

NGS Analysis Basics

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Overview

Sequence Analysis in R and Bioconductor

R Base

- Some basic string handling utilities. Wide spectrum of numeric data analysis tools.

Bioconductor

Bioconductor packages provide much more sophisticated string handling utilities for sequence analysis (Lawrence et al. 2013, Huber et al. (2015)).

- Biostrings: general sequence analysis environment
- ShortRead: pipeline for short read data
- IRanges: low-level infrastructure for range data
- GenomicRanges: high-level infrastructure for range data
- GenomicFeatures: managing transcript centric annotations
- GenomicAlignments: handling short genomic alignments
- Rsamtools: interface to **samtools**, **bcftools** and **tabix**
- BSgenome: genome annotation data
- biomaRt: interface to BioMart annotations
- rtracklayer: Annotation imports, interface to online genome browsers
- HelloRanges: Bedtools semantics in Bioc's Ranges infrastructure

Package Requirements

Several Bioconductor packages are required for this tutorial. To install them, execute the following lines in the R console. Please also make sure that you have a recent R version installed on your system. R versions 3.3.x or higher are recommended.

```
source("https://bioconductor.org/biocLite.R")
biocLite(c("Biostrings", "GenomicRanges", "GenomicRanges", "rtracklayer", "systemPipeR", "seqLogo", "Sh
```

Strings in R Base

Basic String Matching and Parsing

String matching

Generate sample sequence data set

```
myseq <- c("ATGCAGACATAGTG", "ATGAACATAGATCC", "GTACAGATCAC")
```

String searching with regular expression support

```
myseq[grep("ATG", myseq)]
```

```
## [1] "ATGCAGACATAGTG" "ATGAACATAGATCC"
```

Searches myseq for first match of pattern “AT”

```
pos1 <- regexpr("AT", myseq)
```

```
as.numeric(pos1); attributes(pos1)$match.length # Returns position information of matches
```

```
## [1] 1 1 7
```

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

Searches myseq for all matches of pattern “AT”

```
pos2 <- gregexpr("AT", myseq)
```

```
as.numeric(pos2[[1]]); attributes(pos2[[1]])$match.length # Returns positions of matches in first sequence
```

```
## [1] 1 9
```

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

String substitution with regular expression support

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

```
## [1] "atgCAGACATAGTG" "atgAACATAGATCC" "GTACAGATCAC"
```

Positional parsing

```
nchar(myseq) # Computes length of strings
```

```
## [1] 14 14 11
```

```
substring(myseq[1], c(1,3), c(2,5)) # Positional parsing of several fragments from one string
```

```
## [1] "AT" "GCA"
```

```
substring(myseq, c(1,4,7), c(2,6,10)) # Positional parsing of many strings
```

```
## [1] "AT" "AAC" "ATCA"
```

Random Sequence Generation

Random DNA sequences of any length

```
rand <- sapply(1:100, function(x) paste(sample(c("A","T","G","C"), sample(10:20), replace=T), collapse=  
rand[1:3])
```

```
## [1] "CAGTTCATGA" "TATTTTCACCGCATAAAA" "TTGTAGTCGTGAAAT"
```

Count identical sequences

```
table(c(rand[1:4], rand[1]))
```

```
##
##          CAGTTCATGA          GATAGTACAC TATTTTCACCGCATAAAA          TTGTAGTCGTGAAAT
##                      2                      1                      1                      1
```

Extract reads from reference

Note: this requires Biostrings package.

```
library(Biostrings)
ref <- DNAString(paste(sample(c("A","T","G","C"), 100000, replace=T), collapse=""))
randstart <- sample(1:(length(ref)-15), 1000)
randreads <- Views(ref, randstart, width=15)
rand_set <- DNAStringSet(randreads)
unlist(rand_set)
```

```
## 15000-letter "DNAString" instance
```

```
## seq: ACATGATTTTCGTGCTTGGTCGCGTTGTCTCAATACGGGGCGTGTAT...AGTCGAAGGAGCTCAACGTCCTTAAGCTTTCAACAATCGTTATTG
```

Sequences in Bioconductor

Important Data Objects of Biostrings

XString for single sequence

- DNAString: for DNA
- RNAString: for RNA
- AAString: for amino acid
- BString: for any string

XStringSet for many sequences

- ‘DNAStringSet’: for DNA
- RNAStringSet: for RNA
- AAStringSet: for amino acid
- BStringSet: for any string

QualityScaledXStringSet for sequences with quality data

- QualityScaledDNAStringSet: for DNA
- QualityScaledRNAStringSet: for RNA
- QualityScaledAAStringSet: for amino acid
- QualityScaledBStringSet: for any string

Sequence Import and Export

Download the following sequences to your current working directory and then import them into R: ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Bacteria/Halobacterium_sp_uid217/AE004437.ffn

```
dir.create("data", showWarnings = FALSE)
# system("wget ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Bacteria/Halobacterium_sp_uid217/
download.file("ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Bacteria/Halobacterium_sp_uid217/
```

Import FASTA file with readDNASTringSet

```
myseq <- readDNASTringSet("data/AE004437.ffn")
myseq[1:3]
```

```
## A DNASTringSet instance of length 3
## width seq names
## [1] 1206 ATGACTCGGCGGTCTCGTGTGCGTGCCGGCCTC...GTCGTCGTTGTTTCGACGCTGGCGGAACCCATGA gi|12057215|gb|AE...
## [2] 666 ATGAGCATCATCGAACTCGAAGGCGTGGTCAAA...GTCAACCTCGTCGATGGGGTGTTACACACGTGA gi|12057215|gb|AE...
## [3] 1110 ATGGCGTGCGGAACCTCGGGCGGAACCGCGTG...AACGATCCGCCGTCGAGGCGCTCGGCGAATGA gi|12057215|gb|AE...
```

Subset sequences with regular expression on sequence name field

```
sub <- myseq[grep("99.*", names(myseq))]
length(sub)
```

```
## [1] 170
```

Export subsetted sequences to FASTA file

```
writeXStringSet(sub, file="./data/AE004437sub.ffn", width=80)
```

Now inspect exported sequence file AE004437sub.ffn in a text editor

Working with XString Containers

The XString stores the different types of biosequences in dedicated containers

```
library(Biostrings)
d <- DNASTring("GCATAT-TAC")
d
```

```
## 10-letter "DNASTring" instance
## seq: GCATAT-TAC
```

```
d[1:4]
```

```
## 4-letter "DNASTring" instance
## seq: GCAT
```

RNA sequences

```
r <- RNASTring("GCAUAU-UAC")
r <- RNASTring(d) # Converts d to RNASTring object
r
```

```
## 10-letter "RNASTring" instance
## seq: GCAUAU-UAC
```

Protein sequences

```
p <- AASTring("HCWYHH")
p
```

```
## 6-letter "AAString" instance
## seq: HCWYHH
```

Any type of character strings

```
b <- BString("I store any set of characters. Other XString objects store only the IUPAC characters.")
b

## 85-letter "BString" instance
## seq: I store any set of characters. Other XString objects store only the IUPAC characters.
```

Working with XStringSet Containers

XStringSet containers allow to store many biosequences in one object

```
dset <- DNASTringSet(c("GCATATTAC", "AATCGATCC", "GCATATTAC"))
names(dset) <- c("seq1", "seq2", "seq3") # Assigns names
dset[1:2]

## A DNASTringSet instance of length 2
## width seq names
## [1] 9 GCATATTAC seq1
## [2] 9 AATCGATCC seq2
```

Important utilities for XStringSet containers

```
width(dset) # Returns the length of each sequences

## [1] 9 9 9

d <- dset[[1]] # The [[ subsetting operator returns a single entry as XString object
dset2 <- c(dset, dset) # Appends/concatenates two XStringSet objects
dsetchar <- as.character(dset) # Converts XStringSet to named vector
dsetone <- unlist(dset) # Collapses many sequences to a single one stored in a DNASTring container
```

Sequence subsetting by positions:

```
DNASTringSet(dset, start=c(1,2,3), end=c(4,8,5))

## A DNASTringSet instance of length 3
## width seq names
## [1] 4 GCAT seq1
## [2] 7 ATCGATC seq2
## [3] 3 ATA seq3
```

Multiple Alignment Class

The XMultipleAlignment class stores the different types of multiple sequence alignments:

```
origMAlign <- readDNAMultipleAlignment(filepath = system.file("extdata",
  "msx2_mRNA.aln", package = "Biostrings"), format = "clustal")
origMAlign

## DNAMultipleAlignment with 8 rows and 2343 columns
## aln names
## [1] -----TCCCGTCTCCGCAGCAAAAAAGTTTGAGTCG...TTGTCCAAACTCACAATTAATAAAAAAAAAAAAAAAAAA gi|84452153|ref|N...
## [2] -----..... gi|208431713|ref|...
## [3] -----..... gi|118601823|ref|...
## [4] -----AAAAGTTGGAGTCT... gi|114326503|ref|...
## [5] -----..... gi|119220589|ref|...
```

```
## [6] -----...----- gi|148540149|ref|...
## [7] -----CGGCTCCGCAGCGCCTCACTCG...----- gi|45383056|ref|N...
## [8] GGGGGGAGACTTCAGAAATTGTTGTCCTCTCCGCTGA...----- gi|213515133|ref|...
```

