

Controlling the False Discovery Rate

A Practical and Powerful Approach to Multiple Testing

Benjamini Y and Hochberg Y (1995) Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society. Series B (Methodological), Vol. 57, No. 1, pp. 289-300

Acknowledgement: [Lecture10_MultipleTesting.ppt \(washington.ehttps://www.gs.washington.edu/academics/courses/akey/56008/lecture/lecture10.pdfdu\)](https://www.gs.washington.edu/academics/courses/akey/56008/lecture/lecture10.pdf)

Background and Setting

Assume we are testing H_1, H_2, \dots, H_m

m_0 = number of true hypotheses

R = number of rejected hypotheses

V = number of type I errors [false positives]

$$Q = \begin{cases} V/R & R > 0 \\ 0 & \text{otherwise} \end{cases}$$

We further assume:

- m is known
- R is an observable random variable
- U, V, S and T are unobservable random variables

Number of errors committed when testing m null hypotheses

	declared non-significant	declared significant	total
True null hypotheses	U Correct	V Type I error	m_0
Non-true null hypotheses	T Type II error	S Correct	$m - m_0$
	$m - R$	R	m

Simple example for the hapo_metabolomics_2020:

We want to test the correlation of **all** metabolites in the data set with the value of FPG.

Conducting $m = 51$ tests independently we get $R = 28$ significant ones (at a 0.05 level). We can expect by chance 2-3 wrong discoveries.

How we “weed out” false discoveries depends on the type of error rate we choose and the approach to control it.

[BH-demo/BH-FDR-control-implementation.pdf at main · amuzikansky/BH-demo \(github.com\)](#)

Multiple Testing Type 1 Error Rates

- **Per comparison error rate (PCER):**

$$\text{PCER} = E(\mathbf{V}/m)$$

- **Per-family error rate (PFER):**

$$\text{PFER} = E(\mathbf{V}).$$

- **Family-wise error rate (FWER):**

$$\text{FEWR} = P(\mathbf{V} \geq 1)$$

- **Generalized FWER (k-FWER):**

$$\text{gFEWR}(k) = P(\mathbf{V} > k)$$

- **False discovery rate (FDR)**

$$\text{FDR} = E(\mathbf{V}/\mathbf{R}) = E(\mathbf{V}/\mathbf{R} \mid \mathbf{R} > 0) P(\mathbf{R} > 0)$$

- **Positive false discovery rate (pFDR)**

$$\text{pFDR} = E(\mathbf{V}/\mathbf{R} \mid \mathbf{R} > 0) \text{ - next week.}$$

	declared non-signifi cant	declared significant	total
True null hypotheses	U	V	m_0
Non-true null hypotheses	T	S	$m - m_0$
	$m - \mathbf{R}$	R	m

Controlling the Error Rate: Multiple Comparison Procedures (MCP)

- $\text{FWER} \leq 1 - (1 - \alpha)^m$ (strictly equal for independent tests)
- For $m=100$, $\text{FWER} = 99\%$ ($\alpha = 0.05$)
- MCP goal is to “control the probability of any type I error in families of comparisons under simultaneous consideration”.
- Many procedures have been developed to control FWER (Sidak, Dunnett, Scheffe, Tukey’s HSD, Hsu’s Best, etc.)
- Two general types of FWER correction:
 - Single-step procedure: each p-value gets the same adjustment - e.g. Bonferroni correction
{if each hypothesis is tested at α/m , $\text{FWER} \leq \alpha$ }
 - Sequential (step-up/step-down): broadly speaking, these are order based adjustments - e.g. Hochberg (1988), Holm-Bonferroni (2018), uniformly more powerful than single step procedures.
- Problems with MCP for FWER:
 - mostly assume test statistics are MVN (or t)
 - controlling FWER can be too stringent - depending on context, some false positive tests can be acceptable.
 - **can result in dramatic loss of power.**

Important properties of FDR

1. If all null hypothesis are true: $m_0 = m$

→ FDR is equivalent to FWER

$\{v = 0 \rightarrow v/r = 0$
 $v > 0 \rightarrow v/r = 1$
 $E(V/R) = 0 \cdot P(V=0) + 1 \cdot P(V \geq 1) = P(V \geq 1) = \text{FWER}\}$

