

Hypothesis testing and statistical tests

MOL518, Lecture #11

Outline

- What is a statistical test?
- p -values
- Types of statistical tests
- Multiple hypothesis testing

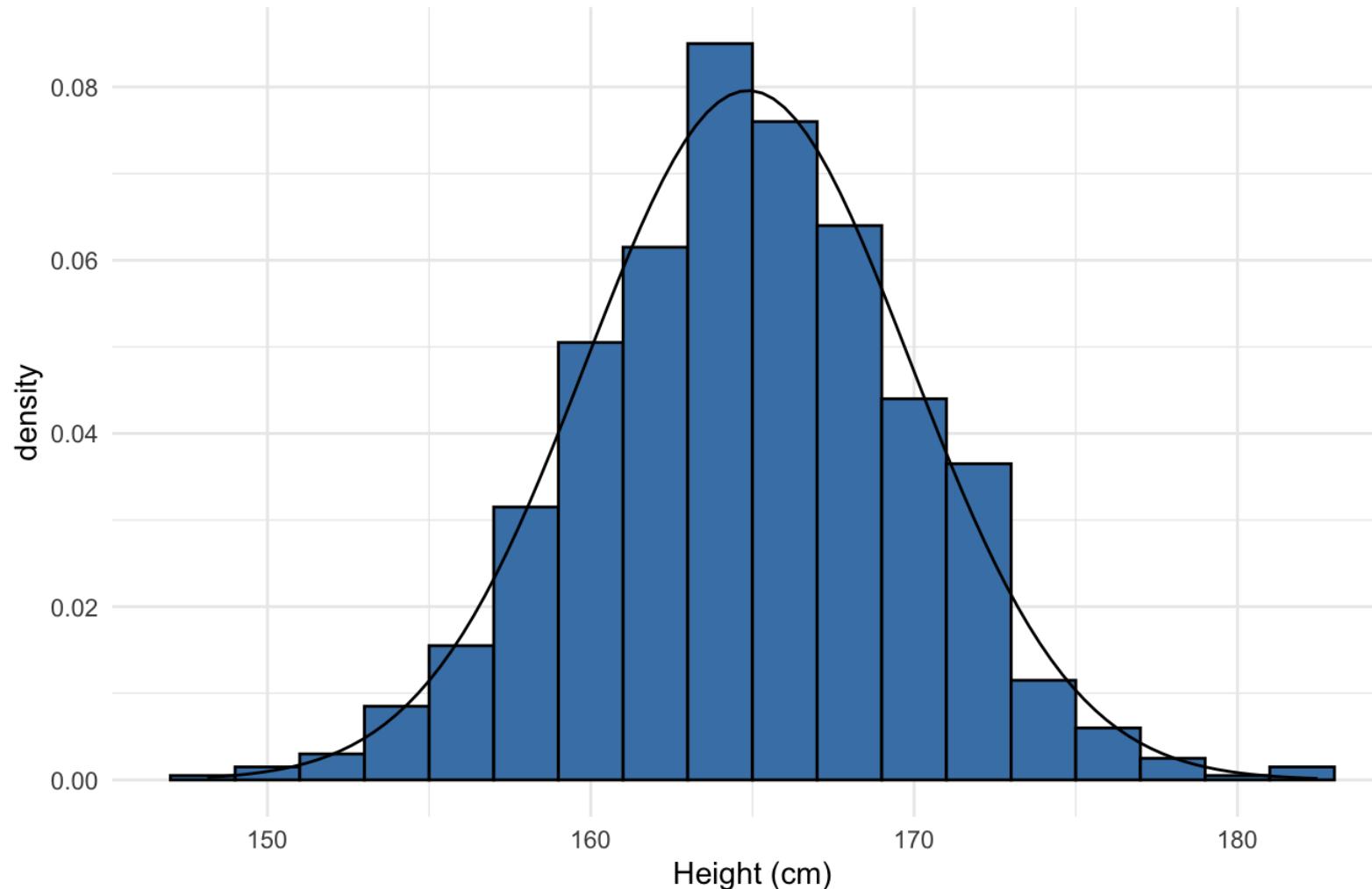
Two motivating problems for today

- Assume we have a gene with two alleles, Y and y
- Is the gene under selection, or segregating randomly?
- Assume we have a wild-type (x_1) and a mutant (x_2) bacterium and want to compare the expression level of a GFP reporter
- How do we compare GFP expression between these groups x_1 and x_2 ?

