

# Today

- Model checking: likelihood and Bayesian
- Good model for DGP?
  - are our assumptions good?
- Can we improve the model?
- After: please take a moment to do FCQ

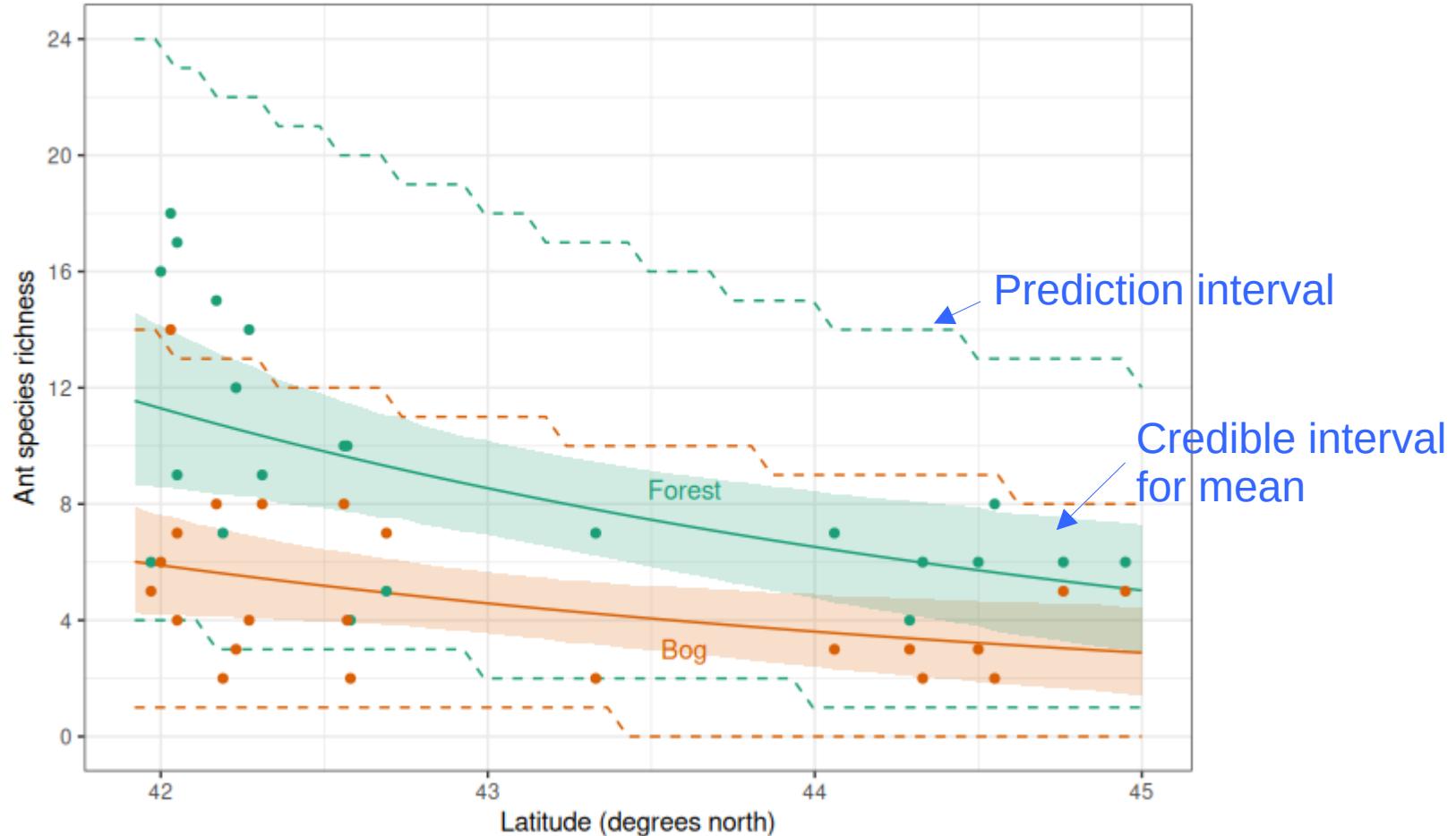
# Thursday

- Prerecorded lecture:
  - model comparison
  - intro to cross validation, key algorithm for machine learning
- Individual project meetings

# Week 16

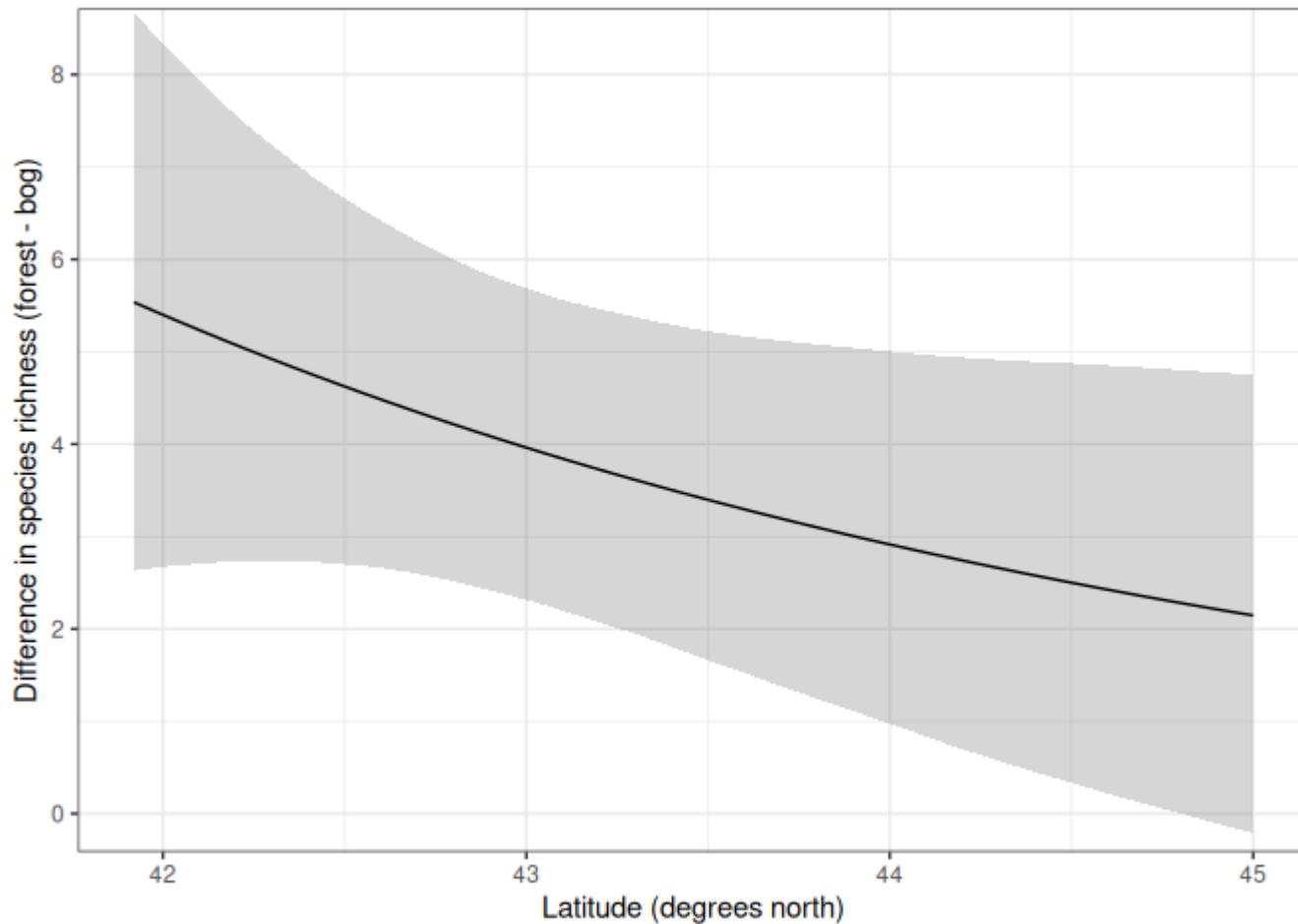
- The missing week
  - Populate with material for self study
- Thu: 4-7 PM “exam”
  - presentations

# Bayes ants



# Bayes ants

How different is species richness between habitats?



# Model checking

- Not much advice (in literature) for general likelihood approaches
- Not commonly done for non-standard models (i.e. not standard regression)
- Examining diagnostics is standard practice for linear Normal models
- It should be standard for all models!

