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 procedure based on Bayesian hierarchical model to estimate and shrink gene- or CpG site-specific dispersions, then conduct Wald tests for detecting differential expression/methylation.

1 Introduction

Recent advances in various high-throughput sequencing technologies have revolutionized genomics research. Among them, RNA-seq is designed to measure the the abundance of RNA products, and Bisulfite sequencing (BS-seq) is for measuring DNA methylation. A fundamental question in functional genomics research is whether gene expression or DNA methylation vary under different biological contexts. Thus, identifying differential expression genes (DEGs) or differential methylation loci/regions (DML/DMRs) are key tasks in RNA-seq or BS-seq data analyses.

The differential expression (DE) or differential methylation (DM) analyses are often based on gene- or CpG-specific statistical test. A key limitation in RNA- or BS-seq experiments is that the number of biological replicates is usually limited 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 applied in DE analyses in microarray data to improve the estimation of gene-specific within group variances. These 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.

A distinct feature of RNA-seq or BS-seq data is that the measurements are in the form of counts and have to be modeld by discrete distributions. Unlike continuous distributions (such as Gaussian), the variances depend on means in these discrete distributions. This implies that the sample variances do not account for biological variation, and shrinkage cannot be applied on variances directly. In DSS, we assume that the count data are from the Gamma-Poisson (for RNA-seq) or Beta-Binomial (for BS-seq) distribution. We then parameterize the distributions by a mean and a dispersion parameters. The dispersion parameters, which represent the biological variation for replicates within a treatment group, play a central role in the differential analyses.

DSS implements a series of DE/DM detection algorithms based on the dispersion shrinkage method followed by Wald statistical test to test each gene/CpG site for differential expression/methylation. It provides functions for RNA-seq DE analysis for both two group comparision and multi-factor design, BS-seq DM analysis for two group comparision, multi-factor design, and data without biological replicate. Simulation and real data results show that the methods provides excellent performance compared to existing methods, especially when the overall dispersion level is high or the number of replicates is small.

For more details of the data model, the shrinkage method, and test procedures, please read [4] for differential expression from RNA-seq, [1] for differential methylation for two-group comparison from BS-seq, [2] for differential methylation for data without biological replicate, and [3] for differential methylation for general experimental design.

2 Using DSS for differential expression analysis

2.1 Input data preparation

DSS requires a count table (a matrix of **integers**) for gene expression values (rows are for genes and columns are for samples). This is different from the isoform expression based analysis such as in cufflink/cuffdiff, where the gene expressions are represented as non-integers values. There are a number of ways to obtain the count table from raw sequencing data (fastq file), here we provide some example codes using several Bioconductor packages (the codes require installation of `GenomicFeatures`, `Rsamtools`, and `GenomicRanges` packages).

1. Sequence alignment. There are several RNA-seq aligner, for example, `tophat` or `STAR`. Assume the alignment result is saved in a BAM file `data.bam`.
2. Choose a gene annotation. `GenomicFeatures` package provides a convenient way to access different gene annotations. For example, if one wants to use RefSeq annotation for human genome build hg19, one can use following codes:

```
> library(GenomicFeatures)
> txdb = makeTranscriptDbFromUCSC(genom="hg19",tablename="refGene")
> genes = genes(txdb)
```

3. Obtain count table based on the alignment results and gene annotation. This can be done in several steps. First read in the BAM file using the `Rsamtools` package:

```
> bam=scanBam("data.bam")
```

Next, create `GRanges` object for the aligned sequence reads.

```
> IRange.reads=GRanges(seqnames=Rle(bam$rname), ranges=IRanges(bam$pos, width=bam$qwidth))
```

Finally, use the `countOverlaps` function in `GenomicRanges` function to obtain the read counts overlap each gene.

```
> counts = countOverlaps(genes, IRange.reads)
```

There are other ways to obtain the counts, for example, using `QuasR` or `easyRNASeq` Bioconductor package. Please refer to the package vignettes for more details.

