

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

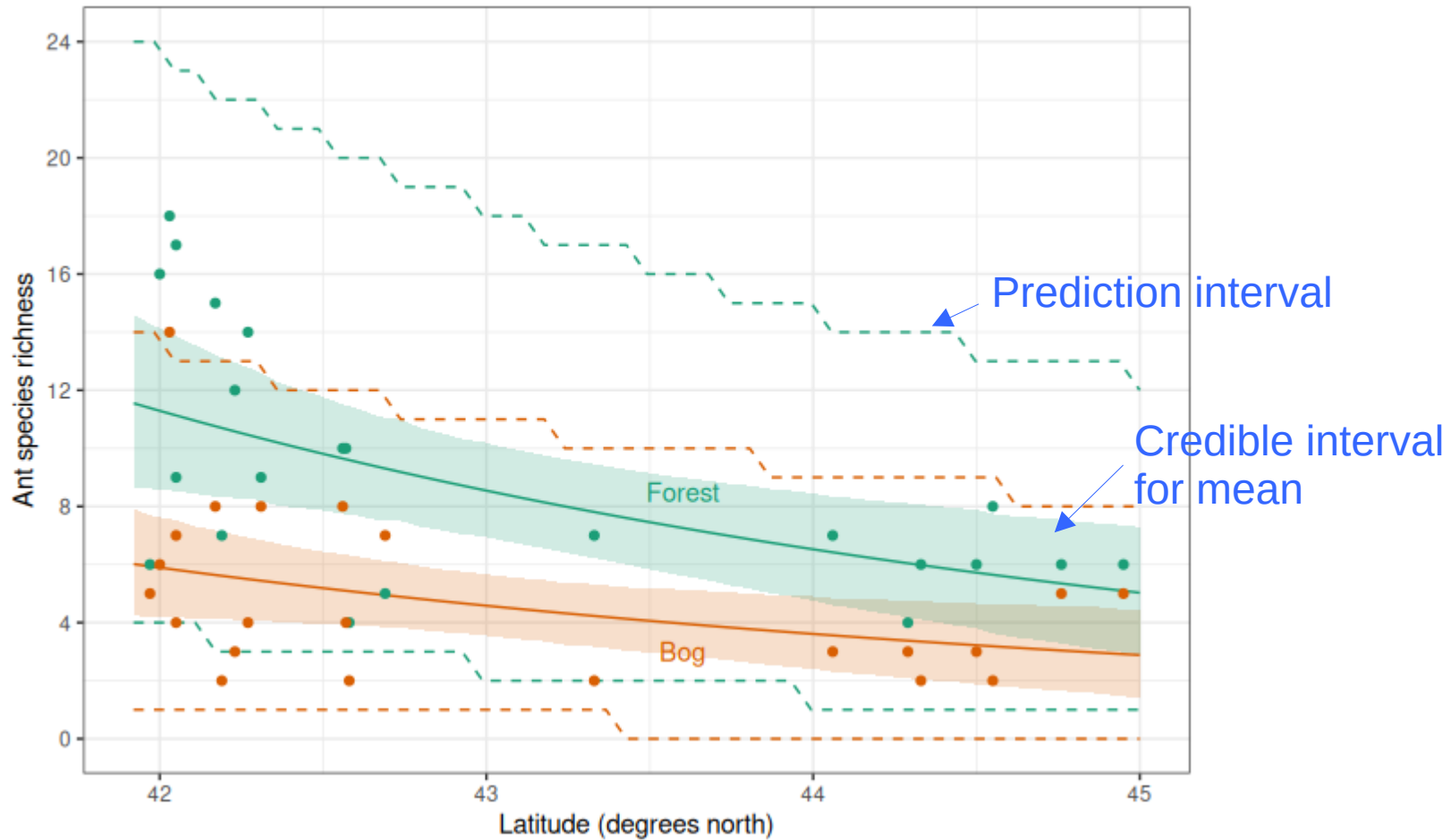
Thursday

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

Week 16

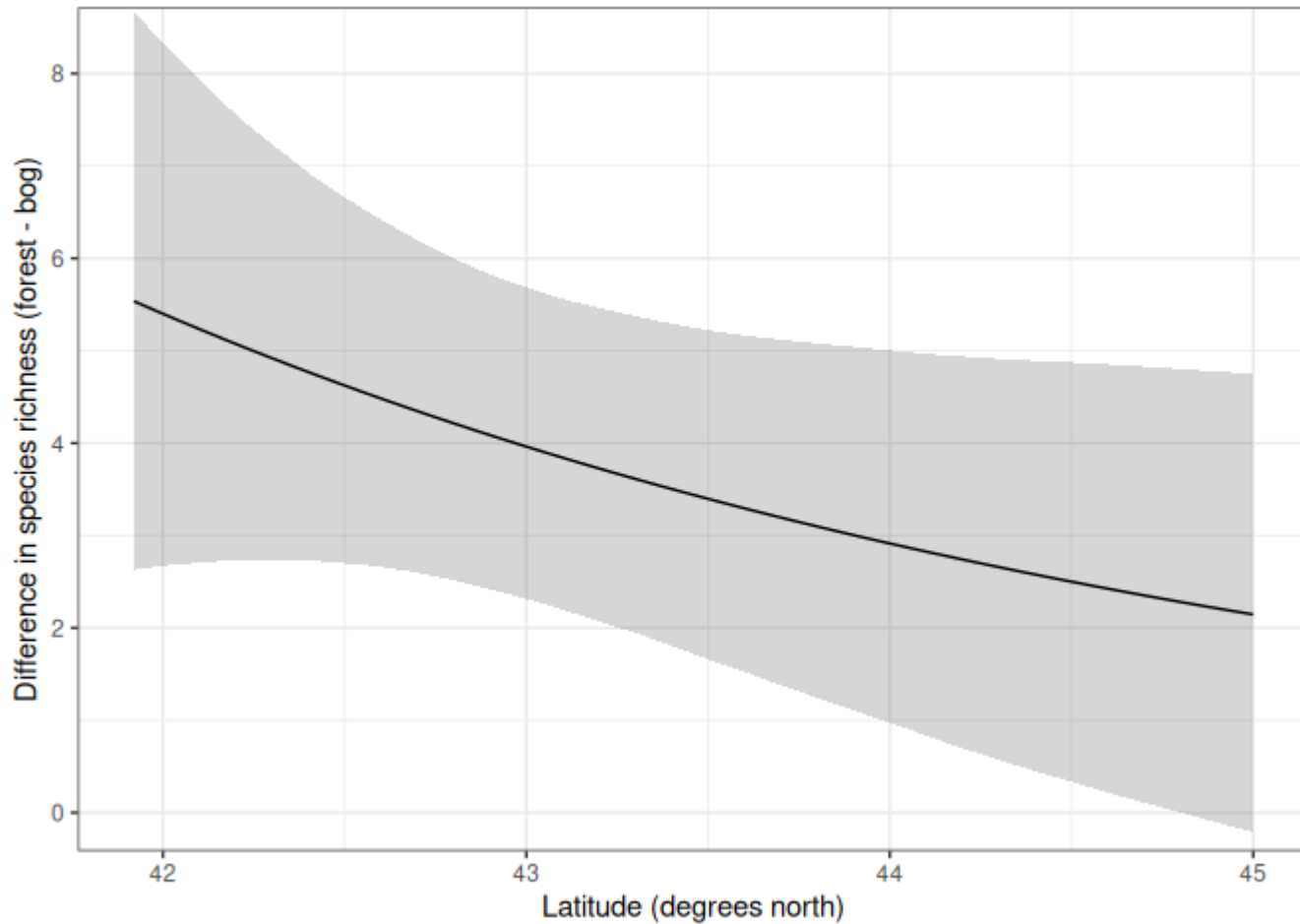
- The missing week
 - Populate with material for self study
- Thu: 4-7 PM “exam”
 - presentations

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)