Therefore controlling the FDR implies control of FWER
1. If $m_0 < m$

→ $\text{FDR} \leq \text{FWER}$

$\{v > 0 \rightarrow v/r < 1$
 $E(V/R) = E(V/R \mid v = 0) \cdot P(V=0) + E(V/R \mid V \geq 1) \cdot P(V \geq 1) \leq P(V \geq 1)\}$

Procedures controlling the FWER also controls FDR

	declared non-significant	declared significant	total
True null hypotheses	U	V	m_0
Non-true null hypotheses	T	S	$m - m_0$
	$m - R$	R	m

BH proposed approach to multiple testing: control the FDR

Let p_1, p_2, \dots, p_m be the set of p-values corresponding to the hypotheses H_1, H_2, \dots, H_m

To control the FDR at level q^* follow this procedure:

- i. order all p-values for the hypothesis tested from smallest to largest, that is, $p_{(1)} \leq p_{(2)} \leq \dots \leq p_{(m)}$
- ii. Let k be the largest value of i for which $p_{(i)} \leq (i / m)q^*$
- iii. reject all $H_{(i)}$, $i = 1, 2, \dots, k$

BH procedure control levels assumes **independent** test statistics.

Benjamini and Yekutieli expanded on the approach for cases of dependency

[The Control of the False Discovery Rate in Multiple Testing under Dependency. The Annals of Statistics, Aug., 2001, Vol. 29, No. 4 (Aug., 2001), pp. 1165-1188]

BH Example:

- A group of $m=15$ tests.
- Controlling FWER with Bonferroni - reject all hypotheses $< 0.05/15=0.0033$
- Controlling the FDR at $q^*=0.05 \rightarrow$

```
> pvec <- c(0.0001,0.0004,0.0019,0.0095,0.0201,0.0278,0.0298,0.0344,0.0459,  
+          0.3240,0.4262,0.5719,0.6528,0.7590,1.000)  
> round(cbind("pval"=pvec,  
+            'BH'=p.adjust(pvec,method='BH'),  
+            'bon'=p.adjust(pvec,method='bonferroni')),4)  
      pval    BH    bon  
[1,] 0.0001 0.0015 0.0015  
[2,] 0.0004 0.0030 0.0060  
[3,] 0.0019 0.0095 0.0285  
[4,] 0.0095 0.0356 0.1425  
[5,] 0.0201 0.0603 0.3015  
[6,] 0.0278 0.0639 0.4170  
[7,] 0.0298 0.0639 0.4470  
[8,] 0.0344 0.0645 0.5160  
[9,] 0.0459 0.0765 0.6885  
[10,] 0.3240 0.4860 1.0000  
[11,] 0.4262 0.5812 1.0000  
[12,] 0.5719 0.7149 1.0000  
[13,] 0.6528 0.7532 1.0000  
[14,] 0.7590 0.8132 1.0000  
[15,] 1.0000 1.0000 1.0000  
>
```

