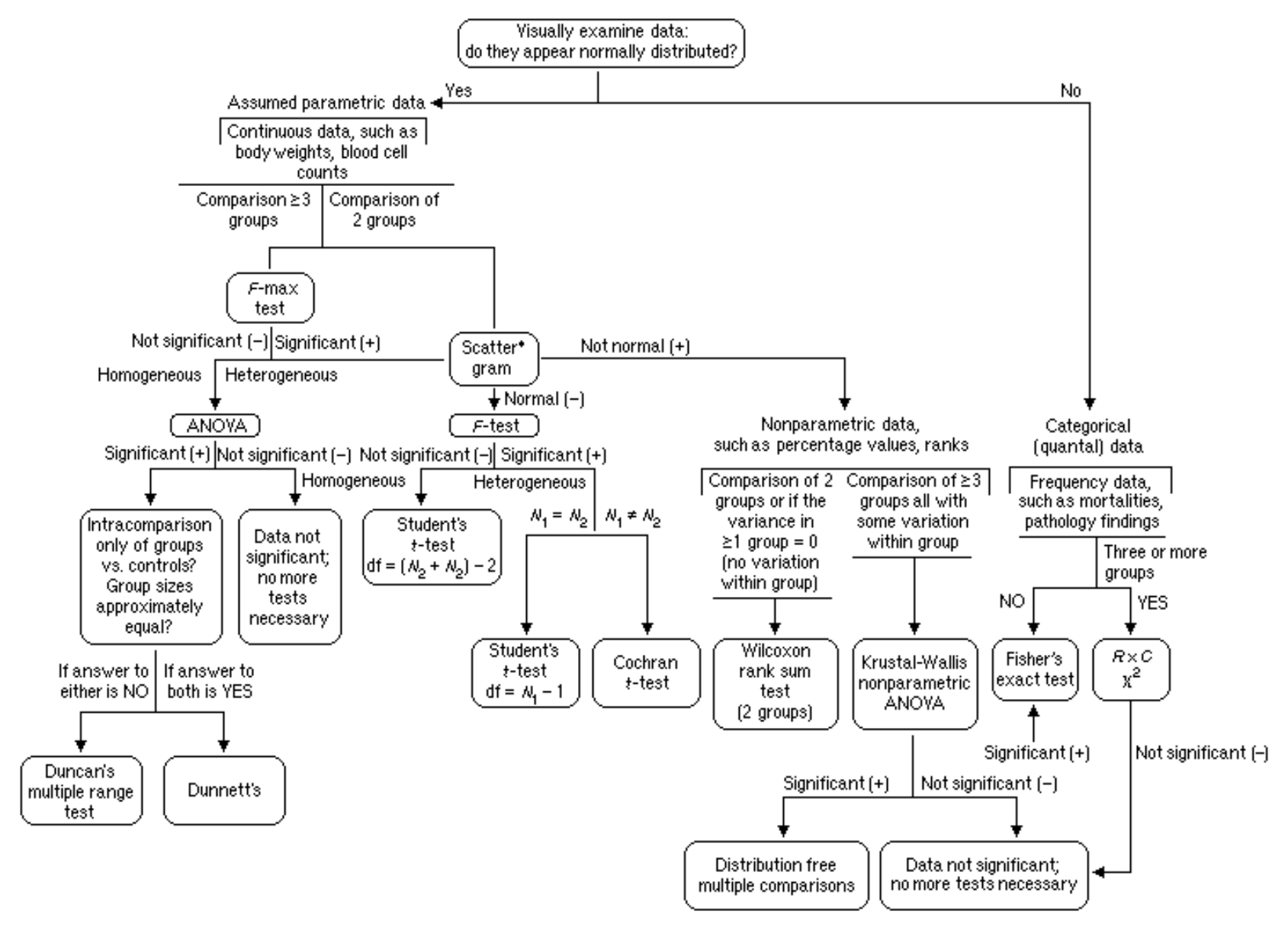
GLM as a unified framework for data analysis

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

How I was taught statistics



So many questions

- **Why** should we really use analysis Y over Z?

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- **Why** should we really use analysis Y over Z?
- What if my data are **not Normal**?
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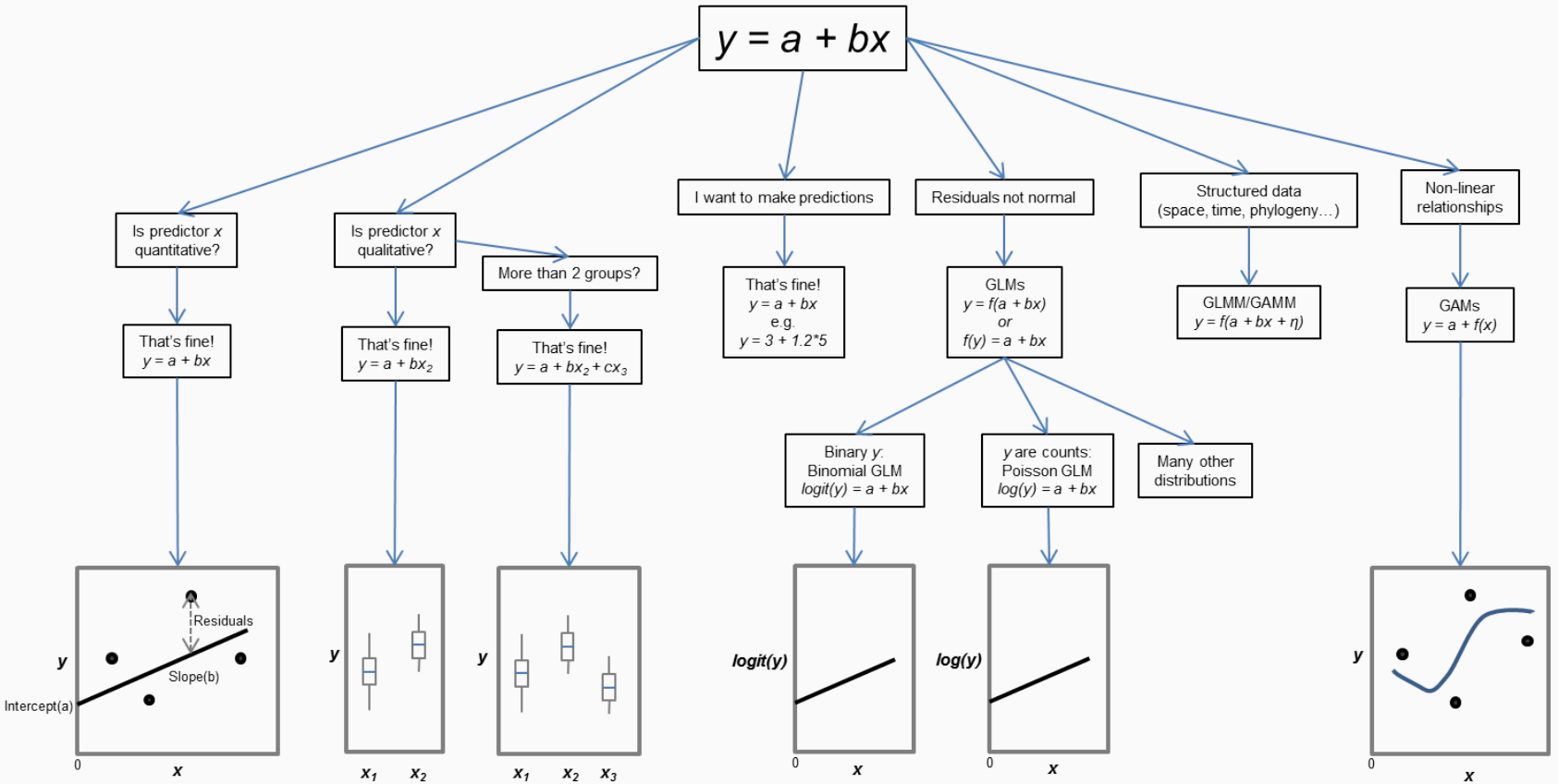
- Why am I getting **different p-values** with different tests?
- What even is a **p-value**?
- How can I take **different factors** into account?

So many questions

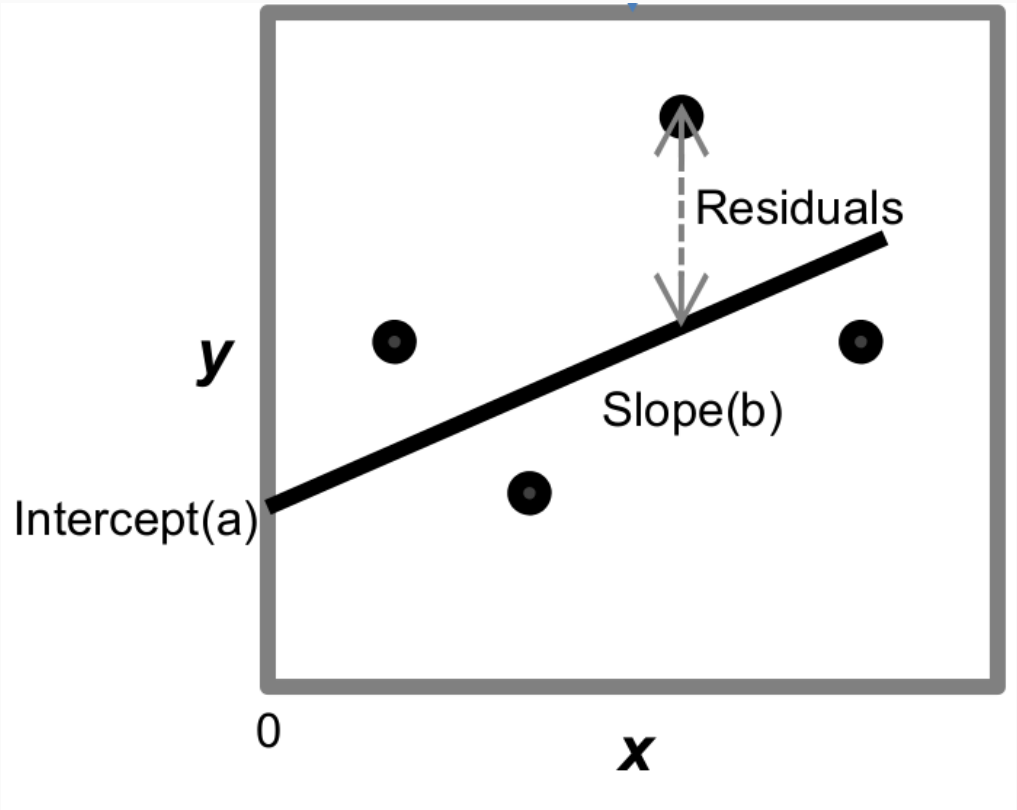
- **Why** should we really use analysis Y over Z?
- What if my data are **not Normal**?
- What if they are **not independent**?
- Why am I getting **different p-values** with different tests?
- What even is a **p-value**?
- How can I take **different factors** into account?
- Can I make **predictions**?

A unified framework



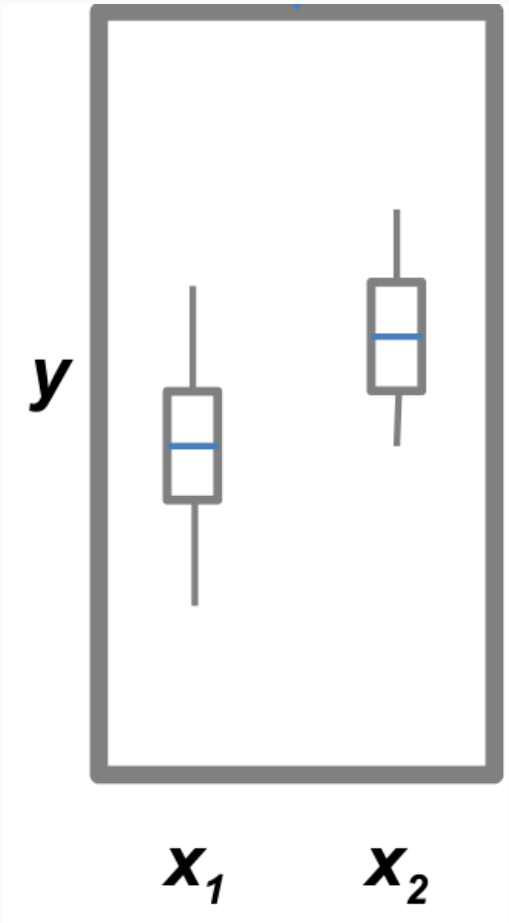
Linear regression

$$y = a + bx$$



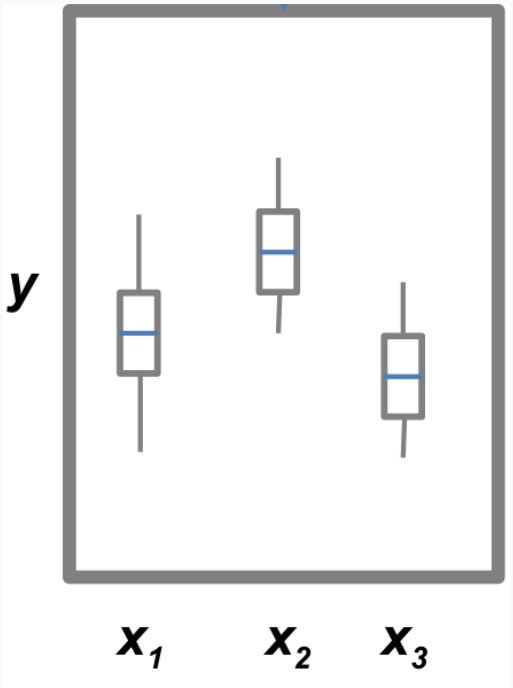
Is predictor X qualitative?

$$y = a + bx_2$$



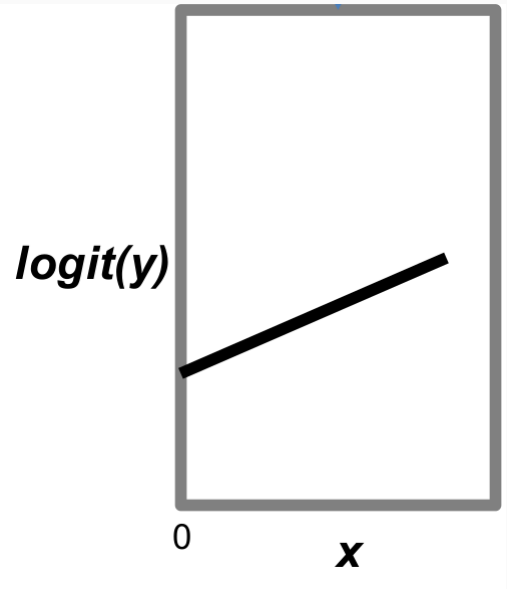
More than 2 groups?

$$y = a + bx_2 + cx_3$$



My data (residuals) are not Normal

$$y = f(a + bx)$$

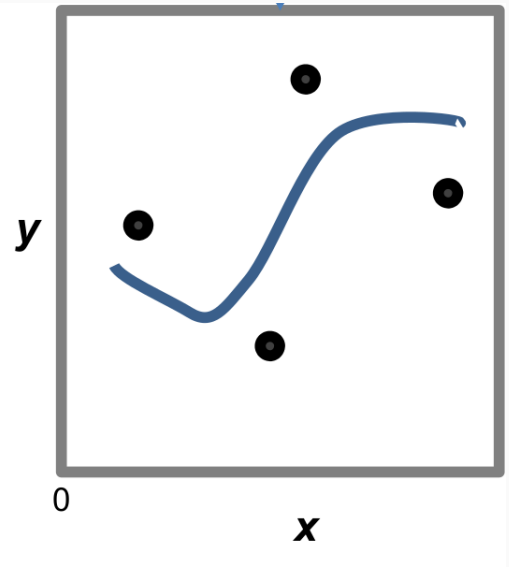


My data are structured (space, time, phylogeny)

$$y = f(a + bx + \eta)$$

Relationships are not linear

$$y = a + f(x)$$



t-tests

ANOVA

regression

...

are special cases of GLM

With GLM we can analyse

many different types of data

using many predictors

(quantitative & qualitative)

Unified, coherent framework for data analysis with many extensions:

- **GLMM** (mixed models): accomodate data structure & variation (space, time, phylogeny)

Unified, coherent framework for data analysis with many extensions:

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Unified, coherent framework for data analysis with many extensions:

- **GLMM** (mixed models): accomodate data structure & variation (space, time, phylogeny)
- **GAMM** (generalised additive models): non-linear relationships
- **Model-based multivariate** statistics

Unified, coherent framework for data analysis with many extensions:

- **GLMM** (mixed models): accomodate data structure & variation (space, time, phylogeny)
- **GAMM** (generalised additive models): non-linear relationships
- **Model-based multivariate** statistics
- **Bayesian** modelling

The Generalised Linear Model (GLM) is a particularly reasonable vantage point on statistical analyses, as **many tests and procedures are special cases** of the GLM. The downside of that (and any other) vantage point is that **we first have to climb it**. There are the morass of unfamiliar terminology, the scree slopes of probability and the cliffs of distributions. **The vista, however, is magnificent**. From the GLM, t-test, ANOVA and regression neatly arrange themselves into regular patterns, and we can see the paths leading towards the horizon: to time series analyses, Bayesian statistics, spatial statistics and so forth.

Dormann 2020

Introduction to linear models

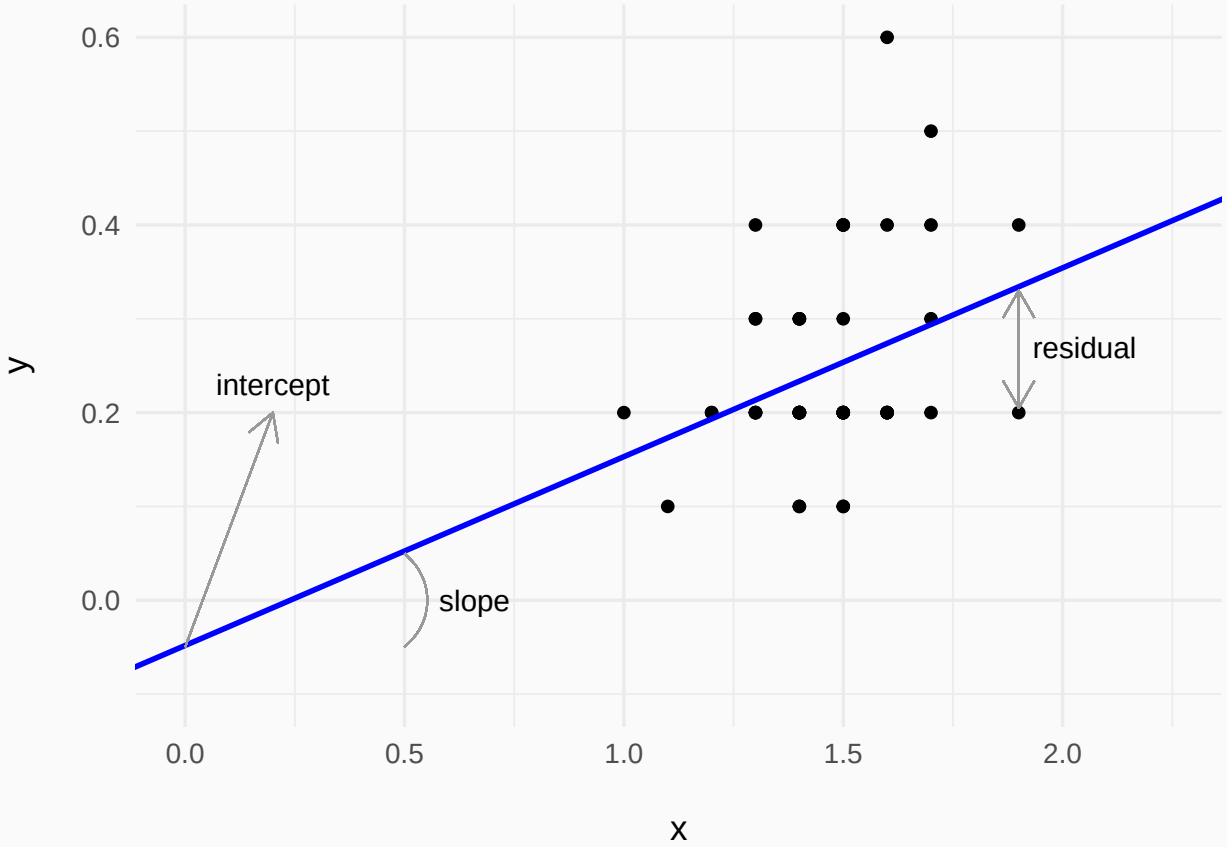
Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Our unified regression framework (GLM)

$$y_i = a + bx_i + \varepsilon_i$$

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$



Data

y = response variable

x = predictor

Parameters

a = intercept

b = slope

σ = residual variation

ε = residuals

What's the intercept?