Basic Sequence Manipulations

Reverse and Complement

```
randset <- DNASTringSet(rand)
complement(randset[1:2])

## A DNASTringSet instance of length 2
## width seq
## [1] 10 GTCAAGTACT
## [2] 18 ATAAAAGTGGCGTATTTT

reverse(randset[1:2])

## A DNASTringSet instance of length 2
## width seq
## [1] 10 AGTACTTGAC
## [2] 18 AAAATACGCCACTTTTAT

reverseComplement(randset[1:2])

## A DNASTringSet instance of length 2
## width seq
## [1] 10 TCATGAACTG
## [2] 18 TTTTATGCGGTGAAAATA
```

Translate DNA into Protein

```
translate(randset[1:2])

## Warning in .Call2("DNASTringSet_translate", x, skip_code, dna_codes[codon_alphabet], : in 'x[[1]]':
## last base was ignored

## A AAStringSet instance of length 2
## width seq
## [1] 3 QFM
## [2] 6 YFHRIK
```

Pattern Matching

Pattern matching with mismatches

Find pattern matches in reference

```
myseq1 <- readDNASTringSet("./data/AE004437.ffn")
mypos <- matchPattern("ATGGTG", myseq1[[1]], max.mismatch=1)
```

Count only the corresponding matches

```
countPattern("ATGGCT", myseq1[[1]], max.mismatch=1)
```

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

Count matches in many sequences

```
vcountPattern("ATGGCT", myseq1, max.mismatch=1)[1:20]
```

```
## [1] 3 0 5 4 1 2 2 1 4 3 0 0 1 2 0 1 4 0 0 1
```

Results shown in DNASTringSet object

```
tmp <- c(DNASTringSet("ATGGTG"), DNASTringSet(mypos))
```

Return a consensus matrix for query and hits

```
consensusMatrix(tmp)[1:4,]
```

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

Find all pattern matches in reference

```
myvpos <- vmatchPattern("ATGGCT", myseq1, max.mismatch=1)
myvpos # The results are stored as MIndex object.
```

```
## MIndex object of length 2058
## $`gi|12057215|gb|AE004437.1|:248-1453 Halobacterium sp. NRC-1, complete genome`
## IRanges object with 3 ranges and 0 metadata columns:
##           start      end      width
##      <integer> <integer> <integer>
## [1]          1         6         6
## [2]        383        388         6
## [3]        928        933         6
##
## $`gi|12057215|gb|AE004437.1|:1450-2115 Halobacterium sp. NRC-1, complete genome`
## IRanges object with 0 ranges and 0 metadata columns:
##           start      end      width
##      <integer> <integer> <integer>
##
## $`gi|12057215|gb|AE004437.1|:2145-3254 Halobacterium sp. NRC-1, complete genome`
## IRanges object with 5 ranges and 0 metadata columns:
##           start      end      width
##      <integer> <integer> <integer>
## [1]          1         6         6
## [2]         94         99         6
## [3]        221        226         6
## [4]        535        540         6
## [5]        601        606         6
##
## ...
## <2055 more elements>
```

```
Views(myseq1[[1]], start(myvpos[[1]]), end(myvpos[[1]])) # Retrieves the result for single entry
```

```
## Views on a 1206-letter DNASTring subject
```

```
## subject: ATGACTCGGCGGTCTCGTGTCTCGGTGCCGGCCTCGCAGCCATTGT...TTGCGATCGTCGTCGTTGTTTCGACGCTGGCGGAACCCATGA
## views:
##      start end width
## [1]      1   6     6 [ATGACT]
## [2]    383 388     6 [ATGGCA]
## [3]    928 933     6 [ATGACT]
```

Return all matches

```
sapply(seq(along=myseq1), function(x)
  as.character(Views(myseq1[[x]], start(myvpos[[x]]), end(myvpos[[x]]))))[1:4]
```

Pattern matching with regular expression support

```
myseq <- DNASTringSet(c("ATGCAGACATAGTG", "ATGAACATAGATCC", "GTACAGATCAC"))
myseq[grep("^ATG", myseq, perl=TRUE)] # String searching with regular expression support
```

```
## A DNASTringSet instance of length 2
##      width seq
## [1]     14 ATGCAGACATAGTG
## [2]     14 ATGAACATAGATCC
```

```
pos1 <- regexpr("AT", myseq) # Searches 'myseq' for first match of pattern "AT"
as.numeric(pos1); attributes(pos1)$match.length # Returns position information of matches
```

```
## [1] 1 1 7
```

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

```
pos2 <- gregexpr("AT", myseq) # Searches 'myseq' for all matches of pattern "AT"
as.numeric(pos2[[1]]); attributes(pos2[[1]])$match.length # Match positions in first sequence
```

```
## [1] 1 9
```

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

```
DNASTringSet(gsub("^ATG", "NNN", myseq)) # String substitution with regular expression support
```

```
## A DNASTringSet instance of length 3
##      width seq
## [1]     14 NNNCAGACATAGTG
## [2]     14 NNNAACATAGATCC
## [3]     11 GTACAGATCAC
```

PWM Viewing and Searching

Plot with seqLogo

```
library(seqLogo)
```

```
## Loading required package: grid
```

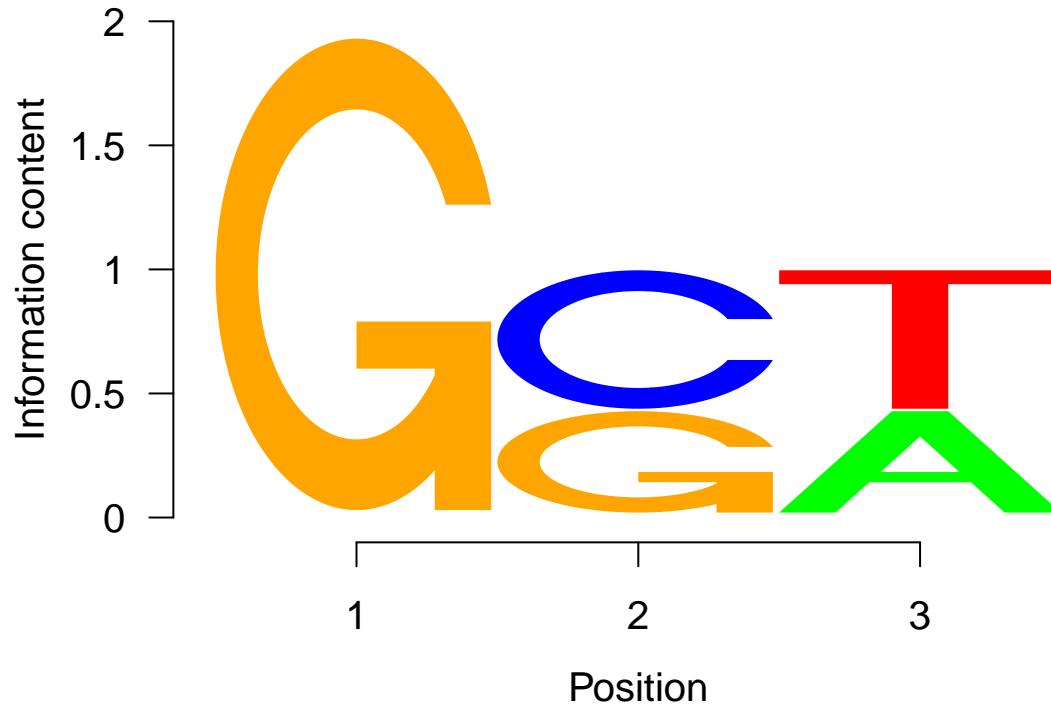
```
pwm <- PWM(DNASTringSet(c("GCT", "GGT", "GCA")))
pwm
```

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



```
## A 0.0000000 0.0000000 0.2312611
## C 0.0000000 0.3157205 0.0000000
## G 0.3685591 0.2312611 0.0000000
## T 0.0000000 0.0000000 0.3157205
```

```
seqLogo(t(t(pwm) * 1/colSums(pwm)))
```



Plot with ggseqlogo

The `ggseqlogo` package (manual) provides many customization options for plotting sequence logos. It also supports various alphabets including sequence logos for amino acid sequences.

```
library(ggplot2); library(ggseqlogo)
pwm <- PWM(DNAStringSet(c("GCT", "GGT", "GCA")))
ggseqlogo(pwm)
```



Search sequence for PWM matches with score better than `min.score`

```
chr <- DNASTring("AAAGCTAAAGGTAAAGCAAAA")
matchPWM(pwm, chr, min.score=0.9)
```

```
## Views on a 21-letter DNASTring subject
## subject: AAAGCTAAAGGTAAAGCAAAA
## views:
##      start end width
## [1]      4   6     3 [GCT]
## [2]     10  12     3 [GGT]
## [3]     16  18     3 [GCA]
```

NGS Sequences

Sequence and Quality Data: FASTQ Format

Four lines per sequence:

1. ID
2. Sequence
3. ID
4. Base call qualities (Phred scores) as ASCII characters

The following gives an example of 3 Illumina reads in a FASTQ file. The numbers at the beginning of each line are not part of the FASTQ format. They have been added solely for illustration purposes.

