScatalog\_UCSC

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

---

**Description**

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

**Usage**

```
GWAScatalog_UCSC(gen, chr, start, end, title="GWAS Catalog", 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)
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjtrdrFAy6dn&c=chr6&g=gwa](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjtrdrFAy6dn&c=chr6&g=gwa)  
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

**See Also**

[ISCA\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

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

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

---

HiCdata2matrix	<i>Creates a HiC matrix from a file (Rao et al., 2014)</i>
----------------	--

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

Got to BindingMotifsBiomart binding motif biomart

**Examples**

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

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

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

```

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

```

---

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

```

### Arguments

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
mySession	the object session from the function browserSession of rtracklayer
pattern	The cell type
track.name	the name of the track, for example: "Broad Histone"
table.name	the name of the table from the track

### Value

A list of AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

**See Also**

[HistoneOne\\_UCSC](#),

**Examples**

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

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

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

---

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

---

**Description**

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

**Usage**

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

**Arguments**

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)

<code>mySession</code>	the object session from the function <code>browserSession</code> of <code>rtracklayer</code>
<code>title</code>	Name of tracks
<code>track.name</code>	the name of the track, for example: "Broad Histone"
<code>table.name</code>	the name of the table from the track

**Value**

An `AnnotationTrack` object of `Gviz`

**Author(s)**

Tiphaine Martin

**References**

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

**See Also**

[HistoneAll\\_UCSC](#)

**Examples**

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

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

---

imprintedGenes\_GTEx *Creates a imprinted genes track from GTEx*

---

### Description

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

### Usage

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

### Arguments

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

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

### Examples

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

```

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

  imprintinglist <- list(allIGtrack,allimprintedIGtrack,
    StomachIGtrack,PancreasIGtrack,PancreasimprintedIGtrack)

  plotTracks(imprintinglist, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")

} else {

  data(allIGtrack)
  data(allimprintedIGtrack)
  data(StomachIGtrack)
  data(PancreasIGtrack)
  data(PancreasimprintedIGtrack)

  imprintinglist <- list(allIGtrack,allimprintedIGtrack,
    StomachIGtrack,PancreasIGtrack,PancreasimprintedIGtrack)

  plotTracks(imprintinglist, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
}

```

---

interestGenes\_ENSEMBL *Create one track of the genes in the genomic regions of interest from EMSEMBL*

---

### Description

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

### Usage

```
interestGenes_ENSEMBL(gen, chr, start, end, interestfeatures,interestcolor,
  showId=FALSE,title="genes (ENSEMBL)")
```



**Arguments**

<code>gen</code>	the name of the genome
<code>chr</code>	the chromosome of interest
<code>start</code>	the first position in the region of interest (the smallest value)
<code>end</code>	the last position in the region of interest (the largest value)
<code>interestfeatures</code>	A data frame with 3 columns: start of features, end of features, and type of features
<code>interestcolor</code>	A list with the color for each new features defined
<code>showId</code>	Show the ID of the genetic elements
<code>title</code>	Name of tracks

**Value**

A `BiomartGeneRegionTrack` object of `Gviz`

**Author(s)**

Tiphaine Martin

**References**

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

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

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

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

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

```
fontfamily="sans",fontfamily.title="sans")
}
```

---

`interestTranscript_ENSEMBL`

*Create a track of transcripts from ENSEMBL*

---

### **Description**

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

### **Usage**

```
interestTranscript_ENSEMBL(gen, chr, start, end,interestfeatures,
interestcolor,showId = FALSE, title="transcripts ENSEMBL")
```

### **Arguments**

<code>gen</code>	the name of the genome
<code>chr</code>	the chromosome of interest
<code>start</code>	the first position in the region of interest (the smallest value)
<code>end</code>	the last position in the region of interest (the largest value)
<code>interestfeatures</code>	A data frame with 3 columns: start of features, end of features, and type of features
<code>interestcolor</code>	A list with the color for each new features defined
<code>showId</code>	Show the ID of the genetic elements
<code>title</code>	Name of tracks

