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 $\geq start$, 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

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

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
</tr>
<tr>
<td>[1] ch1</td>
<td>16-20</td>
<td>+</td>
</tr>
<tr>
<td>[2] ch1</td>
<td>17-20</td>
<td>-</td>
</tr>
<tr>
<td>[3] chMT</td>
<td>18-20</td>
<td>*</td>
</tr>
<tr>
<td>[5] chMT</td>
<td>20</td>
<td>-</td>
</tr>
<tr>
<td>[6] chMT</td>
<td>21-20</td>
<td>*</td>
</tr>
</tbody>
</table>

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
  Levels: ch1 chMT

> ranges(gr1)
IRanges object with 6 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>20</td>
<td>5</td>
</tr>
<tr>
<td>17</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td>18</td>
<td>20</td>
<td>3</td>
</tr>
<tr>
<td>19</td>
<td>20</td>
<td>2</td>
</tr>
<tr>
<td>20</td>
<td>20</td>
<td>1</td>
</tr>
<tr>
<td>21</td>
<td>20</td>
<td>0</td>
</tr>
</tbody>
</table>
GRanges accessors: `start()`, `end()`, `width()`, `strand()`

```r
> 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
</tr>
<tr>
<td>E</td>
<td>chMT</td>
<td>20</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
</tr>
</tbody>
</table>

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:

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

GRanges object with 6 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20+</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>E</td>
<td>chMT</td>
<td>20</td>
<td>-</td>
<td>15</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20+</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome; no seqlengths

> mcols(gr1)

DataFrame with 6 rows and 2 columns

<table>
<thead>
<tr>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>15</td>
<td>0.2</td>
</tr>
<tr>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>
GRanges accessors: `seqinfo()`, `seqlevels()`, `seqlengths()`

```r
> 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
```
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

```r
> gr1[, c("F", "A")]
GRanges object with 2 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome

> gr1[strand(gr1) == "+"]
GRanges object with 2 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome
```
Vector operations on `GRanges` objects: Single-bracket subsetting

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

GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome
Vector operations on GRanges objects: Combining

```r
> 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
```
Vector operations on GRanges objects: Comparing

> gr12[length(gr12)] == gr12
[1] FALSE 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
<tr>
<td></td>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
</tr>
<tr>
<td></td>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
Vector operations on GRanges objects: Ordering

```r
> sort(gr12)

GRanges object with 8 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td></td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td></td>
<td>14</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td></td>
<td>15</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td></td>
<td>13</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
Splitting a GRanges object

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

- **ir0**
- **shift(ir0, 5)**
- **reduce(ir0)**
- **disjoin(ir0)**
Range-based operations on GRanges objects

```r
> 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome

> resize(gr1, 12)

GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>9-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>9-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-29</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>9-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-32</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome
Range-based operations on GRanges objects (continued)

> gr1

GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>16-20</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>21-20</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome

> flank(gr1, 3)

GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>21-23</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>21-23</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>15-17</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>21-23</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>18-20</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome
Range-based operations on GRanges objects (continued)

```r
> 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 - 
[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  -
[4]  chMT     19-20      -
-------
seqinfo: 2 sequences from an unspecified genome
```
### Range-based operations on GRanges objects (continued)

```r
> gr3
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35016-35020</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

```

seqinfo: 2 sequences from an unspecified genome

```r
> gaps(gr3)
GRanges object with 10 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>ch1 1-50000</td>
<td>+</td>
</tr>
<tr>
<td>[2]</td>
<td>ch1 1-16</td>
<td>-</td>
</tr>
<tr>
<td>[3]</td>
<td>ch1 21-35015</td>
<td>-</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td>...</td>
</tr>
<tr>
<td>[8]</td>
<td>chMT 1-18</td>
<td>-</td>
</tr>
<tr>
<td>[9]</td>
<td>chMT 21-800</td>
<td>-</td>
</tr>
<tr>
<td>[10]</td>
<td>chMT 1-800</td>
<td>*</td>
</tr>
</tbody>
</table>

```

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 +
[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.
> 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)

```r
> mean(cvg12)
  ch1    chMT    ch2
0.000180 0.006250 2.571429

> max(cvg12)
  ch1    chMT    ch2
   2      2      3
```
Slicing the coverage

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

Load aligned reads from a BAM file:

```r
> library(pasillaBamSubset)
> untreated1_chr4()
[1] "/home/biocbuild/bbs-3.18-bioc/R/site-library/pasillaBamSubset/extdata/untreated1_chr4.bam"
> library(GenomicAlignments)
> reads <- readGAlignments(untreated1_chr4())
```

and store them in a `GRanges` object:

```r
> 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 

```
> 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:

<table>
<thead>
<tr>
<th>queryHits</th>
<th>subjectHits</th>
</tr>
</thead>
<tbody>
<tr>
<td>6296</td>
<td>11499</td>
</tr>
<tr>
<td>6304</td>
<td>11499</td>
</tr>
<tr>
<td>6305</td>
<td>11499</td>
</tr>
<tr>
<td>6310</td>
<td>11499</td>
</tr>
<tr>
<td>6311</td>
<td>11499</td>
</tr>
<tr>
<td>6312</td>
<td>11499</td>
</tr>
</tbody>
</table>
```

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

```r
> grl <- GRangesList(gr3, gr2)
> grl

GRangesList object of length 2:
[[1]]
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35016-35020</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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

[[2]]
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

-------
seqinfo: 3 sequences from an unspecified genome
GRangesList accessors

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

