segmentSeq: methods for identifying small RNA loci from high-throughput sequencing data

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1 Introduction

High-throughput sequencing technologies allow the production of large volumes of short sequences, which can be aligned to the genome to create a set of *matches* to the genome. By looking for regions of the genome which to which there are high densities of matches, we can infer a segmentation of the genome into regions of biological significance. The methods we propose allows the simultaneous segmentation of data from multiple samples, taking into account replicate data, in order to create a consensus segmentation. This has obvious applications in a number of classes of sequencing experiments, particularly in the discovery of small RNA loci and novel mRNA transcriptome discovery.

We approach the problem by considering a large set of potential *segments* upon the genome and counting the number of tags that match to that segment in multiple sequencing experiments (that may or may not contain replication). We then adapt the empirical Bayesian methods implemented in the `baySeq` package [1] to establish, for a given segment, the likelihood that the count data in that segment is similar to background levels, or that it is similar to the regions to the left or right of that segment. We then rank all the potential segments in order of increasing likelihood of similarity and reject those segments for which there is a high likelihood of similarity with the background or the regions to the left or right of the segment. This gives us a large list of overlapping segments. We reduce this list to identify non-overlapping loci by choosing, for a set of overlapping segments, the segment which has the lowest likelihood of similarity with either background or the regions to the left or right of that segment and rejecting all other segments that overlap with this segment. For fuller details of the method, see Hardcastle *et al.* [2].

2 Preparation

We begin by loading the `segmentSeq` package.

```
>    library(segmentSeq)
```

Note that because the experiments that `segmentSeq` is designed to analyse are usually massive, we should use (if possible) parallel processing as implemented by the `parallel` package. If using this approach, we need to begin by define a *cluster*. The following command will use eight processors on a single machine; see the help page for 'makeCluster' for more information. If we don't want to parallelise, we can proceed anyway with a `NULL` cluster.

```
> if(require("parallel"))
+ {
+     numCores <- min(8, detectCores())
+     cl <- makeCluster(numCores)
+ } else {
+     cl <- NULL
+ }
```

The `readGeneric` function is able to read in tab-delimited files which have appropriate column names, and create an `alignmentData` object. Alternatively, if the appropriate column names are not present, we can specify which columns to use for the data. In either case, to use this function we pass a character vector of files, together with information on which data are to be treated as replicates to the function. We also need to define the lengths of

the chromosome and specifiy the chromosome names as a character. The data here, drawn from text files in the 'data' directory of the segmentSeq package are taken from the first million bases of an alignment to chromosome 1 and the first five hundred thousand bases of an alignment to chromosome 2 of *Arabidopsis thaliana* in a sequencing experiment where libraries 'SL9' and 'SL10' are replicates, as are 'SL26' and 'SL32'. Libraries 'SL9' and 'SL10' are sequenced from an Argonaute 6 IP, while 'SL26' and 'SL32' are an Argonaute 4 IP.

