

# Differential analyses with DSS

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### Abstract

This vignette introduces the use of the Bioconductor package DSS (Dispersion Shrinkage for Sequencing data), which is designed for differential analysis based on high-throughput sequencing data. It performs differential expression analyses for RNA-seq, and differential methylation analyses for bisulfite sequencing (BS-seq) data. The core of DSS is a new procedure to estimate and shrink gene- or CpG site-specific dispersions, then conduct Wald tests for differential expression/methylation. Compared with existing methods, DSS provides excellent statistical and computational performance.

## 1 Introduction

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Recent advances in high-throughput sequencing technology have revolutionized genomic research. For example, RNA-seq is a new technology for measuring the abundance of RNA products. Compared to gene expression microarrays, it provides a better dynamic range and lower signal-to-noise ratio. Bisulfite sequencing (BS-seq) is a new technology for measuring DNA methylation. Compared to capture-based methods such as MeDIP-seq, it provides single-base resolution and eliminates biases associated with CpG density.

Fundamental questions for RNA-seq or BS-seq data analyses are whether gene expression regulation or DNA methylation dynamics vary under different biological contexts. Identifying sites or regions exhibiting differential expression (DE) or differential methylation (DM) are thus key tasks in functional genomics research.

RNA- or BS-seq experiments typically have a limited number of biological replicates due to cost constraints. This can lead to unstable estimation of within group variance, and subsequently undesirable results from hypothesis testing. Variance shrinkage methods have been widely used in DE analyses based on microarray data. The methods are typically based on a Bayesian hierarchical model, with a prior imposed on the gene-specific variances to provide a basis for information sharing across all genes/CpG sites. In these models, shrinkage is achieved for variance estimation. Using shrunk variance in hypothesis tests has been shown to provide better results.

A distinct feature of RNA-seq or BS-seq data is that the measurements are in the form of counts. These data are often assumed to be from the Poisson (for RNA-seq) or Binomial (for BS-seq) distributions. Unlike continuous distributions such as the Gaussian distribution, the variances depend on means in these discrete distributions. This implies that the sample variances do not account for biological variation between replicates, and shrinkage cannot be applied on variances directly.

In contrast, we assume that our count data come from the Gamma-Poisson (RNA-seq) or Beta-Binomial (BS-seq) distribution. These distributions can be parameterized by a mean and an over dispersion parameter. The over dispersion parameters, which represent the biological variation for replicates within a treatment group, play a central role in the differential analyses.

Here we present a new DE/DM detection algorithm, where shrinkage is performed on the dispersion parameters. We first impose a log-normal prior on the dispersions, and then combine data from all genes/CpG sites to shrink dispersions through a penalized likelihood approach. Finally, we construct Wald tests to test each gene/site for differential expression/methylation. Our results show that the new method provides excellent performance compared to existing methods, especially when the overall dispersion level is high or the number of replicates is small.

For details of the hierarchical model, the shrinkage method and test procedure, please read [3] for differential expression from RNA-seq, and [1] for differential methylation from BS-seq.

## 2 Using DSS for differential expression analysis

---

### 2.1 Single factor experiment

Required inputs for DSS are (1) gene expression values as a matrix of integers, rows are for genes and columns are for samples; and (2) a vector representing experimental designs. The length of the design vector must match the number of

columns of input counts. Optionally, normalization factors or additional annotation for genes can be supplied.

The basic data container in the package is `SeqCountSet` class, which is directly inherited from `ExpressionSet` class defined in `Biobase`. An object of the class contains all necessary information for a DE analysis: gene expression values, experimental designs, and additional annotations.

A typical DE analysis contains the following simple steps.

1. Create a `SeqCountSet` object using `newSeqCountSet`.
2. Estimate normalization factor using `estNormFactors`.
3. Estimate and shrink gene-wise dispersion using `estDispersion`
4. Two-group comparison using `waldTest`.

The usage of DSS is demonstrated in the simple simulation below.

