

# GenomicRanges HOWTOs

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## 1 Introduction

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### 1.1 Purpose of this document

This document is a collection of *HOWTOs*. Each *HOWTO* is a short section that demonstrates how to use the containers and operations implemented in the *GenomicRanges* and related packages (*IRanges*, *Biostrings*, *Rsamtools*, *GenomicAlign-*

[ments](#), [BSgenome](#), and [GenomicFeatures](#)) to perform a task typically found in the context of a high throughput sequence analysis.

Unless stated otherwise, the *HOWTOs* are self contained, independent of each other, and can be studied and reproduced in any order.

## 1.2 Prerequisites and additional recommended reading

We assume the reader has some previous experience with *R* and with basic manipulation of *GRanges*, *GRangesList*, *Rle*, *RleList*, and *DataFrame* objects. See the “An Introduction to Genomic Ranges Classes” vignette located in the [GenomicRanges](#) package (in the same folder as this document) for an introduction to these containers.

Additional recommended readings after this document are the “Software for Computing and Annotating Genomic Ranges” paper [Lawrence et al. (2013)] and the “Counting reads with summarizeOverlaps” vignette located in the [GenomicAlignments](#) package.

To display the list of vignettes available in the [GenomicRanges](#) package, use `browseVignettes("GenomicRanges")`.

## 1.3 Input data and terminology used across the HOWTOs

In order to avoid repetition, input data, concepts and terms used in more than one *HOWTO* are described here:

- **The [pasillaBamSubset](#) data package:** contains both a BAM file with single-end reads (`untreated1_chr4`) and a BAM file with paired-end reads (`untreated3_chr4`). Each file is a subset of chr4 from the “Pasilla” experiment.  

```
> library(pasillaBamSubset)
> untreated1_chr4()
[1] "/home/biobuild/bbs-3.3-bioc/R/library/pasillaBamSubset/extdata/untreated1_chr4.bam"
> untreated3_chr4()
[1] "/home/biobuild/bbs-3.3-bioc/R/library/pasillaBamSubset/extdata/untreated3_chr4.bam"
See ?pasillaBamSubset for more information.
> ?pasillaBamSubset
```
- **Gene models and TxDb objects:** A *gene model* is essentially a set of annotations that describes the genomic locations of the known genes, transcripts, exons, and CDS, for a given organism. In *Bioconductor* it is typically represented as a *TxDb* object but also sometimes as a *GRanges* or *GRangesList* object. The [GenomicFeatures](#) package contains tools for making and manipulating *TxDb* objects.

# 2 HOWTOs

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## 2.1 How to read single-end reads from a BAM file

As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> un1 <- untreated1_chr4() # single-end reads
```

Several functions are available for reading BAM files into *R*:

```
readGAlignments()
readGAlignmentPairs()
readGAlignmentsList()
scanBam()
```

`scanBam` is a low-level function that returns a list of lists and is not discussed further here. See `?scanBam` in the [Rsamtools](#) package for more information.

Single-end reads can be loaded with the `readGAlignments` function from the [GenomicAlignments](#) package.

```
> library(GenomicAlignments)
> gal <- readGAlignments(un1)
```

Data subsets can be specified by genomic position, field names, or flag criteria in the `ScanBamParam`. Here we input records that overlap position 1 to 5000 on the negative strand with `flag` and `cigar` as metadata columns.

```
> what <- c("flag", "cigar")
> which <- GRanges("chr4", IRanges(1, 5000))
> flag <- scanBamFlag(isMinusStrand = TRUE)
> param <- ScanBamParam(which=which, what=what, flag=flag)
> neg <- readGAlignments(un1, param=param)
> neg
```

GAlignments object with 37 alignments and 2 metadata columns:

	seqnames	strand	cigar	qwidth	start	end
	<Rle>	<Rle>	<character>	<integer>	<integer>	<integer>
[1]	chr4	-	75M	75	892	966
[2]	chr4	-	75M	75	919	993
[3]	chr4	-	75M	75	967	1041
...	...	...	...	...	...	...
[35]	chr4	-	75M	75	4997	5071
[36]	chr4	-	75M	75	4998	5072
[37]	chr4	-	75M	75	4999	5073

  

	width	njunc	flag	cigar
	<integer>	<integer>	<integer>	<character>
[1]	75	0	16	75M
[2]	75	0	16	75M
[3]	75	0	16	75M
...	...	...	...	...
[35]	75	0	16	75M
[36]	75	0	16	75M
[37]	75	0	16	75M

-----  
seqinfo: 8 sequences from an unspecified genome

Another approach to subsetting the data is to use `filterBam`. This function creates a new BAM file of records passing user-defined criteria. See `?filterBam` in the [Rsamtools](#) package for more information.

## 2.2 How to read paired-end reads from a BAM file

As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> un3 <- untreated3_chr4() # paired-end reads
```

Paired-end reads can be loaded with the `readGAlignmentPairs` or `readGAlignmentsList` function from the [GenomicAlignments](#) package. These functions use the same mate pairing algorithm but output different objects.

Let's start with `readGAlignmentPairs`:

```
> un3 <- untreated3_chr4()
> gapairs <- readGAlignmentPairs(un3)
```

The `GAlignmentPairs` class holds only pairs; reads with no mate or with ambiguous pairing are discarded. Each list element holds exactly 2 records (a mated pair). Records can be accessed as the `first` and `last` segments in a template or as `left` and `right` alignments. See `?GAlignmentPairs` in the [GenomicAlignments](#) package for more information.

```
> gapairs
```

GAlignmentPairs object with 75346 pairs, strandMode=1, and 0 metadata columns:

	seqnames	strand	:	ranges	--	ranges
	<Rle>	<Rle>	:	<IRanges>	--	<IRanges>
[1]	chr4	+	:	[169, 205]	--	[ 326, 362]
[2]	chr4	+	:	[943, 979]	--	[1086, 1122]
[3]	chr4	+	:	[944, 980]	--	[1119, 1155]
...	...	...	...	...	...	...
[75344]	chr4	+	:	[1348217, 1348253]	--	[1348215, 1348251]
[75345]	chr4	+	:	[1349196, 1349232]	--	[1349326, 1349362]
[75346]	chr4	+	:	[1349708, 1349744]	--	[1349838, 1349874]

-----  
seqinfo: 8 sequences from an unspecified genome

For readGAlignmentsList, mate pairing is performed when asMates is set to TRUE on the BamFile object, otherwise records are treated as single-end.

```
> galist <- readGAlignmentsList(BamFile(un3, asMates=TRUE))
```

GAlignmentsList is a more general 'list-like' structure that holds mate pairs as well as non-mates (i.e., singletons, records with unmapped mates etc.) A mates\_status metadata column (accessed with mcols) indicates which records were paired.

```
> galist
```

GAlignmentsList object of length 96636:

```
[[1]]
```

GAlignments object with 2 alignments and 0 metadata columns:

	seqnames	strand	cigar	qwidth	start	end	width	njunc
[1]	chr4	+	37M	37	169	205	37	0
[2]	chr4	-	37M	37	326	362	37	0

```
[[2]]
```

GAlignments object with 2 alignments and 0 metadata columns:

	seqnames	strand	cigar	qwidth	start	end	width	njunc
[1]	chr4	+	37M	37	946	982	37	0
[2]	chr4	-	37M	37	986	1022	37	0

```
[[3]]
```

GAlignments object with 2 alignments and 0 metadata columns:

	seqnames	strand	cigar	qwidth	start	end	width	njunc
[1]	chr4	+	37M	37	943	979	37	0
[2]	chr4	-	37M	37	1086	1122	37	0

```
...
```

```
<96633 more elements>
```

```
-----
```

seqinfo: 8 sequences from an unspecified genome

Non-mated reads are returned as groups by QNAME and contain any number of records. Here the non-mate groups range in size from 1 to 9.

```
> non_mates <- galist[unlist(mcols(galist)$mate_status) == "unmated"]
```

```
> table(elementNROWS(non_mates))
```

1	2	3	4	5	6	7	8	9
18191	2888	69	60	7	8	2	1	1

## 2.3 How to read and process a big BAM file by chunks in order to reduce memory usage

A large BAM file can be iterated through in chunks by setting a `yieldSize` on the *BamFile* object. As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> un1 <- untreated1_chr4()
> bf <- BamFile(un1, yieldSize=100000)
```

Iteration through a BAM file requires that the file be opened, repeatedly queried inside a loop, then closed. Repeated calls to `readGAlignments` without opening the file first result in the same 100000 records returned each time.

