

Counting with `summarizeOverlaps`

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Edited: October 2011; Compiled: August 27, 2012

Contents

1	Introduction	1
2	A First Example	1
3	Counting Modes	2
4	Counting Features	3
5	pasilla Data	6
5.1	source files	6
5.2	Exon counts	7
5.3	Gene counts	9
6	References	9

1 Introduction

This vignette illustrates how reads mapped to a genome can be counted with `summarizeOverlaps`. Different "modes" of counting are provided to resolve reads that overlap multiple features. The built-in count modes are fashioned after the "Union", "IntersectionStrict", and "IntersectionNotEmpty" methods found in the HTSeq package by Simon Anders (see references).

2 A First Example

In this example reads are counted from a list of BAM files and returned in a `matrix` for use in further analysis such as those offered in DESeq and edgeR.

```
> library(Rsamtools)
> library(DESeq)
> library(edgeR)
> fls = list.files(system.file("extdata", package="GenomicRanges"),
```

```

+     recursive=TRUE, pattern="*bam$", full=TRUE)
> bfl <- BamFileList(fls)
> features <- GRanges(
+     seqnames = Rle(c("chr2L", "chr2R", "chr2L", "chr2R", "chr2L", "chr2R",
+     "chr2L", "chr2R", "chr2R", "chr3L", "chr3L")),
+     strand = strand(rep("+", 11)),
+     ranges = IRanges(start=c(1000, 2000, 3000, 3600, 7000, 7500, 4000, 4000,
+     3000, 5000, 5400), width=c(500, 900, 500, 300, 600, 300, 500, 900, 500,
+     500, 500))
+ )
> olap <- summarizeOverlaps(features, bfl)
> deseq <- newCountDataSet(countData=assays(olap)$counts,
+     conditions=rownames(colData(olap)))
> edger <- DGEList(counts=assays(olap)$counts, group=rownames(colData(olap)))

```

3 Counting Modes

The modes of "Union", "IntersectionStrict" and "IntersectionNotEmpty" provide different approaches to resolving reads that overlap multiple features. Figure 1 illustrates how both simple and gapped reads are handled by the modes. Note that a read is counted a maximum of once; there is no double counting. These methods do not currently handle paired-end reads. For additional detail on the counting modes see the `summarizeOverlaps` man page.

	Union	IntersectionStrict	IntersectionNotEmpty
	Feature 1	Feature 1	Feature 1
	Feature 1	No hit	Feature 1
	Feature 1	No hit	Feature 1
	Feature 1	Feature 1	Feature 1
	Feature 1	Feature 1	Feature 1
	No hit	Feature 1	Feature 1
	No hit	No hit	No hit

* Picture reproduced from HTSeq web site :
<http://www-huber.embl.de/users/anders/HTSeq/doc/count.html>

Figure 1: Counting Modes

4 Counting Features

Features can be exons, transcripts, genes or any region of interest. The number of ranges that define a single feature is specified in the **features** argument.

When annotation regions of interest are defined by a single range a *GRanges* should be used as the **features** argument. With a *GRanges* it is assumed that each row (i.e., each range) represents a distinct feature. If **features** was a *GRanges* of exons, the result would be counts per exon.

When the region of interest is defined by one or more ranges the **features** argument should be a *GRangesList*. In practice this could be a list of exons by gene or transcripts by gene or other similar relationships. The count result will

be the same length as the *GRangesList*. For a list of exons by genes, the result would be counts per gene.

The combination of defining the features as either *GRanges* or *GRangesList* and choosing a counting mode controls how `summarizeOverlaps` assigns hits. Regardless of the mode chosen, each read is assigned to at most a single feature. These options are intended to provide flexibility in defining different biological problems.

This next example demonstrates how the same read can be counted differently depending on how the `features` argument is specified. We use a single read that overlaps two ranges, `gr1` and `gr2`.

```
> rd <- GappedAlignments("a", seqnames = Rle("chr1"), pos = as.integer(100),
+   cigar = "300M", strand = strand("+"))
> gr1 <- GRanges("chr1", IRanges(start=50, width=150), strand="+")
> gr2 <- GRanges("chr1", IRanges(start=350, width=150), strand="+")
```

