

The NanoStringDiff package

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Abstract

This vignette introduces the use of the Bioconductor package NanoStringDiff, which is designed for differential analysis based on NanoString nCounter Data. NanoStringDiff considers a generalized linear model of the negative binomial family to characterize count data and allows for multi-factor design. Data normalization is incorporated in the model framework by including data normalization parameters estimated from positive controls, negative controls and housekeeping genes embedded in the nCounter system. Present method propose an empirical Bayes shrinkage approach to estimate the dispersion parameter and a likelihood ratio test to identify differential expression genes.

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1 Citation

The package NanoStringDiff implements statistical methods from the following publication. If you use NanoStringDiff in the published research, please cite:

Hong Wang, Craig Horbinski, Hao Wu, Yinxing Liu, Arnold J. Stromberg and Chi Wang: A Negative Binomial Model-Based Method for Differential Expression Analysis Based on NanoString nCounter Data. (Manuscript)

2 Quick Start

This section show the most basic steps for a differential expression analysis for NanoString nCounter Data:

1. Create a NanoStringSet object using `createNanoStringSet` or `createNanoStringSetFromCsv` (see examples in the Data Input section). In this section we use `NanoStringData` directly, which is an object of `NanoStringSet` contained in the package.
2. Make a design matrix to describe treatment conditions.
3. Estimate normalization factors including positive size factors, housekeeping size factors and background noise using `estNormalizationFactors`
4. Perform a likelihood ratio test using `glm.LRT`.

```
> library("Biobase")
> library("NanoStringDiff")
> data(NanoStringData)
> pheno=pData(NanoStringData)
> design.full=model.matrix(~0+pheno$group)
> NanoStringData=estNormalizationFactors(NanoStringData)
> result=glm.LRT(NanoStringData,design.full,contrast=c(1,-1))
```

Here, the data `NanoStringData` contained in the package is an animal data, we called `MoriData`[\[1\]](#). Mori et al tried to study the possible reasons responsible for the widespread miRNA repression observed in cancer, global microRNA expression in mouse liver normal tissues and liver tumors induced by deletion of Nf2 (merlin) profiled by nCounter Mouse miRNA Expression Assays. Expressions of 599 miRNAs were profiled for two replicates in each group.

3 Data Input

NanoStringDiff works on matrix of integer read counts from NanoString nCounter analyzer with endogenous genes, positive control genes, negative control genes and housekeeping control genes. For the matrix, rows corresponding to genes and columns to independent samples or replicates. The counts represent the total number of reads aligning to each gene (or other genomic locus).

The count values must be raw counts of NanoString nCounter data, since data normalization is incorporated in the model framework by including data normalization parameters estimated from positive controls, negative controls and housekeeping genes using function `estNormalizationFactors`. Hence, please do not supply normalized counts.

There must be six positive control genes order by different concentrations from high to low, since NanoString nCounter analyzer provide six different small positive controls with six different concentrations in the 30 uL hybridization: 128 fM, 32 fM, 8 fM, 2 fM, 0.5 fM, and 0.125 fM. No such restriction for negative control genes and housekeeping control genes. Nanostring recommends at least three housekeeping genes, but the more that are included, the more accurate the normalization will be.

3.1 Create NanoStringSet from csv.file

The data produced by the nCounter Digital Analyzer are exported as a Reporter Code Count (RCC) file. RCC files are comma-separated text(.csv) files that contain the counts for each gene in a sample and the data for each sample hybridization are contained in a separate RCC file. So before you call `createNanoStringSetFromCsv` to create a `NanoStringSet` object, you should create a csv.file to combine all interesting samples together, and the first three columns should be "CodeClass", "Name" and "Accession", the counts data contained from the 4th column to the last column.

Note:

1. The 1st column "CodeClass" should specify the function of genes as "Positive", "Negative", "Housekeeping" or "Endogenous".
2. Some data set have "Spikein" genes, you need delete these "spikein" genes or you could just leave there if you use `createNanoStringSetFromCsv` to create `NanoStringSet` object (See example in the Data Input section). But NanoStringDiff only works with "positive", "negative", housekeeping" and "endogenous".