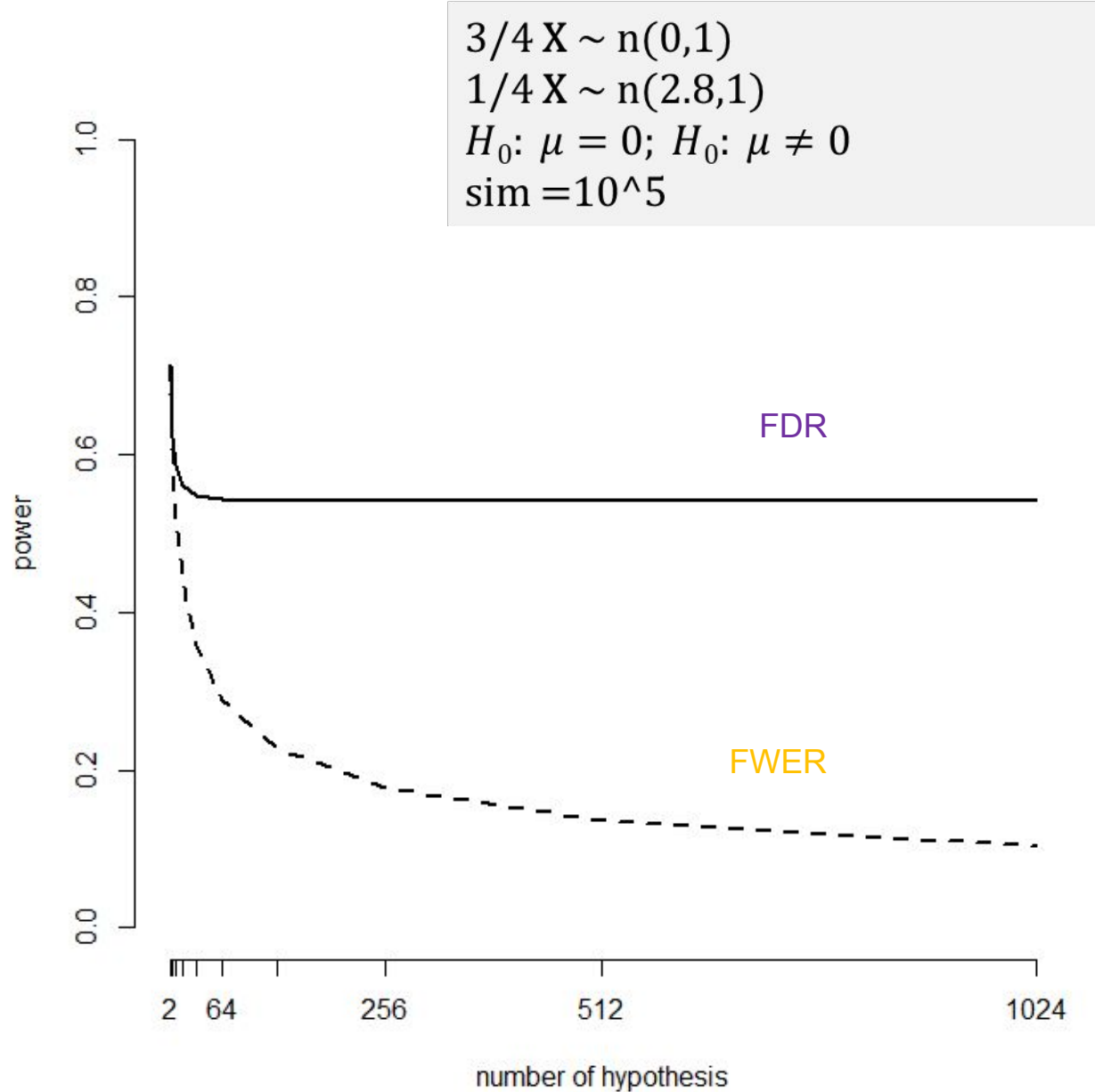
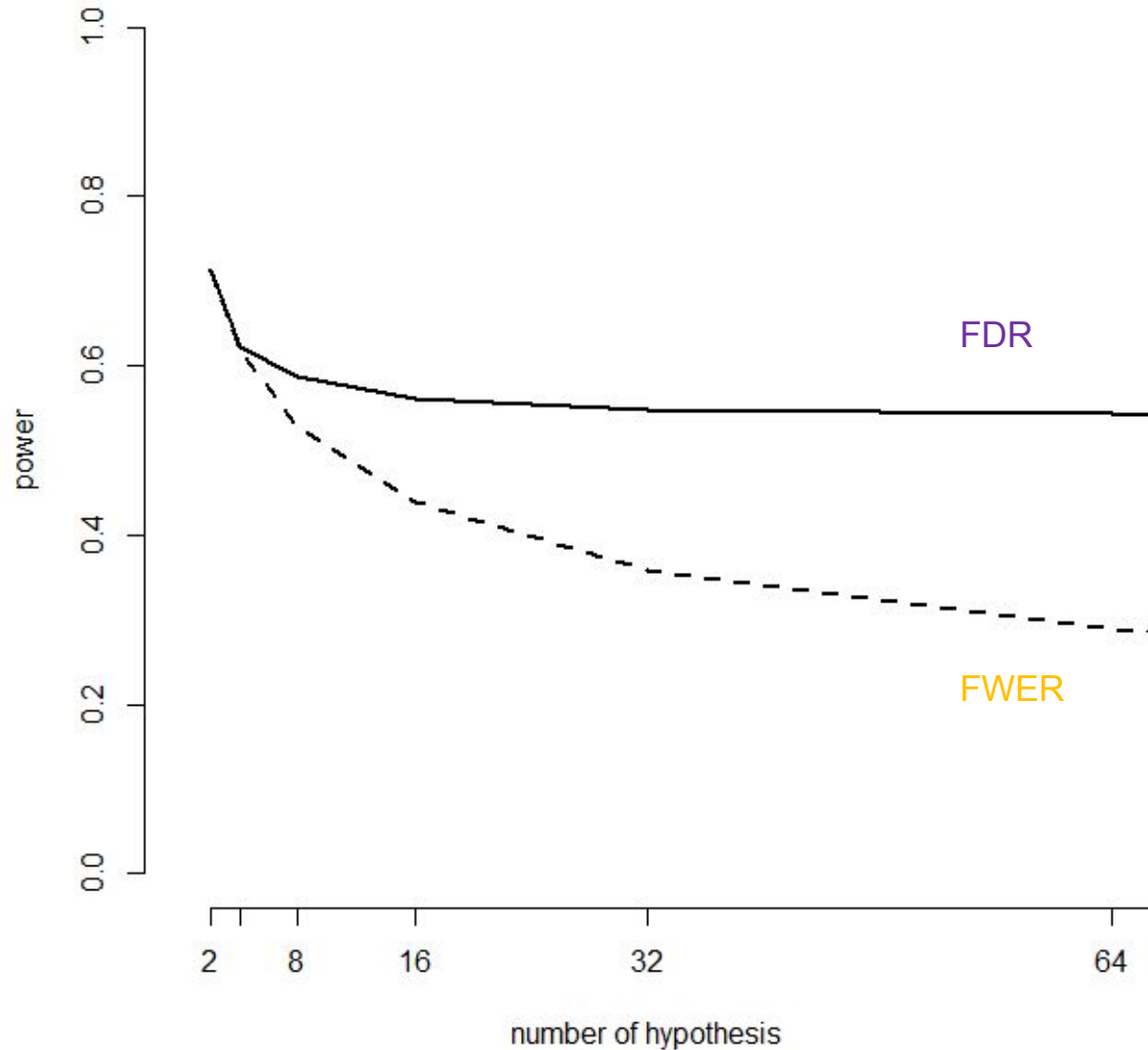
rank = i	$p_{(i)}$	$(i/m) q^*$	$q = p_{(i)} * m/i$
1	0.0001	0.0033	0.0015
2	0.0004	0.0067	0.003
3	0.0019	0.01	0.0095
4	0.0095	0.0133	0.0356
5	0.0201	0.0167	0.0603
6	0.0278		0.0695
7	0.0298		0.0639
8	0.0344		0.0645
9	0.0459		0.0765
10	0.3240		0.486
11	0.4262		0.5811
12	0.5719		0.714
13	0.6528		0.722
14	0.7590		0.813
15	1.000		1.000

