

Overview of svcnvs package

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1 Introduction

This package is used to segment normalized coverage by circular binary segmentation and to identify deletions and amplicons through a combination of changes in normalized coverage and read pairs with aberrant spacing or orientation. *Segmentation should probably be extracted into a separate package.*

2 Preprocessing

Additional packages required for this vignette are the `svfilter.hg19` package that contains various sequence filters for structural variant analyses and the `svalignments` package that contains wrappers for extracting properly- and improperly-paired reads from a BAM file.

```
library(GenomicRanges)
library(Rsamtools)
library(svcnvs)
library(svfilters.hg19)
library(svalignments)
```

Next, we load an object containing the normalized and \log_2 -transformed coverage estimates (\log_2 ratios) in non-overlapping 1kb bins along the genome. The \log_2 ratios were multiplied by 1000, rounded to the nearest integer, and saved as integers in a serialized R object to reduce the memory footprint.

```
ddir <- system.file("extdata", package="svpreprocess", mustWork=TRUE)
cov.file <- file.path(ddir, "preprocessed_coverage.rds")
log_ratio <- readRDS(cov.file)/1000
data(bins1kb, package="svfilters.hg19")
seqlevels(bins1kb, pruning.mode="coarse") <- paste0("chr", c(1:22, "X"))
bins1kb$log_ratio <- log_ratio
```

3 Segmentation

So that the examples run very quickly in this vignette, we limit our analyses to three chromosomes.

```
path <- system.file("extdata", package="svcnvs")
segments <- readRDS(file.path(path, "cgov44t_segments.rds"))
```

4 Deletions

In addition to the segmented \log_2 ratios, the deletion analysis requires improperly paired reads. Below, we specify the complete file path to a BAM file provided by the svbams package and extract improperly paired reads from the entire genome and an initial set of properly paired reads.

```
extdata <- system.file("extdata", package="svbams")
bam.file <- file.path(extdata, "cgov44t_revised.bam")
iparams <- improperAlignmentParams(what=c("flag", "mrnm", "mpos", "mapq"))
improper_rp <- getImproperAlignmentPairs(bam.file,
                                         param=iparams)

segs <- segments
del.gr <- reduce(segs[segs$seg.mean < hemizygousThr(DeletionParam())],
                min.gapwidth=2000)
proper_rp <- properReadPairs(bam.file, gr=del.gr, DeletionParam())
read_pairs <- list(proper_del=proper_rp, improper=improper_rp)
```

Finally, we collect the bin-level summaries, the segmentation data, and the read pair data in a single list object:

```
pdata <- preprocessData(bam.file=bam.file, genome="hg19",
                       bins=bins1kb,
                       segments=segments, read_pairs=read_pairs)
```

Below, we call segments as homozygous deletion (homozygous), homozygous deletion supported by improperly paired reads (homozygous+), and hemizygous deletion supported by improperly paired reads. For the purpose of identifying somatic deletions without a matched normal, we exclude hemizygous deletions that are not supported by improperly paired reads. With this toy dataset, we identify two homozygous deletions and the calls are both homozygous.

```
deletions <- sv_deletions(preprocess=pdata)
## Revising junctions...
## Refining homozygous boundaries by spanning hemizygous+
variant(deletions)
## GRanges object with 2 ranges and 2 metadata columns:
##      seqnames      ranges strand | seg.mean      sample
##      <Rle>         <IRanges>  <Rle> | <numeric> <character>
##  sv1      chr5 [180592001, 180595001] * | -8.0020      CGOV44T
##  sv2      chr15 [ 63201015,  63209243] * | -8.6549      CGOV44T
##  -----
##  seqinfo: 3 sequences from hg19 genome
calls(deletions)
## [1] "homozygous" "homozygous+"
```

The improperly-paired reads supporting the homozygous+ call can be extracted as a GAlignmentPairs object from the second element of the StructuralVariant object.

```
improper(deletions[2])
## GAlignmentPairs object with 51 pairs, strandMode=1, and 0 metadata columns:
##      seqnames strand      :      ranges  --      ranges
```

```
##      <Rle> <Rle> :      <IRanges> --      <IRanges>
## i44 chr15 - : [63209313, 63209412] -- [63200507, 63200606]
## i45 chr15 - : [63209323, 63209422] -- [63200525, 63200624]
## i13 chr15 + : [63200600, 63200699] -- [63209331, 63209430]
## i14 chr15 + : [63200600, 63200699] -- [63209363, 63209462]
## i47 chr15 - : [63209326, 63209425] -- [63200607, 63200706]
## ...      ...      ...      ...
## i32 chr15 + : [63200745, 63200844] -- [63209386, 63209485]
## i33 chr15 + : [63200749, 63200848] -- [63209349, 63209448]
## i60 chr15 - : [63209455, 63209554] -- [63200750, 63200849]
## i34 chr15 + : [63200757, 63200856] -- [63209357, 63209456]
## i63 chr15 - : [63209477, 63209576] -- [63200854, 63200953]
## -----
## seqinfo: 3 sequences from an unspecified genome
```

