

# sSeq: A Simple and Shrinkage Approach of Differential Expression Analysis for RNA-Seq experiments.

Danni Yu, Wolfgang Huber and Olga Vitek

April 16, 2015

The sSeq package introduced in this manual provides a simple and efficient approach to discover differentially expressed (DE) genes based on the counts of transcripts from RNA-seq experiments. It regularizes the per-gene dispersion estimates with the common information across genes so that the bias and the variability in variance estimation are maintained at the low level.

## 1 Simple comparison between two conditions.

In this section, we will use the Hammer *et. al.* data [1] to illustrate how to use the functions in the sSeq package. The two conditions are control Sprague Dawley after 2 months (Condition A) and L5 SNL Sprague Dawley after 2 months (Condition B). There are two samples within each condition. This data is included in the sSeq package as an example, and can be imported as follows. “countsTable” is a matrix or data frame in which a column represents a sample and a row represents a gene. “conds.Hammer” is a characteristic vector, and used to define the conditions corresponding to the samples in columns. After defining the input counts table and the groups for conditions, the function “nbTestSH” can be utilized to obtain the regularized dispersion estimates and perform the exact tests. The output is a data frame in which the “pval” column includes the p-values of the exact tests.

```
> library(sSeq);
> data(Hammer2months);
> head(countsTable);
```

	A 1	A 2	B 1	B 2
ENSRNOG000000000001	2	4	18	24
ENSRNOG000000000007	4	1	3	1
ENSRNOG000000000008	0	1	4	2
ENSRNOG000000000009	0	0	0	0
ENSRNOG000000000010	19	10	19	13
ENSRNOG000000000012	7	5	1	0

```
> conds.Hammer=c("A","A","B","B");

> #exact test to get differential expressed genes
> res1 = nbTestSH( countsTable, conds.Hammer, "A", "B");

[1] "Shrinkage estimates on dispersion are used for the tests."
[1] "The shrink target is 0.543981062963739"
[1] "The shrink quantile is 0.963"
[1] "30% processed."
[1] "50% processed."
[1] "70% processed."
[1] "90% processed."
[1] "100% processed."
Time difference of 37.11988 secs

> head(res1);
```

	Mean	rawMeanA	rawMeanB	rawLog2FoldChange	dispMM
ENSRNOG000000000001	11.611882	3.0	21.0	-2.8073549	0.655085689
ENSRNOG000000000007	2.207431	2.5	2.0	0.3219281	0.000000000
ENSRNOG000000000008	1.722050	0.5	3.0	-2.5849625	0.329805247
ENSRNOG000000000009	0.000000	0.0	0.0	NaN	0.000000000
ENSRNOG000000000010	15.041505	14.5	16.0	-0.1420190	0.001213686
ENSRNOG000000000012	3.323526	6.0	0.5	3.5849625	0.707503560

	dispSH	pval
ENSRNOG000000000001	0.6294031	0.01235650
ENSRNOG000000000007	0.1257451	0.76135252
ENSRNOG000000000008	0.3793135	0.18544609
ENSRNOG000000000009	0.1257451	1.00000000
ENSRNOG000000000010	0.1266782	1.00000000
ENSRNOG000000000012	0.6697042	0.01880579

## 1.1 ASD plot and Dispersion plot

In the sSeq package, the testing is based on the shrinkage estimator  $\hat{\phi}^{sSeq} = (1 - \delta)\hat{\phi}^{MM} + \delta\xi$  that regularizes the method of moment estimates  $\hat{\phi}^{MM}$  to a shrinkage target  $\xi$  for the dispersion parameter. The averaged squared difference (ASD) between the method of moment estimates and the shrinkage estimates is used to estimate the shrinkage target. The smallest target value that minimizes the ASD value is selected as the estimate.

