To determine whether our mixed effects model is significant, we need to know whether it differs from what we'd expect if Condition didn't influence Reaction Times.

```
mixed_model_null <- lmer(rt ~ (1 | subject) + (1 | item), data = fulldata)</pre>
```

• This model which we call mixed_model_null removes Condition as a predictor - in other words, it simply contains our random effects.

We can now compare the two models with each other using the anova function:

> anova(mixed_model, mixed_model_null)

This performs a likelihood ratio test on our 2 models and tells us whether they are significantly different from each other - this test only works with **nested** models - i.e., when one model is a subset of the other.