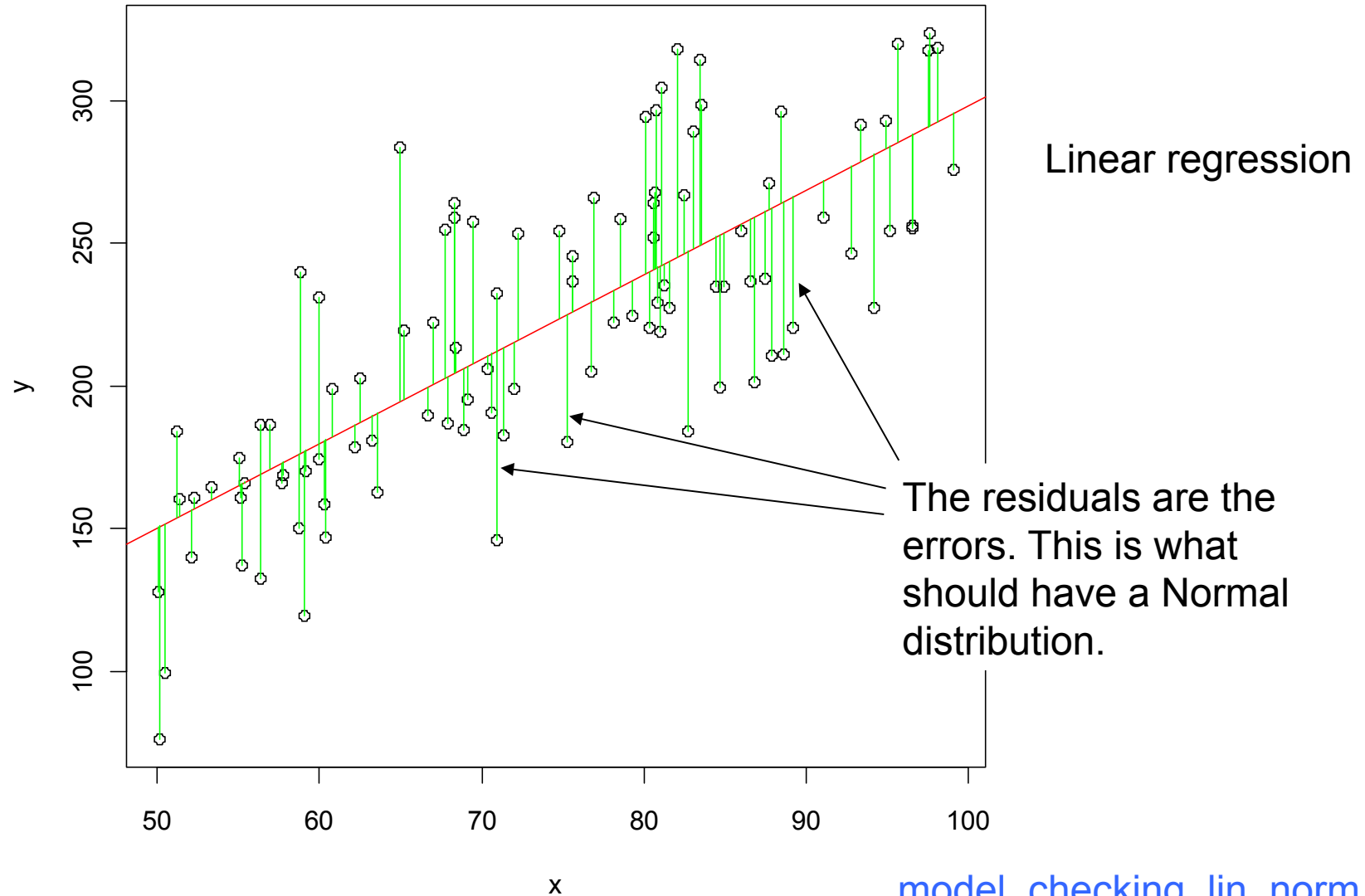
What are the issues?

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

Tools

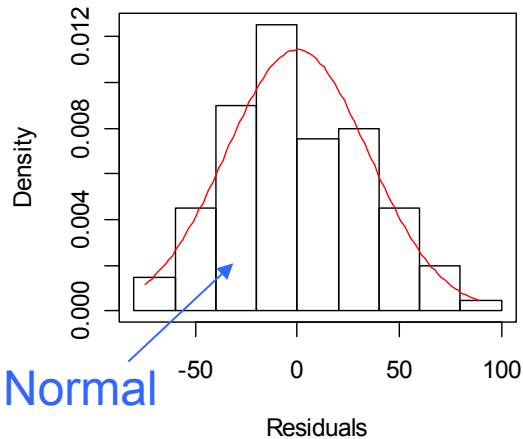
- Plot the fitted model with the data
- Generative model check
 - simulate data using the fitted model
- Residuals vs fitted values
- QQ plot, histogram of residuals
- Leave one out (LOO) influence algorithm
- How can I know what to look for in a diagnostic plot?
 - Simulate it! Make diagnostic plots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

Normal likelihood diagnostics



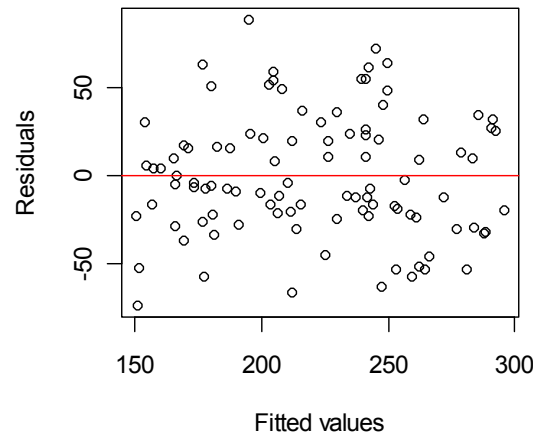
Normal likelihood diagnostics

Histogram of residuals



Looks Normal

Residuals vs fitted

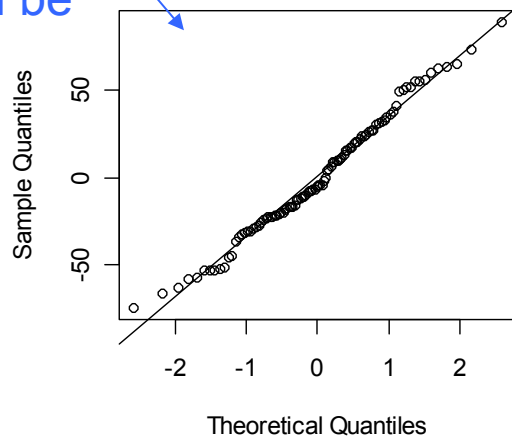


Linear regression

This is what it should look like

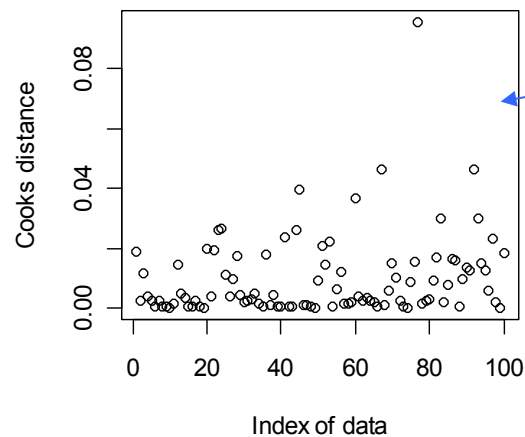
A special plot for the Normal distribution

Normal Q-Q Plot



Should be linear

Influence



A special plot for linear models incl. GLM.

