

Bioconductor for Sequence Analysis

Martin T. Morgan*

27-28 February 2014

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Common file formats The 'big data' component of high-throughput sequence analyses seems to be a tangle of transformations between file types; common files are summarized in Table~1. FASTQ and BAM (sometimes CRAM) files are the primary formats for representing raw sequences and their alignments. VCF are used to summarize called variants in DNA-seq; BED and sometimes WIG files are used to represent ChIP and other regulatory peaks and 'coverage'. GTF / GFF files are important for providing feature annotations, e.g., of exons organization into transcripts and genes.

1 Short reads: FASTQ files

1.1 FASTQ files

The Illumina GAI and HiSeq technologies generate sequences by measuring incorporation of florescent nucleotides over successive PCR cycles. These sequencers produce output in a variety of formats, but *FASTQ* is ubiquitous. Each read is represented by a record of four components:

```
## @ERR127302.200 HWI-EAS350_0441:1:1:1196:1175#0/2
## CTCAGCGACACCAATCTCCTTGAAGTGCACGTGGACAGGCCCTCCGCCGACGGCGGGAGTTGGGGAG
## +
## B<BGGADEAB>73A/(?BD8EBAAA<?>>BAAA<+*<8:,-5&E>??;B#####
```

*mtmorgan@fhcrc.org

Table 1: Common [file types](#) and *Bioconductor* packages used for input.

File	Description	Package
FASTQ	Unaligned sequences: identifier, sequence, and encoded quality score tuples	ShortRead
BAM	Aligned sequences: identifier, sequence, reference sequence name, strand position, cigar and additional tags	Rsamtools
VCF	Called single nucleotide, indel, copy number, and structural variants, often compressed and indexed (with Rsamtools <code>bgzip</code> , <code>indexTabix</code>)	VariantAnnotation
GFF, GTF	Gene annotations: reference sequence name, data source, feature type, start and end positions, strand, etc.	rtracklayer
BED	Range-based annotation: reference sequence name, start, end coordinates.	rtracklayer
WIG, bigWig	'Continuous' single-nucleotide annotation.	rtracklayer
2bit	Compressed FASTA files with 'masks'	

The first and third lines (beginning with @ and + respectively) are unique identifiers. The identifier produced by the sequencer typically includes a machine id followed by colon-separated information on the lane, tile, x, and y coordinate of the read. The example illustrated here also includes the SRA accession number, added when the data was submitted to the archive. The machine identifier could potentially be used to extract information about batch effects. The spatial coordinates (lane, tile, x, y) are often used to identify optical duplicates; spatial coordinates can also be used during quality assessment to identify artifacts of sequencing, e.g., uneven amplification across the flow cell, though these spatial effects are rarely pursued.

The second and fourth lines of the FASTQ record are the nucleotides and qualities of each cycle in the read. This information is given in 5' to 3' orientation as seen by the sequencer. A letter N in the sequence is used to signify bases that the sequencer was not able to call. The fourth line of the FASTQ record encodes the quality (confidence) of the corresponding base call. The quality score is encoded following one of several conventions, with the general notion being that letters later in the visible ASCII alphabet

```
## ! " # $ % & ' ( ) * + , - . / 0 1 2 3 4 5 6 7 8 9 : ; < = >
## 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
## ? @ A B C D E F G H I J
## 30 31 32 33 34 35 36 37 38 39 40 41
```

are of higher quality. Letters map to numbers, and numbers correspond (most commonly) to $-10 \log_{10} p$. In the encoding above, I corresponds to a phred score of 40, hence $p = 0.0001$. Both the sequence and quality scores may span multiple lines.

1.2 Basic Manipulations of a FASTQ file

Exercise 1

Here we take a first look at FASTQ files from the ArrayExpress repository E-MTAB-1147¹ [1].

- Load the [ShortRead](#) and [BiocParallel](#) packages.
- Create a character vector `dirPath` to the 'bigdata/fastq' directory containing the files 'ERR127302.1.fastq.gz', 'ERR127302.2.fastq.gz'.
- Read in a representative sample from 'ERR127302.1.fastq.gz'
- simple manipulations on a FASTQ file -id, reads and quality
- summarize use of nucleotides at each cycle
- Analyzing nucleotides per cycle, gc content and quality score per cycle
- Construct histogram of the GC content of individual reads