```
> open(bf)
> cvg <- NULL
> repeat {
+   chunk <- readGAlignments(bf)
+   if (length(chunk) == 0L)
+     break
+   chunk_cvg <- coverage(chunk)
+   if (is.null(cvg)) {
+     cvg <- chunk_cvg
+   } else {
+     cvg <- cvg + chunk_cvg
+   }
+ }
> close(bf)
> cvg

RleList of length 8
$chr2L
integer-Rle of length 23011544 with 1 run
  Lengths: 23011544
  Values :      0

$chr2R
integer-Rle of length 21146708 with 1 run
  Lengths: 21146708
  Values :      0

$chr3L
integer-Rle of length 24543557 with 1 run
  Lengths: 24543557
  Values :      0

$chr3R
integer-Rle of length 27905053 with 1 run
  Lengths: 27905053
  Values :      0

$chr4
integer-Rle of length 1351857 with 122061 runs
  Lengths: 891  27  5  12  13  45 ... 106  75 1600  75 1659
  Values :  0  1  2  3  4  5 ...  0  1  0  1  0

...
<3 more elements>
```

## 2.4 How to compute read coverage

The “read coverage” is the number of reads that cover a given genomic position. Computing the read coverage generally consists in computing the coverage at each position in the genome. This can be done with the `coverage()` function.

As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> un1 <- untreated1_chr4() # single-end reads
> library(GenomicAlignments)
> reads1 <- readGAlignments(un1)
> cvg1 <- coverage(reads1)
> cvg1

RleList of length 8
$chr2L
integer-Rle of length 23011544 with 1 run
  Lengths: 23011544
  Values :      0

$chr2R
integer-Rle of length 21146708 with 1 run
  Lengths: 21146708
  Values :      0

$chr3L
integer-Rle of length 24543557 with 1 run
  Lengths: 24543557
  Values :      0

$chr3R
integer-Rle of length 27905053 with 1 run
  Lengths: 27905053
  Values :      0

$chr4
integer-Rle of length 1351857 with 122061 runs
  Lengths: 891 27 5 12 13 45 ... 106 75 1600 75 1659
  Values : 0 1 2 3 4 5 ... 0 1 0 1 0

...
<3 more elements>

Coverage on chr4:
> cvg1$chr4

integer-Rle of length 1351857 with 122061 runs
  Lengths: 891 27 5 12 13 45 ... 106 75 1600 75 1659
  Values : 0 1 2 3 4 5 ... 0 1 0 1 0

Average and max coverage:
> mean(cvg1$chr4)
[1] 11.33746
> max(cvg1$chr4)
[1] 5627
```

Note that `coverage()` is a generic function with methods for different types of objects. See `?coverage` for more information.

## 2.5 How to find peaks in read coverage

ChIP-Seq analysis usually involves finding peaks in read coverage. This process is sometimes called “peak calling” or “peak detection”. Here we’re only showing a naive way to find peaks in the object returned by the `coverage()` function. *Bioconductor* packages [BayesPeak](#), [bumphunter](#), [Starr](#), [CexoR](#), [exomePeak](#), [RIPSeeker](#), and others, provide sophisticated peak calling tools for ChIP-Seq, RIP-Seq, and other kind of high throughput sequencing data.

Let’s assume `cvg1` is the object returned by `coverage()` (see previous *HOWTO* for how to compute it). We can use the `slice()` function to find the genomic regions where the coverage is greater or equal to a given threshold.

```
> chr4_peaks <- slice(cvg1$chr4, lower=500)
> chr4_peaks
```

Views on a 1351857-length Rle subject

views:

	start	end	width	
[1]	86849	87364	516	[ 525  538  554  580  583  585  589 ...]
[2]	87466	87810	345	[4924 4928 4941 4943 4972 5026 5039 ...]
[3]	340791	340798	8	[508 512 506 530 521 519 518 501]
[4]	340800	340885	86	[500 505 560 560 565 558 564 559 555 ...]
[5]	348477	348483	7	[503 507 501 524 515 513 512]
[6]	348488	348571	84	[554 554 559 552 558 553 549 550 559 ...]
[7]	692512	692530	19	[502 507 508 518 520 522 524 526 547 ...]
[8]	692551	692657	107	[ 530  549  555  635  645  723  725 ...]
[9]	692798	692800	3	[503 500 503]
...	...	...	...	...
[34]	1054306	1054306	1	[502]
[35]	1054349	1054349	1	[501]
[36]	1054355	1054444	90	[510 521 525 532 532 539 549 555 557 ...]
[37]	1054448	1054476	29	[502 507 516 517 508 517 525 528 532 ...]
[38]	1054479	1054482	4	[504 503 506 507]
[39]	1054509	1054509	1	[500]
[40]	1054511	1054511	1	[502]
[41]	1054521	1054623	103	[529 521 529 530 524 525 547 540 536 ...]
[42]	1054653	1054717	65	[520 519 516 528 526 585 591 589 584 ...]

```
> length(chr4_peaks) # nb of peaks
```

```
[1] 42
```

The weight of a given peak can be defined as the number of aligned nucleotides that belong to the peak (a.k.a. the area under the peak in mathematics). It can be obtained with `sum()`:

```
> sum(chr4_peaks)
```

[1]	1726347	1300700	4115	52301	3575	51233	10382	95103
[9]	1506	500	2051	500	5834	10382	92163	500
[17]	88678	1512	500	11518	14514	5915	3598	7821
[25]	511	508	503	500	1547	8961	43426	22842
[33]	503	502	501	51881	15116	2020	500	502
[41]	67010	40496						

## 2.6 How to retrieve a gene model from the UCSC genome browser

See introduction for a quick description of what *gene models* and *TxDb* objects are. We can use the `makeTranscriptDbFromUCSC()` function from the *GenomicFeatures* package to import a UCSC genome browser track as a *TxDb* object.

```
> library(GenomicFeatures)
> ### Internet connection required! Can take several minutes...
> txdb <- makeTxDbFromUCSC(genome="sacCer2", tablename="ensGene")
```

See `?makeTxDbFromUCSC` in the *GenomicFeatures* package for more information.

Note that some of the most frequently used gene models are available as *TxDb* packages. A *TxDb* package consists of a pre-made *TxDb* object wrapped into an annotation data package. Go to [http://bioconductor.org/packages/release/BiocViews.html#\\_\\_\\_TxDb](http://bioconductor.org/packages/release/BiocViews.html#___TxDb) to browse the list of available *TxDb* packages.

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

*TxDb* object:

```
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: UCSC
# Genome: hg19
# Organism: Homo sapiens
# Taxonomy ID: 9606
# UCSC Table: knownGene
# Resource URL: http://genome.ucsc.edu/
# Type of Gene ID: Entrez Gene ID
# Full dataset: yes
# miRBase build ID: GRCh37
# transcript_nrow: 82960
# exon_nrow: 289969
# cds_nrow: 237533
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2015-10-07 18:11:28 +0000 (Wed, 07 Oct 2015)
# GenomicFeatures version at creation time: 1.21.30
# RSQLite version at creation time: 1.0.0
# DBSCHEMAVERSION: 1.1
```

Extract the transcript coordinates from this gene model:

```
> transcripts(txdb)
```

GRanges object with 82960 ranges and 2 metadata columns:

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	chr1	[11874, 14409]	+	1	uc001aaa.3
[2]	chr1	[11874, 14409]	+	2	uc010nxq.1
[3]	chr1	[11874, 14409]	+	3	uc010nxr.1
...	...	...	...	...	...
[82958]	chrUn_g1000243	[11501, 11530]	+	82958	uc011mgw.1
[82959]	chrUn_g1000243	[13608, 13637]	+	82959	uc022brq.1
[82960]	chrUn_g1000247	[ 5787, 5816]	-	82960	uc022brr.1

-----

seqinfo: 93 sequences (1 circular) from hg19 genome



## 2.7 How to retrieve a gene model from Ensembl

See introduction for a quick description of what *gene models* and *TxDb* objects are. We can use the `makeTranscriptDbFromBiomart()` function from the *GenomicFeatures* package to retrieve a gene model from the Ensembl Mart.

```
> library(GenomicFeatures)
> ### Internet connection required! Can take several minutes...
> txdb <- makeTxDbFromBiomart(biomart="ensembl",
+                             dataset="hsapiens_gene_ensembl")
```

See `?makeTxDbFromBiomart` in the *GenomicFeatures* package for more information.