2.2 Single factor experiment

In single factor RNA-seq experiment, DSS also requires a vector representing experimental designs. The length of the design vector must match the number of columns of the count table. 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
61        61 4.000000 58.08963 -2.566480 -54.08963 -5.955113 2.598923e-09
89        89 6.000000 66.07358 -2.326506 -60.07358 -5.888428 3.898853e-09
99        99 9.000000 67.02983 -1.961278 -58.02983 -5.534586 3.119635e-08
78        78 7.000000 57.44535 -2.044597 -50.44535 -5.506439 3.661642e-08
44        44 7.666667 56.57150 -1.944244 -48.90484 -5.437989 5.388525e-08
      local.fdr          fdr
61 2.873373e-05 2.873373e-05
89 3.060904e-05 2.873373e-05
99 6.606128e-05 5.096362e-05
78 7.022337e-05 5.096362e-05
44 8.161496e-05 5.823975e-05
```

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
28        28  4.000000 12.03661 -1.0245761 -8.036614 -3.061671 0.002201053
54        54 12.333333  5.85164  0.7033329  6.481693  2.215855 0.026701410
88        88  9.333333  4.56776  0.6628790  4.765573  1.948688 0.051332696
98        98  6.333333 11.72801 -0.5819164 -5.394674 -1.922225 0.054577394
8          8 11.666667  6.49358  0.5537074  5.173086  1.835296 0.066461789
23        23  7.333333 12.75273 -0.5258157 -5.419400 -1.804982 0.071077505
     local.fdr         fdr
28 0.001475807 0.001475807
54 0.201510079 0.176498431
88 0.412878437 0.339160677
98 1.000000000 0.203016651
8  0.547609219 0.400764037
23 1.000000000 0.282197213
```

2.3 Multifactor experiment

DSS provides functionalities for dispersion shrinkage for multifactor experimental designs. Downstream model fitting (through genearlized 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 -0.2790497 21.17391 0.5305006 0.46639647
2 -0.2498857 21.01397 0.3989214 0.52764682
3  0.6806753 21.26523 3.2610244 0.07094479
4 -0.1323667 21.38564 0.1387687 0.70950816
5 -0.1386056 21.06558 0.1206494 0.72833128
6  0.2300513 21.17648 0.3763040 0.53958793
```

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 sequencing 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 sequencing depth. Sometimes arbitrary filtering are implemented: loci with depth lower than an arbitrary threshold are filtered out, which results in information loss

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 (characterized by dispersion parameter) as well as the sequencing 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]. An advantage of DSS is that the test can be performed even when there is no biological replicates. That's because by smoothing, the neighboring CpG sites can be viewed as "pseudo-replicates", and the dispersion can still be estimated with reasonable precision.

DSS also works for general experimental design, based on a beta-binomial regression model with "arcsine" link function. Model fitting is performed on transformed data with generalized least square method, which achieves much improved computational performance compared with methods based on generalized linear model.

DSS 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 preparation

DSS requires data from each BS-seq experiment to be 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
```

One can follow below steps to obtain such data from raw sequence file (fastq file), using `bismark` (version 0.10.0, commands for newer versions could be different) for BS-seq alignment and count extraction. These steps require installation of `bowtie` or `bowtie2`, `bismark`, and the fasta file for reference genome.

1. Prepare Bisulfite reference genome. This can be done using the `bismark_genome_preparation` function (details in bismark manual). Example command is:
   `bismark_genome_preparation -path_to_bowtie /usr/local/bowtie/ -verbose /path/to/refgenomes/`
2. BS-seq alignment. Example command is:
   `bismark -q -n 1 -l 50 -path_to_bowtie /path/bowtie/ BS-refGenome reads.fastq`
   This step will produce two text files `reads.fastq_bismark.sam` and `reads.fastq_bismark_SE_report.txt`.
3. Extract methylation counts using `bismark_methylation_extractor` function:
   `bismark_methylation_extractor -s -bedGraph reads.fastq_bismark.sam`. This will create multiple txt files to summarize methylation call and cytosine context, a bedGraph file to display methylation percentage, and a coverage file containing counts information. The count file contain following columns:`chr, start, end, methylation%, count methylated, count unmethylated`. This file can be modified to make the input file for DSS.

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.

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") )[1:1000,]
> BSobj

An object of type 'BSseq' with
  1000 methylation loci
  4 samples
has not been smoothed
All assays are in-memory
```

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
1 chr18 3014904 0.3817233 0.4624549 -0.08073162 0.24997034 -0.3229648
2 chr18 3031032 0.3380579 0.1417008  0.19635711 0.11086362  1.7711592
3 chr18 3031044 0.3432172 0.3298853  0.01333190 0.12203116  0.1092500
4 chr18 3031065 0.4369377 0.3649218  0.07201587 0.10099395  0.7130711
5 chr18 3031069 0.2933572 0.5387464 -0.24538920 0.13178800 -1.8619996
6 chr18 3031082 0.3526311 0.3905718 -0.03794068 0.07847999 -0.4834440
         phi1       phi2       pval       fdr
1 0.300542998 0.01706260 0.74672190 0.9985094
2 0.008911745 0.04783892 0.07653423 0.6792127
3 0.010409029 0.01994821 0.91300423 0.9985094
4 0.010320888 0.01603200 0.47580174 0.9985094
5 0.012537553 0.02320887 0.06260315 0.6158797
6 0.007665696 0.01145531 0.62878051 0.9985094
```