[BH-demo/Demo2.pdf at main · amuzikansky/BH-demo \(github.com\)](#)

[control-implementation.pdf at main · amuzikansky/BH-demo \(github.com\)](#)

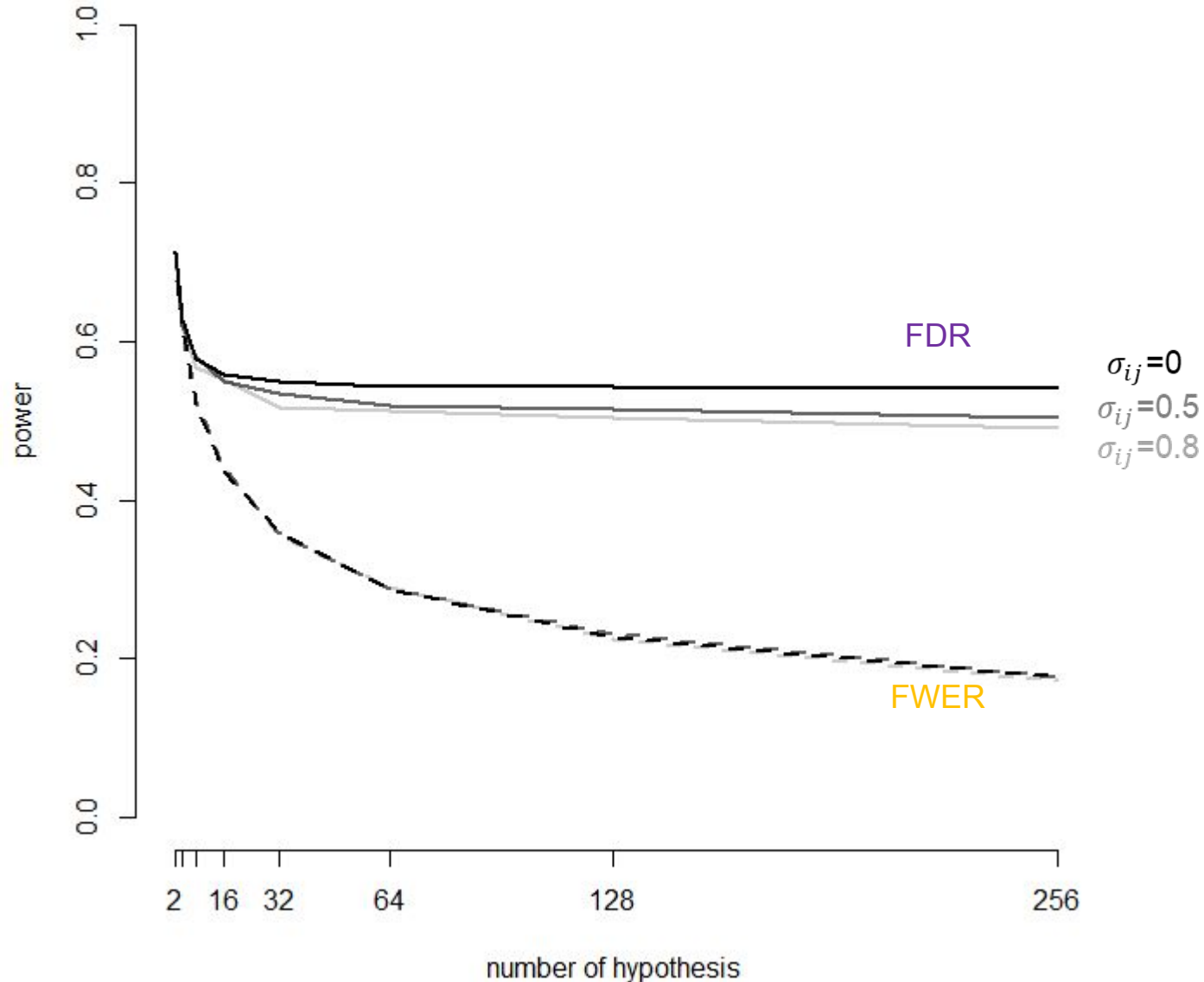
Simulation-based estimates of power

Independent hypothesis



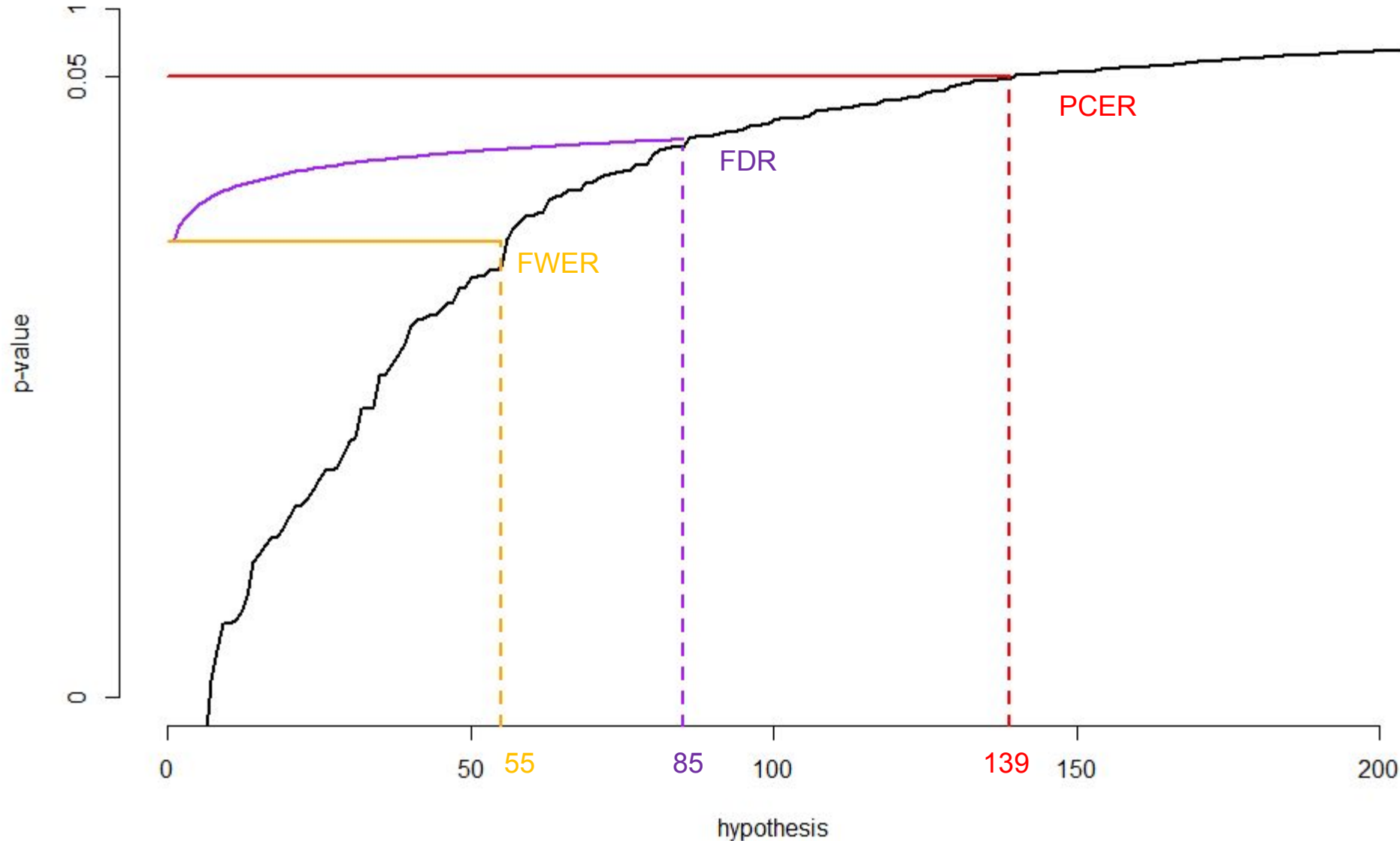