1. First load in the library, and make a `SeqCountSet` object from some counts for 2000 genes and 6 samples.

```
> library(DSS)
> counts1=matrix(rnbinom(300, mu=10, size=10), ncol=3)
> counts2=matrix(rnbinom(300, mu=50, size=10), ncol=3)
> X1=cbind(counts1, counts2) ## these are 100 DE genes
> X2=matrix(rnbinom(11400, mu=10, size=10), ncol=6)
> X=rbind(X1,X2)
> designs=c(0,0,0,1,1,1)
> seqData=newSeqCountSet(X, designs)
> seqData
```

```
SeqCountSet (storageMode: lockedEnvironment)
```

```
assayData: 2000 features, 6 samples
```

```
  element names: exprs
```

```
protocolData: none
```

```
phenoData
```

```
  sampleNames: 1 2 ... 6 (6 total)
```

```
  varLabels: designs
```

```
  varMetadata: labelDescription
```

```
featureData: none
```

```
experimentData: use 'experimentData(object)'
```

```
Annotation:
```

2. Estimate normalization factor.

```
> seqData=estNormFactors(seqData)
```

3. Estimate and shrink gene-wise dispersions

```
> seqData=estDispersion(seqData)
```

4. With the normalization factors and dispersions ready, the two-group comparison can be conducted via a Wald test:

```
> result=waldTest(seqData, 0, 1)
```

```
> head(result,5)
```

	geneIndex	muA	muB	lfc	difExpr	stats	pval	local.fdr
14	14	3.666667	66.98335	-2.784765	-63.31668	-5.765322	8.150222e-09	0.0002141899

```

94      94 5.666667 56.78839 -2.228940 -51.12173 -5.435560 5.462466e-08 0.0003256136
61      61 4.333333 45.50451 -2.253203 -41.17118 -5.341391 9.223627e-08 0.0003747546
59      59 7.333333 59.81217 -2.041146 -52.47884 -5.327595 9.952159e-08 0.0003830699
28      28 5.333333 50.17023 -2.161750 -44.83690 -5.297494 1.174027e-07 0.0004012137
      fdr
14 0.0002141899
94 0.0002803702
61 0.0003030798
59 0.0003030798
28 0.0003292965

```

A higher level wrapper function `DSS.DE` is provided for simple RNA-seq DE analysis in a two-group comparison. User only needs to provide a count matrix and a vector of 0's and 1's representing the design, and get DE test results in one line. A simple example is listed below:

```

> counts = matrix(rpois(600, 10), ncol=6)
> designs = c(0,0,0,1,1,1)
> result = DSS.DE(counts, designs)
> head(result)

```

	geneIndex	muA	muB	lfc	difExpr	stats	pval	local.fdr
76	76	6.666667	12.830246	-0.6205949	-6.163579	-2.043231	0.04102955	0.6435678
68	68	12.000000	6.593915	0.5664913	5.406085	1.849229	0.06442482	0.5477304
5	5	14.333333	8.260582	0.5266146	6.072752	1.833451	0.06673558	0.5477304
8	8	11.333333	6.581790	0.5133938	4.751544	1.666157	0.09568223	0.6749023
98	98	6.333333	10.866622	-0.5088685	-4.533288	-1.634250	0.10220633	0.9862480
1	1	9.333333	14.854496	-0.4456304	-5.521163	-1.599526	0.10970379	1.0000000

```

      fdr
76 0.6435678
68 0.7338878
5  0.7524176
8  0.7589466
98 0.7463392
1  0.7521756

```

## 2.2 Multifactor experiment

DSS provides functionalities for dispersion shrinkage for multifactor experimental designs. Downstream model fitting (through generalized linear model) and hypothesis testing can be performed using other packages such as `edgeR`, with the dispersions estimated from DSS.

Below is an example, based a simple simulation, to illustrate the DE analysis of a crossed design.

1. First simulate data for a 2x2 crossed experiments. Note the counts are randomly generated.

```

> library(DSS)
> library(edgeR)
> counts=matrix(rpois(800, 10), ncol=8)
> design=data.frame(gender=c(rep("M",4), rep("F",4)), strain=rep(c("WT", "Mutant"),4))
> X=model.matrix(~gender+strain, data=design)
2. make SeqCountSet, then estimate size factors and dispersion
> seqData=newSeqCountSet(counts, as.data.frame(X))
> seqData=estNormFactors(seqData)
> seqData=estDispersion(seqData)
3. Using edgeR's function to do glm model fitting, but plugging in the estimated size factors and dispersion from DSS.
> fit.edgeR <- glmFit(counts, X, lib.size=normalizationFactor(seqData),
+                     dispersion=dispersion(seqData))
4. Using edgeR's function to do hypothesis testing on the second parameter of the model (gender).
> lrt.edgeR <- glmLRT(glmfit=fit.edgeR, coef=2)
> head(lrt.edgeR$table)
      logFC  logCPM      LR  PValue
1  0.18515866 21.21148 0.271176429 0.6025437
2  0.16573687 21.10779 0.198338613 0.6560652
3  0.01149793 21.19907 0.001038751 0.9742889
4  0.01684743 20.93833 0.001834012 0.9658407
5 -0.04025179 21.30986 0.012919268 0.9095050
6  0.36915160 21.05711 0.941973404 0.3317708