Expected value of y when predictors (x) = 0

If x = 0:

- y = a + b*0

What's the intercept?

Expected value of y when predictors (x) = 0

If x = 0:

- y = a + b*0
- y = a

What's the slope?

How much y increases (or decreases) when x increases in 1 unit

If we have model

$y = 0.5 + 2*x$

If x increases 1 unit, y increases **2 units**

- If x = 10 —> $y = 0.5 + 2 * 10 = 20.5$

What's the slope?

How much y increases (or decreases) when x increases in 1 unit

If we have model

$y = 0.5 + 2*x$

If **x** increases 1 unit, **y** increases **2 units**

- If x = 10 —> $y = 0.5 + 2 * 10 =$ **20.5**
- If x = 11 —> $y = 0.5 + 2 * 11 =$ **22.5**

Slopes can be negative

If we have model

$y = 0.5$**- 2*x**

If **x** increases 1 unit, **y** decreases 2 units

- If x = 10 -> $y = 0.5 - 2 * 10 =$ **-19.5**

Slopes can be negative

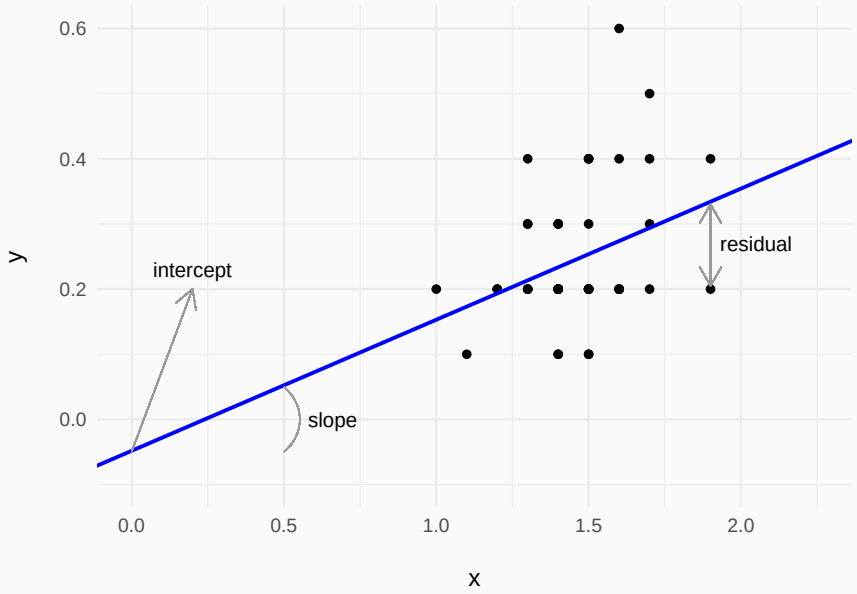
If we have model

$y = 0.5$**- 2*x**

If **x** increases 1 unit, **y** decreases 2 units

- If x = 10 -> $y = 0.5 - 2 * 10 =$ **-19.5**
- If x = 11 -> $y = 0.5 - 2 * 11 =$ **-21.5**

What are residuals?



How far points fall from the regression line

Difference between **observed values** and values **predicted** by model (regression line)

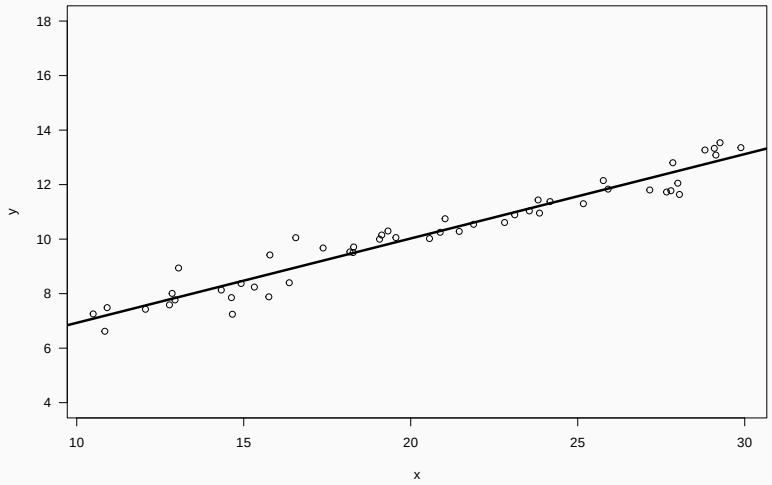
If sigma is large, residuals are larger

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

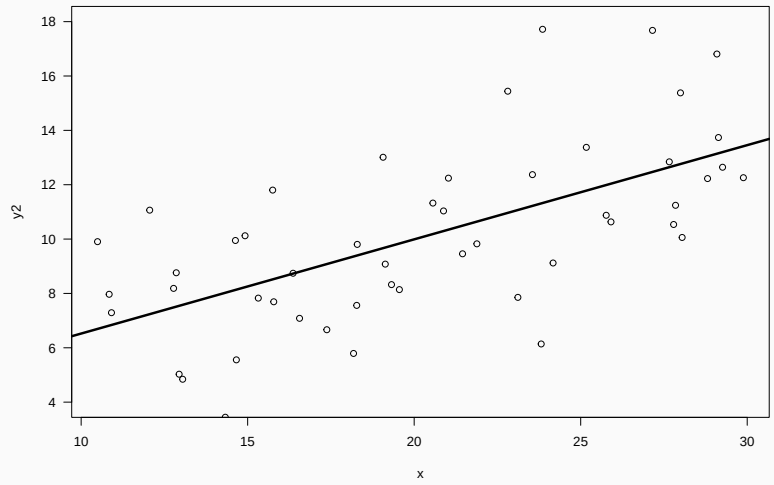
If sigma is larger:

- points farther from regression line
- larger difference of observed - predicted values

small sigma

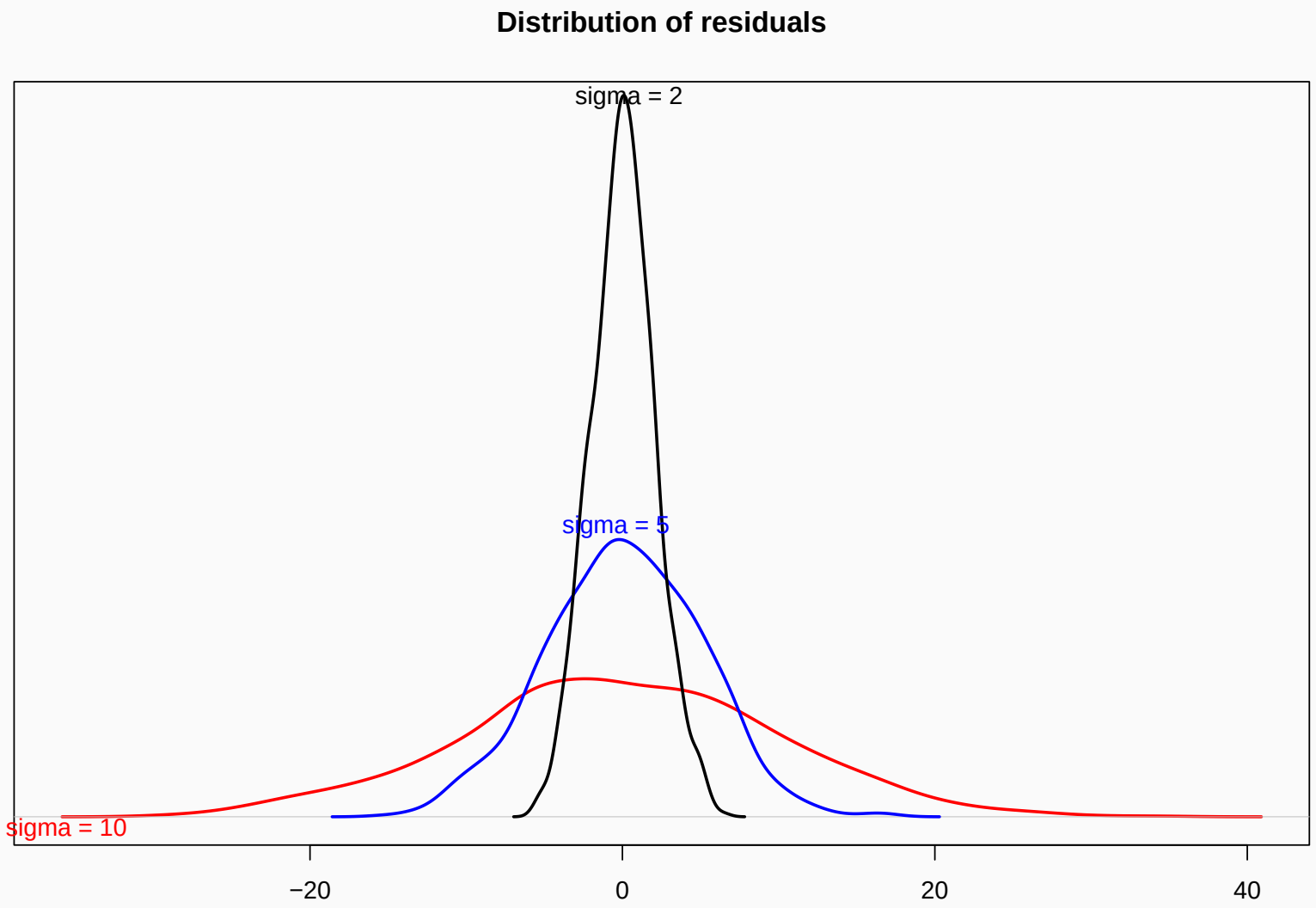


large sigma



Residual variation (sigma) is the Std. Dev. of residuals

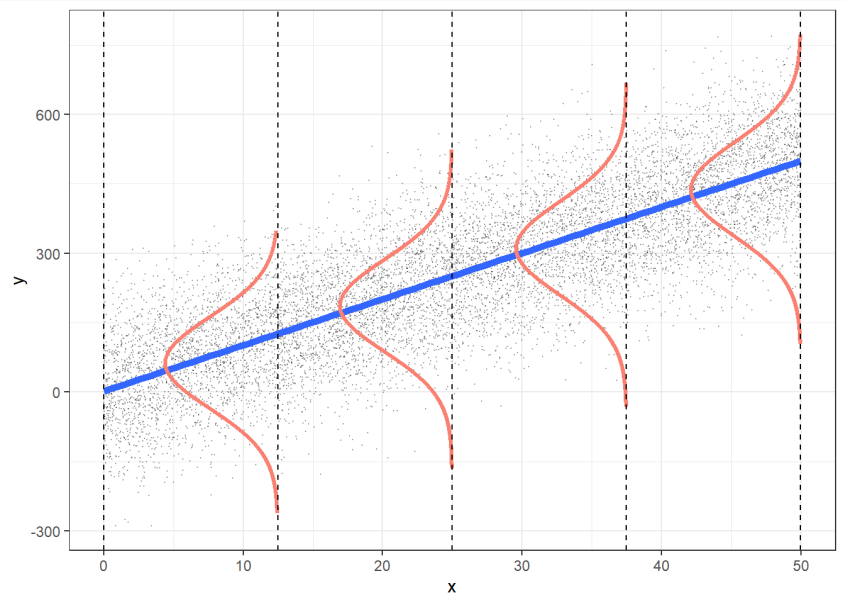
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$



In a general linear model we assume residuals are

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

- Normal

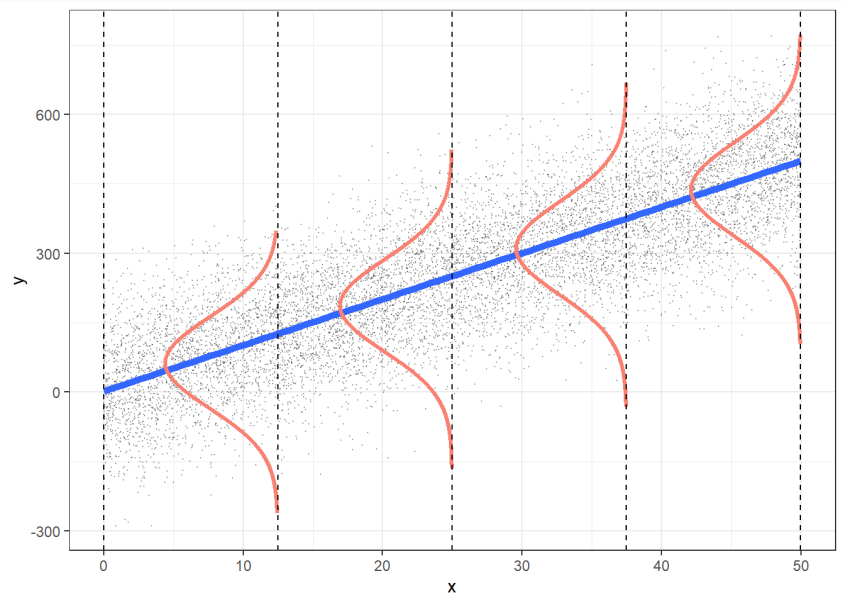


Roback & Legler 2021

In a general linear model we assume residuals are

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

- Normal
- Centred on 0 (no bias)

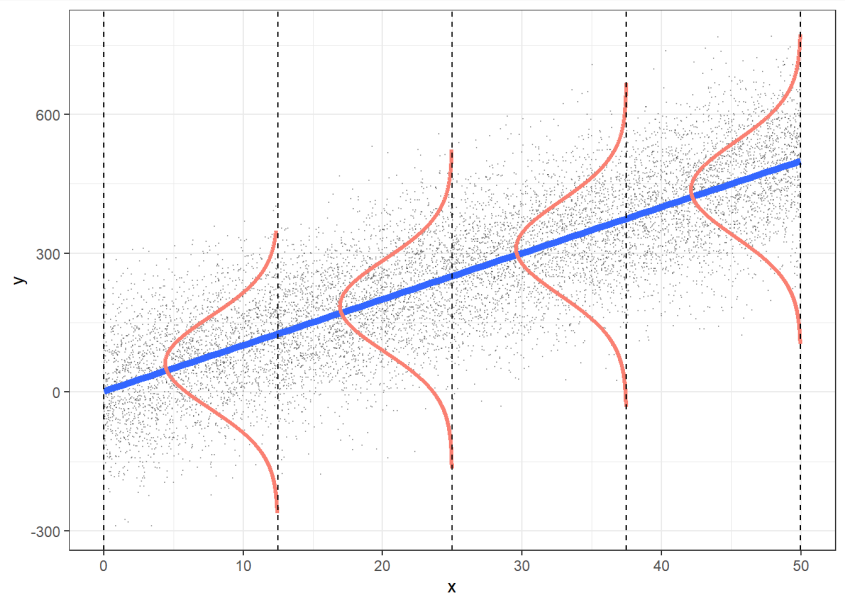


Roback & Legler 2021

In a general linear model we assume residuals are

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

- Normal
- Centred on 0 (no bias)
- Homogeneous variance (*homoscedasticity*)



Roback & Legler 2021

Different ways to write same model

$$y_i = a + bx_i + \varepsilon_i$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

$$y_i \sim N\left(\mu_i, \sigma^2\right)$$
$$\mu_i = a + bx_i$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Quiz

https://pollev.com/franciscorod726

Linear models

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https://frodriguezsanchez.net