When provided as a *GRanges* both `gr1` and `gr2` are considered distinct features. In this case none of the modes count the read as a hit. Mode `Union` discards the read because more than 1 feature is overlapped. `IntersectionStrict` requires the read to fall completely within a feature which is not the case for either `gr1` or `gr2`. `IntersectionNotEmpty` requires the read to overlap a single unique disjoint region of the features. In this case `gr1` and `gr2` do not overlap so each range is considered a unique disjoint region. However, the read overlaps both `gr1` and `gr2` so a decision cannot be made and the read is discarded.

```
> gr <- c(gr1, gr2)
> data.frame(union = assays(summarizeOverlaps(gr, rd))$counts,
+   intStrict = assays(summarizeOverlaps(gr, rd,
+   mode="IntersectionStrict"))$counts,
+   intNotEmpty = assays(summarizeOverlaps(gr, rd,
+   mode="IntersectionNotEmpty"))$counts)

  union intStrict intNotEmpty
1     0          0           0
2     0          0           0
```

Next we count with `features` as a *GRangesList*; this is list of length 1 with 2 elements. Modes `Union` and `IntersectionNotEmpty` both count the read for the single feature.

```
> grl <- GRangesList(c(gr1, gr2))
> data.frame(union = assays(summarizeOverlaps(grl, rd))$counts,
+   intStrict = assays(summarizeOverlaps(grl, rd,
+   mode="IntersectionStrict"))$counts,
+   intNotEmpty = assays(summarizeOverlaps(grl, rd,
+   mode="IntersectionNotEmpty"))$counts)

  union intStrict intNotEmpty
1     1          0           1
```

In this more complicated example we have 7 reads, 5 are simple and 2 have gaps in the CIGAR. There are 12 ranges that will serve as the **features**.

```
> group_id <- c("A", "B", "C", "C", "D", "D", "E", "F", "G", "G", "H", "H")
> features <- GRanges(
+   seqnames = Rle(c("chr1", "chr2", "chr1", "chr1", "chr2", "chr2",
+     "chr1", "chr1", "chr2", "chr2", "chr1", "chr1")),
+   strand = strand(rep("+", length(group_id))),
+   ranges = IRanges(
+     start=c(1000, 2000, 3000, 3600, 7000, 7500, 4000, 4000, 3000, 3350, 5000, 5400),
+     width=c(500, 900, 500, 300, 600, 300, 500, 900, 150, 200, 500, 500)),
+   DataFrame(group_id)
+ )
> reads <- GappedAlignments(
+   names = c("a", "b", "c", "d", "e", "f", "g"),
+   seqnames = Rle(c(rep(c("chr1", "chr2"), 3), "chr1")),
+   pos = as.integer(c(1400, 2700, 3400, 7100, 4000, 3100, 5200)),
+   cigar = c("500M", "100M", "300M", "500M", "300M", "50M200N50M", "50M150N50M"),
+   strand = strand(rep.int("+", 7L)))
>
```

Using a *GRanges* as the **features** all 12 ranges are considered to be different features and counts are produced for each row,

```
> data.frame(union = assays(summarizeOverlaps(features, reads))$counts,
+   intStrict = assays(summarizeOverlaps(features, reads,
+     mode="IntersectionStrict"))$counts,
+   intNotEmpty = assays(summarizeOverlaps(features, reads,
+     mode="IntersectionNotEmpty"))$counts)
```

	union	intStrict	intNotEmpty
1	1	0	1
2	1	1	1
3	0	0	0
4	0	0	0
5	0	1	1
6	0	0	0
7	0	0	0
8	0	0	0
9	0	0	0
10	0	0	0
11	0	1	1
12	0	0	0

When the data are split by group to create a *GRangesList* the highest list-levels are treated as different features and the multiple list elements are considered part of the same features. Counts are returned for each group.

```

> lst <- split(features, values(features)[["group_id"]])
> length(lst)

[1] 8

> data.frame(union = assays(summarizeOverlaps(lst, reads))$counts,
+           intStrict = assays(summarizeOverlaps(lst, reads,
+           mode="IntersectionStrict"))$counts,
+           intNotEmpty = assays(summarizeOverlaps(lst, reads,
+           mode="IntersectionNotEmpty"))$counts)

```

	union	intStrict	intNotEmpty
A	1	0	1
B	1	1	1
C	1	0	1
D	1	1	1
E	0	0	0
F	0	0	0
G	1	1	1
H	1	1	1

If desired, users can supply their own counting function as the `mode` argument and take advantage of the infrastructure for counting over multiple BAM files and parsing the results into a *SummarizedExperiment*. See `?BamViews-class` or `?BamFile-class` in *Rsamtools*.

5 pasilla Data

In this exercise we use the *pasilla* data to create an *ExonCountSet* and *CountDataSet* similar to those available in the *pasilla* data package. These objects can be used in differential expression methods offered in the *DESeq* or *DEXSeq* packages. Details of read alignment and the creation of the annotation file are available in the *pasilla* package vignette.