1. @SRR038845.3 HWI-EAS038:6:1:0:1938 length=36
2. CAACGAGTTCACACCTTGGCCGACAGGCCCGGTAA
3. +SRR038845.3 HWI-EAS038:6:1:0:1938 length=36

```

4. BA@7>B=>:>>7@7@>>9=BAA?;>52;>:9=8.=A
1. @SRR038845.41 HWI-EAS038:6:1:0:1474 length=36
2. CCAATGATTTTTTTTCCGTGTTTCAGAATACGGTTAA
3. +SRR038845.41 HWI-EAS038:6:1:0:1474 length=36
4. BCCBA@BB@BBBBAB@B9B@=BABA@A:@693:@B=
1. @SRR038845.53 HWI-EAS038:6:1:1:360 length=36
2. GTTCAAAAAGAACTAAATTGTGTCAATAGAAAACCTC
3. +SRR038845.53 HWI-EAS038:6:1:1:360 length=36
4. BBCBBBBBB@B@B@?BBBBBCBC>BBBAA8>BBBAA@

```

Sequence and Quality Data: QualityScaleXStringSet

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

Phred score interconversion

```

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
```

Construct QualityScaledDNAStringSet from scratch

```

dset <- DNAStringSet(sapply(1:100, function(x) paste(sample(c("A","T","G","C"), 20, replace=T), collapse="")))
myqlist <- lapply(1:100, function(x) sample(1:40, 20, replace=T)) # Creates random Phred score list.
myqual <- sapply(myqlist, function(x) toString(PhredQuality(x))) # Converts integer scores into ASCII c
myqual <- PhredQuality(myqual) # Converts to a PhredQuality object.
dsetq1 <- QualityScaledDNAStringSet(dset, myqual) # Combines DNAStringSet and quality data in QualitySc
dsetq1[1:2]

```

```
## A QualityScaledDNAStringSet instance containing:
```

```
##
```

```
## A DNAStringSet instance of length 2
```

```
## width seq
```

```
## [1] 20 CCTTATAAATAAGACCGTA
```

```
## [2] 20 TTGCGACAAGCTATTGCCTC
```

```
##
```

```
## A PhredQuality instance of length 2
```

```
## width seq
```

```
## [1] 20 +>IFBGC*#0I@##%,&0C<
```

```
## [2] 20 3&D?*@*.9&$I+H89,90%
```

Processing FASTQ Files with ShortRead

The following explains the basic usage of `ShortReadQ` objects. To make the sample code work, download and unzip this file to your current working directory. The following code performs the download for you.

```

library(ShortRead)
download.file("http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rsequen
unzip("data.zip")

```

Important utilities for accessing FASTQ files

```
fastq <- list.files("data", "*.fastq$"); fastq <- paste("data/", fastq, sep="")
names(fastq) <- paste("flowcell6_lane", 1:length(fastq), sep="_")
(fq <- readFastq(fastq[1])) # Imports first FASTQ file

## class: ShortReadQ
## length: 1000 reads; width: 36 cycles

countLines(dirPath="./data", pattern=".fastq$")/4 # Counts numbers of reads in FASTQ files

## SRR038845.fastq SRR038846.fastq SRR038848.fastq SRR038850.fastq
##           1000           1000           1000           1000

id(fq)[1] # Returns ID field

## A BStringSet instance of length 1
## width seq
## [1] 43 SRR038845.3 HWI-EAS038:6:1:0:1938 length=36

sread(fq)[1] # Returns sequence

## A DNAStringSet instance of length 1
## width seq
## [1] 36 CAACGAGTTCACACCTTGCCGACAGGCCCGGGTAA

quality(fq)[1] # Returns Phred scores

## class: FastqQuality
## quality:
## A BStringSet instance of length 1
## width seq
## [1] 36 BA@7>B=>:>>7@7@>>9=BAA?;>52;>:9=8.=A

as(quality(fq), "matrix")[1:4,1:12] # Coerces Phred scores to numeric matrix

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
## [1,] 33  32  31  22  29  33  28  29  25  29  29  22
## [2,] 33  34  34  33  32  31  33  33  31  33  33  33
## [3,] 33  33  34  33  33  33  33  33  33  31  31  33
## [4,] 33  33  33  33  31  33  28  31  28  32  33  33

ShortReadQ(sread=sread(fq), quality=quality(fq), id=id(fq)) # Constructs a ShortReadQ from components

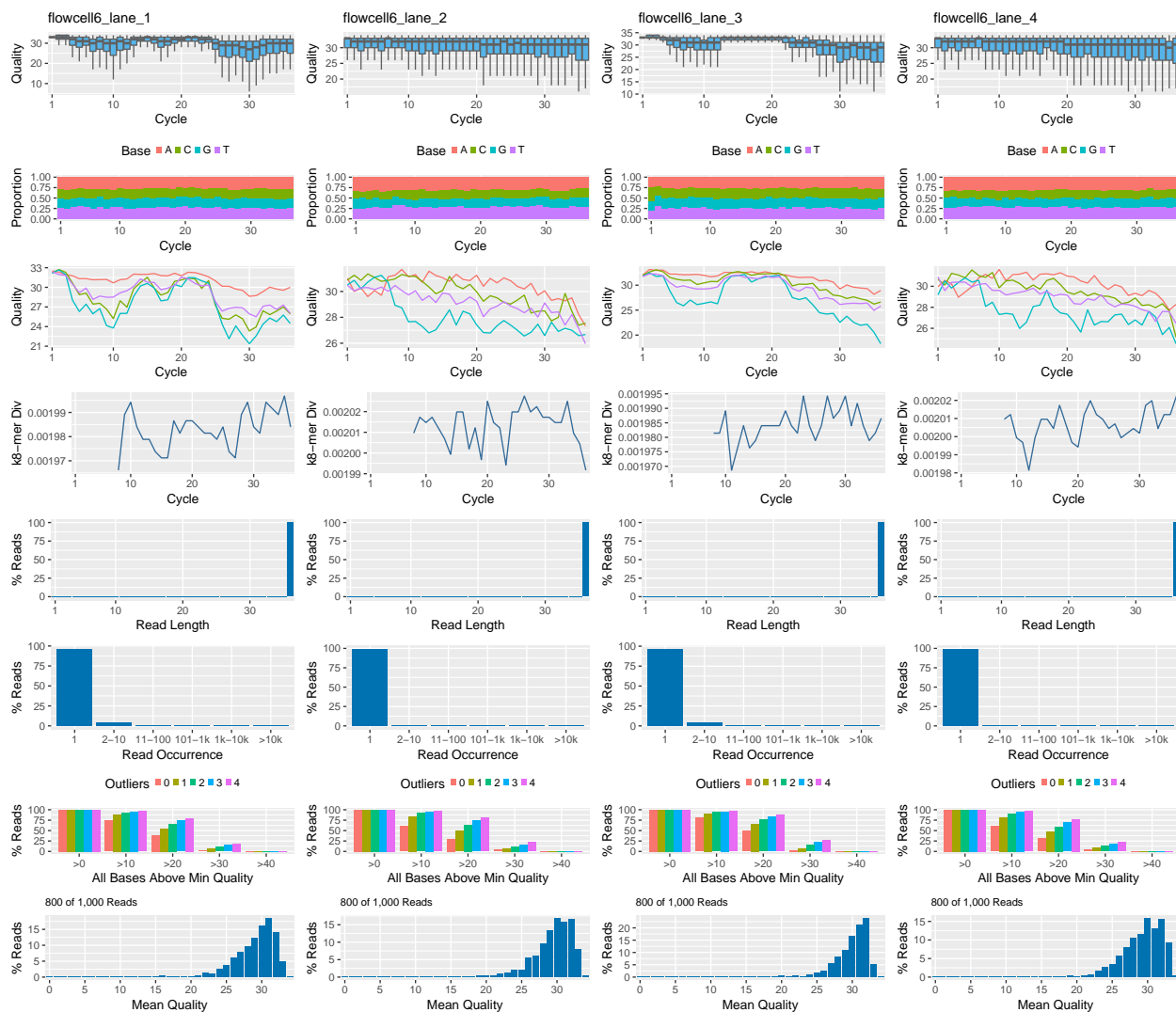
## class: ShortReadQ
## length: 1000 reads; width: 36 cycles
```

FASTQ Quality Reports

Using systemPipeR

The following `seeFastq` and `seeFastqPlot` functions generate and plot a series of useful quality statistics for a set of FASTQ files.

```
library(systemPipeR)
fqlist <- seeFastq(fastq=fastq, batchsize=800, klength=8) # For real data set batchsize to at least 10^3
seeFastqPlot(fqlist)
```



Handles many samples in one PDF file. For more details see [here](#)

Using ShortRead

The ShortRead package contains several FASTQ quality reporting functions.

```
sp <- SolexaPath(system.file('extdata', package='ShortRead'))
fl <- file.path(analysisPath(sp), "s_1_sequence.txt")
fls <- c(fl, fl)
coll <- QACollate(QAFastqSource(fls), QAReadQuality(), QAAdapterContamination(),
  QANucleotideUse(), QAQualityUse(), QASequenceUse(), QAFrequentSequence(n=10),
  QANucleotideByCycle(), QAQualityByCycle())
x <- qa2(coll, verbose=TRUE)
res <- report(x)
if(interactive())
  browseURL(res)
```

