A quick introduction to GRanges and GRangesList objects

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GRanges objects

- The GRanges() constructor
- GRanges accessors
- Vector operations on GRanges objects
- Range-based operations on GRanges objects

GRangesList objects

- The GRangesList() constructor
- GRangesList accessors
- Vector operations on GRangesList objects
- List operations on GRangesList objects
- Range-based operations on GRangesList objects

Other resources

The `GRanges` class is a container for...

... storing a set of *genomic ranges* (a.k.a. *genomic regions* or *genomic intervals*).

- Each genomic range is described by a chromosome name, a *start*, an *end*, and a strand.
- *start* and *end* are both **1-based** positions relative to the 5' end of the plus strand of the chromosome, even when the range is on the minus strand.
- *start* and *end* are both considered to be included in the interval (except when the range is empty).
- The *width* of the range is the number of genomic positions included in it. So *width* = *end* - *start* + 1.
- *end* is always >= *start*, except for empty ranges (a.k.a. zero-width ranges) where *end* = *start* - 1.

Note that the *start* is always the leftmost position and the *end* the rightmost, even when the range is on the minus strand.
Gotcha: A TSS is at the *end* of the range associated with a transcript located on the minus strand.

The `GRanges()` constructor

```
> library(GenomicRanges)
> gr1 <- GRanges(seqnames=Rle(c("ch1", "chMT"), c(2, 4)),
+                ranges=IRanges(16:21, 20),
+                strand=rep(c("+", "-", "*"), 2))
> gr1
```

```
GRanges object with 6 ranges and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]      ch1     16-20      +
  [2]      ch1     17-20      -
  [3]     chMT     18-20      *
  [4]     chMT     19-20      +
  [5]     chMT        20      -
  [6]     chMT     21-20      *
  -------
  seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

GRanges accessors: `length()`, `seqnames()`, `ranges()`

```
> length(gr1)

[1] 6

> seqnames(gr1)

factor-Rle of length 6 with 2 runs
  Lengths:    2    4
  Values : ch1  chMT
Levels(2): ch1 chMT

> ranges(gr1)

IRanges object with 6 ranges and 0 metadata columns:
          start       end     width
      <integer> <integer> <integer>
  [1]        16        20         5
  [2]        17        20         4
  [3]        18        20         3
  [4]        19        20         2
  [5]        20        20         1
  [6]        21        20         0
```

GRanges accessors: start(), end(), width(), strand()

```
> start(gr1)

[1] 16 17 18 19 20 21

> end(gr1)

[1] 20 20 20 20 20 20

> width(gr1)

[1] 5 4 3 2 1 0

> strand(gr1)

factor-Rle of length 6 with 6 runs
  Lengths: 1 1 1 1 1 1
  Values : + - * + - *
Levels(3): + - *

> strand(gr1) <- c("-", "-", "+")
> strand(gr1)

factor-Rle of length 6 with 4 runs
  Lengths: 2 1 2 1
  Values : - + - +
Levels(3): + - *
```

GRanges accessors: names()

```
> names(gr1) <- LETTERS[1:6]
> gr1
GRanges object with 6 ranges and 0 metadata columns:
    seqnames    ranges strand
       <Rle> <IRanges>  <Rle>
  A      ch1     16-20      -
  B      ch1     17-20      -
  C     chMT     18-20      +
  D     chMT     19-20      -
  E     chMT        20      -
  F     chMT     21-20      +
  -------
  seqinfo: 2 sequences from an unspecified genome; no seqlengths
> names(gr1)
[1] "A" "B" "C" "D" "E" "F"
```

GRanges accessors: `mcols()`

Like with most *Bioconductor* vector-like objects, *metadata columns* can be added to a GRanges object:

```
> mcols(gr1) <- DataFrame(score=11:16, GC=seq(1, 0, length=6))
> gr1
GRanges object with 6 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  E     chMT        20      - |        15       0.2
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome; no seqlengths
> mcols(gr1)
DataFrame with 6 rows and 2 columns
      score        GC
  <integer> <numeric>
A        11       1.0
B        12       0.8
C        13       0.6
D        14       0.4
E        15       0.2
F        16       0.0
```

GRanges accessors: `seqinfo(), seqlevels(), seqlengths()`

```
> seqinfo(gr1)

Seqinfo object with 2 sequences from an unspecified genome; no seqlengths:
  seqnames seqlengths isCircular genome
  ch1              NA         NA   <NA>
  chMT             NA         NA   <NA>

> seqlevels(gr1)

[1] "ch1"  "chMT"

> seqlengths(gr1)

 ch1 chMT
  NA   NA

> seqlengths(gr1) <- c(50000, 800)
> seqlengths(gr1)

  ch1  chMT
50000   800
```

Vector operations on GRanges objects

What we call *vector operations* are operations that work on any ordinary vector:

- `length()`, `names()`
- Single-bracket subsetting: `[`
- Combining: `c()`
- `split()`, `relist()`
- Comparing: `==`, `!=`, `match()`, `%in%`, `duplicated()`, `unique()`
- Ordering: `<=`, `>=`, `<`, `>`, `order()`, `sort()`, `rank()`

`GRanges` objects support all these *vector operations* ==> They're considered *vector-like* objects.

Vector operations on GRanges objects: Single-bracket subsetting

```
> gr1[c("F", "A")]
GRanges object with 2 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  F     chMT     21-20      + |        16         0
  A      ch1     16-20      - |        11         1
  -------
  seqinfo: 2 sequences from an unspecified genome
> gr1[strand(gr1) == "+"]
GRanges object with 2 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  C     chMT     18-20      + |        13       0.6
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Vector operations on GRanges objects: Single-bracket subsetting

```
> gr1 <- gr1[-5]
> gr1

GRanges object with 5 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Vector operations on GRanges objects: Combining

```
> gr2 <- GRanges(seqnames="ch2",
+                ranges=IRanges(start=c(2:1,2), width=6),
+                score=15:13,
+                GC=seq(0, 0.4, length=3))
> gr12 <- c(gr1, gr2)
> gr12

GRanges object with 8 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  .      ...       ...    ... .       ...       ...
         ch2       2-7      * |        15       0.0
         ch2       1-6      * |        14       0.2
         ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Vector operations on GRanges objects: Comparing

```
> gr12[length(gr12)] == gr12
[1] FALSE FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE
> duplicated(gr12)
[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE
> unique(gr12)
GRanges object with 7 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  F     chMT     21-20      + |        16       0.0
         ch2       2-7      * |        15       0.0
         ch2       1-6      * |        14       0.2
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Vector operations on GRanges objects: Ordering

```
> sort(gr12)
GRanges object with 8 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  .      ...       ...    ... .       ...       ...
         ch2       1-6      * |        14       0.2
         ch2       2-7      * |        15       0.0
         ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Splitting a GRanges object

```
> split(gr12, seqnames(gr12))
GRangesList object of length 3:
$ch1
GRanges object with 2 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  -------
  seqinfo: 3 sequences from an unspecified genome

$chMT
GRanges object with 3 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$ch2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
```

Exercise 1

a. Load the *GenomicRanges* package.

b. Open the man page for the `GRanges` class and run the examples in it.

c. Extract from `GRanges` object `gr` the elements (i.e. ranges) with a score between 4 and 8.

d. Split `gr` by strand.