```

### 3 Using DSS for differential methylation analysis

---

#### 3.1 Overview

To detect differential methylation, statistical tests are conducted at each CpG site, and then the differential methylation loci (DML) or differential methylation regions (DMR) are called based on user specified threshold. A rigorous statistical tests should account for biological variations among replicates and the coverage depth. Most existing methods for DM analysis are based on *ad hoc* methods. For example, using Fisher's exact ignores the biological variations, using t-test on estimated methylation levels ignores the coverage depth. Sometimes arbitrary filtering are recommended: loci with coverages lower than an arbitrary threshold are filtered out.

The DM detection procedure implemented in DSS is based on a rigorous Wald test for beta-binomial distributions. The test statistics depend on the biological variations (captured by dispersion parameter) as well as the coverage depth. An important part of the algorithm is the estimation of dispersion parameter, which is achieved through a shrinkage estimator based on a Bayesian hierarchical model [1].

A great advantage of DSS is that the test can be performed even when there is no biological replicates. That's because by smoothing procedure, the neighboring CpG sites can be viewed as "pseudo-replicates", and the dispersion can still be

estimated with reasonable precision.

This package depends on `bsseq` Bioconductor package, which has neat definition of data structures and many useful utility functions. In order to use the DM detection functionalities, `bsseq` needs to be pre-installed.

### 3.2 Input data

For one BS-seq experiments, after sequence alignment and some processing, the BS-seq data are usually summarized into following information for each CG position: chromosome number, genomic coordinate, total number of reads, and number of reads showing methylation. For a sample, this information are saved in a simple text file, with each row representing a CpG site. Below shows an example of a small part of such a file:

chr	pos	N	X
chr18	3014904	26	2
chr18	3031032	33	12
chr18	3031044	33	13
chr18	3031065	48	24
chr18	3031069	17	4
chr18	3031082	93	37
chr18	3031089	76	25
chr18	3031092	76	28

DML/DMR detection using DSS starts from several such text files. A typical DML detection contains two simple steps. First one conduct DM test at each CpG site, then DML/DMR are called based on the test result and user specified threshold. We will use example data distributed with DSS to illustrate the procedure.

### 3.3 DML/DMR detection from two-group comparison

Below are the steps to call DML or DMR for BS-seq data in two-group comparison setting.

1. Load in library. Read in text files and create an object of `BSseq` class, which is defined in `bsseq` Bioconductor package. This step requires `bsseq` Bioconductor package. `BSseq` class is defined in that package.

```
> library(DSS)
> require(bsseq)
> path <- file.path(system.file(package="DSS"), "extdata")
> dat1.1 <- read.table(file.path(path, "cond1_1.txt"), header=TRUE)
> dat1.2 <- read.table(file.path(path, "cond1_2.txt"), header=TRUE)
> dat2.1 <- read.table(file.path(path, "cond2_1.txt"), header=TRUE)
> dat2.2 <- read.table(file.path(path, "cond2_2.txt"), header=TRUE)
> BSobj <- makeBSseqData( list(dat1.1, dat1.2, dat2.1, dat2.2),
+   c("C1", "C2", "N1", "N2") )[1:10000,]
> BSobj
```

An object of type 'BSseq' with  
10000 methylation loci

4 samples

has not been smoothed

2. Perform statistical test for DML by calling `DMLtest` function. This function basically performs following steps: (1) estimate mean methylation levels for all CpG site; (2) estimate dispersions at each CpG sites; (3) conduct Wald test. For the first step, there's an option for smoothing or not. Because the methylation levels show strong spatial correlations, smoothing can help obtain better estimates of mean methylation when the CpG sites are dense in the data (such as from the whole-genome BS-seq). However for data with sparse CpG, such as from RRBS or hydroxyl-methylation, smoothing is not recommended.

