

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.

```

> anova(mixed_model, mixed_model_null)
refitting model(s) with ML (instead of REML)
Data: fulldata
Models:
mixed_model_null: rt ~ (1 | subject) + (1 | item)
mixed_model: rt ~ condition + (1 | subject) + (1 | item)

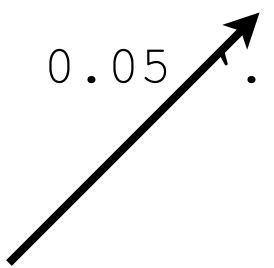
```

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
mixed_model_null	4	1336.4	1346.8	-664.18	1328.4				
mixed_model	5	1303.8	1316.8	-646.91	1293.8	34.534		1	4.19e-09 ***

```

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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



This is the important bit as the chi-squared test tells us whether our models differ from each other. It does. Note the AIC, BIC, and deviance values are all lower for the model with our fixed effect.

Note, deviance equals the residual sum of squares in linear models.