

# Microarray Analysis

Chao-Jen Wong  
Fred Hutchinson Cancer Research Center

9-10 December, 2010

Basics

Moderated  $t$ -tests

Using limma

$p$ -value Correction

Resources

# Introduction

- ▶ Identify differentially expressed genes associated with biological or experimental conditions.
- ▶ Primarily concerned with two-class problems.
- ▶ Data with  $n$  samples and  $p$  probes ( $p \gg n$ ).

A	A	A	A	A	B	B	B	B	B
$x_{1,1}$	$x_{1,2}$	$x_{1,3}$	$x_{1,4}$	$x_{1,5}$	$x_{1,6}$	$x_{1,7}$	$x_{1,8}$	$x_{1,9}$	$x_{1,10}$
$x_{2,1}$	$x_{2,2}$	$x_{2,3}$	$x_{2,4}$	$x_{2,5}$	$x_{2,6}$	$x_{2,7}$	$x_{2,8}$	$x_{2,9}$	$x_{2,10}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$x_{p,1}$	$x_{p,2}$	$x_{p,3}$	$x_{p,4}$	$x_{p,5}$	$x_{p,6}$	$x_{p,7}$	$x_{p,8}$	$x_{p,9}$	$x_{p,10}$

# Approaches

- ▶ Gene-by-gene hypothesis testing
  - ▶ Treating each gene independently of others.
  - ▶ Goal: find statistically significant associations of biological conditions.
  - ▶ Genes are deemed to be interesting if the  $p$ -value is small.
  - ▶ Method:  $t$ -tests, moderated  $t$ -tests, ROC,  $F$ -test.
- ▶ Machine learning

## t-tests

$$t_g = \frac{\mu_x - \mu_y}{\sqrt{\sigma_x^2 - \sigma_y^2}}$$

Drawback:

- ▶ Parametric assumptions hard to justify with few arrays.
- ▶ The variance in small samples might be noisy.
- ▶ Genes with small fold-change might be significant from statistical, not biological point of view.

# Moderated $t$ -statistics

- ▶ Rather than estimating within-group variability for each gene, pool the global information from all other genes.
- ▶ Advantage: eliminate occurrence of accidentally large  $t$ -statistics due to accidentally small within-group variance.

# Moderated $t$ -statistics

Using empirical Bayesian approach to estimate:

- ▶ Overall estimate variation  $s_0^2$ .
- ▶ Per-gene deviation variation  $s_g^2$ .
- ▶ Shrinkage variation

$$\tilde{s}_g^2 = \frac{d_0 s_0^2 + d_g s_g^2}{d_0 + d_g}$$

- ▶ Contrast estimator  $\hat{\beta}_g$  – the difference in means between two classes.
- ▶ Moderated  $t$ -statistics:

$$\tilde{t}_g = \frac{\hat{\beta}_g}{\tilde{s}_g \sqrt{\nu_g}}$$

# Using limma

1. Define a design matrix to establish parameters of linear model `model.matrix`.
2. Fit a linear model for each gene based on the given design matrix (and a contrast matrix): `lmFit()`.
3. Use function `eBayes` to get moderated  $t$ -statistics and relevant statistics.



## Deriving linear models

Suppose we define a design matrix as the following:

sample $i$	(intercept)	mol.biolNEG
NEG	1	1
BCR/ABL	1	0
NEG	1	1
$\vdots$	$\vdots$	$\vdots$

Each gene  $Y_j$  for all sample  $i$ , the expression level can be expressed by

$$\begin{bmatrix} Y_{NEG_{i,j}} \\ Y_{BCR/ABL_{i,j}} \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} \beta_{intercept} \\ \beta_{mol.biolNEG} \end{bmatrix} + \epsilon$$

$$\Rightarrow \beta_{mol.biolNEG} = Y_{BCR/ABL_{i,j}} - Y_{NEG_{i,j}} + \epsilon$$

$$y_j = \beta_{intercept} + \beta_{mol.biolNEG} a_{ij} + \epsilon$$

$$\Rightarrow y_j = \beta_0 + \beta_1 a_{ij} + \epsilon$$

# Using limma

Step 1:

Code: define design matrix and contrast model

```
> library(limma)
> design <- model.matrix( ~mol.biol, ALLfilt_bcrneg)
>
```

Step 2:

Code: linear models and eBayes

```
> fit1 <- lmFit(exprs(ALLfilt_bcrneg), design)
> fit2 <- eBayes(fit1)
> topTable(fit2, coef=2, adjust.method="BH",
+          number=5)
```

# Deriving linear models

Suppose we define a design matrix as the following:

sample $i$	mol.biolBCR	mol.biolNEG
BCR/ABL	1	0
BCR/ABL	1	0
BCR/ABL	1	0
$\vdots$	$\vdots$	$\vdots$
NEG	0	1
NEG	0	1
NEG	0	1
$\vdots$	$\vdots$	$\vdots$

$$y_i = \beta_1 a_{ij} + \beta_2 b_{ij} + \varepsilon_i$$

# Using limma

Step 1:

