

# Visualizing\_genome

Paulyna Magana

19/05/2022

## Libraries

```
library(Gviz)
```

```
## Loading required package: S4Vectors
```

```
## Loading required package: stats4
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
```

```
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
```

```
##
```

```
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,  
##   clusterExport, clusterMap, parApply, parCapply, parLapply,  
##   parLapplyLB, parRapply, parSapply, parSapplyLB
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##   IQR, mad, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames,  
##   dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,  
##   grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,  
##   order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,  
##   rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,  
##   union, unique, unsplit, which.max, which.min
```

```
##
```

```
## Attaching package: 'S4Vectors'
```

```
## The following object is masked from 'package:base':
##
##   expand.grid
```

```
## Loading required package: IRanges
```

```
## Loading required package: GenomicRanges
```

```
## Loading required package: GenomeInfoDb
```

```
## Loading required package: grid
```

```
library(GenomicRanges)
```

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

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

```
chr <- as.character(unique(seqnames(cpgIslands)))
gen <- genome(cpgIslands)
atrack <- AnnotationTrack(cpgIslands, name= "CpG")
```

## 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_1.4.2	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	gridExtra_2.3
##	[19]	tidyselect_1.1.2	prettyunits_1.1.1
##	[21]	bit_4.0.4	curl_4.3.2
##	[23]	compiler_4.0.5	cli_3.3.0
##	[25]	Biobase_2.50.0	htmlTable_2.4.0
##	[27]	xml2_1.3.3	DelayedArray_0.16.3
##	[29]	rtracklayer_1.50.0	checkmate_2.1.0
##	[31]	scales_1.2.0	askpass_1.1
##	[33]	rappdirs_0.3.3	stringr_1.4.0
##	[35]	digest_0.6.29	Rsamtools_2.6.0
##	[37]	foreign_0.8-82	rmarkdown_2.13
##	[39]	XVector_0.30.0	dichromat_2.0-0.1
##	[41]	base64enc_0.1-3	jpeg_0.1-9
##	[43]	pkgconfig_2.0.3	htmltools_0.5.2
##	[45]	MatrixGenerics_1.2.1	ensemldb_2.14.1
##	[47]	dbplyr_2.1.1	fastmap_1.1.0
##	[49]	BSgenome_1.58.0	htmlwidgets_1.5.4
##	[51]	rlang_1.0.2	rstudioapi_0.13
##	[53]	RSQLite_2.2.11	generics_0.1.2
##	[55]	BiocParallel_1.24.1	dplyr_1.0.8
##	[57]	VariantAnnotation_1.36.0	RCurl_1.98-1.6
##	[59]	magrittr_2.0.3	GenomeInfoDbData_1.2.4
##	[61]	Formula_1.2-4	Matrix_1.4-1
##	[63]	Rcpp_1.0.8.3	munsell_0.5.0
##	[65]	fansi_1.0.3	lifecycle_1.0.1
##	[67]	stringi_1.7.6	yaml_2.3.5
##	[69]	SummarizedExperiment_1.20.0	zlibbioc_1.36.0
##	[71]	BiocFileCache_1.14.0	blob_1.2.2
##	[73]	crayon_1.5.1	lattice_0.20-45
##	[75]	Biostrings_2.58.0	splines_4.0.5
##	[77]	GenomicFeatures_1.42.3	hms_1.1.1
##	[79]	knitr_1.38	pillar_1.7.0
##	[81]	biomaRt_2.46.3	XML_3.99-0.9
##	[83]	glue_1.6.2	evaluate_0.15
##	[85]	biovizBase_1.38.0	latticeExtra_0.6-29
##	[87]	data.table_1.14.2	vctrs_0.4.0
##	[89]	png_0.1-7	gtable_0.3.0
##	[91]	openssl_2.0.1	purrr_0.3.4
##	[93]	assertthat_0.2.1	cachem_1.0.6
##	[95]	ggplot2_3.3.5	xfun_0.31
##	[97]	AnnotationFilter_1.14.0	survival_3.3-1
##	[99]	tibble_3.1.6	GenomicAlignments_1.26.0
##	[101]	AnnotationDbi_1.52.0	memoise_2.0.1
##	[103]	cluster_2.1.3	ellipsis_0.3.2