Example dataset: forest trees

- Download this dataset (or the entire zip file)

```
trees <- read.csv('data/trees.csv')
head(trees)
```

```
  site   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
3    2 28.03   41.9 female    0
4    5 39.86   46.5 female    0
5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Example dataset: forest trees

- Download this dataset (or the entire zip file)
- Import:

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Questions

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- Do taller trees have bigger trunks?

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- What is the relationship between DBH and height?
- Do taller trees have bigger trunks?
- Can we predict height from DBH? How well?

Plot your data!

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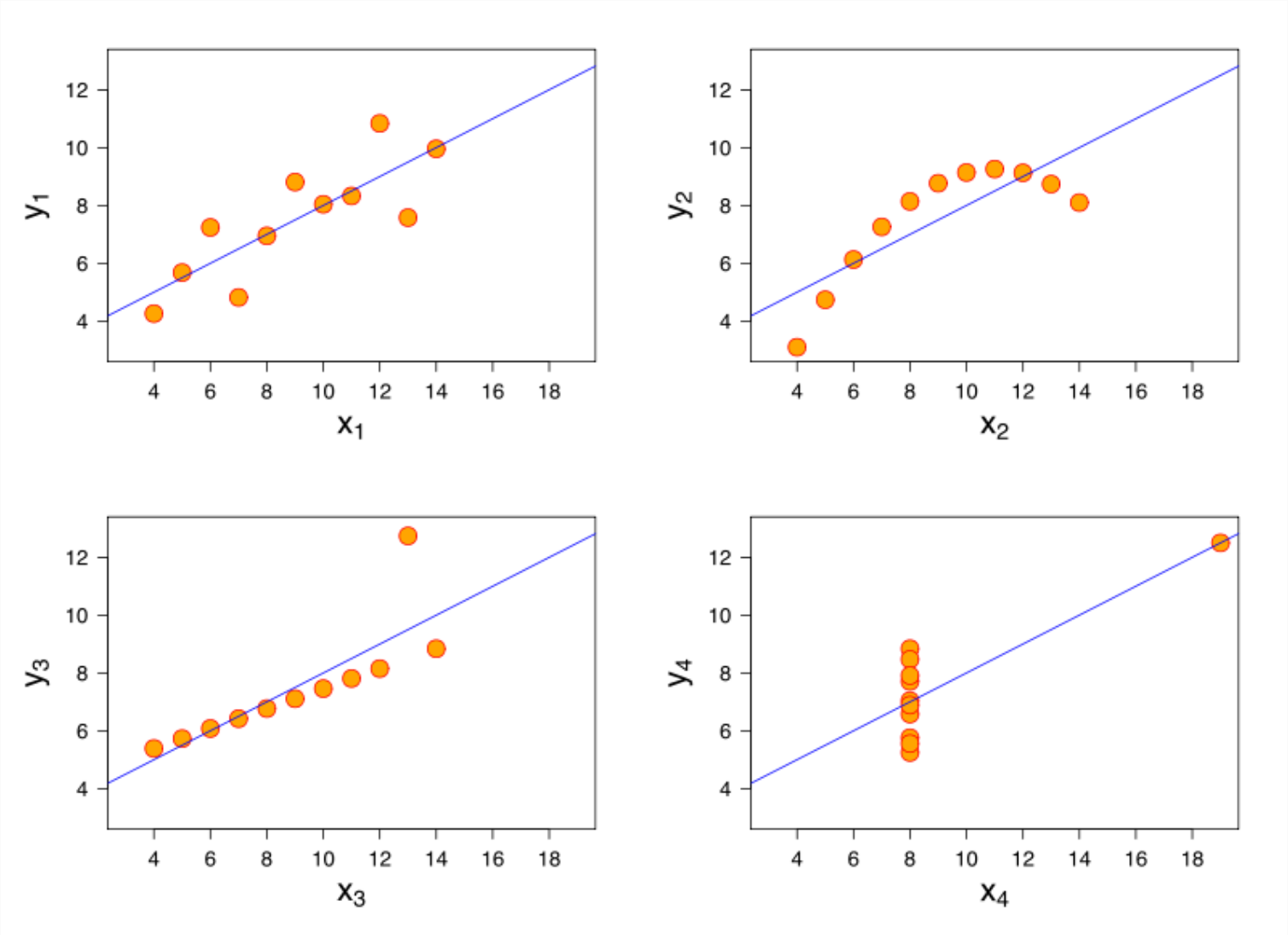
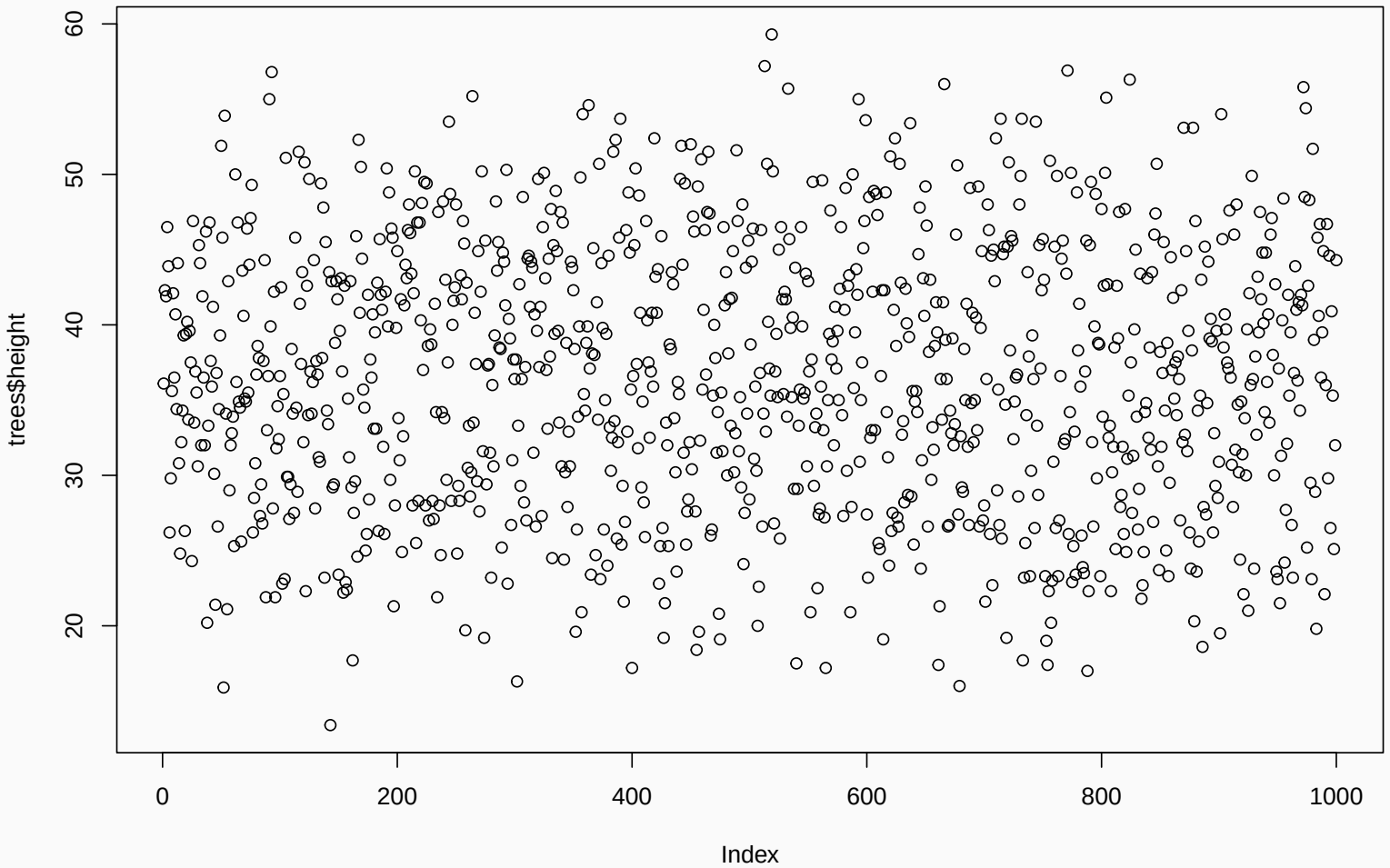
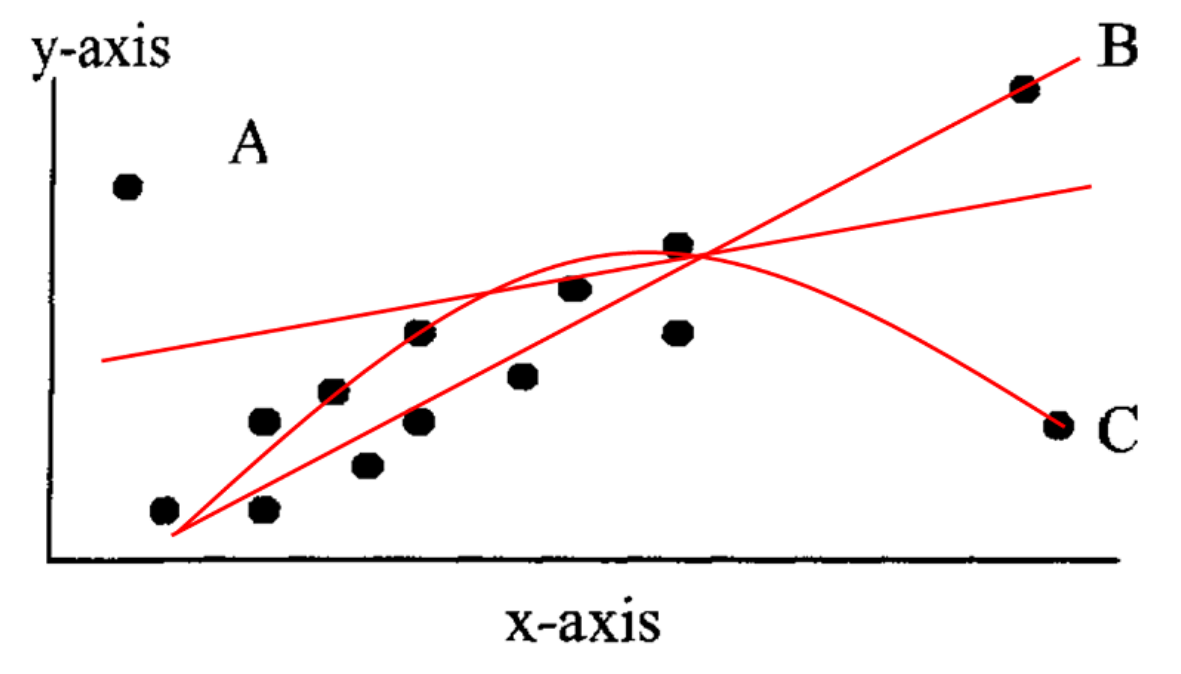


Outliers

```
plot(trees$height)
```



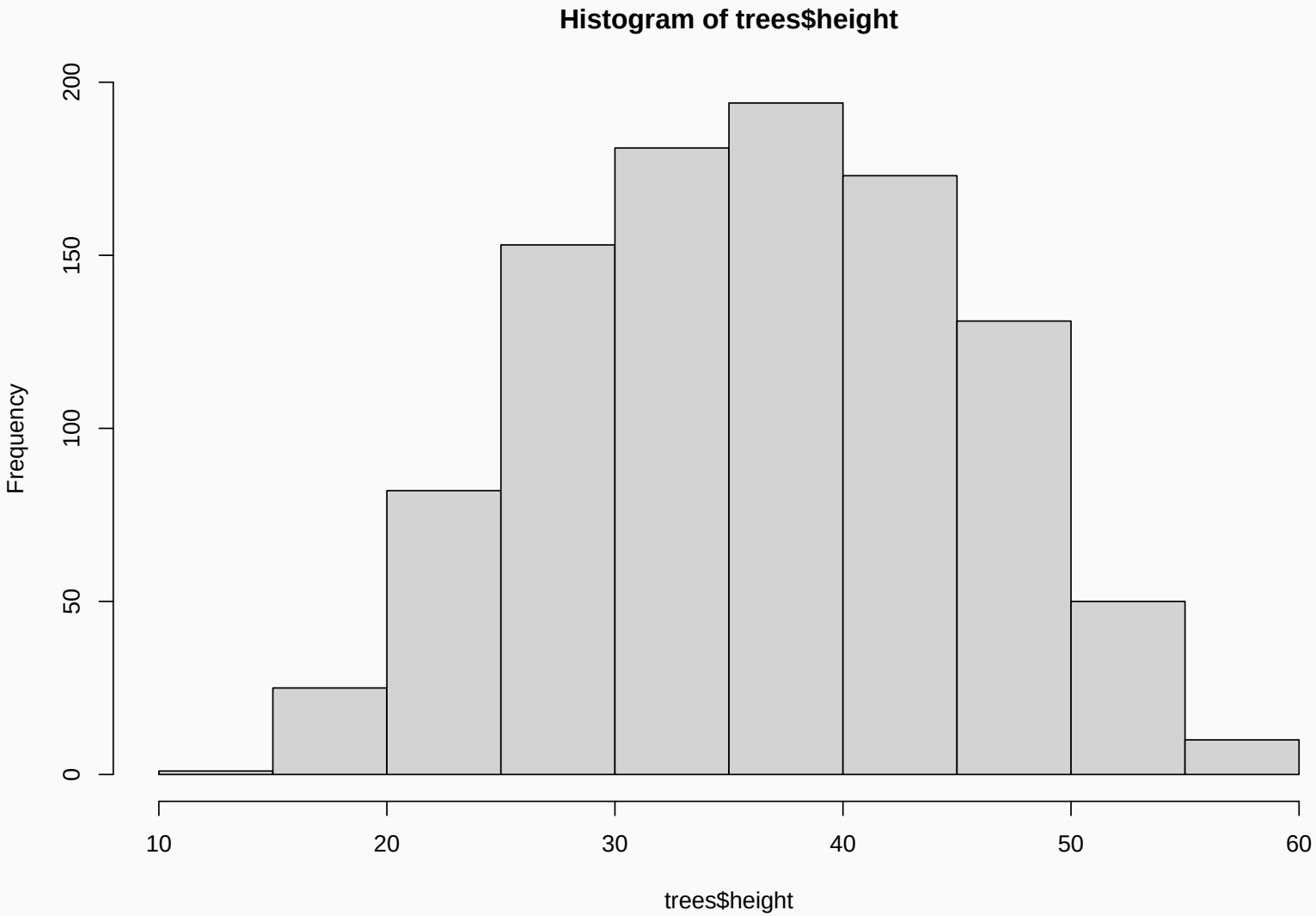
Outliers impact on regression



See http://rpsychologist.com/d3/correlation/

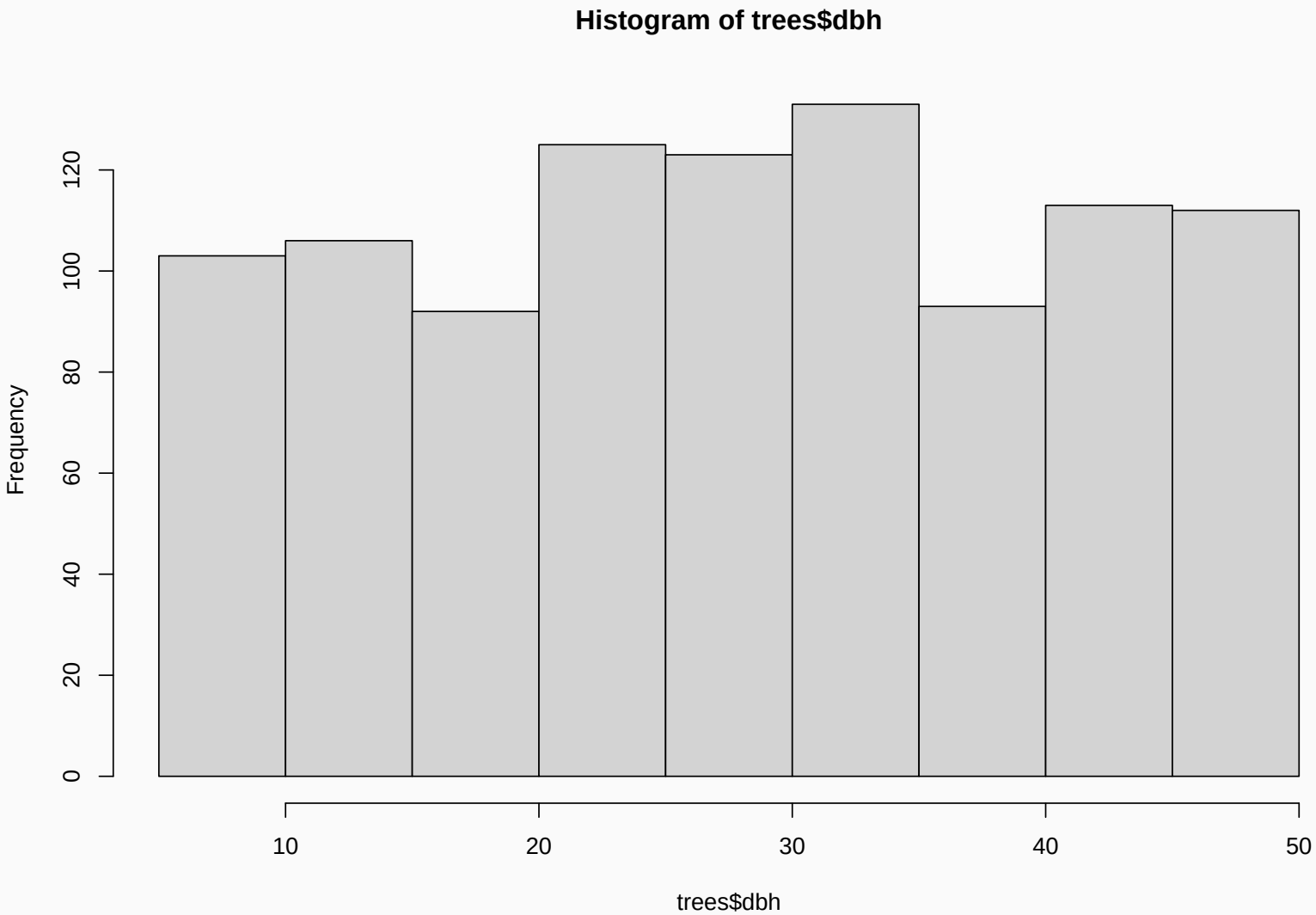
Histogram of response variable

```
hist(trees$height)
```



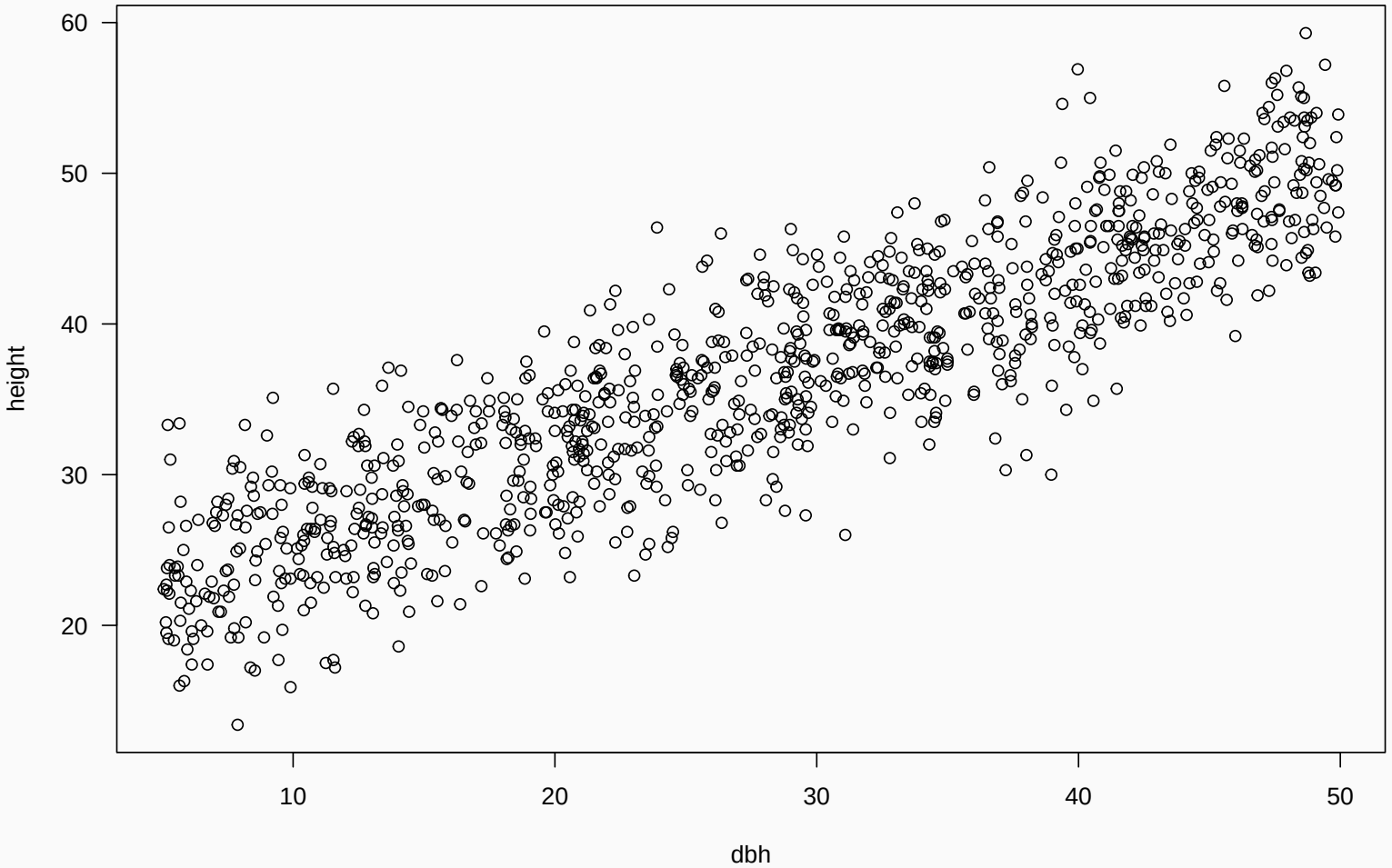
Histogram of predictor variable