# Model checking: issues

- Systematic departures of the deterministic skeleton from the data
- Poor stochastic distribution(s)
- Mistakes in data
- Outliers
- Influential data points

# What are the issues?

- **Systematic departures** of the deterministic skeleton from the data
  - e.g. proposed biological model is linear whereas the true model is nonlinear
- **Poor stochastic distribution(s)**
  - e.g. proposed error distribution is Normal whereas the true error distribution is lognormal

# What are the issues?

- **Mistakes** in the data
  - Incorrect entries, broken instruments etc
  - Rule of thumb: 1-5% of data points
- **Outliers**
  - Data points that lie unexpectedly far from the prediction
  - Could be mistakes (oops)
  - Could be biological exceptions (interesting)

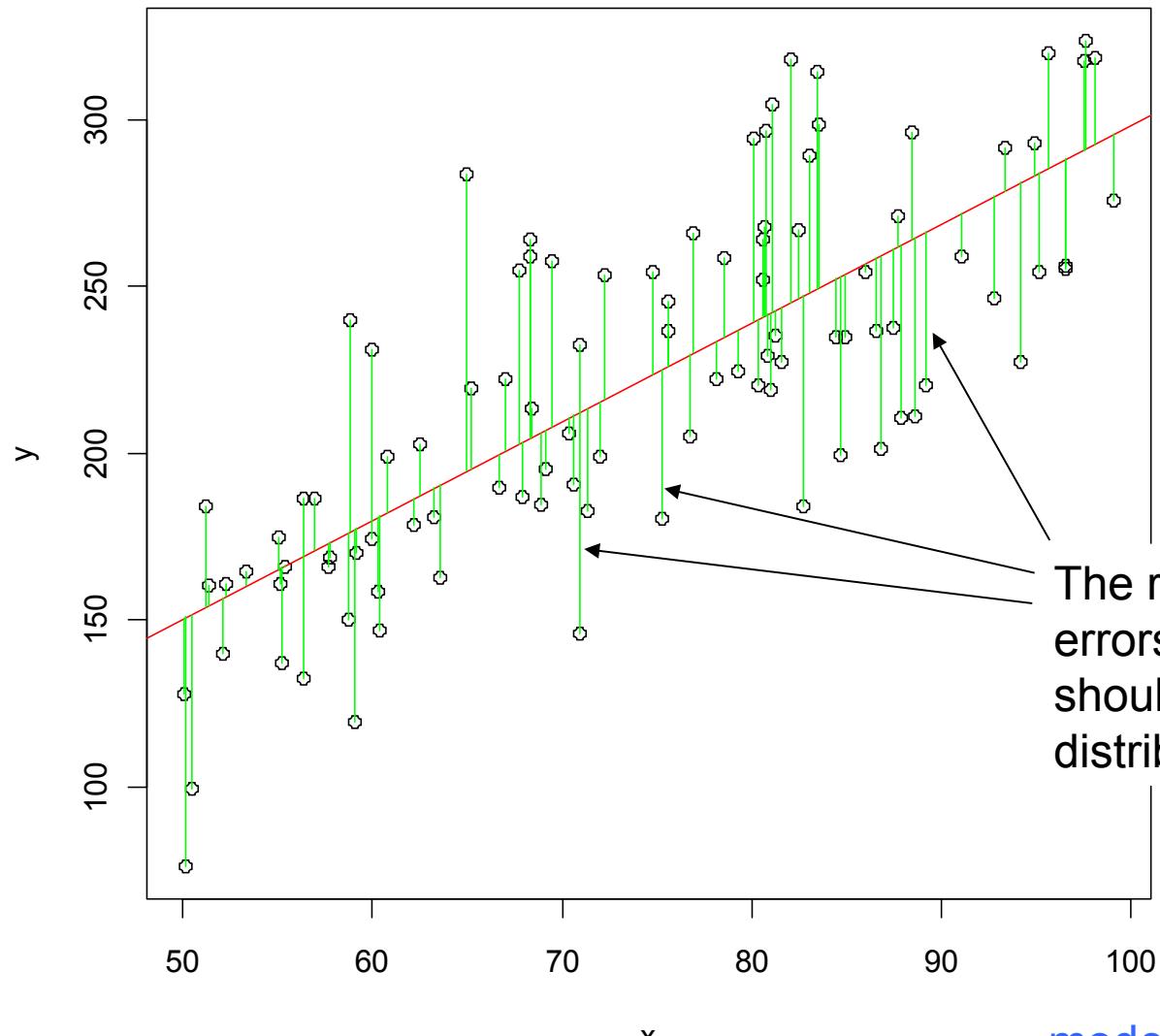
# What are the issues?

- Influential data points
  - Data points that cause markedly different parameter estimates

# Tools

- Plot the fitted model with the data
- Generative model check
  - simulate data using the fitted model
- Residuals vs fitted values
- QQ plot, histogram of residuals
- Leave one out (LOO) influence algorithm
- How can I know what to look for in a diagnostic plot?
  - Simulate it! Make diagnostic plots for simulated data using the fitted model

# Normal likelihood diagnostics

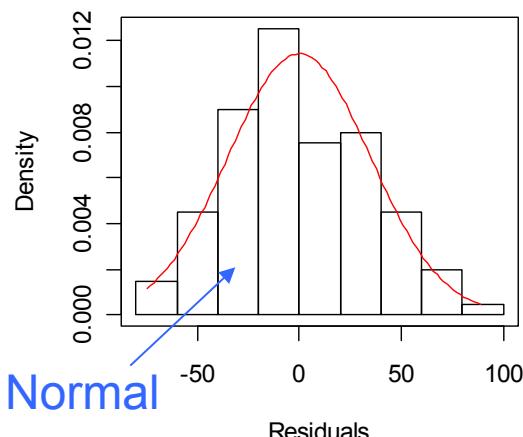


Linear regression

The residuals are the errors. This is what should have a Normal distribution.

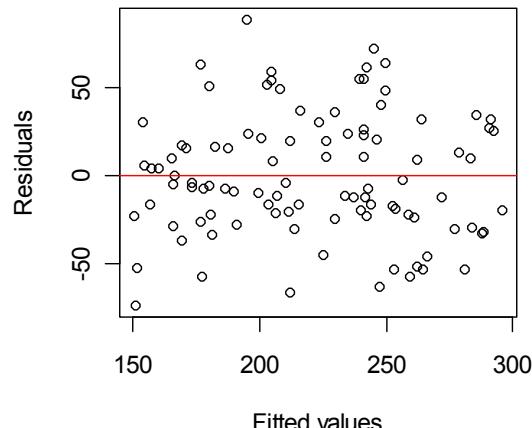
# Normal likelihood diagnostics

Histogram of residuals



Looks Normal

Residuals vs fitted

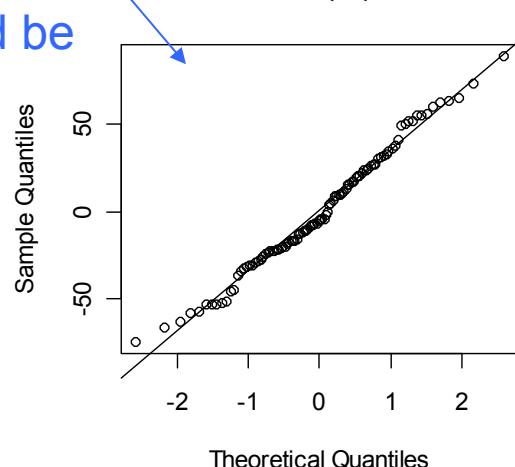


Linear regression

This is what it should look like

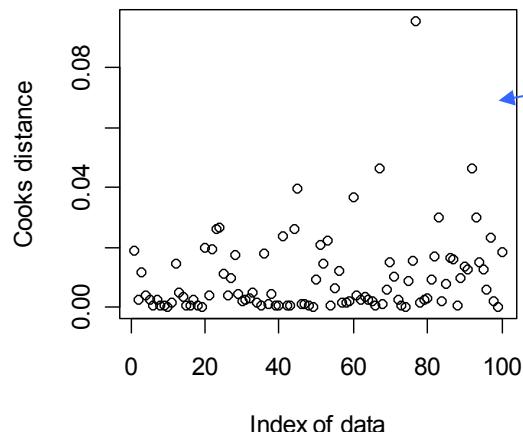
A special plot for the Normal distribution