Filtering and Trimming FASTQ Files with ShortRead

Adaptor trimming

```
fqtrim <- trimLRPatterns(Rpattern="GCCCAGGTAA", subject=fq)
sread(fq)[1:2] # Before trimming

## A DNAStringSet instance of length 2
## width seq
## [1] 36 CAACGAGTTCACACCTTGGCCGACAGGCCCGGTAA
## [2] 36 CCAATGATTTTTTTCCGTGTTTCAGAATACGGTTAA

sread(fqtrim)[1:2] # After trimming

## A DNAStringSet instance of length 2
## width seq
## [1] 26 CAACGAGTTCACACCTTGGCCGACAG
## [2] 36 CCAATGATTTTTTTCCGTGTTTCAGAATACGGTTAA
```

Read counting and duplicate removal

```
tables(fq)$distribution # Counts read occurrences

## nOccurrences nReads
## 1 1 948
## 2 2 26

sum(srduplicated(fq)) # Identifies duplicated reads

## [1] 26

fq[!srduplicated(fq)]

## class: ShortReadQ
## length: 974 reads; width: 36 cycles
```

Trimming low quality tails

```
cutoff <- 30
cutoff <- rawToChar(as.raw(cutoff+33))
sread(trimTails(fq, k=2, a=cutoff, successive=FALSE))[1:2]

## A DNAStringSet instance of length 2
## width seq
## [1] 4 CAAC
## [2] 20 CCAATGATTTTTTTCCGTGT
```

Removal of reads with Phred scores below a threshold value

```
cutoff <- 30
qcount <- rowSums(as(quality(fq), "matrix") <= 20)
fq[qcount == 0] # Number of reads where all Phred scores >= 20
```

```
## class: ShortReadQ
## length: 349 reads; width: 36 cycles
```

Removal of reads with x Ns and/or low complexity segments

```
filter1 <- nFilter(threshold=1) # Keeps only reads without Ns
filter2 <- polynFilter(threshold=20, nuc=c("A","T","G","C")) # Removes reads with >=20 of one nucleotide
filter <- compose(filter1, filter2)
fq[filter(fq)]
```

```
## class: ShortReadQ
## length: 989 reads; width: 36 cycles
```

Memory Efficient FASTQ Processing

Streaming through FASTQ files with `FastqStreamer` and random sampling reads with `FastqSampler`

```
fq <- yield(FastqStreamer(fastq[1], 50)) # Imports first 50 reads
fq <- yield(FastqSampler(fastq[1], 50)) # Random samples 50 reads
```

Streaming through a FASTQ file while applying filtering/trimming functions and writing the results to a new file here `SRR038845.fastq_sub` in data directory.

```
f <- FastqStreamer(fastq[1], 50)
while(length(fq <- yield(f))) {
  fqsub <- fq[grep("^TT", sread(fq))]
  writeFastq(fqsub, paste(fastq[1], "sub", sep="_"), mode="a", compress=FALSE)
}
close(f)
```

Range Operations

Important Data Objects for Range Operations

- `IRanges`: stores range data only (`IRanges` library)
- `GRanges`: stores ranges and annotations (`GenomicRanges` library)
- `GRangesList`: list version of `GRanges` container (`GenomicRanges` library)

Range Data Are Stored in `IRanges` and `GRanges` Containers

Construct `GRanges` Object

```
library(GenomicRanges); library(rtracklayer)
gr <- GRanges(seqnames = Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)), ranges = IRanges(1:10, c(100, 200, 300, 400)))
```

Import GFF into `GRanges` Object

```
gff <- import.gff("http://faculty.ucr.edu/~tgirke/Documents/R_BioCond/Samples/gff3.gff") # Imports a si
seqlengths(gff) <- end(ranges(gff[which(values(gff)[,"type"]=="chromosome"),]))
names(gff) <- 1:length(gff) # Assigns names to corresponding slot
gff[1:4,]
```

```
## GRanges object with 4 ranges and 10 metadata columns:
##      seqnames      ranges strand |   source      type      score      phase      ID
##      <Rle>        <IRanges> <Rle> | <factor>    <factor> <numeric> <integer>    <character>
##  1      Chr1 [ 1, 30427671]      + |   TAIR10 chromosome    <NA>    <NA>      Chr1
##  2      Chr1 [3631, 5899]      + |   TAIR10      gene    <NA>    <NA>      AT1G01010
##  3      Chr1 [3631, 5899]      + |   TAIR10      mRNA    <NA>    <NA>      AT1G01010.1
##  4      Chr1 [3760, 5630]      + |   TAIR10      protein  <NA>    <NA> AT1G01010.1-Protein
##      Name          Note          Parent      Index Derives_from
##      <character>    <CharacterList> <CharacterList> <character> <character>
##  1      Chr1
##  2  AT1G01010 protein_coding_gene
##  3 AT1G01010.1
##  4 AT1G01010.1
##  -----
##  seqinfo: 7 sequences from an unspecified genome
```

Coerce GRanges object to data.frame

```
as.data.frame(gff)[1:4, 1:7]
```

```
##      seqnames start      end      width strand source      type
##  1      Chr1      1 30427671 30427671      + TAIR10 chromosome
##  2      Chr1 3631      5899      2269      + TAIR10      gene
##  3      Chr1 3631      5899      2269      + TAIR10      mRNA
##  4      Chr1 3760      5630      1871      + TAIR10      protein
```

Coerce GRanges to RangedData object and vice versa

```
gff_rd <- as(gff, "RangedData")
gff_gr <- as(gff_rd, "GRanges")
```

Utilities for Range Containers

Accessor and subsetting methods for GRanges objects

Subsetting and replacement

```
gff[1:4]
```

```
## GRanges object with 4 ranges and 10 metadata columns:
##      seqnames      ranges strand |   source      type      score      phase      ID
##      <Rle>        <IRanges> <Rle> | <factor>    <factor> <numeric> <integer>    <character>
##  1      Chr1 [ 1, 30427671]      + |   TAIR10 chromosome    <NA>    <NA>      Chr1
##  2      Chr1 [3631, 5899]      + |   TAIR10      gene    <NA>    <NA>      AT1G01010
##  3      Chr1 [3631, 5899]      + |   TAIR10      mRNA    <NA>    <NA>      AT1G01010.1
##  4      Chr1 [3760, 5630]      + |   TAIR10      protein  <NA>    <NA> AT1G01010.1-Protein
```



```
##           Name           Note           Parent           Index Derives_from
##   <character>   <CharacterList> <CharacterList> <character> <character>
## 1      Chr1
## 2 AT1G01010 protein_coding_gene
## 3 AT1G01010.1
## 4 AT1G01010.1
## -----
## seqinfo: 7 sequences from an unspecified genome
gff[1:4, c("type", "ID")]
```

```
## GRanges object with 4 ranges and 2 metadata columns:
##   seqnames      ranges strand |      type      ID
##   <Rle>        <IRanges> <Rle> | <factor>    <character>
## 1      Chr1 [ 1, 30427671] + | chromosome    Chr1
## 2      Chr1 [3631, 5899] + | gene            AT1G01010
## 3      Chr1 [3631, 5899] + | mRNA            AT1G01010.1
## 4      Chr1 [3760, 5630] + | protein AT1G01010.1-Protein
## -----
## seqinfo: 7 sequences from an unspecified genome
gff[2] <- gff[3]
```

GRanges objects can be concatenated with the c function

```
c(gff[1:2], gff[401:402])
```

```
## GRanges object with 4 ranges and 10 metadata columns:
##   seqnames      ranges strand | source      type      score      phase
##   <Rle>        <IRanges> <Rle> | <factor>    <factor> <numeric> <integer>
## 1      Chr1 [ 1, 30427671] + | TAIR10 chromosome <NA> <NA>
## 2      Chr1 [3631, 5899] + | TAIR10 mRNA <NA> <NA>
## 401     Chr5 [5516, 5769] - | TAIR10 protein <NA> <NA>
## 402     Chr5 [5770, 5801] - | TAIR10 five_prime_UTR <NA> <NA>
##           ID           Name           Note           Parent           Index Derives_from
##   <character> <character> <CharacterList> <CharacterList> <character> <character>
## 1      Chr1      Chr1
## 2 AT1G01010.1 AT1G01010.1
## 401 AT5G01015.2-Protein AT5G01015.2
## 402 <NA> <NA>
## -----
## seqinfo: 7 sequences from an unspecified genome
```