Simulation-based estimates of power

Correlated hypothesis



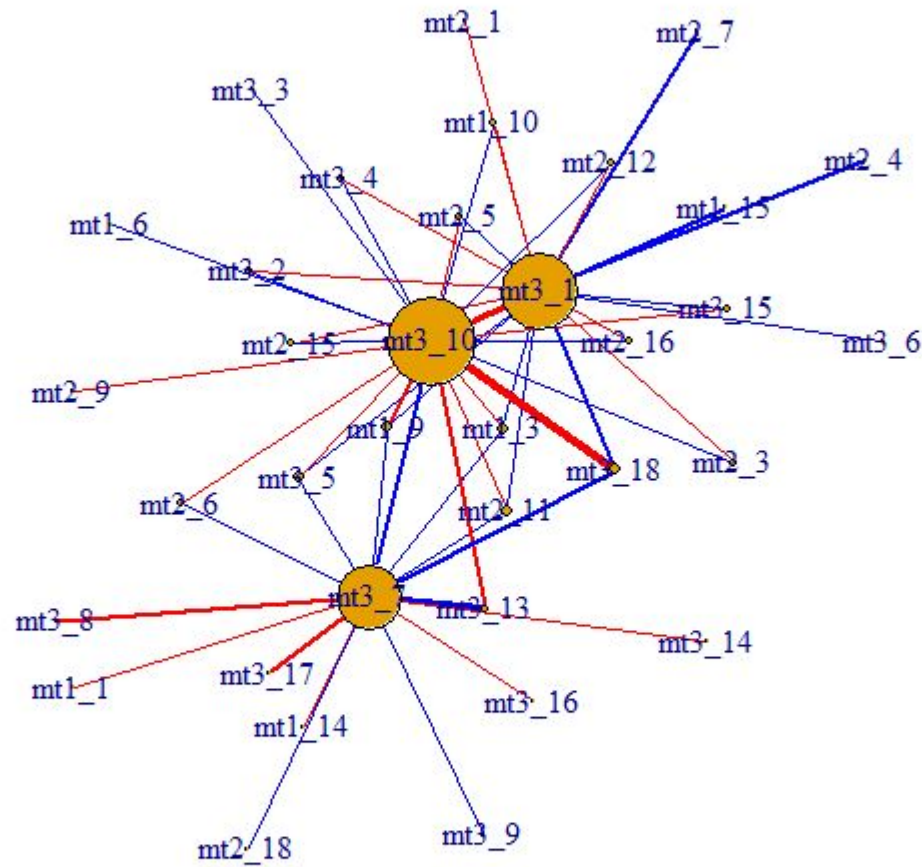
$X \sim \text{mvn}(\mu, \Sigma)$
 $3/4 \mu = 0$
 $1/4 \mu = 2.8$
 $\sigma_{ij} = 1$ for $i = j$
 $\sigma_{ij} = \{0, .5, .8\}$ for $i \neq j$
 $H_0: \mu = 0; H_0: \mu \neq 0$
 $\text{sim} = 10^4$

