Midterm Proposals

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Overview

- 16 projects
- 10 singles, 6 pairs
- Wide range:
 - Medicine (microbiome, lung cancer, genetics)

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- Environment (seafood, global warming)
- Sports (basketball and baseball)
- Conflict predictions in the Congo
- Police killings
- University rankings
- Virtual Architecture
- Digital humanities
- Natural language processing
- Linear smoothers
- Finance

Overview

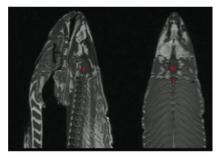
- Very creative, some a bit too ambitious
- Try to start simple, and make it more complicated as you go along
- Do it stepwise, so that you always know which step doesn't work
- Otherwise, in the end you won't know where the problem is, and you'll have to start from scratch

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A Dead Fish Can See

- Scientists put a dead fish in a fMRI scanner
- They measured brain activation of the dead fish while showing photos of human faces

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Source: Bennet et al. (2009)

- What happened? Random noise from scanner
- The problem is that we are testing around 130,000 voxels in a typical fMRI scan

- Using the common significance level $\alpha = 0.05$, we will see 6,500 discoveries just by chance alone
- We have to adjust for this multiple testing problem
- Here are the common tools and R functions
- For detailed treatment take for instance Stats 300C

• We have four types of outcomes in multiple testing:

	H_0 accepted	H_0 rejected	Total
H ₀ true	U	V	<i>n</i> ₀
H_0 false	Т	S	<i>n</i> – <i>n</i> ₀
	n-R	R	n

- ► U, V, S, T are unobserved random variables
- R is an observed random variable
- Familywise Error Rate: Classical multiple comparison procedures aim to control

$$\mathsf{FWER} = P(V \ge 1)$$

- Holm's procedure is not as conservative as Bonferroni; we typically make more rejections (have more power)
- Holm's procedure can always be used instead of Bonferroni

- The FWER makes sense when we are testing a small number of hypotheses
- For example, in comparing six or ten different treatments, it is very reasonable to control the probability of returning even one ineffective treatment
- If we are testing millions of hypotheses at once, for example in genome-wide association studies, and making a false discovery is not the end of the world
- We prefer to return some false positives along with many potentially interesting genes, because this enables scientists to follow these leads and to distinguish the important genes from the false discoveries

	H_0 accepted	H_0 rejected	Total
H_0 true	U	V	<i>n</i> 0
H_0 false	Т	S	$n - n_0$
	n-R	R	n

False discovery proportion (FDP):

$$\mathsf{FDP} = egin{cases} V/R & ext{if } R \geq 1 \ 0 & ext{otherwise} \end{cases}$$

- ▶ We observe R, we do not observe V, and so FDP is an unobserved random variable
- False Discovery Rate controls the expectation

$$FDR = E(FDP)$$

- Consider what it means to control FDR: if we repeat our experiment many times, on average we control the FDP
- This is not a statement about our individual experiment, and does not say much about the chance of having our FDP exceed a certain threshold
- FWER, on the other hand, does control for an individual experiment

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Reproducible Reserach

- Create a github repository for your project
- Do version control every day
- Keep track of everything
- Do all the anlaysis in a Rmd
- Never try out things without writing them down in a script!

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Some examples: (link)

References

- Candes (2016). Lecture Notes (link)
- R function: p.adjust
- Bennet et al. (2009). Salmon Poster. (link)

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