

Strings and Ranges in R and Bioconductor

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November 2, 2013

Outline

Aims

Introduction

Strings

- Strings in R

- Biostrings

- Representing reads

- Representing reads

Ranges

- IRanges

- Dealing with alignments - Rsamtools

Aims

By the end of this lecture and practical you should be familiar with

- ▶ How DNA sequences are represented in R
- ▶ How to create and compare genomic intervals
- ▶ How to read fastq and bam files into R
- ▶ Interactions between the packages

Previously....

- ▶ Whistle-stop tour of sequencing.
 - ▶ fastq
 - ▶ bam
- ▶ Recap of R and Bioconductor
 - ▶ Vectors, data.frames, lists
 - ▶ Functions
 - ▶ How to get help

Introduction

Sequencing produces millions of reads. e.g in fastq format

Read 1

CTAAGAAAGGAGTTGAGTTTAGTTAAAAGAGGGTTTGCATCGAGATATTAGATTTGGGATAGACATGTACC

Read 2

CTAAGAAAGGAGTTGAGTTTAGTTAAAANAGNGTTTGCATCGAGATATTAGATNTNGGNTNGACATGTNCC

Read 3

TAAGAAAGGAGTTGAGTTTAGTTAAAAGAGGGTTTGCATCCAGATATTAGATTTGGGATAGACATGTACCT

Read 4

AAAGGAGTTGAGTTTAGTTAAAAGAGGGTTTGCATCGAGATATTAGATTTGGGATAGACATGTACCTTTTA

Read 5

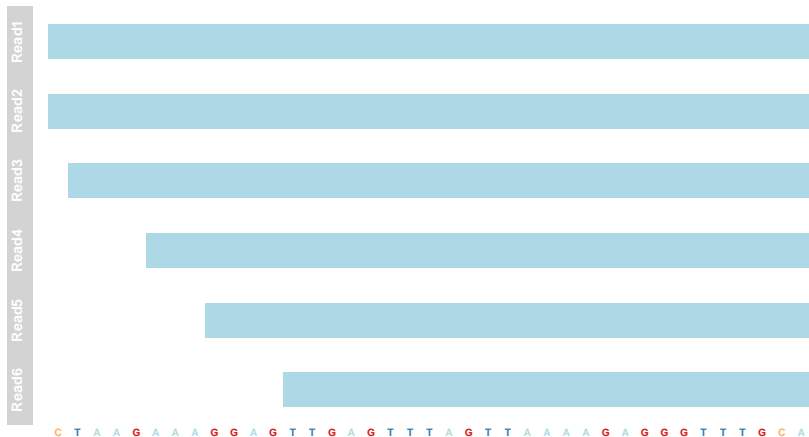
GGAGTTGAGTTTAGTTAAAAGAGGGTTTGCATCGAGATATTAGATTTGGGATAGACATGTACCTTTTACAG

Read 6

TTGAGTTTAGTTAAAAGAGGGTTTGCATCGAGATATTAGATTTGGGATAGACATGTACCTTTTACAGCATT

These need to be compared to the genome (aligned) and we record the chromosome and coordinates that each sequence aligns to, often with quality information.

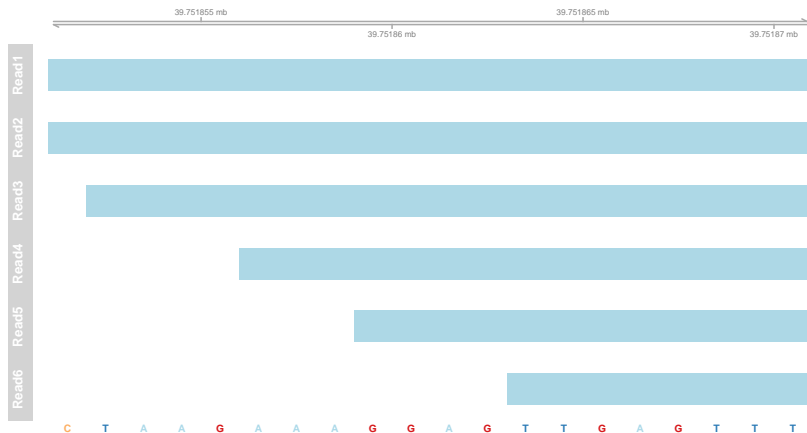
Need consistent representation of (1) genome and (2) reads



Reads come with quality score and IDs that also need to be captured

Associating reads with positions

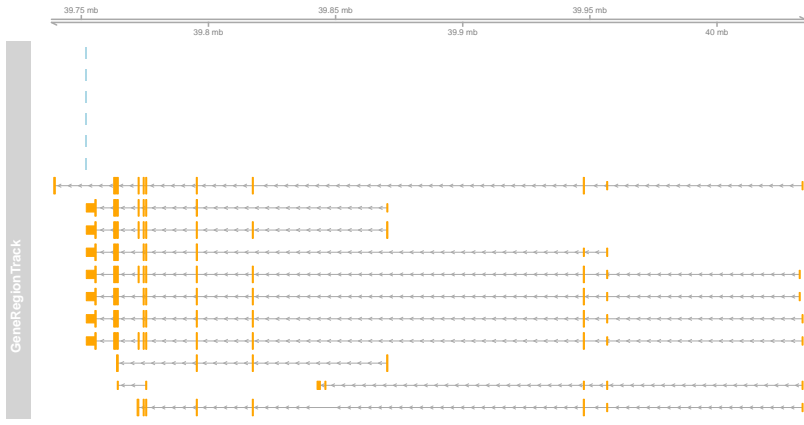
Often we are given the mapped location of reads



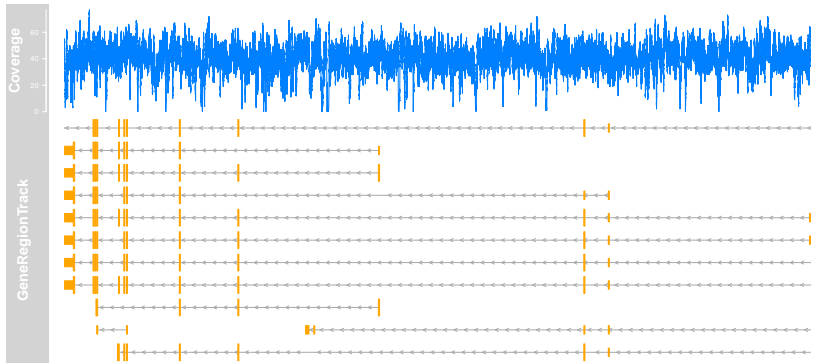
Need a way of representing alignments and associated qualities

Associating with Genomic Features

We will often want to find information about the genomic region around the reads



Or use definitions of genomic regions to interrogate the data



Need representation of genomic regions of interest

Why bother doing these things in R?

