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

```r
> 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>ch1</td>
<td>16-20</td>
<td>+</td>
</tr>
<tr>
<td>ch1</td>
<td>17-20</td>
<td>-</td>
</tr>
<tr>
<td>chMT</td>
<td>18-20</td>
<td>*</td>
</tr>
<tr>
<td>chMT</td>
<td>19-20</td>
<td>+</td>
</tr>
<tr>
<td>chMT</td>
<td>20</td>
<td>-</td>
</tr>
<tr>
<td>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
  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 accessor: names()

```r
> 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></td>
<td></td>
<td></td>
</tr>
<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)

Data Frame 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
```
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

```r
> 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

```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 16-20</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 18-20</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 21-20</td>
<td>+</td>
<td>16</td>
<td>0.0</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>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>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

```r
> gr12[length(gr12)] == gr12
[1] FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE TRUE 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 16-20</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 18-20</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 21-20</td>
<td>+</td>
<td>16</td>
<td>0.0</td>
</tr>
<tr>
<td></td>
<td>ch2 2-7</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td></td>
<td>ch2 1-6</td>
<td>*</td>
<td>14</td>
<td>0.2</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>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;integer&gt;</td>
<td>&lt;numeric&gt;</td>
</tr>
<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>14</td>
<td>0.2</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>2-7</td>
<td>*</td>
<td>13</td>
<td>0.4</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

-------
```
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

> gr2

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: 1 sequence from an unspecified genome; no seqlengths

> shift(gr2, 50)

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>52-57</td>
<td>*</td>
<td>15</td>
<td>0.0</td>
</tr>
<tr>
<td>ch2</td>
<td>51-56</td>
<td>*</td>
<td>14</td>
<td>0.2</td>
</tr>
<tr>
<td>ch2</td>
<td>52-57</td>
<td>*</td>
<td>13</td>
<td>0.4</td>
</tr>
</tbody>
</table>

seqinfo: 1 sequence from an unspecified genome; no seqlengths
Range-based operations on GRanges objects (continued)

```r
> 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)

```r
> 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:

<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

> range(gr3)

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] ch1</td>
<td>17-35020</td>
<td>-</td>
</tr>
<tr>
<td>[3] chMT</td>
<td>19-20</td>
<td>-</td>
</tr>
</tbody>
</table>

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:

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

> 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>[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)

```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

> disjoin(gr3)

GRanges object with 6 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>ranges</th>
</tr>
</thead>
<tbody>
<tr>
<td>17-20</td>
</tr>
<tr>
<td>35016-35020</td>
</tr>
<tr>
<td>18-120</td>
</tr>
<tr>
<td>121-134</td>
</tr>
<tr>
<td>135-237</td>
</tr>
<tr>
<td>19-20</td>
</tr>
</tbody>
</table>

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)

<table>
<thead>
<tr>
<th></th>
<th>ch1</th>
<th>chMT</th>
<th>ch2</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean</td>
<td>0.000180</td>
<td>0.006250</td>
<td>2.571429</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>ch1</th>
<th>chMT</th>
<th>ch2</th>
</tr>
</thead>
<tbody>
<tr>
<td>max</td>
<td>2</td>
<td>2</td>
<td>3</td>
</tr>
</tbody>
</table>
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
```
Load aligned reads from a BAM file:

```r
> library(pasillaBamSubset)
> untreated1_chr4()
> 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:

```

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr4</td>
<td>892-966</td>
<td>-</td>
</tr>
<tr>
<td>chr4</td>
<td>919-993</td>
<td>-</td>
</tr>
<tr>
<td>chr4</td>
<td>924-998</td>
<td>+</td>
</tr>
<tr>
<td>chr4</td>
<td>936-1010</td>
<td>+</td>
</tr>
</tbody>
</table>
```

seqinfo: 8 sequences from an unspecified genome
Load the gene ranges from a \textit{TxDb} package:

\begin{verbatim}
> library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
> txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
> dm3_genes <- genes(txdb)
\end{verbatim}

and find the overlaps between the reads and the genes:

\begin{verbatim}
> 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>&lt;integer&gt;</td>
<td>&lt;integer&gt;</td>
</tr>
</tbody>
</table>

[1]    6296   11499
[2]    6304   11499
[3]    6305   11499
[4]    6310   11499
[5]    6311   11499
[6]    6312   11499

-------
queryLength: 204355 / subjectLength: 15682
\end{verbatim}
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

