Multiple testing (in R)

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Outline for the course

- Introduction to statistics
- Hypothesis testing (in R)
- Regression analysis (in R)
- Multiple testing (in R)

Often, the aim of the analysis is not only **estimation**.

For example,

- ▶ Is the treatment effective?
- Is a gene differentially expressed?
- ► Is there an association between genotype and phenotype?



These questions can be translated as hypothesis testing problems

No test is exact:

	Null hypothesis does not hold	Null hypothesis holds
Reject null	Correct	Wrong
hypothesis	True positive	False positive
Do not reject	Wrong	Correct
null hypothesis	False negative	True negative

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For example, Genome Wide Association Studies (GWAS):

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- Usually framed as a regression problem
- ▶ Outcome: disease (yes/no), biomarker value, height, etc.
- Covariates: SNPs in the genome (millions!)

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- \triangleright Y_i : response variable (e.g. biomarker value) for person i
- $x_i^{(j)}$: observed value for SNP j, person i

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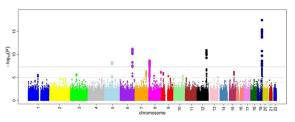
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$$H_0: \beta_j = 0$$
 vs $H_1: \beta_j \neq 0$

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There are as many tests as SNPs in the genome!

No test is exact:

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What happens to these errors when we run more multiple tests?

What is the probability of obtaining 1 or more false positives (i.e. Reject H_0 when H_0 is true) among T independent tests?

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= 1 - (1 - \alpha)^T
```

P(At least 1 FP in
$$T$$
 tests) = $1 - (1 - \alpha)^T$; $\alpha = 0.05$

1.0

0.8

0.6

0.4

0.2

0 20 40 60 80 100

Number of tests

For T=100 tests, the probability of at least 1 FP is almost 1!

What is the probability of obtaining 1 or more false positives (i.e. Reject H_0 when H_0 is true) among T independent tests?

We need to correct for multiple testing to control error rates

To control the **Family-Wise Error Rate** (FWER)

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Bonferroni's solution is to use:

$$\alpha^* = \min\{\alpha/T, 1\}$$

Doing this for each test ensures that FWER $\leq \alpha$

Bonferroni's correction:

$$\alpha^* = \min\{\alpha/T, 1\}$$

For example, for 1 million tests and $\alpha = 0.05$, this leads to

$$\alpha^* = 5 \times 10^{-8}$$

This is commonly used as a p-value threshold in GWAS

Bonferroni's correction:

▶ It can be too conservative ⇒ too many false negatives

► Holm's method is less conservative while still controlling FWER

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Benjamini and Hochberg's method controls the FDR