- ▶ Interactivity and data exploration
- ▶ Quality assessment
- ▶ Access to existing statistical and visualisation techniques (e.g. limma)
- ▶ Reproducibility

We will not do alignment of reads in R

Packages we will meet

- ▶ Biostrings - Manipulation of DNA sequences in R
- ▶ ShortRead - Input / output of fastq files and quality assessment
- ▶ IRanges - Low-level classes and functions for dealing with intervals of consecutive values
- ▶ GRanges - Functions for representing ranges with sequence and strand information
- ▶ Rsamtools - Input of bam files

DNA Sequences

```
## [1] "AGTCTGCTCCAG"  
## [2] "CGCAGTCGCGG"  
## [3] "TGGTCTTTGTTCACTCTT"  
## [4] "AGAAAAAGCCCTTCG"
```

We can represent sequences of A, T, C, G. Several useful operations are possible

```
myseq
```

```
## [1] "AGTCTGCTCCAG"  
## [2] "CGCAGTCGCGG"  
## [3] "TGGTCTTTGTTCACTCTT"  
## [4] "AGAAAAAGCCCTTCG"
```

```
gsub("ATG", "atg", myseq)
```

```
## [1] "AGTCTGCTCCAG"  
## [2] "CGCAGTCGCGG"  
## [3] "TGGTCTTTGTTCACTCTT"  
## [4] "AGAAAAAGCCCTTCG"
```

Biostrings package

However, the Biostrings package is specifically-designed for biological sequences

```
library(Biostrings)
myseq <- DNASTringSet(randomStrings)
```

Biostrings operations

```
myseq
```

```
##      A DNAStringSet instance of length 100
##      width seq
##      [1]      12 AGTCTGCTCCAG
##      [2]      11 CGCAGTCGCGG
##      [3]      18 TGGTCTTTGTTCACTCTT
##      [4]      15 AGAAAAAGCCCTTCG
##      [5]      17 GTTAAGATGCTTACTGA
##      ...      ...      ...
##      [96]      13 ACTTCCTTTTCTG
##      [97]      12 TAATGTCAAGAG
##      [98]      10 TGA CTCTCAA
##      [99]      14 TTATAGACTCTGGA
##     [100]      13 GATCACAGCGCGG
```

Biostrings operations

```
myseq[1:2, ]  
  
##      A DNASTringSet instance of length 2  
##      width seq  
## [1]      12 AGTCTGCTCCAG  
## [2]      11 CGCAGTCGCGG
```

This doesn't work!

```
myseq[, 1:2]
```

```
subseq(myseq, 1, 3)
```

```
##      A DNAStringSet instance of length 100
##           width seq
##      [1]      3 AGT
##      [2]      3 CGC
##      [3]      3 TGG
##      [4]      3 AGA
##      [5]      3 GTT
##      ...      ... ...
##     [96]      3 ACT
##     [97]      3 TAA
##     [98]      3 TGA
##     [99]      3 TTA
##    [100]      3 GAT
```

Similar to substr

Biostrings operations

Accessor functions must be used to retrieve the data

```
width(myseq)[1:2]
```

```
## [1] 12 11
```

```
length(width(myseq))
```

```
## [1] 100
```

```
table(width(myseq))
```

```
##
```

```
## 10 11 12 13 14 15 16 17 18 19 20
```

```
## 15 13 7 9 8 7 6 6 8 15 6
```

Can subset based on properties of the set

```
myseq[width(myseq) > 19]

##      A DNAStringSet instance of length 6
##      width seq
## [1]      20 ATTAGCCAGTGTTATGTACT
## [2]      20 CAGGTTGCAATTCATTGGCA
## [3]      20 ACACATGTGTCCTTCTTAAG
## [4]      20 ATGTCGATGAACGTATGGTC
## [5]      20 TTTAGGAAGCAGATGTTCTA
## [6]      20 CCCTCTCGGCAGAACGAGGG

myseq[as.character(substr(myseq, 1, 3)) ==
      "TTC"]

##      A DNAStringSet instance of length 1
##      width seq
## [1]      12 TTCCAGGGTTAC
```

Some useful string operation functions are provided

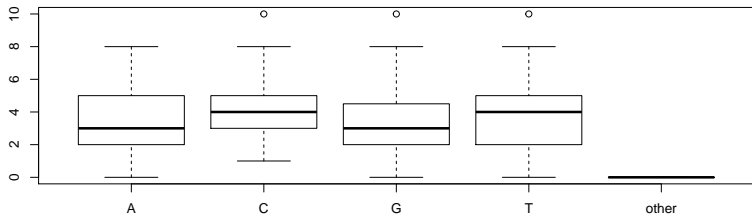
```
alphabetFrequency(myseq[1:4, ], baseOnly = TRUE)
```

```
##      A C G  T other
## [1,] 2 4 3  3      0
## [2,] 1 4 5  1      0
## [3,] 1 4 3 10      0
## [4,] 6 4 3  2      0
```

```
af <- alphabetFrequency(myseq, baseOnly = TRUE)
myseq[af[, 1] == 0, ]
```

```
##      A DNAStringSet instance of length 3
##      width seq
## [1]      10 CTCCTGGTCC
## [2]      11 TCGCCGCCCT
## [3]      19 CGGGTGCTCGCTTCCGCCT
```

```
boxplot(af)
```



More-specialised features

```
myseq[1:2, ]
```

```
##      A DNAStringSet instance of length 2
##      width seq
## [1]      12 AGTCTGCTCCAG
## [2]      11 CGCAGTCGCGG
```

```
reverse(myseq[1:2, ])
```

```
##      A DNAStringSet instance of length 2
##      width seq
## [1]      12 GACCTCGTCTGA
## [2]      11 GGCGCTGACGC
```

```
reverseComplement(myseq[1:2, ])
```

```
##      A DNAStringSet instance of length 2
##      width seq
## [1]      12 CTGGAGCAGACT
## [2]      11 CCGCGACTGCG
```

```
translate(myseq[1:4, ])
```

```
##    A AAStringSet instance of length 4  
##      width seq  
## [1]      4 SLLQ  
## [2]      3 RSR  
## [3]      6 WSLFTL  
## [4]      5 RKSPS
```

The genome as a string - BSgenome

```
library(BSgenome)
head(available.genomes())

## [1] "BSgenome.Alyrata.JGI.v1"
## [2] "BSgenome.Amellifera.BeeBase.assembly4"
## [3] "BSgenome.Amellifera.UCSC.apiMel2"
## [4] "BSgenome.Athaliana.TAIR.04232008"
## [5] "BSgenome.Athaliana.TAIR.TAIR9"
## [6] "BSgenome.Btaurus.UCSC.bosTau3"

available.genomes()[23:25]

## Bioconductor version 2.12
## (BiocInstaller 1.10.4), ?biocLite for
## help
## A newer version of Bioconductor is
## available for this version of R,
## ?BiocUpgrade for help

## [1] "BSgenome.Hsapiens.UCSC.hg17"
## [2] "BSgenome.Hsapiens.UCSC.hg18"
## [3] "BSgenome.Hsapiens.UCSC.hg19"
```

The human genome

```
library(BSgenome.Hsapiens.UCSC.hg19)
hg19 <- BSgenome.Hsapiens.UCSC.hg19::Hsapiens
hg19

## Human genome
## |
## | organism: Homo sapiens (Human)
## | provider: UCSC
## | provider version: hg19
## | release date: Feb. 2009
## | release name: Genome Reference Consortium GRCh37
## |
## | single sequences (see '?seqnames'):
```

##	chr1
##	chr2
##	chr3
##	chr4
##	chr5
##	chr6
##	chr7
##	chr8
##	chr9

Retrieve Sequences

```
tp53 <- getSeq(hg19, "chr17", 7577851, 7590863)
tp53
```

```
## 13013-letter "DNAString" instance
## seq: TTGTATTTTTCAGTAG...GGGGAAAACCCCAATC
```

```
as.character(tp53)
```

```
## [1] "TTGTATTTTTCAGTAGAGACGGGGTTTCACCGTTAGCCAGGATGGTCTCGATCTCCCAACCTC
```

```
alphabetFrequency(tp53, baseOnly = TRUE)
```

```
##      A      C      G      T other
## 3102  3375  3025  3511      0
```

```
subseq(tp53, 1000, 1010)
```

```
## 11-letter "DNAString" instance
## seq: TATAGGTGTGC
```

Timings

Don't need to load the whole genome into memory, so reading a particular sequence is **fast**

```
system.time(tp53 <- getSeq(hg19, "chr17",  
                           7577851, 7598063))
```

```
##      user  system elapsed  
##    0.900    0.031    0.935
```

Manipulating sequences

We can now use Biostrings operations to manipulate the sequence

```
translate(subseq(tp53, 1000, 1010))  
  
##    3-letter "AAString" instance  
## seq: YRC  
  
reverseComplement(subseq(tp53, 1000, 2000))  
  
##    1001-letter "DNAString" instance  
## seq: CCTATGGAACTGTGA...GTGGTGCACACCTATA
```