Accessor functions

```
seqnames(gff)
```

```
## factor-Rle of length 449 with 7 runs
## Lengths: 72 22 38 118 172 13 14
## Values : Chr1 Chr2 Chr3 Chr4 Chr5 ChrC ChrM
## Levels(7): Chr1 Chr2 Chr3 Chr4 Chr5 ChrC ChrM
```

```
ranges(gff)
```

```
## IRanges object with 449 ranges and 0 metadata columns:
##   start      end      width
##   <integer> <integer> <integer>
## 1      1      30427671 30427671
```

```
##      2      3631      5899      2269
##      3      3631      5899      2269
##      4      3760      5630      1871
##      5      3631      3913      283
##      ...      ...      ...      ...
## 445    11918    12241      324
## 446    11918    12241      324
## 447    11918    12241      324
## 448    11918    12241      324
## 449    11918    12241      324
```

```
strand(gff)
```

```
## factor-Rle of length 449 with 13 runs
##  Lengths:  18  54  28  21  12 117  1 171  1 12  1  8  5
##  Values :   +   -   +   -   +   -   +   -   +   -   +   -   +
## Levels(3): + - *
```

```
seqlengths(gff)
```

```
##      Chr1      Chr2      Chr3      Chr4      Chr5      ChrC      ChrM
## 30427671 19698289 23459830 18585056 26975502  154478  366924
```

```
start(gff[1:4])
```

```
## [1]      1 3631 3631 3760
```

```
end(gff[1:4])
```

```
## [1] 30427671      5899      5899      5630
```

```
width(gff[1:4])
```

```
## [1] 30427671      2269      2269      1871
```

Accessing metadata component

```
values(gff) # or elementMetadata(gff)
```

```
## DataFrame with 449 rows and 10 columns
##      source      type      score      phase      ID      Name      Note
##      <factor> <factor> <numeric> <integer> <character> <character> <CharacterList>
## 1      TAIR10 chromosome      NA      NA      Chr1      Chr1
## 2      TAIR10      mRNA      NA      NA      AT1G01010.1 AT1G01010.1
## 3      TAIR10      mRNA      NA      NA      AT1G01010.1 AT1G01010.1
## 4      TAIR10      protein      NA      NA AT1G01010.1-Protein AT1G01010.1
## 5      TAIR10      exon      NA      NA      NA      NA
## ...      ...      ...      ...      ...      ...      ...
## 445    TAIR10      gene      NA      NA      ATMG00030  ATMG00030 protein_coding_gene
## 446    TAIR10      mRNA      NA      NA      ATMG00030.1 ATMG00030.1
## 447    TAIR10      protein      NA      NA ATMG00030.1-Protein ATMG00030.1
## 448    TAIR10      exon      NA      NA      NA      NA
## 449    TAIR10      CDS      NA      0      NA      NA
##
##      Parent      Index Derives_from
##      <CharacterList> <character> <character>
## 1      NA      NA
## 2      AT1G01010      1      NA
## 3      AT1G01010      1      NA
## 4      NA      AT1G01010.1
```

```
## 5          AT1G01010.1          NA          NA
## ...          ...          ...          ...
## 445          NA          NA
## 446          ATMG00030          1          NA
## 447          NA          ATMG00030.1
## 448          ATMG00030.1          NA          NA
## 449 ATMG00030.1,ATMG00030.1-Protein          NA          NA
```

```
values(gff)[, "type"][1:20]
```

```
## [1] chromosome      mRNA          mRNA          protein       exon          five_prime_UTR
## [7] CDS              exon          CDS           exon          CDS           exon
## [13] CDS              exon          CDS           exon          CDS           three_prime_UTR
## [19] gene            mRNA
```

```
## Levels: chromosome gene mRNA protein exon five_prime_UTR CDS three_prime_UTR rRNA tRNA
```

```
gff[values(gff)[, "type"] == "gene"]
```

```
## GRanges object with 21 ranges and 10 metadata columns:
```

##	seqnames	ranges	strand	source	type	score	phase	ID
##	<Rle>	<IRanges>	<Rle>	<factor>	<factor>	<numeric>	<integer>	<character>
## 19	Chr1	[5928, 8737]	-	TAIR10	gene	<NA>	<NA>	AT1G01020
## 64	Chr1	[11649, 13714]	-	TAIR10	gene	<NA>	<NA>	AT1G01030
## 74	Chr2	[1025, 2810]	+	TAIR10	gene	<NA>	<NA>	AT2G01008
## 84	Chr2	[3706, 5513]	+	TAIR10	gene	<NA>	<NA>	AT2G01010
## 87	Chr2	[5782, 5945]	+	TAIR10	gene	<NA>	<NA>	AT2G01020
##
## 427	ChrC	[383, 1444]	-	TAIR10	gene	<NA>	<NA>	ATCG00020
## 432	ChrC	[1717, 4347]	-	TAIR10	gene	<NA>	<NA>	ATCG00030
## 437	ChrM	[273, 734]	-	TAIR10	gene	<NA>	<NA>	ATMG00010
## 442	ChrM	[8848, 11415]	-	TAIR10	gene	<NA>	<NA>	ATMG00020
## 445	ChrM	[11918, 12241]	+	TAIR10	gene	<NA>	<NA>	ATMG00030

##	Name	Note	Parent	Index	Derives_from
##	<character>	<CharacterList>	<CharacterList>	<character>	<character>
## 19	AT1G01020	protein_coding_gene		<NA>	<NA>
## 64	AT1G01030	protein_coding_gene		<NA>	<NA>
## 74	AT2G01008	protein_coding_gene		<NA>	<NA>
## 84	AT2G01010	rRNA		<NA>	<NA>
## 87	AT2G01020	rRNA		<NA>	<NA>
##
## 427	ATCG00020	protein_coding_gene		<NA>	<NA>
## 432	ATCG00030	tRNA		<NA>	<NA>
## 437	ATMG00010	protein_coding_gene		<NA>	<NA>
## 442	ATMG00020	rRNA		<NA>	<NA>
## 445	ATMG00030	protein_coding_gene		<NA>	<NA>

```
## -----
## seqinfo: 7 sequences from an unspecified genome
```

Useful utilities for GRanges objects

Remove chromosome ranges

```
gff <- gff[values(gff)$type != "chromosome"]
```

Erase the strand information

```
strand(gff) <- "*"
```

Collapses overlapping ranges to continuous ranges.

```
reduce(gff)
```

```
## GRanges object with 22 ranges and 0 metadata columns:
```

```
##      seqnames      ranges strand
##      <Rle>      <IRanges> <Rle>
## [1]   Chr1 [ 3631,  5899]      *
## [2]   Chr1 [ 5928,  8737]      *
## [3]   Chr1 [11649, 13714]      *
## [4]   Chr2 [ 1025,  2810]      *
## [5]   Chr2 [ 3706,  5513]      *
## ...      ...      ...      ...
## [18]  ChrC [   383,  1444]      *
## [19]  ChrC [ 1717,  4347]      *
## [20]  ChrM [   273,   734]      *
## [21]  ChrM [ 8848, 11415]      *
## [22]  ChrM [11918, 12241]      *
```

```
## -----
```

```
## seqinfo: 7 sequences from an unspecified genome
```

Return uncovered regions

```
gaps(gff)
```

```
## GRanges object with 43 ranges and 0 metadata columns:
```

```
##      seqnames      ranges strand
##      <Rle>      <IRanges> <Rle>
## [1]   Chr1 [    1, 30427671]      +
## [2]   Chr1 [    1, 30427671]      -
## [3]   Chr1 [    1,    3630]      *
## [4]   Chr1 [5900,    5927]      *
## [5]   Chr1 [8738,   11648]      *
## ...      ...      ...      ...
## [39]  ChrM [    1, 366924]      -
## [40]  ChrM [    1,    272]      *
## [41]  ChrM [  735,   8847]      *
## [42]  ChrM [11416, 11917]      *
## [43]  ChrM [12242, 366924]      *
```

```
## -----
```

```
## seqinfo: 7 sequences from an unspecified genome
```

More intuitive way to get uncovered regions

```
setdiff(as(seqinfo(gff), "GRanges"), gff)
```

```
## GRanges object with 29 ranges and 0 metadata columns:
```

```
##      seqnames      ranges strand
##      <Rle>      <IRanges> <Rle>
## [1]   Chr1 [    1,    3630]      *
## [2]   Chr1 [ 5900,    5927]      *
## [3]   Chr1 [ 8738,   11648]      *
## [4]   Chr1 [13715, 30427671]      *
## [5]   Chr2 [    1,    1024]      *
## ...      ...      ...      ...
```

```
## [25] ChrC [ 4348, 154478] *
## [26] ChrM [    1,    272] *
## [27] ChrM [  735,   8847] *
## [28] ChrM [11416, 11917] *
## [29] ChrM [12242, 366924] *
## -----
## seqinfo: 7 sequences from an unspecified genome
```

Return disjoint ranges

```
disjoin(gff)
```

```
## GRanges object with 211 ranges and 0 metadata columns:
##      seqnames      ranges strand
##      <Rle>      <IRanges> <Rle>
## [1] Chr1 [3631, 3759] *
## [2] Chr1 [3760, 3913] *
## [3] Chr1 [3914, 3995] *
## [4] Chr1 [3996, 4276] *
## [5] Chr1 [4277, 4485] *
## ...    ...      ...    ...
## [207] ChrC [ 1752,  4310] *
## [208] ChrC [ 4311,  4347] *
## [209] ChrM [  273,   734] *
## [210] ChrM [ 8848, 11415] *
## [211] ChrM [11918, 12241] *
## -----
## seqinfo: 7 sequences from an unspecified genome
```