Introducing histograms!

Histogram of adult height and normal curve

N = 1000, mean = 164.87, variance = 25.13



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What is a statistical test?

- Statistical tests allow us to decide whether the data support a particular hypothesis (typically we construct null and alternative hypotheses):
- Null hypothesis examples:
 - The coin is fair
 - The gene is not under selection
 - The mutation **does not affect** GFP expression
- Alternative hypothesis examples:
 - The coin is biased
 - The gene is under selection
 - The mutation **does affect** GFP expression

A very simple example

- Suppose we measure 10 pea plants, and all of them are green (yy)
- Null hypothesis is that yy should occur with probability 0.25: $(1/2)*(1/2)$
- $P(10 \text{ green}) = 0.25^{10} \approx 10^{-6}$
- This is very unlikely, so we can safely reject the null hypothesis
- It gets hard to directly compute probabilities for larger sample sizes and more complex distributions

How do we perform a statistical test?

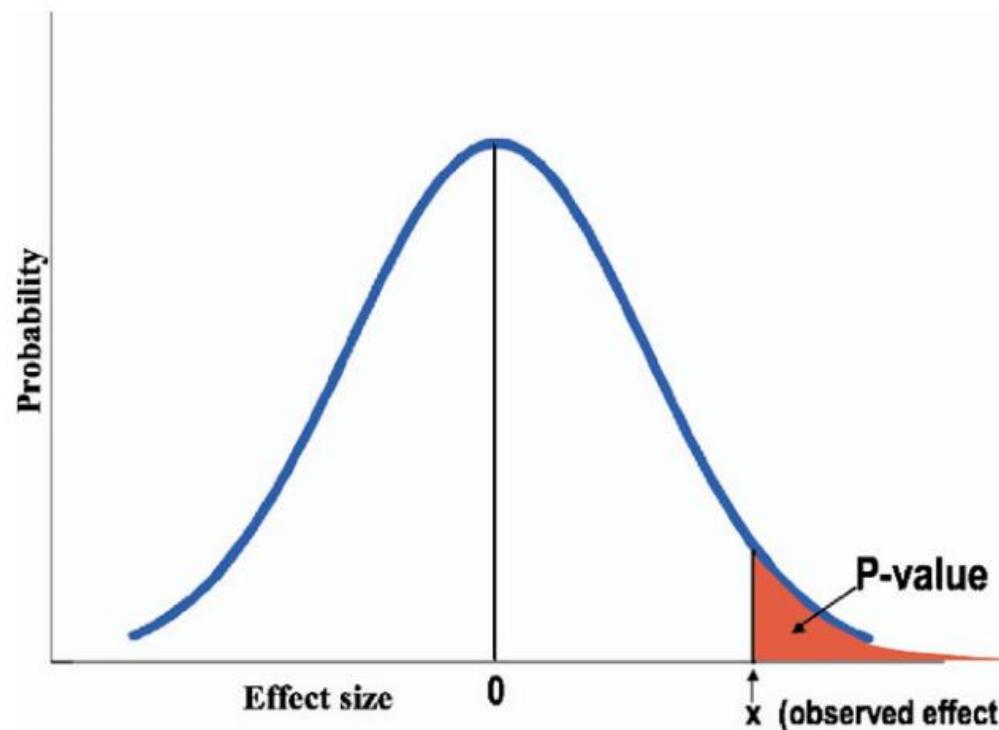
1. Define a null hypothesis (and typically an alternative hypothesis)
 - Goal is to reject the null hypothesis (we cannot prove the alternative hypothesis!)
2. Select a relevant statistical test with a test statistic T
3. Select a significance level α (maximum acceptable false-positive rate), typically 5% or 1%
4. Using the data, compute the test statistic and the p -value
5. Reject the null hypothesis if $p \geq \alpha$

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What is a *p*-value?

