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, 20]      -
  [6]     chMT  [21, 20]      *
  -------
  seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

GRanges accessors

```
> 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 of length 6
    start end width
[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 (continued)

```
> 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 (continued)

```
> names(gr1) <- LETTERS[1:6]
> names(gr1)

[1] "A" "B" "C" "D" "E" "F"

> mcols(gr1) <- DataFrame(score=11:16, GC=seq(1, 0, length=6))
> mcols(gr1)

DataFrame with 6 rows and 2 columns
      score        GC
  <integer> <numeric>
1        11       1.0
2        12       0.8
3        13       0.6
4        14       0.4
5        15       0.2
6        16       0.0

> 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
  B      ch1  [17, 20]      - |        12       0.8
  C     chMT  [18, 20]      + |        13       0.6
  D     chMT  [19, 20]      - |        14       0.4
  E     chMT  [20, 20]      - |        15       0.2
  F     chMT  [21, 20]      + |        16         0
  -------
  seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

GRanges accessors (continued)

```
> 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 (continued)

```
> 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
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Vector operations on GRanges objects (continued)

```
> 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
  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
  -------
  seqinfo: 2 sequences from an unspecified genome
```

Vector operations on GRanges objects (continued)

```
> 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
    B      ch1  [17, 20]      -   |        12       0.8
    C     chMT  [18, 20]      +   |        13       0.6
  ...      ...       ...    ... ...       ...       ...
           ch2    [2, 7]      *   |        15         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 (continued)

```
> 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
    B      ch1  [17, 20]      -   |        12       0.8
    C     chMT  [18, 20]      +   |        13       0.6
  ...      ...       ...    ... ...       ...       ...
    F     chMT  [21, 20]      +   |        16         0
          ch2  [ 2,  7]      *   |        15         0
          ch2  [ 1,  6]      *   |        14       0.2
  -------
  seqinfo: 3 sequences from an unspecified genome
```

Vector operations on GRanges objects (continued)

```
> 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
    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
           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
  B      ch1  [17, 20]      - |        12       0.8

$chMT
GRanges object with 3 ranges and 2 metadata columns:
    seqnames   ranges strand | score  GC
  C     chMT [18, 20]      + |    13 0.6
  D     chMT [19, 20]      - |    14 0.4
  F     chMT [21, 20]      + |    16   0

$ch2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   0
        ch2 [1, 6]      * |    14 0.2
        ch2 [2, 7]      * |    13 0.4

-------
seqinfo: 3 sequences from an unspecified genome
```

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()`

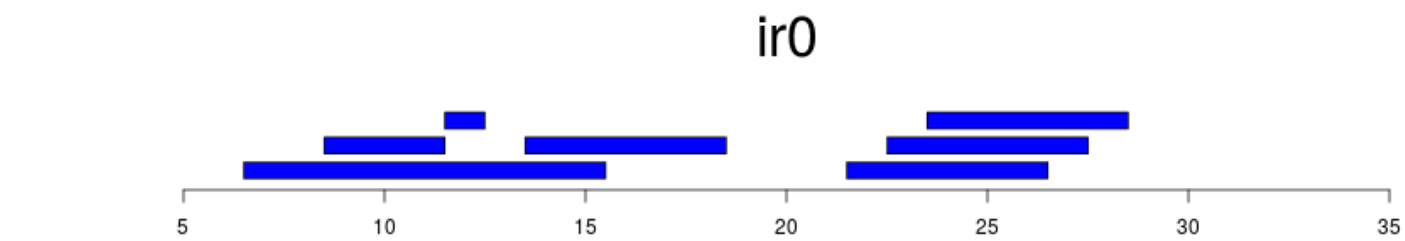
Coverage and slicing
`coverage()`, `slice()`

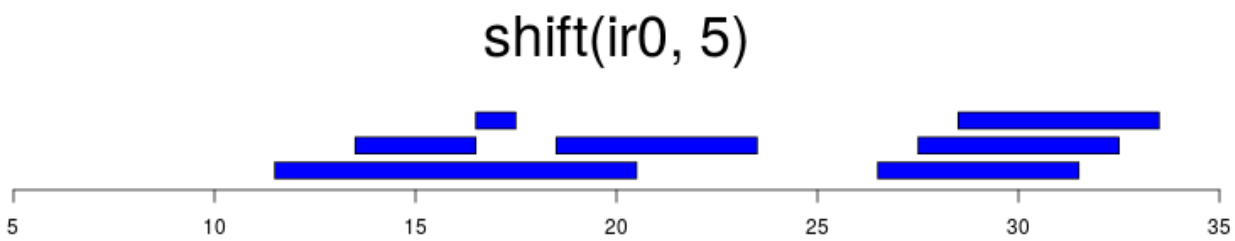
Finding/counting overlapping ranges
`findOverlaps()`, `countOverlaps()`