```
hist(trees$dbh)
```



Scatterplot

```
plot(height ~ dbh, data = trees, las = 1)
```



Scatterplot

```
ggplot(trees) +
  geom_point(aes(x = dbh, y = height))
```

Model fitting

Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

```
m1 <- lm(height ~ dbh, data = trees)
```

which corresponds to

$$Height_i = a + b \cdot DBH_i + \varepsilon_i$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Package `equatiomatic` returns model structure

```
library('equatiomatic')
m1 <- lm(height ~ dbh, data = trees)
equatiomatic::extract_eq(m1)
```

$$\text{height} = \alpha + \beta_1(\text{dbh}) + \epsilon \tag{1}$$

```
equatiomatic::extract_eq(m1, use_coefs = TRUE)
```

$$\widehat{\text{height}} = 19.34 + 0.62(\text{dbh}) \tag{2}$$

To preview LaTeX:

```
library(texPreview)
tex_preview(equatiomatic::extract_eq(m1))
```

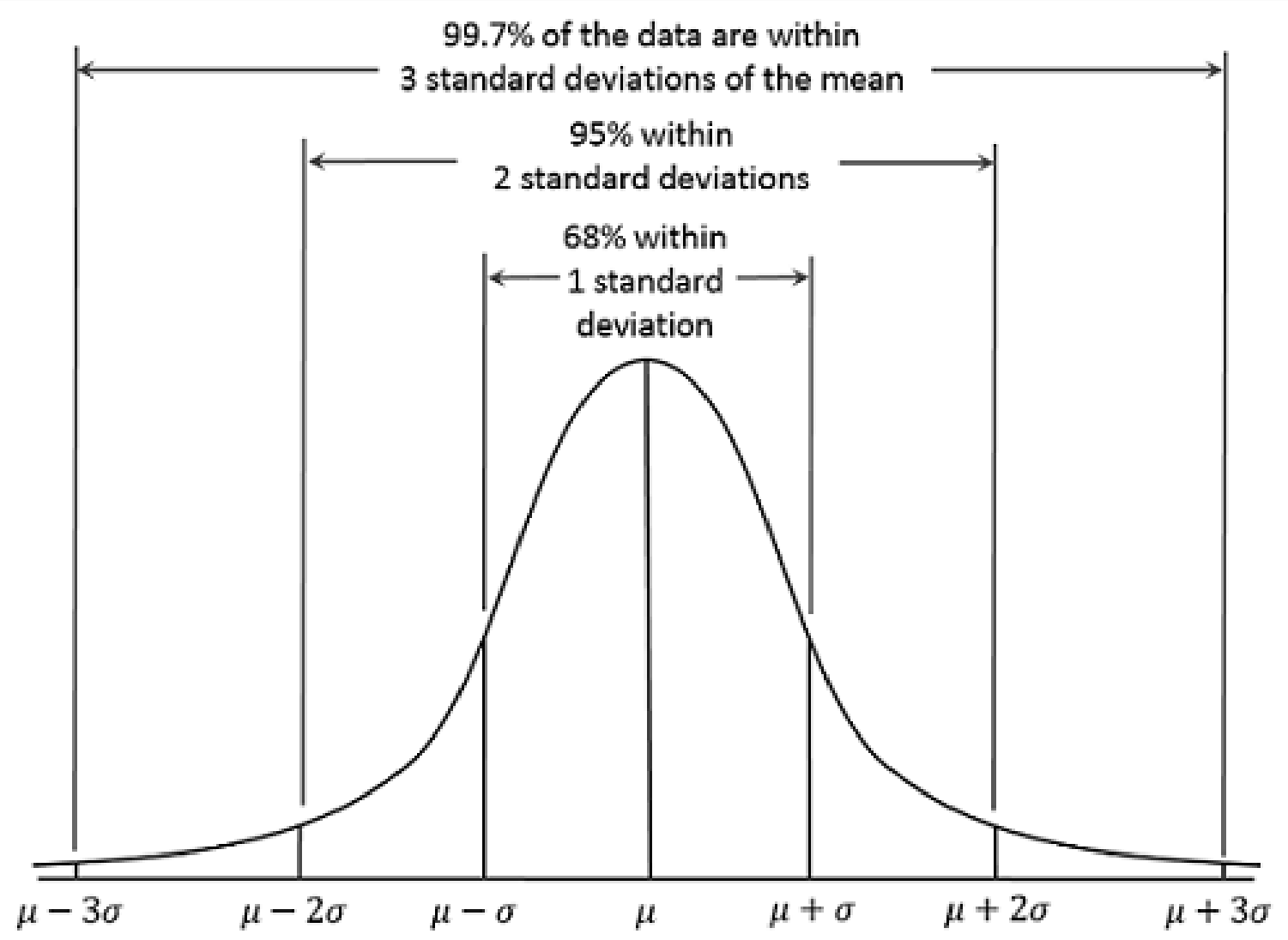
Model interpretation

What does this mean?

```
summary(m1)
```

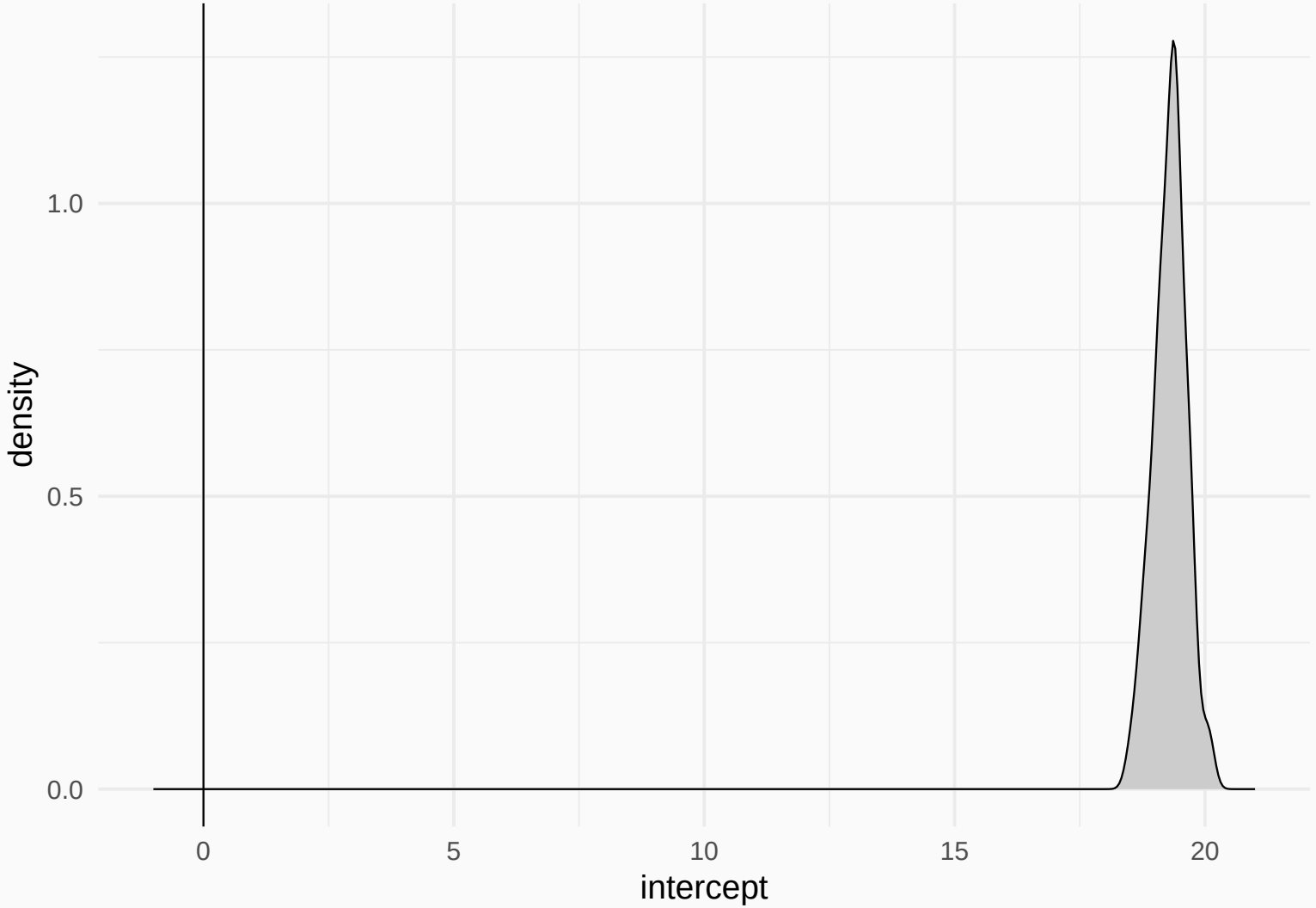
```
Call:
lm(formula = height ~ dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-13.3270  -2.8978   0.1057   2.7924  12.9511

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 19.33920    0.31064   62.26   <2e-16 ***
dbh          0.61570    0.01013   60.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.093 on 998 degrees of freedom
Multiple R-squared:  0.7874,    Adjusted R-squared:  0.7871
F-statistic:  3695 on 1 and 998 DF,  p-value: < 2.2e-16
```

Remember that in a Normal distribution



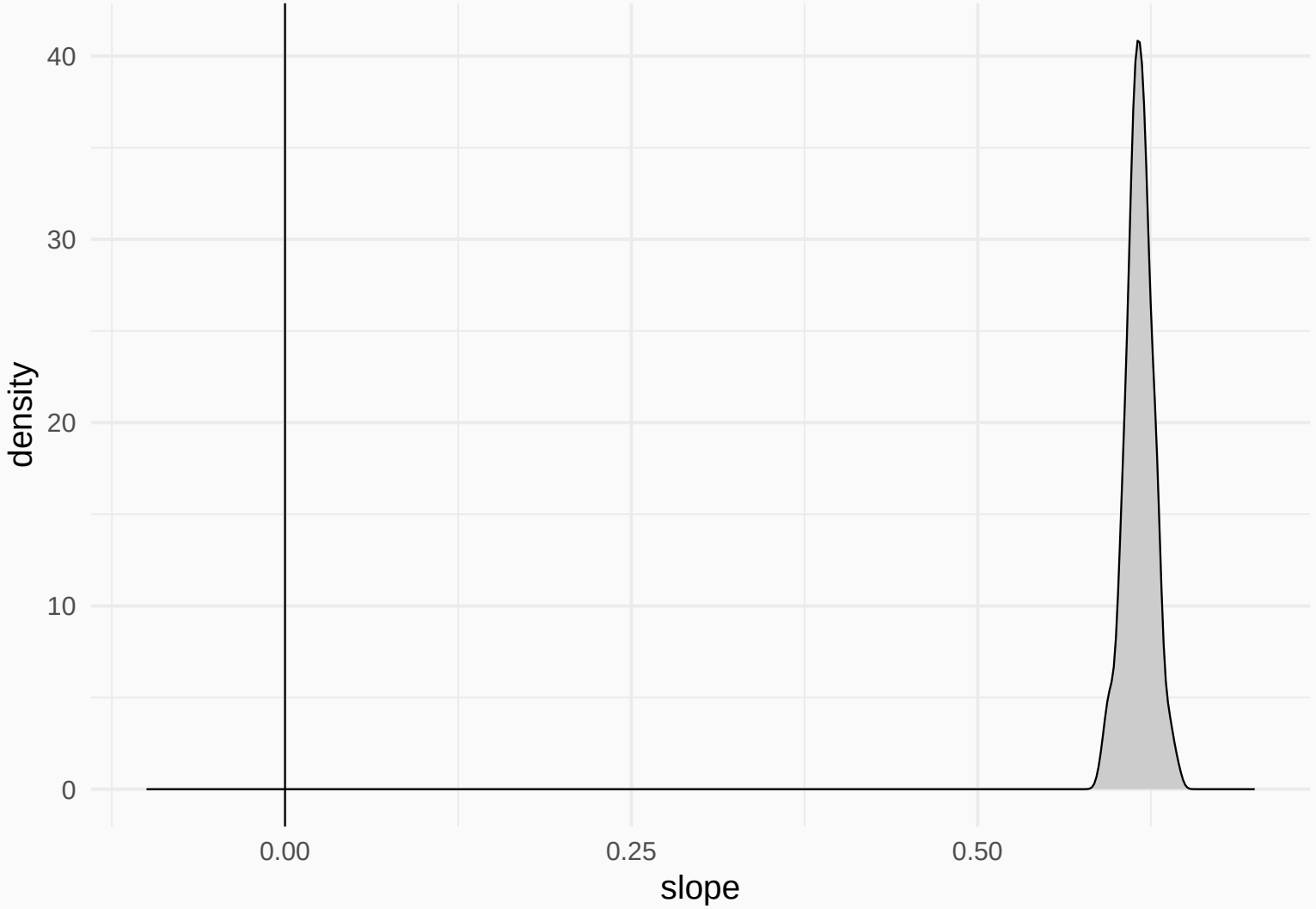
Estimated distribution of the intercept parameter

Parameter	Coefficient	SE	95% CI	t(998)	p
(Intercept)	19.34	0.31	[18.73, 19.95]	62.26	< .001

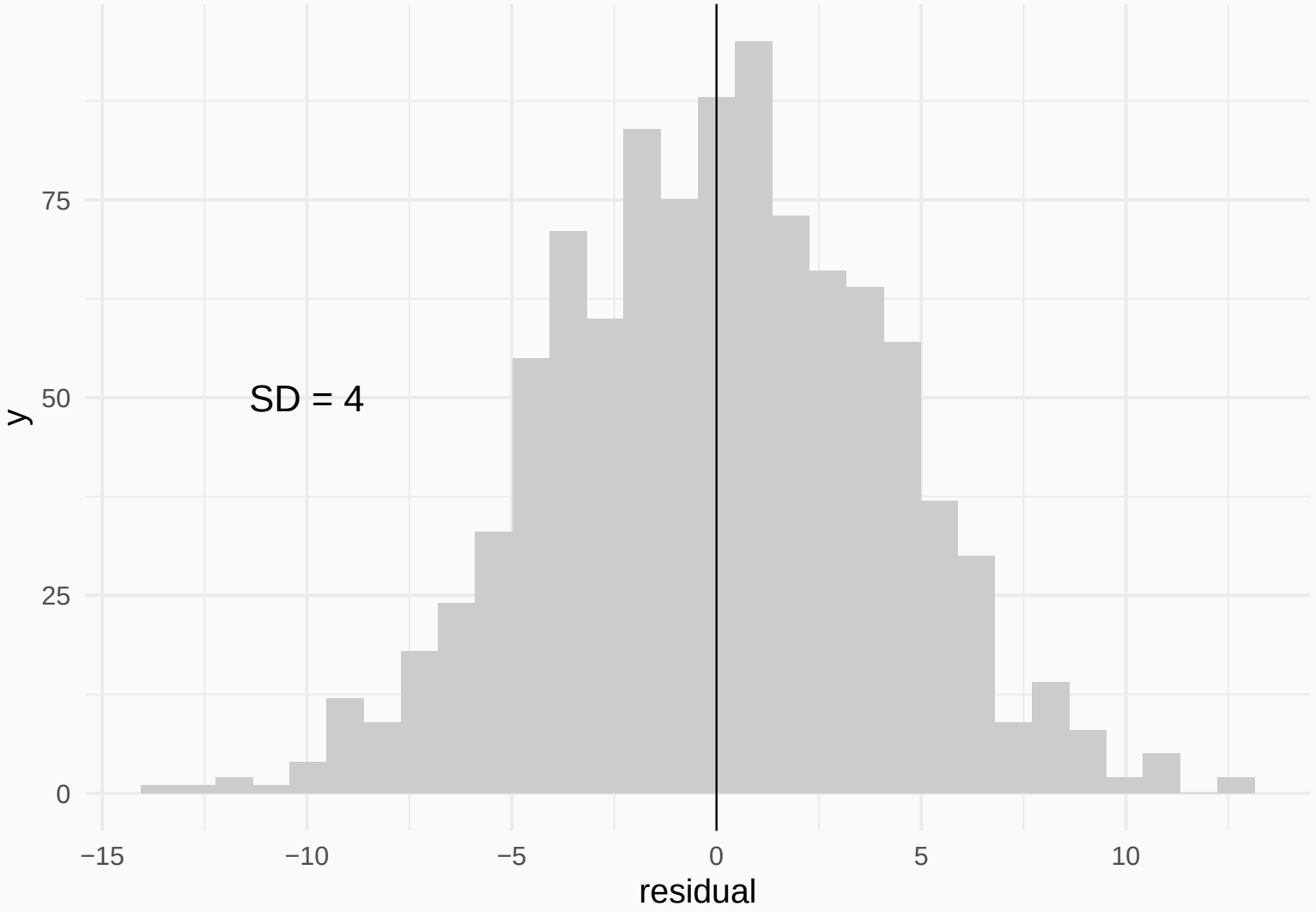


Estimated distribution of the slope parameter

Parameter	Coefficient	SE	95% CI	t(998)	p
dbh	0.62	0.01	[0.60, 0.64]	60.79	< .001



Distribution of residuals



Degrees of freedom

$DF = n - p$

n = sample size

p = number of estimated parameters

Proportion of ‘explained’ variance

$$R^2 = 1 - \frac{Residual\ Variation}{Total\ Variation}$$

Adjusted R-squared

Accounts for model complexity

(number of parameters)

$$R^2_{adj} = 1 - (1 - R^2)\frac{n-1}{n-p-1}$$

Quiz

https://pollev.com/franciscorod726

Centering continuous predictors

Centering continuous predictors

- Helps interpretation
- Helps (complex) model convergence
- Centering usually around the mean, but can be any suitable reference point

Centering continuous predictors

```
mean(trees$dbh)
```

```
[1] 27.88209
```

```
trees$dbh.c <- trees$dbh - 30
```

```
summary(trees$dbh)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   5.06   17.69   28.62   27.88   38.97   49.92 
```

```
summary(trees$dbh.c)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
-24.940 -12.312  -1.380  -2.118   8.965  19.920 
```

Centering continuous predictors

```
m1.c <- lm(height ~ dbh.c, data = trees)
```

```
Call:
lm(formula = height ~ dbh.c, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-13.3270  -2.8978   0.1057   2.7924  12.9511

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 37.81030    0.13119  288.22   <2e-16 ***
dbh.c        0.61570    0.01013   60.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.093 on 998 degrees of freedom
Multiple R-squared:  0.7874,    Adjusted R-squared:  0.7871
F-statistic:  3695 on 1 and 998 DF,  p-value: < 2.2e-16
```

Extracting model info

Retrieving model coefficients

```
coef(m1)
```

```
(Intercept)         dbh
 19.3391968   0.6157036
```

Confidence intervals for parameters

```
confint(m1)
```

```
                 2.5 %    97.5 %
(Intercept) 18.7296053 19.948788
dbh          0.5958282  0.635579
```

Tidy up model coefficients with broom

```
library('broom')
tidy(m1)
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic p.value
  <chr>          <dbl>     <dbl>     <dbl>   <dbl>
1 (Intercept)   19.3      0.311       62.3       0
2 dbh            0.616    0.0101      60.8       0
```

```
glance(m1)
```

```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>
1     0.787         0.787  4.09     3695.       0     1 -2827. 5660. 5675.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

https://broom.tidymodels.org/

Retrieving model parameters with `parameters` package

```
library('easystats')   # parameters package
parameters(m1)
```

```
Parameter   | Coefficient |   SE |         95% CI | t(998) |      p
-------------------------------------------------------------------
(Intercept) |       19.34 | 0.31 | [18.73, 19.95] |  62.26 | < .001
dbh         |        0.62 | 0.01 | [ 0.60,  0.64] |  60.79 | < .001
```

https://easystats.github.io/parameters/

Communicating results

Avoid dichotomania of statistical significance

- 'Never conclude there is **'no difference'** or 'no association' just because **p > 0.05 or CI includes zero**'

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- Estimate and communicate **effect sizes and their uncertainty**

Avoid dichotomania of statistical significance

- 'Never conclude there is **'no difference'** or 'no association' just because **p > 0.05 or CI includes zero**'
- Estimate and communicate **effect sizes and their uncertainty**
- https://doi.org/10.1038/d41586-019-00857-9

Communicating results

- We found a **significant relationship** between DBH and Height **($p<0.05$)**.

