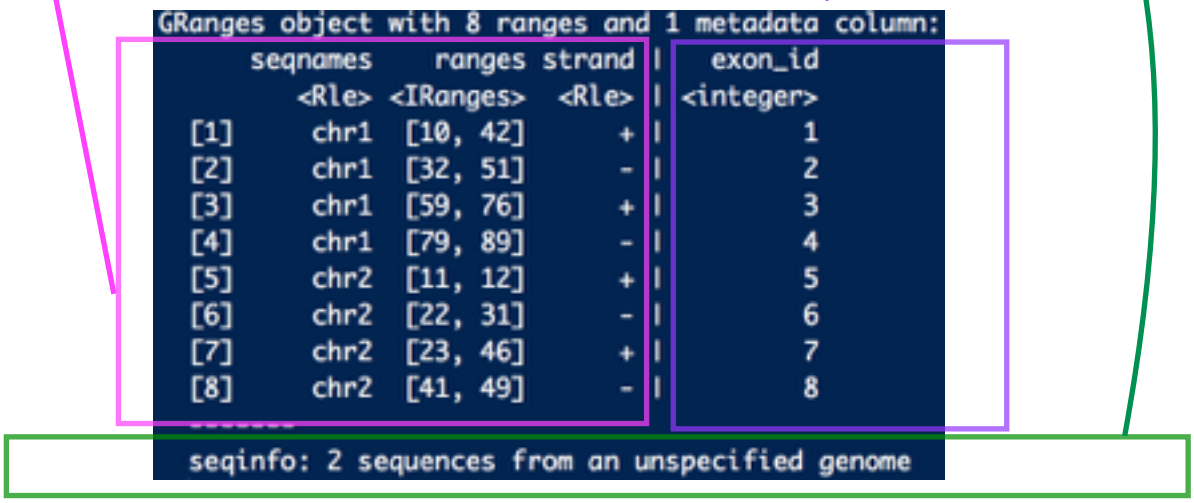
GenomicRanges cheatsheets

Explore the contents of “GRanges" object

Granges
length(gr)
seqnames(gr)
start(gr)
end(gr)
width(gr)
strand(gr)

metadata
mcols(gr)
gr$exon_id

seqinfo
seqlevels(gr)
seqlengths(gr)
genome(gr)



create a GRanges object:
gr <- GRanges(**seqnames** = ,
ranges = IRanges(start= , end =),
strand = , …)

subset: [ ]
gr[gr$exon_id == 1]
gr[2:3, “exon_id”]

split:
split(gr, seqnames(gr))

How to extract the chromosome seq from a BSgenome data?
library(“BSgenome.Hsapiens.UCSC.hg19")
genome<-BSgenome.Hsapiens.UCSC.hg19
ch1<-getSeq(genome,”chr1")
Get the first 20 bases of each chromosome:
getSeq(genome,start=1, end=20)
Get the first 20 bases of chr1
getSeq(genome,"chr1",end=20)
Use GRanges to specify where to get
getSeq(genome,gr)

Ranges : operations
reduce(gr, ignore.strand=T)

coverage(gr)
coverage(gr)$chr1
findOverlaps(gr1, gr2)

(optional:)
shift(gr, -5)
shift(gr, 1:8)
flank(gr, 3)
resize(gr,10)
disjoin(gr)
disjoin(gr, ignore.strand=T)

* gr here is the name of the GRanges object.