

# Machine Learning and Statistics in Genetics and Genomics

III: Introduction to hypothesis testing

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Microsoft  
**Research**

Current topics in computational biology

UCLA

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## Hypothesis Testing

Introduction

$P$ -values and significance

$t$ -test in linear regression

Likelihood ratio test

Multiple Hypothesis Testing

Model checking - useful heuristics

# Outline

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## Hypothesis Testing

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Likelihood ratio test

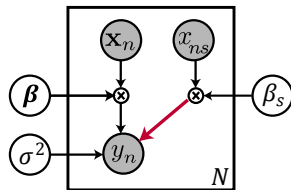
Multiple Hypothesis Testing

Model checking - useful heuristics

# Testing in Linear Regression

$$p(\mathbf{y} | \mathbf{X}) = \prod_{n=1}^N \mathcal{N}(y_n | \mathbf{x}_n \cdot \boldsymbol{\beta}, \sigma^2)$$

- ▶  $x_{n,s}$ : SNP to be tested
- ▶ remaining  $\mathbf{x}_n$ : regression covariates (including bias term)
  - ▶ Race
  - ▶ Known background SNPs
  - ▶ Environment



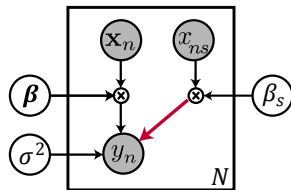
Equivalent graphical model

$x_n$ : regression covariates

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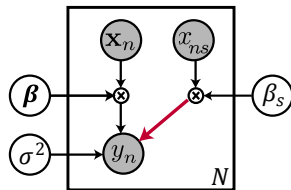
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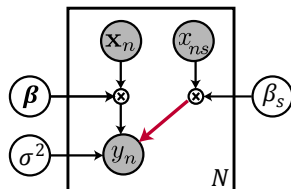
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- ▶ Use the estimate  $\beta_{s\text{ML}}$  as a test statistic.
- ▶ **Intuition:** The larger the absolute value of the estimate  $\beta_{s\text{ML}}$ , the less likely is  $\mathcal{H}_0 : \beta_s = 0$ .



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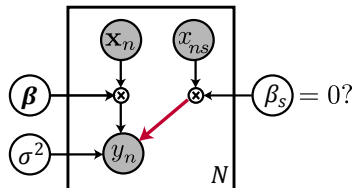


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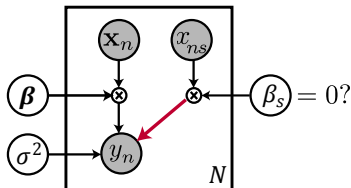
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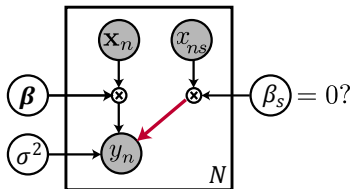
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# Hypothesis Testing

## Some definitions

Example:

- ▶ Given a sample  
 $\mathcal{D} = \{x_1, \dots, x_N\}$ .
- ▶ Test whether  $\mathcal{H}_0 : \beta_s = 0$  (null hypothesis) or  $\mathcal{H}_1 : \beta_s \neq 0$  (alternative hypothesis) is true.
- ▶ To show that  $\beta_s \neq 0$  we can perform a statistical test that tries to reject  $\mathcal{H}_0$ .
- ▶ **type 1 error:**  $\mathcal{H}_0$  is rejected but does hold.
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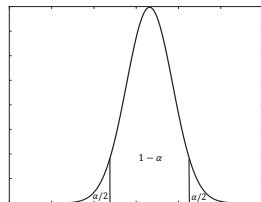
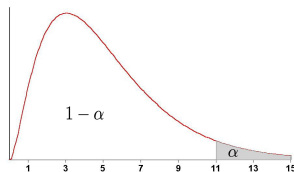
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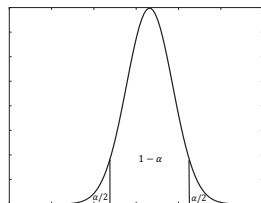
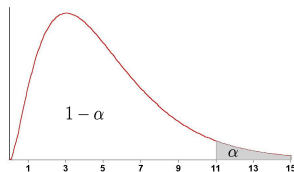
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- ▶ Usually decision is based on a **test statistic**.
- ▶ The **critical region**  $\mathcal{R}_\alpha$  defines the values of the test statistic that lead to a rejection of the test at significance  $\alpha$ .