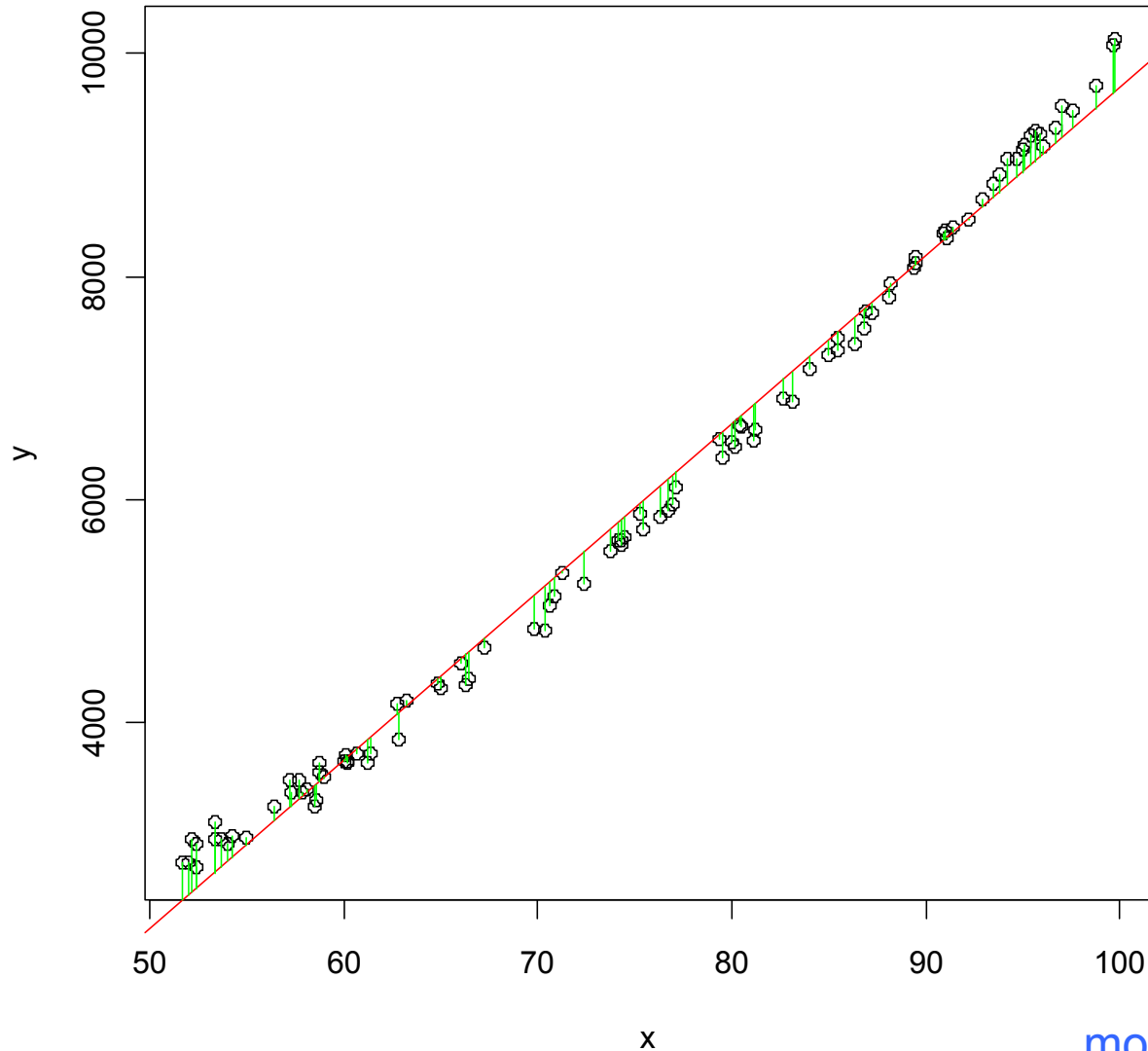
A measure of the influence of individual points

`model_checking_lin_norm.R`

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

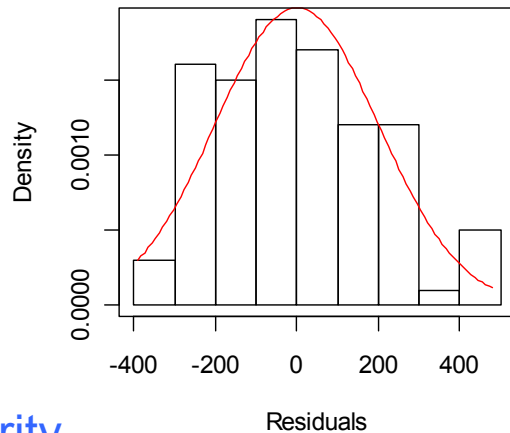
Normal likelihood diagnostics



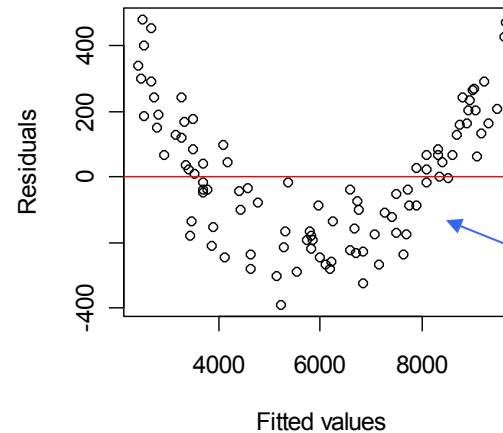
Linear regression

Normal likelihood diagnostics

Histogram of residuals



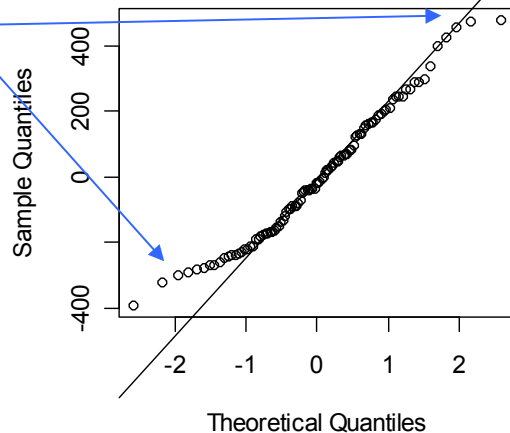
Residuals vs fitted



Linear regression

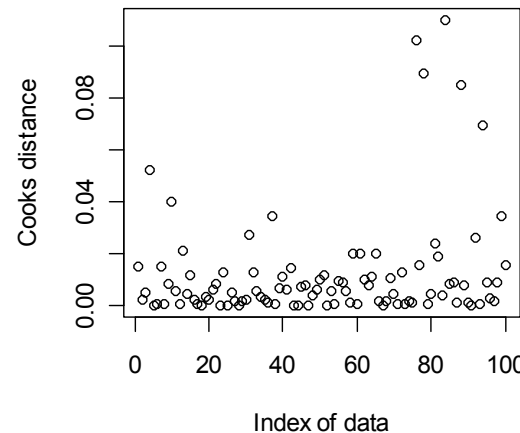
Nonlinearity
clearly seen

Normal Q-Q Plot

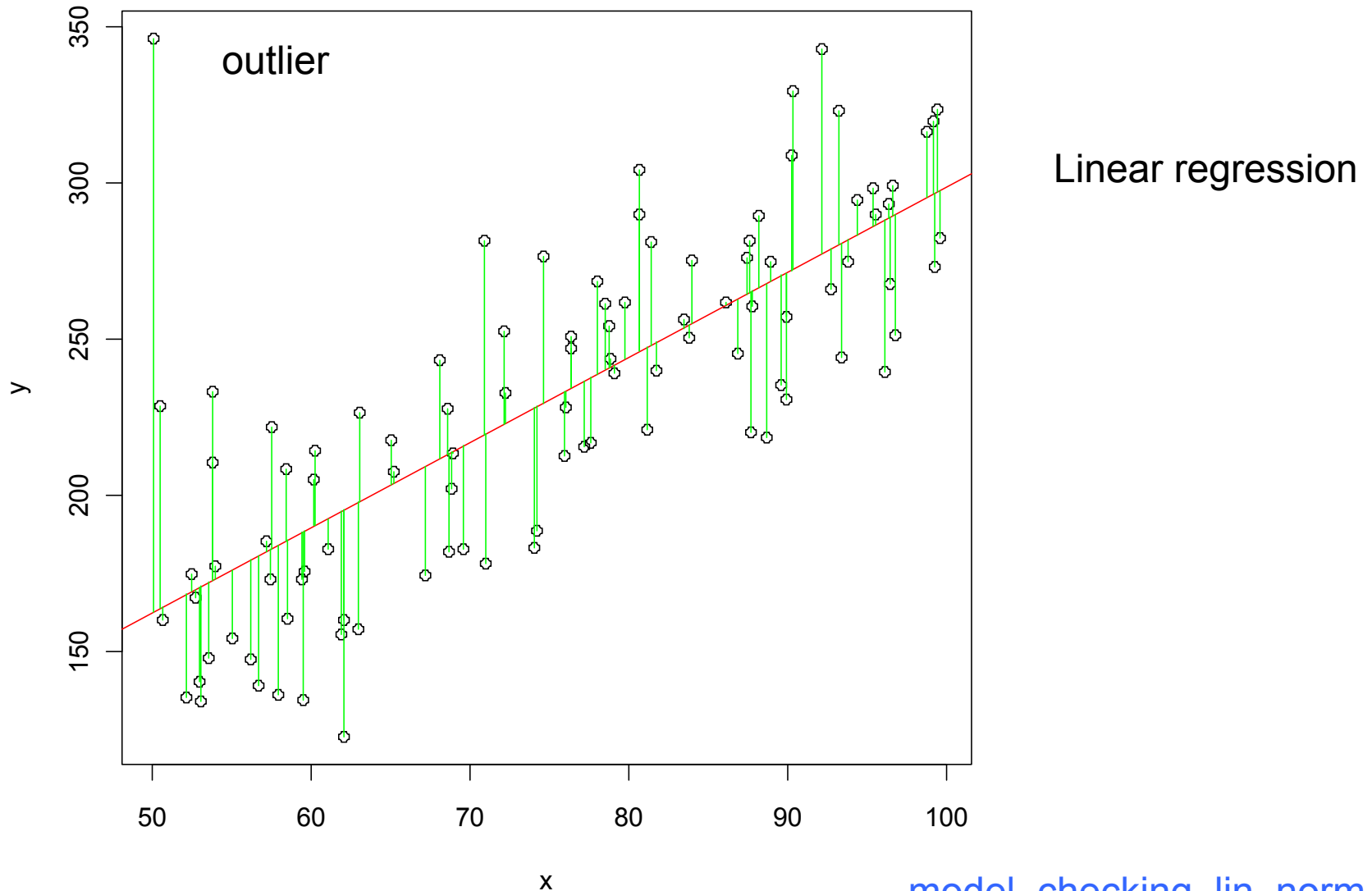


Nonlinearity
clearly seen.
Curves off the
ends.