Communicating results

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- We found a {*significant*} **positive** relationship between DBH and Height {*(p<0.05)*} **(b = 0.61, SE = 0.01)**.

Communicating results

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- We found a {*significant*} **positive** relationship between DBH and Height {*(p<0.05)*} **(b = 0.61, SE = 0.01)**.
- (add p-value if you wish)

Models that describe themselves

```
library('report')
report(m1)
```

We fitted a linear model (estimated using OLS) to predict height with dbh (formula: height ~ dbh). The model explains a statistically significant and substantial proportion of variance (R2 = 0.79, F(1, 998) = 3695.40, p < .001, adj. R2 = 0.79). The model's intercept, corresponding to dbh = 0, is at 19.34 (95% CI [18.73, 19.95], t(998) = 62.26, p < .001). Within this model:

- The effect of dbh is statistically significant and positive (beta = 0.62, 95% CI [0.60, 0.64], t(998) = 60.79, p < .001; Std. beta = 0.89, 95% CI [0.86, 0.92])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

https://easystats.github.io/report/

Generating table with model results: `report_table`

```
report_table(m1, include_effectsize = FALSE)
```

Parameter	Coefficient	95% CI	t(998)	p	Fit
(Intercept)	19.34	[18.73, 19.95]	62.26	< .001	
dbh	0.62	[0.60, 0.64]	60.79	< .001	
AIC					5660.25
AICc					5660.27
BIC					5674.97
R2					0.79
R2 (adj.)					0.79
Sigma					4.09

Generating table with model results: `gtsummary`

```
library('gtsummary')
tbl_regression(m1, intercept = TRUE)
```

Characteristic	Beta	95% CI[1]	p-value
(Intercept)	19	19, 20	<0.001
dbh	0.62	0.60, 0.64	<0.001

[1]CI = Confidence Interval

https://www.danieldsjoberg.com/gtsummary

Generating table with model results: `modelsummary`

```
library('modelsummary')
modelsummary(m1, output = 'markdown')  # Word, PDF, PowerPoint, png...
```

	(1)
(Intercept)	19.339
	(0.311)
dbh	0.616
	(0.010)
Num.Obs.	1000
R2	0.787
R2 Adj.	0.787
AIC	5660.3
BIC	5675.0
Log.Lik.	-2827.125
F	3695.395
RMSE	4.09

https://modelsummary.com/

Generating table with model results: `modelsummary`

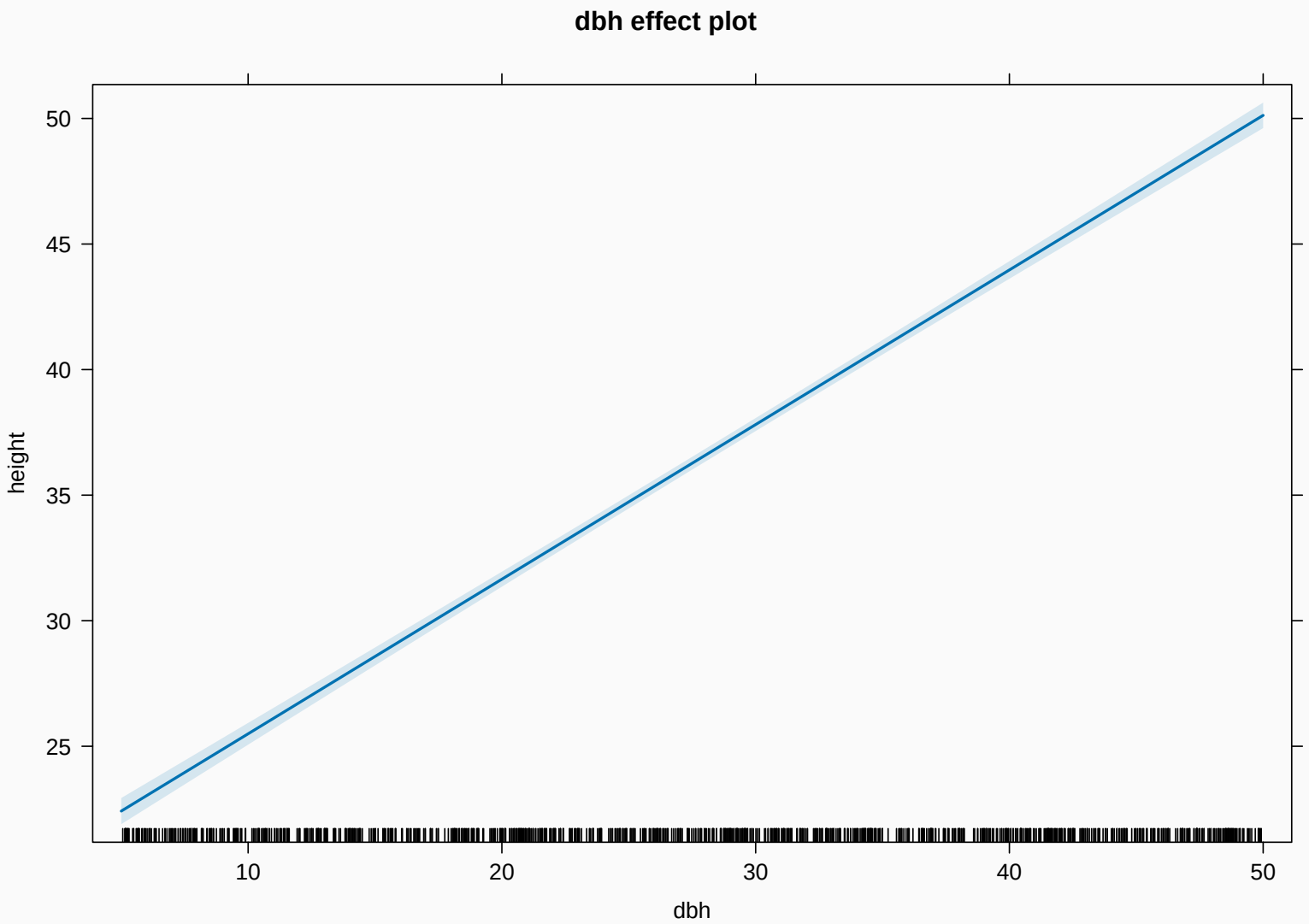
```
modelsummary(m1, fmt = 2,
             estimate = '{estimate} ({std.error})',
             statistic = NULL,
             gof_map = c('nobs', 'r.squared', 'rmse'),
             output = 'markdown')  # Word, PDF, PowerPoint, png...
```

	(1)
(Intercept)	19.34 (0.31)
dbh	0.62 (0.01)
Num.Obs.	1000
R2	0.787
RMSE	4.09

Visualising fitted model

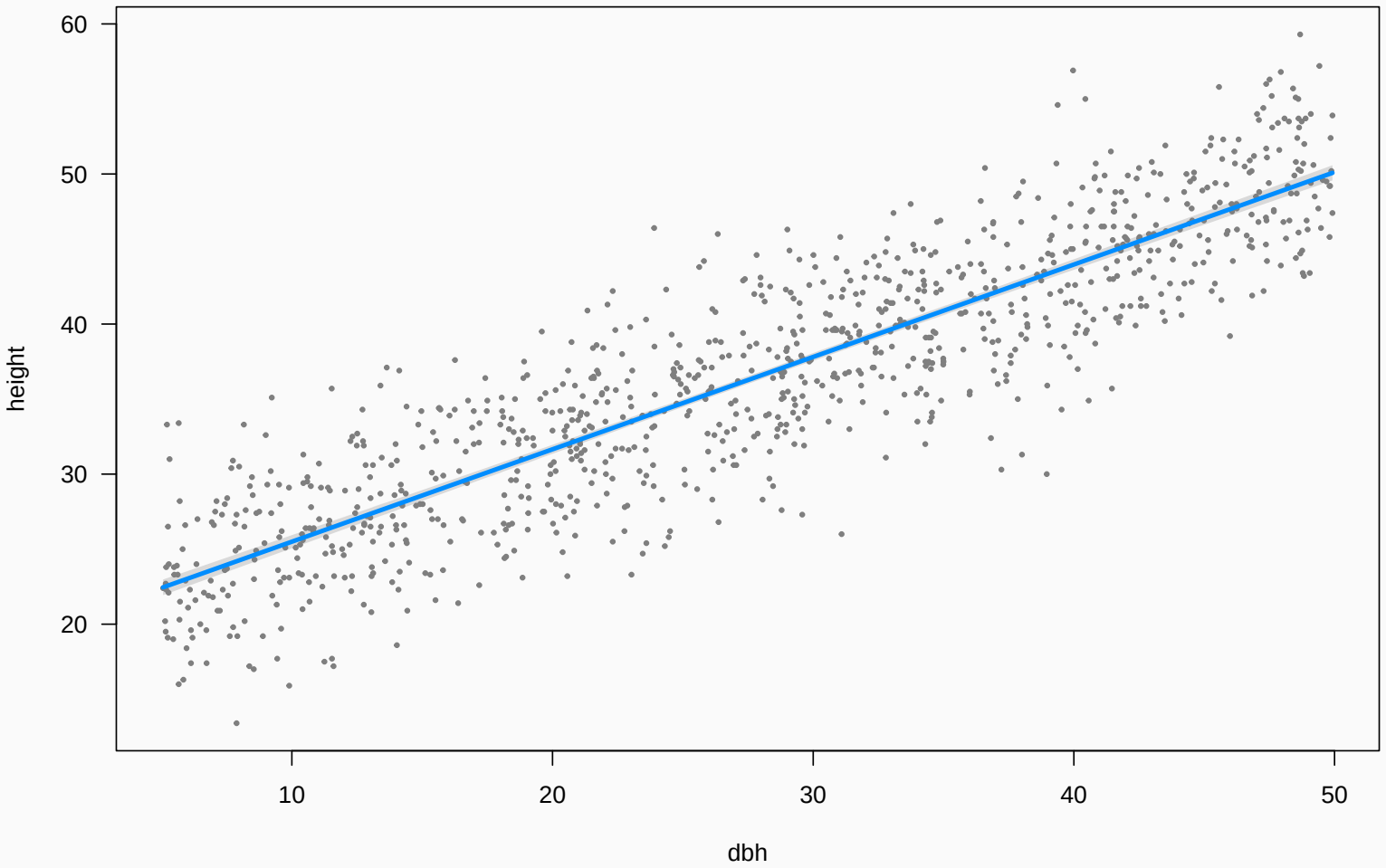
Plot model: `effects` package

```
library('effects')
plot(allEffects(m1))
```



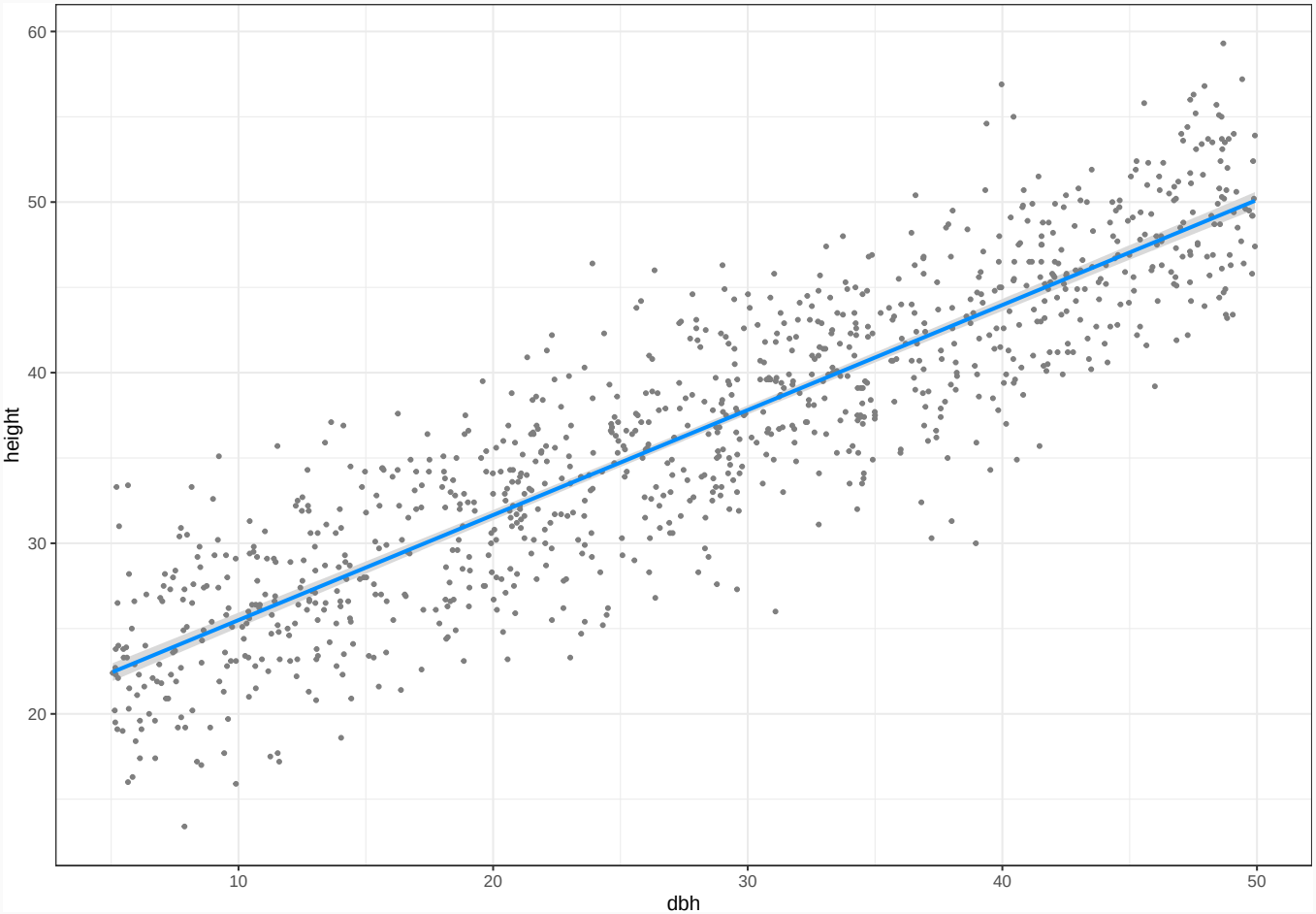
Plot model: visreg

```
library('visreg')
visreg(m1)
```



visreg can use ggplot2 too

```
visreg(m1, gg = TRUE) + theme_bw()
```

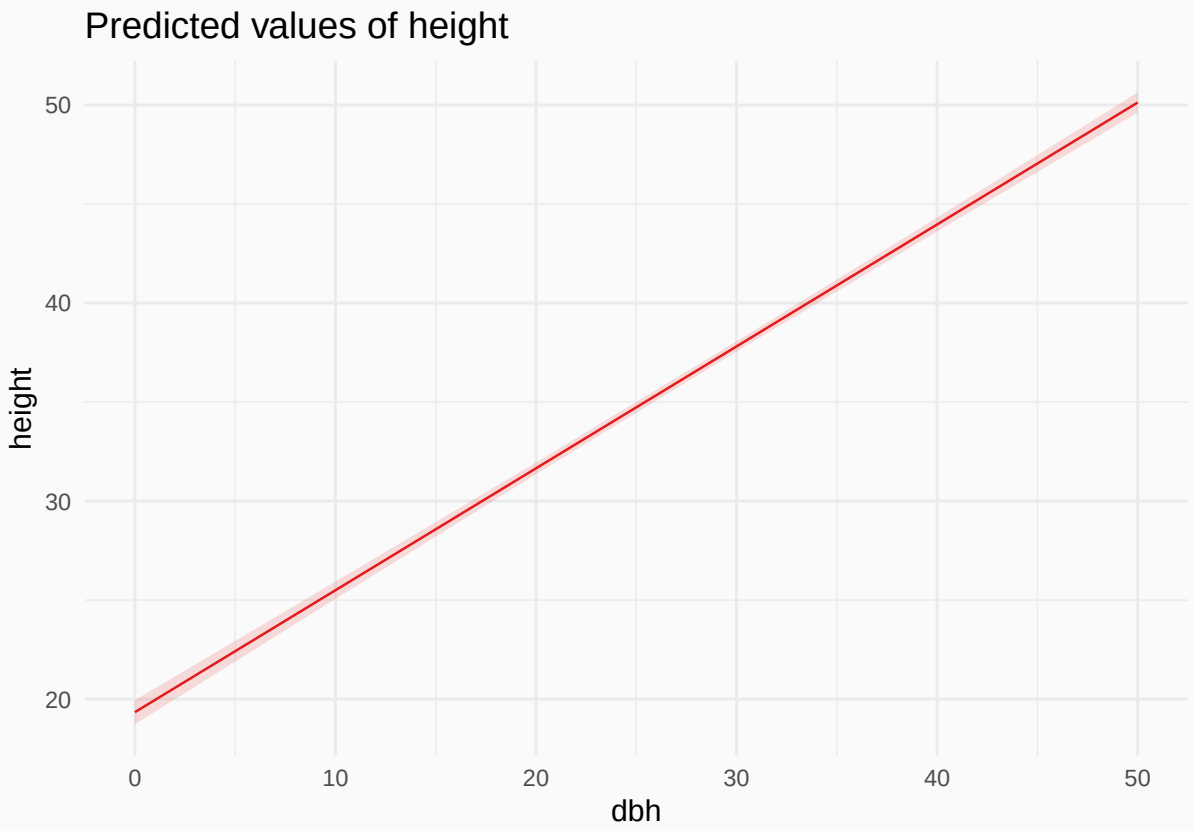


https://pbreheny.github.io/visreg

```
library('easystats')
plot(estimate_expectation(m1))
```

