Visualizing_genome

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Libraries

```r
library(Gviz)
library(GenomicRanges)
```

```r
data(cpgIslands)
class(cpgIslands)
```

```
## [1] "GRanges"
## attr(,"package")
## [1] "GenomicRanges"
```

```r
chr <- as.character(unique(seqnames(cpgIslands)))
gen <- genome(cpgIslands) #plot the single CpG islands annotation track.
```

```r
atrack <- AnnotationTrack(cpgIslands, name= "CpG") #plot cpgislands
gtrack <- GenomeAxisTrack() #to add a genomic axis to the plot
ideoTrack <- IdeogramTrack(genome = "hg19", chromosome = "chr6")# ideogram
```

```r
#plot
# showbandId - chromosome bands in the ideogram
# turn off the explicit plotting of the chromosome name by setting the showId display parameter to FALSE
plotTracks(ideoTrack, from = 85e6, to = 129e6, showId = FALSE,
           showBandId = TRUE, cex.bands = 0.5)
```
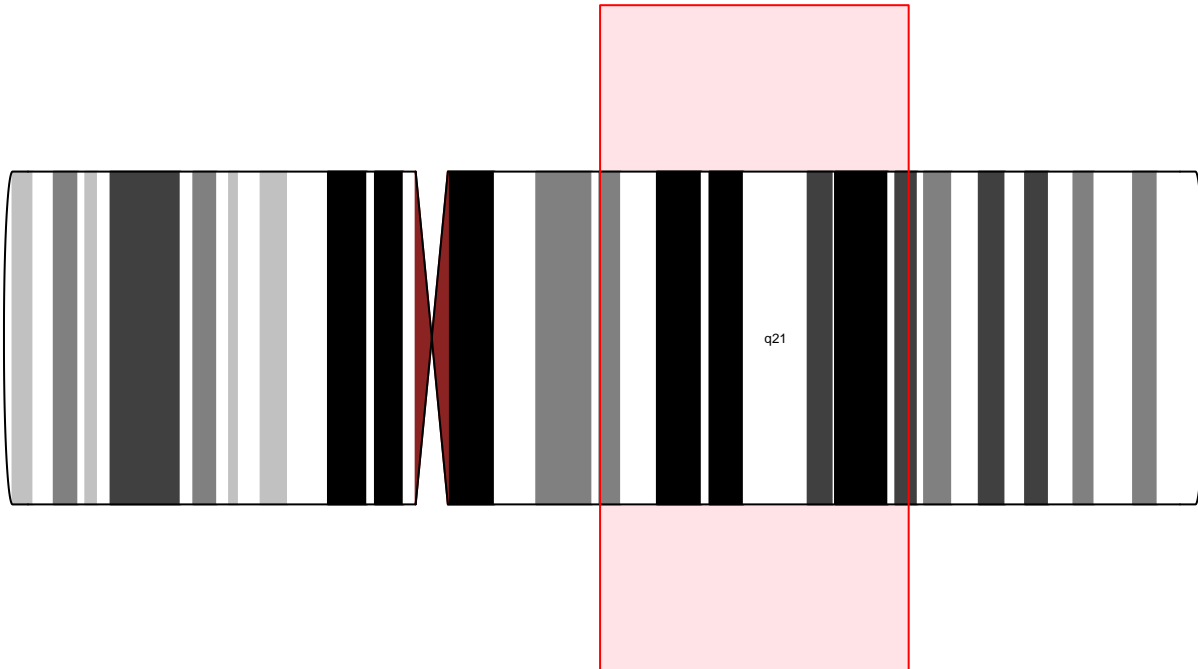
```
###Simple annotation tracks:

from <- 160120744
to <- 160128417
cpgIslands <- UcscTrack(genome="hg38", chromosome="chr6",
                        track="cpgIslandExt", from=from, to=to,
                        trackType="AnnotationTrack", start="chromStart", end="chromEnd",
                        id="name", shape="box", fill="#006400", name="CpG Islands")


snpLocations <- UcscTrack(genome="hg38", chromosome="chr6",
                          track="All SNPs(144)", from=from, to=to, trackType="AnnotationTrack",
                          start="chromStart", end="chromEnd", id="name", feature="func",
                          strand="strand", shape="box", stacking="dense", fill="black",
                          name="SNPs")

##Gene model type tracks:

knownGenes <- UcscTrack(genome="hg38", chromosome="chr6",
                        track="knownGene", from=from, to=to, trackType="GeneRegionTrack",
