Comparing models

Jeff Leek

@jtleek

www.jtleek.com

Common goal: Identify associations after adjusting for some confounders

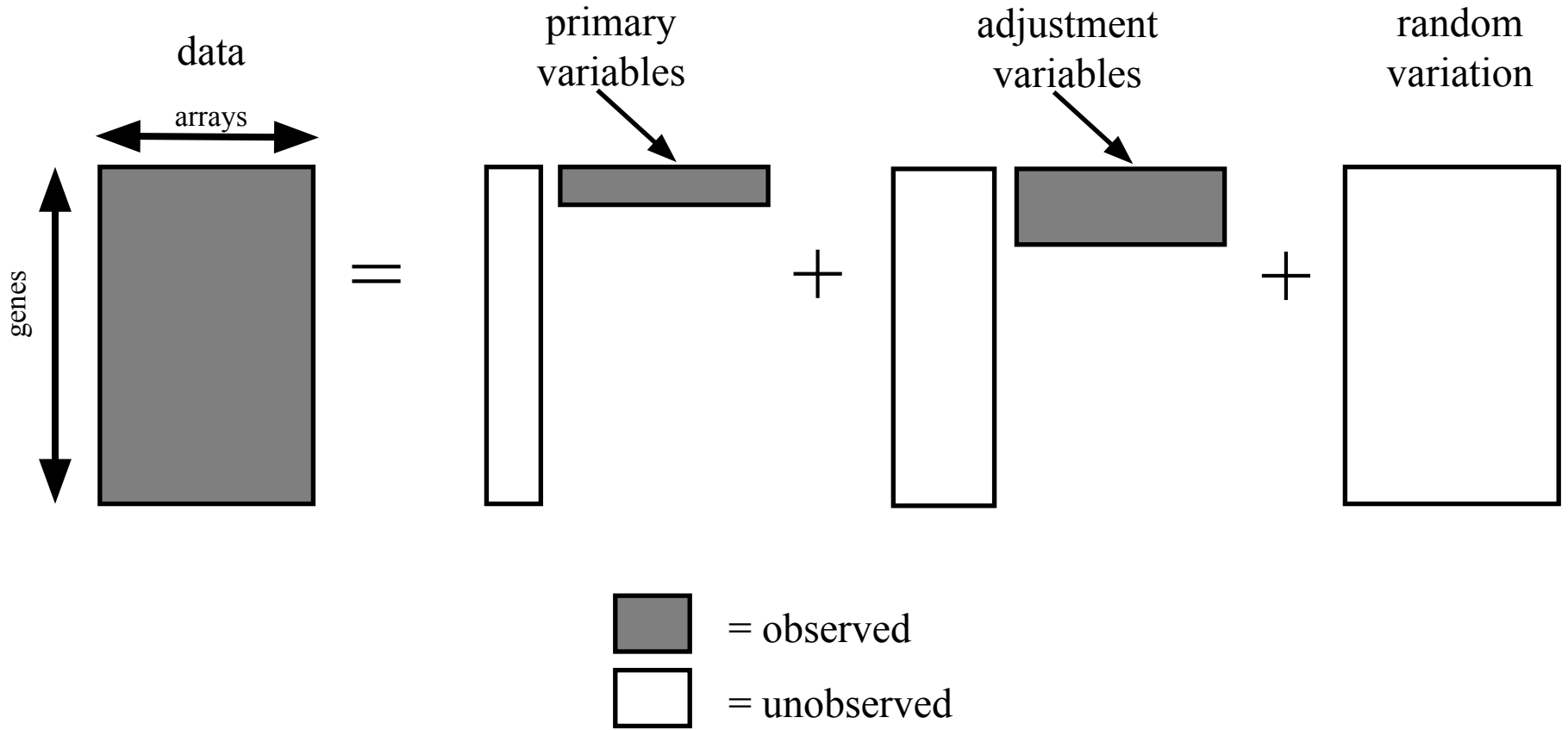
$$Y = b_0 + b_1 P + b_2 B + e$$

P = Phenotype you care about

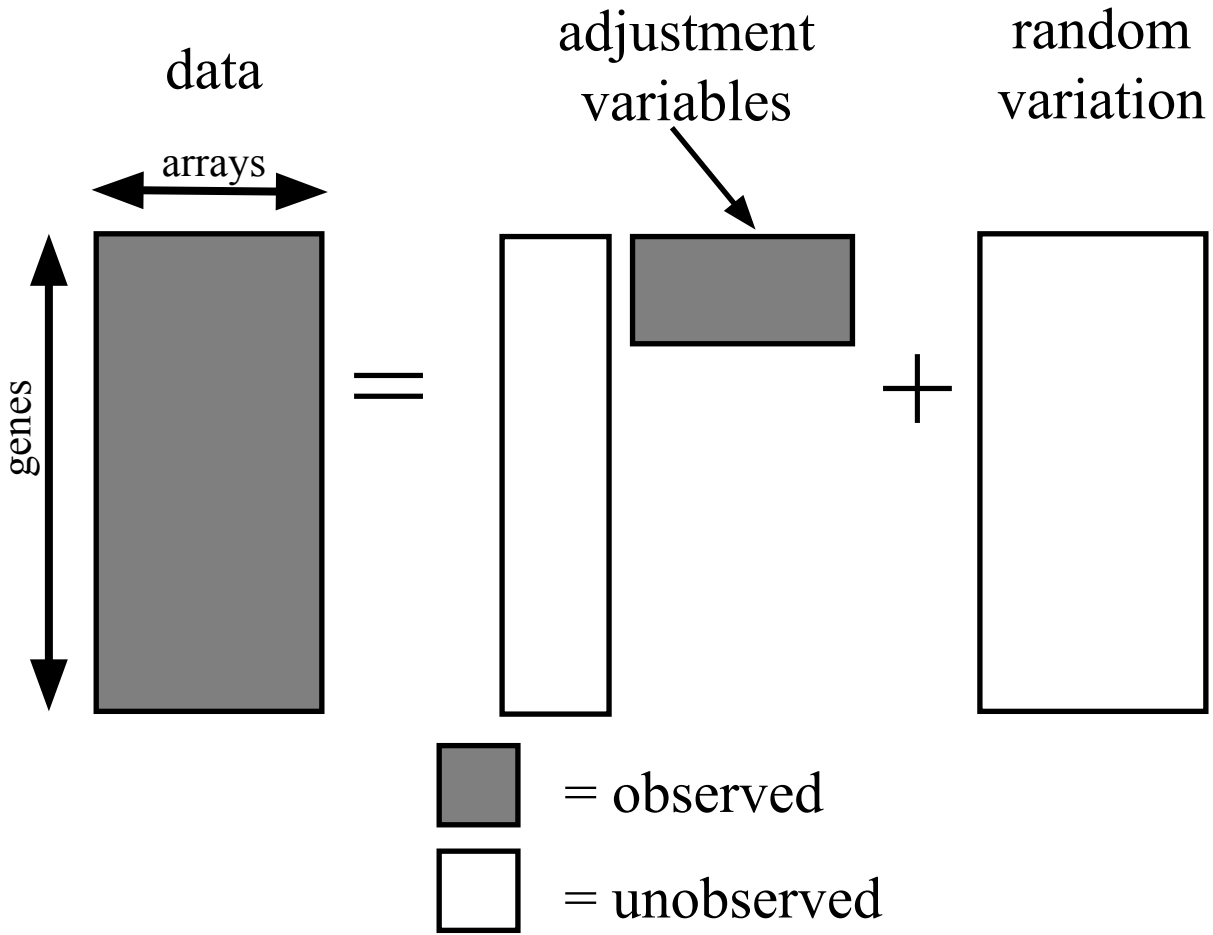
B = Batch

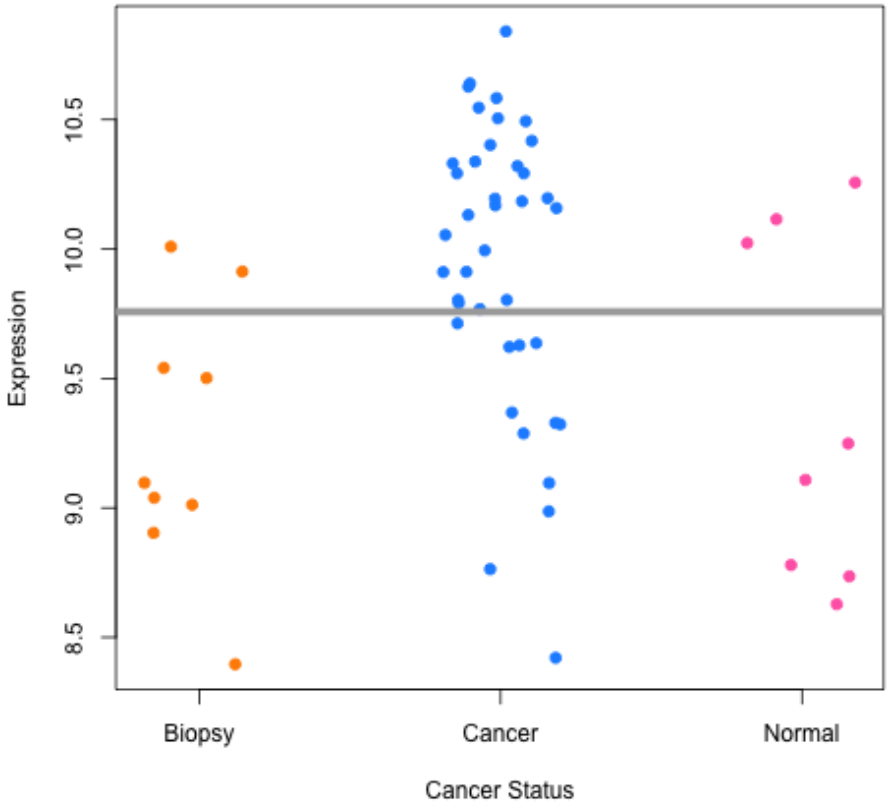
Compare two models

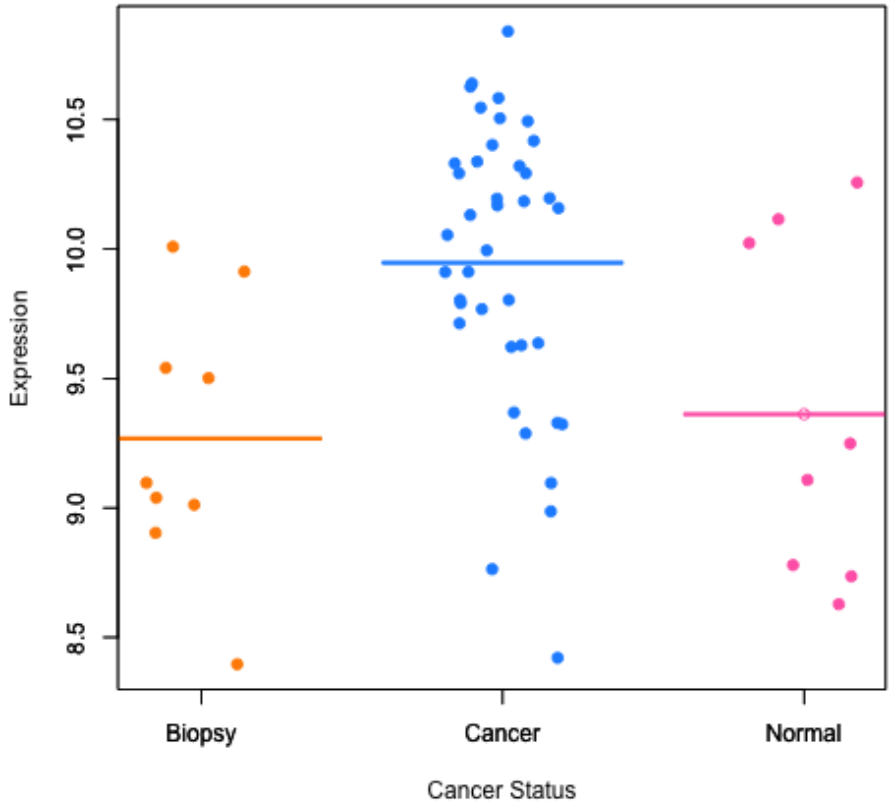