An overview of *range-based* operations

Intra range transformations
`shift()`, `narrow()`, `resize()`, `flank()`

Inter range transformations
`range()`, `reduce()`, `gaps()`, `disjoin()`

Range-based set operations
`union()`, `intersect()`, `setdiff()`, `punion()`, `pintersect()`, `psetdiff()`, `pgap()`

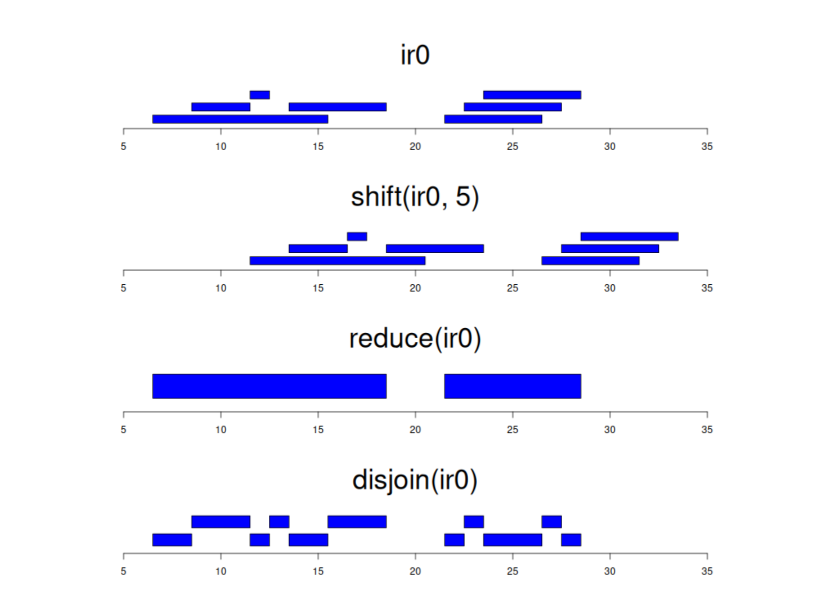
Coverage and slicing
`coverage()`, `slice()`

Finding/counting overlapping ranges
`findOverlaps()`, `countOverlaps()`

Finding the nearest range neighbor
`nearest()`, `precede()`, `follow()`

and more...

Examples of some common *range-based* operations



Range-based operations on GRanges objects

```
> gr2
GRanges object with 3 ranges and 2 metadata columns:
      seqnames    ranges strand |     score        GC
         <Rle> <IRanges>  <Rle> | <integer> <numeric>
  [1]      ch2       2-7      * |        15       0.0
  [2]      ch2       1-6      * |        14       0.2
  [3]      ch2       2-7      * |        13       0.4
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths
> shift(gr2, 50)
GRanges object with 3 ranges and 2 metadata columns:
      seqnames    ranges strand |     score        GC
         <Rle> <IRanges>  <Rle> | <integer> <numeric>
  [1]      ch2     52-57      * |        15       0.0
  [2]      ch2     51-56      * |        14       0.2
  [3]      ch2     52-57      * |        13       0.4
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

Range-based operations on GRanges objects (continued)

```
> gr1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> resize(gr1, 12)
GRanges object with 5 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1      9-20      - |        11       1.0
  B      ch1      9-20      - |        12       0.8
  C     chMT     18-29      + |        13       0.6
  D     chMT      9-20      - |        14       0.4
  F     chMT     21-32      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Range-based operations on GRanges objects (continued)

```
> gr1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     16-20      - |        11       1.0
  B      ch1     17-20      - |        12       0.8
  C     chMT     18-20      + |        13       0.6
  D     chMT     19-20      - |        14       0.4
  F     chMT     21-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> flank(gr1, 3)
GRanges object with 5 ranges and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  A      ch1     21-23      - |        11       1.0
  B      ch1     21-23      - |        12       0.8
  C     chMT     15-17      + |        13       0.6
  D     chMT     21-23      - |        14       0.4
  F     chMT     18-20      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Range-based operations on GRanges objects (continued)