- Mathematical definition: $p = P(\text{Data}|\text{Null})$
- Not just probability of the observed data, but also for more extreme data!



How do we interpret a *p*-value?

- Common misconceptions:
 - Probability the null hypothesis is true (Fisher himself got this wrong!)
 - Non-significance (e.g. $p > 0.05$) means there is no difference between groups
 - Statistical significance equals importance
- Actually, context matters:
 - What is the effect size?
 - What is the sample size?

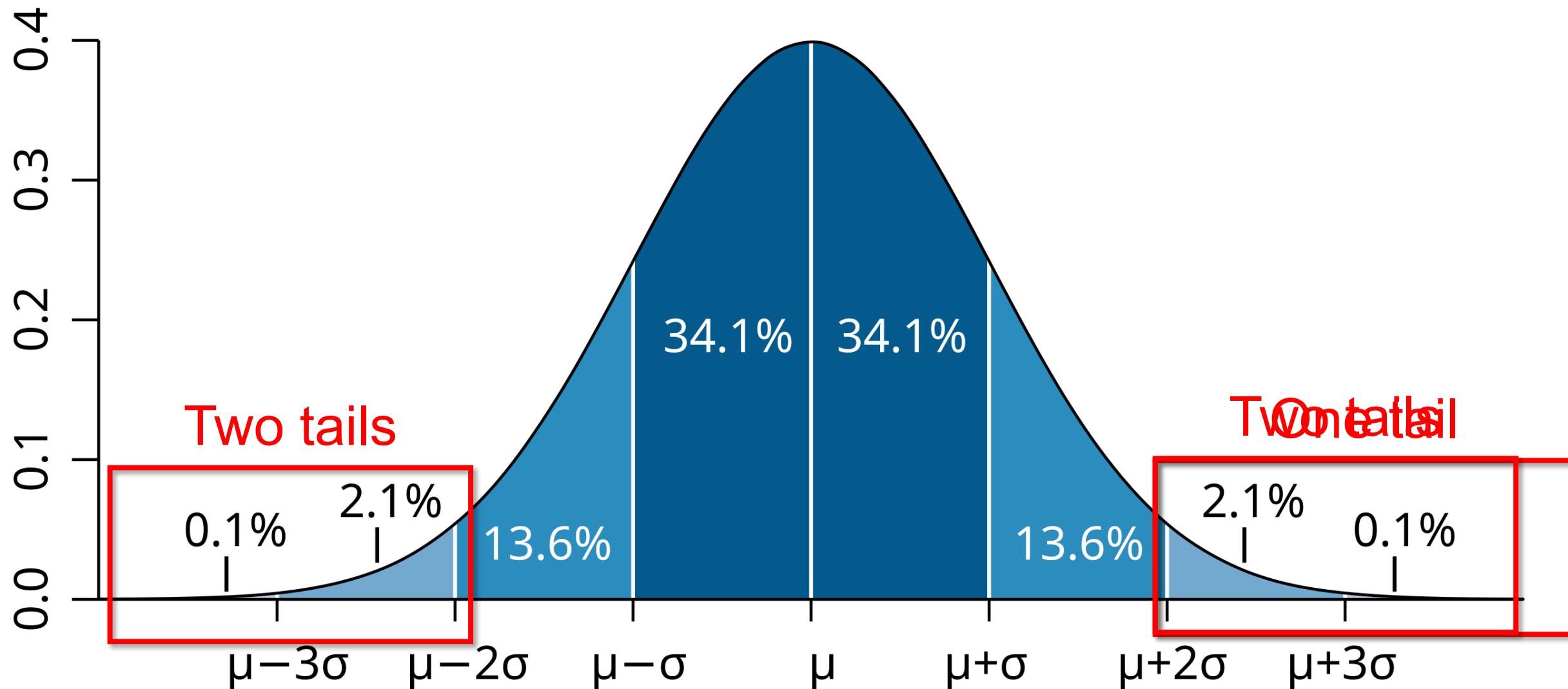
Scientists are obsessed with $p < 0.05$

<u>P-VALUE</u>	<u>INTERPRETATION</u>
0.001	
0.01	
0.02	HIGHLY SIGNIFICANT
0.03	
0.04	
0.049	SIGNIFICANT
0.050	OH CRAP. REDO CALCULATIONS.
0.051	ON THE EDGE
0.06	OF SIGNIFICANCE
0.07	HIGHLY SUGGESTIVE,
0.08	SIGNIFICANT AT THE $p < 0.10$ LEVEL
0.09	
0.099	HEY, LOOK AT
≥ 0.1	THIS INTERESTING SUBGROUP ANALYSIS

p-values can be one-tailed and two-tailed

- One-tailed: consider the possibility that a coin is biased towards **heads**
 - Two-tailed: consider the possibility that a coin is biased towards **heads or tails**
-
- One-tailed: consider that the mean of the mutant is **greater than** the wild-type
 - Two-tailed: consider that the mean of the mutant could be **greater or less than** the wild-type

Visualizing one- vs. two-tailed p-values



When should you use one vs. two tails?

- It depends on the outcomes you are interested in
- Often in science we care about both significant increases *and* decreases
- Examples:
 - A mutation could cause a GFP reporter to go up or down
 - Selection for a gene could be positive or negative
 - A treatment could make a disease better or worse(!)
- One-tailed tests should be used only if the distribution has a single tail:
 - Exponential
 - Chi-squared test

Some key caveats to remember

- No statistical test is perfect, we expect false-positive results some fraction of the time
- A 5% significance threshold is totally arbitrary
- Significance testing does not consider the effect size!
- As a result, significance testing (and p values) are somewhat controversial

Defining one more term: SEM

- Standard error of the mean, or SEM
