

# Testing against a high-dimensional alternative

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Statistical Learning

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# Testing against a high-dimensional alternative

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# Outline

- 1 **High-Dimensional Alternatives**
- 2 **A Locally Most Powerful Test**
  - A random regression coefficient model
  - Derivation of the test statistic
- 3 **Applications**
  - Theoretical: the linear model
- 4 **Summary**

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# Testing in a high-dimensional model

## Testing in linear regression

- Response vector  $y$  ( $n \times 1$ ) and design matrix  $X$  ( $n \times p$ )
- Model:  $y \sim \mathcal{N}(X\beta, \sigma^2 I)$
- Regression coefficients  $\beta$  ( $p \times 1$ ) and variance  $\sigma^2$  unknown
- How to test  $H_0 : \beta = \mathbf{0}$  against  $H_A : \beta \neq \mathbf{0}$ ?

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  - What if  $p$  is close to  $n$ ?

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  - What if  $p$  is larger than  $n$ ?





# What is a microarray?

- Microarray measures 'gene expression'
- Central dogma of molecular biology

DNA  $\rightarrow$  RNA  $\rightarrow$  protein

- DNA is the same in every cell at every time  
But need for proteins is different  
 $\rightarrow$  amount of RNA is different
- Gene expression  $\approx$  concentration of RNA of a specific gene
- Microarray: simultaneous measurement of gene expression of around 20,000 genes in one tissue

# A typical microarray experiment

- Make microarrays of tissue samples of  $n$  patients
- Sample size  $n$  usually between 10 and 300.
- Typical research question:  
Which genes are associated with the response?

## Typical procedure

- 1 Do 20,000 univariate tests
- 2 Correct for multiple testing
- 3 Report a list of associated genes

# Alternative: focus on pathways

- Pathway = set of genes with a similar function in the cell
  - Apoptosis: programmed cell death
  - Cell Cycle: the process of cell division
  - Angiogenesis: generation of blood vessels
- Our research question:
 

which “pathways” are associated with  $y$ ?
- More general: take any predefined set of genes
  - Genes with similar annotation in Gene Ontology / KEGG
  - Genes with similar chromosomal location
  - All genes on the microarray
- $p = \# \text{genes}$ : anything from 1 to 20,000 or more

# Testing association of a pathway with a response

- Gene set = a set of covariates  $(x_1, \dots, x_p)$   
→ design matrix  $X$  ( $n \times p$ )
- How to test for association  $(x_1, \dots, x_p)$  and  $y$ ?
- $(x_1, \dots, x_p)$  and  $y$  are associated  $\iff$   
part of the variance of  $y$  can be predicted using  $(x_1, \dots, x_p)$
- In a linear model:  $y \sim \mathcal{N}(X\beta, \sigma^2 I)$
- No association:

$$H_0 : \beta = \mathbf{0}$$

- Some association:

$$H_A : \beta \neq \mathbf{0}$$

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# The alternative hypothesis

Alternative: “at least one  $\beta_i \neq 0$ ”: very general if  $p$  large

## Statistical problems

- Classical tests break down if  $p > n$
- There are  $\beta \neq \mathbf{0}$  which have  $\mathbf{r} = X\beta = \mathbf{0}$   
→ it is impossible to have power against all alternatives

# Focus the power

- Focus the power using a distribution on  $\beta$ :
- Larger density of  $\beta$   
= alternative  $\beta$  is more interesting to detect

## General Unprejudicedness Assumptions:

- 1 Alternative  $\beta$  as interesting as  $-\beta$
- 2 Alternative  $\beta$  as interesting as permutation  $\pi(\beta)$



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  - 2 Alternative  $\beta$  as interesting as permutation  $\pi(\beta)$
- Consequence: take  $\beta$  with  $E(\beta) = \mathbf{0}$  and  $E(\beta\beta') = \tau^2 I$
  - The distribution of  $\beta$  may have any shape  
→ We don't want to assume any shape

# A model with random regression coefficients

Inference via the marginal model: integrate  $\beta$  out

→  $p$  parameters in  $\beta$  become one parameter  $\tau^2$

## New alternative

Test  $H_0 : \tau^2 = 0$  against  $H_A : \tau^2 > 0$

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## Model interpretation 1: Empirical Bayes

Look at the distribution of  $\beta$  as a prior

to Inference on  $\beta$  goes through hyperparameter  $\tau^2$

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## Model interpretation 2: Penalized likelihood

- The distribution of  $\beta$  gives a penalty to the likelihood
- Do maximum likelihood on penalized likelihood
- Normal  $\beta$ : Ridge regression
- Double exponential  $\beta$ : LASSO

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## Model interpretation 3: Random effects model

- $\beta$  random  $\rightarrow$  linear predictor  $\mathbf{r} = X\beta$  random
- Moments:  $E(\mathbf{r}) = \mathbf{0}$ ;  $E(\mathbf{r}\mathbf{r}') = XX'$
- Look at  $r_1, \dots, r_n$  as a random subject effect
- Similar gene expressions  $\rightarrow$  correlated random effect
- Similar gene expressions  $\rightarrow$  correlated response

# The Neyman Pearson Lemma

- Why integrate out the  $\beta$  parameters?

