Gviz visualization: plot with GeneModel

Iris Raes

30-4-2020

Installation of BiocManager and Gviz (= Bioconductor package)

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

Loading Gviz package

```r
library(Gviz) # Version 1.30.3
library(GenomicRanges)

setwd("C:/Users/irisr/Desktop/CSV")
```

Function to create a table with GRCh37 coordinates

```r
## separate function requires tidyr package
library(tidyr)
Gviz_table <- function(filename) {
  X <- read.csv(file=filename, header = TRUE, sep=";")
  # GRCh37 coordinates in first assembly
  tablepart1 <- X[grep("^GRCh37", X$assembly1),]
  id1 <- tablepart1[1]
  Chr_1a <- tablepart1[["Chr_1"]]
  Chr_1a <- gsub("[A-Za-z]", "", Chr_1a)
  Chr_1a <- sub("", "chr", Chr_1a)
  assembly1 <- tablepart1[["assembly1"]]
  assembly1 <- gsub(".*?:", "", assembly1)
  assembly1 <- separate(data = as.data.frame(assembly1), col = assembly1,
                        into = c("start", "end"), sep = "-")
  GRCh37_assembly1 <- data.frame(id1,Chr_1a,assembly1)
  names(GRCh37_assembly1)[names(GRCh37_assembly1) == "assembly1"] <- "assembly"
  names(GRCh37_assembly1)[names(GRCh37_assembly1) == "Chr_1a"] <- "chr"
```

```
  # GRCh37 coordinates in second assembly
  tablepart2 <- X[grep("^GRCh37", X$assembly2),]
  id2 <- tablepart2[1]
  Chr_1b <- tablepart2[["Chr_2"]]
  Chr_1b <- gsub("[A-Za-z]", "", Chr_1b)
  Chr_1b <- sub("", "chr", Chr_1b)
  assembly2 <- tablepart2[["assembly2"]]
  assembly2 <- gsub(".*?:", "", assembly2)
  assembly2 <- separate(data = as.data.frame(assembly2), col = assembly2,
                        into = c("start", "end"), sep = "-")
  GRCh37_assembly2 <- data.frame(id2,Chr_1b,assembly2)
  names(GRCh37_assembly2)[names(GRCh37_assembly2) == "assembly2"] <- "assembly"
  names(GRCh37_assembly2)[names(GRCh37_assembly2) == "Chr_1b"] <- "chr"
  # Gviz table
  GRCh37_Gviz <- rbind(GRCh37_assembly1,GRCh37_assembly2)
}


### results-CNV-dbVar.csv
CNVdbVar <- Gviz_table("results-CNV-dbVAR.csv")
CNVdbVar_GR <- makeGRangesFromDataFrame(CNVdbVar)
```
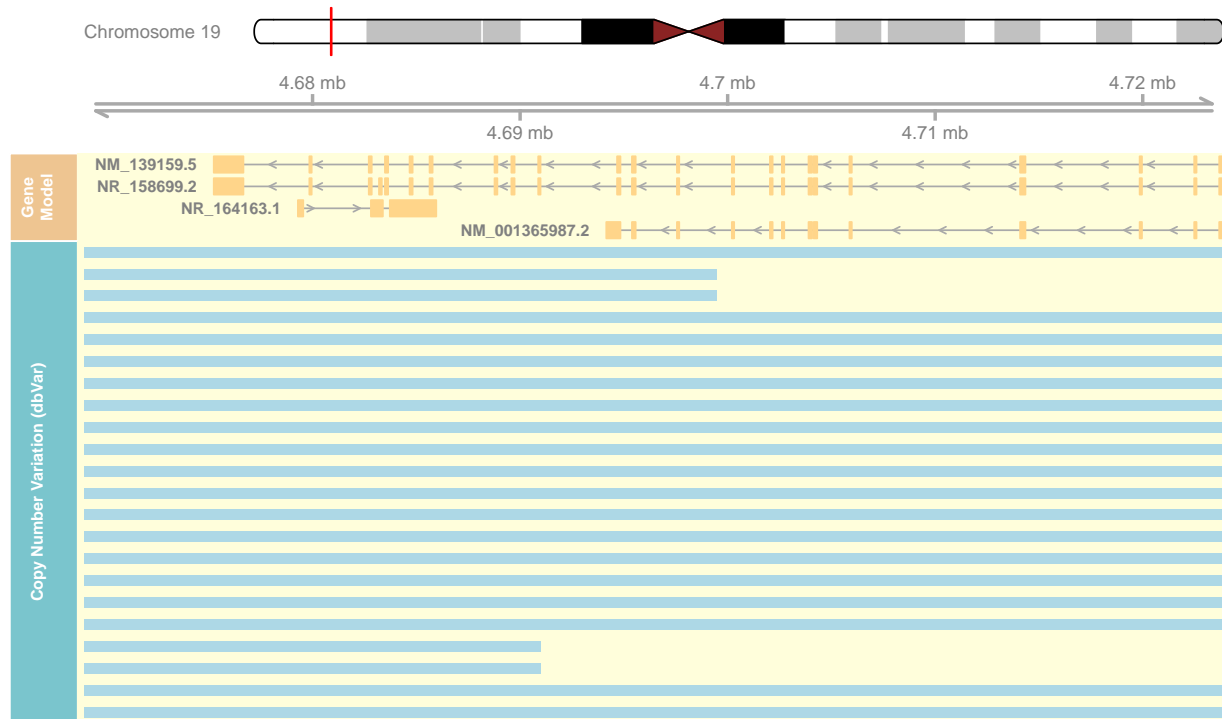
Gene Model with CNVs - DPP9

```
GeneModel <- read.csv(file="results-transcripts-UCSC.csv", header = TRUE, sep=";")
grtrack1 <- GeneRegionTrack(GeneModel, genome = "hg19", chromosome = "chr19",
                            name = "Gene Model",
                            transcriptAnnotation = "symbol",
                            background.title = "#EEC591",
                            background.panel = "#FFFEDB")
gtrack1 <- GenomeAxisTrack()
atrack1 <- AnnotationTrack(CNVdbVar_GR,
                            name = "Copy Number Variation (dbVar)",
                            background.title = "#7AC5CD",
                            background.panel = "#FFFEDB")
chr1 <- as.character(unique(seqnames(CNVdbVar_GR)))
itrack1 <- IdeogramTrack(genome = "hg19", chromosome = chr1)
plotTracks(list(itrack1,gtrack1,grtrack1,atrack1),
           from = 4669000, to = 4723900,
           col = NULL)
```

Documentation to create nice plots

Usage: https://www.bioconductor.org/packages/devel/bioc/vignettes/Gviz/inst/doc/Gviz.html

Color Chart: https://github.com/EarlGlynn/colorchart/wiki/Color-Chart-in-R