Later, we will show how the sequences for genomic features can be extracted

Fastq Recap

Recall that sequence reads are represented in text format

```
readLines(sampleFq(), n = 10)
```

```
## [1] "@SRR020521.1 EAS139_33_FC301DUAAXX_0_2_1_206_461/1"  
## [2] "GTCTATAGTTCTCAAGTTTATGTCCATTGAGCTC"  
## [3] "+"  
## [4] ">>>>>>>>>>>>>>>>>>>><>>>>+:48<"  
## [5] "@SRR020521.3188018 EAS139_33_FC301DUAAXX_0_2_33_1708_1368/1"  
## [6] "CTTGAGAAGATCATCATTGTAAAGAGGCCAAACTTG"  
## [7] "+"  
## [8] ">>>>4>>>>>>>>>>>>>><>><<<<<<<>"  
## [9] "@SRR020521.3332221 EAS139_33_FC301DUAAXX_0_2_35_514_899/1"  
## [10] "ATCAAATGGAATCGAATGGAATCTTCATCAATTGG"
```

It should be possible to represent these as **Biostrings** objects

The Short Read package

Has convenient functions for reading fastq files and performing quality assessment

```
library(ShortRead)
fq <- readFastq(sampleFQ())
fq

## class: ShortReadQ
## length: 1000000 reads; width: 35 cycles
```

```
sread(fq)[1:3, ]
```

```
##      A DNAStringSet instance of length 3
##      width seq
## [1]      35 GTCTATAGTTCTCA...TCCATTTGAGCTC
## [2]      35 CTTGAGAAGATCAT...AGAGGCAAACCTG
## [3]      35 ATCAAATGGAATCG...CTTCATCAATTGG
```

```
quality(fq)[1:3, ]
```

```
## class: FastqQuality
## quality:
##      A BStringSet instance of length 3
##      width seq
## [1]      35 >>>>>>>>>>>>...>>>>+>+:48><
## [2]      35 >>>>4>>>>>>>>...<>>><<<><<><>
## [3]      35 9>>>6>>49>>>>:...2>>4<<:-:<70%
```

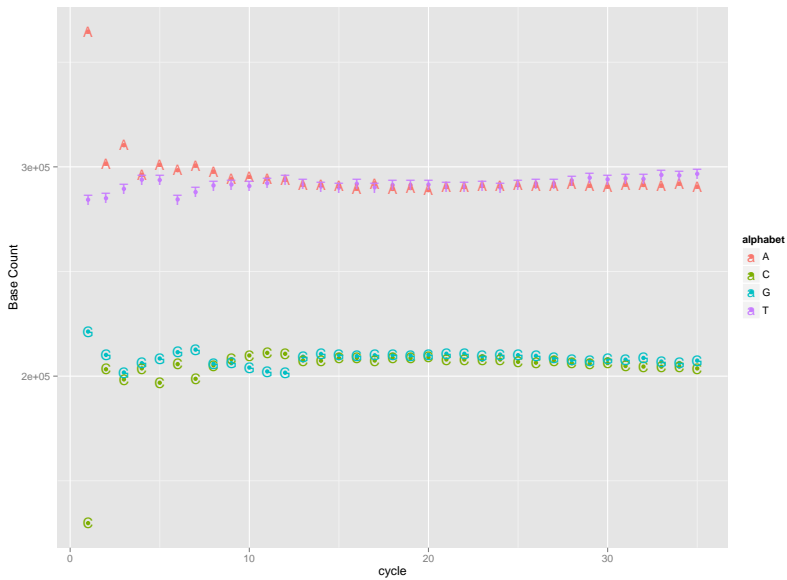
```
id(fq)[1:3]
```

```
##    A BStringSet instance of length 3  
##      width seq  
## [1]    49 SRR020521.1 EA...2_1_206_461/1  
## [2]    58 SRR020521.3188...3_1708_1368/1  
## [3]    56 SRR020521.3332..._35_514_899/1
```

Could parse the ID for run names, lanes, tiles etc

```
abc <- alphabetByCycle(sread(fq))
abc[1:4, 1:8]
```

```
##           cycle
## alphabet  [,1]  [,2]  [,3]  [,4]
##           A 364639 301566 310341 296242
##           C 129777 203283 198450 203706
##           G 221299 210142 201737 206191
##           T 284285 285009 289472 293861
##           cycle
## alphabet  [,5]  [,6]  [,7]  [,8]
##           A 301006 298385 300656 297781
##           C 196845 205745 198741 205139
##           G 208434 211436 212665 205970
##           T 293715 284434 287938 291110
```

Conversion of qualities

Phred quality scores are integers from 0 to 50 that are stored as ASCII characters after adding 33. The basic R functions `rawToChar` and `charToRaw` can be used to convert

```
phred <- 1:9
phreda <- paste(sapply(as.raw((phred) + 33),
  rawToChar), collapse = "")
phreda

## [1] "\"#$%&'()*\"

as.integer(charToRaw(phreda)) - 33

## [1] 1 2 3 4 5 6 7 8 9
```

```
quality(fq) [1]
```

```
## class: FastqQuality
```

```
## quality:
```

```
##      A BStringSet instance of length 1
```

```
##      width seq
```

[illegible]

```
as.integer(charToRaw(">>>>>>>>>>>>>>>>>><>>>>+:+:48><")) -
```

33

```
## [1] 29 29 29 29 29 29 29 29 29 29 29 29 29
```

```
## [13] 29 29 29 29 29 29 29 29 29 27 29 29
```

```
## [25] 29 29 29 10 29 10 25 19 23 29 27
```

A shortcut

```
qual <- as(quality(fq), "matrix")  
dim(qual)
```

```
## [1] 1000000      35
```

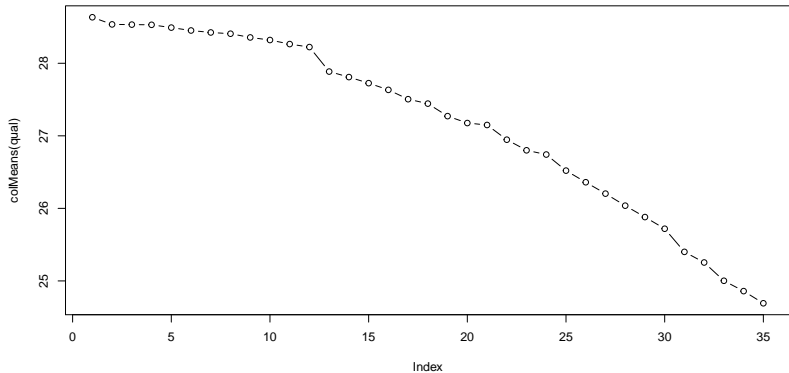
```
qual[1, ]
```

```
## [1] 29 29 29 29 29 29 29 29 29 29 29 29 29
```

```
## [13] 29 29 29 29 29 29 29 29 29 27 29 29
```

```
## [25] 29 29 29 10 29 10 25 19 23 29 27
```

```
plot(colMeans(qual), type = "b")
```



Read Occurrence

```
tbl <- tables(fq)
names(tbl)

## [1] "top"          "distribution"

tbl$top[1:5]

## AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
##                                     37
## GAATGGAATGGAATGGAATGGAATGGAATG
##                                     37
## ATTCCATTCCATTCCATTCCATTCCATTCC
##                                     36
## GGAATGGAATGGAATGGAATGGAATGGAATG
##                                     32
## AACCTAACCTAACCTAACCTAACCTAACCT
##                                     27
```

```
head(tbl$distribution)
```

```
##      nOccurrences nReads  
## 1                1 977827  
## 2                2  6801  
## 3                3  1428  
## 4                4   496  
## 5                5   180  
## 6                6    72
```

977827 sequences appear only once, 6801 appear twice, etc.