Influence

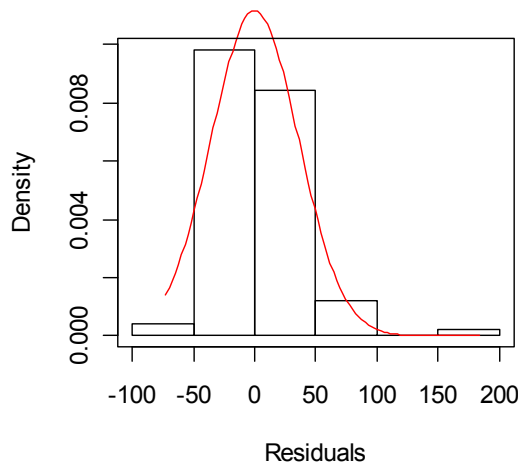


Normal likelihood diagnostics

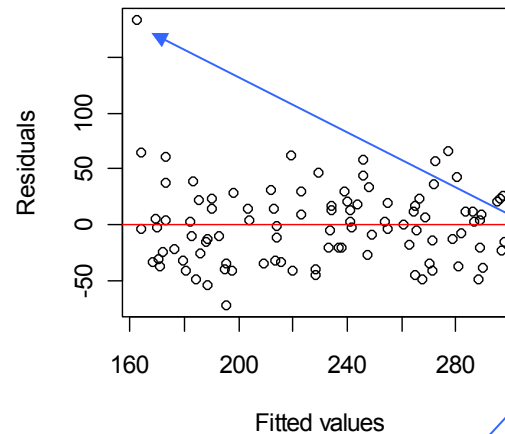


Normal likelihood diagnostics

Histogram of residuals



Residuals vs fitted

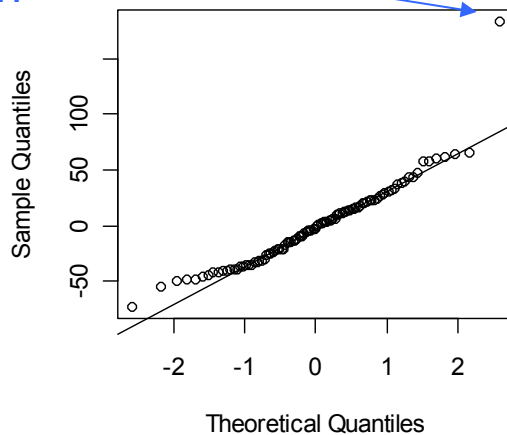


Linear regression

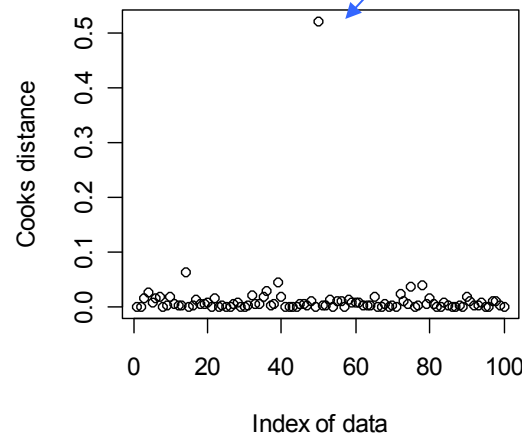
Outlier
clearly seen

Outlier
clearly seen

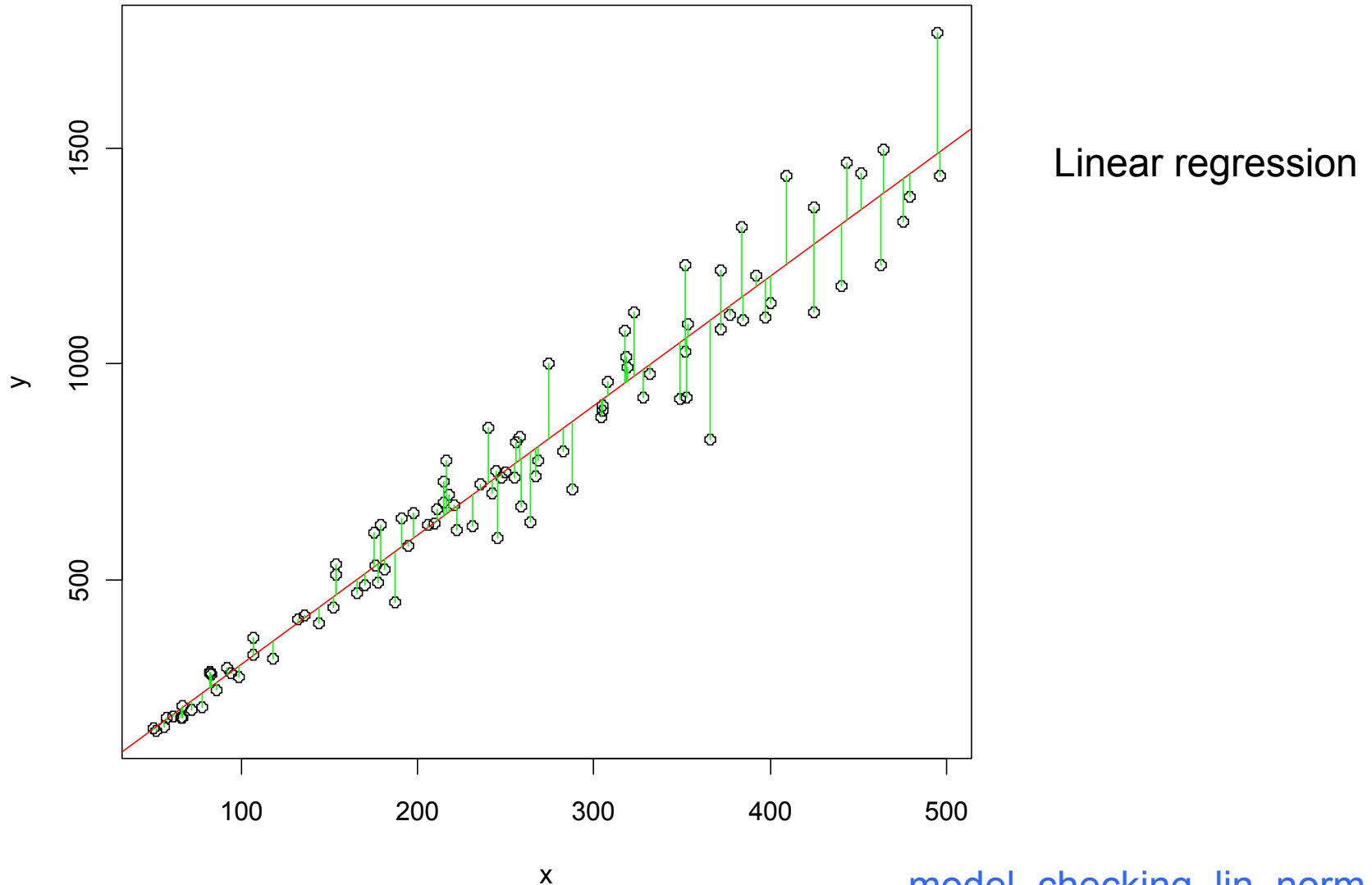
Normal Q-Q Plot



Influence

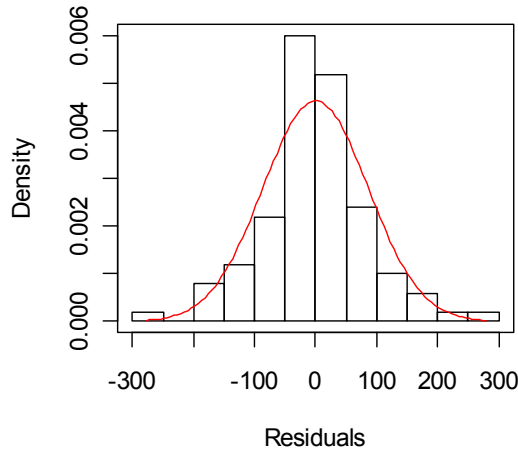