```r
> 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
```

```r
> 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)

```r
> 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
```

```r
> start(grl)
IntegerList of length 2
[[1]] 35016 17 18 19 121
[[2]] 2 1 2
```

```r
> end(grl)
IntegerList of length 2
[[1]] 35020 20 134 20 237
[[2]] 7 6 7
```

```r
> width(grl)
IntegerList of length 2
[[1]] 5 4 117 2 117
[[2]] 6 6 6
```
GRangesList accessors (continued)

```r
> names(grl) <- c("TX1", "TX2")
> grl

GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th></th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35016-35020</td>
<td>-</td>
<td></td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20</td>
<td>-</td>
<td></td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134</td>
<td>+</td>
<td></td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20</td>
<td>-</td>
<td></td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237</td>
<td>+</td>
<td></td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th></th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>2-7 *</td>
<td></td>
<td></td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6 *</td>
<td></td>
<td></td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7 *</td>
<td></td>
<td></td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
```
GRangesList accessors (continued)

```r
gcols(grl)$geneid <- c("GENE1", "GENE2")
gcols(grl)

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

grl
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>35016-35020</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-134</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>121-237</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
```
GRangesList accessors (continued)

> seqinfo(grl)

Seqinfo object with 3 sequences from an unspecified genome:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>seqlengths</th>
<th>isCircular</th>
<th>genome</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch1</td>
<td>50000</td>
<td>NA</td>
<td>&lt;NA&gt;</td>
</tr>
<tr>
<td>chMT</td>
<td>800</td>
<td>NA</td>
<td>&lt;NA&gt;</td>
</tr>
<tr>
<td>ch2</td>
<td>NA</td>
<td>NA</td>
<td>&lt;NA&gt;</td>
</tr>
</tbody>
</table>
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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;integer&gt;</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

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

$TX1
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;integer&gt;</td>
</tr>
<tr>
<td>A</td>
<td>ch1</td>
<td>35016-35020</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-134</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>121-237</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

-------
seqinfo: 3 sequences from an unspecified genome
Vector operations on GRangesList objects (continued)

```r
> c(gr1, GRangesList(gr3))

GRangesList object of length 3:

$TX1
GRanges object with 5 ranges and 2 metadata columns:

- seqnames: [A, B, C, D, F]
- ranges: [35016-35020, 17-20, 18-134, 19-20, 121-237]
- strand: [-, -, +, -, +]
- score: [11, 12, 13, 14, 16]
- GC: [1.0, 0.8, 0.6, 0.4, 0.0]

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:

- seqnames: [ch2, ch2, ch2]
- ranges: [2-7, 1-6, 2-7]
- strand: [*]
- score: [15, 14, 13]
- GC: [0.0, 0.2, 0.4]

seqinfo: 3 sequences from an unspecified genome

[[3]]
GRanges object with 5 ranges and 2 metadata columns:

- seqnames: [A, B, C, D, F]
- ranges: [35016-35020, 17-20, 18-134, 19-20, 121-237]
- strand: [-, -, +, -, +]
- score: [11, 12, 13, 14, 16]
- GC: [1.0, 0.8, 0.6, 0.4, 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()

```r
> 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
```
> 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
> grl100b <- endoapply(grl, shift, 100)
> grl100b
GRangesList object of length 2:
$TX1
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35116-35120</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 117-120</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 118-234</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 119-120</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 221-337</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>102-107</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>101-106</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>102-107</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

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
  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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35016-35020</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

-------
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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35116-35120</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 117-120</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 118-234</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 119-120</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 221-337</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>102-107</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>101-106</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>102-107</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

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

shift(grl, 100) is equivalent to endoapply(grl, shift, 100)
Range-based operations on GRangesList objects (continued)

```r
> 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>
  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

> 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>
  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
```

`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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1</td>
<td>35016-35020</td>
<td>-</td>
<td>11</td>
</tr>
<tr>
<td>B</td>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td>C</td>
<td>chMT</td>
<td>18-134</td>
<td>+</td>
<td>13</td>
</tr>
<tr>
<td>D</td>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
<td>14</td>
</tr>
<tr>
<td>F</td>
<td>chMT</td>
<td>121-237</td>
<td>+</td>
<td>16</td>
</tr>
</tbody>
</table>

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

$TX2
GRanges object with 3 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>ch1</td>
<td>17-35020</td>
</tr>
<tr>
<td>[3]</td>
<td>chMT</td>
<td>19-20</td>
</tr>
</tbody>
</table>

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

> range(grl)
GRangesList object of length 2:
$TX1
GRanges object with 3 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>ch1</td>
<td>17-35020</td>
</tr>
<tr>
<td>[3]</td>
<td>chMT</td>
<td>19-20</td>
</tr>
</tbody>
</table>

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

$TX2
GRanges object with 1 range and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>ch2</td>
<td>1-7</td>
</tr>
</tbody>
</table>

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

range(grl) is equivalent to endoapply(grl, range)
Range-based operations on GRangesList objects (continued)

```r
> grl
GRangesList object of length 2:

$TX1
GRanges object with 5 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>ch1 35016-35020</td>
<td>-</td>
<td>11</td>
<td>1.0</td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20</td>
<td>-</td>
<td>12</td>
<td>0.8</td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134</td>
<td>+</td>
<td>13</td>
<td>0.6</td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20</td>
<td>-</td>
<td>14</td>
<td>0.4</td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>1-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

> reduce(grl)
GRangesList object of length 2:

$TX1
GRanges object with 4 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
</tr>
<tr>
<td>ch1</td>
<td>35016-35020</td>
<td>-</td>
</tr>
<tr>
<td>chMT</td>
<td>18-237</td>
<td>+</td>
</tr>
<tr>
<td>chMT</td>
<td>19-20</td>
<td>-</td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome

$TX2
GRanges object with 1 range and 0 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch2</td>
<td>1-7</td>
<td>*</td>
</tr>
</tbody>
</table>

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

> setdiff(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/