¹<http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1147/>

```
library(ShortRead)
library(BiocParallel)
```

```
dirPath <- "~/bigdata/fastq"
sampler <- FastqSampler(file.path(dirPath, "ERR127302_1.fastq.gz"), 1000000)
reads <- yield(sampler)
```

```
# outputs read ids as a list as BStringSet
head( id(reads) )

##      A BStringSet instance of length 6
##      width seq
## [1] 55 ERR127302.26848518 HWI-EAS350_0441:1:109:18347:2925#0/1
## [2] 54 ERR127302.25150153 HWI-EAS350_0441:1:103:7039:6996#0/1
## [3] 53 ERR127302.15238353 HWI-EAS350_0441:1:63:2526:7358#0/1
## [4] 53 ERR127302.19869862 HWI-EAS350_0441:1:82:5829:7822#0/1
## [5] 54 ERR127302.19322838 HWI-EAS350_0441:1:80:1683:14418#0/1
## [6] 54 ERR127302.5738751 HWI-EAS350_0441:1:23:12911:18925#0/1
```

```
# outputs read sequences as a list as DNAStringSet
head(sread(reads) )

##      A DNAStringSet instance of length 6
##      width seq
## [1]      72 AATGAAGCAAACATTTTCTAACACTACGAACATCAGAATTACAGTGAAATACAGCATTTTTCCTATGCTTG
## [2]      72 GTTCGGTGTCCTTTATGTCAACAAGGACGCTATCGCTGATCTTGTGCAGGTGTTCAATAGCAACACGAGCAG
## [3]      72 CTTGGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGCAGCTACCAAGAGGCTCA
## [4]      72 CTTTATCAAGTGGGCAGCACTCAACTCAATCTTCCCACCCTCATTGATGTCAAAGTCCAATTCAATGTTAC
## [5]      72 CTGCGCTCGTGGACACCTGCCACCGGGCCATGAGGACCACCTTCCTCCACATCTCCAAGACCCCCCAGGAGA
## [6]      72 GTCCATATCACATTGGCAGCAGTGTGGAATTTGATTGGTGTGCTGTCTCTAGTATCCGCACACTGCGTCAAC
```

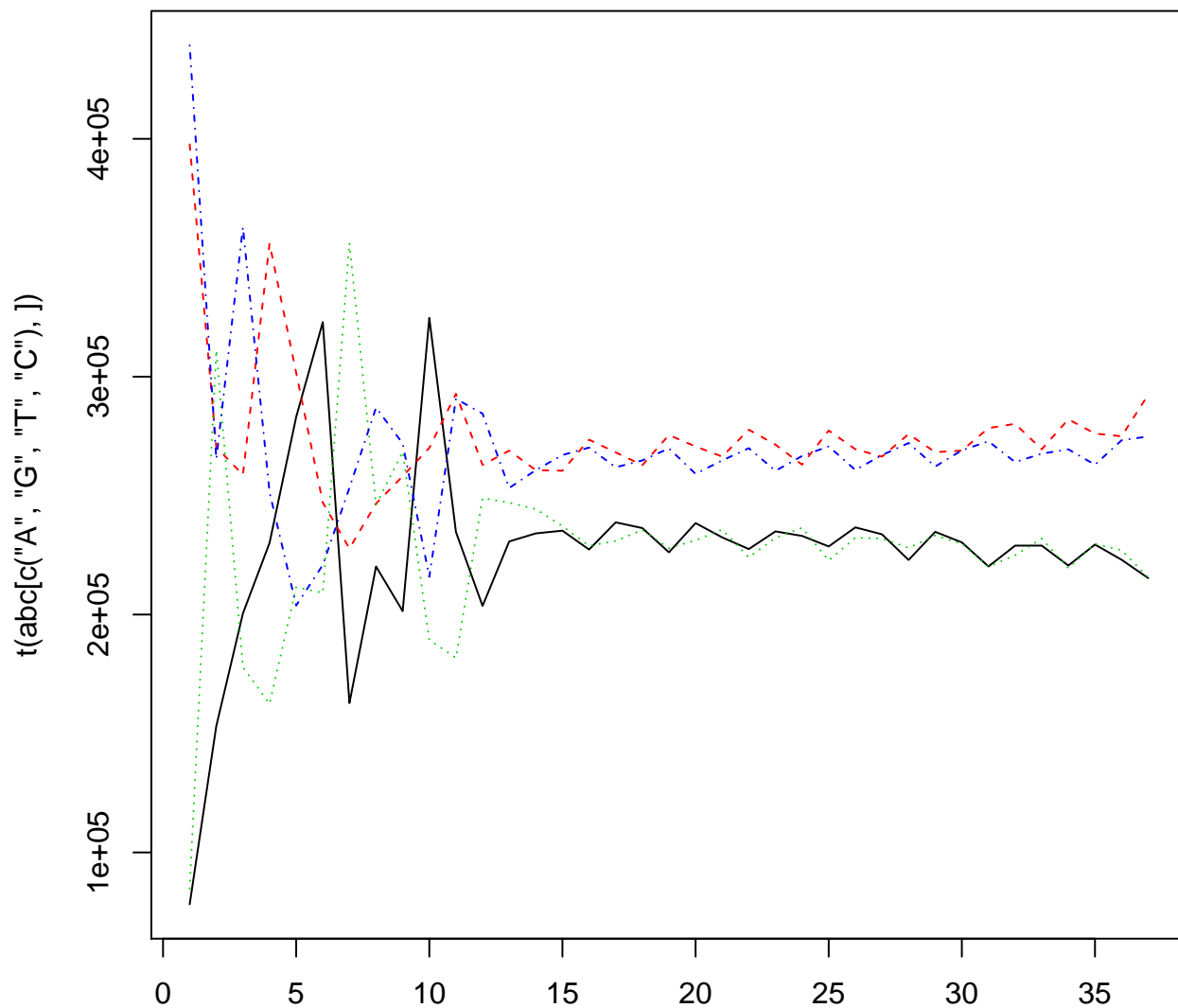
```
# outputs list of quality scores as BStringSet
head(quality(reads))

## class: FastqQuality
## quality:
##      A BStringSet instance of length 6
##           width seq
## [1]    72 BIIIIIHHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIHIIIIIIHHIFIDIHB
## [2]    72 IIIIIIIIIIIIIIIHIIIIIIIIIIHIGIIIIIIIIIIIHFQGGGGGIIIIIDIIIGFGIIDIQHEGD
## [3]    72 HHHHBHHFFGDBGEGGBGGGDGDG<GGEgg>GDGD>G@GDGHFHHFE@DGGB>D@D5; :==BGDG8; :B::DA
## [4]    72 EEEE*GGGGGIIIIIIIIIIIIIHIIIIIIIIIIIIIIIIIIIIIIIIHGIIDIIIIHIIIBIIHHIE
## [5]    72 HHHHHHHHHHHHGHHHGHHHHHHHHHHGHHGHHHHHHHHHHHHHHHD<GFBHHHHGHCHHFDDB@DDE
## [6]    72 HHHHHHHHHHHHGHHHHGBHHGGDBGGGGGGHHHHHHHDHHCHEGHEHHHHHHHHHHHHHHHHHDHGHGFCF
```