### **Value**

A `BiomartGeneRegionTrack` object of Gviz

### **Author(s)**

Tiphaine Martin

### **References**

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=ens](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=ens)

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#),

**Examples**

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

if(interactive()){
  interesttransENSMBltrack<-interestTranscript_ENSEMBL(gen,chr,start,end,
  interestfeatures,interestcolor,showId=TRUE)
  plotTracks(interesttransENSMBltrack, from=start, to=end,
             fontfamily="sans", fontfamily.title="sans")
} else {
  data(interesttransENSMBltrack)
  plotTracks(interesttransENSMBltrack, from=start, to=end,
             fontfamily="sans", fontfamily.title="sans")
}
```

---

ISCA\_UCSC

*Create one track of the genomic positions of variants from ISCA [obselete database]*

---

**Description**

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

**Usage**

```
ISCA_UCSC(gen, chr, start, end, mySession, table.name, title="ISCA", 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
title	The name of the annotation track
showId	Show the ID of the genetic elements

**Value**

An UcsTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

**See Also**

[GWScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

```
# Oboelet function

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

if(interactive()){
  BROWSER.SESSION="UCSC"
  mySession <- browserSession(BROWSER.SESSION)
  genome(mySession) <- gen
  iscatrack <- ISCA_UCSC(gen,chrom,start,end,mySession,title="ISCA", table="iscaPathogenic")
  plotTracks(iscatrack, from = start, to =end,
             fontfamily="sans", fontfamily.title="sans")
} else {
  data(ISCAtrack_Grch38)
  plotTracks(iscatrack, from = start, to =end,
             fontfamily="sans", fontfamily.title="sans")
}
```

---

knownGenes_UCSC	<i>Create a track of known genes from the UCSC genome browser</i>
-----------------	---

---

**Description**

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

**Usage**

```
knownGenes_UCSC(gen, chr, start, end, title="UCSC known Genes", showId=TRUE)
```

**Arguments**

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

**Value**

An UcscTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=knownGenes\\_UCSC](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=knownGenes_UCSC)  
<http://bioconductor.org/packages/release/bioc/html/Gviz.html>

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#),

**Examples**

```

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

if(interactive()) {
  genesUcsctrack<-knownGenes_UCSC(gen,chr,start,end,showId=TRUE)
  plotTracks(genesUcsctrack, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
}else {
  data(genesUcsctrack)
  plotTracks(genesUcsctrack, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
}

```

metQTL

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

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

**Usage**

```
metQTL(gen, chr, start, end, bedFilePath, featureDisplay, showId=FALSE,
       type_stacking="squish",just_group="above", title="metQTL")
```

**Arguments**

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

showId	Allows the visualization of the Id of metQTL group.
type_stacking	Sets the type of stacking used by Gviz for plots. By default this is set to 'squish'. For more information see Gviz user guide.
just_group	position. say where we write the name of group (choice in c("above","right","left"))
title	The name of the annotation track

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**Examples**

```
library("Gviz")

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

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

if(interactive()){
  metQTLTrackSingle <- metQTL(gen,chr,start, end,mqlbedFilePath,
    featureDisplay = featureDisplay )
  plotTracks(metQTLTrackSingle, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
} else {
  data(metQTLTrackSingle)
  plotTracks(metQTLTrackSingle, from = start, to = end,
    fontfamily="sans",fontfamily.title="sans")
}

###

library("Gviz")

gen <- 'hg19'
```

```

chr <- "chr15"
start <- 74889136
end <- 75018200

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

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

if(interactive()){
  metQTLTrackMultiple <- metQTL(gen,chr,start, end, bedFilePath,
    featureDisplay = featureDisplay )
  plotTracks(metQTLTrackMultiple, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
} else {
  data(metQTLTrackMultiple)
  plotTracks(metQTLTrackMultiple, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
}

#####

library("Gviz")

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

featureDisplay <- "all"

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

if(interactive()){
  metQTLTrackAll <- metQTL(gen,chr,start, end, bedFilePath,
    featureDisplay = featureDisplay )
  plotTracks(metQTLTrackAll, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
} else {
  data(metQTLTrackAll)
  plotTracks(metQTLTrackAll, from = start, to = end,
    fontfamily="sans", fontfamily.title="sans")
}