Normal likelihood diagnostics

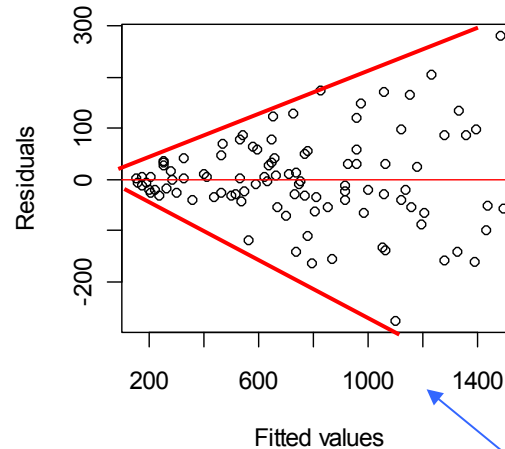


Normal likelihood diagnostics

Histogram of residuals



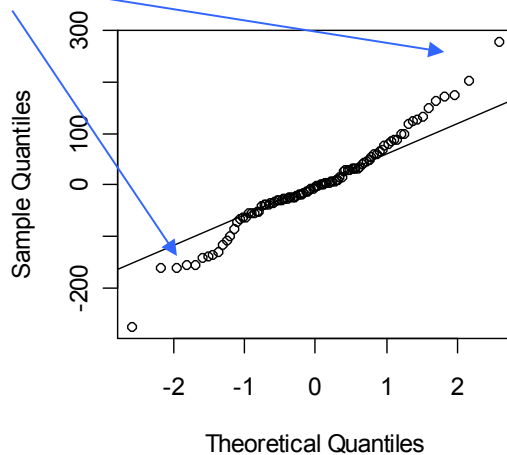
Residuals vs fitted



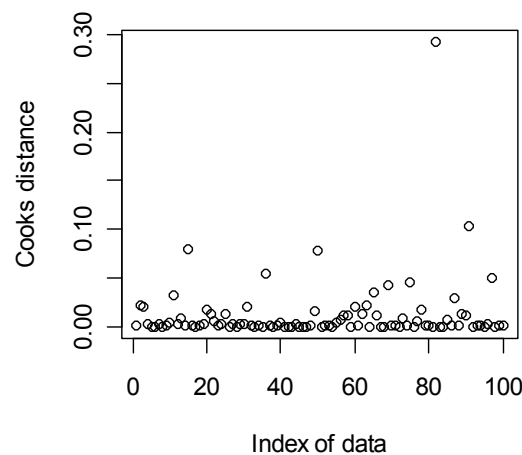
Linear regression

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

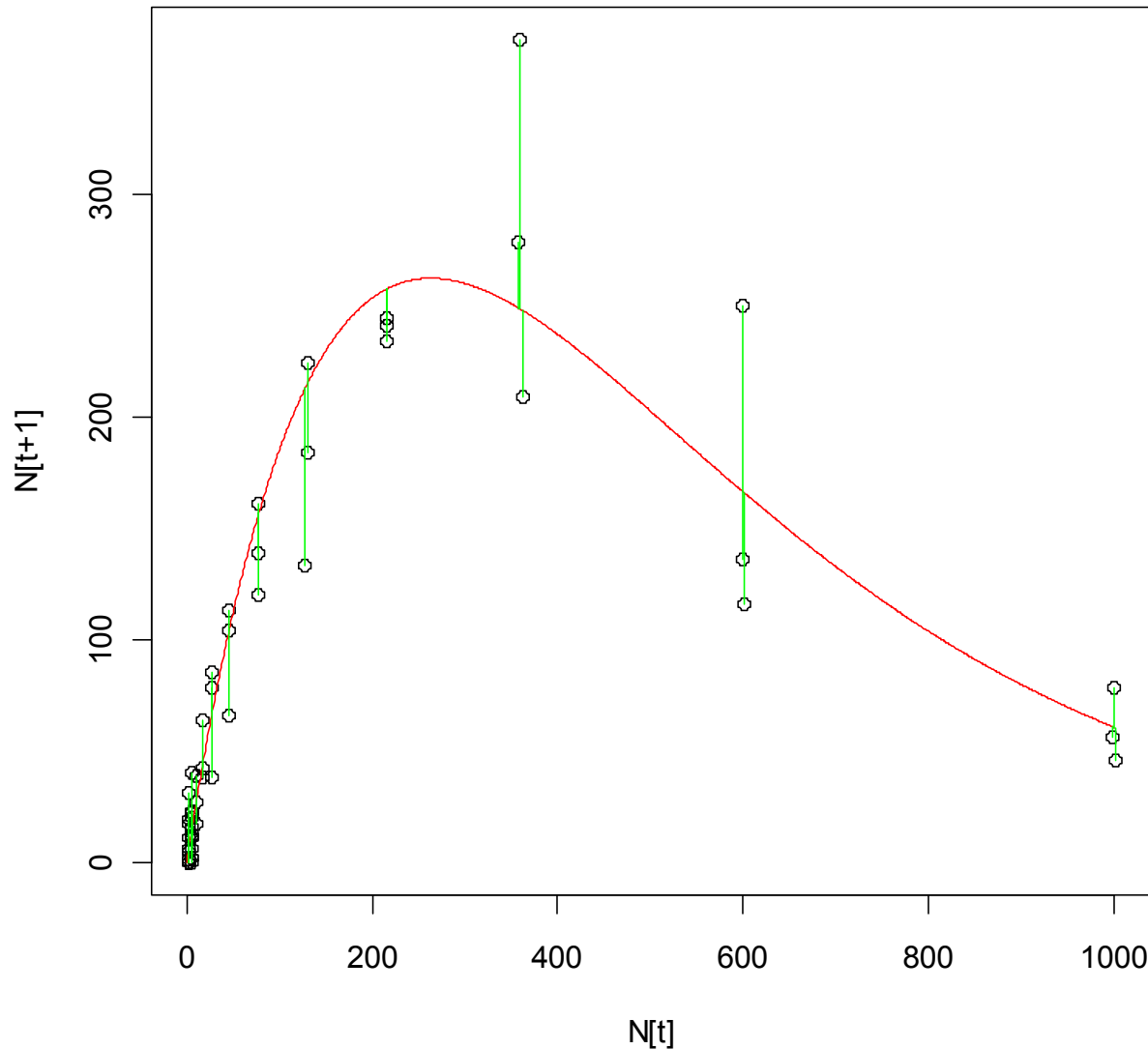
Notice LD is a
likelihood ratio

- Parameter sensitivity

– percent change in parameter estimate by leaving out the data point

