

Gviz visualization: installation

Iris Raes

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Installation of BiocManager and Gviz (= Bioconductor package)

```
if (!requireNamespace("BiocManager", quietly = TRUE)){  
  install.packages("BiocManager")}  
if (! requireNamespace("Gviz", quietly = TRUE)) {  
  BiocManager::install("Gviz")  
}  
library(BiocManager)
```

Loading of Gviz package and others

```
#install.packages("RCurl")  
library(RCurl)  
#install.packages("Rcpp")  
library(Rcpp)  
#install.packages("bit")  
library(bit)  
#install.packages("rlang")  
library(rlang)  
#install.packages("vctrs")  
library(vctrs)  
#install.packages("tibble")  
library(tibble)  
#install.packages("dplyr")  
library(dplyr)  
#install.packages("backports")  
library(backports)  
  
library(Gviz)  
library(GenomicRanges)
```

Links to documentation

About mapsnp: <https://bioinformaticshome.com/tools/descriptions/Mapsnp.html> Usage and features:
<https://www.bioconductor.org/packages/devel/bioc/vignettes/Gviz/inst/doc/Gviz.html>

```
browseVignettes("Gviz")
```

Test: Example found on the internet

```
data(cpgIslands)
chr <- as.character(unique(seqnames(cpgIslands)))
gen <- genome(cpgIslands)
# Plot first track
atrack <- AnnotationTrack(cpgIslands, name = "CpG")
# Genome region track and ideogram
gtrack <- GenomeAxisTrack()
itrack <- IdeogramTrack(genome = gen, chromosome = chr)
plotTracks(list(itrack, gtrack, atrack))
```