```

---

miRNATargetRegionsBiomart\_ENSEMBL

*Creates a track of miRNA target regions from ENSEMBL*

---



**Description**

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

**Usage**

```
miRNATargetRegionsBiomart_ENSEMBL(gen, chr, start, end, showId=FALSE,
  datasetEnsembl = "hsapiens_mirna_target_feature",
  title="miRNA Target Regions ENSEMBL")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**Examples**

```
library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 1000000
end <- 2000000

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

```

                                fontfamily="sans",fontfamily.title="sans")
} else {
  data(miRNATargetRegionsBiomartTrack)
  plotTracks(miRNATargetRegionsBiomartTrack, from = start, to = end,
                                fontfamily="sans",fontfamily.title="sans")
}

```

---

otherRegulatoryRegionsBiomart\_ENSEMBL

*Creates a track of other regulatory regions from ENSEMBL*

---

### Description

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

### Usage

```

otherRegulatoryRegionsBiomart_ENSEMBL(gen, chr, start, end,
featureDisplay = "all",datasetEnsembl = "hsapiens_external_feature",
title="Other Regulatory Regions ENSEMBL")

```

### Arguments

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

### Value

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**Examples**

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

if(interactive()){
  otherRegulatoryRegionsTrackSingle<-otherRegulatoryRegionsBiomart_ENSEMBL(gen,
  chr,start,end,featureDisplay)
  plotTracks(otherRegulatoryRegionsTrackSingle, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(otherRegulatoryRegionsTrackSingle)
  plotTracks(otherRegulatoryRegionsTrackSingle, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}

#####

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

if(interactive()){
  otherRegulatoryRegionsTrackAll<-otherRegulatoryRegionsBiomart_ENSEMBL(gen,
  chr,start,end,featureDisplay)
  plotTracks(otherRegulatoryRegionsTrackAll, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(otherRegulatoryRegionsTrackAll)
  plotTracks(otherRegulatoryRegionsTrackAll, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}
```

---

psiQTL\_GTEEx

*Creates a psiQTL track from GTEEx*


---

### Description

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

### Usage

```
psiQTL_GTEEx(gen,chr,start, end, bedFilePath, featureDisplay = 'all',
showId=FALSE, type_stacking="squish",just_group="above", title="psiQTL GTEEx")
```

### Arguments

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

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

## References

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

Got to BindingMotifsBiomart binding motif biomart

## Examples

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

```
if(interactive()){
  psiGTexTrackall<- psiQTL_GTex(gen,chr,start, end, psiQTLFilePath,
    featureDisplay = 'all', showId=TRUE, type_stacking="squish",
    just_group="above" )
  plotTracks(psiGTexTrackall, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(psiGTexTrackall)
  plotTracks(psiGTexTrackall, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}
```

```
if(interactive()){
  psiGTexTrackSNP<- psiQTL_GTex(gen,chr,start, end, psiQTLFilePath,
    featureDisplay = 'SNP', showId=TRUE, type_stacking="squish",
    just_group="left")
  plotTracks(psiGTexTrackSNP, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(psiGTexTrackSNP)
  plotTracks(psiGTexTrackSNP, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}
```

---

refGenes\_UCSC

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

---

## Description

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

**Usage**