```
> gr3 <- shift(gr1, c(35000, rep(0, 3), 100))
> width(gr3)[c(3,5)] <- 117
> gr3
GRanges object with 5 ranges and 2 metadata columns:
    seqnames       ranges strand |     score        GC
       <Rle>    <IRanges>  <Rle> | <integer> <numeric>
  A      ch1  35016-35020      - |        11       1.0
  B      ch1        17-20      - |        12       0.8
  C     chMT       18-134      + |        13       0.6
  D     chMT        19-20      - |        14       0.4
  F     chMT      121-237      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> range(gr3)
GRanges object with 3 ranges and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]      ch1  17-35020      -
  [2]     chMT    18-237      +
  [3]     chMT     19-20      -
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Range-based operations on GRanges objects (continued)

```
> gr3
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> reduce(gr3)
GRanges object with 4 ranges and 0 metadata columns:
      seqnames      ranges strand
         <Rle>   <IRanges>  <Rle>
  [1]      ch1       17-20      -
  [2]      ch1 35016-35020      -
  [3]     chMT      18-237      +
  [4]     chMT       19-20      -
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Range-based operations on GRanges objects (continued)

```
> gr3
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> gaps(gr3)
GRanges object with 10 ranges and 0 metadata columns:
       seqnames    ranges strand
          <Rle> <IRanges>  <Rle>
   [1]      ch1   1-50000      +
   [2]      ch1      1-16      -
   [3]      ch1  21-35015      -
   ...      ...       ...    ...
   [8]     chMT      1-18      -
   [9]     chMT    21-800      -
  [10]     chMT     1-800      *
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Range-based operations on GRanges objects (continued)

```
> gr3
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 2 sequences from an unspecified genome
> disjoin(gr3)
GRanges object with 6 ranges and 0 metadata columns:
      seqnames      ranges strand
         <Rle>   <IRanges>  <Rle>
  [1]      ch1       17-20      -
  [2]      ch1 35016-35020      -
  [3]     chMT      18-120      +
  [4]     chMT     121-134      +
  [5]     chMT     135-237      +
  [6]     chMT       19-20      -
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Exercise 2

Using `GRanges` object `gr` created at Exercise 1:

a. Shift the ranges in `gr` by 1000 positions to the right.

b. What method is called when doing `shift()` on a `GRanges` object? Find the man page for this method.

Coverage

```
> cvg12 <- coverage(gr12)
> cvg12
RleList of length 3
$ch1
integer-Rle of length 50000 with 4 runs
  Lengths:    15     1     4 49980
  Values :     0     1     2     0

$chMT
integer-Rle of length 800 with 4 runs
  Lengths:  17   1   2 780
  Values :   0   1   2   0

$ch2
integer-Rle of length 7 with 3 runs
  Lengths: 1 5 1
  Values : 1 3 2
```

Coverage (continued)

```
> mean(cvg12)

     ch1      chMT       ch2
0.000180 0.006250 2.571429

> max(cvg12)

 ch1 chMT  ch2
   2    2    3
```

Slicing the coverage

```
> sl12 <- slice(cvg12, lower=1)
> sl12

RleViewsList object of length 3:
$ch1
Views on a 50000-length Rle subject

views:
    start end width
[1]    16  20     5 [1 2 2 2 2]

$chMT
Views on a 800-length Rle subject

views:
    start end width
[1]    18  20     3 [1 2 2]

$ch2
Views on a 7-length Rle subject

views:
    start end width
[1]     1   7     7 [1 3 3 3 3 3 2]

> elementNROWS(sl12)

 ch1 chMT  ch2
   1    1    1

> sl12$chMT

Views on a 800-length Rle subject
```

findOverlaps()

Load aligned reads from a BAM file:

```
> library(pasillaBamSubset)
> untreated1_chr4()

[1] "/home/biocbuild/bbs-3.22-bioc/R/site-library/pasillaBamSubset/extdata/untreated1_chr4

> library(GenomicAlignments)
> reads <- readGAlignments(untreated1_chr4())
```

and store them in a GRanges object:

```
> reads <- as(reads, "GRanges")
> reads[1:4]