If “plotASD=TRUE” is specified in the function “nbTestSH”, a plot (Fig.1) of ASD values when varying the shrinkage targets is generated. In Fig.1, the dotted vertical and horizontal lines represent the estimated shrinkage target  $\hat{\xi}$  and the corresponding ASD value. The argument “SHonly=TRUE” is used to only calculate the dispersion estimates without running the exact tests.

```
> disp1 <- nbTestSH( countsTable, conds.Hammer, "A", "B", SHonly=TRUE, plotASD=TRUE);
```

```
[1] "Shrinkage estimates on dispersion are used for the tests."
[1] "The shrink target is 0.543981062963739"
[1] "The shrink quantile is 0.963"
```

After running the function “nbTestSH” with the argument “SHonly=TRUE”, we obtain an object (named as “disp1” in the following R scripts) that includes the dispersion estimates and the mean estimates. Using this object, a scatter plot (Fig.2) visualizing the relationship between the dispersion estimates and the mean estimates can be generated with the function “plot.dispersion”.

```
> head(disp1);
```

	SH	raw	mus
1	0.6294031	0.655085689	11.611882
2	0.1257451	0.000000000	2.207431
3	0.3793135	0.329805247	1.722050
4	0.1257451	0.000000000	0.000000
5	0.1266782	0.001213686	15.041505
6	0.6697042	0.707503560	3.323526

```
> plotDispersion(disp1, legPos="bottomright")
```

Sometimes, a user may like to define the shrinkage target instead of letting the package automatically find an estimate. The sSeq package is flexible for the requirement. For example, the method of moment estimates will be shrunk toward the target 1 when the argument “shrinkTarget=1” is added in the function “nbTestSH”. If the target needs to be defined as a quantile (e.g. 0.975) of the method of moment estimates across genes, then “shrinkQuantile=0.975” should be only added in the function “nbTestSH”. When both the arguments are added, the sSeq package uses the pre-defined target value, not the quantile, and shrinks the method of moment estimates toward the target 1.

## 1.2 Variance plot

To visualize the dependence between the variance estimates and the mean estimates, the following R scripts are used to generate a scatter plot (Fig.3) of log variance estimates versus log mean estimates. The black dots are the



Figure 1: The plot of ASD varying the shrinkage target. The smallest target value that minimizes the ASD value is represented by the vertical dotted line, and the corresponding ASD value is represented by the horizontal dotted line.

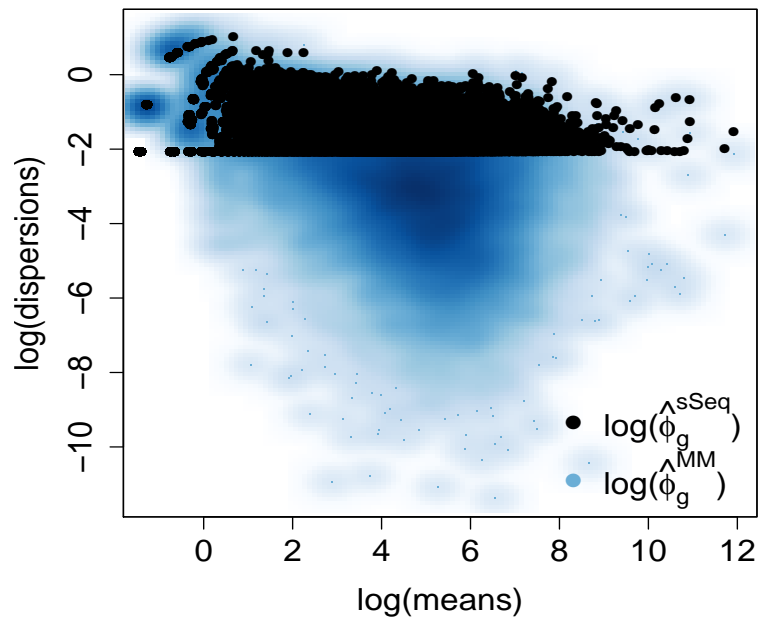


Figure 2: Dispersion plot.

