

# segmentSeq: methods for detecting methylation loci and differential methylation

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October 24, 2023

## 1 Introduction

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This vignette introduces analysis methods for data from high-throughput sequencing of bisulphite treated DNA to detect cytosine methylation. The `segmentSeq` package was originally designed to detect siRNA loci [1] and many of the methods developed for this can be used to detect loci of cytosine methylation from replicated (or unreplicated) sequencing data.

## 2 Preparation

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Preparation of the `segmentSeq` package proceeds as in siRNA analysis. 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. Results may be slightly different depending on whether or not a cluster is used owing to the non-deterministic elements of the method.

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

The `segmentSeq` package is designed to read in output from the YAMA (Yet Another Methylation Aligner) program. This is a perl-based package using either `bowtie` or `bowtie2` to align bisulphite treated reads (in an unbiased manner) to a reference and identify the number of times each cytosine is identified as methylated or unmethylated. Unlike most other aligners, YAMA does not require that reads that map to more than one location are discarded, instead it reports the number of alternate matches to the reference for each cytosine. This is then used by `segmentSeq` to weight the observed number of methylated/un-methylated cytosines at a location. The files used here have been compressed to save space.

```

> datadir <- system.file("extdata", package = "segmentSeq")
> files <- c("short_18B_C24_C24_trim.fastq_CG_methCalls.gz",
+ "short_Sample_17A_trimmed.fastq_CG_methCalls.gz",
+ "short_13_C24_col_trim.fastq_CG_methCalls.gz",
+ "short_Sample_28_trimmed.fastq_CG_methCalls.gz")
> mD <- readMeths(files = files, dir = datadir,
+ libnames = c("A1", "A2", "B1", "B2"), replicates = c("A", "A", "B", "B"),
+ nonconversion = c(0.004777, 0.005903, 0.016514, 0.006134))

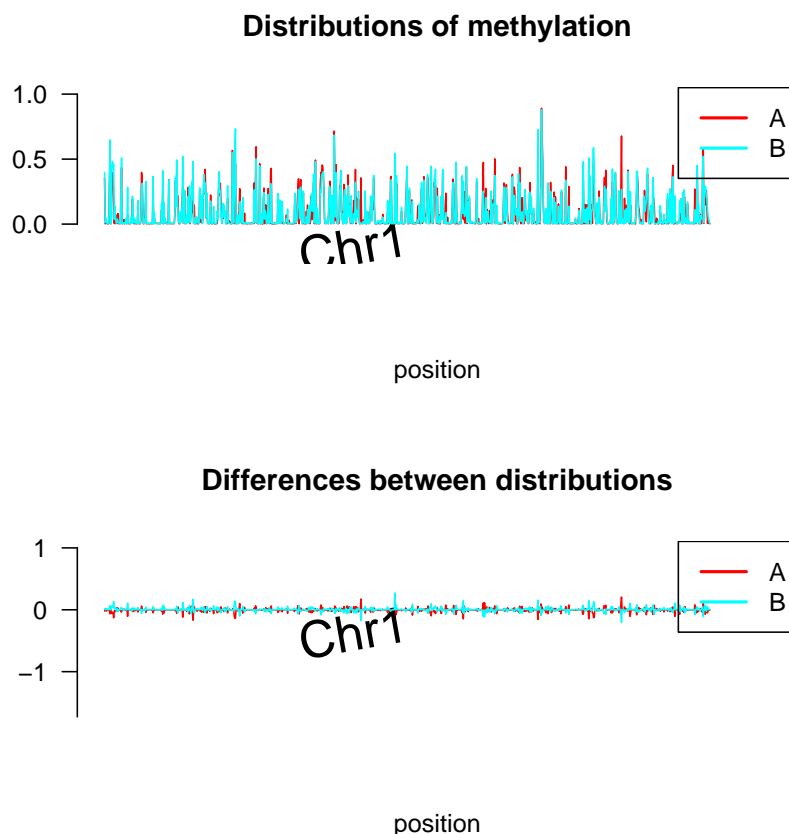
```

We can begin by plotting the distribution of methylation for these samples. The distribution can be plotted for each sample individually, or as an average across multiple samples. We can also subtract one distribution from another to visualise patterns of differential methylation on the genome.

```

> par(mfrow = c(2,1))
> dists <- plotMethDistribution(mD, main = "Distributions of methylation", chr = "Chr1")
> plotMethDistribution(mD,
+                      subtract = rowMeans(sapply(dists, function(x) x[,2])),
+                      main = "Differences between distributions", chr = "Chr1")

```



**Figure 1:** Distributions of methylation on the genome (first two million bases of chromosome 1).

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(mD, cl = cl)
```

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

## Segmentation by heuristic Bayesian methods

A fast method of segmentation can be achieved by assuming a binomial distribution on the data with an uninformative beta prior, and identifying those potential segments which have a sufficiently large posterior likelihood that the proportion of methylation exceeds some critical value. This value can be determined by examining the data using the 'thresholdFinder' function, but expert knowledge is likely to provide a better guess as to where methylation becomes biologically significant.