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

##           cycle
```

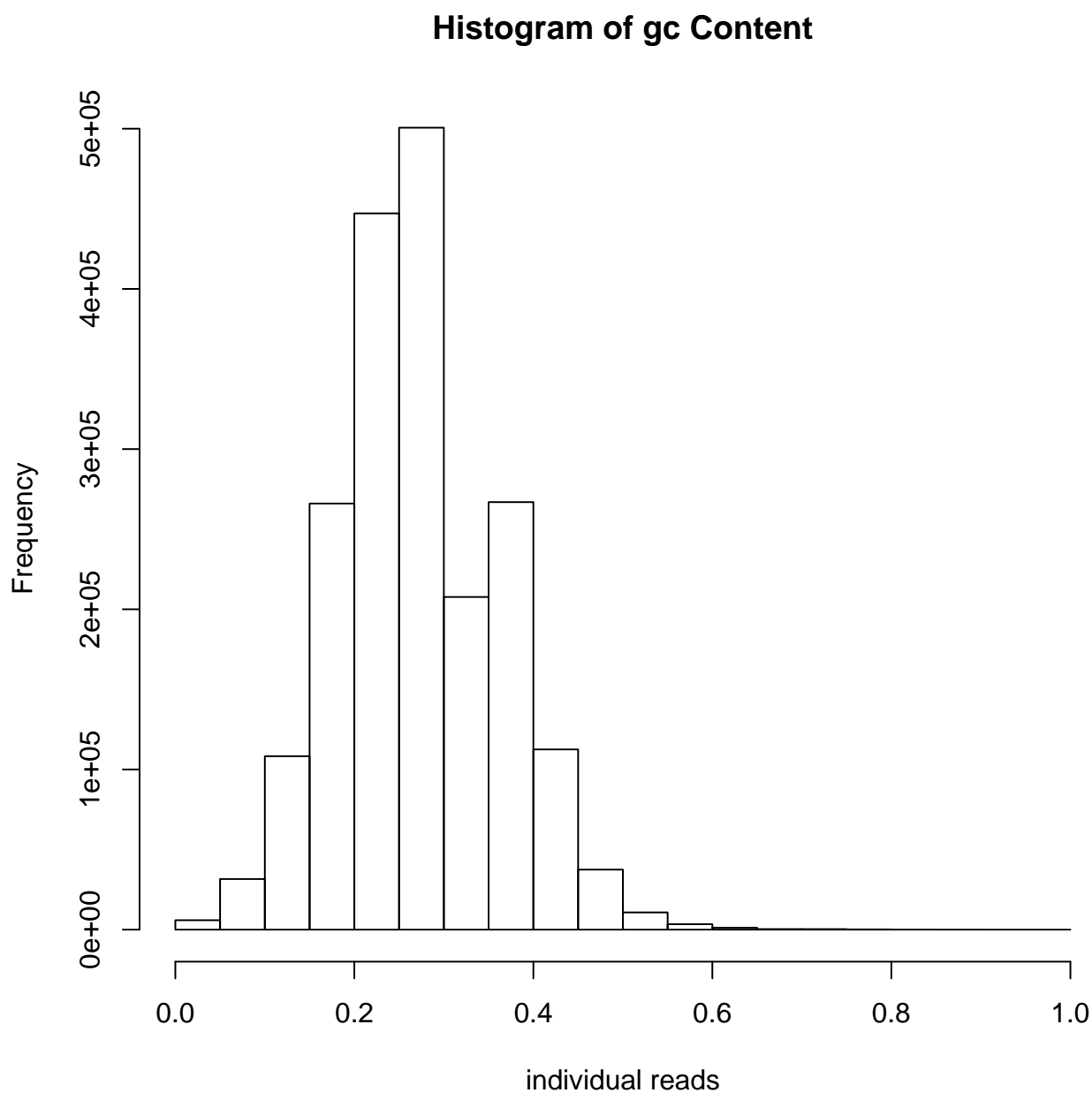
```
## alphabet  [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8]
##          A  78194 153156 200468 230120 283083 322913 162766 220205
##          C  439302 265338 362839 251434 203787 220855 253245 287010
##          G  397671 270342 258739 356003 301640 247090 227811 246684
##          T   84833 311164 177954 162443 211490 209142 356178 246101
matplot(t(abc[c("A","G","T","C"),]), type="l")
```



A histogram of the GC content of individual reads is obtained with:

```
alf0 <- alphabetFrequency(sread(reads), as.prob=TRUE)
hist(alf0[,c("G", "C")],
```

```
main = "Histogram of gc Content",  
xlab="individual reads" )
```



1.3 Quality assessment

Exercise 2

Here we create a quality assessment report of FASTQ files from the ArrayExpress repository E-MTAB-1147² [1].

²<http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1147/>

- Create a quality report for these two files using the `ShortRead::qa` function, e.g., `qa <- qa(dirPath, "ERR*", type="fastq")`.
- View the quality report in a web browser with `browseURL(report(qa))`
- View the QA report for all fastq files in the full experiment. Do this by loading the prepared data object 'E-MTAB-1147-qa_report.Rda'. Discuss the meaning of each plot with your neighbor. What technology arti

Solution: Create the QA report from two sample files

```
qa <- qa(dirPath, "ERR*", type="fastq")
```

View the report

```
browseURL(report(qa))
```

Load the report for all lanes

```
(load(file.path(dirPath, "E-MTAB-1147-qa_report.Rda")))  
## [1] "qa"
```

View the report

```
browseURL(report(qa))
```

1.4 Trimming

Exercise 3

This exercise explores trimming, then applies a trimming filter to several FASTQ files.

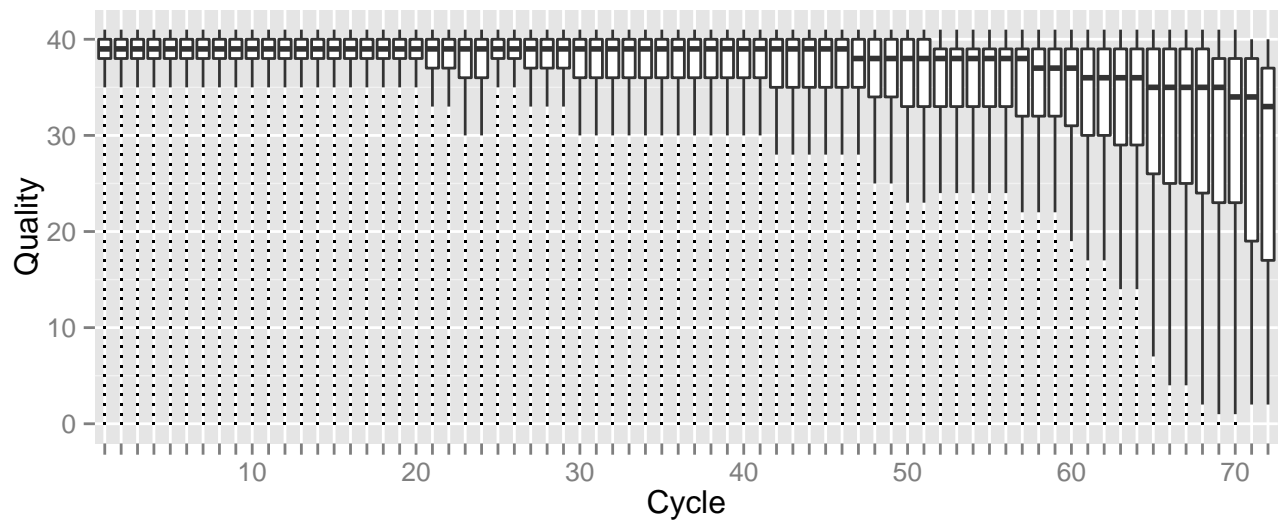
Start by loading the BiocIntro package