Plot model: sjPlot

```
library('sjPlot')
plot_model(m1, type = 'eff', terms = 'dbh')
```



https://strengejacke.github.io/sjPlot

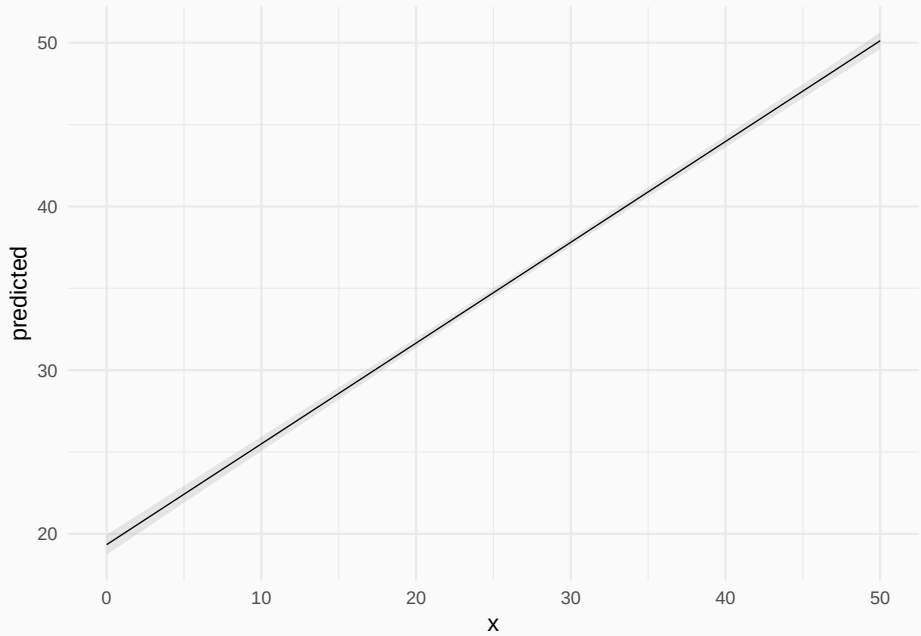
ggeffects

```
library('ggeffects')
```

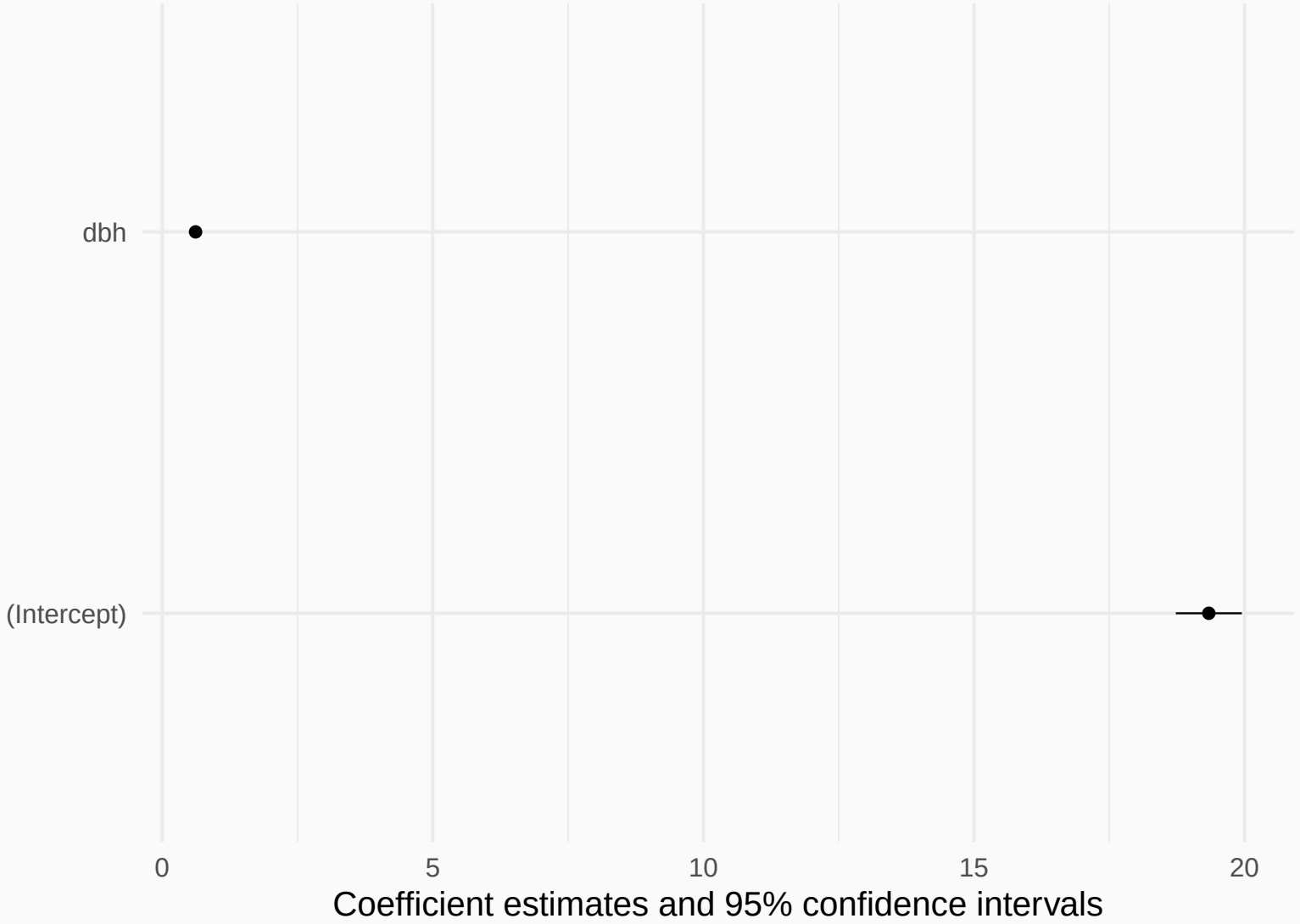
```
mydf <- ggpredict(m1, terms = 'dbh')
dplyr::glimpse(mydf, width = 40)
```

```
Rows: 6
Columns: 6
$ x         <dbl> 0, 10, 20, 30, 40, 50
$ predicted <dbl> 19.33920, 25.49623, ~
$ std.error <dbl> 0.3106446, 0.2226051~
$ conf.low  <dbl> 18.72961, 25.05941, ~
$ conf.high <dbl> 19.94879, 25.93306, ~
$ group     <fct> 1, 1, 1, 1, 1, 1
```

```
ggplot(mydf, aes(x, predicted)) +
  geom_line() +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high),
              alpha = 0.1)
```

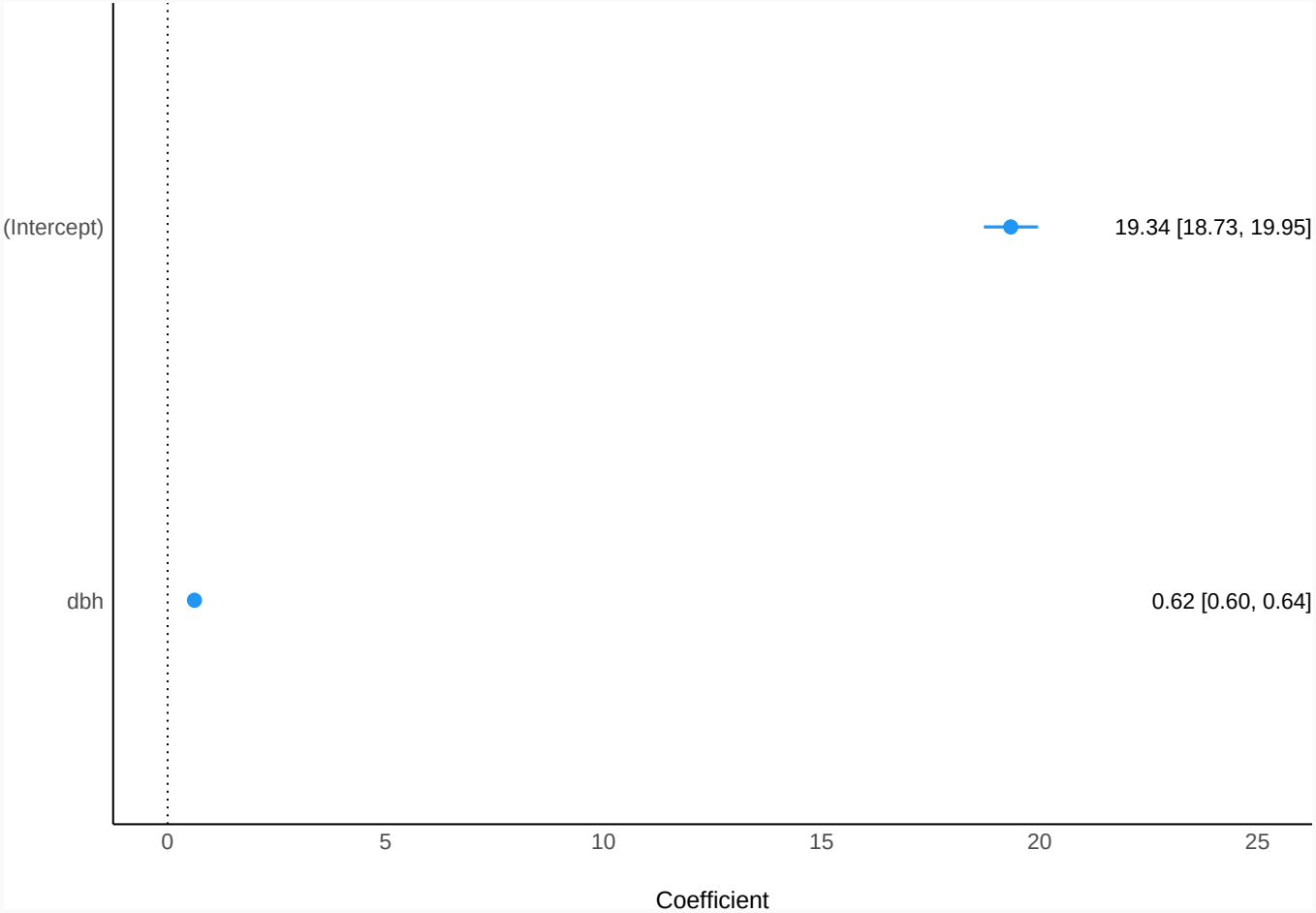


```
modelplot(m1)
```



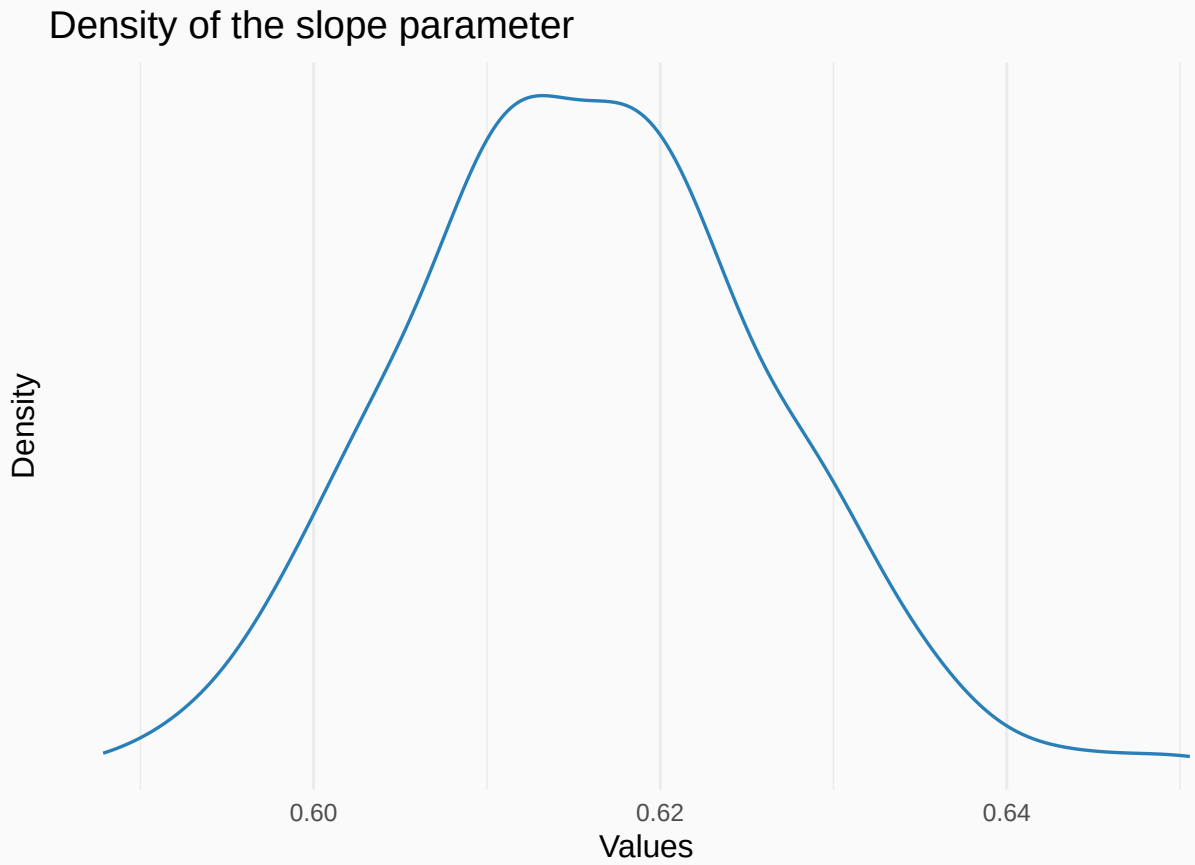
Plot model parameters with easystats (see package)

```
library('easystats')
plot(parameters(m1), show_intercept = TRUE, show_labels = TRUE)
```



Plot parameters' estimated distribution

```
plot(simulate_parameters(m1)) +
  labs(title = 'Density of the slope parameter')
```



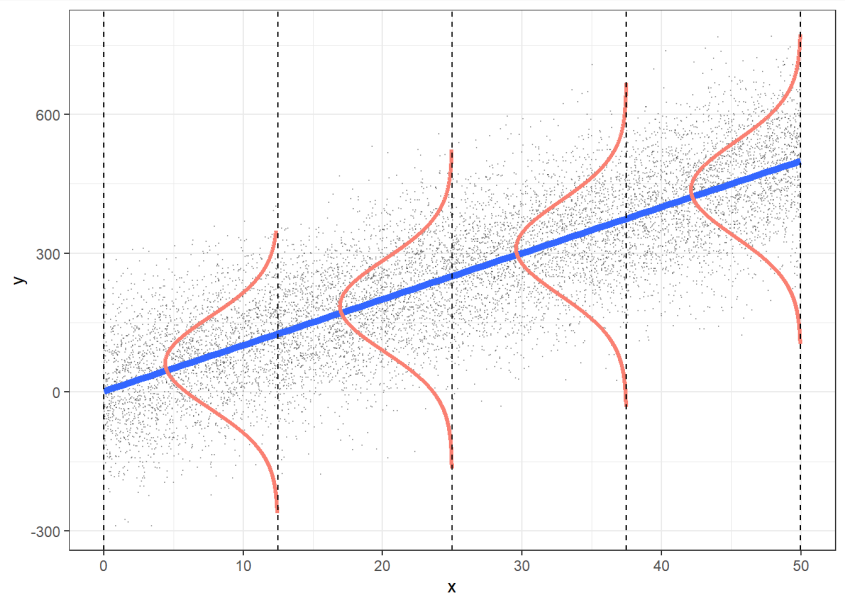
Model checking

Linear model assumptions

- **Linearity** (transformations, GAM...)

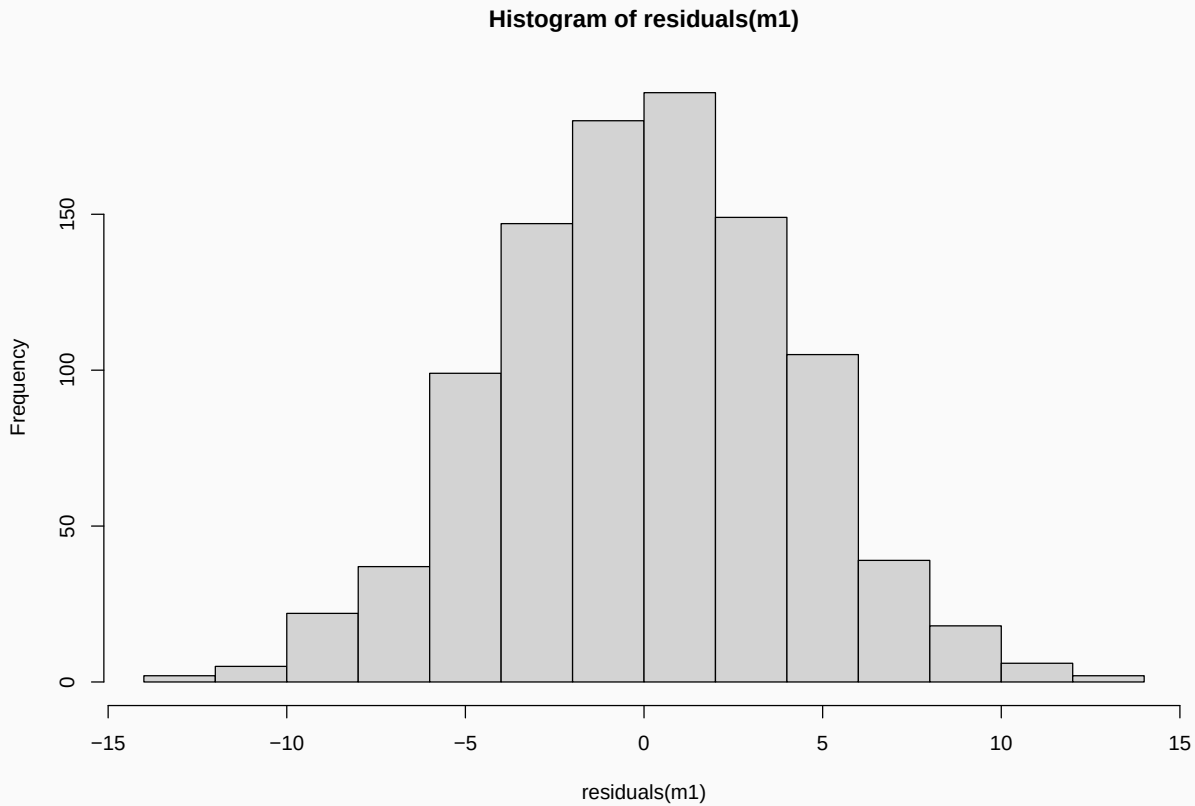
- **Residuals**:
  - Independent
  - Equal variance
  - Normal

- Negligible **measurement error** in predictors



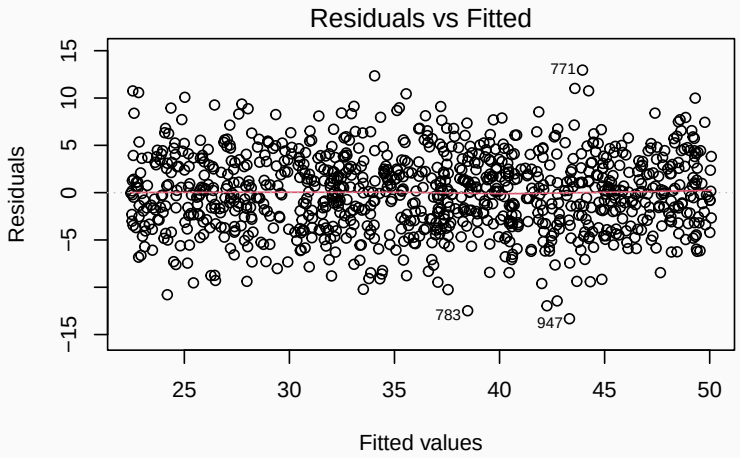
Are residuals normal?