```
> thresh = 0.2
> hS <- heuristicSeg(sD = sD, aD = mD, prop = thresh, cl = cl, gap = 100, getLikes = FALSE)
> hS
```

GRanges object with 2955 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	Chr1	108-948	*
[2]	Chr1	5449-5465	*
[3]	Chr1	6452	*
[4]	Chr1	6520	*
[5]	Chr1	7020-7034	*
...	...	...	...
[2951]	Chr1	1993118-1993128	*
[2952]	Chr1	1993149	*
[2953]	Chr1	1993335	*
[2954]	Chr1	1994611	*
[2955]	Chr1	1994857-1994886	*

-----

seqinfo: 1 sequence from an unspecified genome; no seqlengths

An object of class "lociData"

2955 rows and 4 columns

Slot "replicates"

A A B B

Slot "groups":

list()

Slot "data":

	[,1]	[,2]	[,3]	[,4]
[1,]	247:169	175:133	165:149	28:31
[2,]	0:49	1:86	23:36	2:2
[3,]	2:0	5:3	0:3	0:1
[4,]	0:3	0:9	2:1	0:0

```
[5,] 0:119  2:78  20:37  0:2
2950 more rows...

Slot "annotation":
data frame with 0 columns and 2955 rows

Slot "locLikelihoods" (stored on log scale):
Matrix with 2955 rows.
      A B
1     1 1
2     0 1
3     1 0
4     0 1
5     0 1
... ..
2951  1 1
2952  1 1
2953  1 0
2954  1 0
2955  0 1

Expected number of loci in each replicate group
      A B
1968 2168
```

Within a methylation locus, it is not uncommon to find completely unmethylated cytosines. If the coverage of these cytosines is too high, it is possible that these will cause the locus to be split into two or more fragments. The `mergeMethSegs` function can be used to overcome this splitting by merging loci with identical patterns of expression that are not separated by too great a gap. Merging in this manner is optional, but recommended.

```
> hS <- mergeMethSegs(hS, mD, gap = 5000, cl = cl)
```

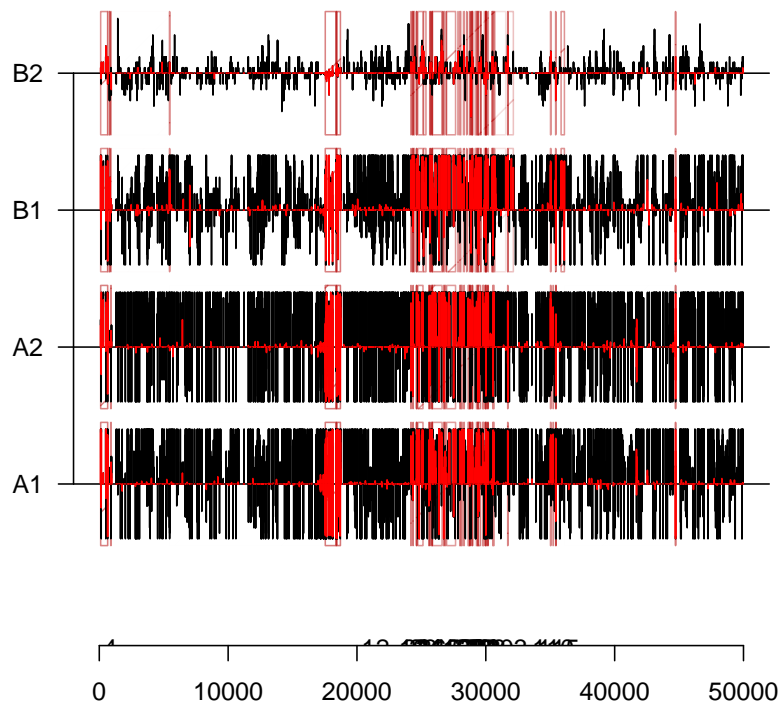
We can then estimate posterior likelihoods on the defined loci by applying empirical Bayesian methods. These will not change the locus definition, but will assign likelihoods that the identified loci represent a true methylation locus in each replicate group.

```
> hSL <- lociLikelihoods(hS, mD, cl = cl)
```

## Visualising loci

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

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



**Figure 2:** Methylation and identified loci on the first ten thousand bases of chromosome 1.

```
> plotMeth(mD, hSL, chr = "Chr1", limits = c(1, 50000), cap = 10)
```

## Differential Methylation analysis

We can also examine the `methData` object for differentially methylated regions using the beta-binomial methods [2] implemented in `baySeq`. We first define a group structure on the data.

```
> groups(hSL) <- list(NDE = c(1,1,1,1), DE = c("A", "A", "B", "B"))
```

The `methObservables` function pre-calculates a set of data to improve the speed of prior and posterior estimation (at some minor memory cost).

```
> hSL <- methObservables(hSL)
```

The density function used here is a composite of the beta-binomial and a binomial distribution that accounts for the reported non-conversion rates.