To perform DML test without smoothing, do:

```
> dmlTest <- DMLtest(BSobj, group1=c("C1", "C2"), group2=c("N1", "N2"))
```

Estimating dispersion for each CpG site, this will take a while ...

```
> head(dmlTest)
```

	chr	pos	mu1	mu2	diff	diff.se	stat	phi1
1	chr18	3014904	0.3850276	0.4623677	-0.07734011	0.24899738	-0.3106061	0.286610813
2	chr18	3031032	0.3384423	0.1416667	0.19677555	0.11402507	1.7257217	0.009525212
3	chr18	3031044	0.3436302	0.3299846	0.01364560	0.12508174	0.1090935	0.010959806
4	chr18	3031065	0.4372540	0.3646882	0.07256585	0.10435917	0.6953471	0.010846613
5	chr18	3031069	0.2939132	0.5397749	-0.24586172	0.13554689	-1.8138499	0.012965376
6	chr18	3031082	0.3529066	0.3903499	-0.03744333	0.08197055	-0.4567900	0.008246131

	phi2	pval	fdr
1	0.01964971	0.75610007	0.9999077
2	0.05282909	0.08439748	0.7175525
3	0.02285714	0.91312835	0.9999077
4	0.01849672	0.48683778	0.9999077
5	0.02658296	0.06970083	0.6313442
6	0.01338446	0.64782202	0.9999077

To perform statistical test for DML with smoothing, do:

```
> dmlTest.sm <- DMLtest(BSobj, group1=c("C1", "C2"), group2=c("N1", "N2"), smoothing=TRUE)
```

Smoothing ...

Estimating dispersion for each CpG site, this will take a while ...

There are two options for smoothing: a simple moving average, or the `BSmooth` method implemented in `bsseq` package. The `BSmooth` method produces much smoother curve, which is good for visualization purpose. However, it is very computationally intensive, and the results are not very different from moving average in terms of DMR calling. So we recommend using moving average. Smoothing span is an important parameter in smoothing procedure and have non-trivial impact on DMR calling. We use 500 bp as default, and think that it performs well in real data tests.

3. With the test results, one can call DML by using `callDML` function. The results DMLs are sorted by the significance.

```
> dmls <- callDML(dmlTest, p.threshold=0.001)
```

```
> head(dmls)
```

	chr	pos	mu1	mu2	diff	diff.se	stat	phi1
450	chr18	3976129	0.01048590	0.93773387	-0.9272480	0.06785915	-13.664303	0.04319795
451	chr18	3976138	0.01048590	0.93773387	-0.9272480	0.06785915	-13.664303	0.04319795

```

582 chr18 4340682 0.96365233 0.03162952 0.9320228 0.09947722 9.369209 0.06181184
583 chr18 4340709 0.96365233 0.03162952 0.9320228 0.09947722 9.369209 0.06181184
638 chr18 4431501 0.01325735 0.94195478 -0.9286974 0.09390549 -9.889704 0.04380187
639 chr18 4431511 0.01321013 0.94195478 -0.9287446 0.09387324 -9.893604 0.04377619

```

```

      phi2 pval fdr postprob.overThreshold
450 0.02756948 0 0 1
451 0.02756948 0 0 1
582 0.05147878 0 0 1
583 0.05147878 0 0 1
638 0.08184949 0 0 1
639 0.08184949 0 0 1

```

By default, the test is based on the null hypothesis that the difference in methylation levels is 0. Alternatively, users can specify a threshold for difference. For example, to detect loci with difference greater than 0.1, do:

```

> dm1s2 <- callDML(dm1Test, delta=0.1, p.threshold=0.001)
> head(dm1s2)
      chr    pos      mu1      mu2      diff      diff.se      stat      phi1
450 chr18 3976129 0.01048590 0.93773387 -0.9272480 0.06785915 -13.664303 0.04319795
451 chr18 3976138 0.01048590 0.93773387 -0.9272480 0.06785915 -13.664303 0.04319795
582 chr18 4340682 0.96365233 0.03162952 0.9320228 0.09947722 9.369209 0.06181184
583 chr18 4340709 0.96365233 0.03162952 0.9320228 0.09947722 9.369209 0.06181184
638 chr18 4431501 0.01325735 0.94195478 -0.9286974 0.09390549 -9.889704 0.04380187
639 chr18 4431511 0.01321013 0.94195478 -0.9287446 0.09387324 -9.893604 0.04377619

```

```

      phi2 pval fdr postprob.overThreshold
450 0.02756948 0 0 1
451 0.02756948 0 0 1
582 0.05147878 0 0 1
583 0.05147878 0 0 1
638 0.08184949 0 0 1
639 0.08184949 0 0 1

```

When delta is specified, the function will compute the posterior probability that the difference of the means is greater than delta. So technically speaking, the threshold for p-value here actually refers to the threshold for 1-posterior probability, or the local FDR. Here we use the same parameter name for the sake of the consistence of function syntax.

