

A decorative graphic on the left side of the slide, consisting of a network of white lines and small circles on a blue gradient background, resembling a circuit board or a neural network.

# THE BASICS OF MULTIPLE TESTING

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# RECAP: HYPOTHESIS TESTING

- Statistical method used to decide whether the data provides significant evidence to reject a hypothesis
- Null hypothesis ( $H_0$ ): a gene is NOT related to colon cancer
- Alternative hypothesis ( $H_1$ ): a gene is related to colon cancer
- Type 1 error (false positive): rejecting  $H_0$  when  $H_0$  is true
  - By construction, valid tests satisfy:  $P(\text{FP}) \leq \alpha$
- Type 2 error (false negative): failing to reject  $H_0$  when  $H_0$  is false

# WHAT IS MULTIPLE TESTING?

- Testing many hypotheses on the same dataset
  - Each hypothesis test has its own p-value ( $p_1, p_2, \dots$ )
- Ex: Genome-wide association studies (GWAS) with 278,869 SNPs
  - Each SNP is associated with a separate hypothesis

# THE BIG PROBLEM WITH DOING SO MANY TESTS

- If  $\alpha = 0.05$  for each test, then:
  - For one test  $\rightarrow$  5% chance of a false positive
  - For 20 independence tests  $\rightarrow$  chance of at least one FP  $\approx 1 - (1 - 0.05)^{20} \approx 0.64$ 
    - 64% chance of getting a wrong “significant” result?! TOO HIGH!
- The more tests you run, the more likely to “discover” something that’s just “random noise”
- Back to the GWAS example:
  - With a  $p < 0.05$  threshold, 13,943 false positives are expected even if no true associations exist.

# FWER OR FDR

- **Family Wise Error Rate (FWER):** Probability of making at least one FP among all tests
  - $\text{FWER} = P(\text{at least one } H_0^{(k)} \text{ rejected for } k = 1, 2, \dots, m \mid H_0^{(k)} \text{ true for all } k = 1, \dots, m)$
- **False Discovery Rate (FDR):** expected proportion of FP of the total number of positive findings (rejection of a null)
  - An FDR of 5% = among all discoveries (rejections of a null), 5% are expected to be FP (null is actually true)

# FWER OR FDR

- Controlling FWER is best for:
  - When you hope not to have any false positives (having FP too costly)
  - The # of hypotheses is small – controlling FWER is more conservative
- Controlling FDR is best for:
  - When you have a very large # of tests, and controlling FWER is too stringent
  - When some number of false positives is acceptable

# CONTROLLING FWER - BONFERRONI

- If given the significance level  $\alpha$  and  $k$  tests, then...
- Bonferroni-adjusted threshold  $\alpha^* = \alpha/k$
- Example:  $p_1 = 0.004$ ,  $p_2 = 0.021$ ,  $p_3 = 0.037$ ,  $p_4 = 0.056$ ,  $p_5 = 0.093$ ,  $\alpha = 0.05$ 
  - $\alpha^* = 0.05/5 = 0.01$
  - Before Bonferroni: reject  $H_1, H_2, H_3$
  - After Bonferroni: reject  $H_1$

# CONTROLLING FWER – HOLM'S STEP DOWN

- Given  $m$  hypotheses with p-values  $p_1, p_2, \dots, p_m$ 
  1. Order them from lowest to highest:  $p_{(1)} \leq p_{(2)} \leq \dots \leq p_{(m)}$  with hypotheses  $H_{(1)}, H_{(2)}, \dots, H_{(m)}$ 
    - Note: Not always  $p_1 \neq p_{(1)}$ 
      - Ex: If  $p_1 = 0.021, p_2 = 0.05, p_3 = 0.004$ , then  $p_{(1)} = p_3 \leq p_{(2)} = p_1 \leq p_{(3)} = p_2$
  2. For each p-value from lowest to highest, test whether  $p_{(k)} \leq \alpha/(m+1-k)$
  3. If so, reject  $H_{(k)}$ , otherwise EXIT
  4. Continue to examine the next large p-value until EXIT or last p-value is examined
    - If  $p_{(1)} \leq \alpha/m$ , reject  $H_{(1)}$  and continue, otherwise EXIT
    - If  $p_{(2)} \leq \alpha/(m - 1)$ , reject  $H_{(2)}$  and continue, otherwise EXIT
    - And so on...



# CONTROLLING FWER – HOCHBERG'S STEP UP

- Similar procedure as Holm's, but instead of starting from the smallest p-value, we begin from the **largest** p-value
  - If  $p_{(m)} \leq \alpha$ , reject  $H_{(m)}$  and below and EXIT, otherwise continue
  - If  $p_{(m-1)} \leq \alpha/2$ , reject  $H_{(m-1)}$  and below and EXIT, otherwise continue
  - And so on...

# CONTROLLING FDR – BENJAMINI-HOCHBERG

- Given  $m$  hypotheses with p-values  $p_1, p_2, \dots, p_m$ 
  1. Order them from lowest to highest:  $p_{(1)} \leq p_{(2)} \leq \dots \leq p_{(m)}$  with hypotheses  $H_{(1)}, H_{(2)}, \dots, H_{(m)}$
  2. Choose a target FDR level/desired FDR threshold (e.g.  $\alpha = 0.05$ )
  3. For each p-value from lowest to highest, test whether  $p_{(k)} \leq (k * \alpha)/m$
  4. If so, reject  $H_{(k)}$ , otherwise EXIT
  5. Continue to examine the next large p-value until EXIT or last p-value is examined
    - If  $p_{(1)} \leq \alpha/m$ , reject  $H_{(1)}$  and continue, otherwise EXIT
    - If  $p_{(2)} \leq 2\alpha/m$ , reject  $H_{(2)}$  and continue, otherwise EXIT
    - And so on...

# CONCLUSION

- Here, we have discussed a few methods for controlling FWER or FDR:
  - FWER – Bonferroni, Holm's, Hochberg's
  - FDR – Benjamini-Hochberg
- These corrections allow us to make more meaningful statements when we conduct many hypothesis tests.
- There are many, *MANY* more methods out there!
- Some methods will take into account **dependence** between hypotheses, hypotheses conducted **sequentially**, and many other situations.