The "csv.file" should look like as following Figure:

Code Class	Name	Accession	Normal 1	Normal 2	Tumor 1	Tumor 2
Positive	POS_A(128)	nmiR00813.1	4869	4416	10069	8018
Positive	POS_B(32)	nmiR00809.1	1427	1171	2809	2289
Positive	POS_C(8)	nmiR00811.1	277	213	400	318
Positive	POS_D(2)	nmiR00822.1	111	91	262	191
Positive	POS_E(0.5)	nmiR00801.1	33	25	56	33
Positive	POS_F(0.125)	nmiR00825.1	9	8	24	10
Negative	NEG_B(0)	nmiR00828.1	3	8	6	9
Negative	NEG_C(0)	nmiR00803.1	11	5	3	12
Negative	NEG_A(0)	nmiR00810.1	7	10	5	8
Negative	NEG_F(0)	nmiR00805.1	5	7	9	2
Negative	NEG_E(0)	nmiR00827.1	16	7	5	5
Negative	NEG_D(0)	nmiR00823.1	11	9	17	10
Housekeeping	B2m 0	NM_009735.3	874	698	3591	2377
Housekeeping	Rpl19 0	NM_009078.1	175	180	1099	1103
Housekeeping	Actb 0	NM_007393.1	356	332	1608	1651
Housekeeping	Gapdh 0	NM_008084.1	147	126	348	212
Endogenous1	mmu-miR-18a 0	MIMAT0000528	2	4	5	7
Endogenous1	mmu-miR-880 0	MIMAT0004844	3	6	15	10
Endogenous1	mmu-miR-686 0	MIMAT0003464	3	7	8	4
Endogenous1	mmu-miR-466f-5p 0	MIMAT0004881	8	5	4	5
Endogenous1	mmu-miR-106b 0	MIMAT0000386	30	26	310	106
Endogenous1	mmu-miR-1969 0	MIMAT0009442	3	4	5	1
Endogenous1	mmu-miR-193 0	MIMAT0000223	39	33	81	58

Figure 1: Example of csv.file pattern

When you created a csv.file, you will specify a variable which points on the directory in which your csv.file is located

```
> directory <- "/path/to/your/files/"
```

However, for demonstration purposes only, the following line of code points to the directory for the "Mori.csv" in the NanoStringDiff package.

```
> directory <- system.file("extdata", package="NanoStringDiff", mustWork=TRUE)
> path<-paste(directory,"Mori.csv",sep="/")
```

The phenotype informations of the data should be stored as data frame.

```
> designs=data.frame(group=c("Normal","Normal","Tumor","Tumor"))
> designs

  group
1 Normal
2 Normal
```

```

3 Tumor
4 Tumor

> library("NanoStringDiff")
> NanoStringData=createNanoStringSetFromCsv(path,header=TRUE,designs)

There are 4 samples imported;
There are 618 genes imported with:code.class
endogenous1 endogenous2 housekeeping negative positive spikein
          566          33           4           6           6           3

> NanoStringData

NanoStringSet (storageMode: lockedEnvironment)
assayData: 599 features, 4 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: Normal.1 Normal.2 Tumor.1 Tumor.2
  varLabels: group
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:

```

3.2 Create NanoStringSet from matrix

If you already read your positive control genes, negative control genes, housekeeping control genes and endogenous into R session separately and stored as matrix, then you can use `createNanoStringSet` to create a `NanoStringSet` object.

```

> endogenous=matrix(rpois(100,50),25,4)
> colnames(endogenous)=paste("Sample",1:4)
> positive=matrix(rpois(24,c(128,32,8,2,0.5,0.125)*80),6,4)
> colnames(positive)=paste("Sample",1:4)
> negative=matrix(rpois(32,10),8,4)
> colnames(negative)=paste("Sample",1:4)

```

```

> housekeeping=matrix(rpois(12,100),3,4)
> colnames(housekeeping)=paste("Sample",1:4)
> designs=data.frame(group=c("Control","Control","Treatment","Treatment"),
+                       gender=c("Male","Female","Female","Male"),
+                       age=c(20,40,39,37))
> NanoStringData1=createNanoStringSet(endogenous,positive,
+                                     negative,housekeeping,designs)
> NanoStringData1

```

```
NanoStringSet (storageMode: lockedEnvironment)
```

```
assayData: 25 features, 4 samples
```

```
element names: exprs
```

```
protocolData: none
```

```
phenoData
```

```
sampleNames: Sample 1 Sample 2 Sample 3 Sample 4
```

```
varLabels: group gender age
```

```
varMetadata: labelDescription
```

```
featureData: none
```

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

```
Annotation:
```

```
> pData(NanoStringData1)
```

	group	gender	age
Sample 1	Control	Male	20
Sample 2	Control	Female	40
Sample 3	Treatment	Female	39
Sample 4	Treatment	Male	37

```
> head(exprs(NanoStringData1))
```