Returns coverage of ranges

```
coverage(gff)
```

```
## RleList of length 7
## $Chr1
## integer-Rle of length 30427671 with 45 runs
## Lengths:      3630      129      154      82      281 ...      233      161      380 30413957
## Values :        0        4        5        3        5 ...        4        2        4        0
##
## $Chr2
## integer-Rle of length 19698289 with 14 runs
## Lengths:      1024      248      185      53      362 ...      164      625      102 19691617
## Values :        0        5        3        5        3 ...        3        0        5        0
##
## $Chr3
## integer-Rle of length 23459830 with 29 runs
## Lengths:      1652      145      139      111      95 ...      155      148      156 23453781
## Values :        0        4        5        3        5 ...        3        5        4        0
##
## $Chr4
## integer-Rle of length 18585056 with 72 runs
## Lengths:      1179      357      1358      128      872 ...      212      114      74 18571697
## Values :        0        5        0        5        3 ...        3        5        4        0
##
## $Chr5
## integer-Rle of length 26975502 with 64 runs
```

```
## Lengths:      1222      28      28      109      72 ...      76      55      174 26967058
## Values :         0        4        7        13      16 ...        3        5        4        0
##
## ...
## <2 more elements>
```

Return the index pairings for overlapping ranges

```
findOverlaps(gff, gff[1:4])
```

```
## Hits object with 55 hits and 0 metadata columns:
```

```
##      queryHits subjectHits
##      <integer>  <integer>
##      [1]         1         1
##      [2]         1         2
##      [3]         1         4
##      [4]         1         3
##      [5]         2         1
##      ...         ...         ...
##     [51]        16         1
##     [52]        16         2
##     [53]        16         3
##     [54]        17         1
##     [55]        17         2
## -----
```

```
## queryLength: 442 / subjectLength: 4
```

Counts overlapping ranges

```
countOverlaps(gff, gff[1:4])[1:40]
```

```
##  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 30 31 32 33 34
##  4  4  4  4  3  4  3  3  3  3  3  3  3  3  3  3  2  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
## 35 36 37 38 39 40 41
##  0  0  0  0  0  0  0
```

Return only overlapping ranges

```
subsetByOverlaps(gff, gff[1:4])
```

```
## GRanges object with 17 ranges and 10 metadata columns:
```

```
##      seqnames      ranges strand | source      type      score      phase
##      <Rle>      <IRanges> <Rle> | <factor>      <factor> <numeric> <integer>
##      2      Chr1 [3631, 5899]   * | TAIR10      mRNA      <NA>      <NA>
##      3      Chr1 [3631, 5899]   * | TAIR10      mRNA      <NA>      <NA>
##      4      Chr1 [3760, 5630]   * | TAIR10      protein   <NA>      <NA>
##      5      Chr1 [3631, 3913]   * | TAIR10      exon      <NA>      <NA>
##      6      Chr1 [3631, 3759]   * | TAIR10      five_prime_UTR <NA>      <NA>
##      ..      ...      ...      ... | ...      ...      ...      ...
##     14      Chr1 [5174, 5326]   * | TAIR10      exon      <NA>      <NA>
##     15      Chr1 [5174, 5326]   * | TAIR10      CDS      <NA>      0
##     16      Chr1 [5439, 5899]   * | TAIR10      exon      <NA>      <NA>
##     17      Chr1 [5439, 5630]   * | TAIR10      CDS      <NA>      0
##     18      Chr1 [5631, 5899]   * | TAIR10      three_prime_UTR <NA>      <NA>
##
##              ID      Name      Note      Parent      Index
##              <character> <character> <CharacterList> <CharacterList> <character>
##      2      AT1G01010.1 AT1G01010.1      AT1G01010      1
##      3      AT1G01010.1 AT1G01010.1      AT1G01010      1
```

```
## 4 AT1G01010.1-Protein AT1G01010.1 <NA>
## 5 <NA> <NA> AT1G01010.1 <NA>
## 6 <NA> <NA> AT1G01010.1 <NA>
## .. ... ...
## 14 <NA> <NA> AT1G01010.1 <NA>
## 15 <NA> <NA> AT1G01010.1,AT1G01010.1-Protein <NA>
## 16 <NA> <NA> AT1G01010.1 <NA>
## 17 <NA> <NA> AT1G01010.1,AT1G01010.1-Protein <NA>
## 18 <NA> <NA> AT1G01010.1 <NA>
## Derives_from
## <character>
## 2 <NA>
## 3 <NA>
## 4 AT1G01010.1
## 5 <NA>
## 6 <NA>
## .. ...
## 14 <NA>
## 15 <NA>
## 16 <NA>
## 17 <NA>
## 18 <NA>
## -----
## seqinfo: 7 sequences from an unspecified genome
```

GRangesList Objects

```
sp <- split(gff, seq(along=gff)) # Stores every range in separate component of a GRangesList object
split(gff, seqnames(gff)) # Stores ranges of each chromosome in separate component.
```

```
## GRangesList object of length 7:
```

```
## $Chr1
```

```
## GRanges object with 71 ranges and 10 metadata columns:
```

	seqnames	ranges	strand	source	type	score	phase
	<Rle>	<IRanges>	<Rle>	<factor>	<factor>	<numeric>	<integer>
## 2	Chr1	[3631, 5899]	*	TAIR10	mRNA	<NA>	<NA>
## 3	Chr1	[3631, 5899]	*	TAIR10	mRNA	<NA>	<NA>
## 4	Chr1	[3760, 5630]	*	TAIR10	protein	<NA>	<NA>
## 5	Chr1	[3631, 3913]	*	TAIR10	exon	<NA>	<NA>
## 6	Chr1	[3631, 3759]	*	TAIR10	five_prime_UTR	<NA>	<NA>
##
## 68	Chr1	[13335, 13714]	*	TAIR10	exon	<NA>	<NA>
## 69	Chr1	[12941, 13173]	*	TAIR10	five_prime_UTR	<NA>	<NA>
## 70	Chr1	[11864, 12940]	*	TAIR10	CDS	<NA>	0
## 71	Chr1	[11649, 11863]	*	TAIR10	three_prime_UTR	<NA>	<NA>
## 72	Chr1	[11649, 13173]	*	TAIR10	exon	<NA>	<NA>

	ID	Name	Note	Parent	Index
	<character>	<character>	<CharacterList>	<CharacterList>	<character>
## 2	AT1G01010.1	AT1G01010.1		AT1G01010	1
## 3	AT1G01010.1	AT1G01010.1		AT1G01010	1
## 4	AT1G01010.1-Protein	AT1G01010.1			<NA>
## 5	<NA>	<NA>		AT1G01010.1	<NA>
## 6	<NA>	<NA>		AT1G01010.1	<NA>

```
## ..      ...      ...      ...      ...
## 68      <NA>      <NA>      AT1G01030.1      <NA>
## 69      <NA>      <NA>      AT1G01030.1      <NA>
## 70      <NA>      <NA>      AT1G01030.1,AT1G01030.1-Protein      <NA>
## 71      <NA>      <NA>      AT1G01030.1      <NA>
## 72      <NA>      <NA>      AT1G01030.1      <NA>
## Derives_from
##   <character>
## 2      <NA>
## 3      <NA>
## 4 AT1G01010.1
## 5      <NA>
## 6      <NA>
## ..      ...
## 68      <NA>
## 69      <NA>
## 70      <NA>
## 71      <NA>
## 72      <NA>
##
## ...
## <6 more elements>
## -----
## seqinfo: 7 sequences from an unspecified genome
```

```
unlist(sp) # Returns data as GRanges object
```

```
## GRanges object with 442 ranges and 10 metadata columns:
```

```
##      seqnames      ranges strand | source      type      score      phase
##      <Rle>      <IRanges> <Rle> | <factor>      <factor> <numeric> <integer>
## 1.2      Chr1      [3631, 5899] * | TAIR10      mRNA      <NA>      <NA>
## 2.3      Chr1      [3631, 5899] * | TAIR10      mRNA      <NA>      <NA>
## 3.4      Chr1      [3760, 5630] * | TAIR10      protein    <NA>      <NA>
## 4.5      Chr1      [3631, 3913] * | TAIR10      exon       <NA>      <NA>
## 5.6      Chr1      [3631, 3759] * | TAIR10      five_prime_UTR <NA>      <NA>
## ...      ...      ...      ... | ...      ...      ...      ...
## 438.445    ChrM [11918, 12241] * | TAIR10      gene       <NA>      <NA>
## 439.446    ChrM [11918, 12241] * | TAIR10      mRNA      <NA>      <NA>
## 440.447    ChrM [11918, 12241] * | TAIR10      protein    <NA>      <NA>
## 441.448    ChrM [11918, 12241] * | TAIR10      exon       <NA>      <NA>
## 442.449    ChrM [11918, 12241] * | TAIR10      CDS        <NA>      0
##      ID      Name      Note      Parent
##      <character> <character> <CharacterList> <CharacterList>
## 1.2      AT1G01010.1 AT1G01010.1      AT1G01010
## 2.3      AT1G01010.1 AT1G01010.1      AT1G01010
## 3.4 AT1G01010.1-Protein AT1G01010.1
## 4.5      <NA>      <NA>      AT1G01010.1
## 5.6      <NA>      <NA>      AT1G01010.1
## ...      ...      ...      ...
## 438.445    ATMG00030      ATMG00030 protein_coding_gene
## 439.446    ATMG00030.1 ATMG00030.1      ATMG00030
## 440.447 ATMG00030.1-Protein ATMG00030.1
## 441.448    <NA>      <NA>      ATMG00030.1
## 442.449    <NA>      <NA>      ATMG00030.1,ATMG00030.1-Protein
##      Index Derives_from
```



```
##          <character> <character>
##      1.2          1          <NA>
##      2.3          1          <NA>
##      3.4          <NA> AT1G01010.1
##      4.5          <NA>          <NA>
##      5.6          <NA>          <NA>
##      ...          ...          ...
## 438.445          <NA>          <NA>
## 439.446          1          <NA>
## 440.447          <NA> ATMG00030.1
## 441.448          <NA>          <NA>
## 442.449          <NA>          <NA>
## -----
## seqinfo: 7 sequences from an unspecified genome

sp[1:4, "type"] # Subsetting of GRangesList objects is similar to GRanges objects.

## GRangesList object of length 4:
## $1
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand |      type
##      <Rle>      <IRanges> <Rle> | <factor>
##  2      Chr1 [3631, 5899]      * |      mRNA
##
## $2
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand | type
##  3      Chr1 [3631, 5899]      * | mRNA
##
## $3
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand |      type
##  4      Chr1 [3760, 5630]      * | protein
##
## ...
## <1 more element>
## -----
## seqinfo: 7 sequences from an unspecified genome

lapply(sp[1:4], length) # Looping over GRangesList objects similar to lists

## $`1`
## [1] 1
##
## $`2`
## [1] 1
##
## $`3`
## [1] 1
##
## $`4`
## [1] 1
```

