

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)

GRanges object with 8 ranges and 1 metadata column:

	seqnames <Rle>	ranges <IRanges>	strand <Rle>	exon_id <integer>
[1]	chr1	[10, 42]	+	1
[2]	chr1	[32, 51]	-	2
[3]	chr1	[59, 76]	+	3
[4]	chr1	[79, 89]	-	4
[5]	chr2	[11, 12]	+	5
[6]	chr2	[22, 31]	-	6
[7]	chr2	[23, 46]	+	7
[8]	chr2	[41, 49]	-	8

seqinfo: 2 sequences from an unspecified genome

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.