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 ...
```

User has the option to smooth the methylation levels or not. For WGBS data, smoothing is recommended so that information from nearby CpG sites can be combined to improve the estimation of methylation levels. A simple moving average algorithm is implemented for smoothing. In RRBS since the CpG coverage is sparse, smoothing might not alter the results much. If smoothing is requested, smoothing span is an important parameter which has 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
450 chr18 3976129 0.01027497 0.9390339 -0.9287590 0.06544340 -14.19179
451 chr18 3976138 0.01027497 0.9390339 -0.9287590 0.06544340 -14.19179
638 chr18 4431501 0.01331553 0.9430566 -0.9297411 0.09273779 -10.02548
```

```
639 chr18 4431511 0.01327049 0.9430566 -0.9297862 0.09270080 -10.02997
710 chr18 4564237 0.91454619 0.0119300  0.9026162 0.05260037  17.15988
782 chr18 4657576 0.98257334 0.0678355  0.9147378 0.06815000  13.42242
           phi1       phi2 pval fdr postprob.overThreshold
450 0.052591567 0.02428826    0   0                     1
451 0.052591567 0.02428826    0   0                     1
638 0.053172411 0.07746835    0   0                     1
639 0.053121697 0.07746835    0   0                     1
710 0.009528898 0.04942849    0   0                     1
782 0.010424723 0.06755651    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:

```
>   dmls2 <- callDML(dmlTest, delta=0.1, p.threshold=0.001)
>   head(dmls2)

      chr     pos        mu1       mu2       diff    diff.se      stat
450 chr18 3976129 0.01027497 0.9390339 -0.9287590 0.06544340 -14.19179
451 chr18 3976138 0.01027497 0.9390339 -0.9287590 0.06544340 -14.19179
638 chr18 4431501 0.01331553 0.9430566 -0.9297411 0.09273779 -10.02548
639 chr18 4431511 0.01327049 0.9430566 -0.9297862 0.09270080 -10.02997
710 chr18 4564237 0.91454619 0.0119300  0.9026162 0.05260037  17.15988
782 chr18 4657576 0.98257334 0.0678355  0.9147378 0.06815000  13.42242
           phi1       phi2 pval fdr postprob.overThreshold
450 0.052591567 0.02428826    0   0                     1
451 0.052591567 0.02428826    0   0                     1
638 0.053172411 0.07746835    0   0                     1
639 0.053121697 0.07746835    0   0                     1
710 0.009528898 0.04942849    0   0                     1
782 0.010424723 0.06755651    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.

4. 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(dmlTest, p.threshold=0.01)
> head(dmrs)

     chr   start     end length nCG meanMethy1 meanMethy2 diff.Methy areaStat
27 chr18 4657576 4657639     64   4   0.506453   0.318348   0.188105 14.34236
```

   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
31 chr18 4657576 4657639     64   4  0.5064530  0.3183480   0.188105 14.34236
19 chr18 4222533 4222608     76   4  0.7880276  0.3614195   0.426608 12.91667
```