Transcript Ranges

Storing annotation ranges in TranscriptDb databases makes many operations more robust and convenient.

```
library(GenomicFeatures)
download.file("http://faculty.ucr.edu/~tgirke/Documents/R_BioCond/Samples/gff3.gff", "data/gff3.gff")
txdb <- makeTxDbFromGFF(file="data/gff3.gff", format="gff", dataSource="TAIR", organism="Arabidopsis thaliana")

## Warning in .extract_exons_from_GRanges(cds_IDX, gr, ID, Name, Parent, feature = "cds", : The following
##   seqid start end strand ID Parent Name
## 1 Chr1 3760 3913 + <NA> AT1G01010.1-Protein <NA>
## 2 Chr1 3996 4276 + <NA> AT1G01010.1-Protein <NA>
## 3 Chr1 4486 4605 + <NA> AT1G01010.1-Protein <NA>
## 4 Chr1 4706 5095 + <NA> AT1G01010.1-Protein <NA>
## 5 Chr1 5174 5326 + <NA> AT1G01010.1-Protein <NA>
## 6 Chr1 5439 5630 + <NA> AT1G01010.1-Protein <NA>

saveDb(txdb, file="./data/TAIR10.sqlite")

## TxDb object:
## # Db type: TxDb
## # Supporting package: GenomicFeatures
## # Data source: TAIR
## # Organism: Arabidopsis thaliana
## # Taxonomy ID: 3702
## # miRBase build ID: NA
## # Genome: NA
## # transcript_nrow: 28
## # exon_nrow: 113
## # cds_nrow: 99
## # Db created by: GenomicFeatures package from Bioconductor
## # Creation time: 2018-04-25 16:29:04 -0700 (Wed, 25 Apr 2018)
## # GenomicFeatures version at creation time: 1.30.3
## # RSQLite version at creation time: 2.0
## # DBSCHEMAVERSION: 1.2

txdb <- loadDb("./data/TAIR10.sqlite")
transcripts(txdb)

## GRanges object with 28 ranges and 2 metadata columns:
##      seqnames      ranges strand | tx_id tx_name
##      <Rle>      <IRanges> <Rle> | <integer> <character>
## [1] Chr1 [ 3631, 5899] + | 1 AT1G01010.1
## [2] Chr1 [ 5928, 8737] - | 2 AT1G01020.1
## [3] Chr1 [ 6790, 8737] - | 3 AT1G01020.2
## [4] Chr1 [11649, 13714] - | 4 AT1G01030.1
## [5] Chr2 [ 1025, 2810] + | 5 AT2G01008.1
## ...      ...      ...      ... | ...      ...
## [24] ChrC [ 383, 1444] - | 24 ATCG00020.1
## [25] ChrC [ 1717, 4347] - | 25 ATCG00030.1
## [26] ChrM [11918, 12241] + | 26 ATMG00030.1
## [27] ChrM [ 273, 734] - | 27 ATMG00010.1
## [28] ChrM [ 8848, 11415] - | 28 ATMG00020.1
## -----
## seqinfo: 7 sequences (2 circular) from an unspecified genome; no seqlengths
```

```
transcriptsBy(txdb, by = "gene")
```

```
## GRangesList object of length 22:
## $AT1G01010
## GRanges object with 1 range and 2 metadata columns:
##      seqnames      ranges strand |      tx_id      tx_name
##      <Rle>      <IRanges> <Rle> | <integer> <character>
## [1]      Chr1 [3631, 5899]      + |          1 AT1G01010.1
##
## $AT1G01020
## GRanges object with 2 ranges and 2 metadata columns:
##      seqnames      ranges strand | tx_id      tx_name
## [1]      Chr1 [5928, 8737]      - |      2 AT1G01020.1
## [2]      Chr1 [6790, 8737]      - |      3 AT1G01020.2
##
## $AT1G01030
## GRanges object with 1 range and 2 metadata columns:
##      seqnames      ranges strand | tx_id      tx_name
## [1]      Chr1 [11649, 13714]      - |      4 AT1G01030.1
##
## ...
## <19 more elements>
## -----
## seqinfo: 7 sequences (2 circular) from an unspecified genome; no seqlengths
```

```
exonsBy(txdb, by = "gene")
```

```
## GRangesList object of length 22:
## $AT1G01010
## GRanges object with 6 ranges and 2 metadata columns:
##      seqnames      ranges strand | exon_id exon_name
##      <Rle>      <IRanges> <Rle> | <integer> <character>
## [1]      Chr1 [3631, 3913]      + |          1      <NA>
## [2]      Chr1 [3996, 4276]      + |          2      <NA>
## [3]      Chr1 [4486, 4605]      + |          3      <NA>
## [4]      Chr1 [4706, 5095]      + |          4      <NA>
## [5]      Chr1 [5174, 5326]      + |          5      <NA>
## [6]      Chr1 [5439, 5899]      + |          6      <NA>
##
## $AT1G01020
## GRanges object with 12 ranges and 2 metadata columns:
##      seqnames      ranges strand | exon_id exon_name
## [1]      Chr1 [5928, 6263]      - |          7      <NA>
## [2]      Chr1 [6437, 7069]      - |          8      <NA>
## [3]      Chr1 [6790, 7069]      - |          9      <NA>
## [4]      Chr1 [7157, 7232]      - |         10      <NA>
## [5]      Chr1 [7157, 7450]      - |         11      <NA>
## [6]      ...      ...      ...      ...      ...
## [8]      Chr1 [7762, 7835]      - |         14      <NA>
## [9]      Chr1 [7942, 7987]      - |         15      <NA>
## [10]     Chr1 [8236, 8325]      - |         16      <NA>
## [11]     Chr1 [8417, 8464]      - |         17      <NA>
## [12]     Chr1 [8571, 8737]      - |         18      <NA>
##
```

```
## $AT1G01030
## GRanges object with 2 ranges and 2 metadata columns:
##      seqnames      ranges strand | exon_id exon_name
##   [1]      Chr1 [11649, 13173]   - |      19      <NA>
##   [2]      Chr1 [13335, 13714]   - |      20      <NA>
##
## ...
## <19 more elements>
## -----
## seqinfo: 7 sequences (2 circular) from an unspecified genome; no seqlengths
```

txdb from BioMart

Alternative sources for creating txdb databases are BioMart, Bioc annotation packages, UCSC, etc. The following shows how to create a txdb from BioMart.

```
library(GenomicFeatures); library("biomaRt")
txdb <- makeTxDbFromBiomart(biomart = "plants_mart", dataset = "athaliana_eg_gene", host="plants.ensembl.org")
```

The following steps are useful to find out what is available in BioMart.

```
listMarts() # Lists BioMart databases
listMarts(host="plants.ensembl.org")
mymart <- useMart("plants_mart", host="plants.ensembl.org") # Select one, here plants_mart_25
listDatasets(mymart) # List datasets available in the selected BioMart database
mymart <- useMart("plants_mart", dataset="athaliana_eg_gene", host="plants.ensembl.org")
listAttributes(mymart) # List available features
getBM(attributes=c("ensembl_gene_id", "description"), mart=mymart)[1:4,]
```