A similar function, readBAM performs the same operation on files in the BAM format. Please consult the help page for further details.

```
> chrlens <- c(1e6, 2e5)
> datadir <- system.file("extdata", package = "segmentSeq")
> libfiles <- c("SL9.txt", "SL10.txt", "SL26.txt", "SL32.txt")
> libnames <- c("SL9", "SL10", "SL26", "SL32")
> replicates <- c("AGO6", "AGO6", "AGO4", "AGO4")
> aD <- readGeneric(files = libfiles, dir = datadir,
+                   replicates = replicates, libnames = libnames,
+                   chrs = c(">Chr1", ">Chr2"), chrlens = chrlens,
+                   polyLength = 10, header = TRUE, gap = 200)
> aD

An object of class "alignmentData"
13765 rows and 4 columns

Slot "libnames":
[1] "SL9"  "SL10" "SL26" "SL32"

Slot "replicates":
[1] AGO6 AGO6 AGO4 AGO4
Levels: AGO4 AGO6

Slot "alignments":
GRanges object with 13765 ranges and 2 metadata columns:
          seqnames            ranges strand |                      tag multireads
             <Rle>         <IRanges>  <Rle> |              <character>  <numeric>
     [1]     >Chr1      [265, 284]        - |     AAATGAAGATAAACCATCCA          1
     [2]     >Chr1      [405, 427]        - | AAGGAGTAAGAATGACAATAAAT          1
     [3]     >Chr1      [406, 420]        - |          AAGAATGACAATAAA          1
     [4]     >Chr1      [600, 623]        + | AAGGATTGGTGGTTTGAAGACACA          1
     [5]     >Chr1      [665, 688]        + | ATCCTTGTAGCACACATTTTGGCA          1
     ...       ...               ...    ... .                      ...        ...
  [13761]    >Chr2 [179972, 179993]        + |   ATGAATGGCTCTCTCTAGCGGA          1
  [13762]    >Chr2 [179978, 180000]        - |   GAGATTCTCCGCTAGAGAGAGCC          1
  [13763]    >Chr2 [179999, 180022]        - | ATTAATATTAATTCATCGGGAAGA          1
  [13764]    >Chr2 [180002, 180022]        - |    ATTAATATTAATTCATCGGGA          1
  [13765]    >Chr2 [180014, 180037]        + | AATATTAATGGTATTTGTGGAAAA          1
  -------
  seqinfo: 2 sequences from an unspecified genome

Slot "data":
Matrix with  13765  rows.
      SL9 SL10 SL26 SL32
1       1    0    0    0
2       0    0    0    2
3       0    1    0    0
4       0    1    0    0
5       7    1    0    0
...   ...  ...  ...  ...
13761   2    7    0    0
13762   0    1    0    0
13763   0    1    0    0
```

```
13764   0   1   0   0
13765   1   0   0   0
```

```
Slot "libsizes":
[1] 4447 6531 9666 6675
```

Next, we process this `alignmentData` object to produce a `segData` object. This `segData` object contains a set of potential segments on the genome defined by the start and end points of regions of overlapping alignments in the `alignmentData` object. It then evaluates the number of tags that hit in each of these segments.

```
> sD <- processAD(aD, gap = 100, cl = cl)
> sD
```

```
An object of class "segData"
14444 rows and 4 columns
```

```
Slot "replicates":
[1] AGO6 AGO6 AGO4 AGO4
Levels: AGO4 AGO6
```

```
Slot "coordinates":
GRanges object with 14444 ranges and 0 metadata columns:
          seqnames              ranges strand
            <Rle>           <IRanges>  <Rle>
      [1]    >Chr1       [265, 284]       *
      [2]    >Chr1       [405, 427]       *
      [3]    >Chr1       [600, 623]       *
      [4]    >Chr1       [600, 688]       *
      [5]    >Chr1       [600, 830]       *
      ...      ...              ...      ...
  [14440]    >Chr2 [179708, 179872]       *
  [14441]    >Chr2 [179708, 180037]       *
  [14442]    >Chr2 [179738, 179872]       *
  [14443]    >Chr2 [179738, 180037]       *
  [14444]    >Chr2 [179923, 180037]       *
  -------
  seqinfo: 2 sequences from an unspecified genome
```

```
Slot "locLikelihoods" (stored on log scale):
Matrix with  0  rows.
<0 x 0 matrix>
```

```
Slot "data":
Matrix with  0  rows.Matrix with  0  rows.
     SL9 SL10 SL26 SL32
```

```
Slot "libsizes":
[1] 4447 6531 9666 6675
```

We can now construct a segment map from these potential segments.

Segmentation by heuristic methods

A fast method of segmentation can be achieved by exploiting the bimodality of the densities of small RNAs in the potential segments. In this approach, we assign each potential segment to one of two clusters for each replicate group, either as a segment or a null based on the density of sequence tags within that segment. We then combine these clusterings for each replicate group to gain a consensus segmentation map.

```
> hS <- heuristicSeg(sD = sD, aD = aD, RKPM = 1000, largeness = 1e8, getLikes = TRUE, cl = cl)
```

......