	Sample 1	Sample 2	Sample 3	Sample 4
1	49	48	38	54
2	47	49	52	53
3	55	50	51	49
4	48	46	43	42
5	57	35	45	45
6	57	48	42	62

4 Differential Expression Analysis for Single Factor Experiment

For general experiments, once normalization factors obtained using `estNormalizationFactors`, given a design matrix and contrast, we can proceed with testing procedures for determining differential expression using the generalized linear model (GLM) likelihood ratio test. The testing can be done by using the function `glm.LRT` and return a list with a component is table including: `logFC`, `lr`, `pvalue` and `qvalue`(adjust p value using the procedure of Benjamini and Hochberg).

4.1 Two Group Comparisons

The simplest and most common type of experimental design is two group comparison, like treatment group vs control group. As a brief example, consider a simple situation with control group and treatment group, each with two replicates, and the researcher wants to make comparisons between them. Here, we still use `NanoStringData1` we created above to demonstrate this example.

Make design matrix using `model.matrix`:

```
> pheno=pData(NanoStringData1)
> group=pheno$group
> design.full=model.matrix(~0+group)
> design.full
```

```
  groupControl groupTreatment
1           1           0
2           1           0
3           0           1
4           0           1
attr(,"assign")
[1] 1 1
attr(,"contrasts")
attr(,"contrasts")$group
[1] "contr.treatment"
```

Note that there is no intercept column in the design matrix, each column is for each group, since we include `0+` in the model formula.

If the researcher want compare Treatment to Control, that is Treatment- Control, the contrast vector

is try to the comparison $-1 \times \text{Control} + 1 \times \text{Treatment}$, so the contrast is :

```
> contrast=c(-1,1)
```

Estimate normalization factors and return the same object with positiveFactor, negativeFactor and housekeepingFactor slots filled or replaced:

```
> NanoStringData1=estNormalizationFactors(NanoStringData1)
```

```
> positiveFactor(NanoStringData1)
```

```
Sample 1 Sample 2 Sample 3 Sample 4
0.9852634 1.0023264 1.0087207 1.0036896
```

```
> negativeFactor(NanoStringData1)
```

```
Sample 1 Sample 2 Sample 3 Sample 4
      11       8      10       8
```

```
> housekeepingFactor(NanoStringData1)
```

```
Sample 1 Sample 2 Sample 3 Sample 4
1.0262631 0.9156049 1.1027808 0.9850353
```

Generalize linear model likelihood ratio test:

```
> result=glm.LRT(NanoStringData1,design.full,contrast=contrast)
```

```
> head(result$table)
```

	logFC	lr	pvalue	qvalue
1	-0.19109289	0.45145468	0.5016450	0.8264606
2	0.05105675	0.03453376	0.8525760	0.8881000
3	-0.19140497	0.49784774	0.4804473	0.8264606
4	-0.28673939	0.94397022	0.3312589	0.7014756
5	-0.13425242	0.21092560	0.6460429	0.8264606
6	-0.11075106	0.17052068	0.6796495	0.8264606

```
> str(result)
```

List of 11

```
$ table      : 'data.frame':      25 obs. of  4 variables:
..$ logFC : num [1:25] -0.1911 0.0511 -0.1914 -0.2867 -0.1343 ...
..$ lr     : num [1:25] 0.4515 0.0345 0.4978 0.944 0.2109 ...
```

```

..$ pvalue: num [1:25] 0.502 0.853 0.48 0.331 0.646 ...
..$ qvalue: num [1:25] 0.826 0.888 0.826 0.701 0.826 ...
$ dispersion      : num [1:25] 0.00627 0.00625 0.00625 0.00625 0.00626 ...
$ log.dispersion: num [1:25] -5.07 -5.08 -5.08 -5.08 -5.07 ...
$ design.full     : num [1:4, 1:2] 1 1 0 0 0 0 1 1
..- attr(*, "dimnames")=List of 2
.. ..$ : chr [1:4] "1" "2" "3" "4"
.. ..$ : chr [1:2] "groupControl" "groupTreatment"
..- attr(*, "assign")= int [1:2] 1 1
..- attr(*, "contrasts")=List of 1
.. ..$ group: chr "contr.treatment"
$ design.reduce : num [1:4, 1] 0.707 0.707 0.707 0.707
..- attr(*, "dimnames")=List of 2
.. ..$ : chr [1:4] "1" "2" "3" "4"
.. ..$ : NULL
$ Beta.full      : num [1:25, 1:2] 3.7 3.69 3.8 3.66 3.63 ...
$ mean.full      : num [1:25, 1:4] 40.5 40 44.6 38.9 37.6 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : NULL
.. ..$ : chr [1:4] "1" "2" "3" "4"
$ Beta.reduce    : num [1:25] 3.63 3.71 3.73 3.56 3.58 ...
$ mean.reduce    : num [1:25, 1:4] 37.9 40.8 41.7 35.2 35.9 ...
$ m0             : num -5.07
$ sigma          : num 0.1