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

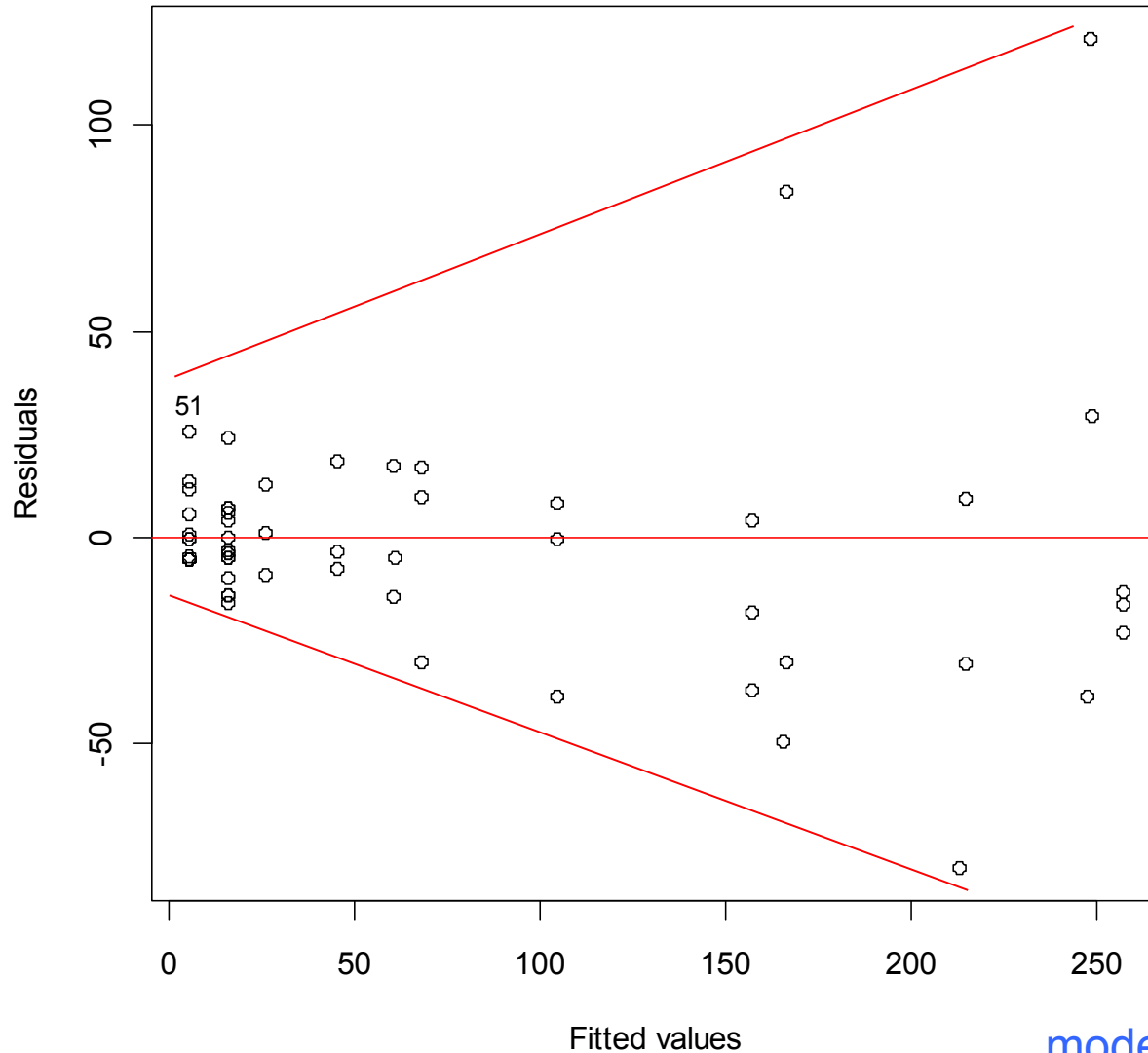
Nonlinear likelihood



Ricker model:

Negative
binomial
error

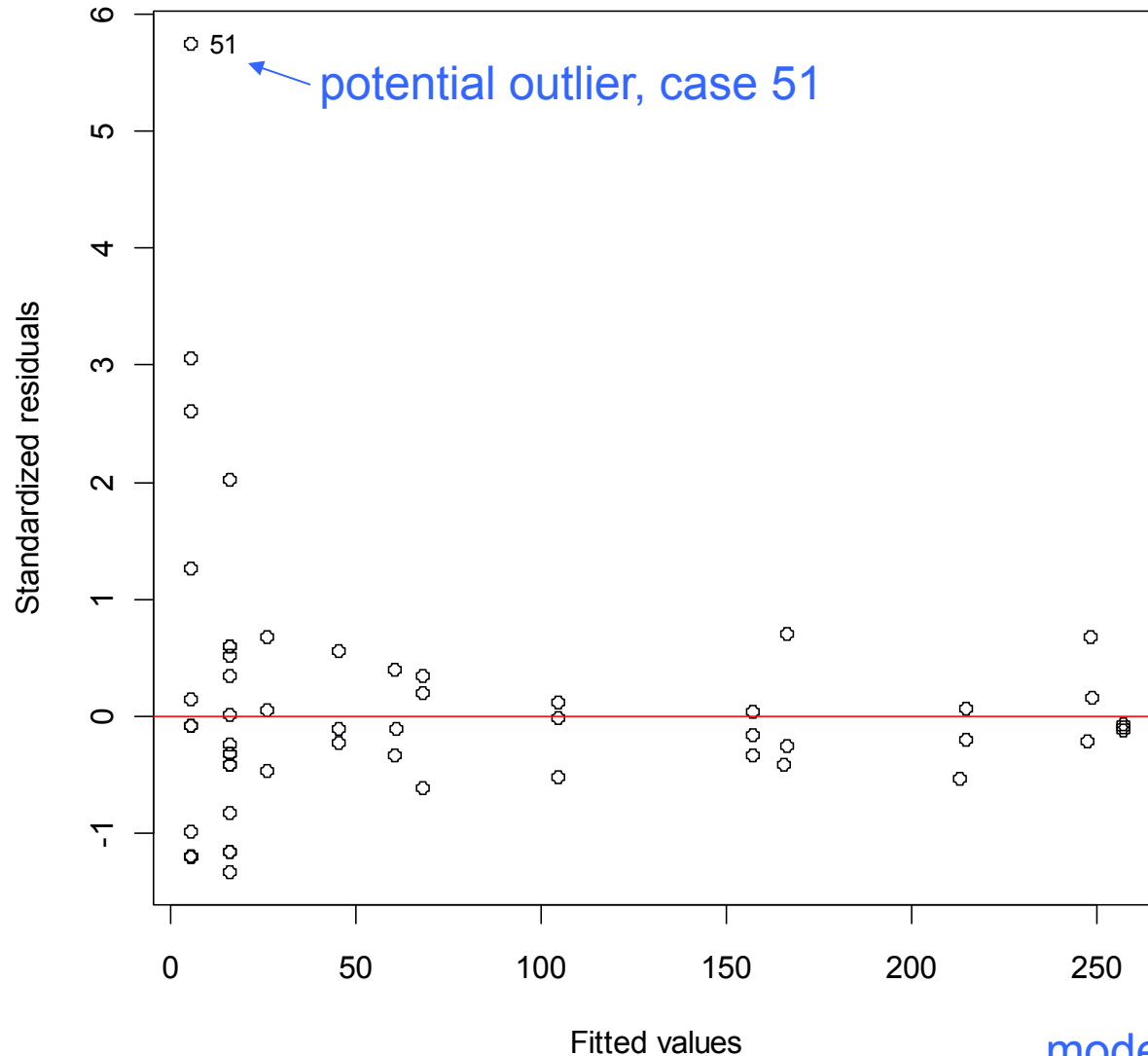
Model checking



Residuals
versus
fitted values

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

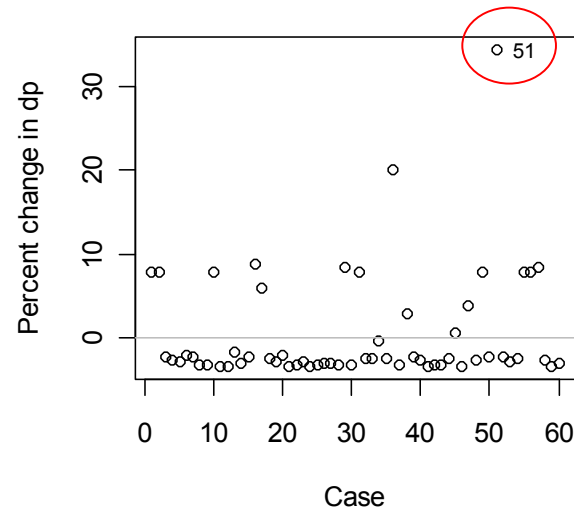
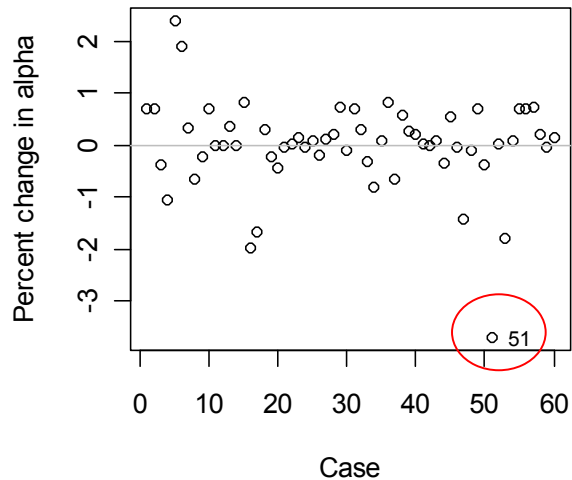
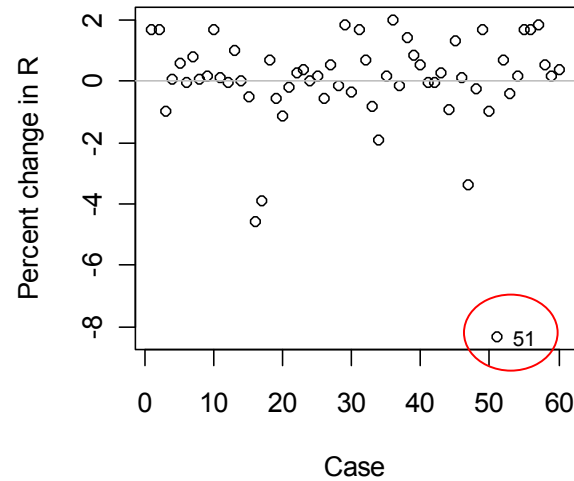
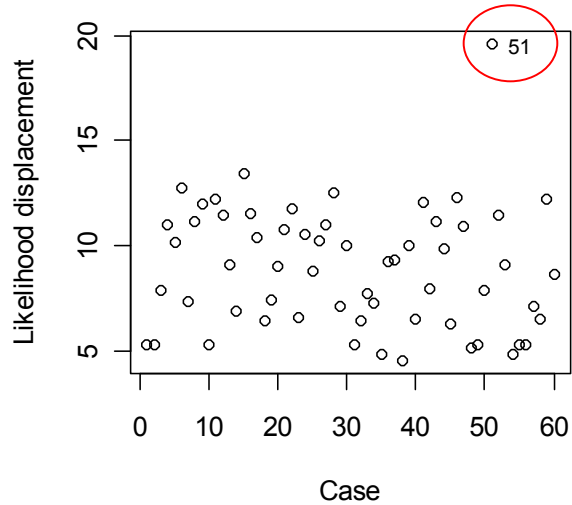
Model checking