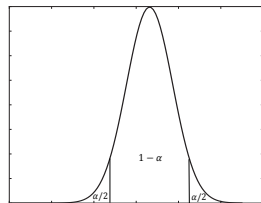
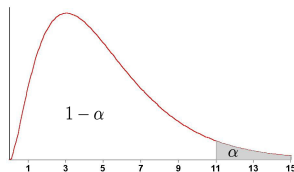
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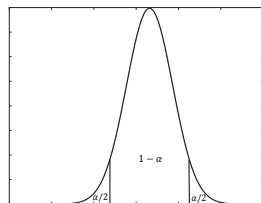
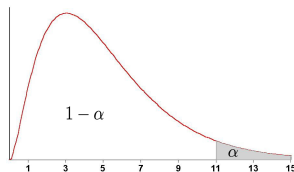
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- ▶  $P$ -value of a test statistic  $x$  is the largest possible  $\alpha$ , such that  $x$  is still rejected.

$$P - \text{value}(x) = \inf_{\alpha} (x \in \mathcal{R}_{\alpha})$$

- ▶ Probability of observing a test statistic at least as extreme as  $x$ , given that  $\mathcal{H}_0$  is true.
- ▶ Significance level  $\alpha$  becomes threshold on  $P$ -value.
- ▶ Need to know the null distribution of test statistics. (usually unknown)
- ▶ For every  $u \in [0, 1]$ ,

$$P_{\mathcal{H}_0}(P - \text{value}(x) \leq u) = P_{\mathcal{H}_0}(x \in \mathcal{R}_u) = u$$

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# $P$ -value

## Permutation procedure

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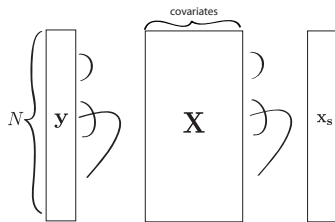
- ▶ Permute phenotype  $y$  and covariates  $x$  jointly over individuals.
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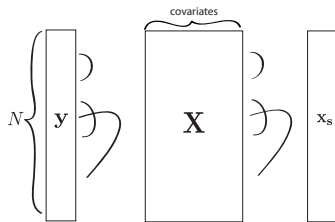


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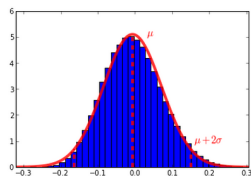
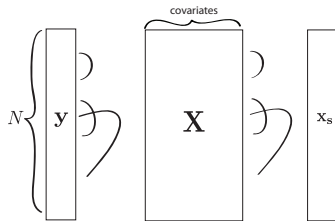


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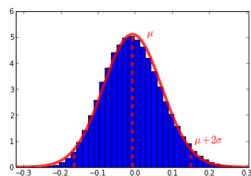
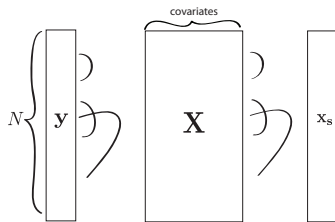
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The  $P$ -value is the **quantile** of real test statistic in artificial null distribution.

- ▶ The quantile is the fraction of the empirical distribution that is more extreme than the test statistic.