- $s = \frac{\sigma}{\sqrt{N}}$, where σ is the standard deviation and N is the sample size
- **SEM is a weighted standard deviation based on sample size!**
- SEMs are useful for estimating the mean of a distribution, which is critical for performing statistical tests

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Some common univariate statistical tests in biology

- *t*-tests are useful for normal distributions
 - Unpaired (Student's) *t*-test
 - Welch's *t*-test
 - Paired *t*-test
- Chi-squared test
 - Useful for proportions or frequencies
- Rank-based tests:
 - Useful when the data are not normal!
 - Mann-Whitney U test (non-parametric analogue of unpaired *t*-test)
 - Wilcoxon signed-rank test (non-parametric analogue of paired *t*-test)

The unpaired (Student's) t -test compares the means of two datasets

- Assumptions:
 - Data (x_1, x_2) are normally distributed
 - x_1, x_2 have equal variances
 - However, it's not too sensitive to these assumptions if the distributions are the same, and the sample sizes are similar between groups
- Null hypothesis: **Equal means**
- Alternative hypothesis: **Different means**
- Formula for equal n : $t = \frac{\bar{x}_1 - \bar{x}_2}{\text{SEM}(x_1, x_2)}$
- Denominator is basically a pooled SEM

Welch's t -test does not require equal variances

- Assumptions:
 - Data (x_1, x_2) are normally distributed
 - ~~x_1, x_2 have equal variances~~
- Null hypothesis: **Equal means**
- Alternative hypothesis: **Different means**
- Formula: $t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s_{\bar{x}_1}^2 + s_{\bar{x}_2}^2}}$, where s denotes the SEM of x_1 and x_2
- **Denominator is not based on pooled data!**

Paired t -tests are great for before and after measurements

- Assumptions:
 - Data (x_1, x_2) **are paired** (therefore have same sample size)
 - Differences $d = x_1 - x_2$ are normally distributed; check with a histogram
- Null hypothesis: **Mean difference is zero**
- Alternative hypothesis: **Mean difference is not zero**
- Formula: $t = \frac{\bar{d}}{s_d}$
- Increased power relative to a standard t -test because each sample now has 2 measurements; cost is having to do 2x the measurements

What if my data are not normal!?!?!