- DMR detection is also Based on the DML test results, by calling `callDMR` function. Regions with many statistically significant CpG sites are identified as DMRs. Some restrictions are provided by users, including the minimum length, minimum number of CpG sites, percentage of CpG site being significant in the region, etc. There are some *post hoc* procedures to merge nearby DMRs into longer ones.

```

> dmrs <- callDMR(dm1Test, p.threshold=0.01)
> head(dmrs)
      chr    start      end length nCG meanMethy1 meanMethy2 diff.Methy areaStat
186 chr18 13131705 13131880    176 6 0.9689797 0.06107942 0.9079003 68.741081
33  chr18 4657576 4657639     64 4 0.5084704 0.31870495 0.1897655 14.421382

```



```
38 chr18 5027578 5027743 166 4 0.7045195 0.38058436 0.3239352 9.109377
```

Here the DMRs are sorted by "areaStat", which is defined in `bsseq` as the sum of the test statistics of all CpG sites within the DMR.

Similarly, users can specify a threshold for difference. For example, to detect regions with difference greater than 0.1, do:

```
> dmrs2 <- callDMR(dmlTest, delta=0.1, p.threshold=0.05)
> head(dmrs2)
      chr      start      end length nCG meanMethy1 meanMethy2 diff.Methy areaStat
229 chr18 13131705 13131880    176   6  0.9689797 0.06107942 0.90790031 68.74108
36  chr18 4657576 4657639     64   4  0.5084704 0.31870495 0.18976548 14.42138
373 chr18 23100427 23100601    175   4  0.5329967 0.43403678 0.09895989 12.76449
22  chr18 4222533 4222608     76   4  0.7882151 0.36126847 0.42694665 12.66181
41  chr18 5027549 5027743    195   5  0.6696348 0.32605410 0.34358066 11.42014
```