Note that some of the most frequently used gene models are available as *TxDb* packages. A *TxDb* package consists of a pre-made *TxDb* object wrapped into an annotation data package. Go to [http://bioconductor.org/packages/release/BiocViews.html#\\_\\_\\_TxDb](http://bioconductor.org/packages/release/BiocViews.html#___TxDb) to browse the list of available *TxDb* packages.

```
> library(TxDb.Athaliana.BioMart.plantsmart22)
> txdb <- TxDb.Athaliana.BioMart.plantsmart22
> txdb
```

*TxDb* object:

```
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: BioMart
# Organism: Arabidopsis thaliana
# Resource URL: www.biomart.org:80
# BioMart database: plants_mart_22
# BioMart database version: ENSEMBL PLANTS 22 (EBI UK)
# BioMart dataset: athaliana_eg_gene
# BioMart dataset description: Arabidopsis thaliana genes (TAIR10 (2010-09-TAIR10))
# BioMart dataset version: TAIR10 (2010-09-TAIR10)
# Full dataset: yes
# miRBase build ID: NA
# transcript_nrow: 41671
# exon_nrow: 171013
# cds_nrow: 147494
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2014-09-26 11:23:54 -0700 (Fri, 26 Sep 2014)
# GenomicFeatures version at creation time: 1.17.17
# RSQLite version at creation time: 0.11.4
# DBSCHEMAVERSION: 1.0
# TaxID: 3702
```

Extract the exon coordinates from this gene model:

```
> exons(txdb)
```

GRanges object with 171013 ranges and 1 metadata column:

	seqnames	ranges	strand	exon_id
	<Rle>	<IRanges>	<Rle>	<integer>
[1]	1	[3631, 3913]	+	1
[2]	1	[3996, 4276]	+	2
[3]	1	[4486, 4605]	+	3
...	...	...	...	...
[171011]	Pt	[137869, 137940]	-	171011
[171012]	Pt	[144921, 145154]	-	171012
[171013]	Pt	[145291, 152175]	-	171013

```
-----
seqinfo: 7 sequences (1 circular) from an unspecified genome
```

## 2.8 How to load a gene model from a GFF or GTF file

See introduction for a quick description of what *gene models* and *TxDb* objects are. We can use the `makeTranscriptDbFromGFF()` function from the [GenomicFeatures](#) package to import a GFF or GTF file as a *TxDb* object.

```
> library(GenomicFeatures)
> gff_file <- system.file("extdata", "GFF3_files", "a.gff3",
+                          package="GenomicFeatures")
> txdb <- makeTxDbFromGFF(gff_file, format="gff3")
> txdb

TxDb object:
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: /home/biocbuild/bbs-3.3-bioc/R/library/GenomicFeatures/extdata/GFF3_files/a.gff3
# Organism: NA
# Taxonomy ID: NA
# miRBase build ID: NA
# Genome: NA
# transcript_nrow: 488
# exon_nrow: 1268
# cds_nrow: 1258
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2016-06-14 19:19:53 -0700 (Tue, 14 Jun 2016)
# GenomicFeatures version at creation time: 1.24.2
# RSQLite version at creation time: 1.0.0
# DBSCHEMAVERSION: 1.1
```

See `?makeTxDbFromGFF` in the [GenomicFeatures](#) package for more information.

Extract the exon coordinates grouped by gene from this gene model:

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

GRangesList object of length 488:
$Slyc00g005000.2
GRanges object with 2 ranges and 2 metadata columns:
      seqnames      ranges strand |   exon_id   exon_name
      <Rle>       <IRanges> <Rle> | <integer>   <character>
[1] SL2.40ch00 [16437, 17275]   + |         1 Slyc00g005000.2.1.1
[2] SL2.40ch00 [17336, 18189]   + |         2 Slyc00g005000.2.1.2

$Slyc00g005020.1
GRanges object with 3 ranges and 2 metadata columns:
      seqnames      ranges strand |   exon_id   exon_name
      <Rle>       <IRanges> <Rle> | <integer>   <character>
[1] SL2.40ch00 [68062, 68211]   + |         3 Slyc00g005020.1.1.1
[2] SL2.40ch00 [68344, 68568]   + |         4 Slyc00g005020.1.1.2
[3] SL2.40ch00 [68654, 68764]   + |         5 Slyc00g005020.1.1.3

$Slyc00g005040.2
GRanges object with 4 ranges and 2 metadata columns:
      seqnames      ranges strand |   exon_id   exon_name
      <Rle>       <IRanges> <Rle> | <integer>   <character>
[1] SL2.40ch00 [550920, 550945] + |         6 Slyc00g005040.2.1.1
```

[2]	SL2.40ch00	[551034, 551132]	+		7	Solyc00g005040.2.1.2
[3]	SL2.40ch00	[551218, 551250]	+		8	Solyc00g005040.2.1.3
[4]	SL2.40ch00	[551343, 551576]	+		9	Solyc00g005040.2.1.4

• • •

```
<485 more elements>
```

-----

```
seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

## 2.9 How to retrieve a gene model from AnnotationHub

When a gene model is not available as a *GRanges* or *GRangesList* object or as a *Bioconductor* data package, it may be available on [AnnotationHub](#). In this *HOWTO*, will look for a gene model for *Drosophila melanogaster* on [AnnotationHub](#). Create a 'hub' and then filter on *Drosophila melanogaster*:

```
> library(AnnotationHub)
> ### Internet connection required!
> hub <- AnnotationHub()
> hub <- subset(hub, hub$species=='Drosophila melanogaster')
```

There are 87 files that match *Drosophila melanogaster*. If you look at the metadata in hub, you can see that the 7th record represents a GRanges object from UCSC

```
> length(hub)
[1] 216

> head(names(hub))
[1] "AH79" "AH80" "AH81" "AH82" "AH83" "AH84"

> head(hub$title, n=10)
[1] "Drosophila_melanogaster.BDGP5.69.cdna.all.fa"
[2] "Drosophila_melanogaster.BDGP5.69.dna.toplevel.fa"
[3] "Drosophila_melanogaster.BDGP5.69.dna_rm.toplevel.fa"
[4] "Drosophila_melanogaster.BDGP5.69.dna_sm.toplevel.fa"
[5] "Drosophila_melanogaster.BDGP5.69.ncrna.fa"
[6] "Drosophila_melanogaster.BDGP5.69.pep.all.fa"
[7] "Assembly"
[8] "GDP Insertions"
[9] "BAC End Pairs"
[10] "FlyBase Genes"

> ## then look at a specific slice of the hub object.
> hub[7]
```

```
AnnotationHub with 1 record
# snapshotDate(): 2016-06-06
# names(): AH6789
# $dataprovder: UCSC
# $species: Drosophila melanogaster
# $rdataclass: GRanges
# $title: Assembly
# $description: GRanges object from on UCSC track ÃĈÃĈñĒĪJAssemblyÃĈÃĈñãĎĎĎ
# $taxonomyid: 7227
# $genome: dm3
# $sourcetype: UCSC track
```

```
# $sourceurl: rtracklayer://hgdownload.cse.ucsc.edu/goldenpath/dm3/d...
# $sourcelastmodifieddate: NA
# $sourcesize: NA
# $tags: gold, UCSC, track, Gene, Transcript, Annotation
# retrieve record with 'object[["AH6789"]]'
```

So you can retrieve that dm3 file as a *GRanges* like this:

```
> gr <- hub[[names(hub)[7]]]
> summary(gr)
```

```
Length Class      Mode
37688 GRanges      S4
```

The metadata fields contain the details of file origin and content.

```
> metadata(gr)
```

```
$AnnotationHubName
[1] "AH6789"
```

```
$`File Name`
[1] "gold"
```

```
$`Data Source`
[1] "rtracklayer://hgdownload.cse.ucsc.edu/goldenpath/dm3/database/gold"
```

```
$Provider
[1] "UCSC"
```

```
$Organism
[1] "Drosophila melanogaster"
```

```
$`Taxonomy ID`
[1] 7227
```

Split the *GRanges* object by gene name to get a *GRangesList* object of transcript ranges grouped by gene.

```
> txbygn <- split(gr, gr$name)
```

You can now use *txbygn* with the *summarizeOverlaps* function to prepare a table of read counts for RNA-Seq differential gene expression.