```
> densityFunction(hSL) <- bbNCDist
```

We can then determine a prior distribution on the parameters of the model for the data.

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

We can then find the posterior likelihoods of the models defined in the groups structure.

```
> hSL <- getLikelihoods(hSL, cl = cl)
```

```
.
```

We can then retrieve the data for the top differentially methylated regions.

```
> topCounts(hSL, "DE")
```

	seqnames	start	end	width	strand	A.1	A.2	B.1	B.2
NA.3932	Chr1	1439804	1440002	199	*	1:239	0:119	102:56	11:5
NA.3064	Chr1	774658	774937	280	*	0:172	0:90	38:16	14:7
NA.3651	Chr1	1192725	1192730	6	*	37:4	15:2	0:55	0:8
NA.3225	Chr1	888560	888590	31	*	423:90	217:56	1:37	0:7
NA.4221	Chr1	1733868	1733987	120	*	0:104	0:150	76:62	11:7
NA.2257	Chr1	25580	25583	4	*	20:2	49:3	0:58	0:3
NA.2517	Chr1	297002	297016	15	*	60:23	48:19	0:48	0:9
NA.3229	Chr1	889432	889508	77	*	2:204	0:131	75:24	9:3
NA.2768	Chr1	526399	526607	209	*	113:148	150:192	0:300	0:15
NA.4179	Chr1	1686726	1686728	3	*	27:2	24:1	0:30	0:5

	likes	DE	FDR.DE	FWER.DE
NA.3932	0.9996911	B>A	0.0003088538	0.0003088538
NA.3064	0.9996891	B>A	0.0003098905	0.0006196849
NA.3651	0.9996146	A>B	0.0003350493	0.0010048132
NA.3225	0.9995707	A>B	0.0003586031	0.0014336461
NA.4221	0.9995685	B>A	0.0003731744	0.0018644872
NA.2257	0.9995677	A>B	0.0003830365	0.0022960279
NA.2517	0.9995407	A>B	0.0003939338	0.0027542913
NA.3229	0.9995296	B>A	0.0004034950	0.0032234190
NA.2768	0.9995007	A>B	0.0004141431	0.0037211375
NA.4179	0.9994950	A>B	0.0004232322	0.0042242918

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

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

## Session Info

```
> sessionInfo()
```

```
R version 4.3.1 (2023-06-16 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2022 x64 (build 20348)
```

Matrix products: default

locale:

- [1] LC\_COLLATE=C
- [2] LC\_CTYPE=English\_United States.utf8
- [3] LC\_MONETARY=English\_United States.utf8
- [4] LC\_NUMERIC=C
- [5] LC\_TIME=English\_United States.utf8

time zone: America/New\_York

tzcode source: internal

attached base packages:

- [1] parallel stats4 stats graphics grDevices utils datasets
- [8] methods base

other attached packages:

- [1] segmentSeq\_2.36.0 ShortRead\_1.60.0
- [3] GenomicAlignments\_1.38.0 SummarizedExperiment\_1.32.0
- [5] Biobase\_2.62.0 MatrixGenerics\_1.14.0
- [7] matrixStats\_1.0.0 Rsamtools\_2.18.0
- [9] Biostrings\_2.70.0 XVector\_0.42.0
- [11] BiocParallel\_1.36.0 baySeq\_2.36.0
- [13] abind\_1.4-5 GenomicRanges\_1.54.0
- [15] GenomeInfoDb\_1.38.0 IRanges\_2.36.0
- [17] S4Vectors\_0.40.0 BiocGenerics\_0.48.0

loaded via a namespace (and not attached):

- [1] Matrix\_1.6-1.1 limma\_3.58.0 BiocStyle\_2.30.0
- [4] compiler\_4.3.1 BiocManager\_1.30.22 crayon\_1.5.2
- [7] Rcpp\_1.0.11 bitops\_1.0-7 png\_0.1-8
- [10] yaml\_2.3.7 fastmap\_1.1.1 statmod\_1.5.0
- [13] lattice\_0.22-5 deldir\_1.0-9 S4Arrays\_1.2.0
- [16] latticeExtra\_0.6-30 knitr\_1.44 DelayedArray\_0.28.0
- [19] interp\_1.1-4 GenomeInfoDbData\_1.2.11 RColorBrewer\_1.1-3
- [22] rlang\_1.1.1 hwriter\_1.3.2.1 xfun\_0.40
- [25] SparseArray\_1.2.0 cli\_3.6.1 zlibbioc\_1.48.0
- [28] digest\_0.6.33 grid\_4.3.1 locfit\_1.5-9.8
- [31] edgeR\_4.0.0 evaluate\_0.22 codetools\_0.2-19
- [34] RCurl\_1.98-1.12 rmarkdown\_2.25 jpeg\_0.1-10
- [37] tools\_4.3.1 htmltools\_0.5.6.1

## References

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

- [2] Thomas J. Hardcastle and Krystyna A. Kelly. *Empirical Bayesian analysis of paired high-throughput sequencing data with a beta-binomial distribution*. BMC Bioinformatics (2013).