```
library(BiocIntro)
```

- Create a character vector pointing to a FASTQ file, `f1 <- file.path(dirPath, "ERR127302_1.fastq.gz")`
- Load a random sample of 100,000 reads from the FASTQ file, using `fq <- FastqSampler()` and `srq <- yield(fq)`
- Plot a histogram of qualities as a function of cycle, `plotByCycle(srq)`.
- Look at how qualities are encoded using `encoding(quality(srq))`.
- Trim reads after the first 3 nucleotides with average quality less than 20 (encoding "5") using `trimTails(srq, 3, "5")`

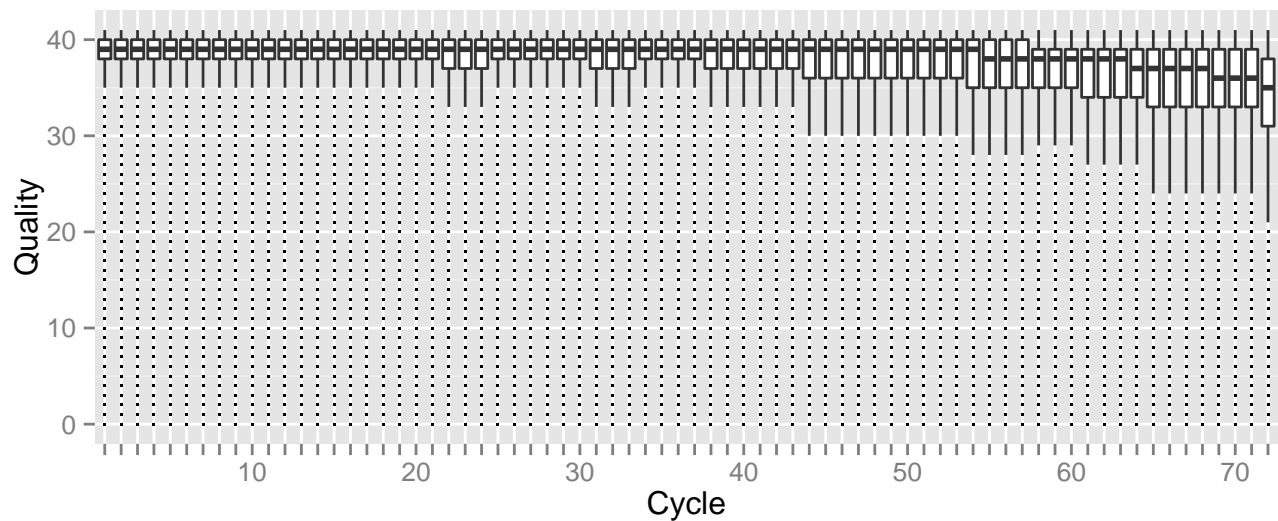
Solution: Load a sample of 100,000 reads and visualize their quality

```
f1 <- file.path(dirPath, "ERR127302_1.fastq.gz")  
fq <- FastqSampler(f1, 100000)  
srq <- yield(fq)  
srq  
  
## class: ShortReadQ  
## length: 100000 reads; width: 72 cycles  
  
plotByCycle(quality(srq))
```



Trim the reads and visualize qualities

```
trimmed <- trimTails(srq, 3, "5")
plotByCycle(quality(trimmed))
```



Exercise 4

(Optional) This exercise trims all reads using our trimming function.

- List the full path to all fastq files using `fls <- dir(dirPath, pattern="fastq.gz", full=TRUE)`.
- Create destination files for each source file, using `destinations <- sub("fastq.gz", "trimmed.fastq", fls)`
- Trim reads as before, but use the file paths and destinations as arguments, `trimTails(fl, 3, "5", FALSE, destinations=destinations)`.

Solution: Identify relevant files

Map the file names to destinations

Perform the trimming

