Stat 145, Wed 10-Mar-2021 -- Wed 10-Mar-2021 Biostatistics Spring 2021

Wednesday, March 10th 2021

Wk 6, We

Topic:: P-values

Topic:: Randomization distributions

From Hesterberg & Chihara:

This is the core idea of statistical significance or classical hypothesis testing—to calculate how often pure random chance would give an effect as large as that observed in the data, in the absence of any real effect. If that probability is small enough, we conclude that the data provide convincing evidence of a real effect.

Randomization distributions: first look

Various distributions:

- A sampling distribution gives the values a sample statistic can take, and their (relative) frequencies. It depends on
 - the population (from which samples are taken)
 - the statistic in question (just what we are computing from the sample: perhaps \overline{x} , \widehat{p} , etc.)
 - the size *n* of samples
- A **null distribution** arises in the context of hypothesis testing. It is
 - like a sampling distribution: it relies on computing a particular sample statistic, from random samples of a particular size n.
 - even more difficult to pin down than a sampling distribution, as it must obey the null hypothesis.
- A randomization distribution uses simulated draws from the original sample to approximate the null distribution.

Some scenarios

Board overview is like that for generating a bootstrap distribution. We

- 1. draw a new sample, called a randomization sample, using data in the original sample, and
- 2. compute a **randomization statistic** from the randomization sample.

Repeating Steps 1 and 2 many (several thousand?) times, and plotting the randomization statistics that arise from Step 2, produces a randomization distribution.

• Case: univariate binary categorical data

Our null hypothesis: \mathbf{H}_0 : $p = p_0$, (p_0 is some number).

• **Case**: bivariate data from independent samples, one binary categorical variable (explanatory; indicates group), other variable is quantitative (response)

Our null hypothesis: \mathbf{H}_0 : $\mu_1 - \mu_2 = 0$, (described as "no effect").

Example¹ Six mice are divided randomly into two groups, with 3 given a drug and the other 3 acting as a control group. Afterward, all 6 mice are timed as they navigate a maze. Let μ_D , μ_C represent the mean finishing time for two populations, mice under the influence of the drug, and mice not so influenced. Suppose the 3 "drug" mice finish in 30, 25 and 18 seconds, while the 3 "control" mice finish in 20, 21, and 22 seconds.

```
mice <- data.frame(time=c(30,25,18,20,21,22), grp = c(rep("Drug",3),rep("Control",3)))
mice

time grp

1 30 Drug
2 25 Drug
3 18 Drug
4 20 Control
5 21 Control
6 22 Control
7

To = (30,25,18,20,21,22), grp = c(rep("Drug",3),rep("Control",3)))

Parameters

A

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```

We look at sample means and their difference:

```
mean(time ~ grp, data=mice) # shows the sample means for the 2 groups

Control Drug
21.00000 24.33333

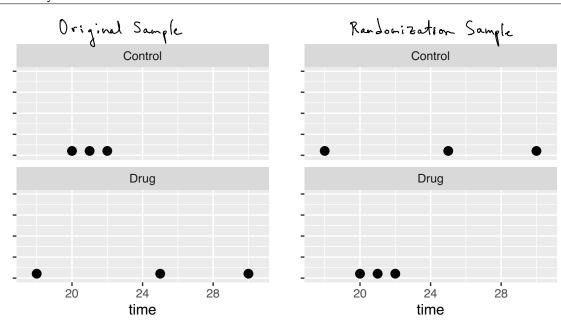
diffmean(time ~ grp, data=mice) # finds the difference in sample means

diffmean
3.3333333
```

Q: What is this difference of means a point estimate for?

In the picture that follows, the left side shows dot plots of time by treatment group as in the actual sampled data. The right side shows dot plots of time by group for a randomization sample.

¹Taken from Chapter 3 of "Mathematical Statistics With Resampling and R", by Chihara and Hesterberg.



• Case: bivariate data, both (explanatory and response) variables are quantitative, and a linear assocation appears plausible

Our null hypothesis: \mathbf{H}_0 : $\rho = 0$.