Differential Network Analysis (Kate's example)

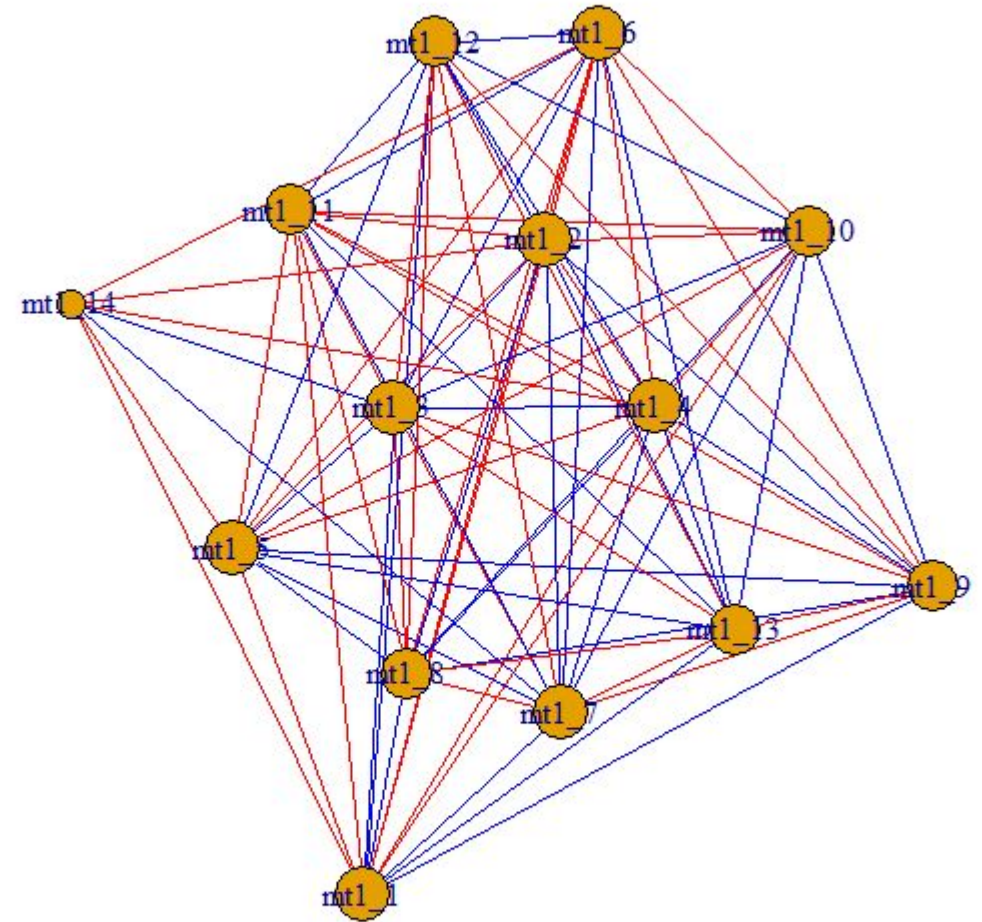


Determine which of the 1275 possible edges (51 choose 2) differs significantly between ancestry group 1 and ancestry group 2

Differential Network Analysis (Kate's example)



FWER (55)



FDR (85)

Conclusions

- FWER maybe ill-suited to
 - Large number of hypothesis
 - The null is unlikely to be true in many instances
- FDR is less stringent and more powerful
- There are improved FDR versions