We can trim the reads if required

```
subseq(sread(fq), 1, 10)
```

```
##      A DNAStringSet instance of length 1000000
##              width seq
##      [1]      10 GTCCTATAGTT
##      [2]      10 CTTGAGAAGA
##      [3]      10 ATCAAATGGA
##      [4]      10 TCATATCCTA
##      [5]      10 CTAAAGTTTT
##      ...      ...      ...
## [999996]      10 TTGTATGTGC
## [999997]      10 ATTTCTGTCTT
## [999998]      10 TAATTGTCTA
## [999999]      10 AAAAACAGAC
## [1000000]      10 TCCTTCTCTC
```

or search for adaptor sequence

```
grep(myAdaptor, sread(fq))
```

And write the resulting files

```
write.XStringSet(...)
```


We could even do some 'aligning' in R

```
system.time(aln <- matchPattern(as.character(sread(fq)[2]),  
  hg19[["chr1"]]))
```

```
##      user  system elapsed  
##    2.481    0.161    3.029
```

```
aln
```

```
##      Views on a 249250621-letter DNAString subject  
## subject: NNNNNNNNNNNNNNN...NNNNNNNNNNNNNNNN  
## views:  
##           start           end width  
## [1] 249066163 249066197      35 [CTT...TG]
```

```
sread(fq)[2]

##      A DNAStringSet instance of length 1
##      width seq
## [1]      35 CTTGAGAAGATCAT...AGAGGCAAACCTTG

getSeq(hg19, "chr1", 249066163, 249066197)

##      35-letter "DNAString" instance
## seq: CTTGAGAAGATCATCATTTGTAAAGAGGCAAACCTTG

identical(as.character(sread(fq)[2]), as.character(getSeq(hg19,
  "chr1", 249066163, 249066197)))

## [1] TRUE
```

We might want to know more about the region between 249066163 and 249066197 on chromosome 1, or find other reads in this region. For this we will need a way of representing genomic ranges

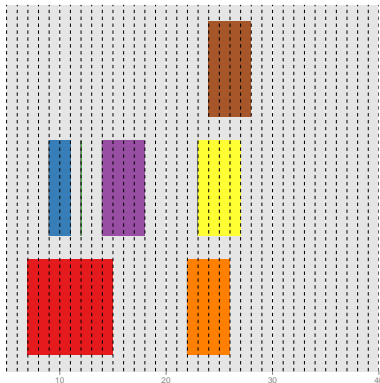
IRanges

- ▶ Genome is typically represented as linear sequence
- ▶ Ranges are an ordered set of consecutive integers defined by a start and end position
- ▶ $\text{start} \leq \text{end}$
- ▶ Ranges are a common scaffold for many genomic analyses
- ▶ Ranges can be associated with genomic information (e.g. gene name) or data derived from analysis (e.g. counts)

Suppose we want to capture information on the following intervals

```
## Object of class "ggbio"
```

Start	End
7	15
9	11
12	12
14	18
22	26
23	27
24	28



```
## NULL
```

```
ir <- IRanges(start = c(7, 9, 12, 14, 22:24),  
              end = c(15, 11, 12, 18, 26, 27, start(ir))
```

```
ir
```

```
## IRanges of length 7
```

```
##      start end width
```

```
## [1]      7  15      9
```

```
## [2]      9  11      3
```

```
## [3]     12  12      1
```

```
## [4]     14  18      5
```

```
## [5]     22  26      5
```

```
## [6]     23  27      5
```

```
## [7]     24  28      5
```

```
## [1]  7  9 12 14 22 23 24
```

```
end(ir)
```

```
## [1] 15 11 12 18 26 27 28
```

```
width(ir)
```

```
## [1] 9 3 1 5 5 5 5
```

Ranges as vectors

```
ir

## IRanges of length 7
##      start end width
## [1]      7  15     9
## [2]      9  11     3
## [3]     12  12     1
## [4]     14  18     5
## [5]     22  26     5
## [6]     23  27     5
## [7]     24  28     5
```

```
ir[1:2]

## IRanges of length 2
##      start end width
## [1]      7  15     9
## [2]      9  11     3

ir[width(ir) == 5]

## IRanges of length 4
##      start end width
## [1]     14  18     5
## [2]     22  26     5
## [3]     23  27     5
## [4]     24  28     5
```

Common Operations

- ▶ shift - move ranges by specified amount
- ▶ resize - change width, anchoring start, end or mid flank -
Regions adjacent to start or end

See GRanges paper

Shifting

We could do this the long way

```
ir2 <- IRanges(start(ir) + 5, end(ir) + 5)
```

But a shortcut is provided by IRanges

```
identical(ir2, shift(ir, 5))
```

```
## [1] TRUE
```


Shifting

e.g. sliding windows

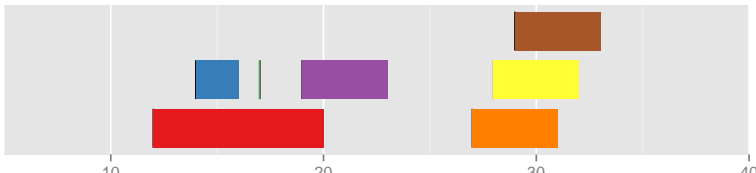
```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7  15     9
## [2]      9  11     3
## [3]     12  12     1
## [4]     14  18     5
## [5]     22  26     5
## [6]     23  27     5
## [7]     24  28     5
```

```
shift(ir, 5)
```

```
## IRanges of length 7
##      start end width
## [1]     12  20     9
## [2]     14  16     3
## [3]     17  17     1
## [4]     19  23     5
## [5]     27  31     5
## [6]     28  32     5
## [7]     29  33     5
```

```
## Object of class "ggbio"
```



Shifting

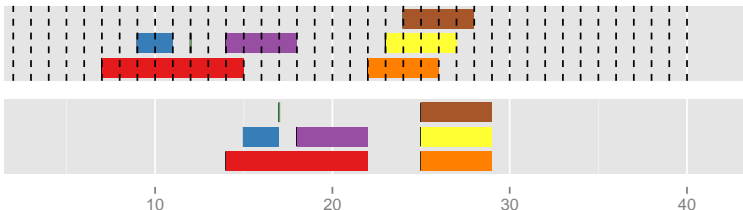
Size of shift doesn't need to be constant

```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7  15      9
## [2]      9  11      3
## [3]     12  12      1
## [4]     14  18      5
## [5]     22  26      5
## [6]     23  27      5
## [7]     24  28      5
```

```
shift(ir, 7:1)
```

```
## IRanges of length 7
##      start end width
## [1]     14  22      9
## [2]     15  17      3
## [3]     17  17      1
## [4]     18  22      5
## [5]     25  29      5
## [6]     25  29      5
## [7]     25  29      5
```



Resize

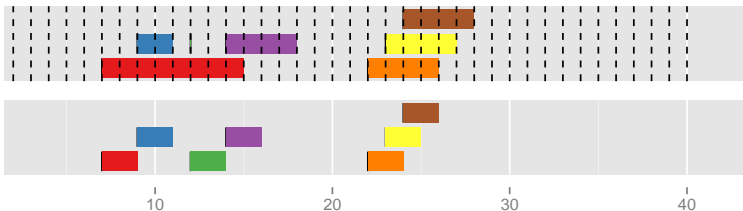
e.g. trimming reads

```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7 15      9
## [2]      9 11      3
## [3]     12 12      1
## [4]     14 18      5
## [5]     22 26      5
## [6]     23 27      5
## [7]     24 28      5
```

```
resize(ir, 3)
```

```
## IRanges of length 7
##      start end width
## [1]      7  9      3
## [2]      9 11      3
## [3]     12 14      3
## [4]     14 16      3
## [5]     22 24      3
## [6]     23 25      3
## [7]     24 26      3
```