# Testing in Linear Regression

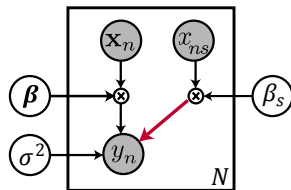
## Analytic solution

$$p(\mathbf{y} | \mathbf{X}) = \prod_{n=1}^N \mathcal{N}(y_n | \mathbf{x}_n \cdot \boldsymbol{\beta}, \sigma^2)$$

- ▶  $\mathcal{H}_0 : \beta_s = 0$ .
- ▶ Can we find an analytic solution for the distribution of the **estimate**  $\beta_{s\text{ML}}$  under  $\mathcal{H}_0$ ?
- ▶ **Intuition:** The estimate is a linear transformation of a Normal distributed variable, namely  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\boldsymbol{\beta}, \sigma^2 \mathbf{I})$ , where  $\boldsymbol{\beta}$  is the value under  $\mathcal{H}_0$  (with  $\beta_s = 0$ ).

$$\beta_{\text{ML}} = \underbrace{\left( \mathbf{X}^\top \mathbf{X} \right)^{-1} \mathbf{X}^\top}_{\text{transformation}} \mathbf{y}$$

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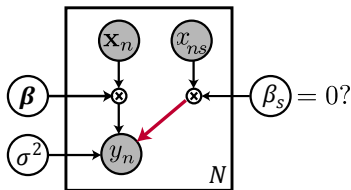
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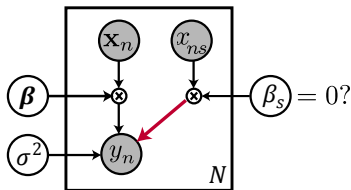
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- ▶  $\mathcal{H}_0 : \beta_s = 0$ .
- ▶ Can we find an analytic solution for the distribution of the **estimate**  $\beta_{s\text{ML}}$  under  $\mathcal{H}_0$ ?

- ▶ **Intuition:** The estimate is a linear transformation of a Normal distributed variable, namely  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\boldsymbol{\beta}, \sigma^2 \mathbf{I})$ , where  $\boldsymbol{\beta}$  is the value under  $\mathcal{H}_0$  (with  $\beta_s = 0$ ).

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Equivalent graphical model

$x_n$ : regression covariates

# Testing in Linear Regression

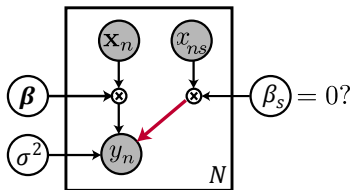
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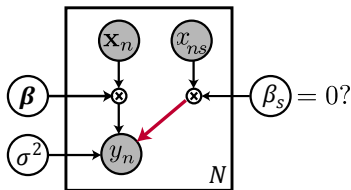
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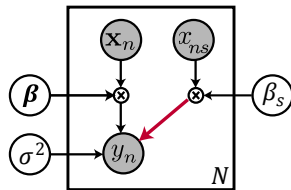
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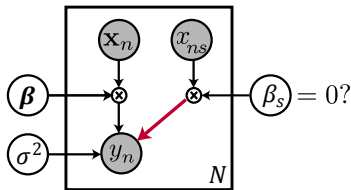
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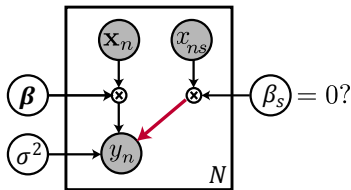
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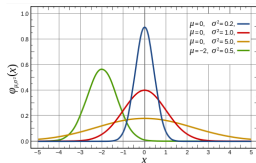
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# Cumulative distribution function

$$\beta_{s\text{ML}} \sim \mathcal{N}\left(0, \sigma^2 \left[ \left( \mathbf{X}^\top \mathbf{X} \right)^{-1} \right]_{ss} \right)$$

- ▶ Now we know the probability distribution of  $\beta_s$ .
- ▶ But the  $P$  value is the probability of observing something at least as extreme.