Segmentation by empirical Bayesian methods

A more refined approach to the problem uses an existing segment map (or, if not provided, a segment map defined by the hS function) to acquire empirical distributions on the density of sequence tags within a segment. We can then estimate posterior likelihoods for each potential segment as being either a true segment or a null. We then identify all potential segments in the with a posterior likelihood of being a segment greater than some value 'lociCutoff' and containing no subregion with a posterior likelihood of being a null greater than 'nullCutoff'. We then greedily select the longest segments satisfying these criteria that do not overlap with any other such segments in defining our segmentation map.

```
> classSegs <- classifySeg(sD = sD, aD = aD, cD = hS, cl = cl)
```

....

```
> classSegs
```

```
GRanges object with 251 ranges and 0 metadata columns:
        seqnames            ranges strand
           <Rle>         <IRanges>  <Rle>
   [1]     >Chr1 [    1,    599]      *
   [2]     >Chr1 [  600,    967]      *
   [3]     >Chr1 [  968,  17054]      *
   [4]     >Chr1 [17055,  18728]      *
   [5]     >Chr1 [18729,  27656]      *
   ...       ...               ...    ...
 [247]     >Chr2 [169231, 178343]      *
 [248]     >Chr2 [178344, 178636]      *
 [249]     >Chr2 [178637, 179707]      *
 [250]     >Chr2 [179708, 180037]      *
 [251]     >Chr2 [180038, 200000]      *
   -------
   seqinfo: 2 sequences from an unspecified genome
An object of class "lociData"
251 rows and 4 columns

Slot "replicates"
AGO6 AGO6 AGO4 AGO4
Slot "groups":
list()

Slot "data":
     AGO6.1 AGO6.2 AGO4.1 AGO4.2
[1,]      1      1      0      2
[2,]     54     46     65     83
[3,]      2      3      0      0
[4,]    682    621   1405   1103
[5,]      0      3      0      0
246 more rows...

Slot "annotation":
data frame with 0 columns and 251 rows

Slot "locLikelihoods" (stored on log scale):
Matrix with  251  rows.
        AGO4     AGO6
1    0.26743  0.10021
2    0.91954  0.97194
```

```
3     0.037959 0.031881
4      0.97847  0.99621
5      0.04024 0.047186
...        ...      ...
247    0.3312 0.062558
248    0.8955  0.98286
249 0.057321 0.060004
250    0.9391  0.97494
251 0.037293  0.02673
```

```
Expected number of loci in each replicate group
     AGO4      AGO6
108.0563 137.2368
```

By one of these methods, we finally acquire an annotated `lociData` object, with the annotations describing the co-ordinates of each segment.

We can use this `lociData` object, in combination with the `alignmentData` object, to plot the segmented genome.

```
> par(mfrow = c(2,1), mar = c(2,6,2,2))
> plotGenome(aD, hS, chr = ">Chr1", limits = c(1, 1e5),
+            showNumber = FALSE, cap = 50)
> plotGenome(aD, classSegs, chr = ">Chr1", limits = c(1, 1e5),
+            showNumber = FALSE, cap = 50)
```
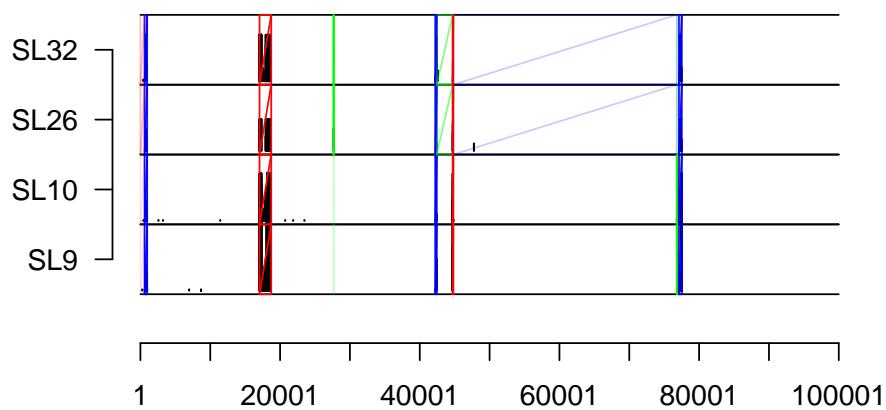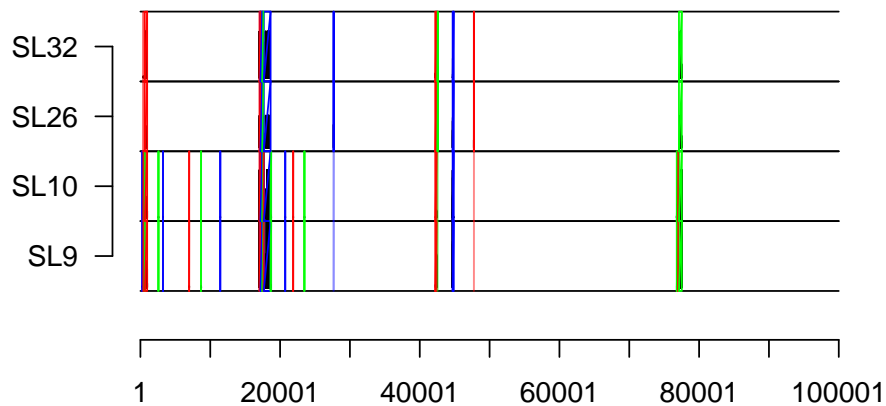