Note that before passing *txbygn* to *summarizeOverlaps*, you should confirm that the *seqlevels* (chromosome names) in it match those in the BAM file. See *?renameSeqlevels*, *?keepSeqlevels* and *?seqlevels* for examples of renaming *seqlevels*.

## 2.10 How to annotate peaks in read coverage

[coming soon...]

## 2.11 How to prepare a table of read counts for RNA-Seq differential gene expression

Methods for RNA-Seq gene expression analysis generally require a table of counts that summarize the number of reads that overlap or 'hit' a particular gene. In this *HOWTO* we count with the *summarizeOverlaps* function from the *GenomicAlignments* package and create a count table from the results.

Other packages that provide read counting are [Rsubread](#) and [easyRNASeq](#). The [parathyroidSE](#) package vignette contains a workflow on counting and other common operations required for differential expression analysis.

As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> reads <- c(untrt1=untreated1_chr4(), # single-end reads
+           untrt3=untreated3_chr4()) # paired-end reads
```

`summarizeOverlaps` requires the name of a BAM file(s) and a gene model to count against. See introduction for a quick description of what a *gene models* is. The gene model must match the genome build the reads in the BAM file were aligned to. For the pasilla data this is dm3 *Dmelanogaster* which is available as a *Bioconductor* package. Load the package and extract the exon ranges grouped by gene:

```
> library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
> exbygene <- exonsBy(TxDb.Dmelanogaster.UCSC.dm3.ensGene, "gene")
```

`exbygene` is a *GRangesList* object with one list element per gene in the gene model.

`summarizeOverlaps` automatically sets a `yieldSize` on large BAM files and iterates over them in chunks. When reading paired-end data set the `singleEnd` argument to `FALSE`. See `?summarizeOverlaps` for details regarding the count modes and additional arguments.

```
> library(GenomicAlignments)
> se <- summarizeOverlaps(exbygene, reads, mode="IntersectionNotEmpty")
```

The return object is a *SummarizedExperiment* with counts accessible with the `assays` accessor:

```
> class(se)
[1] "RangedSummarizedExperiment"
attr(,"package")
[1] "SummarizedExperiment"
> head(table(assays(se)$counts))
      0      1      2      3      4      5
31188      2      6      3      4      4
```

The count vector is the same length as `exbygene`:

```
> identical(length(exbygene), length(assays(se)$counts))
[1] FALSE
```

A copy of `exbygene` is stored in the `se` object and accessible with `rowRanges` accessor:

```
> rowRanges(se)
GRangesList object of length 15682:
$FBgn0000003
GRanges object with 1 range and 2 metadata columns:
      seqnames      ranges strand | exon_id exon_name
      <Rle>        <IRanges> <Rle> | <integer> <character>
[1] chr3R [2648220, 2648518] + | 45123 <NA>

$FBgn0000008
GRanges object with 13 ranges and 2 metadata columns:
      seqnames      ranges strand | exon_id exon_name
[1] chr2R [18024494, 18024531] + | 20314 <NA>
[2] chr2R [18024496, 18024713] + | 20315 <NA>
[3] chr2R [18024938, 18025756] + | 20316 <NA>
...      ...                ...    ...    ...
```

```
[11] chr2R [18059821, 18059938] + | 20328 <NA>
[12] chr2R [18060002, 18060339] + | 20329 <NA>
[13] chr2R [18060002, 18060346] + | 20330 <NA>
```

```
...
<15680 more elements>
```

```
-----
seqinfo: 15 sequences (1 circular) from dm3 genome
```

Two popular packages for RNA-Seq differential gene expression are [DESeq2](#) and [edgeR](#). Tables of counts per gene are required for both and can be easily created with a vector of counts. Here we use the counts from our *SummarizedExperiment* object:

```
> colData(se)$trt <- factor(c("untrt", "untrt"), levels=c("trt", "untrt"))
> colData(se)

DataFrame with 2 rows and 1 column
      trt
  <factor>
untrt1   untrt
untrt3   untrt

> library(DESeq2)
> deseq <- DESeqDataSet(se, design= ~ 1)
> library(edgeR)
> edger <- DGEList(assays(se)$counts, group=rownames(colData(se)))
```

## 2.12 How to summarize junctions from a BAM file containing RNA-Seq reads

As sample data we use the [pasillaBamSubset](#) data package described in the introduction.

```
> library(pasillaBamSubset)
> un1 <- untreated1_chr4() # single-end reads
> library(GenomicAlignments)
> reads1 <- readGAlignments(un1)
> reads1
```

GAlignments object with 204355 alignments and 0 metadata columns:

```
      seqnames strand      cigar  qwidth  start    end
      <Rle>  <Rle> <character> <integer> <integer> <integer>
[1]    chr4      -      75M        75      892     966
[2]    chr4      -      75M        75      919     993
[3]    chr4      +      75M        75      924     998
...      ...      ...      ...      ...      ...
[204353] chr4      +      75M        75 1348268 1348342
[204354] chr4      -      75M        75 1348449 1348523
[204355] chr4      -      75M        75 1350124 1350198

      width  njunc
      <integer> <integer>
[1]         75      0
[2]         75      0
[3]         75      0
...      ...      ...
[204353]    75      0
[204354]    75      0
[204355]    75      0
```

```
-----
seqinfo: 8 sequences from an unspecified genome
```

For each alignment, the aligner generated a CIGAR string that describes its "geometry", that is, the locations of insertions, deletions and junctions in the alignment. See the SAM Spec available on the SAMtools website for the details (<http://samtools.sourceforge.net/>).

The `summarizeJunctions()` function from the [GenomicAlignments](#) package can be used to summarize the junctions in `reads1`.

```
> junc_summary <- summarizeJunctions(reads1)
> junc_summary
```

GRanges object with 910 ranges and 3 metadata columns:

	seqnames	ranges	strand	score	plus_score
	<Rle>	<IRanges>	<Rle>	<integer>	<integer>
[1]	chr4	[ 5246, 11972]	*	3	1
[2]	chr4	[10346, 10637]	*	1	1
[3]	chr4	[27102, 27166]	*	13	11
...	...	...	...	...	...
[908]	chr4	[1333752, 1346734]	*	1	0
[909]	chr4	[1334150, 1347141]	*	1	1
[910]	chr4	[1334557, 1347539]	*	1	0

  

	minus_score
	<integer>
[1]	2
[2]	0
[3]	2
...	...
[908]	1
[909]	0
[910]	1

```
-----
seqinfo: 8 sequences from an unspecified genome
```

See `?summarizeJunctions` in the [GenomicAlignments](#) package for more information.

## 2.13 How to get the exon and intron sequences of a given gene

The exon and intron sequences of a gene are essentially the DNA sequences of the introns and exons of all known transcripts of the gene. The first task is to identify all transcripts associated with the gene of interest. Our sample gene is the human TRAK2 which is involved in regulation of endosome-to-lysosome trafficking of membrane cargo. The Entrez gene id is '66008'.

```
> trak2 <- "66008"
```

The [TxDb.Hsapiens.UCSC.hg19.knownGene](#) data package contains the gene model corresponding to the UCSC 'Known Genes' track.

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

The transcript ranges for all the genes in the gene model can be extracted with the `transcriptsBy` function from the [GenomicFeatures](#) package. They will be returned in a named `GRangesList` object containing all the transcripts grouped by gene. In order to keep only the transcripts of the TRAK2 gene we will subset the `GRangesList` object using the `[]` operator.