- ▶ Cumulative distribution function:

$$CDF(x) = P(X \leq x) = \int_{-\infty}^x p(z) \, dz$$

- ▶ For the univariate normal distribution with mean  $\mu$  and variance  $\sigma^2$ :

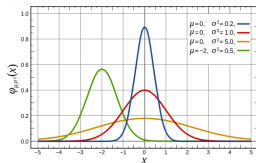
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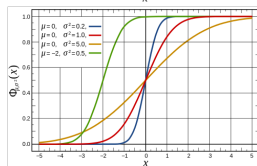
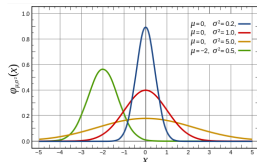
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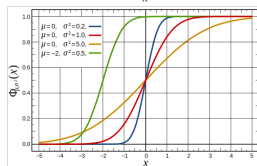
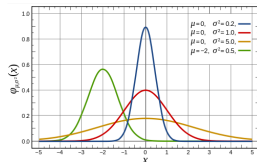
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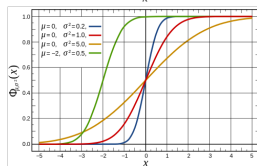
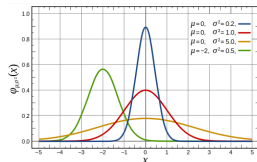
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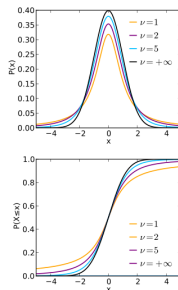
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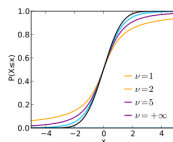
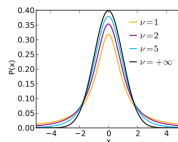
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# Some relationships between distributions

- ▶ Normal distribution

$$x_n \sim \mathcal{N}(\mu, \sigma^2)$$

- ▶  $z$ -score: Standard normal distribution

$$z_n = \frac{x_n - \mu}{\sigma} \sim \mathcal{N}(0, 1)$$

- ▶ Sum of squares of  $N$  iid standard normals:  $\chi^2$  distribution with  $N$  dof

$$\sum_{n=1}^N z_n^2 \sim \chi_N^2$$

- ▶ Ratio of a standard normal and an independent  $\chi_N^2$  variable

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- ▶ Ratio of a  $\chi_{N_1}^2$  and an independent  $\chi_{N_2}^2$ :  $F$ -distribution with  $N_1$  numerator dof and  $N_2$  denominator dof

$$F = \frac{\sum_{n=1}^{N_1} z_n^2}{\sum_{n=N_1+1}^{N_1+N_2} z_n^2} \sim F(N_1, N_2)$$

# Some relationships between distributions

- ▶ Normal distribution

$$x_n \sim \mathcal{N}(\mu, \sigma^2)$$

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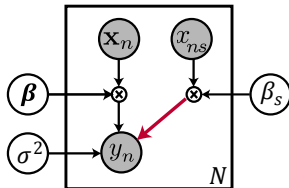
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# Testing in Linear Regression

## Likelihood Ratio Test

$$p(\mathbf{y} | \mathbf{X}) = \prod_{n=1}^N \mathcal{N}(y_n | \mathbf{x}_n \cdot \boldsymbol{\beta}, \sigma^2)$$

- ▶ Test  $\mathcal{H}_0 : \beta_s = 0$  (rest don't matter)
- ▶ The **ratio** of the **likelihood** using the **ML estimator** and the **ML<sub>0</sub> estimator** restricted to  $\mathcal{H}_0$  ( $\beta_s = 0$ ) is another common test statistic.



Equivalent graphical model

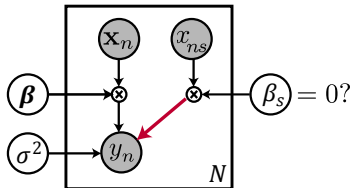
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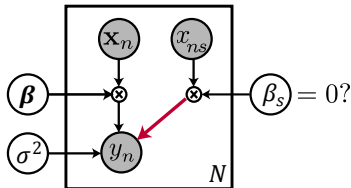
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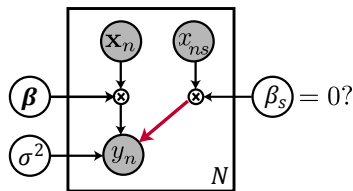
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# Testing in Linear Regression

## Likelihood Ratio Test revisited

- ▶ Can equivalently compute log-likelihood ratio:



Equivalent graphical model

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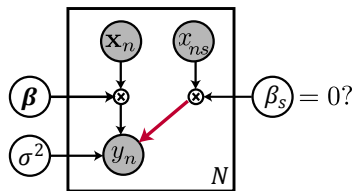
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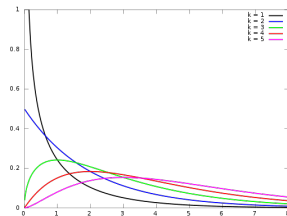
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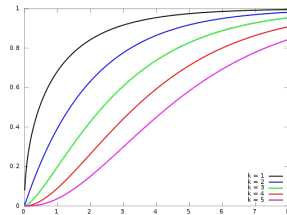
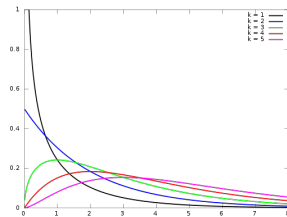
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# Multiple Hypothesis Testing

## Motivation

- ▶ Significance level  $\alpha$  equals probability of type-1 error.
- ▶ In GWAS we perform  $S = 10^6$  tests
- ▶ If all tests are independent we would expect 10000 type-1 errors at  $\alpha = 0.01$ ! ( $S = S_0$ )
- ▶ Probability of at least 1 type-1 error is  $1 - (1 - \alpha)^{S_0} \rightarrow 1$ .
- ▶ Individual  $P$ -values  $< 0.01$  are not significant anymore.

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Need to correct for **multiple hypothesis testing**!

# Multiple Hypothesis Testing

## Family-Wise Error Rate (FWER)

$$\text{FWER} = \Pr \left( \bigcup_{i \in \mathcal{H}_0} P_{(i)} \leq \alpha \right)$$

- ▶ Probability of at least one type-2 error.
- ▶ Correct by bounding the FWER.
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# False Discovery Rate (FDR)

- ▶ FWER based correction (Bonferroni) leads to very conservative significance thresholds.

- ▶ Because of the abundance of tests we might be willing to accept a few false positives.

- ▶ Definition of the FDR:

- ▶  $\mathbb{E} \left[ \frac{FP}{FP + TP} \right]$

- ▶ Note: this can not be bounded when  $\mathcal{H}_0$  always true ( $FN + TP = 0$ ). In this case

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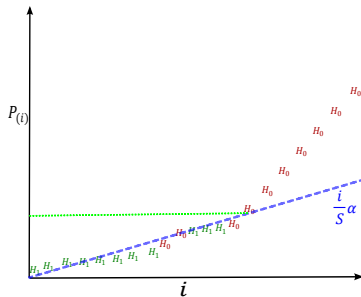
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Algorithm for FDR cutoff  $\alpha$ :

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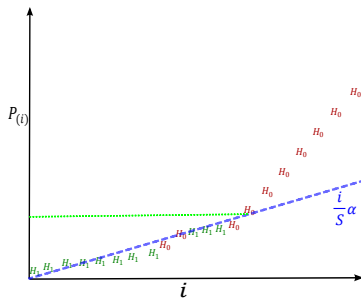
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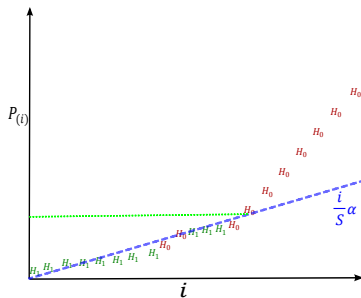
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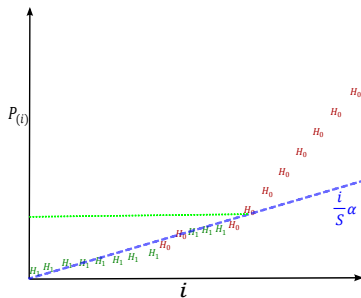
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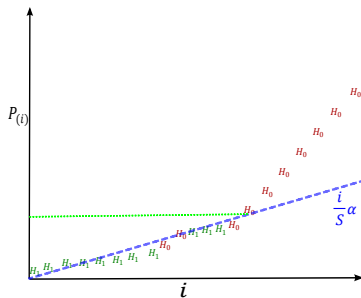
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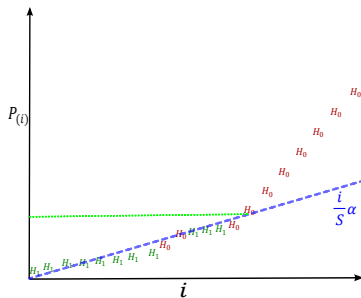