Efficient Sequence Parsing

getSeq

The following parses all annotation ranges provided by a GRanges object (e.g. gff) from a genome sequence stored in a local file.

```
gff <- gff[values(gff)$type != "chromosome"] # Remove chromosome ranges
rand <- DNAStringSet(sapply(unique(as.character(seqnames(gff))), function(x) paste(sample(c("A","T","G"),
writeXStringSet(DNAStringSet(rand), "./data/test")
getSeq(FaFile("./data/test"), gff)
```

```
## A DNAStringSet instance of length 442
##      width seq                                     names
##   [1]  2269 ATGTGTAGGCAATCAGTCACCTTGCATCGATG...CTAGGATAGAGACCACACAGCAAGCGACTTAG Chr1
##   [2]  2269 ATGTGTAGGCAATCAGTCACCTTGCATCGATG...CTAGGATAGAGACCACACAGCAAGCGACTTAG Chr1
##   [3]  1871 GAGGCAATATCTTCATGGAGCAAATAAAAGCT...GATCCGATCGACCACCAAGGGATGGGGCCCCG Chr1
##   [4]   283 ATGTGTAGGCAATCAGTCACCTTGCATCGATG...GAGGCAGATCTTTCAGCGGACTACAGCATAAC Chr1
##   [5]   129 ATGTGTAGGCAATCAGTCACCTTGCATCGATG...CGATCTACCCATCAAGCTCTGGCTCACGCCAT Chr1
##   ...
## [438]   324 CTGTTAGAGATTTTCGGGCACCGACTGGGAGCT...CCACGGTGATCGAACTCGAAAAGCTTTAGTTG ChrM
## [439]   324 CTGTTAGAGATTTTCGGGCACCGACTGGGAGCT...CCACGGTGATCGAACTCGAAAAGCTTTAGTTG ChrM
## [440]   324 CTGTTAGAGATTTTCGGGCACCGACTGGGAGCT...CCACGGTGATCGAACTCGAAAAGCTTTAGTTG ChrM
## [441]   324 CTGTTAGAGATTTTCGGGCACCGACTGGGAGCT...CCACGGTGATCGAACTCGAAAAGCTTTAGTTG ChrM
## [442]   324 CTGTTAGAGATTTTCGGGCACCGACTGGGAGCT...CCACGGTGATCGAACTCGAAAAGCTTTAGTTG ChrM
```

extractTranscriptSeqs

Sequences composed of several ranges, such as transcripts (or CDSs) with several exons, can be parsed with `extractTranscriptSeqs`. Note: the following expects the genome sequence in a file called `mygenome.fasta` and a valid `txdb` defining the ranges for that genome.

```
library(GenomicFeatures); library(Biostrings); library(Rsamtools)
indexFa("mygenome.fasta") # Creates index for genome fasta
txseq <- extractTranscriptSeqs(FaFile("mygenome.fasta"), txdb, use.names=TRUE)
```

Homework 6

HW6a - Demultiplexing

Write a demultiplexing function that accepts any number of barcodes and splits a FASTQ file into as many subfiles as there are barcodes. At the same time the function should remove low quality tails from the reads. The following function accomplishes the first step. Expand this function so that it performs the second step as well.

```
demultiplex <- function(x, barcode, nreads) {
  f <- FastqStreamer(x, nreads)
  while(length(fq <- yield(f))) {
    for(i in barcode) {
      pattern <- paste("^", i, sep="")
      fqsub <- fq[grepl(pattern, sread(fq))]
      if(length(fqsub) > 0) {
        writeFastq(fqsub, paste(x, i, sep="_"), mode="a", compress=FALSE)
      }
    }
  }
  close(f)
}
demultiplex(x=fastq[1], barcode=c("TT", "AA", "GG"), nreads=50)
```

HW6b - Sequence Parsing

- Download GFF from *Halobacterium sp* here
- Download genome sequence from *Halobacterium sp* here
- **Task 1** Extract gene ranges, parse their sequences from genome and translate them into proteins
- **Task 2** Reduce overlapping genes and parse their sequences from genome
- **Task 3** Generate intergenic ranges and parse their sequences from genome

Useful commands

```
download.file("ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Bacteria/Halobacterium_sp_uid217/");
download.file("ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Bacteria/Halobacterium_sp_uid217/");
chr <- readDNASTringSet("data/AE004437.fna")
gff <- import("data/AE004437.gff")
gffgene <- gff[values(gff)[,"type"]=="gene"]
gene <- DNASTringSet(Views(chr[[1]], IRanges(start(gffgene), end(gffgene))))
names(gene) <- values(gffgene)[,"locus_tag"]
pos <- values(gffgene[strand(gffgene) == "+"])[,"locus_tag"]
p1 <- translate(gene[names(gene) %in% pos])
```

```
names(p1) <- names(gene[names(gene) %in% pos])
neg <- values(gffgene[strand(gffgene) == "-"][, "locus_tag"])
p2 <- translate(reverseComplement(gene[names(gene) %in% neg]))
names(p2) <- names(gene[names(gene) %in% neg])
writeXStringSet(c(p1, p2), "./data/mypep.fasta")
```

Homework submission

Submit the homework results in one well structured and annotated R script to the instructor. The script should include instructions on how to use the functions.

Due date

This homework is due on Thu, May 4th at 6:00 PM.

Homework Solutions

See here

Session Info

```
sessionInfo()
```

```
## R version 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C               LC_TIME=en_US.UTF-8
##  [4] LC_COLLATE=en_US.UTF-8    LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8      LC_NAME=C                  LC_ADDRESS=C
## [10] LC_TELEPHONE=C            LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
##  [1] grid      stats4     parallel  methods   stats      graphics  grDevices  utils      datasets
## [10] base
##
## other attached packages:
##  [1] GenomicFeatures_1.30.3      AnnotationDbi_1.40.0        rtracklayer_1.38.3
##  [4] systemPipeR_1.12.0          ShortRead_1.36.1            GenomicAlignments_1.14.2
##  [7] SummarizedExperiment_1.8.1 DelayedArray_0.4.1          matrixStats_0.52.2
## [10] Biobase_2.38.0              Rsamtools_1.30.0            GenomicRanges_1.30.3
## [13] GenomeInfoDb_1.14.0         BiocParallel_1.12.0         ggseqlogo_0.1
## [16] seqLogo_1.44.0              Biostrings_2.46.0           XVector_0.18.0
## [19] IRanges_2.12.0              S4Vectors_0.16.0           BiocGenerics_0.24.0
```

```
## [22] ggplot2_2.2.1          limma_3.34.1          BiocStyle_2.6.0
##
## loaded via a namespace (and not attached):
## [1] Category_2.44.0        bitops_1.0-6          bit64_0.9-7           RColorBrewer_1.1-2
## [5] progress_1.1.2         httr_1.3.1            rprojroot_1.2         Rgraphviz_2.22.0
## [9] tools_3.4.4           backports_1.1.1       R6_2.2.2              DBI_0.7
## [13] lazyeval_0.2.1        colorspace_1.3-2      prettyunits_1.0.2     RMySQL_0.10.14
## [17] bit_1.1-12            compiler_3.4.4        sendmailR_1.2-1       graph_1.56.0
## [21] labeling_0.3           scales_0.5.0          checkmate_1.8.5       BatchJobs_1.7
## [25] genefilter_1.60.0     RBGL_1.54.0          stringr_1.2.0         digest_0.6.12
## [29] rmarkdown_1.8         AnnotationForge_1.20.0 base64enc_0.1-3       pkgconfig_2.0.1
## [33] htmltools_0.3.6       rlang_0.2.0           RSQLite_2.0           BBmisc_1.11
## [37] GOstats_2.44.0        hwriter_1.3.2         RCurl_1.95-4.8        magrittr_1.5
## [41] GO.db_3.5.0           GenomeInfoDbData_1.0.0 Matrix_1.2-14         Rcpp_0.12.13
## [45] munsell_0.4.3         stringi_1.1.6         yaml_2.1.14           edgeR_3.20.1
## [49] zlibbioc_1.24.0       plyr_1.8.4           blob_1.1.0            lattice_0.20-35
## [53] splines_3.4.4         annotate_1.56.1        locfit_1.5-9.1        knitr_1.17
## [57] pillar_1.2.1          rjson_0.2.15          codetools_0.2-15      biomaRt_2.34.2
## [61] XML_3.98-1.9          evaluate_0.10.1       latticeExtra_0.6-28   data.table_1.10.4-3
## [65] gtable_0.2.0          assertthat_0.2.0      xtable_1.8-2          survival_2.42-3
## [69] tibble_1.4.2          pheatmap_1.0.8        memoise_1.1.0         brew_1.0-6
## [73] GSEABase_1.40.0
```

References

Huber, Wolfgang, Vincent J Carey, Robert Gentleman, Simon Anders, Marc Carlson, Benilton S Carvalho, Hector Corrada Bravo, et al. 2015. “Orchestrating High-Throughput Genomic Analysis with Bioconductor.” *Nat. Methods* 12 (2): 115–21. doi:10.1038/nmeth.3252.

Lawrence, Michael, Wolfgang Huber, Hervé Pagès, Patrick Aboyoun, Marc Carlson, Robert Gentleman, Martin T Morgan, and Vincent J Carey. 2013. “Software for Computing and Annotating Genomic Ranges.” *PLoS Comput. Biol.* 9 (8): e1003118. doi:10.1371/journal.pcbi.1003118.