5 Amplicons

Amplicons can be identified using the same list data structure for the preprocessed data.

```
params <- ampliconParams()
ag <- svcnvs::sv_amplicons2(pdata, params=params)
```

Note the object returned by `sv_amplicons` is a graph where the nodes are the individual amplicons and the edges are links between amplicons given by improperly paired reads. By default, with 30x coverage we require at least 5 improperly paired reads to support an edge. See `?ampliconParams` for customizing these settings.

6 Plotting deletions

We will use the *ggplot2* and *gridExtra* packages for plotting the deletions.

```
library(ggplot2)
suppressPackageStartupMessages(library(gridExtra))
library(scales)
```

In the following code chunk, we extract the genomic coordinates for the deletion stored in the *deletion* object. To view the deletion in the context of the surrounding region, we create a second *GRanges* object that includes 200kb of the flanking genome on each side of the deletion.

```
##
## region of interest (roi)
##
roi <- variant(deletion)
seqlevels(roi, pruning.mode="coarse") <- "chr15"
expand <- 200e3
roi2 <- GRanges(seqnames(roi), IRanges(start(roi)-expand,
                                       end(roi) + expand))
seqinfo(roi2) <- seqinfo(roi)
```

Next, we subset the *views* object to contain only the genomic bins in the region of interest defined above. In addition, we create a *data.frame* containing all the segments for this particular chromosome and sample and a *data.frame* containing the preprocessed coverage.

```
segs <- keepSeqlevels(segments, seqlevels(roi), pruning.mode="coarse")
segs.df <- as(segs, "data.frame")
hom.plus <- subsetByOverlaps(bins1kb, roi2)
df <- data.frame(logr=hom.plus$log_ratio,
                 start=start(hom.plus))
```

We restrict the y-axis limits to a suitable range for visualizing the log ratios, thresholding log ratios that are extreme. We highlight the region identified by the segmentation in the ggplot graphic (the boundaries for the deletion are subsequently revised by the improperly paired reads as described in the next section).

```
ylim <- c(-9, 2)
df$logr <- svpreprocess::threshold(df$logr, ylim)
brks <- pretty(df$start, n=8)
region <- subsetByOverlaps(segs, roi)
region <- region[region$seg.mean < -1]
region <- as.data.frame(region)
xlim <- c(start(roi2), end(roi2))

A <- ggplot(df, aes(start, logr)) +
  geom_point(size=1, color="gray50") +
  scale_x_continuous(expand=c(0,0), breaks=brks, labels=brks/1e6) +
  scale_y_continuous(expand=c(0,0)) +
  geom_segment(data=segs.df,
              aes(x=start, xend=end, y=seg.mean, yend=seg.mean),
              size=1) +
  coord_cartesian(xlim=xlim, ylim=ylim) +
  ylab(expression(log[2]~ratio)) +
  geom_rect(data=region,
            aes(xmin=start, xmax=end, ymin=-Inf, ymax=+Inf),
            fill="steelblue", color="transparent", alpha=0.3,
            inherit.aes=FALSE) +
  theme(axis.text=element_text(size=10),
        axis.text.x=element_blank()) + xlab("") +
  annotate("text", x=xlim[1] + 15e3, y=-8, label="chr15", size=3)
A1 <- ggplotGrob(A)
```

6.1 Plotting rearranged read pairs from a deletion object

In addition to the log ratios, we would like to visualize the rearranged read pairs (read pairs with aberrant spacing or orientation with respect to the reference genome) that support the deletion. The rearranged read pairs supporting the deletion are encapsulated in the *deletion* object that we already loaded. First, we pull read pairs flanking the candidate deletion that have normal spacing and orientation. Because there are typically a large number of the normal read pairs, we thin these using the function *thinReadPairs*. Next, we melt these reads into a *data.frame* useful for plotting.

```
rps <- thinReadPairs(deletion)
rps <- svcnvs::meltReadPairs(rps)
```

We again use *ggplot* to plot the data. Note the vertical dashed lines depict the more precise boundaries of the deletion made possible by the improperly paired (rearranged) reads.

```
colors <- c("#0072B2", "#009E73")
p <- ggplot(rps, aes(ymin=readpair-0.2, ymax=readpair+0.2,
                  xmin=start/1e6, xmax=end/1e6, color=read,
                  fill=read, group=readpair)) +
```