                        rstarts="exonStarts", rends="exonEnds", gene="name", symbol="name",
                        transcript="name", strand="strand", fill="#8282d2", name="UCSC Genes")


refGenes <- UcscTrack(genome="hg38", chromosome="chr6",
                      track="xenoRefGene", from=from, to=to,
                      trackType="GeneRegionTrack", rstarts="exonStarts",
                      rends="exonEnds", gene="name", symbol="name2",
                      transcript="name", strand="strand", fill="#8282d2",
```

```r
                    stacking="dense", name="Other RefSeq")

ensGenes <- UcscTrack(genome="hg38", chromosome="chr6",
                    track="All GENCODE V25", from=from, to=to, trackType="GeneRegionTrack",
                    rstarts="exonStarts", rends="exonEnds", gene="name",
                    symbol="name2", transcript="name", strand="strand",
                    fill="#960000", name="Ensembl Genes")


###Data tracks

conservation <- UcscTrack(genome="hg38", chromosome="chr6",
                    track="Conservation", table="phastCons100way", from=from, to=to,
                    trackType="DataTrack", start="start", end="end", data="score",
                    type="hist", window="auto", col.histogram="darkblue",
                    fill.histogram="darkblue", ylim=c(-3.7, 4), name="Conservation")

gcContent <- UcscTrack(genome="hg38", chromosome="chr6",
                    track="GC Percent", table="gc5Base", from=from, to=to,
                    trackType="DataTrack", start="start", end="end", data="score",
                    type="hist", window=-1, windowSize=1500, fill.histogram="black",
                    col.histogram="black", ylim=c(30, 70), name="GC Percent")


###Other tracks and plotting:


axTrack <- GenomeAxisTrack()
idxTrack <- IdeogramTrack(genome="hg38", chromosome="chr6")