Normal Q-Q Plot



Should be linear

Influence

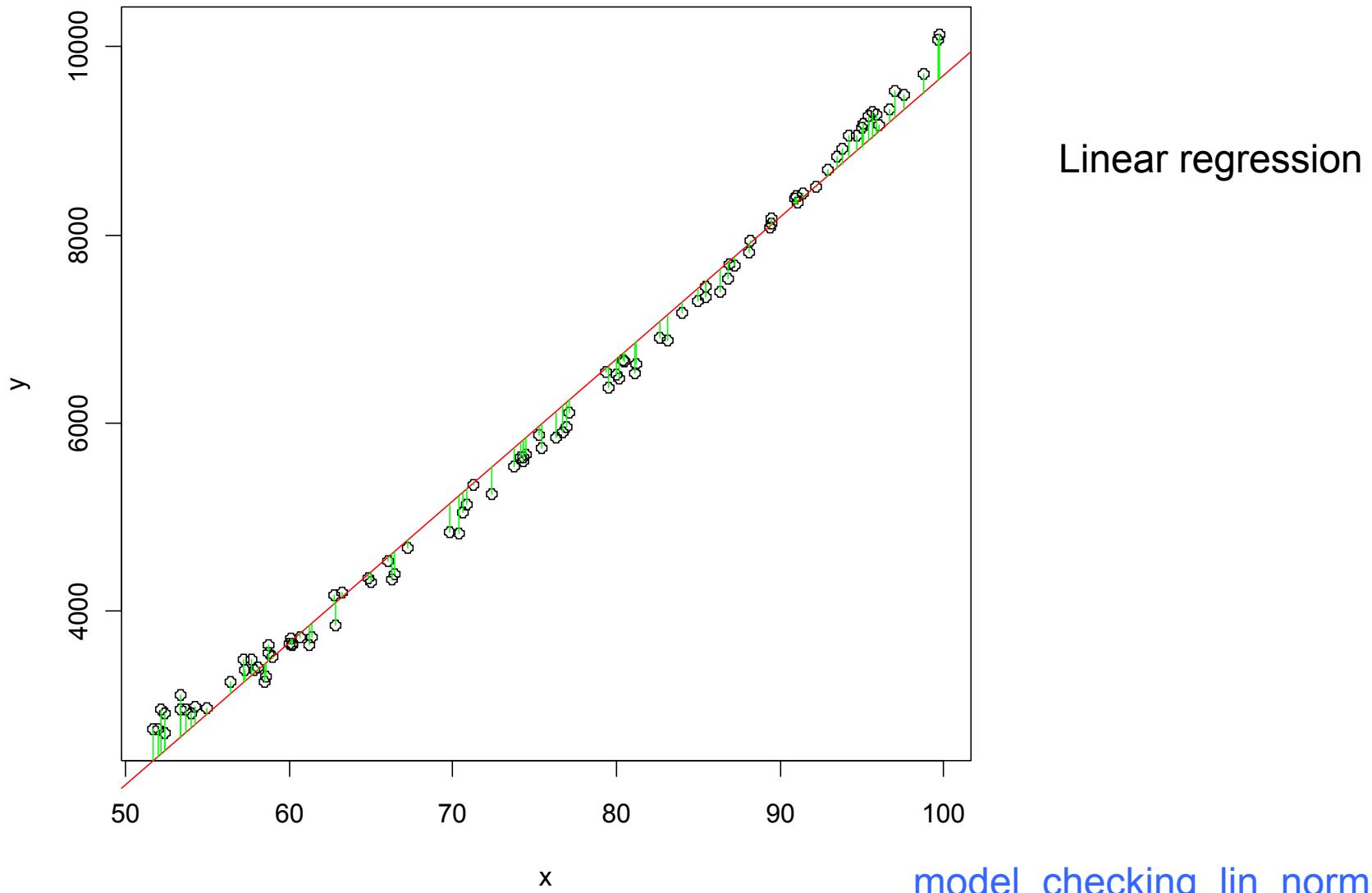


A special plot for linear models incl. GLM.  
A measure of the influence of individual points

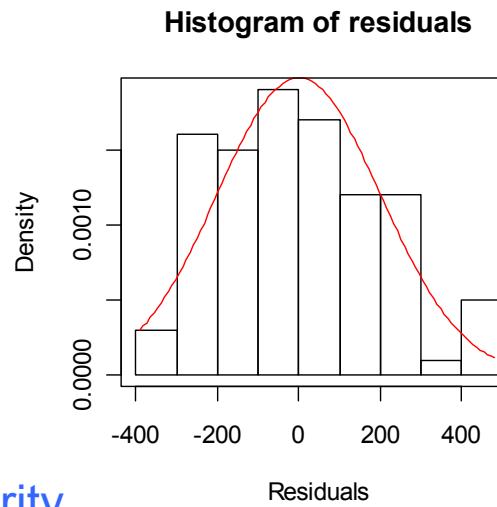
# Linear normal model

- When is **normality of errors** important?
  - Not critical for inference about means
    - Frequentist: sampling distribution will still be approximately normal
    - Bayesian: posterior distribution will still be approximately normal or insensitive
  - Can be important for inference about prediction
    - Because: data generating process
- We could nevertheless improve the model

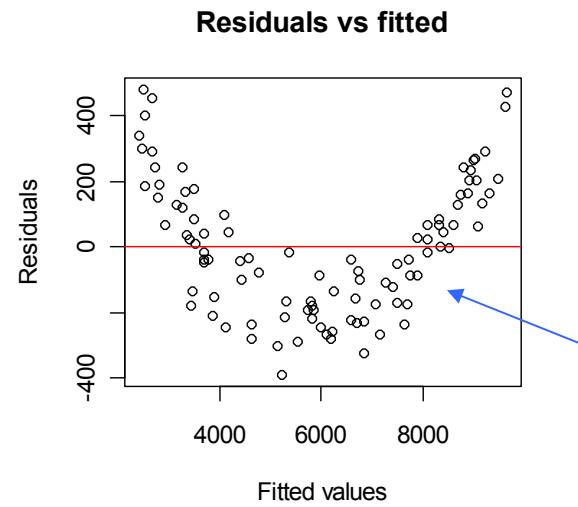
# Normal likelihood diagnostics



# Normal likelihood diagnostics

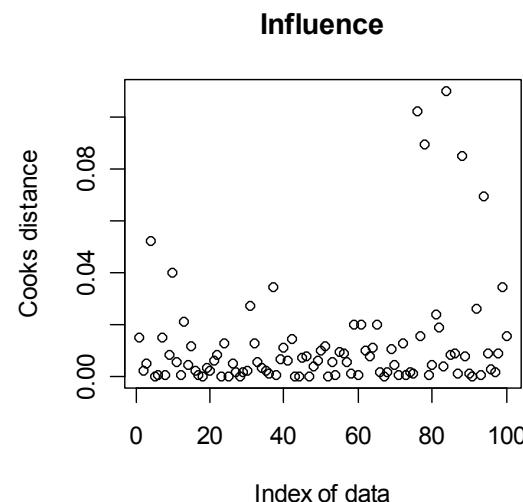
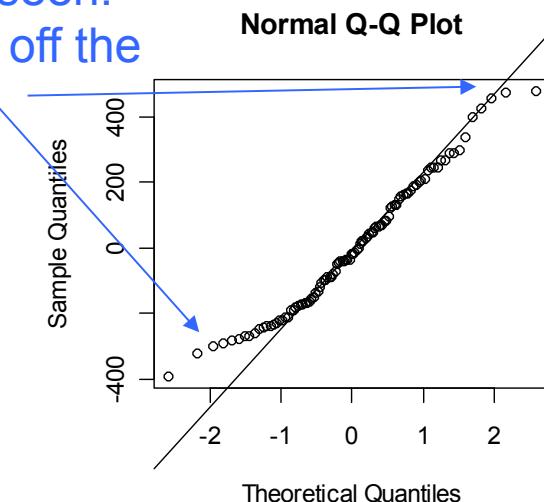


Nonlinearity  
clearly seen.  
Curves off the  
ends.