Figure 1: The segmented genome (first 10^5 bases of chromosome 1.

Given the calculated likelihoods, we can filter the segmented genome by controlling on likelihood, false discovery rate, or familywise error rate

```
> loci <- selectLoci(classSegs, FDR = 0.05)
> loci

GRanges object with 120 ranges and 0 metadata columns:
        seqnames            ranges strand
           <Rle>         <IRanges>  <Rle>
    [1]    >Chr1 [  600,    967]       *
    [2]    >Chr1 [17055,  18728]       *
    [3]    >Chr1 [42217,  42435]       *
    [4]    >Chr1 [44710,  44811]       *
    [5]    >Chr1 [76799,  76890]       *
    ...      ...               ...     ...
  [116]    >Chr2 [152150, 152173]       *
  [117]    >Chr2 [152795, 152877]       *
  [118]    >Chr2 [169196, 169230]       *
  [119]    >Chr2 [178344, 178636]       *
  [120]    >Chr2 [179708, 180037]       *
  -------
  seqinfo: 2 sequences from an unspecified genome
An object of class "lociData"
120 rows and 4 columns

Slot "replicates"
AGO6 AGO6 AGO4 AGO4
Slot "groups":
list()

Slot "data":
     AGO6.1 AGO6.2 AGO4.1 AGO4.2
[1,]     54     46     65     83
[2,]    682    621   1405   1103
[3,]     31     11     48     56
[4,]     73     57     47     21
[5,]      6     19      0      0
115 more rows...

Slot "annotation":
data frame with 0 columns and 120 rows

Slot "locLikelihoods" (stored on log scale):
Matrix with  120  rows.
        AGO4     AGO6
1    0.91954  0.97194
2    0.97847  0.99621
3    0.93562  0.94904
4    0.94711  0.99772
5    0.10403  0.97094
...      ...      ...
116  0.13942   0.9702
117  0.77373  0.94272
118  0.12821  0.98855
119   0.8955  0.98286
120   0.9391  0.97494

Expected number of loci in each replicate group
     AGO4      AGO6
```

```
  79.58033 116.74414
```

The `lociData` objects can now be examined for differential expression with the `baySeq` package.