## The Neyman-Pearson lemma:

*The likelihood ratio test of  $H_0 : \beta = \mathbf{0}$  against  $H_A : \beta = \beta_A$  has optimal power to detect  $H_A$  among all tests of at most the same size*

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## Corollary to Neyman-Pearson:

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- Expectation is taken over the distribution of  $\beta_A$  under  $H_A$

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- Expectation is taken over the distribution of  $\beta_A$  under  $H_A$
- Drawback:** distribution of  $\beta$  must be fully specified



# Score testing

- Score test always one-sided:  $H_0 : \theta = 0$  against  $H_A : \theta > 0$
- Score test = limit for  $\theta_1 \downarrow 0$  of the LR test of  $H_0$  against  $H_A : \theta = \theta_1$

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# The locally most powerful test

- Back to our model with random parameters
- Instead of a Likelihood Ratio test we do a score test

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## Corollary 3 to Neyman-Pearson:

*The score test of  $H_0 : \tau^2 = 0$  against  $H_A : \tau^2 > 0$  has optimal expected slope of the power function in  $\beta = \mathbf{0}$  among all tests of at most the same size*

- Expectation is w.r.t. uniformly choosing a random direction in  $p$ -space
- Practical advantage: no need to estimate  $\tau^2$

# The high dimensional score test statistic

- Test statistic is  $S = S(0)$  with  $S(\tau^2) = \frac{d}{d\tau^2} \log E_{\beta|\tau^2} L(\beta; y)$
- Is equal to:

$$S = \frac{1}{2} s' s - \frac{1}{2} \text{trace}(\mathbf{I})$$

- $s = \frac{\partial}{\partial \beta} \log L(0; y)$ , the score of  $\beta$   
 $\mathbf{I} = -\frac{\partial^2}{\partial \beta \partial \beta'} \log L(0; y)$  is the observed Fisher inform. of  $\beta$
- Nice properties:
  - *Easy: no evaluation of  $p$ -dimensional integrals*
  - *Test statistic only depends on the first two moments of  $\beta$*

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- Nice properties:
  - *Easy: no evaluation of  $p$ -dimensional integrals*
  - *Test statistic only depends on the first two moments of  $\beta$*
- Difficult part: What is the distribution of  $S$ ?
  - Solved for linear (exact), GLM, Cox PH (asymptotic)
  - Alternative: permutations



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# Back to the linear model

- What is the locally most powerful test in the linear model?
- Get rid of the nuisance parameter  $\sigma^2 \rightarrow$  profile likelihood
- For  $\beta$  with  $E\beta = \mathbf{0}$  and  $E(\beta\beta') = \tau^2 I$ :

$$S = \frac{y'XX'y}{y'y}$$

- For  $\beta$  with  $E\beta = \mathbf{0}$  and  $E(\beta\beta') = \tau^2 \Sigma$ :  
Score test statistic:

$$S_{\Sigma} = \frac{y'X\Sigma X'y}{y'y}$$

# The F-test revisited

- The F-test is only defined when  $p < n$
- Equivalent test statistic  $F = \frac{y'X(X'X)^{-1}X'y}{y'y}$  (beta distributed)

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## The F-test as a score test

F-test is equivalent to a score test with  $\Sigma = (X'X)^{-1}$

- $S = F$  in an orthogonal design (i.e.  $X'X \propto I$ )
- F-test optimizes power over a prior for  $\beta$   
with  $E(\beta\beta') = \tau^2(X'X)^{-1}$  (g-prior) for  $\tau^2$  small

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# Discussion: gene expression data

## Analyzing micorarray data in terms of pathways

- Enables use of prior biological knowledge
- Alleviates the multiple testing problem
- Gives better reproducible results across platforms
- Global Test opens door to real inference:  
→ testing hypotheses on biological mechanisms based on theory or past research

# Discussion: high dimensional testing

## A locally most powerful test in high dimensions

- Useable whatever the dimensionality
- Good power against interesting alternatives
- Useful applications in and outside microarray data analysis
- Applicable in survival analysis and generalized linear models

# Read more?



Goeman, Van de Geer, De Kort, Van Houwelingen (2004).

A global test for groups of genes.

*Bioinformatics*, **20** (1) 93–99.



Goeman, Van de Geer and Van Houwelingen (2006).

Testing against a high-dimensional alternative.

*JRSSB*, **68** (3) 477–493.



Goeman and Oosting.

R package: globaltest

[www.bioconductor.org](http://www.bioconductor.org)