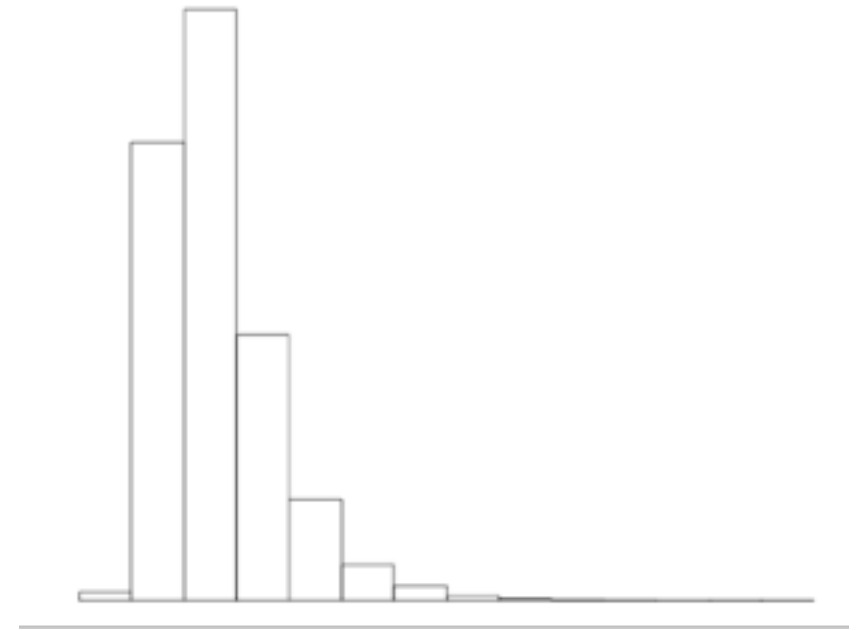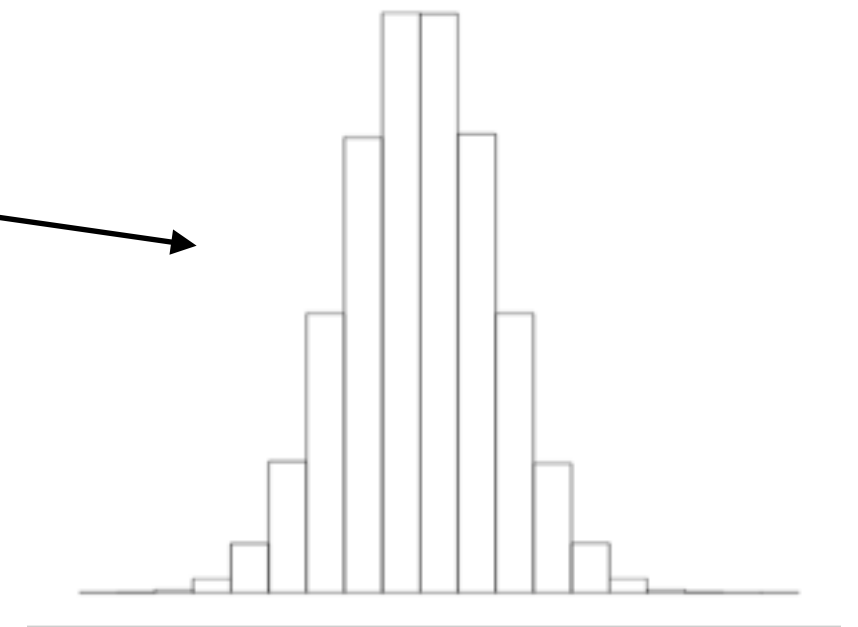# Log transform

Typically, RT data are non-normal and
more often the DV looks like this.

We can log transform our DV to
approximate something that looks a bit more
like the normal distribution (could also look
at inverse RT). But there are risks around
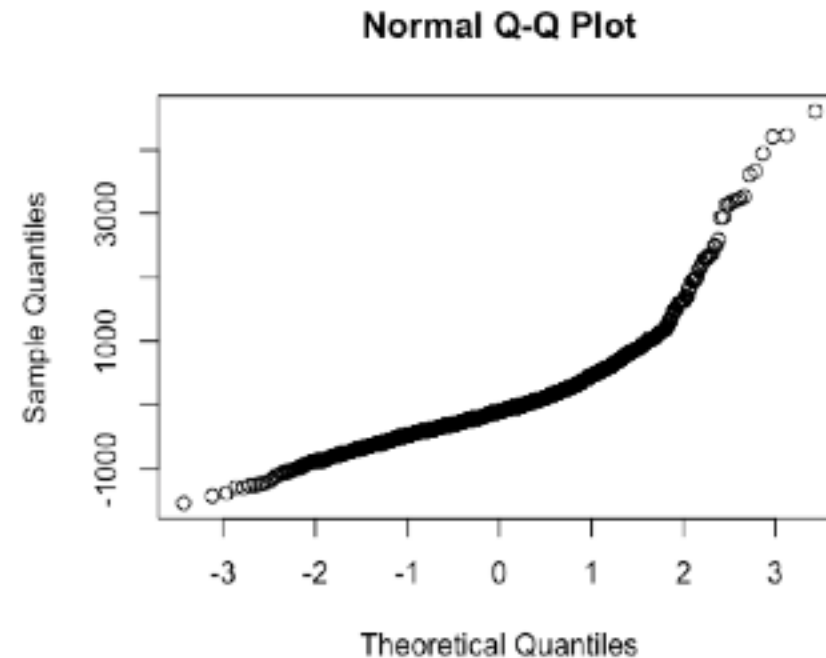transforming data (Lo & Andrews, 2015)

- 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
```


Normal Q-Q Plot

- 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
```


Normal Q-Q Plot