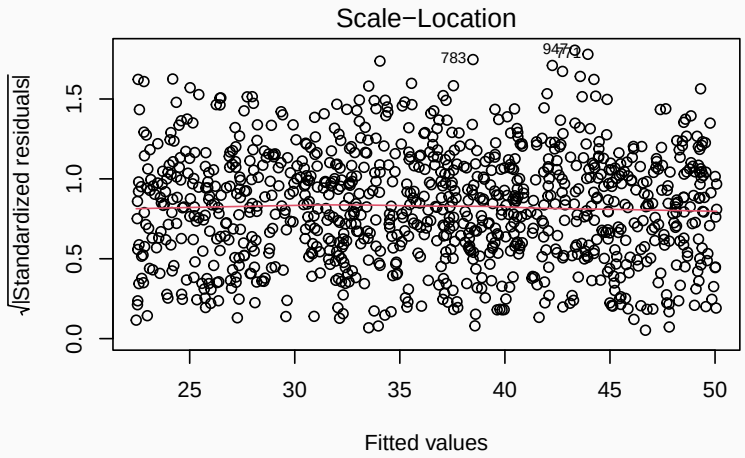
```
hist(residuals(m1))
```

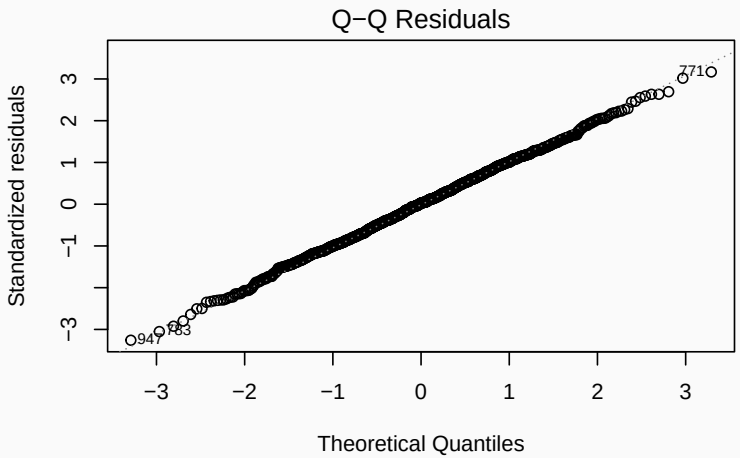


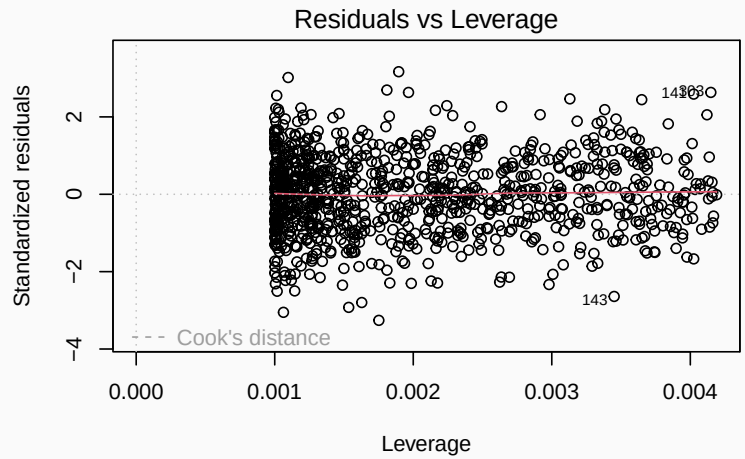
SD = 4.09

Model checking: `plot(model)`



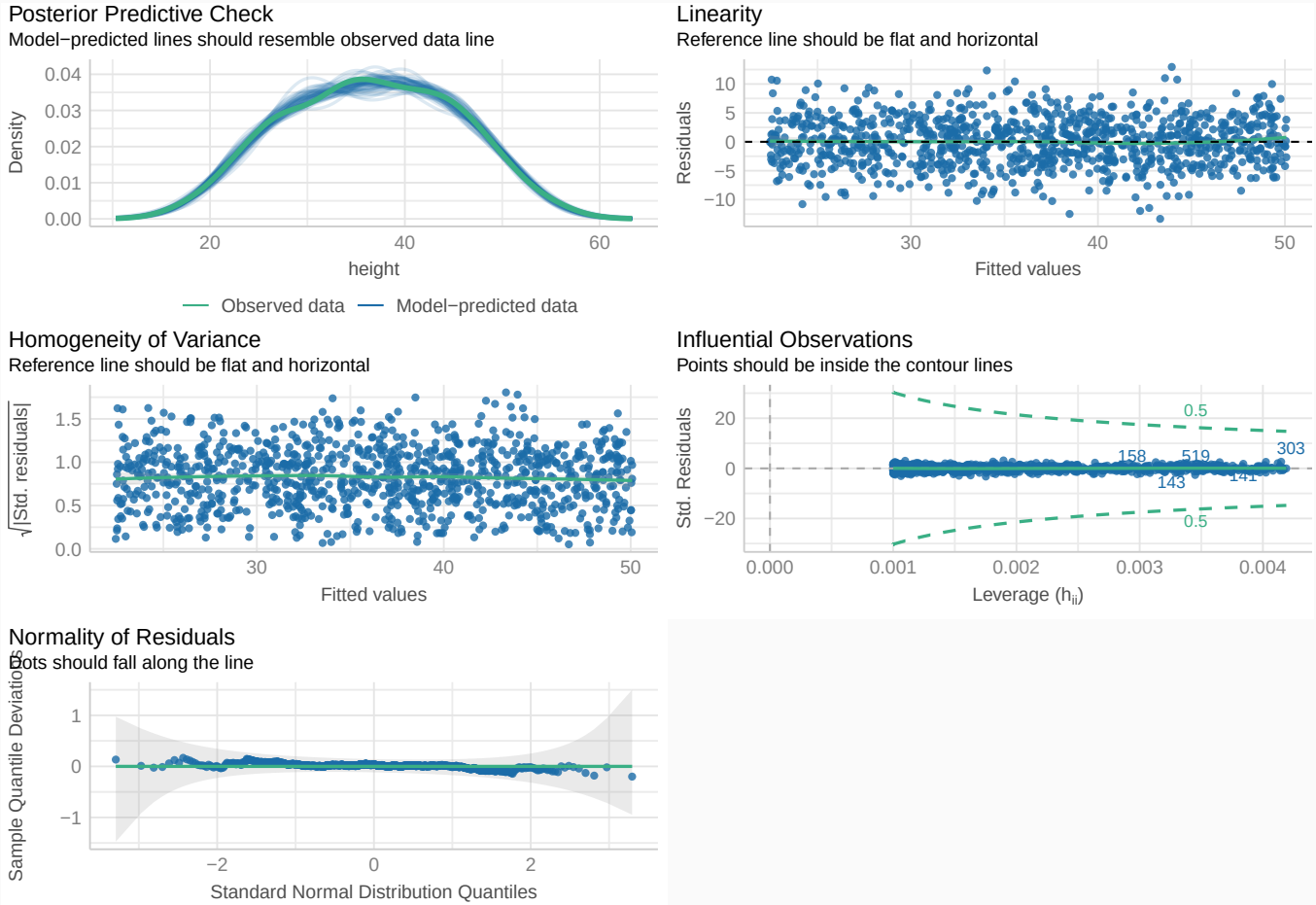






Model checking with `performance` (easystats)

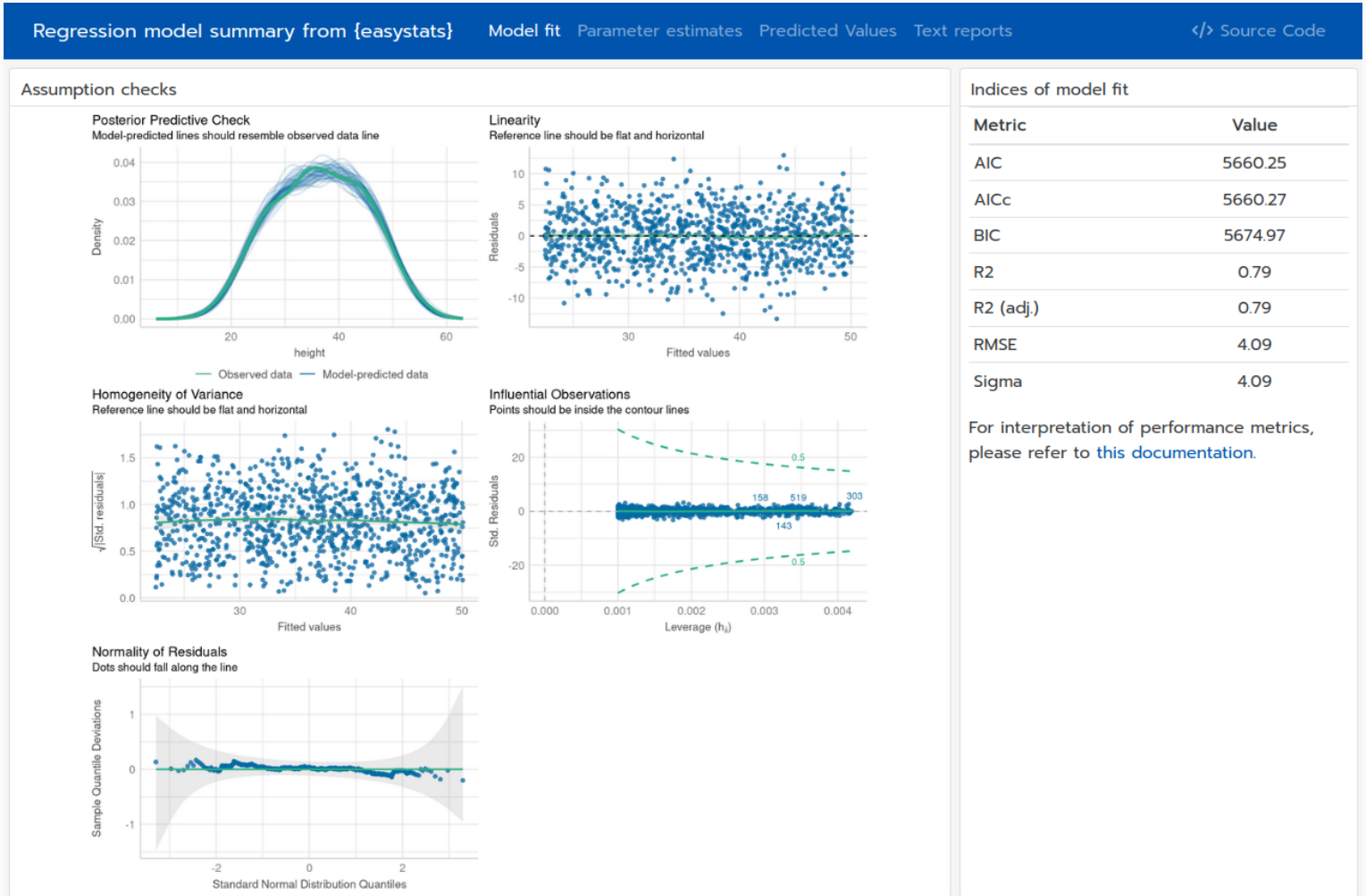
```
library('easystats')
check_model(m1)
```



https://easystats.github.io/performance/articles/check_model.html

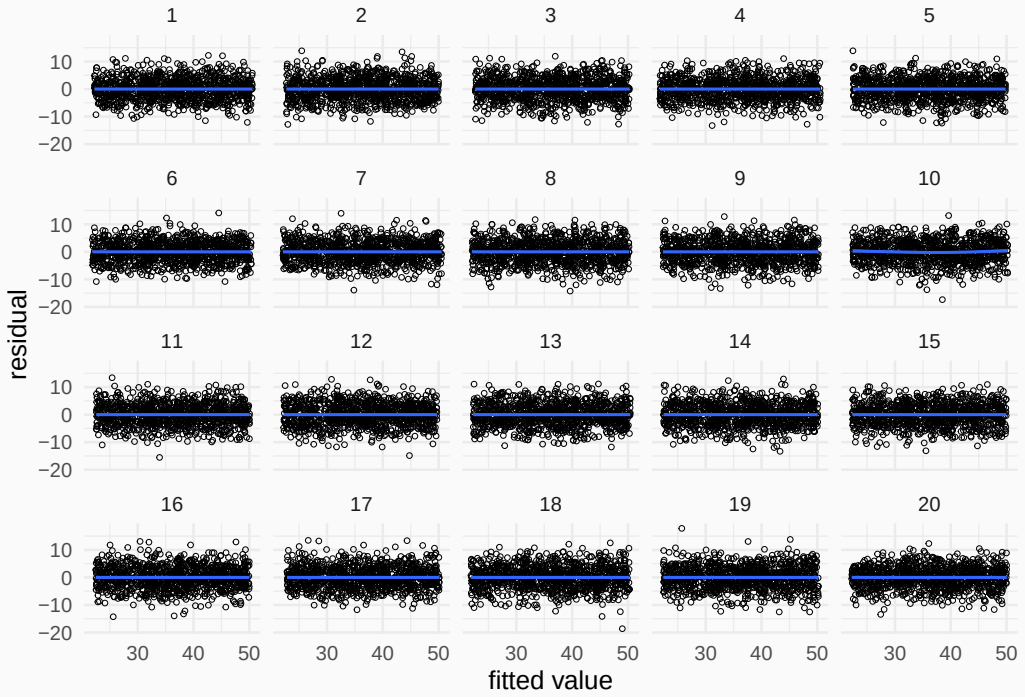
A dashboard to explore the full model

```
library('easystats')
model_dashboard(m1)
```



Can you distinguish model residuals from stochastic noise?

```
library('cannonball')   # https://github.com/janhove/cannonball
lin_plot(parade(m1))
```




```
reveal(parade(m1))
```

```
The true data are in position 12.
```

Using model for prediction

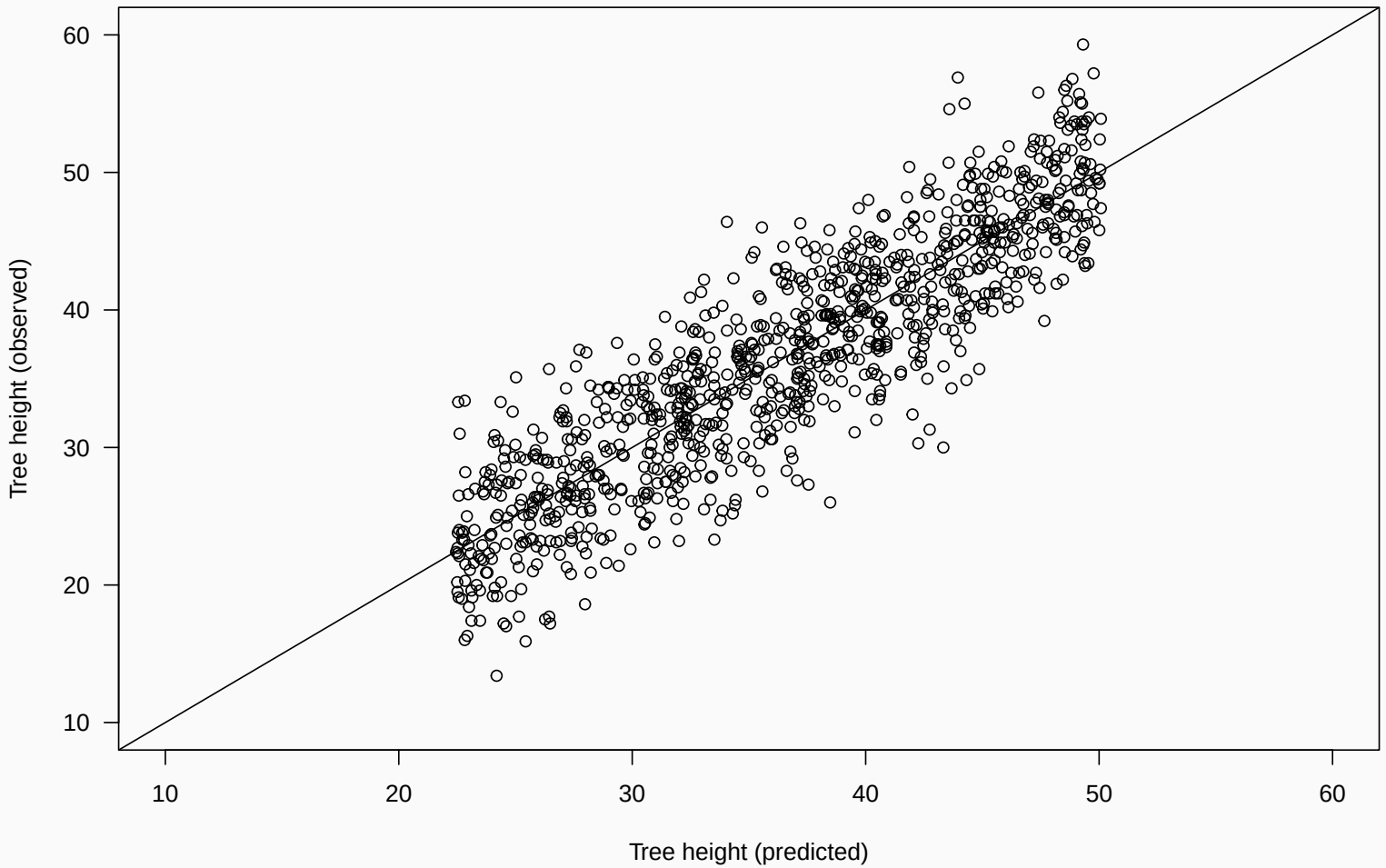
How good is the model in predicting tree height?