```
refGenes_UCSC(gen, chr, start, end, title="Ref Genes UCSC", track = "refGene",
  IdType="Ref", showId=TRUE)
```

**Arguments**

gen	The name of the genome
chr	The chromosome of interest
start	The first position in the region of interest (the smallest value)
end	The last position in the region of interest (the largest value)
title	Name of tracks
track	the name of table in UCSC for the group "Genes and Gene Prediction"
IdType	When set to 'ref' shows the gene reference, when set to "name" shows the gene name
showId	Shows the ID or name of the genetic elements

**Value**

An Ucsctrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**See Also**

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#), [transcript\\_ENSEMBL](#), [knownGenes\\_UCSC](#)

**Examples**

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

if(interactive()) {
  genesUcsctrack<-refGenes_UCSC(gen,chr,start,end,track,IdType)
```

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

---

regulationBiomart\_ENSEMBL

*Create a regulation track from ENSEMBL*

---

### Description

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

### Usage

```
regulationBiomart_ENSEMBL(gen, chr, start, end,title="Regulation ENSEMBL")
```

### 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)
title	Name of tracks

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

Got to ENSEMBLregulation biomart

**Examples**

```

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

if(interactive()){
  regulationENSEMBLtrack<-regulationBiomart_ENSEMBL(gen,chr,start,end)
  plotTracks(regulationENSEMBLtrack, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulationENSEMBLtrack)
  plotTracks(regulationENSEMBLtrack, from = start, to =end,
             fontfamily="sans",fontfamily.title="sans")
}

```

---

```
regulatoryEvidenceBiomart_ENSEMBL
```

*Creates a regulatory feature track from ENSEMBL*

---

**Description**

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

**Usage**

```

regulatoryEvidenceBiomart_ENSEMBL (gen, chr, start, end,
featureDisplay = "all", datasetEnsembl = "hsapiens_annotated_feature",
title="Other Regulatory Regions ENSEMBL")

```

**Arguments**

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



genomic region, achieved by using the word "all" (e.g. `featureDisplay <- "all"`), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.

`datasetEnsembl` Allows the user to manually set which data set is used if required.  
`title` The name of the annotation track

### Value

An AnnotationTrack object of Gviz

### Author(s)

Tiphaine Martin  
 Tom Hardiman

### References

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

### Examples

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

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

#####

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

if(interactive()){
  regulatoryEvidenceBiomartTrackMultiple<-regulatoryEvidenceBiomart_ENSEMBL (gen,
```

```

chr,start,end,featureDisplay)
  plotTracks(regulatoryEvidenceBiomartTrackMultiple, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulatoryEvidenceBiomartTrackMultiple)
  plotTracks(regulatoryEvidenceBiomartTrackMultiple, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
}

#####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 50000
end <- 100000
featureDisplay <- "all"
if(interactive()){
  regulatoryEvidenceBiomartTrackAll<-regulatoryEvidenceBiomart_ENSEMBL (gen,
  chr,start,end,featureDisplay)
  plotTracks(regulatoryEvidenceBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulatoryEvidenceBiomartTrackAll)
  plotTracks(regulatoryEvidenceBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
}

```

---

```
regulatoryFeaturesBiomart_ENSEMBL
```

*Creates a regulatory feature track from ENSEMBL*

---

## Description

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

## Usage