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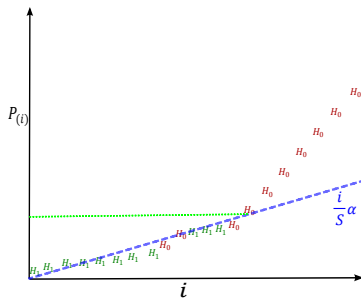
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If tests are independent, then for this procedure:

$$FDR \leq \frac{\overbrace{FP + TN}^{S_0}}{S} \alpha \leq \alpha$$



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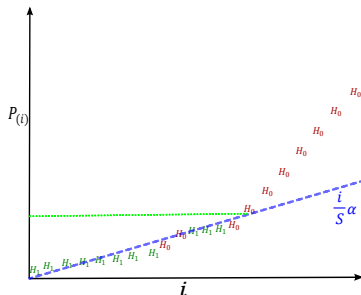
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Definition of a  $q$ -value:

$$q(P_{(s)}) = \min_{t \geq P_{(s)}} \text{FDR}(t)$$

*“minimum FDR that can be attained while calling that feature significant”*  
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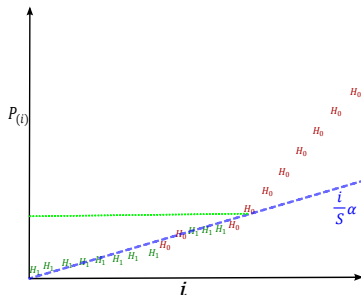
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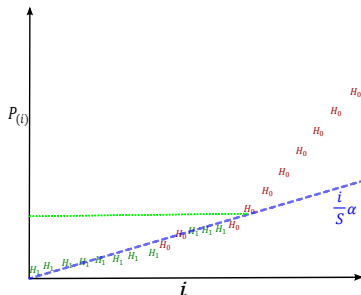
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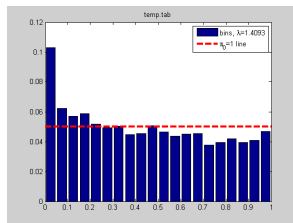
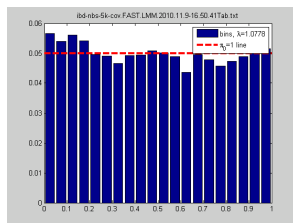
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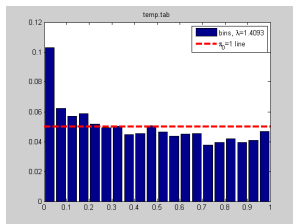
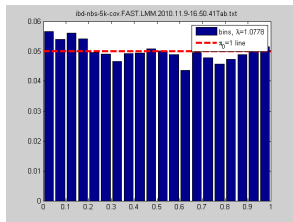
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  - ▶ By definition uniformly distributed under null distribution.
- ▶ Do the empirical results match my assumptions on the null model?
- ▶ In GWAS we perform a large number of tests. (usually in the order of  $10^6$ )
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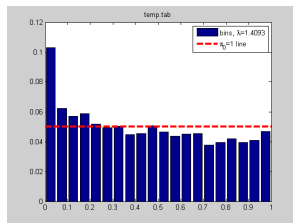
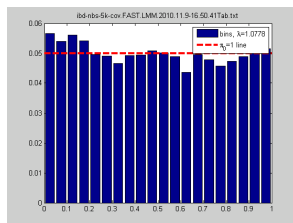
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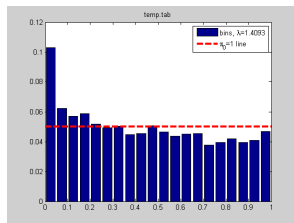
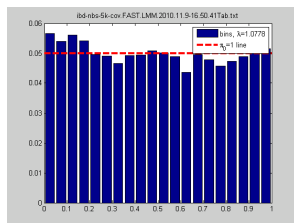
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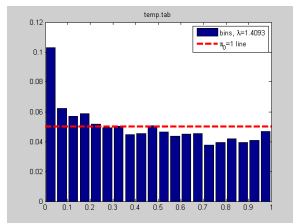
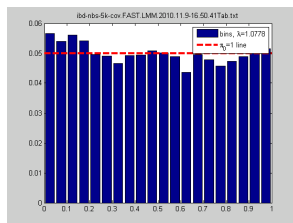
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# Model Checking