- Other approaches:
 - Bootstrapping
 - Rank-based statistical tests
- Bootstrapping resamples your data (with replacement) many times and computes e.g. the mean from the resampled data!
- Then, make a histogram
- Still requires **independence** and a **large sample size**
- Trade-offs:
 - It's computationally intensive, compared to other methods
 - Bootstrapping is largely empirical so some statisticians don't like it

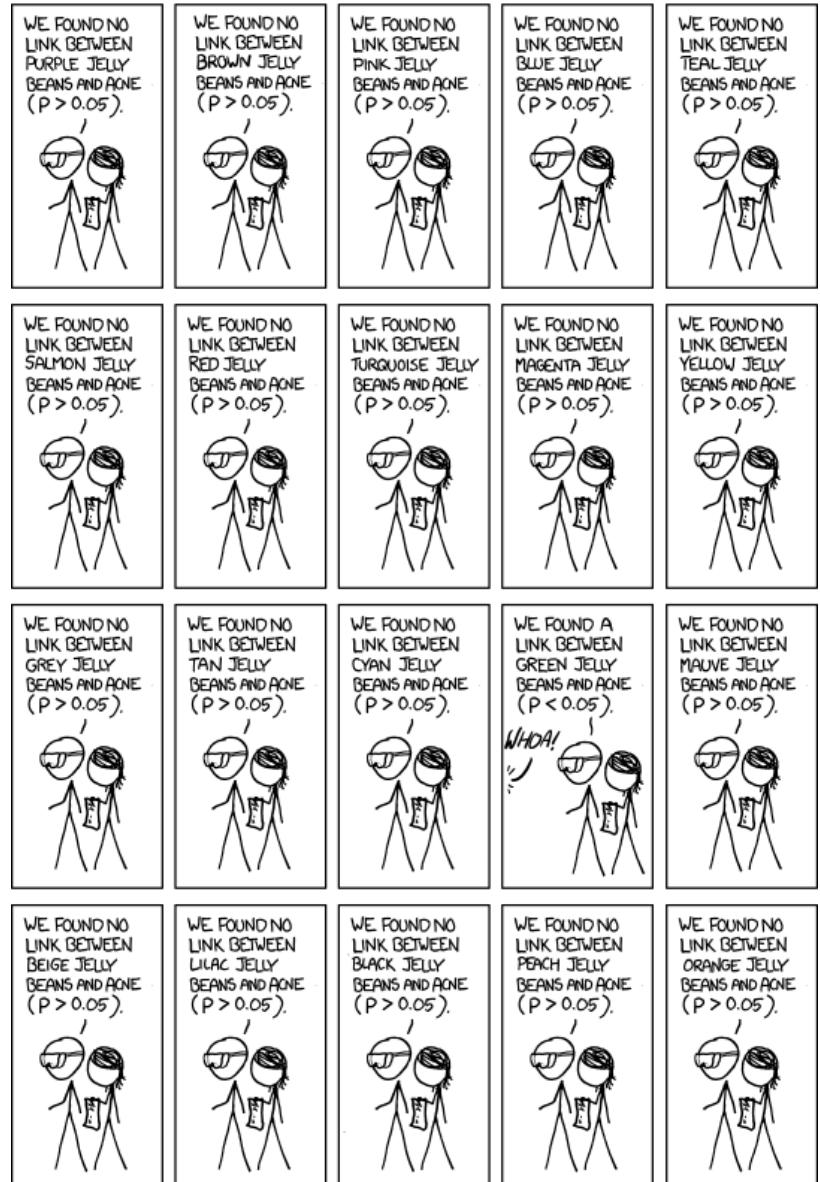
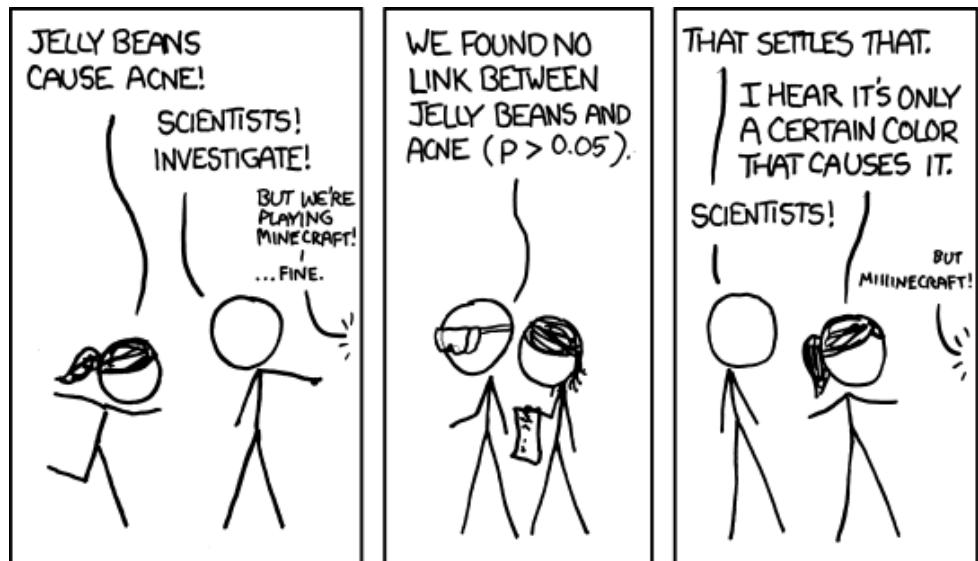
Rank-based tests

