## Benjamini-Hochberg method (1995) for "false discovery rate", http://www.jstor.org/stable/2346101;

implemented in Statistical Analysis of Microarrays (SAM) and BRBTOOLS from the National Cancer Institute's Biometric Research Branch.

## Number of errors committed when testing m null hypotheses

|   | Declared<br>non-significant | Declared<br>significant | Total         |
|---|-----------------------------|-------------------------|---------------|
| True null hypotheses Non-true null hypotheses | U<br>T                      | V<br>S                  | $m_0$ $m-m_0$ |
|   | $m - \mathbf{R}$            | R                       | m             |

B-H is a classical frequentist technique. False discovery rate could be defined as  $FDR = Q_e = E(\mathbf{Q}) = E\{\mathbf{V}/(\mathbf{V} + \mathbf{S})\} = E(\mathbf{V}/\mathbf{R})$ .

Here R = # declared significant.

What if R can equal 0? The  $Q_e$  will be infinite.

And when all null hypotheses are true, then all discoveries are false and FDR=1. Instead B&H define

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

The BH procedure is:

let 
$$k$$
 be the largest  $i$  for which  $P_{(i)} \leq \frac{i}{m}q^*$ ;  
then reject all  $H_{(i)}$   $i = 1, 2, ..., k$ .

Then FDR is no bigger than  $q^*$ .

Example: An randomized clinical trial of treatments rt-PA versus APSAC when myocardial infarction occurs. There are 15 different clinical endpoints. The 15 P values are ranked. Here are the first few with the critical cutoff values with q\*=0.05.

|        | 1      | 2      | 3      | 4      |        |        |        |     |      |
|--------|--------|--------|--------|--------|--------|--------|--------|-----|------|
| Pvalue | 0.0001 | 0.0004 | 0.0019 | 0.0095 | 0.0201 | 0.0278 | 0.0298 | ••• | 1    |
| cutoff | 0.0033 | 0.0067 | 0.0100 | 0.0133 | 0.0167 | 0.0200 | 0.0233 |     | 0.05 |

The first 4 hypotheses are "significant" with this rule. (In bold face)

Suppose we tweak the results. Decrease the 4th P value just a little:

|               | 1      | 2      | 3      | 4      | 5      |        |        |     |      |
|---------------|--------|--------|--------|--------|--------|--------|--------|-----|------|
| <b>Pvalue</b> | 0.0001 | 0.0004 | 0.0019 | 0.0095 | 0.0151 | 0.0278 | 0.0298 | ••• | 1    |
| cutoff        | 0.0033 | 0.0067 | 0.0100 | 0.0133 | 0.0167 | 0.0200 | 0.0233 |     | 0.05 |

Great, now the 5<sup>th</sup> is significant.

Now increase the 4<sup>th</sup> P value slightly:

|        | 1      | 2      | 3      | 4      |        |        |        |     |      |
|--------|--------|--------|--------|--------|--------|--------|--------|-----|------|
| Pvalue | 0.0001 | 0.0004 | 0.0019 | 0.0135 | 0.0151 | 0.0278 | 0.0298 | ••• | 1    |
| cutoff | 0.0033 | 0.0067 | 0.0100 | 0.0133 | 0.0167 | 0.0200 | 0.0233 |     | 0.05 |

Suddenly the 5<sup>th</sup> is ALSO not significant. Why not? Does this make sense? The data for the 5<sup>th</sup> test has not changed at all. That's typical that weird things happen in frequentist approaches to multiple comparisons. It's unsatisfying to many people.