GRanges object with 4 ranges and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]     chr4   892-966      -
  [2]     chr4   919-993      -
  [3]     chr4   924-998      +
  [4]     chr4  936-1010      +
  -------
  seqinfo: 8 sequences from an unspecified genome
```

findOverlaps() (continued)

Load the gene ranges from a *TxDb* package:

```
> library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
> txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
> dm3_genes <- genes(txdb)
```

and find the overlaps between the reads and the genes:

```
> hits <- findOverlaps(reads, dm3_genes)
> head(hits)
Hits object with 6 hits and 0 metadata columns:
      queryHits subjectHits
      <integer>   <integer>
  [1]      6296       11499
  [2]      6304       11499
  [3]      6305       11499
  [4]      6310       11499
  [5]      6311       11499
  [6]      6312       11499
  -------
  queryLength: 204355 / subjectLength: 15682
```

Exercise 3

a. Recreate `GRanges` objects `reads` and `dm3_genes` from previous slides.

b. What method is called when calling `findOverlaps()` on them? Open the man page for this method.

c. Find the overlaps between the 2 objects but this time the strand should be ignored.

Exercise 4

In this exercise we want to get the exon sequences for the dm3 genome.

a. Extract the exon ranges from `txdb`.

b. Load the *BSgenome.Dmelanogaster.UCSC.dm3* package.

c. Use `getSeq()` to extract the exon sequences from the `BSgenome` object in *BSgenome.Dmelanogaster.UCSC.dm3*.

The `GRangesList` class is a container for...

storing a list of *compatible* `GRanges` objects.

compatible means:

- they are relative to the same genome,
- AND they have the same metadata columns (accessible with the `mcols()` accessor).

The GRangesList() constructor

```
> grl <- GRangesList(gr3, gr2)
> grl
GRangesList object of length 2:
[[1]]
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

[[2]]
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

GRangesList accessors

```
> length(grl)
[1] 2
```

```
> seqnames(grl)
RleList of length 2
[[1]]
factor-Rle of length 5 with 2 runs
  Lengths:    2    3
  Values : ch1  chMT
Levels(3): ch1 chMT ch2

[[2]]
factor-Rle of length 3 with 1 run
  Lengths:   3
  Values : ch2
Levels(3): ch1 chMT ch2
```

```
> strand(grl)
RleList of length 2
[[1]]
factor-Rle of length 5 with 4 runs
  Lengths: 2 1 1 1
  Values : - + - +
Levels(3): + - *

[[2]]
factor-Rle of length 3 with 1 run
  Lengths: 3
  Values : *
Levels(3): + - *
```

GRangesList accessors (continued)

```
> ranges(grl)

IRangesList object of length 2:
[[1]]
IRanges object with 5 ranges and 0 metadata
        start       end     width
    <integer> <integer> <integer>
  A     35016     35020         5
  B        17        20         4
  C        18       134       117
  D        19        20         2
  F       121       237       117

[[2]]
IRanges object with 3 ranges and 0 metadata
       start       end     width
   <integer> <integer> <integer>
           2         7         6
           1         6         6
           2         7         6
```

```
> start(grl)

IntegerList of length 2
[[1]] 35016 17 18 19 121
[[2]] 2 1 2

> end(grl)

IntegerList of length 2
[[1]] 35020 20 134 20 237
[[2]] 7 6 7

> width(grl)

IntegerList of length 2
[[1]] 5 4 117 2 117
[[2]] 6 6 6
```

GRangesList accessors (continued)

```
> names(grl) <- c("TX1", "TX2")
> grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

GRangesList accessors (continued)

```
> mcols(grl)$geneid <- c("GENE1", "GENE2")
> mcols(grl)

DataFrame with 2 rows and 1 column
         geneid
    <character>
TX1       GENE1
TX2       GENE2

> grl

GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

GRangesList accessors (continued)

```
> seqinfo(grl)
Seqinfo object with 3 sequences from an unspecified genome:
  seqnames seqlengths isCircular genome
  ch1           50000         NA   <NA>
  chMT            800         NA   <NA>
  ch2              NA         NA   <NA>
```