- Convert each number in your dataset to a rank (e.g. 1, 2, 3, 4...)
- Perform statistics on the ranks rather than the actual data(!)
- **This is basically a test for the median rather than the mean!!!**
- However, you sacrifice some power by converting the data to ranks
- Null hypothesis: distributions are identical
- Alternative hypothesis: distributions are not identical
- Still requires independence

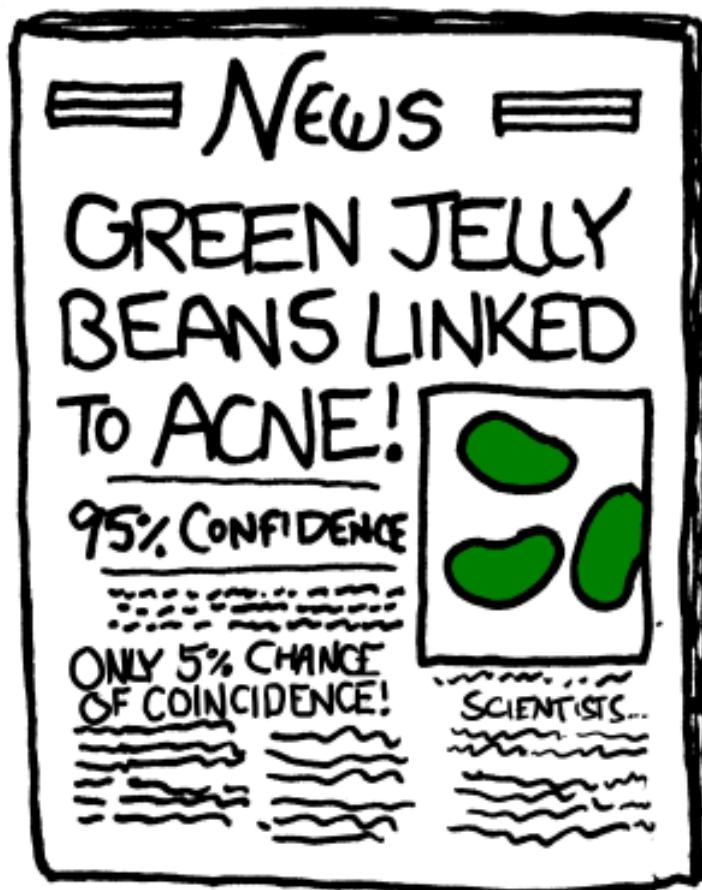
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A poignant example