Standardized
residuals
versus
fitted values

stand res =
residuals /
standard deviation
of neg binomial

Influence



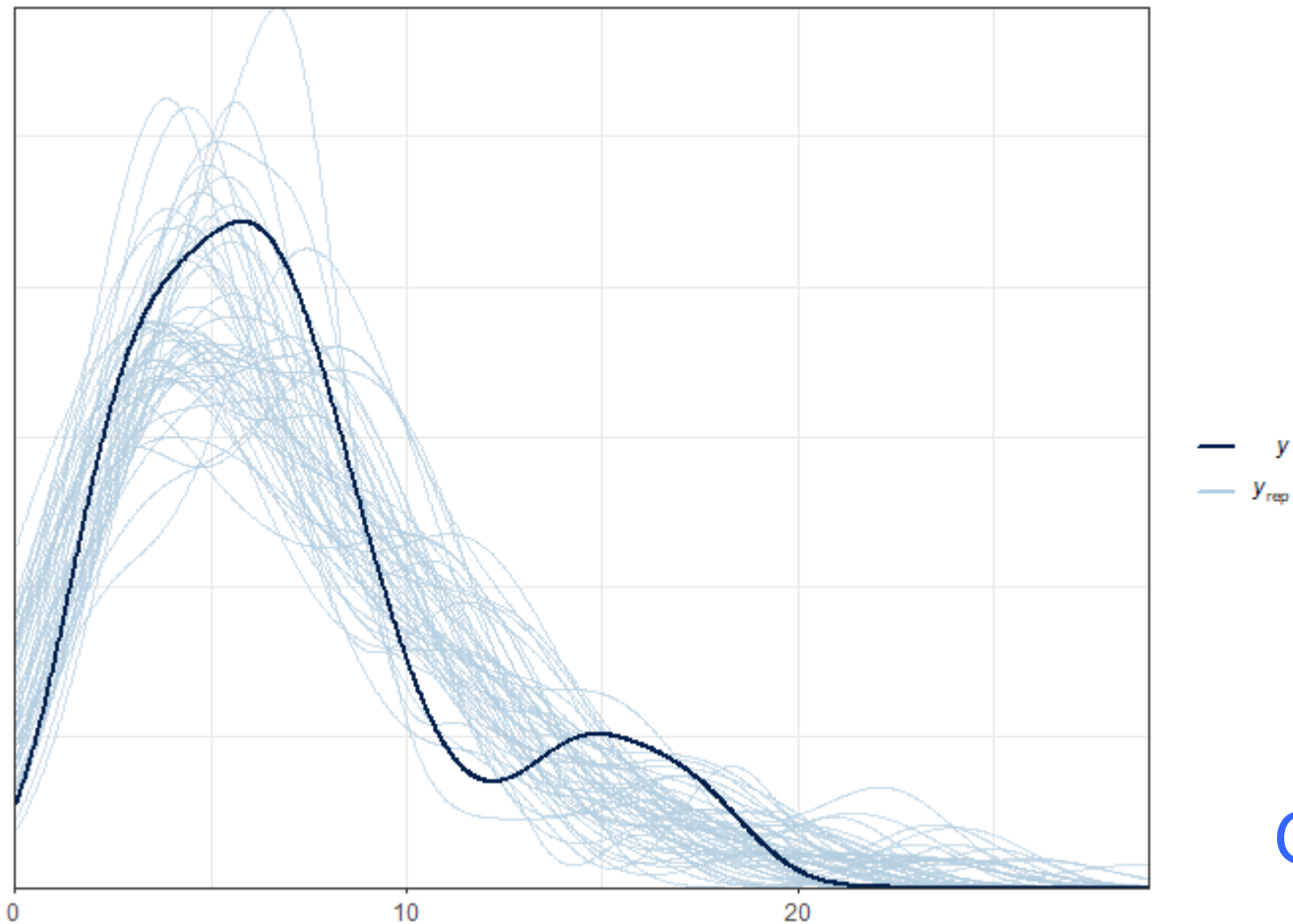
Influence:
Case
deletion
diagnostics

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

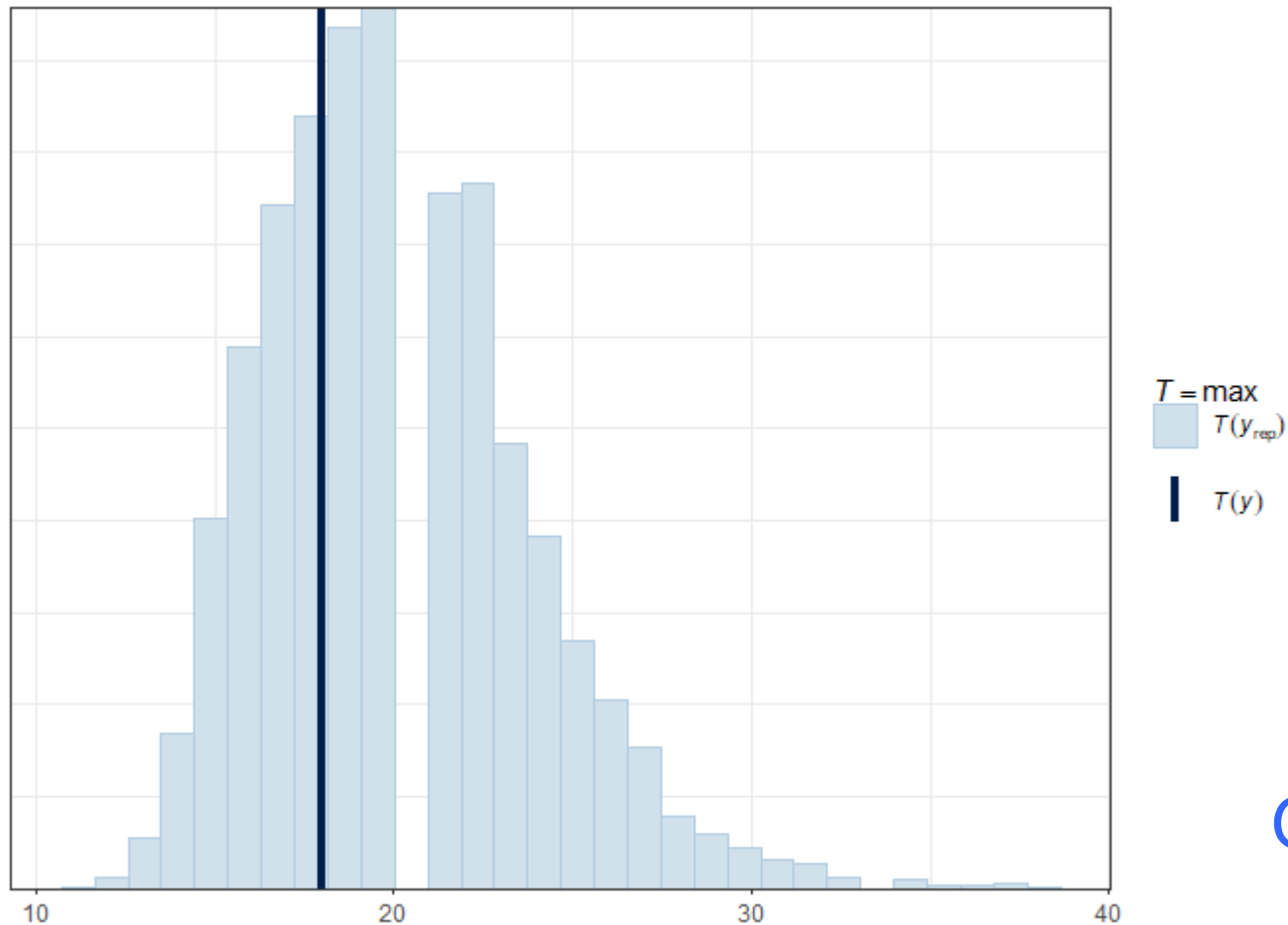
```
pp_check(bayesHLE, plotfun = "dens_overlay")
```