Vector operations on `GRangesList` objects

Only the following *vector operations* are supported on `GRangesList` objects:

- `length()`, `names()`
- Single-bracket subsetting: `[`
- Combining: `c()`

Vector operations on GRangesList objects

```
> grl[c("TX2", "TX1")]
GRangesList object of length 2:
$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Vector operations on GRangesList objects (continued)

```
> c(grl, GRangesList(gr3))
GRangesList object of length 3:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames       ranges strand |     score        GC
       <Rle>    <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1        17-20      - |        12       0.8
  C     chMT       18-134      + |        13       0.6
  D     chMT        19-20      - |        14       0.4
  F     chMT      121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome

[[3]]
GRanges object with 5 ranges and 2 metadata columns:
    seqnames       ranges strand |     score        GC
       <Rle>    <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1        17-20      - |        12       0.8
  C     chMT       18-134      + |        13       0.6
  D     chMT        19-20      - |        14       0.4
  F     chMT      121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome
```

List operations on GRangesList objects

What we call *list operations* are operations that work on an ordinary list:

- Double-bracket subsetting: `[[`
- `elementNROWS()`, `unlist()`
- `lapply()`, `sapply()`, `endoapply()`
- `mendoapply()` (not covered in this presentation)

`GRangesList` objects support all these *list operations* ==> They're considered *list-like* objects.

elementNROWS() and unlist()

```
> grl[[2]]

GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome

> elementNROWS(grl)

TX1 TX2
  5   3

> unlisted <- unlist(grl, use.names=FALSE)  # same as c(grl[[1]], grl[[2]])
> unlisted

GRanges object with 8 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  .      ...         ...    ... .       ...       ...
         ch2         2-7      * |        15       0.0
         ch2         1-6      * |        14       0.2
         ch2         2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

relist()

```
> grl100 <- relist(shift(unlisted, 100), grl)
> grl100
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35116-35120      - |        11       1.0
  B      ch1     117-120      - |        12       0.8
  C     chMT     118-234      + |        13       0.6
  D     chMT     119-120      - |        14       0.4
  F     chMT     221-337      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2   102-107      * |        15       0.0
        ch2   101-106      * |        14       0.2
        ch2   102-107      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

endoapply()

```
> grl100b <- endoapply(grl, shift, 100)
> grl100b

GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35116-35120      - |        11       1.0
  B      ch1     117-120      - |        12       0.8
  C     chMT     118-234      + |        13       0.6
  D     chMT     119-120      - |        14       0.4
  F     chMT     221-337      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2   102-107      * |        15       0.0
        ch2   101-106      * |        14       0.2
        ch2   102-107      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome

> mcols(grl100)

DataFrame with 2 rows and 0 columns

> mcols(grl100b)

DataFrame with 2 rows and 1 column
         geneid
    <character>
TX1       GENE1
TX2       GENE2
```

Range-based operations on GRangesList objects

```
> grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

```
> shift(grl, 100)
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35116-35120      - |        11       1.0
  B      ch1     117-120      - |        12       0.8
  C     chMT     118-234      + |        13       0.6
  D     chMT     119-120      - |        14       0.4
  F     chMT     221-337      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2   102-107      * |        15       0.0
        ch2   101-106      * |        14       0.2
        ch2   102-107      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

`shift(grl, 100)` is equivalent to `endoapply(grl, shift, 100)`

Range-based operations on GRangesList objects (continued)

```
> grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

```
> flank(grl, 10)
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35021-35030      - |        11       1.0
  B      ch1       21-30      - |        12       0.8
  C     chMT        8-17      + |        13       0.6
  D     chMT       21-30      - |        14       0.4
  F     chMT     111-120      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2      -8-1      * |        15       0.0
        ch2      -9-0      * |        14       0.2
        ch2      -8-1      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

`flank(grl, 10)` is equivalent to `endoapply(grl, flank, 10)`

Range-based operations on GRangesList objects (continued)

