Independent Samples $t$ tests

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Background for Independent Samples $t$ test

- In the case of the paired samples $t$ test, we were testing to see if there was a mean difference between two dependent samples.
- MEANING these two means were dependent upon a single sample from which they were drawn. The only thing that was different was the two timepoints.
- In the independent samples $t$ test, we will be comparing the means from two samples which are independent from each other.
- For example, males vs. females, one ethnicity vs. another ethnicity, or students in a treatment vs. students in control.
**H_0** for Independent Samples *t* test

- It is typical that we are trying to detect a mean response change for our different independent samples, although this is not always the case.
- Sometimes, we may want to make sure that our two samples (males and females) have similar mean performance on some instrument.
- Regardless, we test:
  
  \[ H_0 : \mu_1 = \mu_2 \]

- However, since we only have sample approximations of the population mean \( \mu \), we state:
  
  \[ H_0 : \bar{X}_1 = \bar{X}_2 \]

- assuming \( \bar{X}_1 \) and \( \bar{X}_2 \) are random samples drawn from \( \mathcal{N}(\mu_1, \sigma_1^2) \) and \( \mathcal{N}(\mu_2, \sigma_2^2) \) distributions.
Calculating $t$ in the Independent Samples Case

- The calculation of $t_{calc}$ is somewhat different from the paired samples case since our two samples are independent.

$$t_{calc} = \frac{\bar{x}_2 - \bar{x}_1}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

- where $s_j^2$ is the squared standard deviation for group $j$.
- We have additional assumptions to the independent samples case. The most notable is the idea of homogeneity of variance.
- This assumption states that:

$$\sigma_1^2 = \sigma_2^2$$

- The easiest way to do this is through `var.test` (discussed later).
Independent Samples $t$ test in R

```r
> cholest <- data.frame(chol = c(245, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 185, 205, 160, 170, 180, 190, 200, 210, 165), gender = rep(c("female", "male"), c(12, 8)))
> str(cholest)
'data.frame': 20 obs. of 2 variables:
$ chol : num 245 170 180 190 200 210 220 230 240 250 ...  
$ gender: Factor w/ 2 levels "female","male": 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ... 

> boxplot(chol ~ gender, cholest, ylab = "Cholesterol Score")
```
Checking Assumptions of Normality

```r
> par(mfrow = c(1, 2))
> qqnorm(cholest$chol[cholest$gender == "male"],
+       main = "QQNorm for the Males")
> qqnorm(cholest$chol[cholest$gender == "female"],
+       main = "QQNorm for the Females")
```

QQNorm for the Males

QQNorm for the Females
Checking Assumptions of Homogeneity of Variance

- The homogeneity of variance assumption states that the variances of the two independent groups is equal or
  \[ H_0 : \sigma_1^2 = \sigma_2^2 \]
- Because our assumption is that the sample variances are equal we do NOT want to reject this \( H_0 \).
- We can test this assumption with a simple \( F \) test

```r
> var.test(chol ~ gender, cholest)

  F test to compare two variances
  data:  chol by gender
  F = 2.508, num df = 11, denom df = 7, p-value = 0.2319
  alternative hypothesis: true ratio of variances is not equal to 1
  95 percent confidence interval:
  0.5325486 9.4267443
  sample estimates:
  ratio of variances
  2.508021
```
> t.test(chol ~ gender, cholest)

Welch Two Sample t-test
data:  chol by gender
t = 2.7197, df = 17.984, p-value = 0.01406
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
  6.824267 53.175733
sample estimates:
mean in group female  mean in group male
    215           185

• In this case, we would reject the $H_0$ that the mean cholesterol of the females $= \text{the mean cholesterol of the males}$ at the $\alpha = 0.05$ level.
Cohen’s $d$ for the Independent Samples $t$ test

- We have already computed statistical significance through the `t.test` and we found statistically significant results ($p = 0.014$).
- In order to compute “practical” significance, we compute Cohen’s $d$:

$$d = \frac{\bar{X}_1 - \bar{X}_2}{s}$$

- where $s$ is the standard deviation of either group since they are assumed equal.
- Others argue that $s$ should actually be a measure of pooled variance and defined:

$$s = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2}}$$
Glass $\Delta$ Effect Size

- $\Delta$ is typically used in studies where the mean comparison is between some treatment and control.
- For this case, Glass regards the second group as the “control” group and thus defines the effect size as:

$$\Delta = \frac{\bar{X}_1 - \bar{X}_2}{s_2}$$

- where $s_2$ is the standard deviation of the control group.
- This serves to standardize all future treatment effects to a common control group.
- For our “male/female” data, this measure makes little sense.
Hedge’s $g$

- Hedge’s $g$ is very similar to $d$ in that it uses a pooled measure of $s$.
- In this case, $g$ is defined as:

$$g = \frac{X_1 - X_2}{s^*}$$

$$s^* = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

$$= \sqrt{\frac{SS_1 + SS_2}{n_1 + n_2 - 2}}$$
Computing the Effect Size of Our Data

```r
> with(cholest, tapply(chol, gender, mean))

female  male
  215  185

> with(cholest, tapply(chol, gender, sd))

female  male
   30.22642  19.08627

> with(cholest, tapply(chol, gender, length))

female  male
     12      8
```

- Given the above calculations, we can compute the following
- Cohen’s $d$ with female $sd = (215 - 185)/30.23 = 0.992$
- Cohen’s $d$ with male $sd = (215 - 185)/19.09 = 1.572$
- Cohen’s $d$ with pooled $sd = (215 - 185)/25.099 = 1.195$
- Glass’s $\Delta = (215 - 185)/19.09 = 1.572$
- Hedge’s $g = (215 - 185)/26.457 = 1.134$