```
trimTails(fls, 2, "5", destinations=destinations)
```

2.1 BAM files

Alignment formats Most main-stream aligners produce output in SAM (text-based) or BAM format. A SAM file is a text file, with one line per aligned read, and fields separated by tabs. Here is an example of a single SAM line, split into fields.

Fields in a SAM file are summarized in Table~2. We recognize from the FASTQ file the identifier string, read sequence and quality. The alignment is to a chromosome 'seq1' starting at position 1. The strand of alignment is encoded in the 'flag' field. The alignment record also includes a measure of mapping quality, and a CIGAR string describing the nature of the alignment. In this case, the CIGAR is 36M, indicating that the alignment consisted of 36 Matches or mismatches, with no indels or gaps; indels are represented by I and D; gaps (e.g., from alignments spanning introns) by N.

BAM files encode the same information as SAM files, but in a format that is more efficiently parsed by software; BAM files are the primary way in which aligned reads are imported in to *R*.

Table 2: Fields in a SAM record. From <http://samtools.sourceforge.net/samtools.shtml>

Field	Name	Value
1	QNAME	Query (read) NAME
2	FLAG	Bitwise FLAG, e.g., strand of alignment
3	RNAME	Reference sequence NAME
4	POS	1-based leftmost POSition of sequence
5	MAPQ	MAPping Quality (Phred-scaled)
6	CIGAR	Extended CIGAR string
7	MRNM	Mate Reference sequence NaMe
8	MPOS	1-based Mate POSition
9	ISIZE	Inferred insert SIZE
10	SEQ	Query SEQUENCE on the reference strand
11	QUAL	Query QUALity
12+	OPT	OPTional fields, format TAG:VTYPE:VALUE

2.2 Gapped alignments in R

The `readGAlignments` function from the [GenomicAlignments](#) package reads essential information from a BAM file in to R. The result is an instance of the *GappedAlignments* class. The *GappedAlignments* class has been designed to allow useful manipulation of many reads (e.g., 20 million) under moderate memory requirements (e.g., 4 GB).

Exercise 5

This exercise explores the GappedAlignments class.

- Load the [RNAseqData.HNRNPC.bam.chr14](#) and retrieve the names of the BAM files it contains. These BAM files are subsets of a larger experiment.
- Read one BAM file in to R using `readGAlignments`. How many reads are there? What do the first few records look like?
- Use the `strand` accessor and the standard R function `table` to tabulate the number of reads on the plus and minus strand. Use the `width` and `cigar` accessors to summarize the aligned width and to explore the alignment cigars.
- The `readGAlignments` function takes an additional argument, `param`, allowing the user to specify regions of the BAM file (e.g., known gene coordinates) from which to extract alignments, and other data to be extracted from the BAM file. Create a `ScanBamParam` object with argument `what="seq"`, and use this to input the read sequences as well as basic alignment information.
- With larger BAM files we often want to iterate through the file in chunks. Do this by creating a `BamFile` from a file path, specifying a `yieldSize`. Then write a short loop that uses `readGAlignments` to input successive chunks until there are no more records left.

Solution: Load the experiment data library and read in one file, discovering the number of reads present

```
library(GenomicAlignments)
library(RNAseqData.HNRNPC.bam.chr14)
fls <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
basename(fls)

## [1] "ERR127306_chr14.bam" "ERR127307_chr14.bam" "ERR127308_chr14.bam"
## [4] "ERR127309_chr14.bam" "ERR127302_chr14.bam" "ERR127303_chr14.bam"
## [7] "ERR127304_chr14.bam" "ERR127305_chr14.bam"

aln <- readGAlignments(fls[1])
length(aln)

## [1] 800484
```

```
head(aln, 3)
## GAlignments with 3 alignments and 0 metadata columns:
##      seqnames strand      cigar    qwidth    start      end    width    ngap
##      <Rle>   <Rle> <character> <integer> <integer> <integer> <integer> <integer>
## [1]   chr14      +      72M        72  19069583  19069654      72      0
## [2]   chr14      +      72M        72  19363738  19363809      72      0
## [3]   chr14      -      72M        72  19363755  19363826      72      0
## ---
##      seqlengths:
##                chr1                chr10 ...                chrY
##      249250621          135534747 ...          59373566
```

A *GappedAlignments* instance is like a data frame, but with accessors as suggested by the column names. It is easy to query, e.g., the distribution of reads aligning to each strand, the width of reads, or the cigar strings

```
table(strand(aln))
##
##      +      -      *
## 400242 400242      0

range(width(aln))
## [1]      70 404751

head(sort(table(cigar(aln)), decreasing=TRUE))
##
##      72M 35M123N37M 38M670N34M 64M316N8M 36M123N36M 18M123N54M
##      603939      272      264      261      228      225
```

Here we construct a *ScanBamParam* object and indicate that we would also like to input the read sequence.

```
param <- ScanBamParam(what="seq")
aln <- readGAlignments(fls[1], param=param)
```

To iterate through a BAM file, create a *BamFile* instance with appropriate `yieldSize`. We use `yieldSize=200000` in the work below, but in reality this could be one or two orders of magnitude larger.