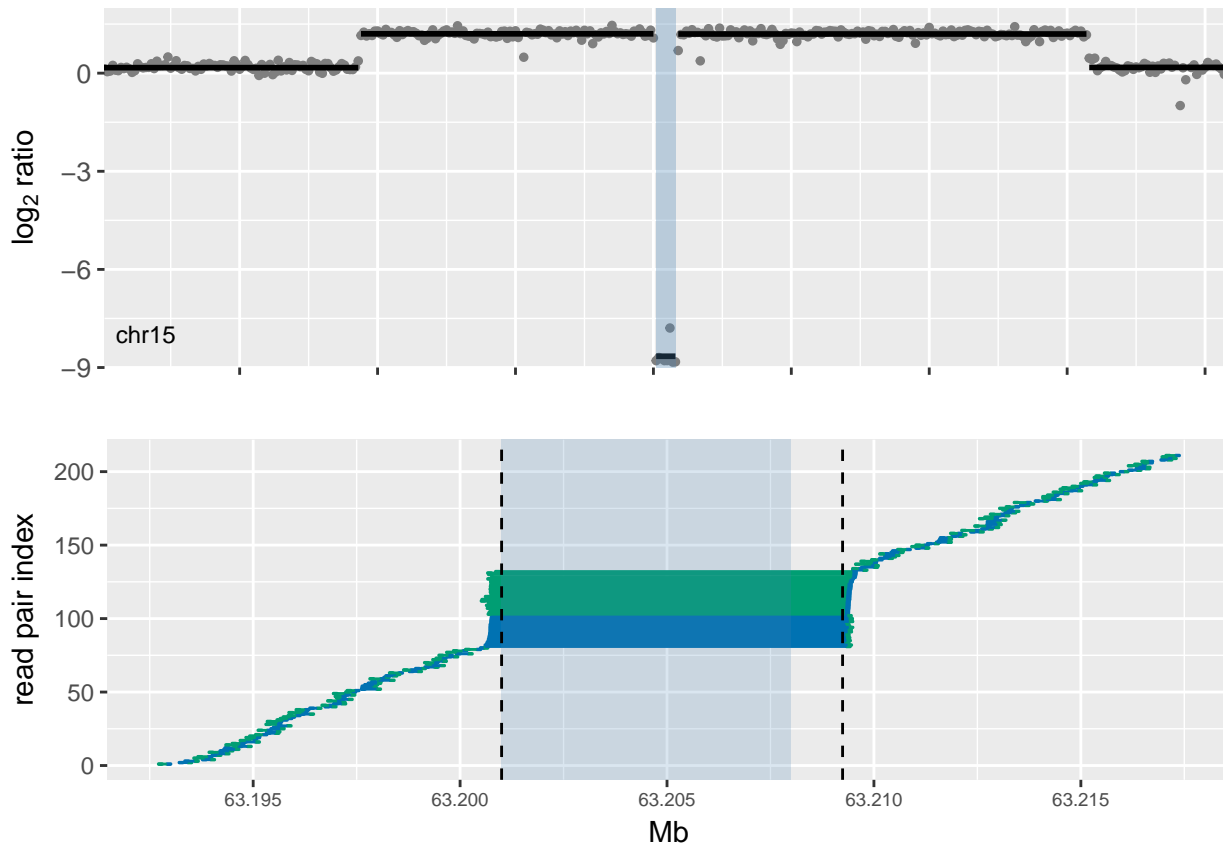
```

geom_rect() +
xlim(c(min(rps$start), max(rps$end))/1e6) +
geom_line(aes(x=start/1e6, y=readpair)) +
ylab("read pair index") +
scale_x_continuous(breaks=pretty_breaks(5)) +
geom_rect(data=region,
          aes(xmin=start/1e6, xmax=end/1e6, ymin=-Inf, ymax=+Inf),
          fill="steelblue", color="transparent", alpha=0.2,
          inherit.aes=FALSE) +
scale_color_manual(values=colors) +
scale_fill_manual(values=colors) +
xlab("Mb") +
theme(axis.text.x=element_text(size=7)) +
guides(fill=FALSE, color=FALSE) +
geom_vline(xintercept=c(start(roi)/1e6, end(roi)/1e6), linetype="dashed")
## Scale for 'x' is already present. Adding another scale for 'x', which
## will replace the existing scale.
B <- ggplotGrob(p)

```

Finally, we make a composite graphic of the log ratios and rearranged reads. Note, the vertical dashed lines show the revised deletion boundaries using the improperly-paired reads that flank the new sequence junction formed as a result of the deletion.

```
grid.arrange(A1, B, ncol=1)
```



7 Plotting amplicon graphs

See the amplicons vignette.