## QQ-plot

Compare quantiles of the empirical test statistic distribution to assumed null distribution.

- ▶ Sort test statistics
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  - ▶ for example: 2LR vs.  $\chi_1^2$
- ▶ If the plot is close to the diagonal, the distributions match up
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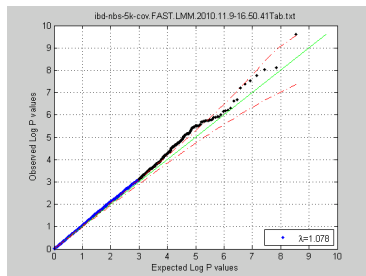
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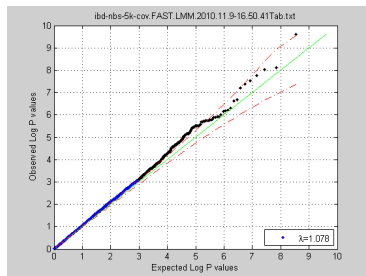


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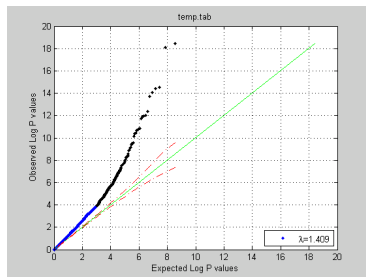


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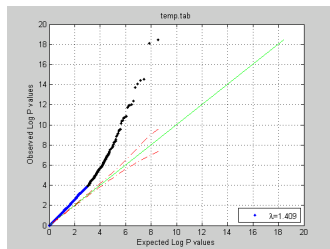
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# Correction for inflation

## Genomic control ( $\lambda_{GC}$ )

- ▶ Ratio of the 50% quantiles between theoretical distribution and test-statistics known as the genomic inflation factor  $\lambda_{GC}$ .
- ▶ **Assumption:**  $\lambda_{GC}$  should be close to 1.
- ▶ Estimate degree of inflation (deflation) from this ratio.
- ▶ Adjust for degree of inflation by dividing all statistics by ratio of the median (50%-quantile).
- ▶ This procedure yields conservative estimates of the  $P$ -value distribution null-distribution.



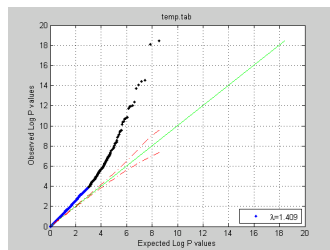
- ▶ GC does not make  $P$ -values uniform, but only **matches one quantile!**
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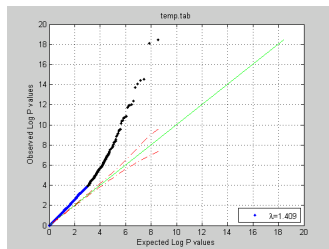
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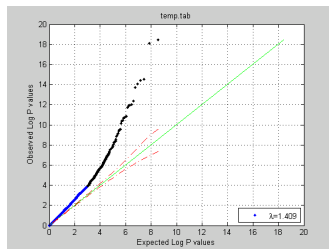


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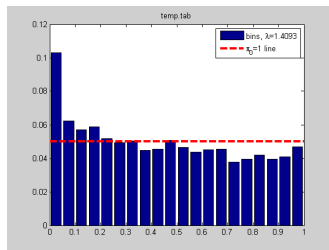


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