Code: define design matrix and contrast model

```
> library(limma)
> design <- model.matrix( ~0+mol.biol, ALLfilt_bcrneg)
> colnames(design) <- c("BCR_ABL", "NEG")
> contr <- makeContrasts(BCR_ABL-NEG, levels=designs)
> # contr <- c(1, -1)
```

Step 2:

Code: linear models and eBayes

```
> fit <- lmFit(exprs(ALLfilt_bcrneg), design)
> fit1 <- contrasts.fit(fit, contr)
> fit2 <- eBayes(fit1)
> topTable(fit2, adjust.method="BH", number=5)
```

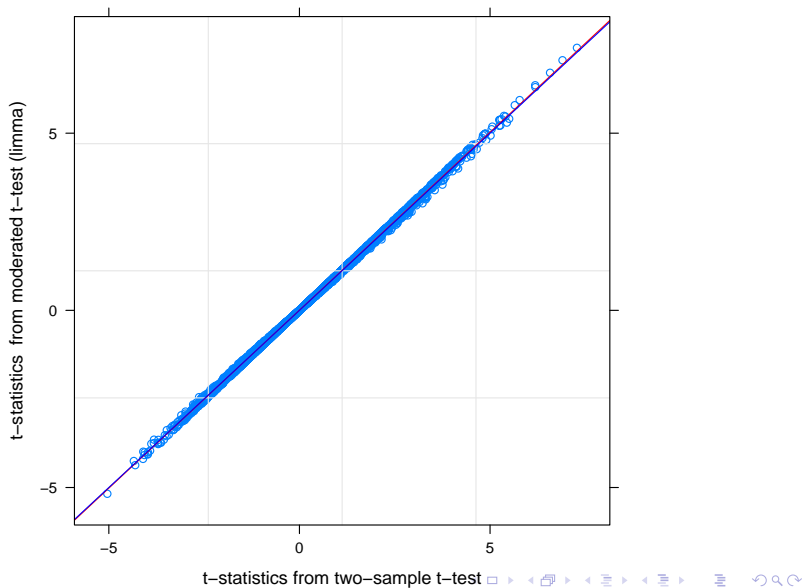
## $t$ -tests vs. moderated $t$ -tests

- ▶ In larger sample size, there is not big difference between the ordinary and the moderated tests.
- ▶ For smaller sample size the difference will be larger.

The empirical Bayes moderation is more useful in cases with fewer replicates.

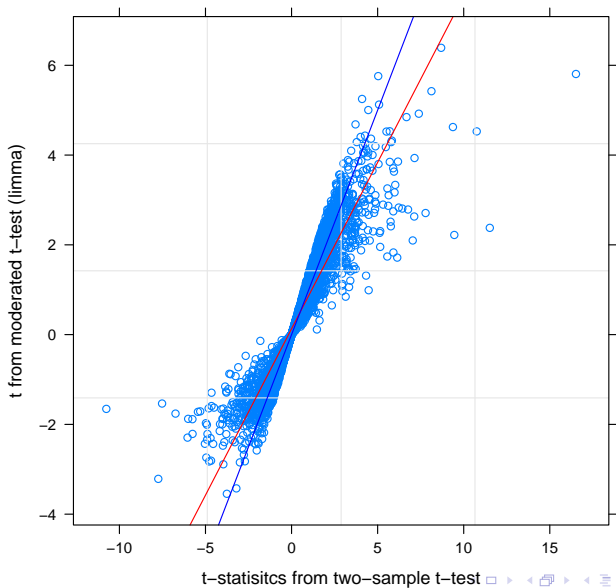
# $t$ -tests vs. moderated $t$ -tests

79 samples



# $t$ -tests vs. moderated $t$ -tests

6 samples -- 3 for each group



# $p$ -value corrections

- ▶ Basic idea: reduce critical value used to reject.
- ▶ Trade-off between sensitivity and specificity.
- ▶ Approaches implemented in the *multtest* package:
  - ▶ criteria for error rate control include family-wise error rate (FWER) and false discovery rate (FDR).
  - ▶ Permutation-based maxT methods.



# Lab activity

- ▶ Chapter 6 and 7 in *Bioconductor Case Studies*.
- ▶ Goals: get familiar with functions provided by *Bioconductor* packages to perform differential expression analysis.

# Resources

- ▶ G.K. Smyth, Linear models and empirical Bayes methods for assessing differential expression in microarray experiments, *Statistical Applications in Genetics and Molecular Biology*, 3(1), 2004.
- ▶ G. K. Smyth, *limma: Linear Models for Microarray Data*, Bioconductor package vignette, 2005.
- ▶ Florian Hahne et. al., *Bioconductor Case Studies*, Springer, 2007.