variance estimates based on the shrinkage (or regularized) estimates of the dispersion. The blue smooth dots are the variance estimates directly obtained from the samples without any regularization. The variability among black dots are much lower than the variability among the blue smooth dots. Fig.3 clearly indicates that the mean-variance dependence is improved by the regularized variance estimates.

```
> rV = rowVars(countsTable);
> mu = rowMeans(countsTable);
> SH.var = (disp1$SH * mu^2 + mu)
> smoothScatter(log(rV)~log(mu), main="Variance Plot", ylab='log(variance)',
+   xlab='log(mean)', col=blues9[5], cex.axis=1.8)
> points( log(SH.var)~log(mu), col="black", pch=16)
> leg1 = expression(paste("log(", hat("V")[g]~"sSeq", ")"), sep='');
> leg2 = expression(paste("log(", hat("V")[g]~"MM", ")"), sep='');
> legend("bottomright", legend=c(leg1,leg2), col=c("black",blues9[5]),
+   pch=c(16, 1), cex=2)
```

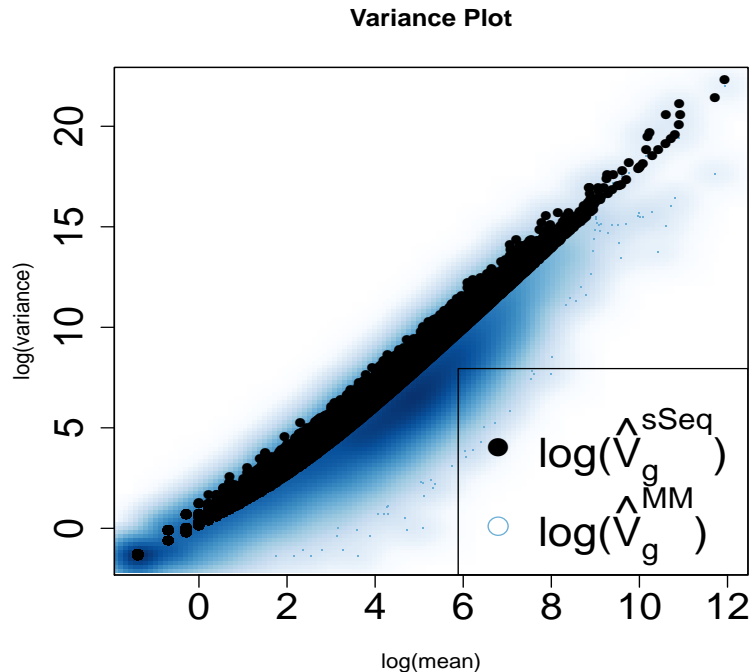


Figure 3: The plot of the variance estimates and the mean estimates.

### 1.3 ECDF plot

The empirical cumulative distribution function (ECDF) is an estimator of the true cumulative distribution function (CDF). It asymptotically converges to the true CDF for large number of points. In RNA-seq experiments, we typically have more than 20,000 p-values, and thus the ECDF of the p-values are very close to the true CDF.

The specificity and the sensitivity can be visualized by drawing the ECDF curves of the p-values for the within-condition comparison and the p-values for the between-condition comparison. When comparing the replicates under the same condition for the specificity, we expect to see that the genes are differentially expressed only by chance. The p-values should follow a uniform distribution (equivalent to the 45 degree line), or most p-values should be large and close to 1. On the other hand, when comparing the samples under two different conditions for the sensitivity, we expect to see that many genes are differentially expressed due to the changes of environment. The p-values should be small and close to 0. When a statistical method is robust for testing, we expect to see that the ECDF curve for the between-condition comparison is toward to the top left corner, and that the ECDF curve for the within-condition

comparison is toward to the 45 degree line or the bottom right corner. An example of this ECDF plot is shown in Fig.4. “AvsA” is for the within-condition comparison and “AvsB” is for the between-condition comparison.

```
> #obtain the p-values for the comparison AvsA.
> conds2.Hammer = c("A","B");
> res1.2 = nbTestSH( countsTable[,1:2], conds2.Hammer, "A", "B");

[1] "Shrinkage estimates on dispersion are used for the tests."
[1] "The shrink target is 0.249603542694111"
[1] "The shrink quantile is 0.972"
[1] "30% processed."
[1] "50% processed."
[1] "70% processed."
[1] "90% processed."
[1] "100% processed."
Time difference of 27.84526 secs

> #draw the ECDF plot;
> dd = data.frame(AvsA=res1.2$pval, AvsB=res1.2$pval);
> ecdfAUC(dd, col.line=c("green", "red"), main = "ECDF, Hammer", drawRef = TRUE, rm1=TRUE)

      AvsA      AvsB
0.4202079 0.6283183
```