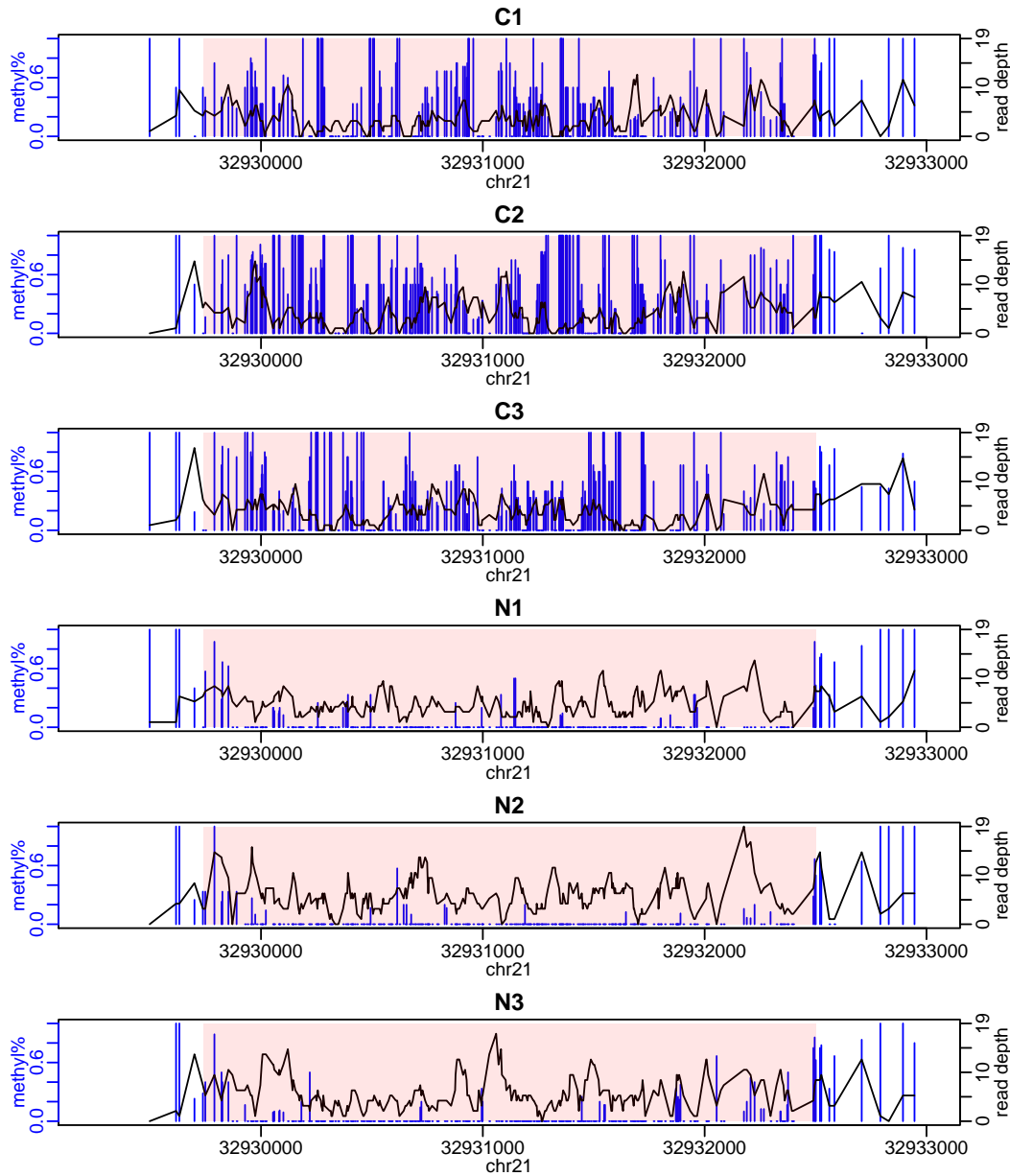
Note that the distribution of test statistics (and p-values) depends on the differences in methylation levels and biological variations, as well as technical factors such as coverage depth. It is very difficult to select a natural and rigorous threshold for defining DMRs. We recommend users try different thresholds in order to obtain satisfactory results.

5. The DMRs can be visualized using `showOneDMR` function. This function provides more information than the `plotRegion` function in `bsseq`. It plots the methylation percentages as well as the coverage depths at each CpG sites, instead of just the smoothed curve. So the coverage depth information will be available in the figure.

To use the function, do

```
> showOneDMR(dmrs[1,], BSobj)
```

The result figure looks like the following. Note that the figure below is not generated from the above example. The example data are from RRBS experiment so the DMRs are much shorter.



### 3.4 DML/DMR detection from general experimental design

In DSS, BS-seq data from a general experimental design (such as crossed experiment, or experiment with covariates) is modeled through a generalized linear model framework. We use arcsine link function instead of the typical logit link for it better deals with data at boundaries (methylation levels close to 0 or 1). Linear model fitting is done through ordinary least square on transformed methylation levels. Standard errors for the estimates are derived with consideration of count data distribution and transformation. A Wald test is applied to perform hypothesis testing.

1. Load in data distributed with DSS. This is a small portion of a set of RRBS experiments. There are 5000 CpG sites and 16 samples. The experiment is a 2 design (2 cases and 2 cell types). There are 4 replicates in each case:cell combination.

```
> data(RRBS)
> RRBS
An object of type 'BSseq' with
  5000 methylation loci
  16 samples
has not been smoothed
> design
```

```
  case cell
1    HC   rN
2    HC   rN
3    HC   rN
4   SLE  aN
5   SLE  rN
6   SLE  aN
7   SLE  rN
8   SLE  aN
9   SLE  rN
10  SLE  aN
11  SLE  rN
12  HC   aN
13  HC   aN
14  HC   aN
15  HC   aN
16  HC   rN
```

2. Fit a linear model using `DMLfit.multiFactor` function, include case, cell, and case:cell interaction.

```
> DMLfit = DMLfit.multiFactor(RRBS, design=design, formula=~case+cell+case:cell)
Fitting DML model for CpG site:
```

3. Use `DMLtest.multiFactor` function to test the cell effect. It is important to note that the `coef` parameter is the index of the coefficient to be tested for being 0. Because the model (as specified by formula in `DMLfit.multiFactor`) include intercept, the cell effect is the 3rd column in the design matrix, so we use `coef=3` here.

```
> DMLtest.cell = DMLtest.multiFactor(DMLfit, coef=3)
```