```
> library(GenomicFeatures)
> trak2_txs <- transcriptsBy(txdb, by="gene")[[trak2]]
> trak2_txs
```

GRanges object with 2 ranges and 2 metadata columns:

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	chr2	[202241930, 202316319]	-	12552	uc002uyb.4
[2]	chr2	[202259851, 202316319]	-	12553	uc002uyc.2

-----  
seqinfo: 93 sequences (1 circular) from hg19 genome

trak2\_txs is a *GRanges* object with one range per transcript in the TRAK2 gene. The transcript names are stored in the tx\_name metadata column. We will need them to subset the extracted intron and exon regions:

```
> trak2_tx_names <- mcols(trak2_txs)$tx_name
> trak2_tx_names
```

```
[1] "uc002uyb.4" "uc002uyc.2"
```

The exon and intron genomic ranges for all the transcripts in the gene model can be extracted with the *exonsBy* and *intronsByTranscript* functions, respectively. Both functions return a *GRangesList* object. Then we keep only the exon and intron for the transcripts of the TRAK2 gene by subsetting each *GRangesList* object by the TRAK2 transcript names.

Extract the exon regions:

```
> trak2_exbytx <- exonsBy(txdb, "tx", use.names=TRUE)[trak2_tx_names]
> elementNROWS(trak2_exbytx)
```

```
uc002uyb.4 uc002uyc.2
      16          8
```

... and the intron regions:

```
> trak2_inbytx <- intronsByTranscript(txdb, use.names=TRUE)[trak2_tx_names]
> elementNROWS(trak2_inbytx)
```

```
uc002uyb.4 uc002uyc.2
      15          7
```

Next we want the DNA sequences for these exons and introns. The *getSeq* function from the *Biostrings* package can be used to query a *BSgenome* object with a set of genomic ranges and retrieve the corresponding DNA sequences.

```
> library(BSgenome.Hsapiens.UCSC.hg19)
```

Extract the exon sequences:

```
> trak2_ex_seqs <- getSeq(Hsapiens, trak2_exbytx)
> trak2_ex_seqs
```

DNASTringSetList of length 2

```
[[ "uc002uyb.4" ]] GCTGGGAGAGTGGCTCTCCTTTGGCTTCCCAATTGTGTGGGGGCTGCCATT...
[[ "uc002uyc.2" ]] GCTGGGAGAGTGGCTCTCCTTTGGCTTCCCAATTGTGTGGGGGCTGCCATT...
```

```
> trak2_ex_seqs[["uc002uyb.4"]]
```

A DNASTringSet instance of length 16

	width	seq
[1]	247	GCTGGGAGAGTGGCTCTCCTTTGGCTTCC...CGGACGACAGAGGATGCCGAACCACTCCA
[2]	290	GTCAATGACTGTCCAAAGTATGATAATCAC...CAATCACAGAGACTCGGAGAGCATCACTG
[3]	195	ATGTCTGCTCCAATGAGGATCTCCCTGAA...CCTTGCTGAAGAGACTTCCGTTACATGA
...	...	...



```
[14] 267 GATCACAACTCTGTATCACTGGCAGCAG...CATTACTTCAGCAGGTGGACCAGTTACAG
[15] 106 TTGCAACCGCCAACCCAGGAAAGTGCCTG...CCCTCTGACATCACTCAGGTTACCCCCAG
[16] 4012 CTCTGGGTTCCCTTCATTATCCTGTGGAA...TTAATAAACATGAGTAGCTGAATTTTCA
```

```
> trak2_ex_seqs[["uc002uyc.2"]]
```

```
A DNASTringSet instance of length 8
width seq
```

```
[1] 247 GCTGGGAGAGTGGCTCTCCTTTGGCTTCCC...CGGACGACAGAGGATGCCGAACCACTCCA
[2] 290 GTCATGACTGTCCAAAGTATGATAATCACA...CAATCACAGAGACTCGGAGAGCATCACTG
[3] 195 ATGTCTGCTCCAATGAGGATCTCCCTGAAG...CCTTGCTGAAGAGACTTTCCGTTACATGA
[4] 77 TTCTAGGCACAGACAGGTGGAGCAGATGA...TCGACATGGTTACACATCTCCTGGCAGAG
[5] 117 AGGGATCGTGATCTGGAACCTGCTGCTCGA...AGGAGCAATTGGGACAAGCCTTTGATCAA
[6] 210 GTTAATCAGCTGCAGCATGAGCTATGCAAG...AAGAAGAGAATATGGCTCTTCGATCCAAG
[7] 79 GCTTGTACATAAAGACAGAACTGTTACC...GCTTGTGAGCGACTGTGTTAAAGAACTTC
[8] 317 GTGAAACAAATGCTCAGATGTCCAGAATGA...AGATATCATGAATAAATACTTTCAAGTCA
```

... and the intron sequences:

```
> trak2_in_seqs <- getSeq(Hsapiens, trak2_inbytx)
> trak2_in_seqs
```

```
DNASTringSetList of length 2
```

```
[["uc002uyb.4"]] GTAAGAGTGCCTGGGAAATCTGGGGCCTCACTTCTTCTCAGCTATATTTT...
[["uc002uyc.2"]] GTGAGTATTAACATATTCTCTTTGTACCTTTTGGACAATTCTTGGTAGG...
```

```
> trak2_in_seqs[["uc002uyb.4"]]
```

```
A DNASTringSet instance of length 15
width seq
```

```
[1] 2892 GTAAGAGTGCCTGGGAAATCTGGGGCCTC...GTCTCCCACTTTTTTTTTTTTTTTTAAAG
[2] 2001 GTGAGAAGAGTGTCTGGTTGAATATGGTA...TGATTTGCTCCCTAAAAATCTATTTTCAG
[3] 1218 GTAATAAATCAGTAAGGGCCCTTACTAAG...TTTCCCCTTCCTTTGTTTTGCATATTCAG
...
[13] 6308 GTGAGTATTTTTTTTACTCTTTTAGTTTG...CTATAAATAGTTGTTTTTAACATATATTAG
[14] 12819 GTAAGTCCAGTTTAATAAATATTGAAGTG...GATTCATTTACATAGACTCTCCTCTTTAG
[15] 30643 GTGAGTAAGCTGTCCGCGCAGAACCCGAAC...GTTCTAGTCACTTGATGTTTTTGTTTTAG
```

```
> trak2_in_seqs[["uc002uyc.2"]]
```

```
A DNASTringSet instance of length 7
width seq
```

```
[1] 2057 GTGAGTATTAACATATTCTCTTTGTACCT...AATTTAAAAAAATTTTTTTTGTCTTCCAAG
[2] 564 GTACGTTCAACCTAATTGCCATTTTCCTTT...ATTGTCACATACTGATTTTTTTCTTGAAG
[3] 1022 GTAAGCCTTTGATCAAATGTCTGCAGTATG...CATGAAAATCAAGCATTTTATATGGACAG
[4] 1524 GTAGGAATATCTTTCTTTCTCCAGTACAA...AAGAAAAGGTGATTTGGTATTTTAAACAG
[5] 6308 GTGAGTATTTTTTTTACTCTTTTAGTTTGT...CTATAAATAGTTGTTTTTAACATATATTAG
[6] 12819 GTAAGTCCAGTTTAATAAATATTGAAGTGC...GATTCATTTACATAGACTCTCCTCTTTAG
[7] 30643 GTGAGTAAGCTGTCCGCGCAGAACCCGAAC...GTTCTAGTCACTTGATGTTTTTGTTTTAG
```

## 2.14 How to get the CDS and UTR sequences of genes associated with colorectal cancer

In this *HOWTO* we extract the CDS and UTR sequences of genes involved in colorectal cancer. The workflow extends the ideas presented in the previous *HOWTO* and suggests an approach for identifying disease-related genes.

### 2.14.1 Build a gene list

We start with a list of gene or transcript ids. If you do not have pre-defined list one can be created with the [KEGG.db](#) and [KEGGgraph](#) packages. Updates to the data in the [KEGG.db](#) package are no longer available, however, the resource is still useful for identifying pathway names and ids.

Create a table of KEGG pathways and ids and search on the term 'cancer'.

```
> library(KEGG.db)
> pathways <- toTable(KEGGPATHNAME2ID)
> pathways[grepl("cancer", pathways$path_name, fixed=TRUE),]
```

	path_id	path_name
370	05200	Pathways in cancer
371	05202	Transcriptional misregulation in cancer
374	05205	Proteoglycans in cancer
375	05206	MicroRNAs in cancer
376	05210	Colorectal cancer
378	05212	Pancreatic cancer
379	05213	Endometrial cancer
381	05215	Prostate cancer
382	05216	Thyroid cancer
385	05219	Bladder cancer
388	05222	Small cell lung cancer
389	05223	Non-small cell lung cancer
390	05230	Central carbon metabolism in cancer
391	05231	Choline metabolism in cancer

Use the "05210" id to query the KEGG web resource (accesses the currently maintained data).