```
regulatoryFeaturesBiomart_ENSEMBL(gen, chr, start, end, featureDisplay = "all",
datasetEnsembl = "hsapiens_regulatory_feature",
title="Regulatory Features ENSEMBL")
```

## Arguments

gen	The name of the genome. Currently only handles human data from either the previous version, GRCh37 (also known as hg19) or the current version, GRCh38 (also known as hg38).
-----	--

chr	The chromosome of interest
start	The starting position in the region of interest (the smallest value)
end	The end position in the region of interest (the largest value)
featureDisplay	A vector of regulatory features to be displayed, such as Promoter. Spelling and capitalisation of features must be identical to those in the user guide. There are three possibilities. First, the visualisation of only one feature (e.g. featureDisplay <- "Promoter"), only the name of the specific feature is required. Second, visualisation of a set of features, for this a vector of features is required (e.g. featureDisplay <- c("TF binding site","Promoter")). Finally, visualisation all features in the genomic region, achieved by using the word "all" (e.g. featureDisplay <- "all"), "all" is set by default. You can find the complete list of features and their associated colours in the user guide.
datasetEnsembl	Allows the user to manually set which data set is used if required. Default=hsapiens_regulatory_feature
title	The name of the annotation track

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin  
Tom Hardiman

**References**

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

**Examples**

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

if(interactive()){
  regulatoryFeaturesBiomartTrackSingle<-regulatoryFeaturesBiomart_ENSEMBL(gen,
  chr,start,end,featureDisplay)
  plotTracks(regulatoryFeaturesBiomartTrackSingle, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulatoryFeaturesBiomartTrackSingle)
  plotTracks(regulatoryFeaturesBiomartTrackSingle, from = start, to = end,
             fontfamily="sans",fontfamily.title="sans")
}
```

```
#####

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

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

#####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "all"
if(interactive()){
  regulatoryFeaturesBiomartTrackAll<-regulatoryFeaturesBiomart_ENSEMBL(gen,
  chr,start,end,featureDisplay)
  plotTracks(regulatoryFeaturesBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulatoryFeaturesBiomartTrackAll)
  plotTracks(regulatoryFeaturesBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
}

}
```

---

regulatorySegmentsBiomart\_ENSEMBL

*Creates a binding motif track from ENSEMBL [obsolete]*

---

### Description

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

**Usage**

```
regulatorySegmentsBiomart_ENSEMBL(gen, chr, start, end, featureDisplay = 'all',
datasetEnsembl = "hsapiens_external_feature",
title="External Regulatory ENSEMBL")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

Tom Hardiman

**References**

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

Got to ENSEMBLregulation binding motif biomart

**Examples**

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

```

featureDisplay <- "CTCF enriched"

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

####

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

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

####

library("Gviz")
gen <- "hg38"
chr <- "chr1"
start <- 10000
end <- 50000
featureDisplay <- "all"
if(interactive()){
  regulatorySegmentsBiomartTrackAll<-regulatorySegmentsBiomart_ENSEMBL(gen,
  chr,start,end,featureDisplay)
  plotTracks(regulatorySegmentsBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
} else {
  data(regulatorySegmentsBiomartTrackAll)
  plotTracks(regulatorySegmentsBiomartTrackAll, from = start, to = end,
              fontfamily="sans",fontfamily.title="sans")
}

```

---

repeatMasker\_UCSC      *Create one track of the genomic positions of regions from repeatMasker\_UCSC*

---

### Description

Create one track of the genomic positions of regions from repeatMasker\_UCSC using the Gviz bioconductor package

### Usage

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

### Arguments

gen	the name of the genome
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
title	The name of the annotation track
showId	Show the ID of the genetic elements
type_stacking	the type of stacking data for this track. More information go to Gviz (the option "stacking")

### Value

An UcsTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=rms](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtDrFAy6dn&c=chr6&g=rms)

### Examples

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

```

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

```

---

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

---

### Description

Create one track of the genomic positions of regions from segmentalDups\_UCSC using the Gviz bioconductor package

### Usage

```
segmentalDups_UCSC(gen, chr, start, end,title="Segmental Dups UCSC")
```

### 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)
title	The name of the annotation track

### Value

An UcsTrack object of Gviz

### Author(s)

Tiphaine Martin  
Tom Hardiman

### References

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



## Examples