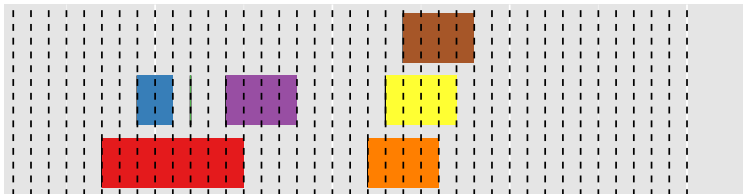
Resize

```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7 15      9
## [2]      9 11      3
## [3]     12 12      1
## [4]     14 18      5
## [5]     22 26      5
## [6]     23 27      5
## [7]     24 28      5
```

```
resize(ir, 3, fix = "end")
```

```
## IRanges of length 7
##      start end width
## [1]     13 15      3
## [2]      9 11      3
## [3]     10 12      3
## [4]     16 18      3
## [5]     24 26      3
## [6]     25 27      3
## [7]     26 28      3
```



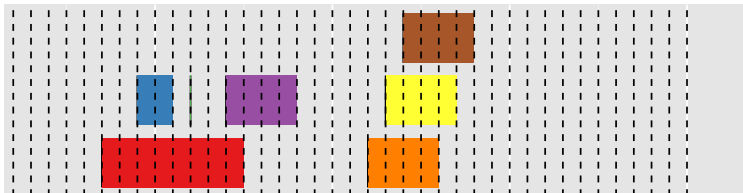
Reducing

```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7  15     9
## [2]      9  11     3
## [3]     12  12     1
## [4]     14  18     5
## [5]     22  26     5
## [6]     23  27     5
## [7]     24  28     5
```

```
reduce(ir)
```

```
## IRanges of length 2
##      start end width
## [1]      7  18    12
## [2]     22  28     7
```



Gaps

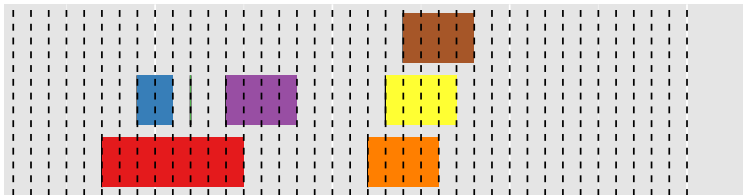
e.g. introns

```
ir

## IRanges of length 7
##      start end width
## [1]      7  15     9
## [2]      9  11     3
## [3]     12  12     1
## [4]     14  18     5
## [5]     22  26     5
## [6]     23  27     5
## [7]     24  28     5
```

```
gaps(ir)
```

```
## IRanges of length 1
##      start end width
## [1]     19  21     3
```



Flanking

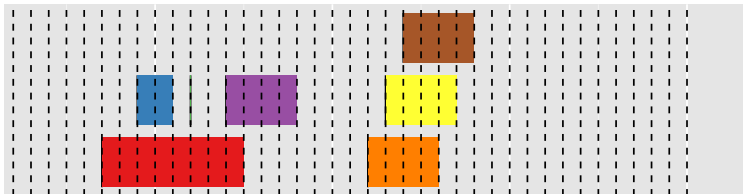
e.g. promoters

```
ir
```

```
## IRanges of length 7
##      start end width
## [1]      7 15      9
## [2]      9 11      3
## [3]     12 12      1
## [4]     14 18      5
## [5]     22 26      5
## [6]     23 27      5
## [7]     24 28      5
```

```
flank(ir, 2)
```

```
## IRanges of length 7
##      start end width
## [1]      5  6      2
## [2]      7  8      2
## [3]     10 11      2
## [4]     12 13      2
## [5]     20 21      2
## [6]     21 22      2
## [7]     22 23      2
```



Coverage

coverage returns a Run Length Encoding - an efficient representation of repeated values

```
cvg <- coverage(ir)
cvg

## integer-Rle of length 28 with 12 runs
##   Lengths: 6 2 4 1 2 3 3 1 1 3 1 1
##   Values  : 0 1 2 1 2 1 0 1 2 3 2 1

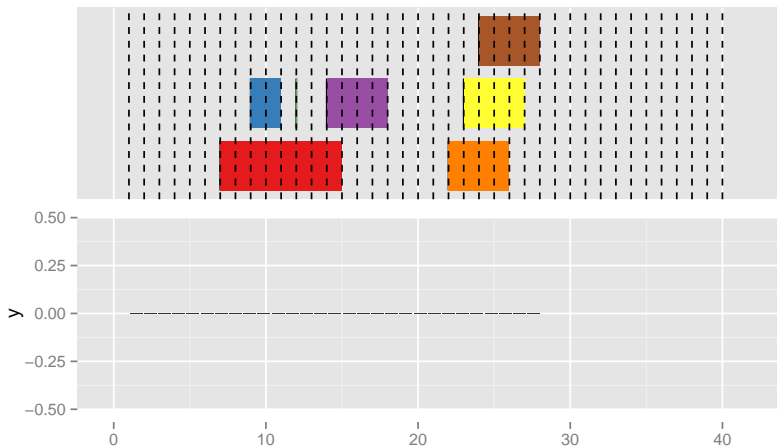
as.vector(cvg[1:12])

##   [1] 0 0 0 0 0 0 0 1 1 2 2 2 2
```



```
## Default use binwidth: range/30
```

```
## Default use binwidth: range/30
```



slice to get peaks

```
ranges(slice(coverage(ir), 2))
```

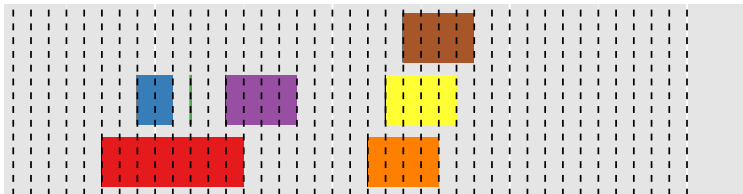
```
## IRanges of length 3  
##      start end width  
## [1]      9  12     4  
## [2]     14  15     2  
## [3]     23  27     5
```

Overlaps...

e.g. counting

```
ir3 <- IRanges(start = c(1, 14, 27), end = c(13,  
18, 30))  
ir3
```

```
## IRanges of length 3  
##      start end width  
## [1]      1  13    13  
## [2]     14  18     5  
## [3]     27  30     4
```



Overlaps

```
query <- ir
subject <- ir3
ov <- findOverlaps(query, subject)
ov
```

```
## Hits of length 7
## queryLength: 7
## subjectLength: 3
##   queryHits subjectHits
##   <integer>   <integer>
## 1         1         1
## 2         1         2
## 3         2         1
## 4         3         1
## 5         4         2
## 6         6         3
## 7         7         3
```

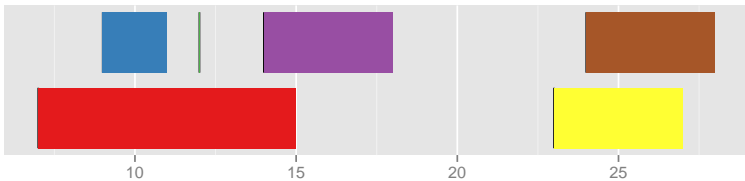
```
query[queryHits(ov)]
```

```
## IRanges of length 7
##      start end width
## [1]      7  15     9
## [2]      7  15     9
## [3]      9  11     3
## [4]     12  12     1
## [5]     14  18     5
## [6]     23  27     5
## [7]     24  28     5
```

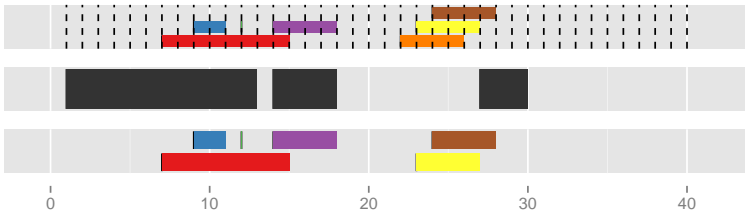
```
subject[subjectHits(ov)]
```

```
## IRanges of length 7
##      start end width
## [1]      1  13    13
## [2]     14  18     5
## [3]      1  13    13
## [4]      1  13    13
## [5]     14  18     5
## [6]     27  30     4
## [7]     27  30     4
```

```
## Object of class "ggbio"
```



```
## NULL
```