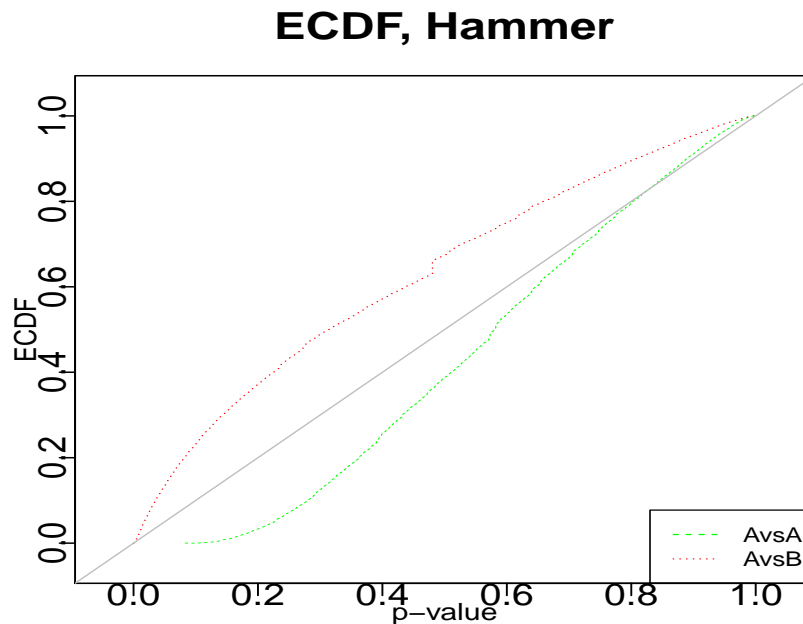


Figure 4: The ECDF plot for the profiles of p-values for the comparison between conditions (*AvsB*) and for the comparison within a condition (*AvsA*).

#### 1.4 MV plot and volcano plot.

A MV plot is a scatter plot between the means ( $M=[\log_2(A)+\log_2(B)]/2$ ) and the differences ( $V=\log_2(A) - \log_2(B)$ ). It helps to detect any dependent structures between the means and the differences in condition A and B. In a MV plot, we expect to see that the dots are roughly distributed on the two sides of the zero horizontal line without any

dependent pattern between M and V. A volcano plot is a scatter plot that visualizes the linear dependence between the statistical changes (e.g.  $-\log_2(\text{p-value})$ ) and the biological changes (e.g.  $\log_2(\text{fold change})$ ). We expect to see that the dots are linearly and evenly distributed on the two sides of the zero vertical line. Both types of the plots are useful for visual inspection on the test results among genes. The function ‘drawMA\_vol’ in the sSeq package can be used to draw the MV plot and the volcano plot. An example is shown in Fig.5. The red dots are the genes that have p-values less than 0.05.

```
> drawMA_vol(countsTable, conds.Hammer, res1$pval, cutoff=0.05);
```



Figure 5: MA plot and volcano plot.

## 2 Comparison between two conditions for paired experimental design.

The sSeq package is also available to perform exact tests for complex designed experiments, such as paired design. The Tuch *et. al.* data [2] is used as an example. In the experiment, there were three patients who had oral squamous cell carcinoma, which is one of the most common cancers in humans. The paired samples from the tumor tissue and the normal tissue for each patient were collected and sequenced with the RNA-seq technology. This data set is included in the sSeq package and shown as follows. We use “normal” and “tumor” to represent the two conditions, and use 1, 2, 3 to represent the three patients. We will simultaneously compare the gene expression between the normal tissue and the tumor tissue within each of the three patients. After specifying the paired samples for each patient by the argument ‘coLevels’, the exact tests for the paired-design experiment are performed. The counts of the genes that have the 25 smallest p-values are also shown as follows.

```
> data(Tuch);
> head(countsTable);
```

