

- Standard linear model assumes a normal distribution of residuals. In the *generalised* linear mixed model, we can assume a distribution in our model that doesn't involve a normal distribution. We have already looked at the binomial.
- Gamma distribution is another possibility (see Kliegl et al. 2010, Lo & Andrews, 2015, for discussion).

```
model1 <- glmer(RT ~ Sentence*Context + (1+Sentence*Context|Subject) + (1+Sentence*Context|Item), data=DV, family=Gamma)
summary(model1)
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	7.28232	0.06731	108.20
Sentence1	0.02284	0.07679	0.30
Context1	0.04276	0.01701	2.51
Sentence1:Context1	-0.10806	0.03403	-3.18

t-value of the
interaction larger than
in previous analysis.

So what to do?

- In this example, all three analyses told basically the same story - there is an effect in our interaction term. They differ in terms of the value of the t-statistic associated with testing this.
- It's an issue - but if each possible way of analysing the data (incl. log transform and GLMM under the Gamma distribution) produces the same story, probably don't need to worry too much.
- Key is to be transparent in the write-up (did you transform the data? If so, how? What distribution do you assume your data come from?). **Most importantly, publicly archive your data and analysis code so it can be examined by others.**