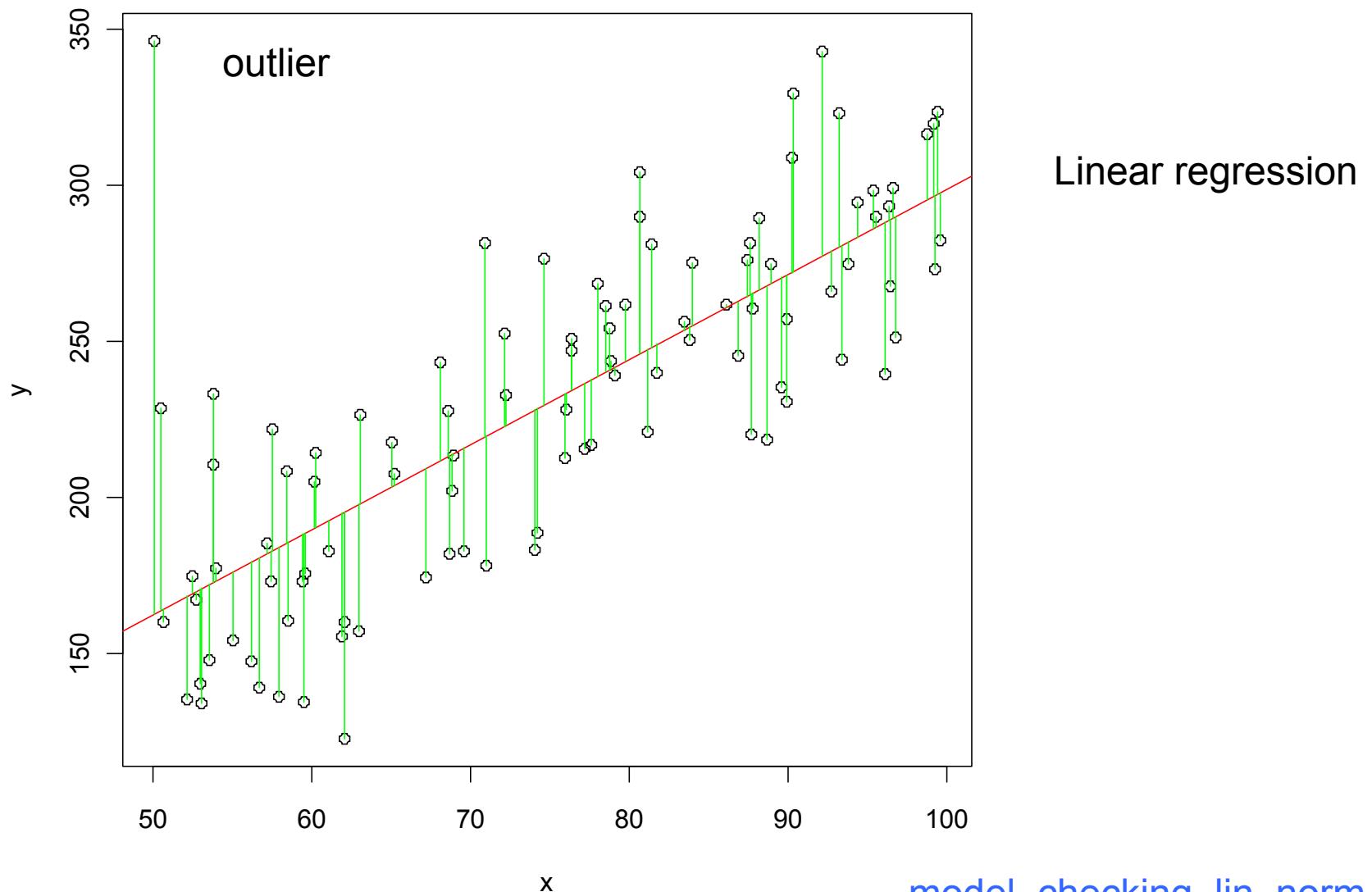


Linear regression

Nonlinearity  
clearly seen

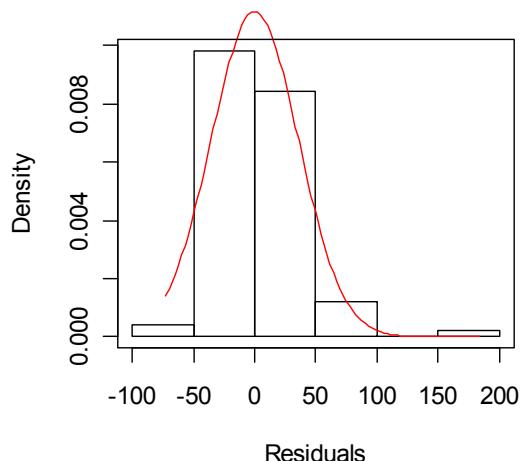


# Normal likelihood diagnostics

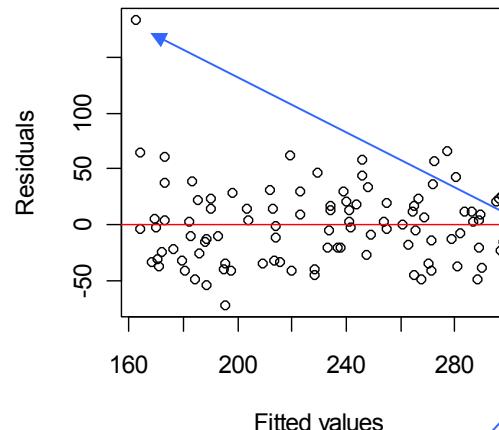


# Normal likelihood diagnostics

Histogram of residuals



Residuals vs fitted

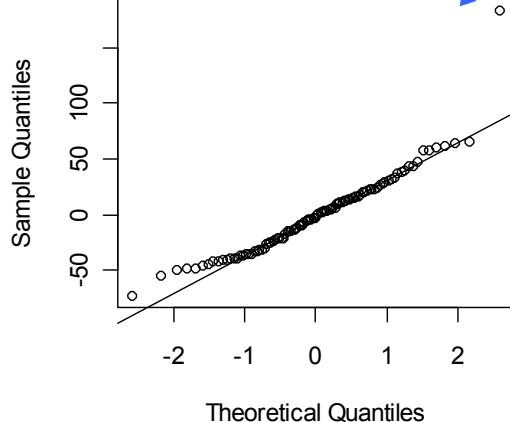


Linear regression

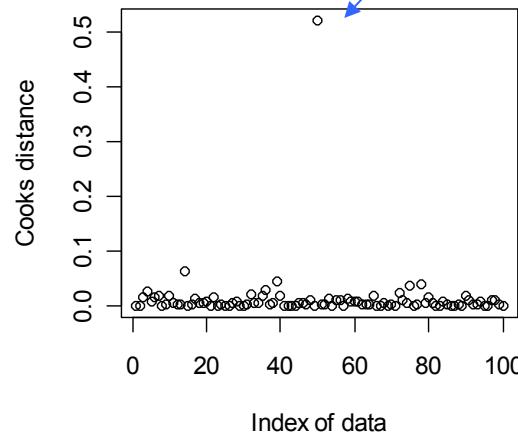
Outlier  
clearly seen

Outlier  
clearly seen

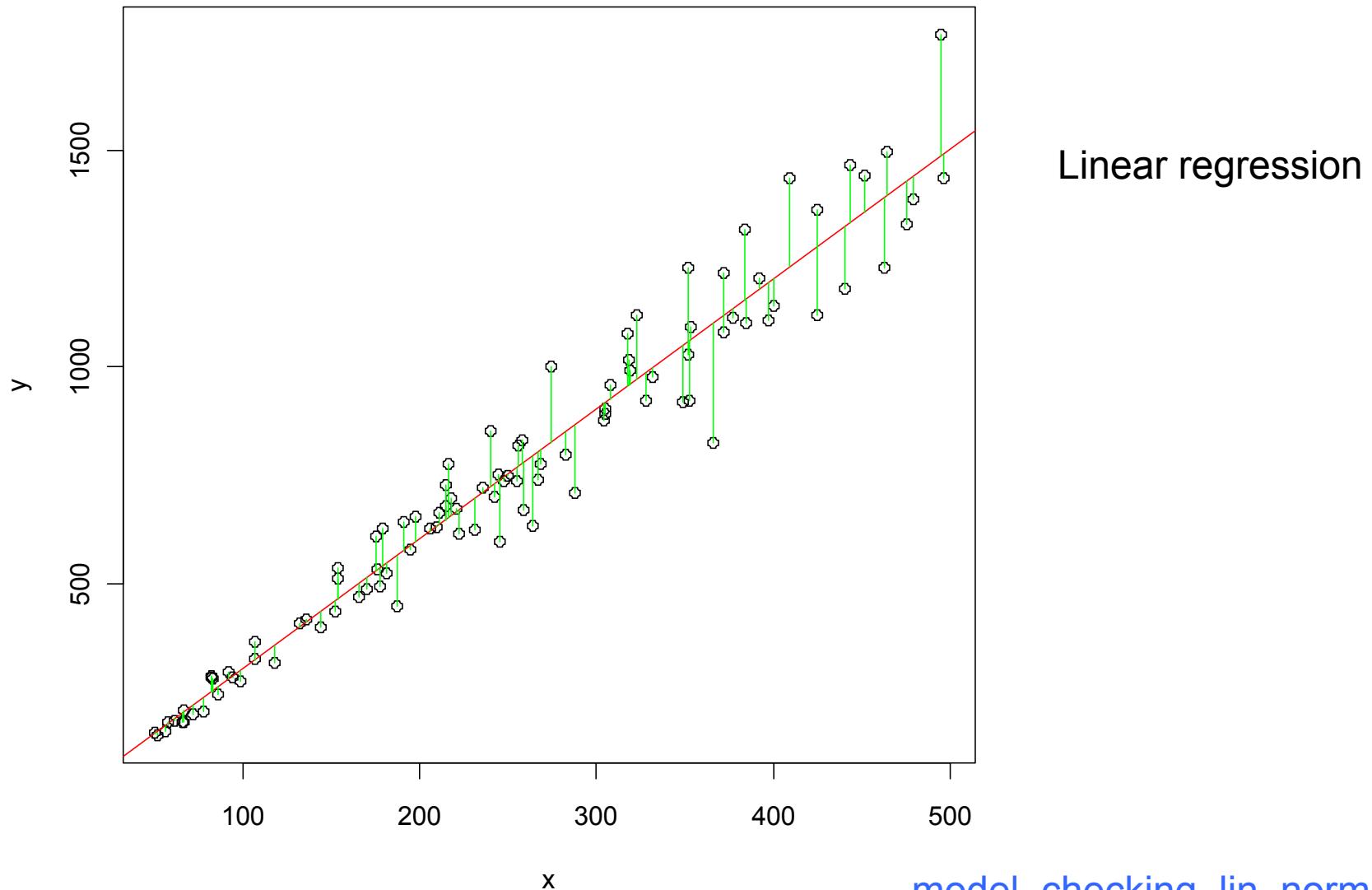
Normal Q-Q Plot



Influence

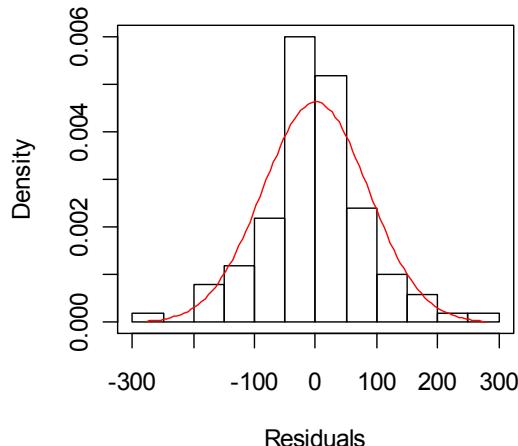


# Normal likelihood diagnostics

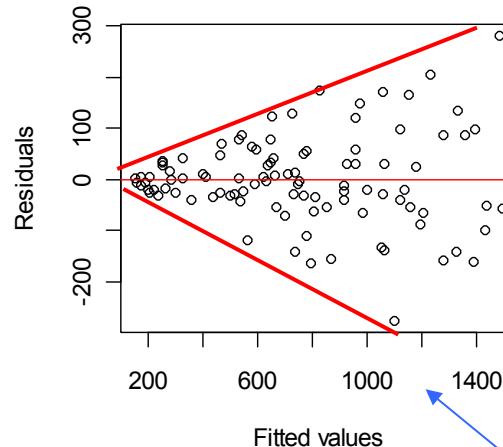


# Normal likelihood diagnostics

Histogram of residuals



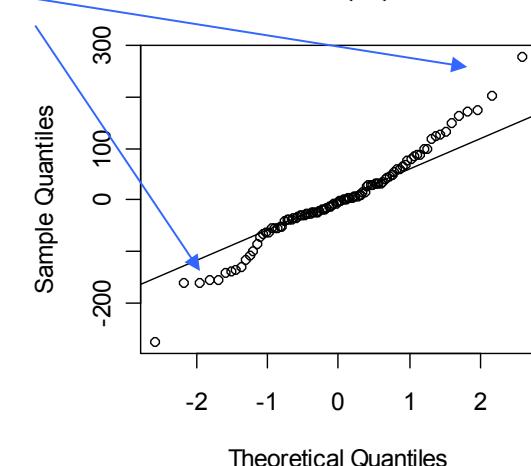
Residuals vs fitted



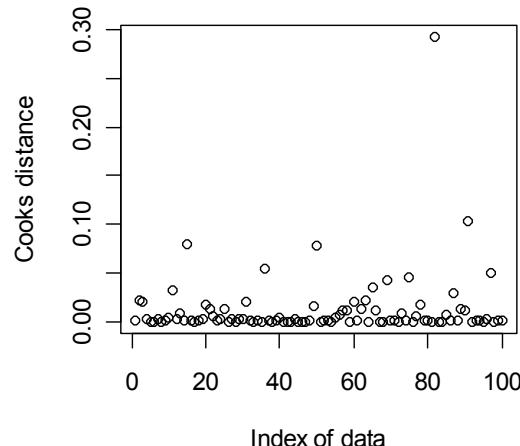
Linear regression