Can make the overlap more stringent

```
findOverlaps(query, subject, type = "within")
```

Intersection

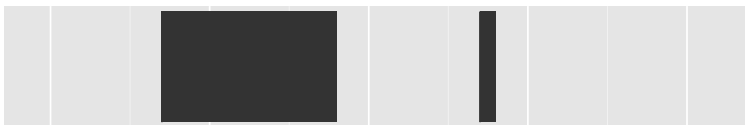
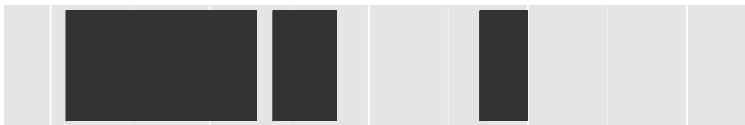
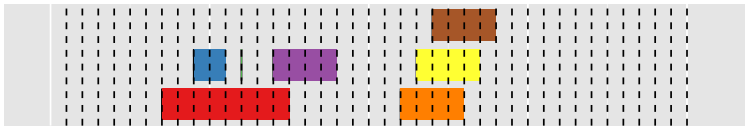
```
intersect(ir, ir3)
```

```
## IRanges of length 2
```

```
##      start end width
```

```
## [1]      7  18    12
```

```
## [2]     27  28     2
```



0

10

20

30

40

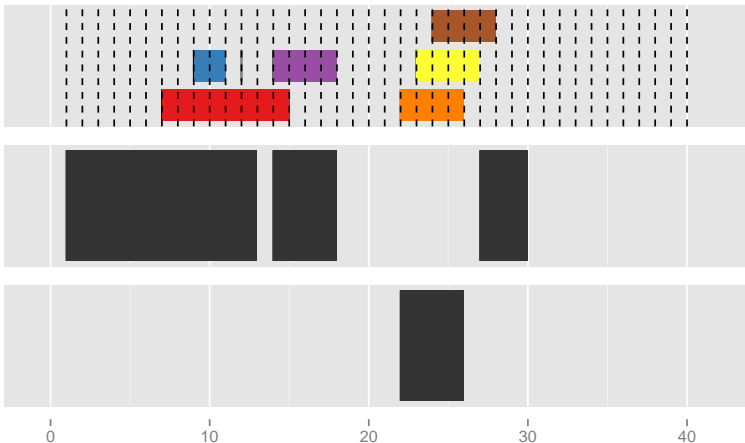
Subtraction

```
setdiff(ir, ir3)
```

```
## IRanges of length 1
```

```
##      start end width
```

```
## [1]    22  26     5
```

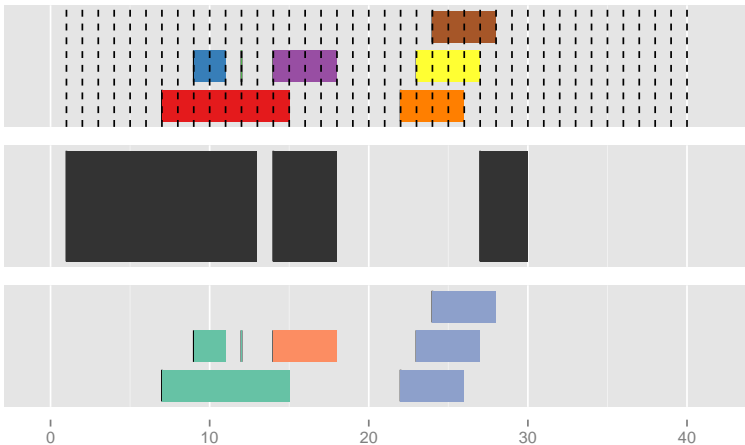


Nearest

e.g. Annotating to features...

```
nearest(ir, ir3)
```

```
## [1] 1 1 1 2 3 3 3
```



GRanges and Genomic Features

- ▶ GRanges provides infrastructure to manipulate genomic intervals in an efficient manner
- ▶ GenomicFeatures provides infrastructure to manipulate databases of genomic features (e.g. transcripts, exons)

GRanges objects are IRanges with additional metadata (e.g. chromosome name, strand)

```
gr <- GRanges(rep("chr1", length(ir)), ranges = ir)
gr
```

```
## GRanges with 7 ranges and 0 metadata columns:
```

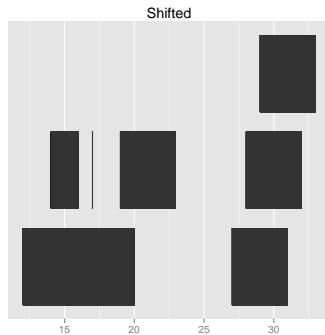
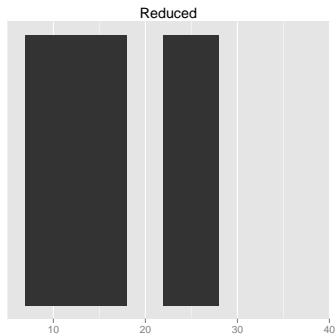
```
##      seqnames      ranges strand
##      <Rle> <IRanges>  <Rle>
## [1]   chr1   [ 7, 15]      *
## [2]   chr1   [ 9, 11]      *
## [3]   chr1  [12, 12]      *
## [4]   chr1  [14, 18]      *
## [5]   chr1  [22, 26]      *
## [6]   chr1  [23, 27]      *
## [7]   chr1  [24, 28]      *
## ---
```

```
## seqlengths:
```

```
##   chr1
##   NA
```

Reducing

```
reduce(gr)  
shift(gr, 5)
```

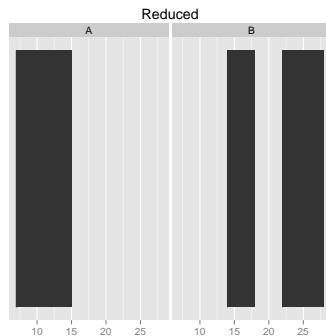
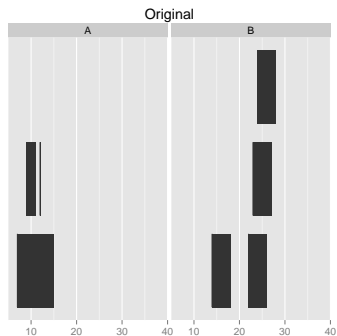


We now define a 'chromosome' for each range

```
gr <- GRanges(c("A", "A", "A", "B", "B",  
               "B", "B"), ranges = ir)  
gr  
  
## GRanges with 7 ranges and 0 metadata columns:  
##           seqnames      ranges strand  
##           <Rle> <IRanges>  <Rle>  
##    [1]          A   [ 7, 15]      *  
##    [2]          A   [ 9, 11]      *  
##    [3]          A  [12, 12]      *  
##    [4]          B  [14, 18]      *  
##    [5]          B  [22, 26]      *  
##    [6]          B  [23, 27]      *  
##    [7]          B  [24, 28]      *  
##    ---  
##    seqlengths:  
##           A  B  
##        NA NA
```