plotTracks(list(idxTrack, axTrack, knownGenes, refGenes,
            ensGenes, cpgIslands, gcContent, conservation,
            snpLocations), from=from, to=to, showTitle=FALSE)
```
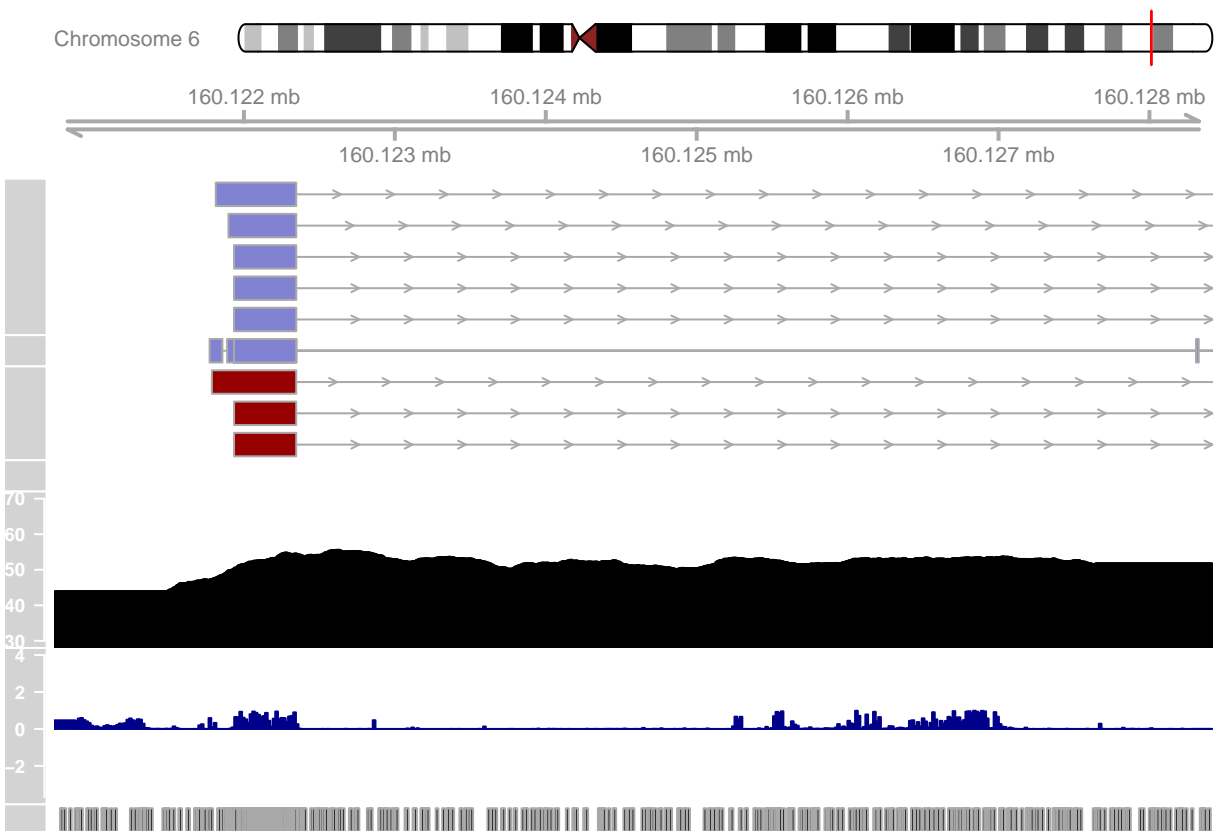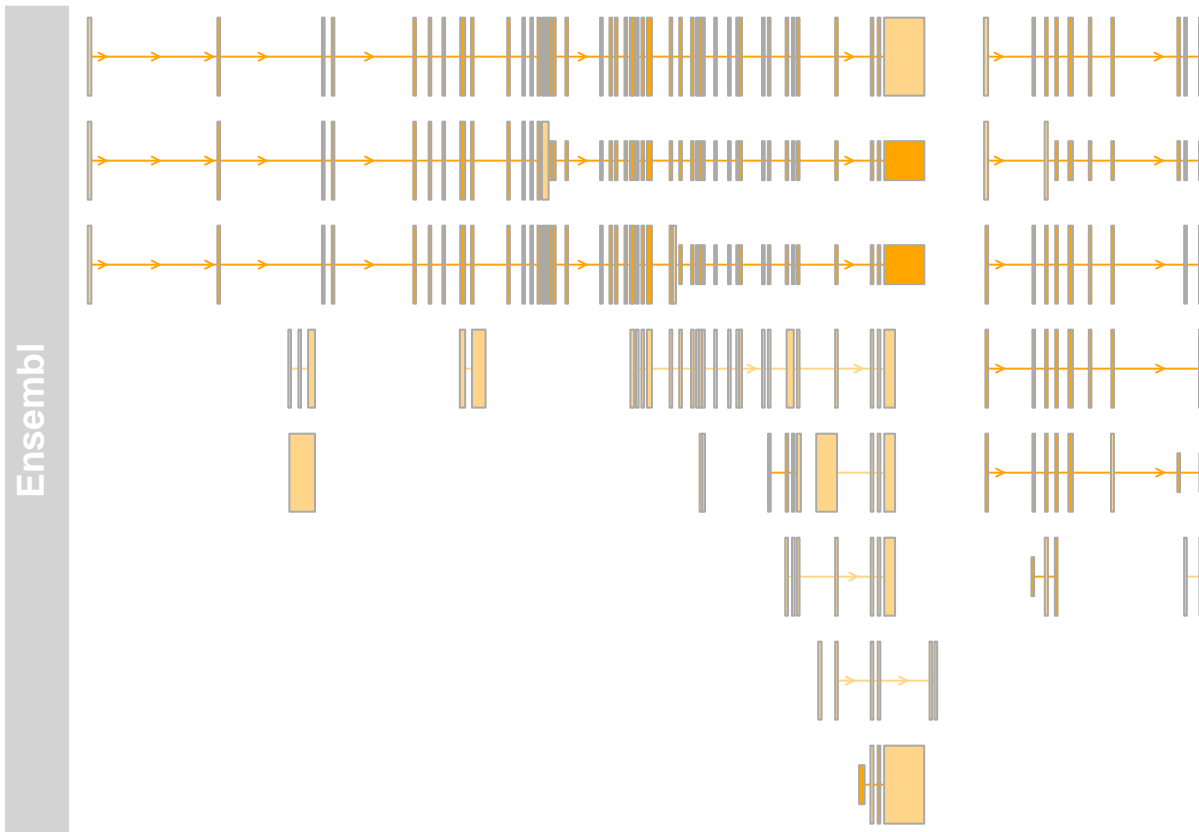
```
biomTrack <- BiomartGeneRegionTrack(genome="hg38", chromosome="chr6",
                                    start=from, end=to, name="Ensembl")
plotTracks(biomTrack)
```

```
plotTracks(biomTrack, col.line=NULL)
```

R Markdown

```
## R version 4.0.5 (2021-03-31)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
##  [1] grid      parallel  stats4    stats     graphics  grDevices utils
##  [8] datasets  methods   base
##
## other attached packages:
## [1] Gviz_1.34.1         GenomicRanges_1.42.0 GenomeInfoDb_1.26.7
## [4] IRanges_2.24.1      S4Vectors_0.28.1     BiocGenerics_0.36.1
##
## loaded via a namespace (and not attached):
##    [1] ProtGenerics_1.22.0       bitops_1.0-7
##    [3] matrixStats_0.62.0        bit64_4.0.5
##    [5] RColorBrewer_1.1-3        progress_1.2.2
```

```
##    [7] httr_1.4.3                backports_1.4.1
##    [9] tools_4.0.5               utf8_1.2.2
##   [11] R6_2.5.1                  rpart_4.1.16
##   [13] lazyeval_0.2.2            Hmisc_4.6-0
##   [15] DBI_1.1.2                 colorspace_2.0-3
##   [17] nnet_7.3-17               withr_2.5.0
##   [19] gridExtra_2.3             tidyselect_1.1.2
##   [21] prettyunits_1.1.1         bit_4.0.4
##   [23] curl_4.3.2                compiler_4.0.5
##   [25] cli_3.3.0                 Biobase_2.50.0
##   [27] htmlTable_2.4.0           xml2_1.3.3
##   [29] DelayedArray_0.16.3       rtracklayer_1.50.0
##   [31] checkmate_2.1.0           scales_1.2.0
##   [33] askpass_1.1               rappdirs_0.3.3
##   [35] stringr_1.4.0             digest_0.6.29