5.1 source files

BAM files were downloaded from <http://www.embl.de/~reyes/Graveley/bam>. Of the seven files available, 3 are single-reads and 4 are paired-end. `summarizeOverlaps` does not currently handle paired-end reads so in this example we use the following 3 single-read files,

- treated1.bam
- untreated1.bam
- untreated2.bam

```
> library(pasilla)
> library(rtracklayer)
> library(Rsamtools)
> gff <- import(system.file("extdata", "Dmel.BDGP5.25.62.DEXSeq.chr.gff",
+   package = "pasilla"), "gff1")
> features <- as(gff, "GRanges")
> head(features[,1])
```

	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
[1]	chr2L	[7529, 9484]	+	
[2]	chr2L	[7529, 8116]	+	
[3]	chr2L	[8193, 8589]	+	
[4]	chr2L	[8590, 8667]	+	
[5]	chr2L	[8668, 9484]	+	
[6]	chr2L	[9836, 21372]	-	

[1] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz
 [2] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz
 [3] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz
 [4] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz
 [5] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz
 [6] *Drosophila_melanogaster*.BDGP5.25.62.gtf.gz

```
chr2L ... chrdmel_mitochondrion_genome
      NA ... NA
```

For counting exons we retain the ranges marked as "exonic_part". The exon and gene id's are extracted from the 'group' metadata column for later use.

7

```
> geneID <- do.call(c,
+                   lapply(st, function(x) {
+                     gsub(" gene_id ", "", x[3]))}))
```

The `params` argument can be used to subset the reads in the bam file on characteristics such as position, unmapped or paired-end reads. Quality scores or the "NH" tag, which identifies reads with multiple mappings, can be included as metadata columns for further subsetting. See `?ScanBamParam` for details about specifying the `param` argument.

```
> param <- ScanBamParam(
+   what='qual',
+   which=GRanges("chr2L", IRanges(1, 1e+6)),
+   flag=scanBamFlag(isUnmappedQuery=FALSE, isPaired=NA))
> bamTag(param) <- "NH"
```

We use `summarizeOverlaps` to count with the default mode of "Union". If a `param` argument is not included all reads from the BAM file are counted.

```
> fls <- c("treated1.bam", "untreated1.bam", "untreated2.bam")
> path <- "pathToBAMFiles"
> bamFiles <- BamFileList(file.path(paste(path, fls, sep="")))
> se_exons <- summarizeOverlaps(exons, bamFiles, mode="Union")
```

An `ExonCountSet` is constructed from the counts and experiment data in *pasilla*.

```
> library(DEXSeq)
> expdata = new("MIAME",
+   name="pasilla knockdown",
+   lab="Genetics and Developmental Biology, University of
+     Connecticut Health Center",
+   contact="Dr. Brenton Graveley",
+   title="modENCODE Drosophila pasilla RNA Binding Protein RNAi
+     knockdown RNA-Seq Studies",
+   url="http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE18508",
+   abstract="RNA-seq of 3 biological replicates of from the Drosophila
+     melanogaster S2-DRSC cells that have been RNAi depleted of mRNAs
+     encoding pasilla, a mRNA binding protein and 4 biological replicates
+     of the the untreated cell line.")
> pubMedIds(expdata) <- "20921232"
> design <- data.frame(
+   condition=c("treated", "untreated", "untreated"),
+   replicate=c(1,1,2),
+   type=rep("single-read", 3),
+   countfiles=colData(se_exons)[,1], stringsAsFactors=TRUE)
> pasillaECS <- newExonCountSet(
+   countData=assays(se_exons)$counts,
+   design=design,
```



```

+             exonIDs=factor(exonID),
+             geneIDs=factor(geneID))
> experimentData(pasillaECS) <- expdata
> sampleNames(pasillaECS) = colnames(se_exons)

```

5.3 Gene counts

The *CountDataSet* will hold counts for the aggregate gene regions. The counts can be obtained by summing the exon hits by gene id using `geneCountTable` in `DEXSeq`,

```

> genetable = geneCountTable(pasillaECS)
> pasillaCDS = newCountDataSet(countData=genetable, conditions=design)
> experimentData(pasillaCDS) = expdata

```

If the primary interest was in counts per gene and counts per exon were not needed an alternative approach could be taken. The annotation file could be subset on "aggregate_gene" ranges and then counted.

```

> genes <- features[values(features)[["type"]] == "aggregate_gene"]
> se_genes <- summarizeOverlaps(genes, bamFiles, mode="Union")
> pasillaCDS_alt <- newCountDataSet(countData=assays(se_genes)$counts,
+   conditions=design)
> experimentData(pasillaCDS_alt) = expdata

```

6 References

<http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html> <http://www-huber.embl.de/users/anders/HTSeq/doc/count.html>