> 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): + - *
> ranges(grl)

IRangesList object of length 2:
[[1]]
IRanges object with 5 ranges and 0 metadata

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>35016</td>
<td>35020</td>
</tr>
<tr>
<td>B</td>
<td>17</td>
<td>20</td>
</tr>
<tr>
<td>C</td>
<td>18</td>
<td>134</td>
</tr>
<tr>
<td>D</td>
<td>19</td>
<td>20</td>
</tr>
<tr>
<td>F</td>
<td>121</td>
<td>237</td>
</tr>
</tbody>
</table>

[[2]]
IRanges object with 3 ranges and 0 metadata

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>7</td>
<td>6</td>
</tr>
<tr>
<td>1</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>2</td>
<td>7</td>
<td>6</td>
</tr>
</tbody>
</table>

> 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
> 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>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
> 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
Using `seqinfo` function:

```r
> 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()`
> 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>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>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
Vector operations on GRangesList objects (continued)

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

GRangesList object of length 3:

$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; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>ch1 35016-35020 -</td>
<td>11</td>
<td>1.0</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20 -</td>
<td>12</td>
<td>0.8</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134 +</td>
<td>13</td>
<td>0.6</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20 -</td>
<td>14</td>
<td>0.4</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237 +</td>
<td>16</td>
<td>0.0</td>
<td></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></td>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt; &lt;Rle&gt;</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

[[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></td>
<td>&lt;Rle&gt; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>ch1 35016-35020 -</td>
<td>11</td>
<td>1.0</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20 -</td>
<td>12</td>
<td>0.8</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134 +</td>
<td>13</td>
<td>0.6</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20 -</td>
<td>14</td>
<td>0.4</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237 +</td>
<td>16</td>
<td>0.0</td>
<td></td>
</tr>
</tbody>
</table>

seqinfo: 3 sequences from an unspecified genome
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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;integer&gt;</td>
<td>&lt;numeric&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

> 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:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>score</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;integer&gt;</td>
<td>&lt;numeric&gt;</td>
</tr>
<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>...</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
> grl100 <- relist(shift(unlisted, 100), grl)
> grl100

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
> 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<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:

<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; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td>&lt;integer&gt; &lt;numeric&gt;</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>ch1 35016-35020 -</td>
<td>11</td>
<td>1.0</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>ch1 17-20 -</td>
<td>12</td>
<td>0.8</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>chMT 18-134 +</td>
<td>13</td>
<td>0.6</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>chMT 19-20 -</td>
<td>14</td>
<td>0.4</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>chMT 121-237 +</td>
<td>16</td>
<td>0.0</td>
<td></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></td>
<td>&lt;Rle&gt; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td>&lt;integer&gt; &lt;numeric&gt;</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>2-7         *</td>
<td>15</td>
<td>0.0</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>1-6         *</td>
<td>14</td>
<td>0.2</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>2-7         *</td>
<td>13</td>
<td>0.4</td>
<td></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></td>
<td>&lt;Rle&gt; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td>&lt;integer&gt; &lt;numeric&gt;</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>ch1 35116-35120 -</td>
<td>11</td>
<td>1.0</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>ch2 117-120 -</td>
<td>12</td>
<td>0.8</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>chMT 118-234 +</td>
<td>13</td>
<td>0.6</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>chMT 119-120 -</td>
<td>14</td>
<td>0.4</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>chMT 221-337 +</td>
<td>16</td>
<td>0.0</td>
<td></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></td>
<td>&lt;Rle&gt; &lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td>&lt;integer&gt; &lt;numeric&gt;</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>102-107     *</td>
<td>15</td>
<td>0.0</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>101-106     *</td>
<td>14</td>
<td>0.2</td>
<td></td>
</tr>
<tr>
<td>ch2</td>
<td>102-107     *</td>
<td>13</td>
<td>0.4</td>
<td></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 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) 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 0 metadata columns:
  seqnames  ranges strand
  <Rle>  <IRanges> <Rle>
[1] ch1  17-35020 -
[3] chMT 19-20 -
-------
seqinfo: 3 sequences from an unspecified genome

$TX
GRangesList object of length 2:
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)

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 -
[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:

<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

> 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>
</table>
[1] ch1    | 17-20  | -      |
[2] ch1    | 35016-35020 | - |
[4] chMT   | 19-20  | -      |

seqinfo: 3 sequences from an unspecified genome

$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
-------
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/