Rolls off  
the ends

Normal Q-Q Plot



Influence



Heteroscedasticity:  
v-shaped residuals

# General likelihood diagnostics

	Normal, linear	Normal, nonlinear	Not Normal
Residual vs fitted	X	X	X standardized
Histogram of residuals	X	X	
Q-Q plot	X	X	some
Case deletion	X Cook's	X	X

# Standardized residuals

$$r^* = \frac{r}{\sigma}$$

Raw residual

Standard deviation of the distribution evaluated at that point

$$\sigma = \sqrt{\text{variance}}$$

# Case deletion diagnostics

- Simple idea: leave out each data point in turn and refit the model
- Likelihood displacement

$$LD = 2(\text{nll}(\theta, y_{-i}) - \text{nll}(\theta, y))$$

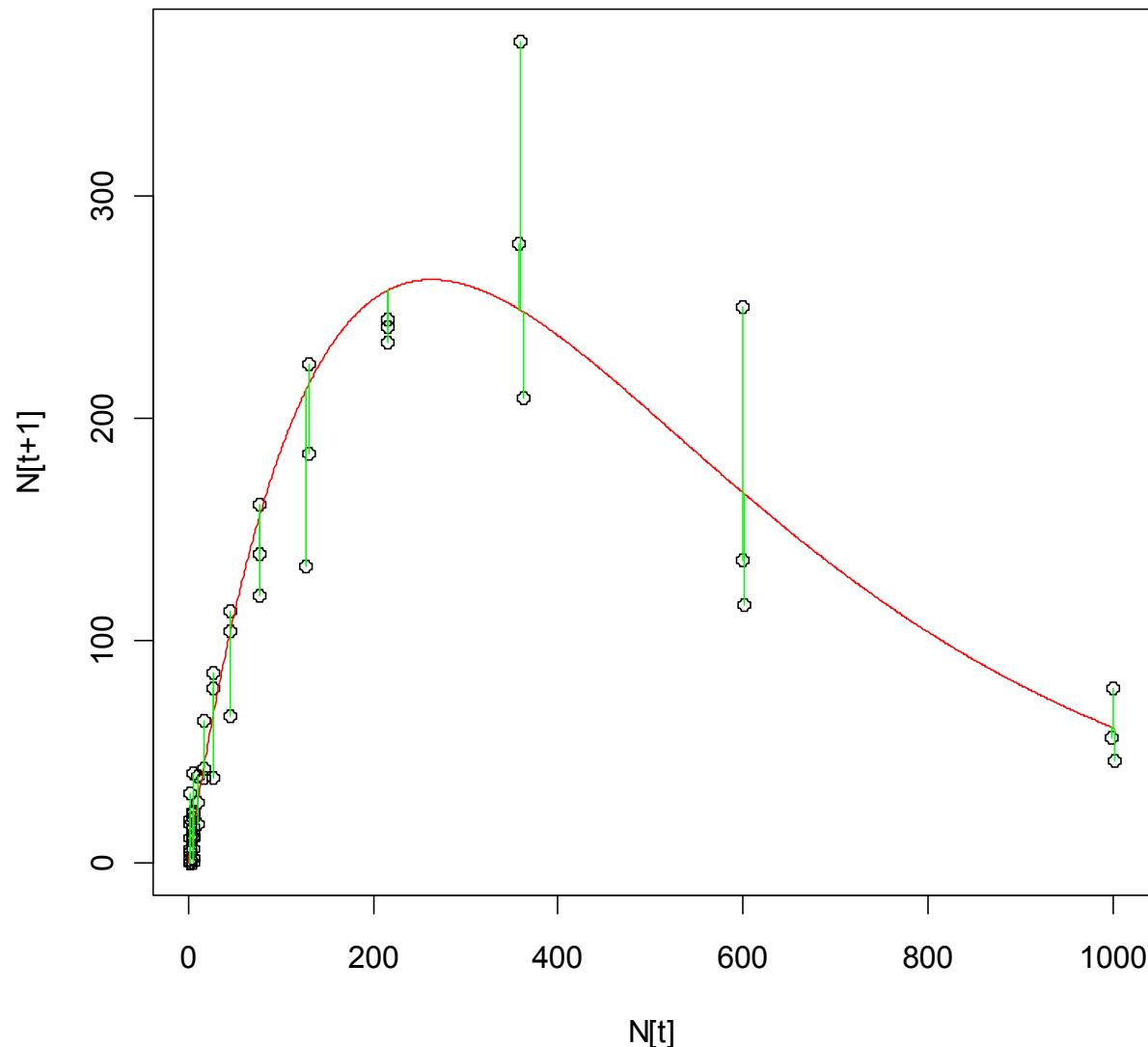
full dataset  
deleting observation i

- Parameter sensitivity
  - percent change in parameter estimate by leaving out the data point

