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 μ, we state:

$$H_0 : \overline{X}_1 = \overline{X}_2$$

- assuming $\overline{X}_1$ and $\overline{X}_2$ 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.

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

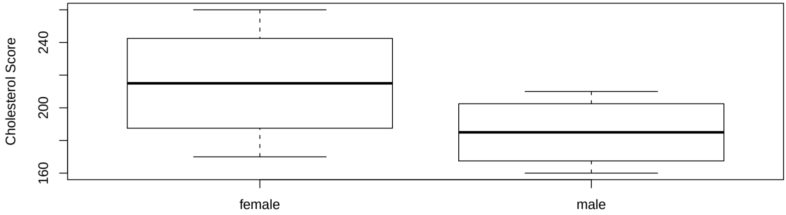
- where s_j^2 is the squared standard deviation for group j.
- We have additional assumptions to the independent samples case. The most notable is the idea of homogeneity of variance.
- This assumption states that:

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

- The easiest way to do this is through `var.test` (discussed later).

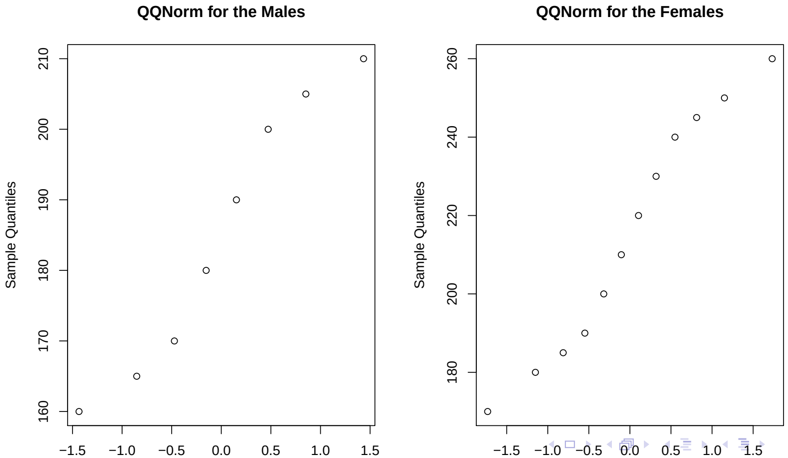
Independent Samples t test in R

```
> 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("f
+       "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 ...

> boxplot(chol ~ gender, cholest, ylab = "Cholesterol Score")
```



Checking Assumptions of Normality

```
> 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")
```



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

```
> 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
```

Running the t test

```
> 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 $=$ 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:

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

- 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 Δ Effect Size

- Δ 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:

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

- 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 is uses a pooled measure of s.
- In this case, g is defined as:

$$
\begin{aligned}
g &= \frac{\overline{X}_1 - \overline{X}_2}{s*} \\
s* &= \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}} \\
&= \sqrt{\frac{SS_1 + SS_2}{n_1 + n_2 - 2}}
\end{aligned}
$$

Computing the Effect Size of Our Data

```
> 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 calcualtions, 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 $g = (215 - 185)/26.457 = 1.134$