Reducing

```
reduce(gr)
```



```
gr
```

```
## GRanges with 7 ranges and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges>  <Rle>
## [1]      A [ 7, 15]      *
## [2]      A [ 9, 11]      *
## [3]      A [12, 12]      *
## [4]      B [14, 18]      *
## [5]      B [22, 26]      *
## [6]      B [23, 27]      *
## [7]      B [24, 28]      *
## ---
##      seqlengths:
##      A      B
##      NA NA
```

```
gr2 <- GRanges("A", ir3)
```

```
gr2
```

```
## GRanges with 3 ranges and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges>  <Rle>
## [1]      A [ 1, 13]      *
## [2]      A [14, 18]      *
## [3]      A [27, 30]      *
## ---
##      seqlengths:
##      A
##      NA
```

```
intersect(gr, gr2)
```

```
## GRanges with 1 range and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges>  <Rle>
## [1]      A [ 7, 15]      *
## ---
##      seqlengths:
##      A      B
```

```
gr
```

```
## GRanges with 7 ranges and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges> <Rle>
## [1]      A [ 7, 15]      *
## [2]      A [ 9, 11]      *
## [3]      A [12, 12]      *
## [4]      B [14, 18]      *
## [5]      B [22, 26]      *
## [6]      B [23, 27]      *
## [7]      B [24, 28]      *
## ---
##      seqlengths:
##      A  B
##      NA NA
```

```
gr3 <- GRanges("B", ir3)
```

```
gr3
```

```
## GRanges with 3 ranges and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges> <Rle>
## [1]      B [ 1, 13]      *
## [2]      B [14, 18]      *
## [3]      B [27, 30]      *
## ---
##      seqlengths:
##      B
##      NA
```

```
intersect(gr, gr3)
```

```
## GRanges with 2 ranges and 0 metadata
##      seqnames      ranges strand
##      <Rle> <IRanges> <Rle>
## [1]      B [14, 18]      *
## [2]      B [27, 28]      *
## ---
##      seqlengths:
```


Naming conventions

Sometimes (well, often) different naming conventions are used for chromosome names

```
seqlevels(gr)

## [1] "A" "B"

gr <- renameSeqlevels(gr, c(A = "chr1", B = "chr2"))
gr

## GRanges with 7 ranges and 0 metadata columns:
##           seqnames      ranges strand
##           <Rle> <IRanges>  <Rle>
## [1]      chr1    [ 7, 15]      *
## [2]      chr1    [ 9, 11]      *
## [3]      chr1   [12, 12]      *
## [4]      chr2   [14, 18]      *
## [5]      chr2   [22, 26]      *
## [6]      chr2   [23, 27]      *
## [7]      chr2   [24, 28]      *
## ---
```

Assigning metadata

GRanges objects can also have metadata associated with them

```
meta <- data.frame(SomeVals = runif(n = length(gr),  
  100, 200), OtherVals = runif(n = length(gr),  
  0, 1), SomeChars = sample(LETTERS, length(gr)))  
values(gr) <- meta
```

```
gr[1:5]
```

```
## GRanges with 5 ranges and 3 metadata columns:
```

```
##      seqnames      ranges strand |
##      <Rle> <IRanges> <Rle> |
## [1]      chr1  [ 7, 15]      * |
## [2]      chr1  [ 9, 11]      * |
## [3]      chr1 [12, 12]      * |
## [4]      chr2 [14, 18]      * |
## [5]      chr2 [22, 26]      * |
##      SomeVals OtherVals SomeChars
##      <numeric> <numeric> <factor>
## [1]      145.6   0.81418      0
## [2]      125.4   0.98168      G
## [3]      105.7   0.03634      U
## [4]      143.5   0.56741      W
## [5]      177.1   0.40172      X
## ---
##      seqlengths:
##      chr1 chr2
##      NA   NA
```

```
gr[values(gr)$SomeVals > 150]
```

```
## GRanges with 2 ranges and 3 metadata columns:
```

```
##      seqnames      ranges strand |  
##      <Rle> <IRanges> <Rle> |  
## [1]      chr2  [22, 26]      * |  
## [2]      chr2  [24, 28]      * |  
##      SomeVals OtherVals SomeChars  
##      <numeric> <numeric> <factor>  
## [1]      177.1      0.4017          X  
## [2]      198.4      0.4033          N  
## ---  
## seqlengths:  
##      chr1 chr2  
##      NA  NA
```

```
gr[order(values(gr)$OtherVals)]
```

```
## GRanges with 7 ranges and 3 metadata columns:
```

```
##      seqnames      ranges strand |
```

```
##      <Rle> <IRanges>  <Rle> |
```

```
## [1]      chr1  [12, 12]      * |
```

```
## [2]      chr2  [22, 26]      * |
```

```
## [3]      chr2  [24, 28]      * |
```

```
## [4]      chr2  [23, 27]      * |
```

```
## [5]      chr2  [14, 18]      * |
```

```
## [6]      chr1  [ 7, 15]      * |
```

```
## [7]      chr1  [ 9, 11]      * |
```

```
##      SomeVals OtherVals SomeChars
```

```
##      <numeric> <numeric>  <factor>
```

```
## [1]      105.7    0.03634      U
```

```
## [2]      177.1    0.40172      X
```

```
## [3]      198.4    0.40332      N
```

```
## [4]      112.9    0.45705      V
```

```
## [5]      143.5    0.56741      W
```

```
## [6]      145.6    0.81418      O
```

```
## [7]      125.4    0.98168      G
```

```
## ---
```

```
##      seqlengths:
```

```
##      chr1 chr2
```

GRanges can be split according to metadata

```
split(gr, values(gr)$SomeChars)

## GRangesList of length 7:
## $G
## GRanges with 1 range and 3 metadata columns:
##      seqnames      ranges strand |
##      <Rle> <IRanges> <Rle> |
## [1]      chr1    [9, 11]      * |
##      SomeVals OtherVals SomeChars
##      <numeric> <numeric> <factor>
## [1]      125.4      0.9817          G
##
## $N
## GRanges with 1 range and 3 metadata columns:
##      seqnames      ranges strand |
## [1]      chr2 [24, 28]      * |
##      SomeVals OtherVals SomeChars
## [1]      198.4      0.4033          N
##
## $O
## GRanges with 1 range and 3 metadata columns:
##      seqnames      ranges strand |
## [1]      chr1 [7, 15]      * |
```

Summary values can be computed

```
lapply(split(gr, values(gr)$SomeChars), function(x) mean(values(x)$Some
```

```
## $G
## [1] 125.4
##
## $N
## [1] 198.4
##
## $O
## [1] 145.6
##
## $U
## [1] 105.7
##
## $V
## [1] 112.9
##
## $W
## [1] 143.5
##
## $X
## [1] 177.1
```

Reading alignments

We will assume that the sequencing reads have been aligned and that we are interested in processing the alignments. Rsamtools provides an interface for doing this. But we will use the `readGappedAlignments` tool in `GenomicRanges` which extracts the essential information from the bam file.

```
bam <- readGappedAlignments(mybam, use.name = TRUE)
```


The result looks a lot like a GRanges object. In fact, a lot of the same operations can be use

```
bam[1:4]
```

```
## GappedAlignments with 4 alignments and 0 metadata columns:
```

```
##           seqnames strand      cigar    qwidth
##           <Rle>  <Rle> <character> <integer>
## SRR031715.1138209   chr4      +      37M       37
## SRR031714.776678    chr4      -      37M       37
## SRR031715.3258011   chr4      -      37M       37
## SRR031715.4791418   chr4      +      37M       37
##           start      end      width      ngap
##           <integer> <integer> <integer> <integer>
## SRR031715.1138209    169      205       37        0
## SRR031714.776678    184      220       37        0
## SRR031715.3258011    187      223       37        0
## SRR031715.4791418    193      229       37        0
```

```
## ---
```

```
## seqlengths:
```

```
##      chr2L      chr2R      chr3L ...      chrM      chrX      chrYHet
## 23011544 21146708 24543557 ... 19517 22422827 347038
```

Querying alignments

```
table(strand(bam))
```

```
##
```

```
##      +      -      *
```

```
## 84871 90475      0
```

```
summary(width(bam))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```