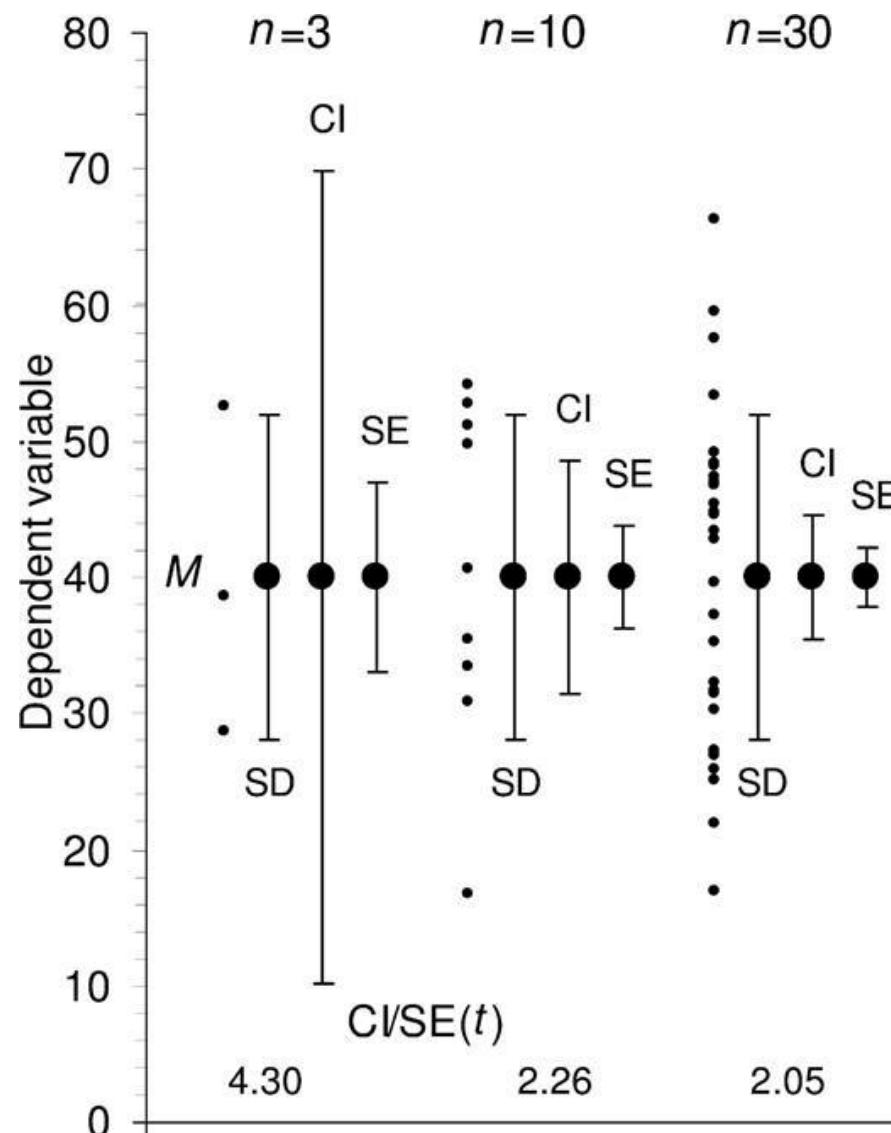
A poignant example



There are several ways to correct for this

- The Bonferroni correction:
 - When performing m tests, divide α by m
 - e.g. for ten tests, use $p < 0.005$
- Instead of adjusting α , you can also adjust p (multiply it by m)
- Other corrections let you specify a false discovery rate independent of α :
 - Benjamini-Hochberg procedure
 - Many other methods
- This will be discussed further in the genomics unit

Reading for next time: Error Bars



Extra Slides