```

Note that the text Treatment compare to Control tells you that the estimates of logFC is $\log_2(\text{Treatment}/\text{Control})$.

4.2 Pairwise Comparisons

Now consider a researcher has three treatment groups say A, B and C, and researcher wants to compare each groups like: B compare to A, C compare to A, and B compare to C.

First create an object of NanoStringSet with pseudo data:

```

> endogenous=matrix(rpois(300,50),25,12)
> colnames(endogenous)=paste("Sample", 1:12)

```

```

> colnames(endogenous)=paste("Sample",1:12)
> positive=matrix(rpois(72,c(128,32,8,2,0.5,0.125)*80),6,12)
> negative=matrix(rpois(96,10),8,12)
> housekeeping=matrix(rpois(36,100),3,12)
> designs=data.frame(group=c(rep("A",4),rep("B",4),rep("C",4)),
+                       gender=rep(c("Male","Male","Female","Female"),3),
+                       age=c(20,40,39,37,29,47,23,45,34,65,35,64))
> NanoStringData2=createNanoStringSet(endogenous,positive,
+                                     negative,housekeeping,designs)
> NanoStringData2

```

```
NanoStringSet (storageMode: lockedEnvironment)
```

```
assayData: 25 features, 12 samples
```

```
element names: exprs
```

```
protocolData: none
```

```
phenoData
```

```
sampleNames: Sample 1 Sample 2 ... Sample 12 (12 total)
```

```
varLabels: group gender age
```

```
varMetadata: labelDescription
```

```
featureData: none
```

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

```
Annotation:
```

```
> pData(NanoStringData2)
```

	group	gender	age
Sample 1	A	Male	20
Sample 2	A	Male	40
Sample 3	A	Female	39
Sample 4	A	Female	37
Sample 5	B	Male	29
Sample 6	B	Male	47
Sample 7	B	Female	23
Sample 8	B	Female	45
Sample 9	C	Male	34
Sample 10	C	Male	65

Sample 11 C Female 35
 Sample 12 C Female 64

Make design matrix only consider one experimental factor group:

```
> pheno=pData(NanoStringData2)
> group=pheno$group
> design.full=model.matrix(~0+group)
> design.full
```

	groupA	groupB	groupC
1	1	0	0
2	1	0	0
3	1	0	0
4	1	0	0
5	0	1	0
6	0	1	0
7	0	1	0
8	0	1	0
9	0	0	1
10	0	0	1
11	0	0	1
12	0	0	1

```
attr("assign")
```

```
[1] 1 1 1
```

```
attr("contrasts")
```

```
attr("contrasts")$group
```

```
[1] "contr.treatment"
```

Estimate normalization factors:

```
> NanoStringData2=estNormalizationFactors(NanoStringData2)
```

B compare to A, the contrast should be (-1,1,0)

```
> result=glm.LRT(NanoStringData2,design.full,contrast=c(-1,1,0))
```

C compare to A, the contrast should be (-1,0,1)

```
> result=glm.LRT(NanoStringData2,design.full,contrast=c(-1,0,1))
```

B compare to c, the contrast should be (0,1,-1)

```
> result=glm.LRT(NanoStringData2,design.full,contrast=c(0,1,-1))
```

The other way to create a design matrix in R is to include an intercept term to represent the base level of the factor. We just omit the 0+ in the model formula when we create design matrix using model.matrix function:

```
> design.full=model.matrix(~group)
```

```
> design.full
```

	(Intercept)	groupB	groupC
1	1	0	0
2	1	0	0
3	1	0	0
4	1	0	0
5	1	1	0
6	1	1	0
7	1	1	0
8	1	1	0
9	1	0	1
10	1	0	1
11	1	0	1
12	1	0	1

```
attr(,"assign")
```

```
[1] 0 1 1
```

```
attr(,"contrasts")
```

```
attr(,"contrasts")$group
```

```
[1] "contr.treatment"
```