```
##         37        37         37         59         37    19400
```

```
range(start(bam))
```

```
## [1]      169 1351760
```

```
cigar(bam)[1:10]
```

```
## [1] "37M" "37M" "37M" "37M" "37M" "37M" "37M" "37M" "37M" "37M"
```

```
## [10] "37M"
```

Manipulation of reads

aligned reads can be manipulated using functions from IRanges

```
shift(ranges(bam), 10)
```

```
## IRanges of length 175346
```

##		start	end	width	names
##	[1]	179	215	37	SRR031715.1138209
##	[2]	194	230	37	SRR031714.776678
##	[3]	197	233	37	SRR031715.3258011
##	[4]	203	239	37	SRR031715.4791418
##	[5]	336	372	37	SRR031715.1138209
##
##	[175342]	1349718	1349754	37	SRR031714.1650928
##	[175343]	1349848	1349884	37	SRR031714.1650928
##	[175344]	1351650	1351686	37	SRR031714.5192891
##	[175345]	1351650	1351686	37	SRR031715.2351056
##	[175346]	1351770	1351806	37	SRR031714.864195

Manipulation of reads

aligned reads can be manipulated using functions from IRanges

```
flank(ranges(bam), 100, both = T)
```

```
## IRanges of length 175346
```

```
##           start      end width      names
## [1]           69      268   200 SRR031715.1138209
## [2]           84      283   200  SRR031714.776678
## [3]           87      286   200 SRR031715.3258011
## [4]           93      292   200 SRR031715.4791418
## [5]          226      425   200 SRR031715.1138209
## ...           ...      ...   ...           ...
## [175342] 1349608 1349807   200 SRR031714.1650928
## [175343] 1349738 1349937   200 SRR031714.1650928
## [175344] 1351540 1351739   200 SRR031714.5192891
## [175345] 1351540 1351739   200 SRR031715.2351056
## [175346] 1351660 1351859   200  SRR031714.864195
```

```
coverage(ranges(bam))
```

```
## integer-Rle of length 1351796 with 104286 runs
```

```
##   Lengths: 168   15    3    6   13 ... 1765   37   83   37
```

Region subset - the naive way

```
bam[start(bam) < 20100 & end(bam) > 20000, ]
```

```
## GappedAlignments with 14 alignments and 0 metadata columns:
```

```
##           seqnames strand      cigar    qwidth
##           <Rle>   <Rle> <character> <integer>
## SRR031714.4100693   chr4      +   31M7704N6M      37
## SRR031715.5248298   chr4      +   29M7704N8M      37
## SRR031714.4092638   chr4      -      37M          37
## SRR031714.4275537   chr4      -      37M          37
## SRR031715.1315719   chr4      -      37M          37
## ...               ...      ...      ...          ...
## SRR031715.3358559   chr4      +      37M          37
## SRR031715.4831822   chr4      +      37M          37
## SRR031715.4459351   chr4      +      37M          37
## SRR031715.2716654   chr4      -      37M          37
## SRR031715.1552693   chr4      +      37M          37
##           start      end      width      ngap
##           <integer> <integer> <integer> <integer>
## SRR031714.4100693   13660    21400    7741      1
## SRR031715.5248298   13662    21402    7741      1
## SRR031714.4092638   19968    20004     37        0
## SRR031714.4275537   19968    20004     37        0
```

The smart way

```
gr <- GRanges("chr4", IRanges(start = 20000, end = 20100))
gr

## GRanges with 1 range and 0 metadata columns:
##      seqnames      ranges strand
##      <Rle>        <IRanges> <Rle>
## [1]      chr4 [20000, 20100]      *
## ---
##      seqlengths:
##      chr4
##      NA
```

```
findOverlaps(gr, bam)
```

```
## Hits of length 12
```

```
## queryLength: 1
```

```
## subjectLength: 175346
```

```
##      queryHits subjectHits
##      <integer>   <integer>
##  1             1         6699
##  2             1         6700
##  3             1         6701
##  4             1         6702
##  5             1         6703
##  ...           ...         ...
##  8             1         6706
##  9             1         6707
## 10             1         6708
## 11             1         6709
## 12             1         6710
```

```
bam[subjectHits(findOverlaps(gr, bam))]
```

```
## GappedAlignments with 12 alignments and 0 metadata columns:
```

```
##           seqnames strand      cigar  qwidth
##           <Rle>  <Rle> <character> <integer>
## SRR031714.4092638   chr4      -      37M      37
## SRR031714.4275537   chr4      -      37M      37
## SRR031715.1315719   chr4      -      37M      37
## SRR031715.1502533   chr4      -      37M      37
## SRR031714.336402    chr4      -      37M      37
## ...                ...      ...      ...      ...
## SRR031715.3358559   chr4      +      37M      37
## SRR031715.4831822   chr4      +      37M      37
## SRR031715.4459351   chr4      +      37M      37
## SRR031715.2716654   chr4      -      37M      37
## SRR031715.1552693   chr4      +      37M      37
##           start      end      width      ngap
##           <integer> <integer> <integer> <integer>
## SRR031714.4092638   19968   20004      37      0
## SRR031714.4275537   19968   20004      37      0
## SRR031715.1315719   19968   20004      37      0
## SRR031715.1502533   19968   20004      37      0
## SRR031714.336402    19971   20007      37      0
## ...                ...      ...      ...      ...
```


Alternative

```
bam.sub <- bam[bam %over% gr]
```

```
bam.sub
```

```
## GappedAlignments with 12 alignments and 0 metadata columns:
```

```
##               seqnames strand      cigar    qwidth
##               <Rle>  <Rle> <character> <integer>
## SRR031714.4092638   chr4      -      37M        37
## SRR031714.4275537   chr4      -      37M        37
## SRR031715.1315719   chr4      -      37M        37
## SRR031715.1502533   chr4      -      37M        37
## SRR031714.336402    chr4      -      37M        37
## ...                ...      ...      ...      ...
## SRR031715.3358559   chr4      +      37M        37
## SRR031715.4831822   chr4      +      37M        37
## SRR031715.4459351   chr4      +      37M        37
## SRR031715.2716654   chr4      -      37M        37
## SRR031715.1552693   chr4      +      37M        37
##               start      end      width      ngap
##               <integer> <integer> <integer> <integer>
## SRR031714.4092638   19968   20004      37        0
## SRR031714.4275537   19968   20004      37        0
## SRR031715.1315719   19968   20004      37        0
```

Read subset of regions

quicker still, we can get the reads directly from the bam file. The region to be read can be specified using the param argument.

```
system.time(bam.sub <- readGappedAlignments(file = mybam, use.names = T,  
      param = ScanBamParam(which = gr)))
```

```
##      user  system elapsed  
##    0.090    0.013    0.136
```

Recap

- ▶ Ranges can be used to represent continuous regions
- ▶ GRanges are special ranges with extra biological context
- ▶ GRanges can be manipulated, compared, overlapped with each other
- ▶ Aligned reads can be represented by Ranges
- ▶ Genome and sequencing reads can be represented efficiently by Biostrings
- ▶ The genome can also be accessed using Ranges

To be continued...

- ▶ Tomorrow, we will go through an RNA-seq analysis workflow
- ▶ We will then look how to relate the regions of interest back to the genome

This talk was brought to you by...

```
sessionInfo()

## R version 3.0.1 (2013-05-16)
## Platform: x86_64-apple-darwin10.8.0 (64-bit)
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] grid      parallel  stats      graphics  grDevices
## [6] utils     datasets  methods    base
##
## other attached packages:
## [1] gridExtra_0.9.1
## [2] reshape_0.8.4
## [3] plyr_1.8
## [4] BSgenome.Hsapiens.UCSC.hg19_1.3.19
## [5] BiocInstaller_1.10.4
## [6] TxDb.Hsapiens.UCSC.hg19.knownGene_2.9.2
## [7] BSgenome.Hsapiens.UCSC.hg18_1.3.19
## [8] Gviz_1.4.4
## [9] ...
```