Good

Posterior predictive check

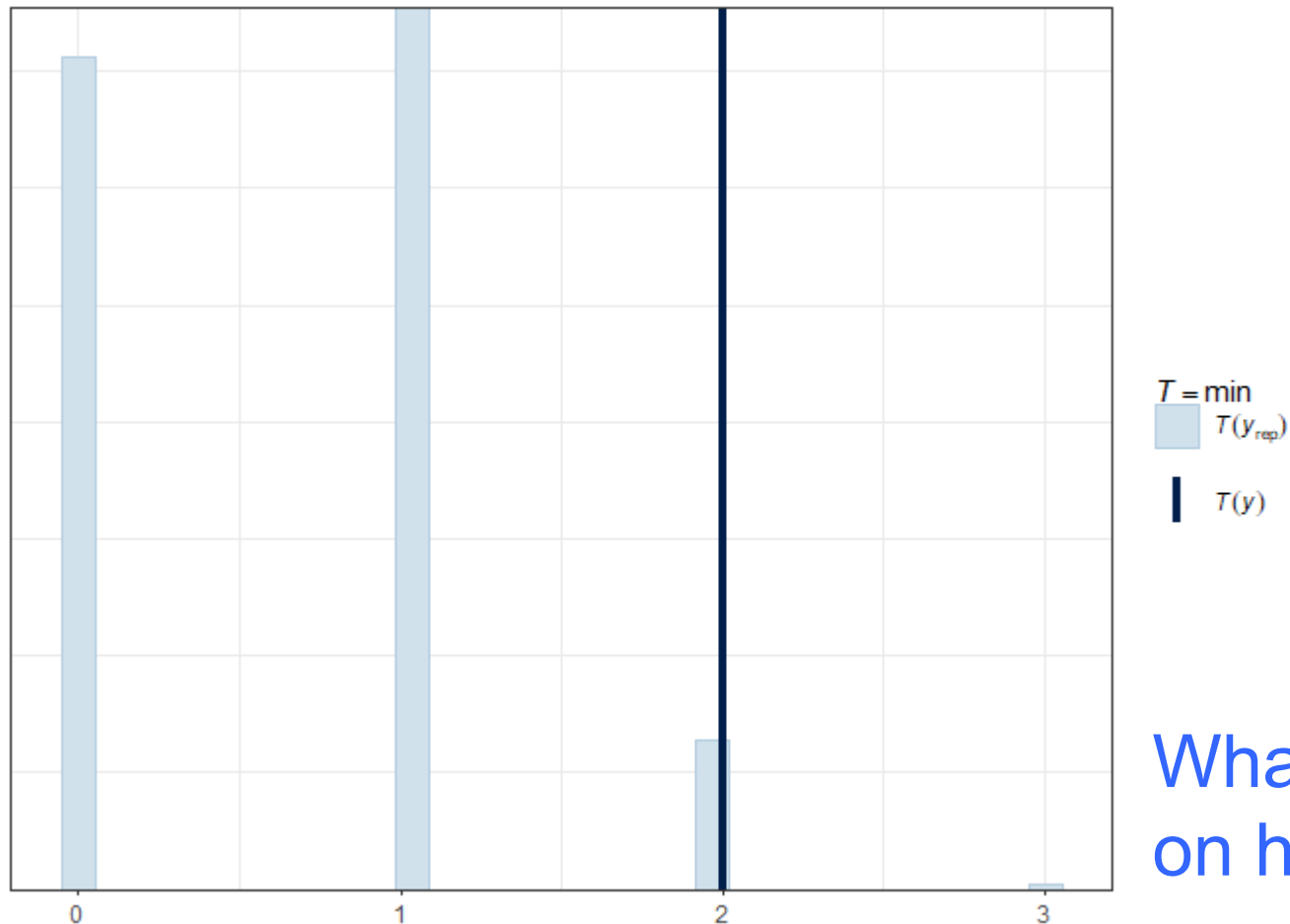
```
pp_check(bayesHLE, plotfun = "stat", stat = "max")
```



Good

Posterior predictive check

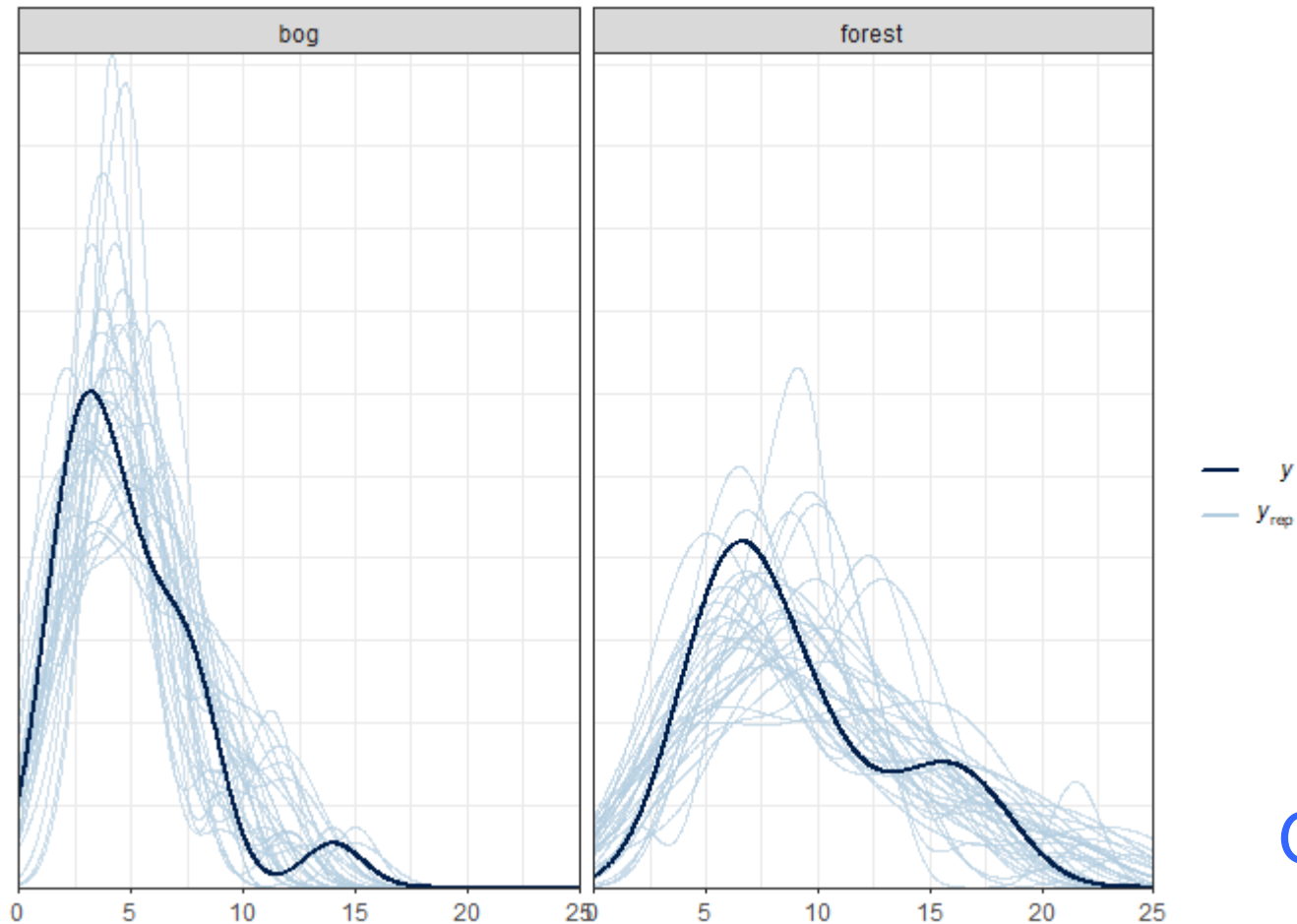
```
pp_check(bayesHLE, plotfun = "stat", stat = "min")
```



What's going on here?

Posterior predictive check

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



Good