In this situation, the first coefficient measures the log scalar of baseline mean expression level in group A, and the second and third columns are now relative to the baseline, not representing the mean expression level in group B and C. So, if we want to compare B to A, now that is equivalent to testing the 2nd coefficient equal to 0.

```
> result=glm.LRT(NanoStringData2,design.full,Beta=2)
```

Beta=3 means compare C to A:

```
> result=glm.LRT(NanoStringData2,design.full,Beta=3)
```

4.3 Multigroup Comparisons

NanoStringDiff can do multigroup comparisons, for example if we want compare group A to the average of group B and C,

```
> design.full=model.matrix(~0+group)
> result=glm.LRT(NanoStringData2,design.full,contrast=c(1,-1/2,-1/2))
```

5 Differential Expression Analysis for Multifactor Experiment

In this section, we still use NanoStringData2 in examples, but the above examples all cotnsider single factor treatment condition , now we include the other experiment factor gender to consider multifactor problems.

5.1 Nested Interactions

First, we form the design matrix use factors group and interaction between group and gender:

```
> design=pData(NanoStringData2)[,c("group","gender")]
> group=design$group
> gender=design$gender
> design.full=model.matrix(~group+group:gender)
> design.full
```

	(Intercept)	groupB	groupC	groupA:genderMale	groupB:genderMale
1	1	0	0	1	0
2	1	0	0	1	0
3	1	0	0	0	0
4	1	0	0	0	0
5	1	1	0	0	1
6	1	1	0	0	1
7	1	1	0	0	0
8	1	1	0	0	0

9	1	0	1	0	0
10	1	0	1	0	0
11	1	0	1	0	0
12	1	0	1	0	0

```
groupC:genderMale
```

1	0
2	0
3	0
4	0
5	0
6	0
7	0
8	0
9	1
10	1
11	0
12	0

```
attr("assign")
```

```
[1] 0 1 1 2 2 2
```

```
attr("contrasts")
```

```
attr("contrasts")$group
```

```
[1] "contr.treatment"
```

```
attr("contrasts")$gender
```

```
[1] "contr.treatment"
```

Here, we consider the mean expression level of female in group A as the baseline expression level, if we want to test the effect of gender in group A, we can use $\text{Beta}=4$,

```
> result=glm.LRT(NanoStringData2,design.full,Beta=4)
```

Compare treatment group B to A ignore the effect the gender,

```
> result=glm.LRT(NanoStringData2,design.full,Beta=2)
```

Consider the interaction effect between gender and group B compare to A:

```
> result=glm.LRT(NanoStringData2,design.full,Beta=c(2,5))
```

5.2 All Interactions

We also can form a design matrix consider all interactions:

```
> design.full=model.matrix(~group+gender+group:gender)
```

Which is equivalent to:

```
> design.full=model.matrix(~group*gender)
```

```
> design.full
```

	(Intercept)	groupB	groupC	genderMale	groupB:genderMale	groupC:genderMale
1	1	0	0	1	0	0
2	1	0	0	1	0	0
3	1	0	0	0	0	0
4	1	0	0	0	0	0
5	1	1	0	1	1	0
6	1	1	0	1	1	0
7	1	1	0	0	0	0
8	1	1	0	0	0	0
9	1	0	1	1	0	1
10	1	0	1	1	0	1
11	1	0	1	0	0	0
12	1	0	1	0	0	0

```
attr("assign")
```

```
[1] 0 1 1 2 3 3
```

```
attr("contrasts")
```

```
attr("contrasts")$group
```

```
[1] "contr.treatment"
```

```
attr("contrasts")$gender
```

```
[1] "contr.treatment"
```

Test the gender effect in Treatment group B:

```
> result=glm.LRT(NanoStringData2,design.full,Beta=4:5)
```


6 Session Info

```
> toLatex(sessionInfo())
```

- R version 3.4.2 (2017-09-28), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: Biobase 2.38.0, BiocGenerics 0.24.0, NanoStringDiff 1.8.0
- Loaded via a namespace (and not attached): compiler 3.4.2, matrixStats 0.52.2, tools 3.4.2

References

- [1] Masaki Mori, Robinson Triboulet, Morvarid Mohseni, Karin Schlegelmilch, Kriti Shrestha, Fernando D Camargo, and Richard I Gregory. Hippo signaling regulates microprocessor and links cell-density-dependent mirna biogenesis to cancer. *Cell*, 156(5):893–906, 2014.