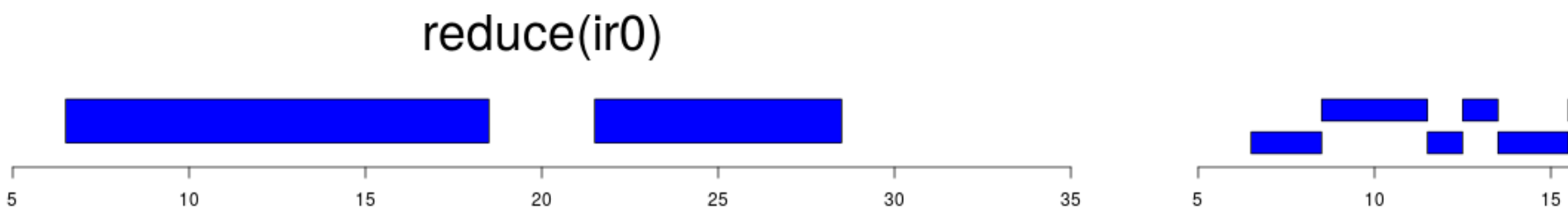
Finding the nearest range neighbor
`nearest()`, `precede()`, `follow()`

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
  [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
  [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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
  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
  -------
  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
```

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 of length 3
names(3): ch1 chMT ch2

> elementLengths(sl12)

 ch1 chMT  ch2
   1    1    1

> sl12$chMT

Views on a 800-length Rle subject

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

> mean(sl12$chMT)

[1] 1.666667

> max(sl12$chMT)

[1] 2
```

findOverlaps()

Load aligned reads from a BAM file:

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

[1] "/home/hpages/R/R-3.2.r67440/library/pasillaBamSubset/extdata/untreated1_chr4.bam"

> 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
```

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
  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

[[2]]
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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 of length 2
[[1]]
IRanges of length 5
    start   end width names
[1] 35016 35020     5     A
[2]    17    20     4     B
[3]    18   134   117     C
[4]    19    20     2     D
[5]   121   237   117     F

[[2]]
IRanges of length 3
    start end width names
[1]     2   7     6
[2]     1   6     6
[3]     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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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>
1       GENE1
2       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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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
        ch2    [1, 6]      * |        14       0.2
        ch2    [2, 7]      * |        13       0.4

$TX1
GRanges object with 5 ranges and 2 metadata columns:
    seqnames          ranges strand | score  GC
  A      ch1 [35016, 35020]      - |    11   1
  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

-------
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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   0
        ch2 [1, 6]      * |    14 0.2
        ch2 [2, 7]      * |    13 0.4

[[3]]
GRanges object with 5 ranges and 2 metadata columns:
    seqnames         ranges strand | score  GC
  A      ch1 [35016, 35020]      - |    11   1
  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

-------
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: `[[`
- `elementLengths()`, `unlist()`
- `lapply()`, `sapply()`, `endoapply()`
- `mendoapply()` (not covered in this presentation)

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

elementLengths() 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
        ch2    [1, 6]      * |        14       0.2
        ch2    [2, 7]      * |        13       0.4
  -------
  seqinfo: 3 sequences from an unspecified genome

> elementLengths(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
    B      ch1 [   17,    20]      -   |        12       0.8
    C     chMT [   18,   134]      +   |        13       0.6
  ...      ...             ...    ... ...       ...       ...
           ch2          [2, 7]      *   |        15         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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames     ranges strand | score  GC
        ch2 [102, 107]      * |    15   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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames     ranges strand | score  GC
        ch2 [102, 107]      * |    15   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>
1       GENE1
2       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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames     ranges strand | score  GC
        ch2 [102, 107]      * |    15   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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames  ranges strand | score  GC
        ch2 [-8, 1]      * |    15   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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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]      -

$TX2
GRanges object with 1 range and 0 metadata columns:
      seqnames ranges strand
  [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
  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

$TX2
GRanges object with 3 ranges and 2 metadata columns:
   seqnames ranges strand | score  GC
        ch2 [2, 7]      * |    15   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]      -

$TX2
GRanges object with 1 range and 0 metadata columns:
      seqnames ranges strand
  [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

$TX2
GRanges object with 1 range and 2 metadata columns:
   seqnames ranges strand | score GC
        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

[[2]]
GRanges object with 1 range and 2 metadata columns:
   seqnames ranges strand | score GC
        ch2 [2, 7]      * |    15  0

-------
seqinfo: 3 sequences from an unspecified genome
```

```
> psetdiff(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]      +

$TX2
GRanges object with 0 ranges and 0 metadata columns:
     seqnames ranges strand

-------
seqinfo: 3 sequences from an unspecified genome
```

`psetdiff(grl2, grl)` is equivalent to `mendoapply(setdiff, grl2, grl)`

Other resources

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/`