Notice LD is a likelihood ratio

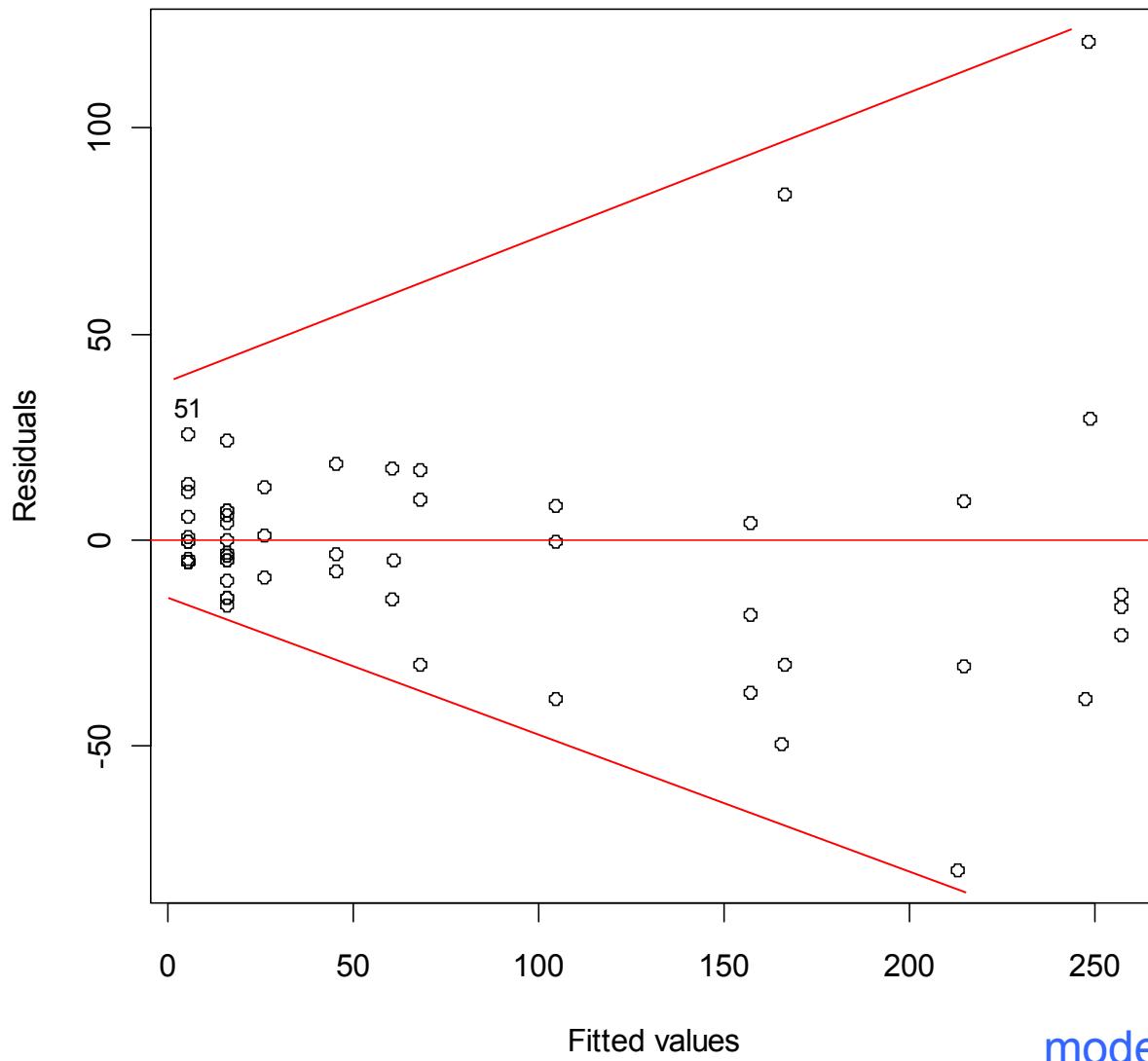
Cook and Weisberg (1982). *Residuals and influence in regression*. Chapman & Hall.