```
library("Gviz")
gen <- "hg38"
chr <- "chr2"
start <- 100000
end <- 200000

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

---

snpBiomart\_ENSEMBL      *Create a short variation track from ENSEMBL*

---

## Description

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

## Usage

```
snpBiomart_ENSEMBL(gen,chr, start, end, dataset, showId=FALSE, title = "SNPs ENSEMBL")
```

## Arguments

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

## Value

An AnnotationTrack object of Gviz

## Author(s)

Tiphaine Martin

**References**

Go to ENSEMBL Biomart

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

**See Also**

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [COSMIC\\_UCSC](#), [CoreillCNV\\_UCSC](#), [ClinVarMain\\_UCSC](#), [ClinVarCnv\\_UCSC](#),

**Examples**

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

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

---

snpLocations\_UCSC      *Create a SNP track from UCSC*

---

**Description**

Create a SNP track from UCSC using the Gviz bioconductor package

**Usage**

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

**Arguments**

gen	the name of the genome. Data is not currently available for GRCh38 (hg38).
chr	the chromosome of interest
start	the first position in the region of interest (the smallest value)
end	the last position in the region of interest (the largest value)
title	Name of tracks
track	The name of the database. Default "All SNPs(142)"

**Value**

An Ucsctrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

[http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739\\_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=snp](http://genome-euro.ucsc.edu/cgi-bin/hgTrackUi?hgsid=202839739_2hYQ1BAOuBMAR620GjrtdrFAy6dn&c=chr6&g=snp)

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

**See Also**

[snpLocations\\_UCSC](#), [structureBiomart\\_ENSEMBL](#), [COSMIC\\_UCSC](#), [CoreilICNV\\_UCSC](#), [ClinVarMain\\_UCSC](#), [ClinVarCnv\\_UCSC](#),

**Examples**

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

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

---

structureBiomart\_ENSEMBL

*Create a structural variation track from ENSEMBL*

---

**Description**

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

**Usage**

```
structureBiomart_ENSEMBL(gen, chr, start, end, strand, dataset,
showId=FALSE, title = "Structural variation")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

Go to ENSEMBL Biomart

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

**See Also**

[snpLocations\\_UCSC](#), [snpBiomart\\_ENSEMBL](#), [COSMIC\\_UCSC](#), [CoreillCNV\\_UCSC](#), [ClinVarMain\\_UCSC](#), [ClinVarCnv\\_UCSC](#),

**Examples**

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

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

---

TFBS_FANTOM	<i>Creates a TFBS motif track from FANTOM</i>
-------------	---

---

**Description**

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

**Usage**

```
TFBS_FANTOM(gen, chr, start, end, bedFilePath, title="TF motif FANTOM5")
```

**Arguments**

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

**Value**

An AnnotationTrack object of Gviz

**Author(s)**

Tiphaine Martin

**References**

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

**Examples**

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

extdata <- system.file("extdata", package="coMET", mustWork=TRUE)
AP1FantomFile <- file.path(extdata, "FANTOM/Fantom_hg19.AP1_MA0099.2.sites_example970.txt")

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

```

plotTracks(tfbsFANTOMtrack, from = start, to = end,
           fontfamily="sans", fontfamily.title="sans")
} else {
  data(tfbsFANTOMtrack)
  plotTracks(tfbsFANTOMtrack, from = start, to = end,
           fontfamily="sans", fontfamily.title="sans")
}

```

---

transcript\_ENSEMBL      *Create a track of transcripts from ENSEMBL*

---

### Description

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

### Usage

```
transcript_ENSEMBL(gen, chr, start, end, showId = FALSE, title="transcripts ENSEMBL")
```

### 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
title	Name of tracks

### Value

A BiomartGeneRegionTrack object of Gviz

### Author(s)

Tiphaine Martin

### References

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

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

### See Also

[ISCA\\_UCSC](#), [GWAScatalog\\_UCSC](#), [knownGenes\\_UCSC](#), [genesName\\_ENSEMBL](#), [GeneReviews\\_UCSC](#), [GAD\\_UCSC](#), [genes\\_ENSEMBL](#), [xenorefGenes\\_UCSC](#),

**Examples**

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

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

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