Slide adapted from: John Storey



Slide adapted from: John Storey




Expression
10.5
10.0
9.5
9.0
8.5
Biopsy
Cancer
Normal
Cancer Status


Expression
10.5
10.0
9.5
9.0
8.5
Biopsy
Cancer
Normal
Cancer Status

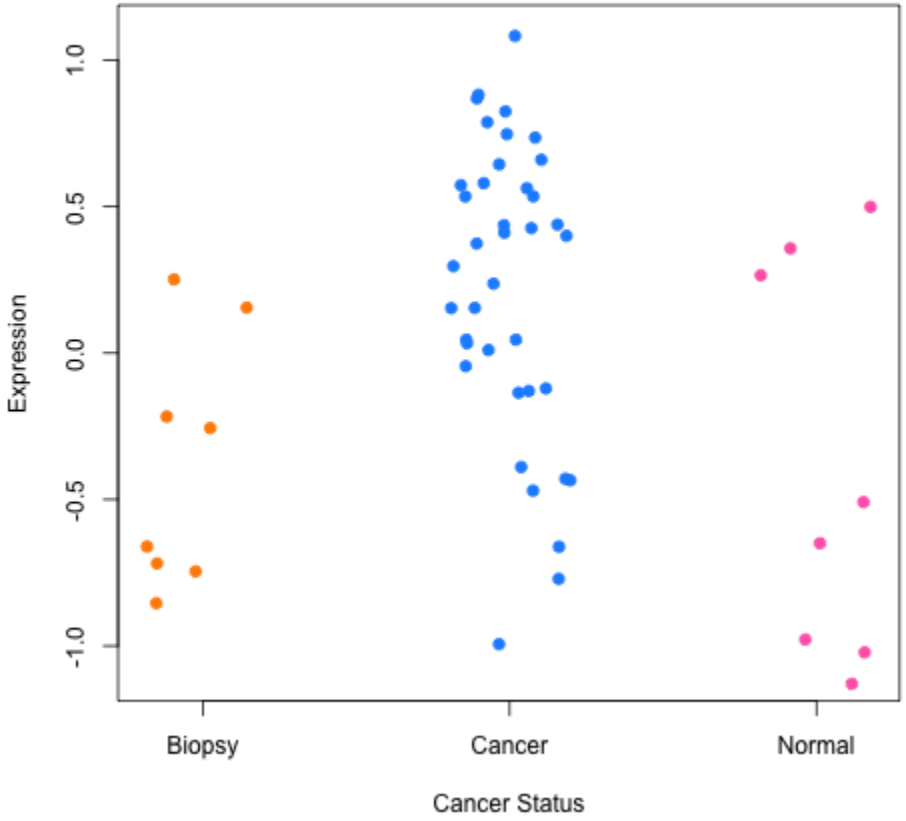
$$R = Y - b_0 - b_1 P - b_2 B$$

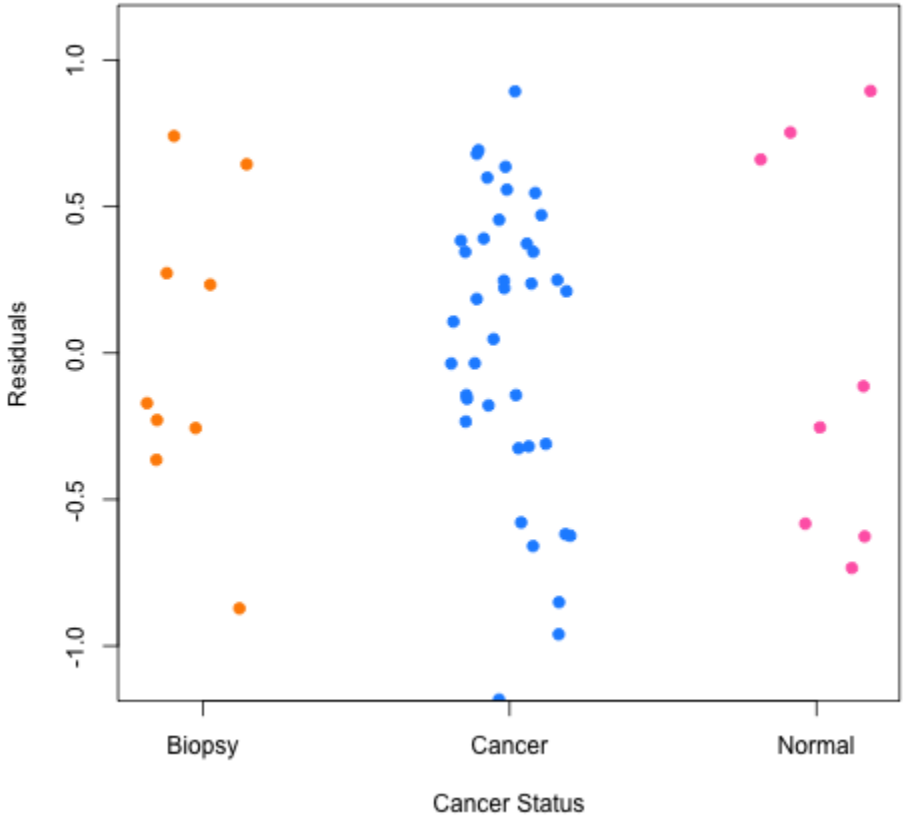
P = Phenotype you care about

B = Batch

$$RSS_0 = \sum_i (y_i - \hat{y}_i^0)^2 \approx 22.05$$

$$RSS_1 = \sum_i (y_i - \hat{y}_i^1)^2 \approx 17.21$$





F-statistic quantifies differences in model fit

$$\frac{n - p_1}{p_1 - p_0} \frac{RSS_0 - RSS_1}{RSS_1}$$

$$RSS_k = \sum_i (y_i - \hat{y}_i^k)^2$$

More variables = smaller residuals

Must account for this in the statistic

To account for the difference in the number of variables

$$\frac{\frac{n-p_1}{p_1-p_0}\left(RSS_0-RSS_1\right)}{RSS_1}$$

$$RSS_k=\sum_i (y_i-\hat{y}_i^k)^2$$

Notes and further reading

- This can be moderated, like the t-statistic
- Linear models for microarray data
  - http://www.statsci.org/smyth/pubs/limma-biocbook-reprint.pdf
- edge package vignette
  - http://bioconductor.org/packages/release/bioc/vignettes/edge/inst/doc/edg