# Nonlinear likelihood



Ricker model:  
Negative  
binomial  
error

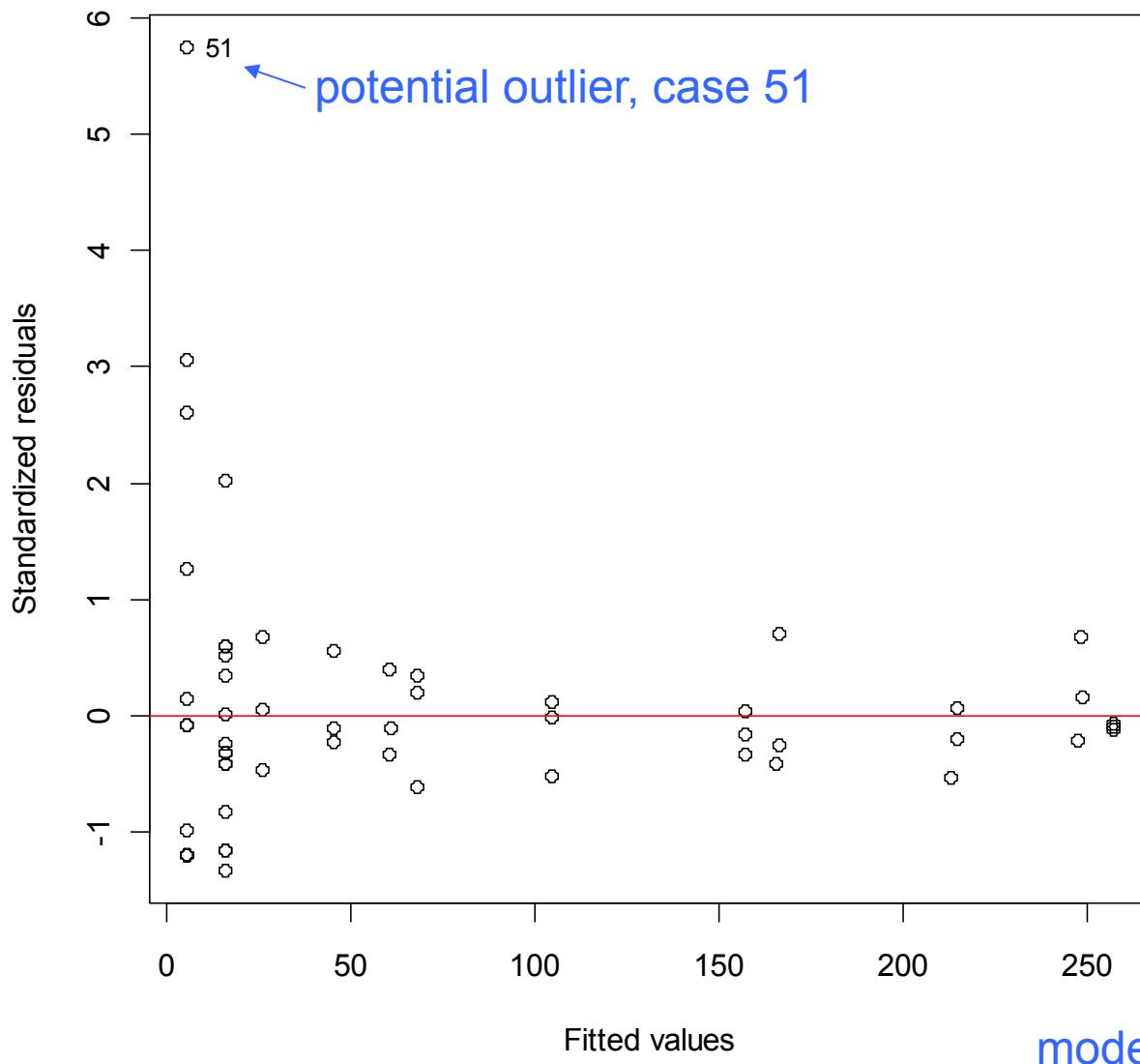
# Model checking



Residuals  
versus  
fitted values

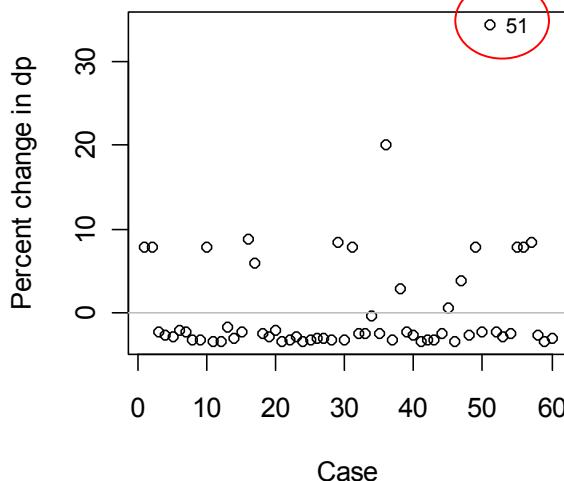
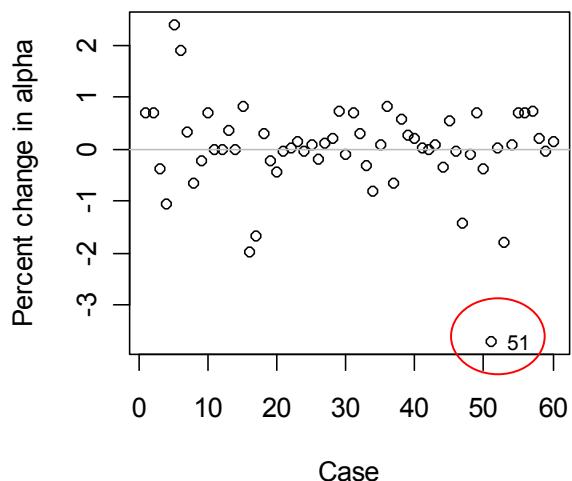
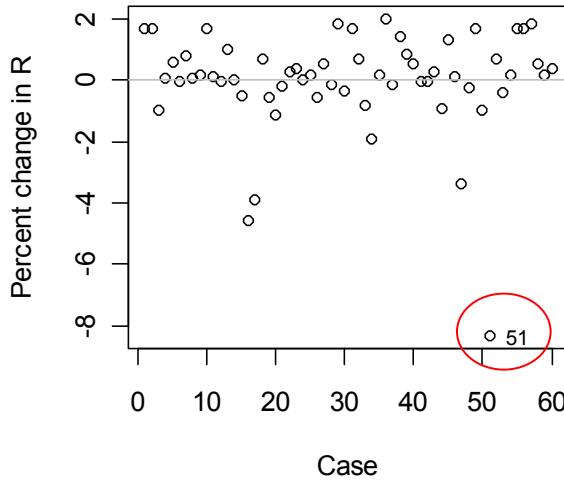
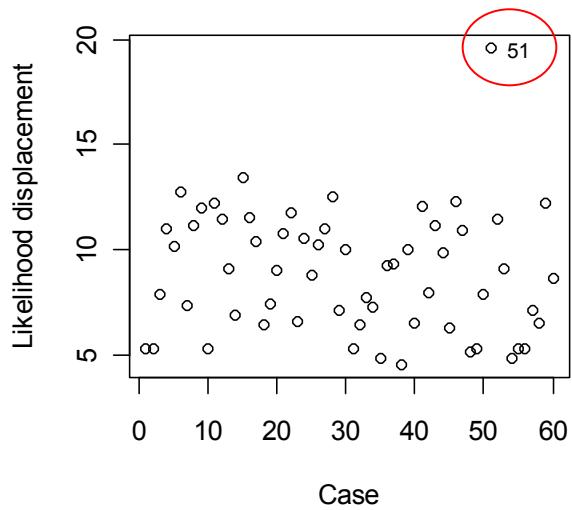
Shows increasing  
variance with  
increasing fv,  
but this is what  
you expect from  
the neg binom

# Model checking



Standardized  
residuals  
versus  
fitted values

# Influence



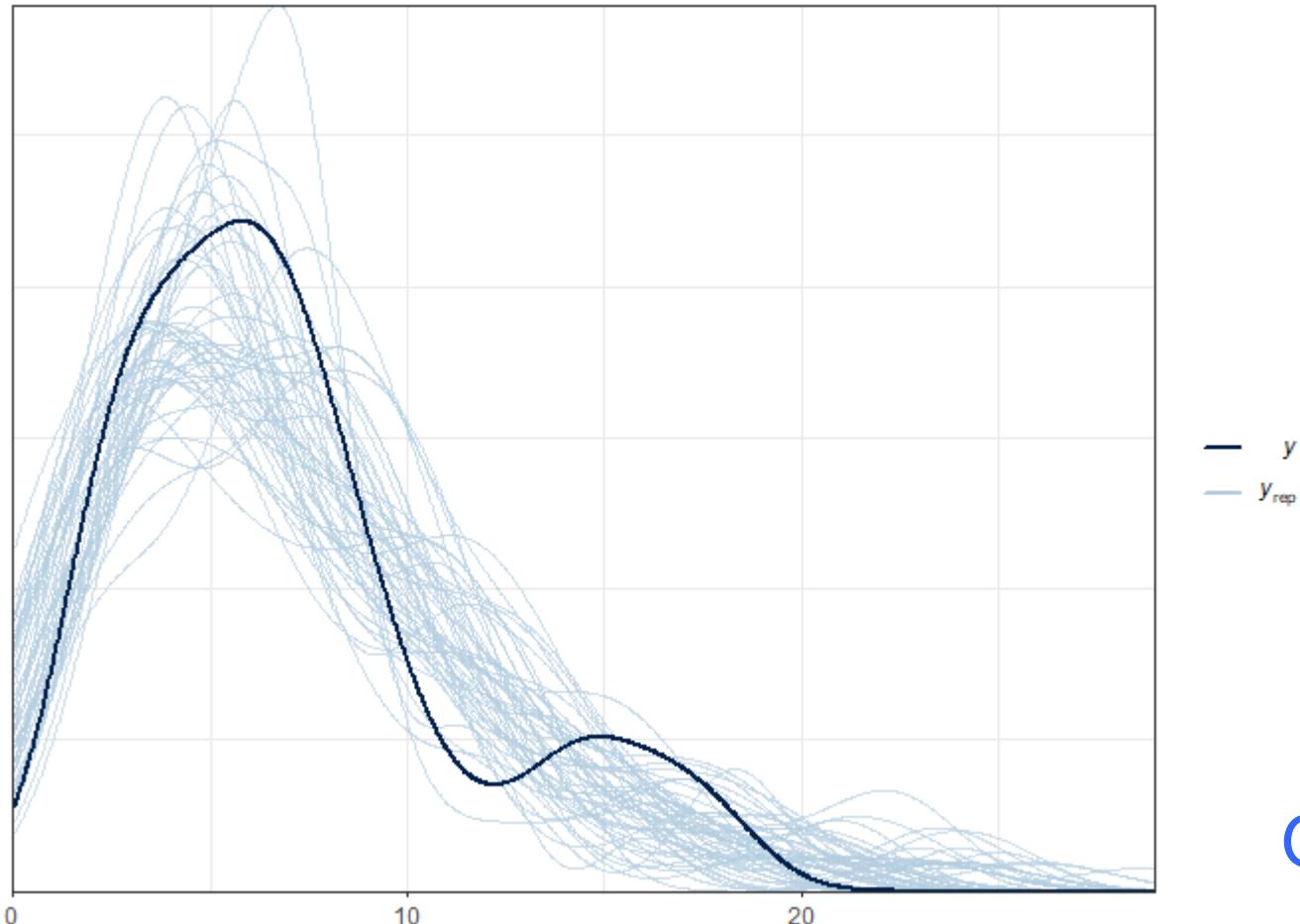
Influence:  
Case  
deletion  
diagnostics