Result from this step is a data frame with chromosome number, CpG site position, test statistics, p-values (from normal distribution), and FDR. Rows are sorted by chromosome/position of the CpG sites. To obtain top ranked CpG sites, one can sort the data frame using following codes:

```
> ix=sort(DMLtest.cell[, "pvals"], index.return=TRUE)$ix
> head(DMLtest.cell[ix,])
```

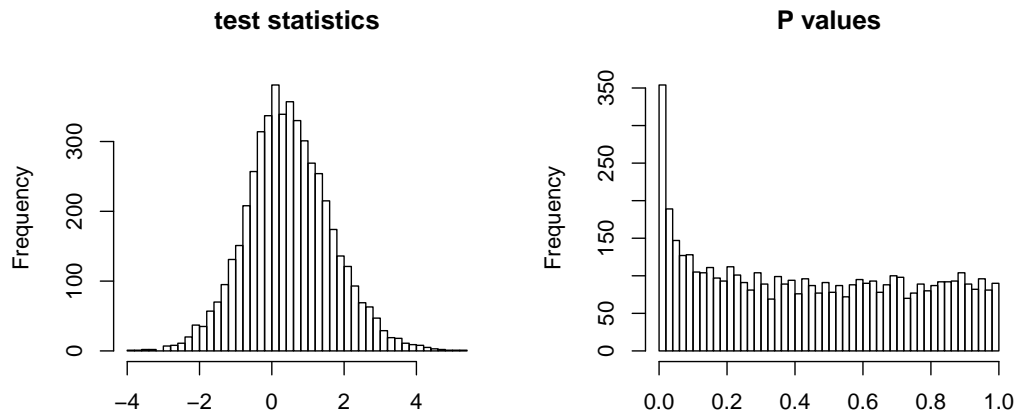
	chr	pos	stat	pvals	fdrs
1273	chr1	2930315	5.280301	1.289720e-07	0.0006448599
4706	chr1	3321251	5.037839	4.708164e-07	0.0011770409
3276	chr1	3143987	4.910412	9.088510e-07	0.0015147517
2547	chr1	3069876	4.754812	1.986316e-06	0.0024828953

```
3061 chr1 3121473 4.675736 2.929010e-06 0.0029290097
```

```
527 chr1 2817715 4.441198 8.945925e-06 0.0065858325
```

Below is a figure showing the distributions of test statistics and p-values from this example dataset

```
> par(mfrow=c(1,2))  
> hist(DMLtest.cell$stat, 50, main="test statistics", xlab="")  
> hist(DMLtest.cell$pvals, 50, main="P values", xlab="")
```



These procedures are computationally very efficient. For a typical RRBS dataset with 4 million CpG sites, it takes around 20 minutes. In comparison, other methods such as RADMeth or BiSeq takes at least 10 times longer.

## 4 Session Info

---

```
> sessionInfo()

R version 3.2.2 Patched (2015-08-16 r69094)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

locale:
[1] LC_COLLATE=C                      LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252 LC_NUMERIC=C
[5] LC_TIME=English_United States.1252

attached base packages:
[1] splines      stats4      parallel     stats        graphics    grDevices    utils        datasets
[9] methods     base

other attached packages:
[1] edgeR_3.12.0          limma_3.26.0          DSS_2.10.0
[4] bsseq_1.6.0           SummarizedExperiment_1.0.0 GenomicRanges_1.22.0
[7] GenomeInfoDb_1.6.0    IRanges_2.4.0         S4Vectors_0.8.0
[10] Biobase_2.30.0        BiocGenerics_0.16.0

loaded via a namespace (and not attached):
[1] Rcpp_0.12.1          XVector_0.10.0        zlibbioc_1.16.0       munsell_0.4.2
[5] colorspace_1.2-6     lattice_0.20-33        plyr_1.8.3            tools_3.2.2
[9] grid_3.2.2           data.table_1.9.6       R.oo_1.19.0           gtools_3.5.0
[13] matrixStats_0.14.2   R.utils_2.1.0          scales_0.3.0          R.methodsS3_1.7.0
[17] locfit_1.5-9.1       BiocStyle_1.8.0        chron_2.3-47
```

## References

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