```
> library(KEGGgraph)
> dest <- tempfile()
> retrieveKGML("05200", "hsa", dest, "internal")
```

The suffix of the KEGG id is the Entrez gene id. The `translateKEGGID2GeneID` simply removes the prefix leaving just the Entrez gene ids.

```
> crids <- as.character(parseKGML2DataFrame(dest)[,1])
> crgenes <- unique(translateKEGGID2GeneID(crids))
> head(crgenes)

[1] "1630" "836" "842" "1499" "51384" "54361"
```

### 2.14.2 Identify genomic coordinates

The list of gene ids is used to extract genomic positions of the regions of interest. The Known Gene table from UCSC will be the annotation and is available as a *Bioconductor* package.

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

If an annotation is not available as a *Bioconductor* annotation package it may be available in [AnnotationHub](#). Additionally, there are functions in [GenomicFeatures](#) which can retrieve data from UCSC and Ensembl to create a TxDb. See `?makeTxDbFromUCSC` for more information.

As in the previous *HOWTO* we need to identify the transcripts corresponding to each gene. The transcript id (or name) is used to isolate the UTR and coding regions of interest. This grouping of transcript by gene is also used to re-group the final sequence results.

The `transcriptsBy` function outputs both the gene and transcript identifiers which we use to create a map between the two. The map is a `CharacterList` with gene ids as names and transcript ids as the list elements.

```
> txbygene <- transcriptsBy(txdb, "gene")[crgenes] ## subset on colorectal genes
> map <- relist(unlist(txbygene, use.names=FALSE)$tx_id, txbygene)
> map
```

```
IntegerList of length 239
[["1630"]] 64962 64963 64964
[["836"]] 20202 20203 20204
[["842"]] 4447 4448 4449 4450 4451 4452
[["1499"]] 13582 13583 13584 13585 13586 13587 13589
[["51384"]] 29319 29320 29321
[["54361"]] 4634 4635
[["7471"]] 46151
[["7472"]] 31279 31280
[["7473"]] 63770
[["7474"]] 16089 16090 16091 16092
...
<229 more elements>
```

Extract the UTR and coding regions.

```
> cds <- cdsBy(txdb, "tx")
> threeUTR <- threeUTRsByTranscript(txdb)
> fiveUTR <- fiveUTRsByTranscript(txdb)
```

Coding and UTR regions may not be present for all transcripts specified in `map`. Consequently, the subset results will not be the same length. This length discrepancy must be taken into account when re-listing the final results by gene.

```
> txid <- unlist(map, use.names=FALSE)
> cds <- cds[names(cds) %in% txid]
> threeUTR <- threeUTR[names(threeUTR) %in% txid]
> fiveUTR <- fiveUTR[names(fiveUTR) %in% txid]
```

Note the different lengths of the subset regions.

```
> length(txid) ## all possible transcripts
[1] 1045
> length(cds)
[1] 960
> length(threeUTR)
[1] 919
> length(fiveUTR)
[1] 947
```

These objects are `GRangesLists` with the transcript id as the outer list element.

```
> cds
```

GRangesList object of length 960:

\$2043

GRanges object with 6 ranges and 3 metadata columns:

seqnames	ranges	strand	cds_id	cds_name
<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1] chr1	[113010160, 113010213]	+	6055	<NA>

```
[2] chr1 [113033633, 113033703] + | 6056 <NA>
[3] chr1 [113057496, 113057716] + | 6058 <NA>
[4] chr1 [113058762, 113059039] + | 6060 <NA>
[5] chr1 [113059743, 113060007] + | 6061 <NA>
[6] chr1 [113062902, 113063131] + | 6062 <NA>
```

```
exon_rank
<integer>
```

```
[1] 1
[2] 2
[3] 3
[4] 4
[5] 5
[6] 6
```

\$2044

GRanges object with 4 ranges and 3 metadata columns:

```
seqnames      ranges strand | cds_id cds_name
[1] chr1 [113057590, 113057716] + | 6059 <NA>
[2] chr1 [113058762, 113059039] + | 6060 <NA>
[3] chr1 [113059743, 113060007] + | 6061 <NA>
[4] chr1 [113062902, 113063131] + | 6062 <NA>
```

```
exon_rank
```

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

\$2045

GRanges object with 5 ranges and 3 metadata columns:

```
seqnames      ranges strand | cds_id cds_name
[1] chr1 [113051885, 113052066] + | 6057 <NA>
[2] chr1 [113057496, 113057716] + | 6058 <NA>
[3] chr1 [113058762, 113059039] + | 6060 <NA>
[4] chr1 [113059743, 113060007] + | 6061 <NA>
[5] chr1 [113062902, 113063131] + | 6062 <NA>
```

```
exon_rank
```

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

...

<957 more elements>

-----

seqinfo: 93 sequences (1 circular) from hg19 genome

### 2.14.3 Extract sequences from BSgenome

The BSgenome packages contain complete genome sequences for a given organism.

Load the BSgenome package for homo sapiens.

```
> library(BSgenome.Hsapiens.UCSC.hg19)
```

```
> genome <- BSgenome.Hsapiens.UCSC.hg19
```

Use `extractTranscriptSeqs` to extract the UTR and coding regions from the `BSgenome`. This function retrieves the sequences for an any `GRanges` or `GRangesList` (i.e., not just transcripts like the name implies).

```
> threeUTR_seqs <- extractTranscriptSeqs(genome, threeUTR)
> fiveUTR_seqs <- extractTranscriptSeqs(genome, fiveUTR)
> cds_seqs <- extractTranscriptSeqs(genome, cds)
```

The return values are `DNAStringSet` objects.

```
> cds_seqs

A DNAStringSet instance of length 960
      width seq                                     names
[1]  1119 ATGTTGGATGGCCTTGA...TGGCTGGACCAACCTGA 2043
[2]   900 ATGCGTTCAGTGGGCGAG...TGGCTGGACCAACCTGA 2044
[3]  1176 ATGCTGAGACCGGGTGGT...TGGCTGGACCAACCTGA 2045
...    ...
[958]  681 ATGTTACGACAAGATTCC...CACAATGAATCAACGTAG 78103
[959]  768 ATGAGTGGAAAGGTGACC...CACAATGAATCAACGTAG 78104
[960]  600 ATGAGTGGAAAGGTGACC...CACAATGAATCAACGTAG 78105
```

Our final step is to collect the coding and UTR regions (currently organized by transcript) into groups by gene id. The `relist` function groups the sequences of a `DNAStringSet` object into a `DNAStringSetList` object, based on the specified `skeleton` argument. The `skeleton` must be a list-like object and only its shape (i.e. its element lengths) matters (its exact content is ignored). A simple form of `skeleton` is to use a partitioning object that we make by specifying the size of each partition. The partitioning objects are different for each type of region because not all transcripts had a coding or 3' or 5' UTR region defined.

```
> lst3 <- relist(threeUTR_seqs, PartitioningByWidth(sum(map %in% names(threeUTR))))
> lst5 <- relist(fiveUTR_seqs, PartitioningByWidth(sum(map %in% names(fiveUTR))))
> lstc <- relist(cds_seqs, PartitioningByWidth(sum(map %in% names(cds))))
```

There are 239 genes in `map` each of which have 1 or more transcripts. The table of element lengths shows how many genes have each number of transcripts. For example, 47 genes have 1 transcript, 48 genes have 2 etc.

```
> length(map)
[1] 239

> table(elementNROWS(map))

 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 21 30
47 48 46 22 17 18 10  4  3  3  5  3  1  1  1  1  4  1  2  1  1
```

The lists of DNA sequences all have the same length as `map` but one or more of the element lengths may be zero. This would indicate that data were not available for that gene. The tables below show that there was at least 1 coding region available for all genes (i.e., none of the element lengths are 0). However, both the 3' and 5' UTR results have element lengths of 0 which indicates no UTR data were available for that gene.