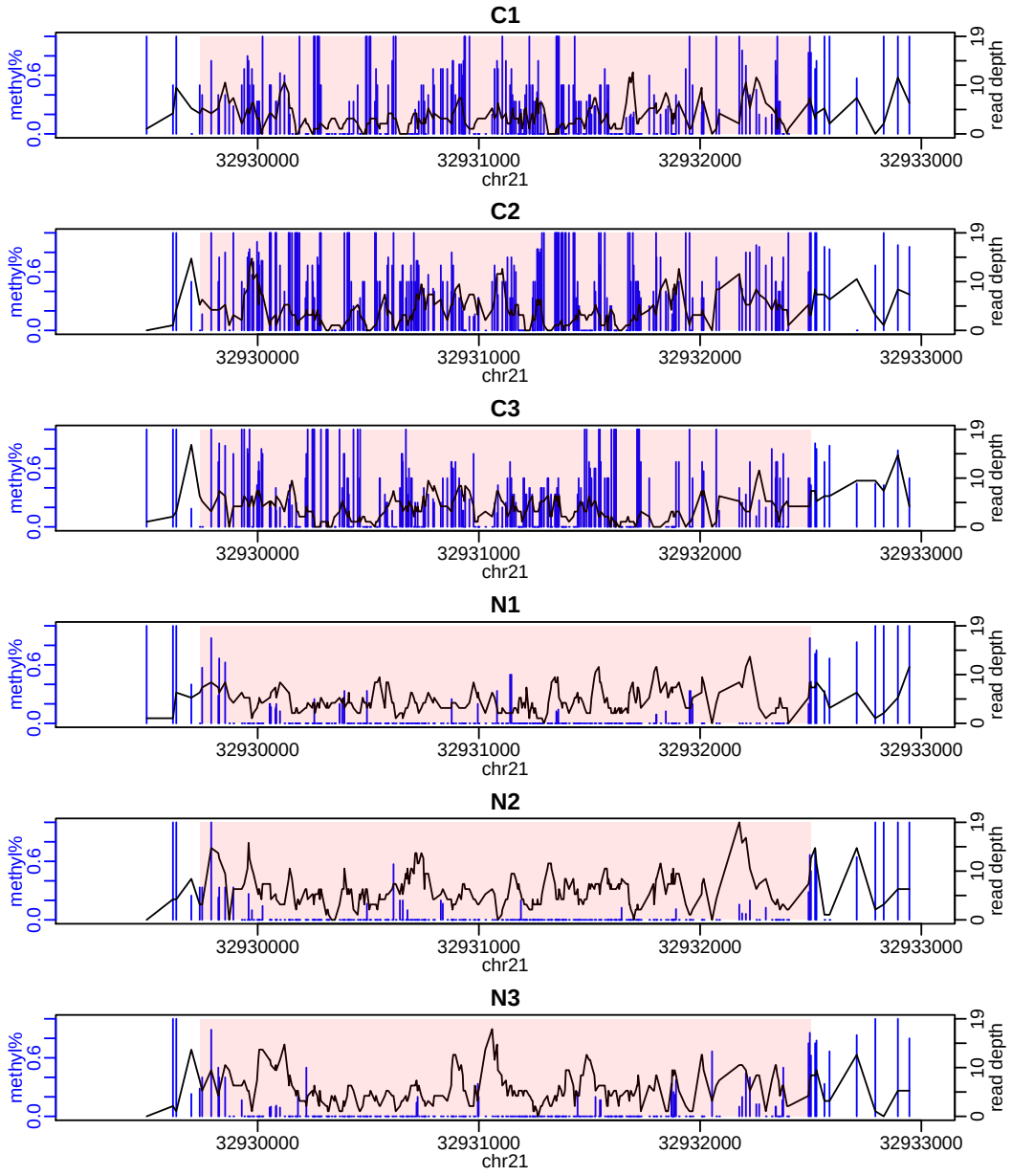
   Note that the distribution of test statistics (and p-values) depends on the differences in methylation levels and biological variations, as well as technical factors such as coverage depth. It is very difficulty to select a natural and rigorous threshold for defining DMRs. We recommend users try different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


C1
C2
C3
N1
N2
N3
methyl%
0.0
0.6
read depth
0
10
19
32930000
32931000
32932000
32933000
chr21

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. Variance/covariance matrices for the estimates are derived with consideration of count data distribution and transformation.

3.4.1 Hypothesis testing in general experimental design

In a general design, the data are modeled through a multiple regression thus there are multiple regression coefficients. In contrast, there is only one parameter in two-group comparison which is the difference between two groups. Under this type of design, hypothesis testing can be performed for one, multiple, or any linear combination of the parameters.

DSS provides flexible functionalities for hypothesis testing. User can test one parameter in the model through a Wald test, or any linear combination of the parameters through an F-test.

The `DMLtest.multiFactor` function provide interfaces for testing one parameter (through `coef` parameter), one term in the model (through `term` parameter), or linear combinations of the parameters (through `Contrast` parameter). We illustrate the usage of these parameters through a simple example below. Assume we have an experiment from three strains (A, B, C) and two sexes (M and F), each has 2 biological replicates (so there are 12 datasets in total).

```
> Strain = rep(c("A", "B", "C"), 4)
> Sex = rep(c("M", "F"), each=6)
> design = data.frame(Strain,Sex)
> design

   Strain Sex
1       A   M
2       B   M
3       C   M
4       A   M
5       B   M
6       C   M
7       A   F
8       B   F
```

```
9       C   F
10      A   F
11      B   F
12      C   F
```

