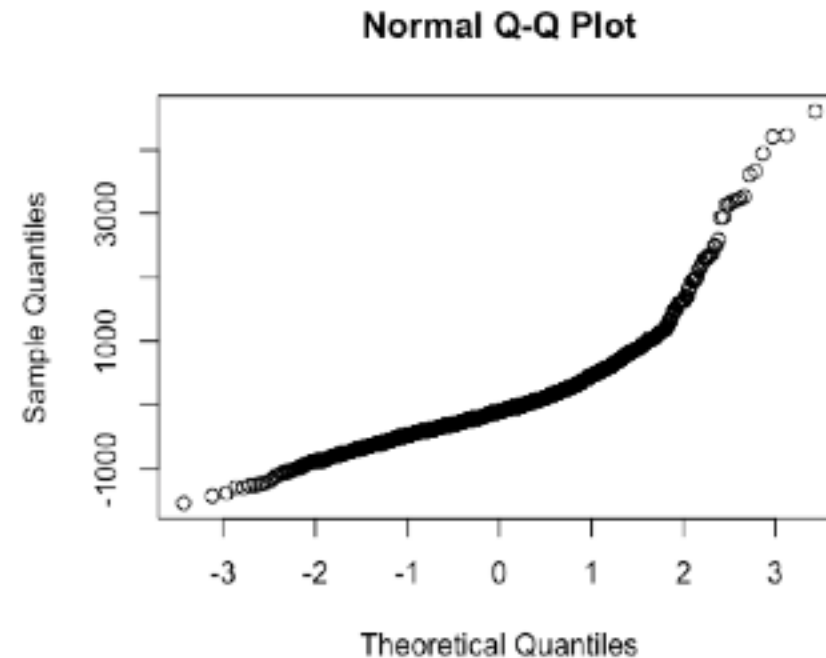


- Normality test on the model residuals from the untransformed data:

```
> qqnorm(residuals(model.full))
> shapiro.test(residuals(model.full))
```

Shapiro-Wilk normality test

```
data: residuals(model.full)
W = 0.84583, p-value < 2.2e-16
```

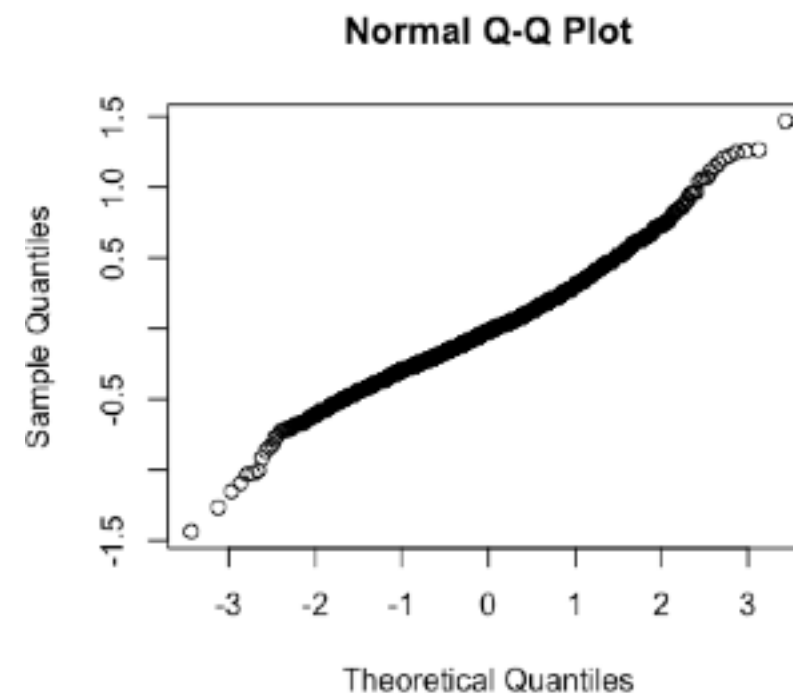


- Normality test on the model residuals from the log transformed data:

```
> model.full <- lmer (log(RT) ~ Sentence*Context + (1+Sentenc
e*Context|Subject) + (1+Sentence*Context |Item), data=DV, REM
L=TRUE)
> qqnorm(residuals(model.full))
> shapiro.test(residuals(model.full))
```

Shapiro-Wilk normality test

```
data: residuals(model.full)
W = 0.98321, p-value = 4.626e-13
```



- **Also need to check the residuals at the random effects level using the `ranef()` function to extract the random effects parameters.**

```
model.full <- lmer(RT ~ Context * Sentence + (1 + Context + Sentence | Subject) +  
                  (1 + Context + Sentence | Item), data = DV, REML = TRUE)
```

```
qqnorm(residuals(model.full))  
summary(model.full)
```

```
# checking residuals  
r_int <- lme4::ranef(model.full)$Subject$(Intercept) `  
qqnorm(r_int)  
qqline(r_int)
```

```
r_slope <- lme4::ranef(model.full)$Subject$Context1  
qqnorm(r_slope)  
qqline(r_slope)
```

```
r_slope <- lme4::ranef(model.full)$Subject$Sentence1  
qqnorm(r_slope)  
qqline(r_slope)
```

- **This is for a crossed design - for nested random effects the above code will need a little modification...**