	N8	N33	N51	T8	T33	T51
NM_000014	2242	2285	15121	261	597	1991
NM_144670	11731	13308	6944	912	3071	1160
NM_017436	162	111	751	296	362	182

```
NM_015665    199    215    512    81    344    342
NM_023928    470    573    690    710    1112    728
NM_024666    298    332    856    203    790    909
```

```
> conds2 = c("normal", "normal", "normal", "tumor", "tumor", "tumor");
> coLevels=data.frame(subjects=c(1,2,3,1,2,3));

> res2 = nbTestSH(countsTable, conds2, "normal", "tumor",
+   coLevels= coLevels, pairedDesign=TRUE, pairedDesign.dispMethod="pooled");
```

```
[1] "Get shrinkage target at level 1"
[1] "For paired design, the aveaged dispersion estimates across paires are used."
[1] "Shrinkage estimates on dispersion are used for the tests."
[1] "The shrink target is 0.82375090107507"
[1] "The shrink quantile is 0.944"
[1] "30% processed."
[1] "50% processed."
[1] "70% processed."
[1] "90% processed."
[1] "100% processed."
Time difference of 1.631247 mins
```

```
> head(res2)
```

	Mean	rawMeanA	rawMeanB	rawLog2FoldChange	dispMM	dispSH
NM_000014	2809.2787	6549.3333	949.6667	2.7858549	1.02097798	0.9805542
NM_144670	6895.8007	10661.0000	1714.3333	2.6366232	1.07008843	1.0195989
NM_017436	286.7446	341.3333	280.0000	0.2857545	0.38780403	0.4771561
NM_015665	252.2928	308.6667	255.6667	0.2717856	0.09804907	0.2467895
NM_023928	734.0457	577.6667	850.0000	-0.5572256	0.08411026	0.2357076
NM_024666	498.6980	495.3333	634.0000	-0.3560831	0.08028615	0.2326673

	pval
NM_000014	0.0031707506
NM_144670	0.0004503366
NM_017436	0.0097131515
NM_015665	0.0813849771
NM_023928	0.0713288404
NM_024666	0.0379905629

```
> countsTable[order(res2$pval),][1:25,]
```

	N8	N33	N51	T8	T33	T51
NM_001100112	4389	7944	9262	7	16	1818
NM_002272	76461	99082	47411	353	20651	31
NM_005181	1840	4180	552	1	35	72
NM_003280	1684	1787	4894	0	7	559
NM_152381	9915	10396	23309	15	48	7181
NM_182502	2592	7805	3372	3	321	9
NM_016190	24146	22026	12480	49	2353	26
NM_001231	519	857	833	0	3	83
NM_002371	2697	3941	1750	3	265	8
NM_001010909	4160	3425	1720	7	516	5
NM_002016	343	3180	713	91	134	0
NM_000257	3118	3767	4001	8	21	724
NM_203378	4114	6544	11279	6	59	1487
NM_145244	432	935	1005	1	6	227
NM_002465	4809	4146	15623	10	14	1311
NM_003063	532	1022	1384	1	6	200
NM_014332	406	688	2347	0	3	318

NM_198060	3741	1990	12531	4	17	1829
NM_207163	449	1032	2138	1	4	272
NM_198271	399	396	1138	2	0	140
NM_014440	367	1824	802	10	45	1
NM_032578	679	656	3256	1	3	321
NM_057088	1069	3774	885	7	358	5
NM_001122853	257	223	559	0	1	83
NM_005416	41809	49781	31185	1155	8036	45

## References

- [1] Hammer, P. and Banck, M.S. and Amberg, R. and Wang, C. and Petznick, G. and Luo, S. and Khrebtukova, I. and Schroth, G.P. and Beyerlein, P. and Beutler, A.S. mRNA-seq with agnostic splice site discovery for nervous system transcriptomics tested in chronic pain. *Genome research*, 20(6):847–860, 2010.
- [2] B.B. Tuch, R.R. Laborde, X. Xu, J. Gu, C.B. Chung, C.K. Monighetti, S.J. Stanley, K.D. Olsen, J.L. Kasperbauer, E.J. Moore, et al. Tumor transcriptome sequencing reveals allelic expression imbalances associated with copy number alterations. *PloS One*, 5:e9317, 2010.