To test the additive effect of Strain and Sex, a design formula is `Strain+Sex`, and the corresponding design matrix for the linear model is:

```
> X = model.matrix(~Strain+ Sex, design)
> X
   (Intercept) StrainB StrainC SexM
1            1       0       0    1
2            1       1       0    1
3            1       0       1    1
4            1       0       0    1
5            1       1       0    1
6            1       0       1    1
7            1       0       0    0
8            1       1       0    0
9            1       0       1    0
10           1       0       0    0
11           1       1       0    0
12           1       0       1    0
attr(,"assign")
[1] 0 1 1 2
attr(,"contrasts")
attr(,"contrasts")$Strain
[1] "contr.treatment"

attr(,"contrasts")$Sex
[1] "contr.treatment"
```

Under this design, we can do different tests using the `DMLtest.multiFactor` function:

- If we want to test the sex effect, we can either specify `coef=4`, `coef="SexM"`, or `term="Sex"`. Notice that when using character for coef, the character must match the column name of the design matrix, cannot do `coef="Sex"`. It is also important to note that using `term="Sex"` only tests a single paramter in the model because sex only has two levels.

- If we want to test the effect of Strain B versus Strain A (this is also testing a single parameter), we do `coef=2` or `coef="StrainB"`.
- If we want to test the whole Strain effect, it becomes a compound test because Strain has three levels. We do `term="Strain"`, which tests `StrainB` and `StrainC` simultaneously. We can also make a Contrast matrix L as following. It's clear that testing $L^T\beta = 0$ is equivalent to testing StrainB=0 and StrainC=0.

```
> L = cbind(c(0,1,0,0),c(0,0,1,0))
> L

     [,1] [,2]
[1,]    0    0
[2,]    1    0
[3,]    0    1
[4,]    0    0
```

- One can perform more general test, for example, to test StrainB=StrainC, or that strains B and C has no difference (but they could be different from Strain A). In this case, we need to make following contrast matrix:

```
> matrix(c(0,1,-1,0), ncol=1)

     [,1]
[1,]    0
[2,]    1
[3,]   -1
[4,]    0
```

3.4.2 Example analysis for data from general experimental design

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
All assays are in-memory
```

```
> 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)
```

Alternatively, one can specify the name of the parameter to be tested. In this case, the input `coef` is a character, and it must match one of the column names in the design matrix. The column names of the design matrix can be viewed by

```
> colnames(DMLfit$X)
[1] "(Intercept)"    "caseSLE"        "cellrN"         "caseSLE:cellrN"
```

The following line also works. Specifying `coef="cellrN"` is the same as specifying `coef=3`.

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

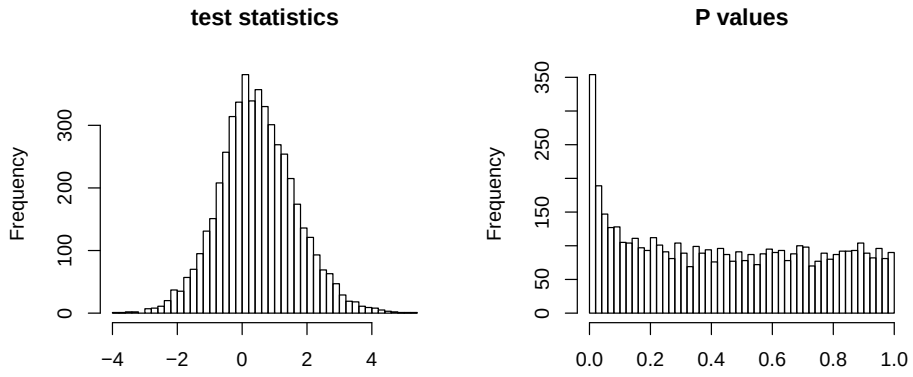
Result from this step is a data frame with chromosome number, CpG site position, test statistics, p-values (from normal distribution), and FDR. Rows are sorted by chromosome/position of the CpG sites. To obtain top ranked CpG sites, one can sort the data frame using following codes:

```
> 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="")
```



4. DMRs for multifactor design can be called using `callDMR` function:

```
> callDMR(DMLtest.cell, p.threshold=0.05)

     chr   start     end length nCG   areaStat
33  chr1 2793724 2793907    184   5  12.619968
413 chr1 3309867 3310133    267   7 -12.093850
250 chr1 3094266 3094486    221   4  11.691413
262 chr1 3110129 3110394    266   5  11.682579
180 chr1 2999977 3000206    230   4  11.508302
121 chr1 2919111 2919273    163   4   9.421873
298 chr1 3146978 3147236    259   5   8.003469
248 chr1 3090627 3091585    959   5  -7.963547
346 chr1 3200758 3201006    249   4  -4.451691
213 chr1 3042371 3042459     89   5   4.115296
169 chr1 2995532 2996558   1027   4  -2.988665
```

Note that for results from for multifactor design, `delta` is NOT supported. This is because in multifactor design, the estimated coefficients in the regression are based on a GLM framework (loosely speaking), thus they don't have clear meaning of methylation level differences. So when the input DMLresult is from `DMLtest.multiFactor`, `delta` cannot be specified.

5. More flexible way to specify a hypothesis test. Following 4 tests should produce the same results, since 'case' only has two levels. However the p-values from F-tests (using term or Contrast) are slightly different, due to normal approximation in Wald test.

```
> ## fit a model with additive effect only
> DMLfit = DMLfit.multiFactor(RRBS, design, ~case+cell)

Fitting DML model for CpG site:

> ## test case effect
> test1 = DMLtest.multiFactor(DMLfit, coef=2)
> test2 = DMLtest.multiFactor(DMLfit, coef="caseSLE")
> test3 = DMLtest.multiFactor(DMLfit, term="case")
> Contrast = matrix(c(0,1,0), ncol=1)
> test4 = DMLtest.multiFactor(DMLfit, Contrast=Contrast)
> cor(cbind(test1$pval, test2$pval, test3$pval, test4$pval))

     [,1] [,2] [,3] [,4]
[1,]    1    1    1    1
[2,]    1    1    1    1
[3,]    1    1    1    1
[4,]    1    1    1    1
```

The model fitting and hypothesis test procedures are computationally very efficient. For a typical RRBS dataset with 4 million CpG sites, it usually takes less than half hour. In comparison, other similar software such as RADMeth or BiSeq takes at least 10 times longer.

4 Session Info

```
> sessionInfo()

R version 3.4.2 (2017-09-28)
Platform: x86_64-apple-darwin15.6.0 (64-bit)
Running under: OS X El Capitan 10.11.6

Matrix products: default
BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib

locale:
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

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

other attached packages:
 [1] edgeR_3.20.0               limma_3.34.0
 [3] DSS_2.26.0                 bsseq_1.14.0
 [5] SummarizedExperiment_1.8.0 DelayedArray_0.4.0
 [7] matrixStats_0.52.2         GenomicRanges_1.30.0
 [9] GenomeInfoDb_1.14.0        IRanges_2.12.0
[11] S4Vectors_0.16.0           Biobase_2.38.0
[13] BiocGenerics_0.24.0

loaded via a namespace (and not attached):
 [1] Rcpp_0.12.13            compiler_3.4.2          plyr_1.8.4
 [4] XVector_0.18.0          R.methodsS3_1.7.1       bitops_1.0-6
 [7] R.utils_2.5.0           tools_3.4.2             zlibbioc_1.24.0
[10] digest_0.6.12           evaluate_0.10.1         lattice_0.20-35
[13] Matrix_1.2-11           yaml_2.1.14             GenomeInfoDbData_0.99.1
[16] stringr_1.2.0           knitr_1.17              gtools_3.5.0
[19] locfit_1.5-9.1          rprojroot_1.2           grid_3.4.2
[22] data.table_1.10.4-3     rmarkdown_1.6           magrittr_1.5
[25] backports_1.1.1         scales_0.5.0            htmltools_0.3.6
[28] permute_0.9-4           BiocStyle_2.6.0         colorspace_1.3-2
```

```
[31] stringi_1.1.5          RCurl_1.95-4.8         munsell_0.4.3
[34] R.oo_1.21.0
```

References

[1] Hao Feng, Karen Conneely and Hao Wu. (2014). A bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data. *Nucleic Acids Research.* **42**(8), e69–e69.

[2] Hao Wu, Tianlei Xu, Hao Feng, Li Chen, Ben Li, Bing Yao, Zhaohui Qin, Peng Jin and Karen N. Conneely. (2015). Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. *Nucleic Acids Research.* doi: 10.1093/nar/gkv715.

[3] Yongseok Park, Hao Wu. (2016). Differential methylation analysis for BS-seq data under general experimental design. *Bioinformatics.* doi:10.1093/bioinformatics/btw026.

[4] Hao Wu, Chi Wang and Zhijing Wu. (2013). A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. *Biostatistics.* **14**(2), 232–243.