```
bf <- open(BamFile(fls[1], yieldSize=200000))
repeat {
  aln <- readGAlignments(bf)
  if (length(aln) == 0)
    break # no more records
  ## do work
  message(length(aln))
}

## 200000
## 200000
## 200000
## 200000
## 484
close(bf)
```

2.3 Summarizing overlaps

Exercise 6

A basic operation in RNA-seq and other work flows is to count the number of times aligned reads overlap features of interest.

- Load the 'transcript db' package that contains the coordinates of each exon of the UCSC 'known genes' track of hg19.
- Extract the exon coordinates grouped by gene; the result is an `GRangesList` object that we will discuss more latter.
- Use the `summarizeOverlaps` function with the exon coordinates and BAM files to generate a count of the number of reads overlapping each gene. Visit the help page `?summarizeOverlaps` to read about the counting strategy used.
- The counts can be extracted from the return value of `summarizeOverlaps` using the function `assay`. This is standard R matrix. How many reads overlapped regions of interest in each sample? How many genes had non-zero counts?

Solution:

```
## library(BiocParallel)
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
ex <- exonsBy(TxDb.Hsapiens.UCSC.hg19.knownGene, "gene")
counts <- summarizeOverlaps(ex, fls)
colSums(assay(counts))

## ERR127306 ERR127307 ERR127308 ERR127309 ERR127302 ERR127303 ERR127304 ERR127305
##      340669      373302      371666      331540      313817      331160      331639      329672

sum(rowSums(assay(counts)) != 0)

## [1] 528
```

3 Variants: VCF files

A major product of DNaseq experiments are catalogs of called variants (e.g., SNPs, indels). We will use the [VariantAnnotation](#) package to explore this type of data. Sample data included in the package are a subset of chromosome 22 from the [1000 Genomes](#) project. Variant Call Format (VCF; [full description](#)) text files contain meta-information lines, a header line with column names, data lines with information about a position in the genome, and optional genotype information on samples for each position.

3.1 Coding consequences

Locating variants in and around genes Variant location with respect to genes can be identified with the `locateVariants` function. Regions are specified in the `region` argument and can be one of the following constructors: `CodingVariants()`, `IntronVariants()`, `FiveUTRVariants()`, `ThreeUTRVariants()`, `IntergenicVariants()`, `SpliceSiteVariants()`, or `AllVariants()`. Location definitions are shown in [Table 3](#).

Exercise 7

Load the `TxDb.Hsapiens.UCSC.hg19.knownGene` annotation package, and read in the `chr22.vcf.gz` example file from the [VariantAnnotation](#) package.

Remembering to re-name sequence levels, use the `locateVariants` function to identify coding variants.

Table 3: Variant locations

Location	Details
coding	Within a coding region
fiveUTR	Within a 5' untranslated region
threeUTR	Within a 3' untranslated region
intron	Within an intron region
intergenic	Not within a transcript associated with a gene
spliceSite	Overlaps any of the first or last 2 nucleotides of an intron

Summarize aspects of your data, e.g., did any coding variants match more than one gene? How many coding variants are there per gene ID?

Solution: Here we open the known genes data base, and read in the VCF file.

```
library(VariantAnnotation)
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene

fl <- system.file("extdata", "chr22.vcf.gz", package="VariantAnnotation")
vcf <- readVcf(fl, "hg19")
vcf <- renameSeqlevels(vcf, c("22"="chr22"))
```

The next lines locate coding variants.

```
rd <- rowData(vcf)
loc <- locateVariants(rd, txdb, CodingVariants())
head(loc, 3)

## GRanges with 3 ranges and 7 metadata columns:
##      seqnames      ranges strand | LOCATION  QUERYID    TXID    CDSID
##      <Rle>        <IRanges> <Rle> | <factor> <integer> <integer> <integer>
## [1] chr22 [50301422, 50301422] - | coding      24      75253      218562
## [2] chr22 [50301476, 50301476] - | coding      25      75253      218562
## [3] chr22 [50301488, 50301488] - | coding      26      75253      218562
##      GENEID      PRECEDEID      FOLLOWID
##      <character> <CharacterList> <CharacterList>
## [1] 79087
## [2] 79087
## [3] 79087
## ---
##      seqlengths:
##      chr22
##      NA
```

To answer gene-centric questions data can be summarized by gene regardless of transcript.

```
## Did any coding variants match more than one gene?
spl1 <- split(loc$GENEID, loc$QUERYID)
table(sapply(spl1, function(x) length(unique(x)) > 1))

##
## FALSE  TRUE
##   965    15

## Summarize the number of coding variants by gene ID
spl2 <- split(loc$QUERYID, loc$GENEID)
```

```
head(sapply(splt, function(x) length(unique(x))), 3)
## 113730 1890 23209
##      22    15    30
```

Amino acid coding changes `predictCoding` computes amino acid coding changes for non-synonymous variants. Only ranges in query that overlap with a coding region in subject are considered. Reference sequences are retrieved from either a BSgenome or fasta file specified in `seqSource`. Variant sequences are constructed by substituting, inserting or deleting values in the `varAllele` column into the reference sequence. Amino acid codes are computed for the variant codon sequence when the length is a multiple of 3.

The query argument to `predictCoding` can be a GRanges or VCF. When a GRanges is supplied the `varAllele` argument must be specified. In the case of a VCF object, the alternate alleles are taken from `alt(<VCF>)` and the `varAllele` argument is not specified.

The result is a modified query containing only variants that fall within coding regions. Each row represents a variant-transcript match so more than one row per original variant is possible.