##   [37] Rsamtools_2.6.0           foreign_0.8-82
##   [39] rmarkdown_2.14            XVector_0.30.0
##   [41] dichromat_2.0-0.1         base64enc_0.1-3
##   [43] jpeg_0.1-9                pkgconfig_2.0.3
##   [45] htmltools_0.5.2           MatrixGenerics_1.2.1
##   [47] highr_0.9                 ensembldb_2.14.1
##   [49] dbplyr_2.1.1              fastmap_1.1.0
##   [51] BSgenome_1.58.0           htmlwidgets_1.5.4
##   [53] rlang_1.0.2               rstudioapi_0.13
##   [55] RSQLite_2.2.14            generics_0.1.2
##   [57] BiocParallel_1.24.1       dplyr_1.0.9
##   [59] VariantAnnotation_1.36.0  RCurl_1.98-1.6
##   [61] magrittr_2.0.3            GenomeInfoDbData_1.2.4
##   [63] Formula_1.2-4             Matrix_1.4-1
##   [65] Rcpp_1.0.8.3              munsell_0.5.0
##   [67] fansi_1.0.3               lifecycle_1.0.1
##   [69] stringi_1.7.6             yaml_2.3.5
##   [71] SummarizedExperiment_1.20.0 zlibbioc_1.36.0
##   [73] BiocFileCache_1.14.0      blob_1.2.3
##   [75] crayon_1.5.1              lattice_0.20-45
##   [77] Biostrings_2.58.0         splines_4.0.5
##   [79] GenomicFeatures_1.42.3    hms_1.1.1
##   [81] knitr_1.39                pillar_1.7.0
##   [83] codetools_0.2-18          biomaRt_2.46.3
##   [85] XML_3.99-0.9              glue_1.6.2
##   [87] evaluate_0.15             biovizBase_1.38.0
##   [89] latticeExtra_0.6-29       data.table_1.14.2
##   [91] vctrs_0.4.1               png_0.1-7
##   [93] gtable_0.3.0              openssl_2.0.1
##   [95] purrr_0.3.4               assertthat_0.2.1
##   [97] cachem_1.0.6              ggplot2_3.3.6
##   [99] xfun_0.31                 AnnotationFilter_1.14.0
##  [101] survival_3.3-1            tibble_3.1.7
##  [103] GenomicAlignments_1.26.0  AnnotationDbi_1.52.0
##  [105] memoise_2.0.1             cluster_2.1.3
##  [107] ellipsis_0.3.2
```