```
> grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

```
> range(grl)
GRangesList object of length 2:
$TX1
GRanges object with 3 ranges and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]      ch1  17-35020      -
  [2]     chMT    18-237      +
  [3]     chMT     19-20      -
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 1 range and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]      ch2       1-7      *
  -------
  seqinfo: 3 sequences from an unspecified genome
```

`range(grl)` is equivalent to `endoapply(grl, range)`

Range-based operations on GRangesList objects (continued)

```
> grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames      ranges strand |     score        GC
       <Rle>   <IRanges>  <Rle> | <integer> <numeric>
  A      ch1 35016-35020      - |        11       1.0
  B      ch1       17-20      - |        12       0.8
  C     chMT      18-134      + |        13       0.6
  D     chMT       19-20      - |        14       0.4
  F     chMT     121-237      + |        16       0.0
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15       0.0
        ch2       1-6      * |        14       0.2
        ch2       2-7      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome
```

```
> reduce(grl)
GRangesList object of length 2:
$TX1
GRanges object with 4 ranges and 0 metadata columns:
      seqnames      ranges strand
         <Rle>   <IRanges>  <Rle>
  [1]      ch1       17-20      -
  [2]      ch1 35016-35020      -
  [3]     chMT      18-237      +
  [4]     chMT       19-20      -
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 1 range and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]      ch2       1-7      *
  -------
  seqinfo: 3 sequences from an unspecified genome
```

`reduce(grl)` is equivalent to `endoapply(grl, reduce)`

Range-based operations on GRangesList objects (continued)

```
> grl2
GRangesList object of length 2:
$TX1
GRanges object with 1 range and 2 metadata columns:
    seqnames    ranges strand |     score        GC
       <Rle> <IRanges>  <Rle> | <integer> <numeric>
  C     chMT    18-134      + |        13       0.6
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 1 range and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15         0
  -------
  seqinfo: 3 sequences from an unspecified genome
> grl3
GRangesList object of length 2:
[[1]]
GRanges object with 1 range and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
       chMT    22-130      + |        13       0.6
  -------
  seqinfo: 3 sequences from an unspecified genome

[[2]]
GRanges object with 1 range and 2 metadata columns:
   seqnames    ranges strand |     score        GC
      <Rle> <IRanges>  <Rle> | <integer> <numeric>
        ch2       2-7      * |        15         0
  -------
  seqinfo: 3 sequences from an unspecified genome
```

```
> setdiff(grl2, grl3)
GRangesList object of length 2:
$TX1
GRanges object with 2 ranges and 0 metadata columns:
      seqnames    ranges strand
         <Rle> <IRanges>  <Rle>
  [1]     chMT     18-21      +
  [2]     chMT   131-134      +
  -------
  seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 0 ranges and 0 metadata columns:
   seqnames    ranges strand
      <Rle> <IRanges>  <Rle>
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Other resources

- Great slides from Michael on ranges sequences and alignments: `http://bioconductor.org/help/course-materials/2014/CSAMA2014/2_Tuesday/lectures/Ranges_Sequences_and_Alignments-Lawrence.pdf`
- Vignettes in the *GenomicRanges* package (`browseVignettes("GenomicRanges")`).
- `GRanges` and `GRangesList` man pages in the *GenomicRanges* package.
- Vignettes and `GAlignments` man page in the *GenomicAlignments* package.
- *Bioconductor* support site: `http://support.bioconductor.org/`
- The *genomic ranges* paper: Michael Lawrence, Wolfgang Huber, Hervé Pagès, Patrick Aboyoun, Marc Carlson, Robert Gentleman, Martin T. Morgan, Vincent J. Carey. Software for Computing and Annotating Genomic Ranges. *PLOS Computational Biology*, 4(3), 2013.