```
> table(elementNROWS(lstc))

 1  2  3  4  5  6  7  8  9 10 11 12 14 15 16 17 18 30
48 54 49 20 17 16  8  5  5  3  1  2  3  1  2  1  3  1

> table(elementNROWS(lst3))

 0  1  2  3  4  5  6  7  8  9 11 12 13 14 15 16 17 18 30
2 49 56 47 19 18 13  9  5  8  2  2  2  1  1  2  1  1  1

> names(lst3)[elementNROWS(lst3) == 0L] ## genes with no 3' UTR data
[1] "2255" "8823"
```

```
> table(elementNROWS(lst5))
 0  1  2  3  4  5  6  7  8  9 10 11 12 14 15 16 17 18 30
 3 48 52 49 19 17 16  8  5  5  3  2  2  3  1  1  1  3  1

> names(lst5)[elementNROWS(lst5) == 0L] ## genes with no 5' UTR data
[1] "2255" "27006" "8823"
```

## 2.15 How to create DNA consensus sequences for read group ‘families’

The motivation for this *HOWTO* comes from a study which explored the dynamics of point mutations. The mutations of interest exist with a range of frequencies in the control group (e.g., 0.1% - 50%). PCR and sequencing error rates make it difficult to identify low frequency events (e.g., < 20%).

When a library is prepared with Nextera, random fragments are generated followed by a few rounds of PCR. When the genome is large enough, reads aligning to the same start position are likely descendant from the same template fragment and should have identical sequences.

The goal is to eliminate noise by grouping the reads by common start position and discarding those that do not exceed a certain threshold within each family. A new consensus sequence will be created for each read group family.

### 2.15.1 Sort reads into groups by start position

Load the BAM file into a GAlignments object.

```
> library(Rsamtools)
> bamfile <- system.file("extdata", "ex1.bam", package="Rsamtools")
> param <- ScanBamParam(what=c("seq", "qual"))
> library(GenomicAlignments)
> gal <- readGAlignments(bamfile, use.names=TRUE, param=param)
```

Use the sequenceLayer function to lay the query sequences and quality strings on the reference.

```
> qseq <- setNames(mcols(gal)$seq, names(gal))
> qual <- setNames(mcols(gal)$qual, names(gal))
> qseq_on_ref <- sequenceLayer(qseq, cigar(gal),
+                             from="query", to="reference")
> qual_on_ref <- sequenceLayer(qual, cigar(gal),
+                             from="query", to="reference")
```

Split by chromosome.

```
> qseq_on_ref_by_chrom <- splitAsList(qseq_on_ref, seqnames(gal))
> qual_on_ref_by_chrom <- splitAsList(qual_on_ref, seqnames(gal))
> pos_by_chrom <- splitAsList(start(gal), seqnames(gal))
```

For each chromosome generate one GRanges object that contains unique alignment start positions and attach 3 metadata columns to it: the number of reads, the query sequences, and the quality strings.

```
> gr_by_chrom <- lapply(seqlevels(gal),
+   function(seqname)
+   {
+     qseq_on_ref2 <- qseq_on_ref_by_chrom[[seqname]]
+     qual_on_ref2 <- qual_on_ref_by_chrom[[seqname]]
+     pos2 <- pos_by_chrom[[seqname]]
+     qseq_on_ref_per_pos <- split(qseq_on_ref2, pos2)
+     qual_on_ref_per_pos <- split(qual_on_ref2, pos2)
```

```
+      nread <- elementNROWS(qseq_on_ref_per_pos)
+      gr_mcols <- DataFrame(nread=unname(nread),
+                             qseq_on_ref=unname(qseq_on_ref_per_pos),
+                             qual_on_ref=unname(qual_on_ref_per_pos))
+      gr <- GRanges(Rle(seqname, nrow(gr_mcols)),
+                     IRanges(as.integer(names(nread)), width=1))
+      mcols(gr) <- gr_mcols
+      seqlevels(gr) <- seqlevels(gal)
+      gr
+    })
```

Combine all the GRanges objects obtained in (4) in 1 big GRanges object:

```
> gr <- do.call(c, gr_by_chrom)
> seqinfo(gr) <- seqinfo(gal)
```

'gr' is a GRanges object that contains unique alignment start positions:

```
> gr[1:6]
```

GRanges object with 6 ranges and 3 metadata columns:

[illegible]

```
seqinfo: 2 sequences from an unspecified genome
```

Look at `qseq_on_ref` and `qual_on_ref`.

```
> qseq_on_ref
```

A DNASTringSet instance of length 3271

	width	seq	names
[1]	36	CACTAGTGGCTCATTGTAAATGTGTGGTTTAACTCG	B7_591:4:96:693:509
[2]	35	CTAGTGGCTCATTGTAAATGTGTGGTTTAACTCGT	EAS54_65:7:152:36...
[3]	35	AGTGGCTCATTGTAAATGTGTGGTTTAACTCGTCC	EAS51_64:8:5:734:57

```
[3269]    35 TTTTTTCTTTTTTTTTTTTTTTTTTTTGCATGCCA      EAS139_11:7:50:12...
[3270]    35 TTTTTTTTTTTTTTTTTTTTTTTTGCATGCCAGAAA   EAS54_65:3:320:20...
[3271]    35 TTTTTTTTTTTTTTTTTTTTTTTCATGCCAGAAAA     EAS114_26:7:37:79...

> qual_on_ref

  A PhredQuality instance of length 3271

width seq                                     names
 [1]    36 <<<<<<<<<<<<<<<<<<<<<<<5<<<<<;<;7 B7_591:4:96:693:509
 [2]    35 <<<<<<<<<<0<<<<655<<7<<<<9<<3/:<6):   EAS54_65:7:152:36...
 [3]    35 <<<<<<<<<<<7;71<<;<;<7;<<3;) ;3*8/5    EAS51_64:8:5:734:57
 ...    ... ..
[3269]    35 <<<<, <&<7<<<<<<<<<<<<<<<<<<<<<<<< EAS139_11:7:50:12...
[3270]    35 +''' /<<<<7:;+<;::<<<;;<<<<<<<<<<<<< EAS54_65:3:320:20...
[3271]    35 3,, ,==6===<====<;===== EAS114_26:7:37:79...
```

2 reads align to start position 13. Let's have a close look at their sequences:

```
> mcols(gr)$qseq_on_ref[[6]]
```

A DNASTringSet instance of length 2

	width	seq	names
[1]	35	ATTGTAATAATGTGTGGTTTAACTCGTCCCTGGCCCA	EAS56_61:6:18:467...
[2]	36	ATTGTAATAATGTGTGGTTTAACTCGTCCATGGCCAG	EAS114_28:5:296:3...

and their qualities:

```
> mcols(gr)$qual_on_ref[[6]]
```

A PhredQuality instance of length 2

	width	seq	names
[1]	35	<<<<<<<<;<<<8<<<<<;8;.;6/686&;(16666	EAS56_61:6:18:467...
[2]	36	<<<<;<<<;<;<<<<<<<<<<<8<8<3<8;<;<0;	EAS114_28:5:296:3...

Note that the sequence and quality strings are those projected to the reference so the first letter in those strings are on top of start position 13, the 2nd letter on top of position 14, etc...

### 2.15.2 Remove low frequency reads

For each start position, remove reads with and under-represented sequence (e.g. threshold = 20% for the data used here which is low coverage). A unique number is assigned to each unique sequence. This will make future calculations easier and a little bit faster.

```
> qseq_on_ref <- mcols(gr)$qseq_on_ref
> tmp <- unlist(qseq_on_ref, use.names=FALSE)
> qseq_on_ref_id <- relist(match(tmp, tmp), qseq_on_ref)
```

Quick look at 'qseq\_on\_ref\_id': It's an IntegerList object with the same length and "shape" as 'qseq\_on\_ref'.

```
> qseq_on_ref_id
IntegerList of length 1934
[[1]] 1
[[2]] 2
[[3]] 3
[[4]] 4
[[5]] 5
[[6]] 6 7
[[7]] 8
[[8]] 9
```



```
[[9]] 10 11
[[10]] 12
...
<1924 more elements>
```

Remove the under represented ids from each list element of 'qseq\_on\_ref\_id':

```
> qseq_on_ref_id2 <- endoapply(qseq_on_ref_id,
+   function(ids) ids[countMatches(ids, ids) >= 0.2 * length(ids)])
```

Remove corresponding sequences from 'qseq\_on\_ref':

```
> tmp <- unlist(qseq_on_ref_id2, use.names=FALSE)
> qseq_on_ref2 <- relist(unlist(qseq_on_ref, use.names=FALSE)[tmp],
+   qseq_on_ref_id2)
```

### 2.15.3 Create a consensus sequence for each read group family

Compute 1 consensus matrix per chromosome:

```
> split_factor <- rep.int(seqnames(gr), elementNROWS(qseq_on_ref2))
> qseq_on_ref2 <- unlist(qseq_on_ref2, use.names=FALSE)
> qseq_on_ref2_by_chrom <- splitAsList(qseq_on_ref2, split_factor)
> qseq_pos_by_chrom <- splitAsList(start(gr), split_factor)
> cm_by_chrom <- lapply(names(qseq_pos_by_chrom),
+   function(seqname)
+     consensusMatrix(qseq_on_ref2_by_chrom[[seqname]],
+       as.prob=TRUE,
+       shift=qseq_pos_by_chrom[[seqname]]-1,
+       width=seqlengths(gr)[[seqname]]))
> names(cm_by_chrom) <- names(qseq_pos_by_chrom)
```

'cm\_by\_chrom' is a list of consensus matrices. Each matrix has 17 rows (1 per letter in the DNA alphabet) and 1 column per chromosome position.