# Bayesian diagnostics

- `launch_shinystan`
- NUTS (plots) “By model parameter”
  - top left: trace; top right: posterior
- `R_hat`, `n_eff`, `se_mean`
- Autocorrelation
- PPcheck – look at all
- LOO diagnostics (see Thu, LOOIC)

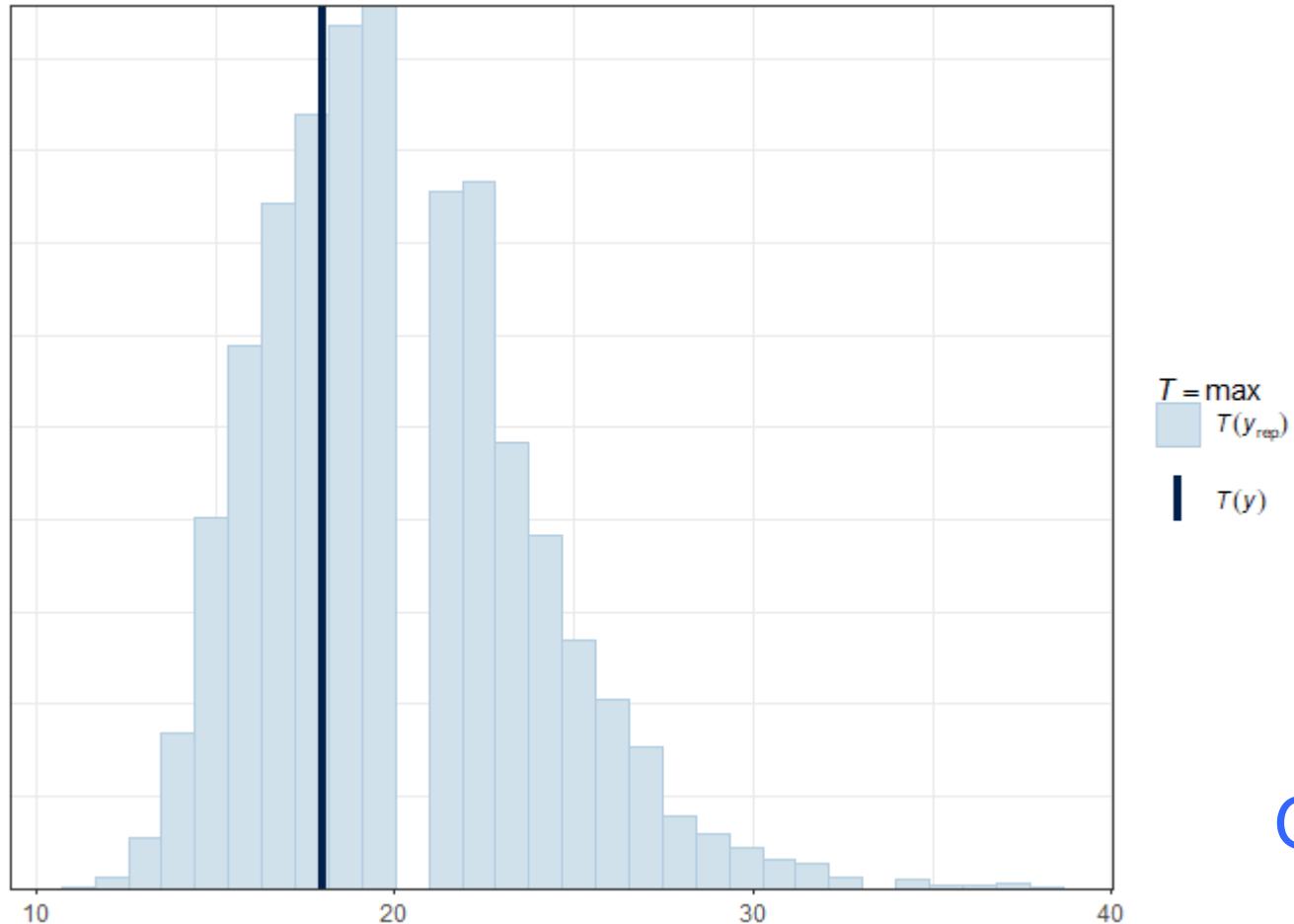
# Posterior predictive check

```
pp_check(bayesHLE, plotfun = "dens_overlay")
```



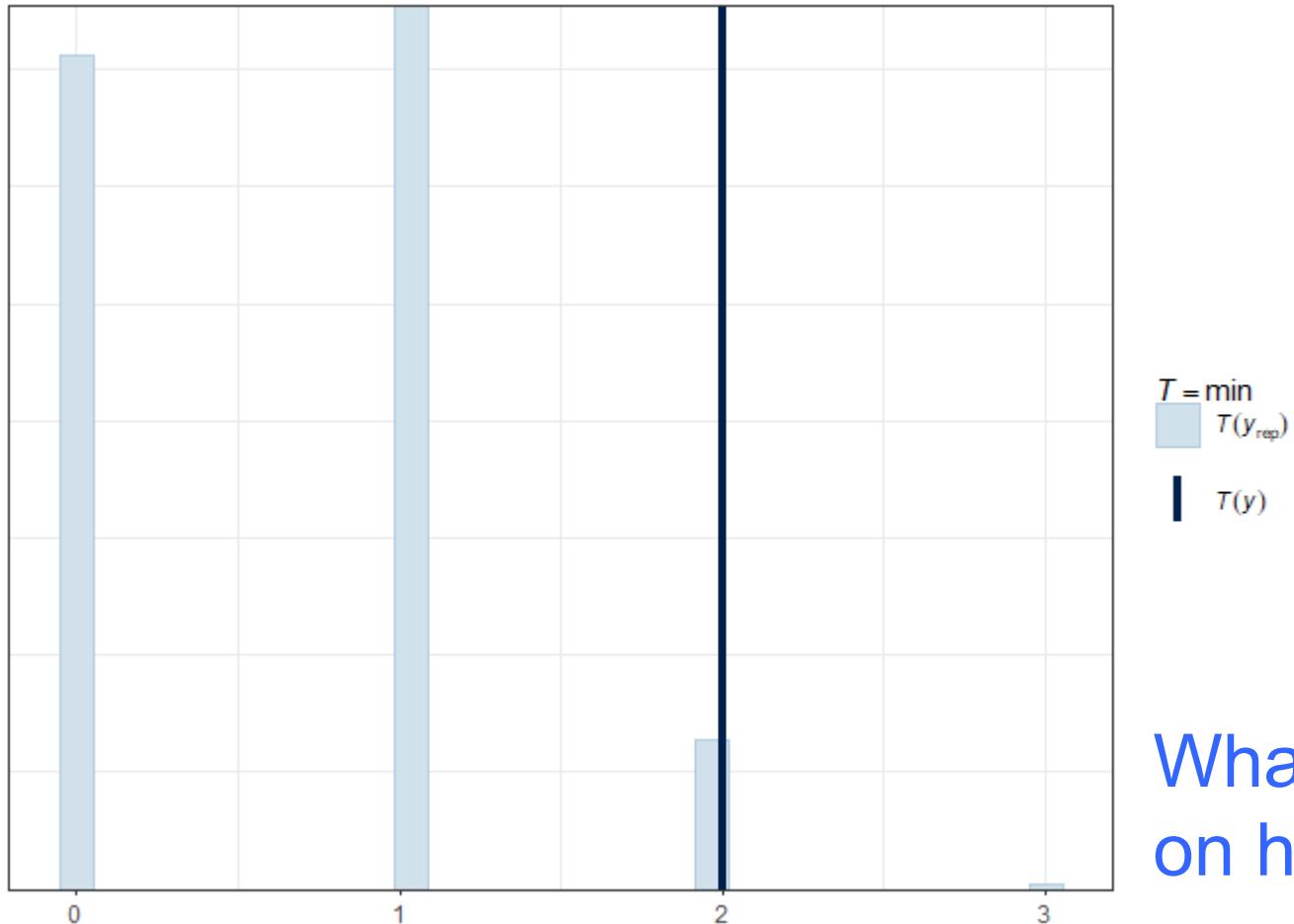
# Posterior predictive check

```
pp_check(bayesHLE, plotfun = "stat", stat = "max")
```



# Posterior predictive check

```
pp_check(bayesHLE, plotfun = "stat", stat = "min")
```



What's going  
on here?

# Posterior predictive check

```
pp_check(bayesHLE, plotfun = "ppc_dens_overlay_grouped",  
         group="habitat", nreps=30)
```