First we define the possible models of differential expression on the data. In this case, the models are of non-differential expression and pairwise differential expression.

```
> groups(classSegs) <- list(NDE = c(1,1,1,1), DE = c("AGO6", "AGO6", "AGO4", "AGO4"))
```

Then we get empirical distributions on the parameter space of the data.

```
> classSegs <- getPriors(classSegs, cl = cl)
```

Then we get the posterior likelihoods of the data conforming to each model. Since the 'classSegs' object contains null regions as well as true loci, we will use the 'nullData = TRUE' option to distinguish between non-differentially expressed loci and non-expressed regions. By default, the loci likelihoods calculated earlier will be used to weight the initial parameter fit in order to detect null data.

```
> classSegs <- getLikelihoods(classSegs, nullData = TRUE, cl = cl)
.
```

We can examine the highest likelihood non-expressed ('null') regions

```
> topCounts(classSegs, NULL, number = 3)
```

	seqnames	start	end	width	strand	AGO6.1	AGO6.2	AGO4.1	AGO4.2	Likelihood	FDR.
1	>Chr1	754198	758593	4396	*	1	0	1	0	0.9321823	0.06781774
2	>Chr1	950796	958752	7957	*	2	4	3	2	0.9302228	0.06879746
3	>Chr1	148877	222440	73564	*	0	0	0	0	0.9277003	0.06996486

	FWER.
1	0.06781774
2	0.13286279
3	0.19555651

The highest likelihood expressed but non-differentially expressed regions

```
> topCounts(classSegs, "NDE", number = 3)
```

	seqnames	start	end	width	strand	AGO6.1	AGO6.2	AGO4.1	AGO4.2	Likelihood	FDR.NDE
1	>Chr2	1554	14423	12870	*	7632	18470	20242	13836	0.9782161	0.02178393
2	>Chr1	446325	447437	1113	*	789	536	1291	1184	0.9402429	0.04077052
3	>Chr1	17055	18728	1674	*	682	621	1405	1103	0.9131513	0.05612990

	FWER.NDE
1	0.02178393
2	0.08023929
3	0.16011929

And the highest likelihood differentially expressed regions

```
> topCounts(classSegs, "DE", number = 3)
```

	seqnames	start	end	width	strand	AGO6.1	AGO6.2	AGO4.1	AGO4.2	Likelihood	ordering
1	>Chr2	52652	53314	663	*	84	86	982	696	0.9988899	AGO4>AGO6
2	>Chr2	58131	59084	954	*	81	83	965	677	0.9986353	AGO4>AGO6
3	>Chr2	49137	50333	1197	*	101	116	992	719	0.9985233	AGO4>AGO6

	FDR.DE	FWER.DE
1	0.001110055	0.001110055
2	0.001237382	0.002473249
3	0.001317159	0.003946311

Finally, to be a good citizen, we stop the cluster we started earlier:

```
> if(!is.null(cl))
+     stopCluster(cl)
```

Session Info

```
> sessionInfo()

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               LC_TIME=en_US.UTF-8
 [4] LC_COLLATE=C               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] stats4    parallel  stats     graphics  grDevices utils     datasets  methods
[9] base

other attached packages:
 [1] segmentSeq_2.6.0          ShortRead_1.30.0          GenomicAlignments_1.8.0
 [4] SummarizedExperiment_1.2.0 Biobase_2.32.0           Rsamtools_1.24.0
 [7] Biostrings_2.40.0         XVector_0.12.0            BiocParallel_1.6.0
[10] baySeq_2.6.0              perm_1.0-0.0              abind_1.4-3
[13] GenomicRanges_1.24.0      GenomeInfoDb_1.8.0        IRanges_2.6.0
[16] S4Vectors_0.10.0          BiocGenerics_0.18.0

loaded via a namespace (and not attached):
[1] lattice_0.20-33    bitops_1.0-6       grid_3.3.0         zlibbioc_1.18.0
[5] hwriter_1.3.2      latticeExtra_0.6-28 BiocStyle_2.0.0    RColorBrewer_1.1-2
[9] tools_3.3.0
```

References

[1] Thomas J. Hardcastle and Krystyna A. Kelly. *baySeq: Empirical Bayesian Methods For Identifying Differential Expression In Sequence Count Data.* BMC Bioinformatics (2010).

[2] Thomas J. Hardcastle and Krystyna A. Kelly and David C. Baulcombe. *Identifying small RNA loci from high-throughput sequencing data.* Bioinformatics (2012).