```
> lapply(cm_by_chrom, dim)
```

```
$seq1
[1] 18 1575
```

```
$seq2
[1] 18 1584
```

Compute the consensus string from each consensus matrix. We'll put "+" in the strings wherever there is no coverage for that position, and "N" where there is coverage but no consensus.

```
> cs_by_chrom <- lapply(cm_by_chrom,
+   function(cm) {
+     ## need to "fix" 'cm' because consensusString()
+     ## doesn't like consensus matrices with columns
+     ## that contain only zeroes (e.g., chromosome
+     ## positions with no coverage)
+     idx <- colSums(cm) == 0L
+     cm["+", idx] <- 1
+     DNAString(consensusString(cm, ambiguityMap="N"))
+   })
```

The new consensus strings.

```
> cs_by_chrom

$seq1
1575-letter "DNAString" instance
seq: NANTAGNNNCTCANTTTAAANNTTNTTTT...AATNATANNTTNTTNTTNTCTGNAC+++++

$seq2
1584-letter "DNAString" instance
seq: ++++++...NNNANANANANCTNNA+++++
```

## 2.16 How to compute binned averages along a genome

In some applications (e.g. visualization), there is the need to compute the average of a variable defined along a genome (a.k.a. genomic variable) for a set of predefined fixed-width regions (sometimes called "bins"). The genomic variable is typically represented as a named RleList object with one list element per chromosome. One such example is coverage. Here we create an artificial genomic variable:

```
> library(BSgenome.Scerevisiae.UCSC.sacCer2)
> set.seed(55)
> my_var <- RleList(
+   lapply(seqlengths(Scerevisiae),
+     function(seqlen) {
+       tmp <- sample(50L, seqlen, replace=TRUE) %/% 50L
+       Rle(cumsum(tmp - rev(tmp)))
+     }
+   ),
+   compress=FALSE)
> my_var

RleList of length 18
$chrI
integer-Rle of length 230208 with 8693 runs
Lengths: 32 33 51 21 22 9 1 36 8 99 ... 8 36 1 9 22 21 51 33 33
Values : 0 1 2 1 0 -1 0 1 0 1 ... 0 1 0 -1 0 1 2 1 0

$chrII
integer-Rle of length 813178 with 31959 runs
Lengths: 56 10 52 12 69 4 48 35 11 1 ... 11 35 48 4 69 12 52 10 57
Values : 0 1 0 1 0 1 2 1 2 3 ... 2 1 2 1 0 1 0 1 0

$chrIII
integer-Rle of length 316617 with 12209 runs
Lengths: 20 116 9 2 21 16 43 ... 43 16 21 2 9 116 21
Values : 0 -1 0 1 0 -1 -2 ... -2 -1 0 1 0 -1 0

$chrIV
integer-Rle of length 1531919 with 60091 runs
Lengths: 39 80 67 22 48 77 19 45 13 3 ... 13 45 19 77 48 22 67 80 40
Values : 0 -1 0 1 2 3 2 1 0 1 ... 0 1 2 3 2 1 0 -1 0

$chrV
integer-Rle of length 576869 with 22903 runs
Lengths: 11 29 7 1 10 29 63 ... 63 29 10 1 7 29 12
Values : 0 -1 -2 -3 -4 -3 -4 ... -4 -3 -4 -3 -2 -1 0
```

```
...
<13 more elements>
```

Use the `tileGenome` function to create a set of bins along the genome.

```
> bins <- tileGenome(seqinfo(Scerevisiae), tilewidth=100,
+                   cut.last.tile.in.chrom=TRUE)
```

Compute the binned average for `my_var`:

```
> binnedAverage(bins, my_var, "binned_var")
```

GRanges object with 121639 ranges and 1 metadata column:

	seqnames	ranges	strand	binned_var
	<Rle>	<IRanges>	<Rle>	<numeric>
[1]	chrI	[ 1, 100]	*	1.03
[2]	chrI	[101, 200]	*	0.75
[3]	chrI	[201, 300]	*	0.92
...	...	...	...	...
[121637]	2micron	[6101, 6200]	*	0.87
[121638]	2micron	[6201, 6300]	*	0.03
[121639]	2micron	[6301, 6318]	*	0

-----

seqinfo: 18 sequences (2 circular) from sacCer2 genome

The bin size can be modified with the `tilewidth` argument to `tileGenome`. See `?binnedAverage` for additional examples.

### 3 Session Information

---

R version 3.3.0 (2016-05-03)

Platform: x86\_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 14.04.4 LTS

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats4      parallel  stats      graphics  grDevices  utils
[7] datasets    methods   base
```

other attached packages:

```
[1] BSgenome.Scerevisiae.UCSC.sacCer2_1.4.0
[2] KEGGgraph_1.30.0
[3] KEGG.db_3.2.3
[4] BSgenome.Hsapiens.UCSC.hg19_1.4.0
[5] BSgenome_1.40.0
[6] rtracklayer_1.32.1
[7] edgeR_3.14.0
[8] limma_3.28.8
```

```

[9] DESeq2_1.12.3
[10] AnnotationHub_2.4.2
[11] TxDb.Athaliana.BioMart.plantmart22_3.0.1
[12] TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2
[13] TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2
[14] GenomicFeatures_1.24.2
[15] AnnotationDbi_1.34.3
[16] GenomicAlignments_1.8.2
[17] Rsamtools_1.24.0
[18] Biostrings_2.40.2
[19] XVector_0.12.0
[20] SummarizedExperiment_1.2.3
[21] Biobase_2.32.0
[22] pasillaBamSubset_0.10.0
[23] GenomicRanges_1.24.2
[24] GenomeInfoDb_1.8.2
[25] IRanges_2.6.0
[26] S4Vectors_0.10.1
[27] BiocGenerics_0.18.0

```

loaded via a namespace (and not attached):

```

[1] locfit_1.5-9.1           Rcpp_0.12.5
[3] lattice_0.20-33          digest_0.6.9
[5] mime_0.4                 R6_2.1.2
[7] plyr_1.8.4               chron_2.3-47
[9] acepack_1.3-3.3          RSQLite_1.0.0
[11] httr_1.1.0               ggplot2_2.1.0
[13] BiocInstaller_1.22.2     zlibbioc_1.18.0
[15] curl_0.9.7               data.table_1.9.6
[17] annotate_1.50.0           rpart_4.1-10
[19] Matrix_1.2-6             splines_3.3.0
[21] BiocParallel_1.6.2       geneplotter_1.50.0
[23] foreign_0.8-66           RCurl_1.95-4.8
[25] biomaRt_2.28.0           munsell_0.4.3
[27] shiny_0.13.2             httpuv_1.3.3
[29] htmltools_0.3.5         nnet_7.3-12
[31] gridExtra_2.2.1          interactiveDisplayBase_1.10.3
[33] Hmisc_3.17-4            XML_3.98-1.4
[35] bitops_1.0-6             grid_3.3.0
[37] xtable_1.8-2             gtable_0.2.0
[39] DBI_0.4-1                scales_0.4.0
[41] graph_1.50.0             genefilter_1.54.2
[43] latticeExtra_0.6-28      Formula_1.2-1
[45] BiocStyle_2.0.2          RColorBrewer_1.1-2
[47] tools_3.3.0              survival_2.39-4
[49] colorspace_1.2-6         cluster_2.0.4
[51] VariantAnnotation_1.18.1

```

## References

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 Computational Biology*, 4(3), 2013.