```
library(BSgenome.Hsapiens.UCSC.hg19)
coding <- predictCoding(vcf, txdb, seqSource=Hsapiens)
coding[5:9]

## GRanges with 5 ranges and 17 metadata columns:
##           seqnames          ranges strand | paramRangeID          REF
##           <Rle>           <IRanges> <Rle> |   <factor> <DNAStringSet>
## 22:50301584_C/T chr22 [50301584, 50301584] - |   <NA>          C
##           ALT          QUAL          FILTER          varAllele          CDSLOC
## <DNAStringSetList> <numeric> <character> <DNAStringSet> <IRanges>
## 22:50301584_C/T          T          100          PASS          A [777, 777]
##           PROTEINLOC  QUERYID          TXID          CDSID          GENEID  CONSEQUENCE
## <IntegerList> <integer> <character> <integer> <character>          <factor>
## 22:50301584_C/T          259          28          75253          218562          79087  synonymous
##           REFCODON          VARCODON          REFAA          VARAA
## <DNAStringSet> <DNAStringSet> <AAStringSet> <AAStringSet>
## 22:50301584_C/T          CCG          CCA          P          P
## [ reached getOption("max.print") -- omitted 4 rows ]
## ---
## seqlengths:
## chr22
## NA
```

Using variant rs114264124 as an example, we see `varAllele` A has been substituted into the `refCodon` CCG to produce `varCodon` CAG. The `refCodon` is the sequence of codons necessary to make the variant allele substitution and therefore often includes more nucleotides than indicated in the range (i.e. the range is 50302962, 50302962, width of 1). Notice it is the second position in the `refCodon` that has been substituted. This position in the codon, the position of substitution, corresponds to genomic position 50302962. This genomic position maps to position 698 in coding region-based coordinates and to triplet 233 in the protein. This is a non-synonymous coding variant where the amino acid has changed from R (Arg) to Q (Gln).

When the resulting `varCodon` is not a multiple of 3 it cannot be translated. The consequence is considered a frameshift and `varAA` will be missing.

```
coding[coding$CONSEQUENCE == "frameshift"]

## GRanges with 2 ranges and 17 metadata columns:
##           seqnames          ranges strand | paramRangeID          REF
```

```
##          <Rle>          <IRanges> <Rle> |      <factor> <DNAStringSet>
## 22:50317001_G/GCACT    chr22 [50317001, 50317001] + |      <NA>          G
##          ALT          QUAL          FILTER          varAllele      CDSLOC
##          <DNAStringSetList> <numeric> <character> <DNAStringSet> <IRanges>
## 22:50317001_G/GCACT    GCACT          233          PASS          GCACT [808, 808]
##          PROTEINLOC  QUERYID          TXID          CDSID          GENEID
##          <IntegerList> <integer> <character> <integer> <character>
## 22:50317001_G/GCACT    270          359          74357          216303          79174
##          CONSEQUENCE  REFCODON          VARCHODON          REFAA
##          <factor> <DNAStringSet> <DNAStringSet> <AAStringSet>
## 22:50317001_G/GCACT  frameshift          GCC          GCC          A
##          VARAA
##          <AAStringSet>
## 22:50317001_G/GCACT
## [ reached getOption("max.print") -- omitted 1 row ]
## ---
## seqlengths:
## chr22
## NA
```

References

- [1] Kathi Zarnack, Julian König, Mojca Tajnik, Iñigo Martincorena, Sebastian Eustermann, Isabelle Stévant, Alejandro Reyes, Simon Anders, Nicholas M Luscombe, and Jernej Ule. Direct competition between hnnp c and u2af65 protects the transcriptome from the exonization of *aluj* elements. *Cell*, 152(3):453–466, 2013. URL: <http://europepmc.org/abstract/MED/23374342>.
- [2] H. Li and R. Durbin. Fast and accurate long-read alignment with Burrows-Wheeler transform. *Bioinformatics*, 26:589–595, Mar 2010.
- [3] H. Li and R. Durbin. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics*, 25:1754–1760, Jul 2009.
- [4] B. Langmead, C. Trapnell, M. Pop, and S. L. Salzberg. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol.*, 10:R25, 2009.
- [5] Michael Lawrence, Wolfgang Huber, Hervé Pagès, Patrick Aboyoun, Marc Carlson, Robert Gentleman, Martin T. Morgan, and Vincent J. Carey. Software for computing and annotating genomic ranges. *PLoS Comput Biol*, 9(8):e1003118, 08 2013. URL: <http://dx.doi.org/10.1371/journal.pcbi.1003118>, doi: 10.1371/journal.pcbi.1003118.