`fitted` gives expected value for each observation

```
trees$height.pred <- fitted(m1)
trees$resid <- residuals(m1)
head(trees)
```

	site	dbh	height	sex	dead	dbh.c	height.pred	resid
1	4	29.68	36.1	male	0	-0.32	37.61328	-1.5132797
2	5	33.29	42.3	male	0	3.29	39.83597	2.4640303
3	2	28.03	41.9	female	0	-1.97	36.59737	5.3026313
4	5	39.86	46.5	female	0	9.86	43.88114	2.6188577
5	1	47.94	43.9	female	0	17.94	48.85603	-4.9560274
6	1	10.82	26.2	male	0	-19.18	26.00111	0.1988903

Calibration plot: Observed vs Predicted values



Making predictions for new data

Q: Expected tree height if DBH = 39 cm?

```
new.dbh <- data.frame(dbh = c(39))
predict(m1, new.dbh, se.fit = TRUE)
```

```
$fit
       1
43.35164

$se.fit
[1] 0.1715514

$df
[1] 998

$residual.scale
[1] 4.092629
```

Confidence vs Prediction Intervals

Q: Expected tree height if DBH = 39 cm?

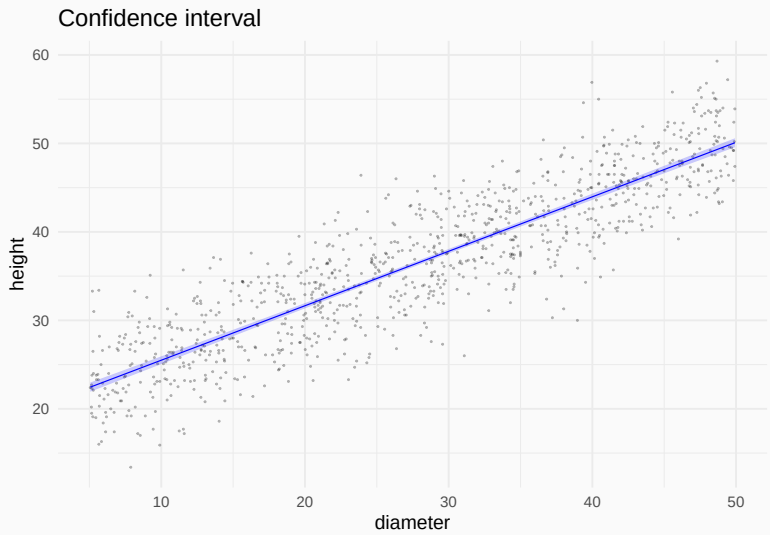
```
predict(m1, new.dbh, interval = 'confidence')
```

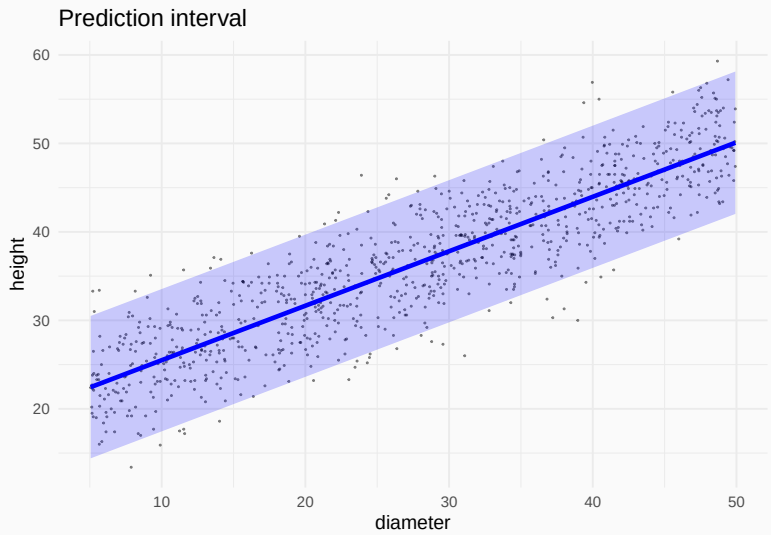
```
       fit      lwr      upr
1 43.35164 43.01499 43.68828
```

```
predict(m1, new.dbh, interval = 'prediction')
```

```
       fit      lwr      upr
1 43.35164 35.31344 51.38983
```

Confidence vs Prediction Intervals





Making predictions with easystats

Estimate expected values

```
pred <- estimate_expectation(m1)
```

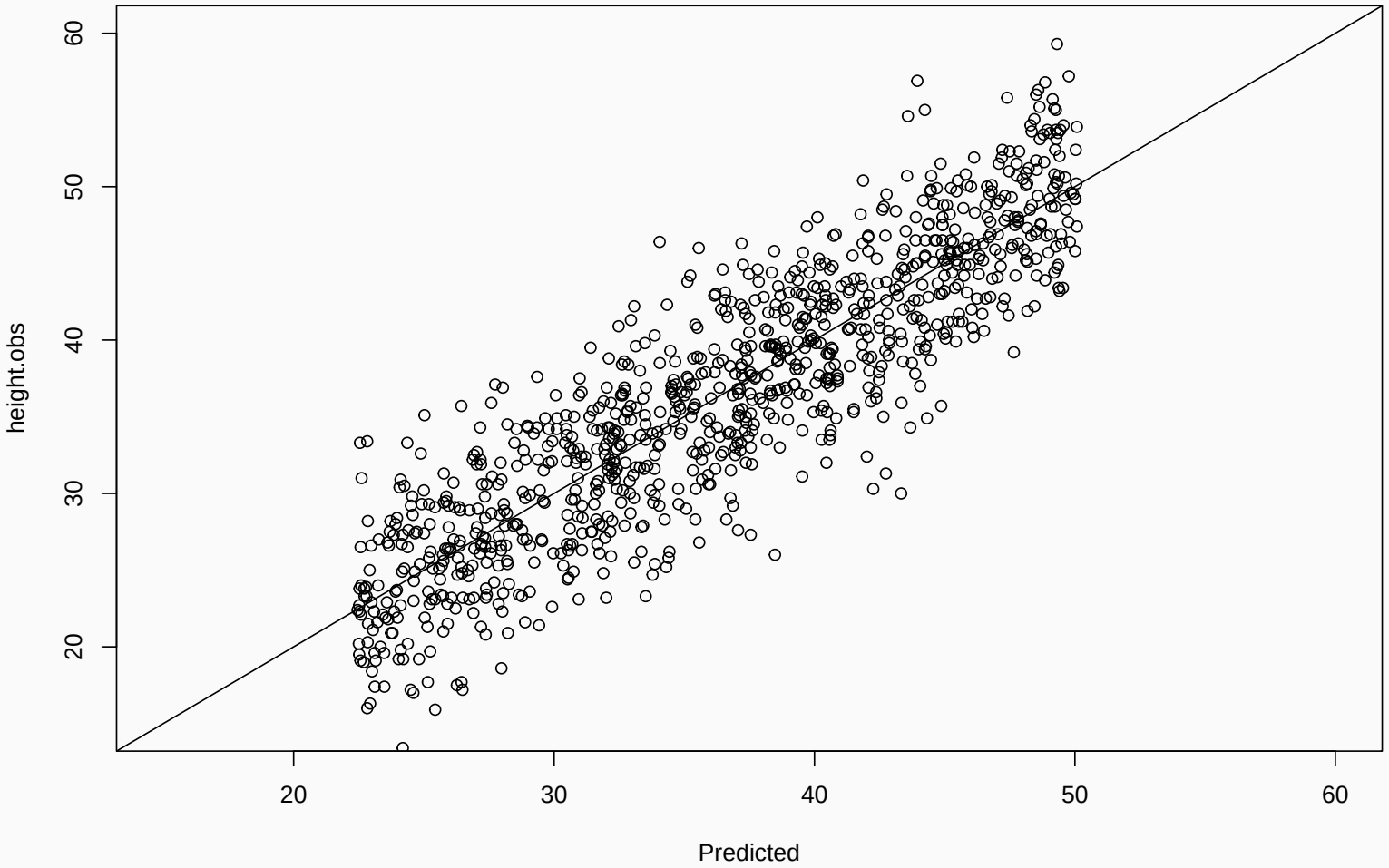
```
Model-based Expectation

dbh   | Predicted |   SE |         95% CI | Residuals
-----------------------------------------------------
29.68 |     37.61 | 0.13 | [37.36, 37.87] |     -1.51
33.29 |     39.84 | 0.14 | [39.56, 40.11] |      2.46
28.03 |     36.60 | 0.13 | [36.34, 36.85] |      5.30
39.86 |     43.88 | 0.18 | [43.53, 44.23] |      2.62
47.94 |     48.86 | 0.24 | [48.38, 49.33] |     -4.96
10.82 |     26.00 | 0.22 | [25.58, 26.42] |      0.20

Variable predicted: height
```

Expected values given DBH

```
plot(estimate_expectation(m1))
```

Calibration plot: observed vs predicted

```
pred$height.obs <- trees$height
plot(height.obs ~ Predicted, data = pred, xlim = c(15, 60), ylim = c(15, 60))
abline(a = 0, b = 1)
```



Estimate prediction interval

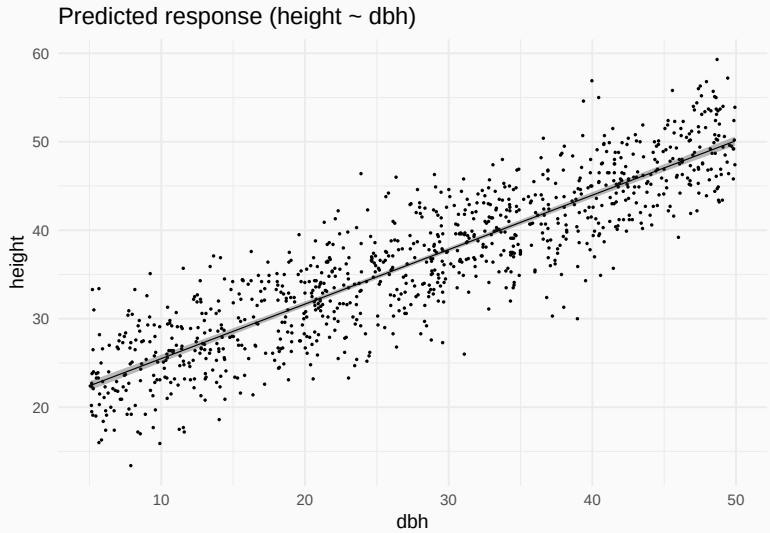
Accounting for residual variation!

```
pred <- estimate_prediction(m1)
head(pred)
```

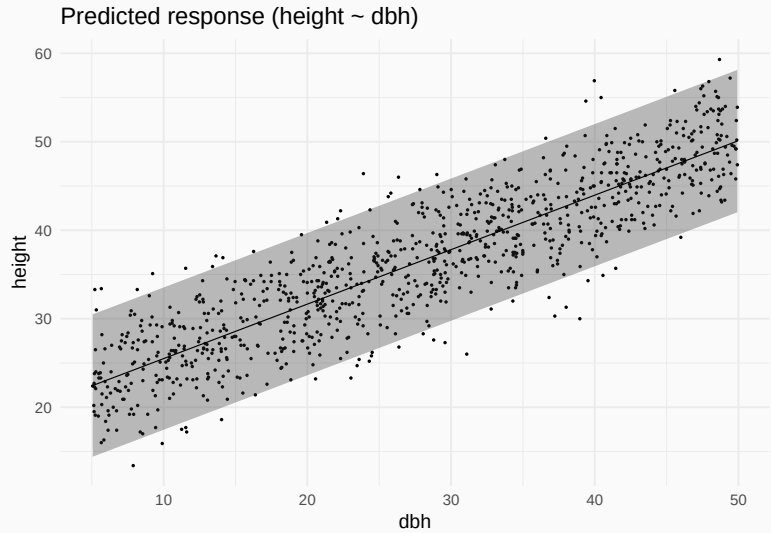
```
Model-based Prediction

dbh   | Predicted |   SE |         95% CI | Residuals
-----------------------------------------------------
29.68 |     37.61 | 4.09 | [29.58, 45.65] |     -1.51
33.29 |     39.84 | 4.10 | [31.80, 47.87] |      2.46
28.03 |     36.60 | 4.09 | [28.56, 44.63] |      5.30
39.86 |     43.88 | 4.10 | [35.84, 51.92] |      2.62
47.94 |     48.86 | 4.10 | [40.81, 56.90] |     -4.96
10.82 |     26.00 | 4.10 | [17.96, 34.04] |      0.20

Variable predicted: height
```

Confidence vs Prediction interval

```
plot(estimate_expectation(m1))
```




```
plot(estimate_prediction(m1))
```



Make predictions for new data

```
estimate_expectation(m1, data = data.frame(dbh = 39))
```

```
Model-based Expectation

dbh   | Predicted |   SE |         95% CI
-----------------------------------------
39.00 |     43.35 | 0.17 | [43.01, 43.69]

Variable predicted: height
```

```
estimate_prediction(m1, data = data.frame(dbh = 39))
```

```
Model-based Prediction

dbh   | Predicted |   SE |         95% CI
-----------------------------------------
39.00 |     43.35 | 4.10 | [35.31, 51.39]
```

Cross-validation

```
performance_cv(m1, method = 'k_fold', metrics = 'common', k = 10)
```

```
# Cross-validation performance (10-fold method)

RMSE |   R2
-----------
4.1  | 0.79
```

Workflow

- Visualise data

Workflow

- Visualise data

- Understand fitted model (`summary`)

Workflow

- Visualise data
- Understand fitted model (`summary`)
- Visualise model (`visreg`...)

Workflow

- Visualise data
- Understand fitted model (`summary`)
- Visualise model (`visreg`...)
- Check model (`plot`, `check_model`, calibration plot...)

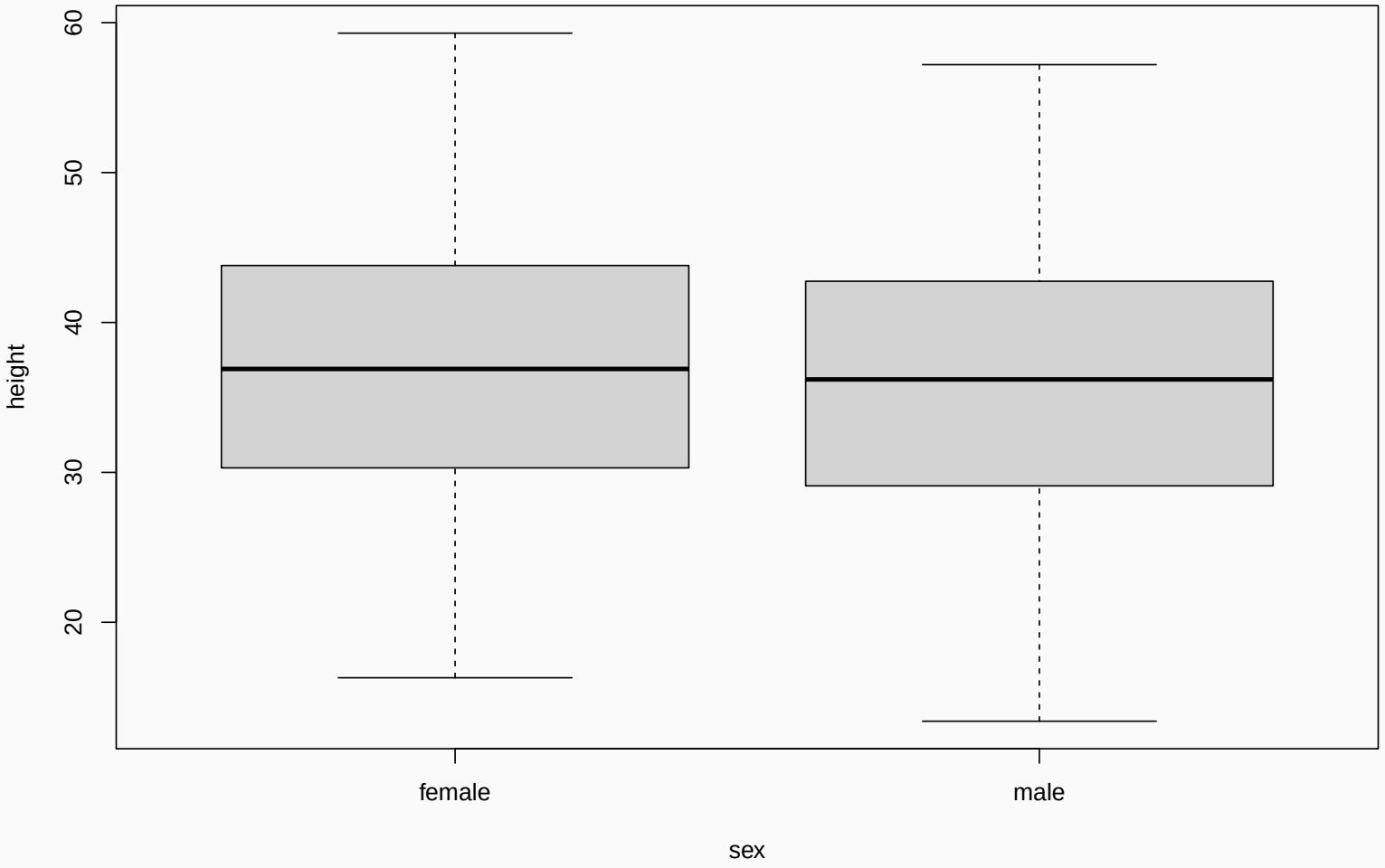
Workflow

- Visualise data
- Understand fitted model (`summary`)
- Visualise model (`visreg`...)
- Check model (`plot`, `check_model`, calibration plot...)
- Predict (`predict`, `estimate_expectation`, `estimate_prediction`)

Categorical predictors (factors)

Q: Does tree height vary with sex?

```
boxplot(height ~ sex, data = trees)
```



Model height ~ sex

```r
m2 <- lm(height ~ sex, data = trees)
```

```
Call:
lm(formula = height ~ sex, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-22.6881  -6.7881  -0.0097   6.7261  22.3687

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  36.9312     0.3981  92.778   <2e-16 ***
sexmale      -0.8432     0.5607  -1.504    0.133
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.865 on 998 degrees of freedom
Multiple R-squared:  0.002261,  Adjusted R-squared:  0.001261
F-statistic: 2.261 on 1 and 998 DF,  p-value: 0.133
```

Linear model with categorical predictors

```r
m2 <- lm(height ~ sex, data = trees)
```

corresponds to

$$Height_i = a + b_{male} + \varepsilon_i$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Model height ~ sex

```r
m2 <- lm(height ~ sex, data = trees)
```

```
Call:
lm(formula = height ~ sex, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-22.6881  -6.7881  -0.0097   6.7261  22.3687

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  36.9312     0.3981  92.778   <2e-16 ***
sexmale      -0.8432     0.5607  -1.504    0.133
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.865 on 998 degrees of freedom
Multiple R-squared:  0.002261,  Adjusted R-squared:  0.001261
F-statistic: 2.261 on 1 and 998 DF,  p-value: 0.133
```

Quiz

https://pollev.com/franciscorod726

Let's read the model report...

```
report(m2)
```

We fitted a linear model (estimated using OLS) to predict height with sex (formula: height ~ sex). The model explains a statistically not significant and very weak proportion of variance (R2 = 2.26e-03, F(1, 998) = 2.26, p = 0.133, adj. R2 = 1.26e-03). The model's intercept, corresponding to sex = female, is at 36.93 (95% CI [36.15, 37.71], t(998) = 92.78, p < .001). Within this model:

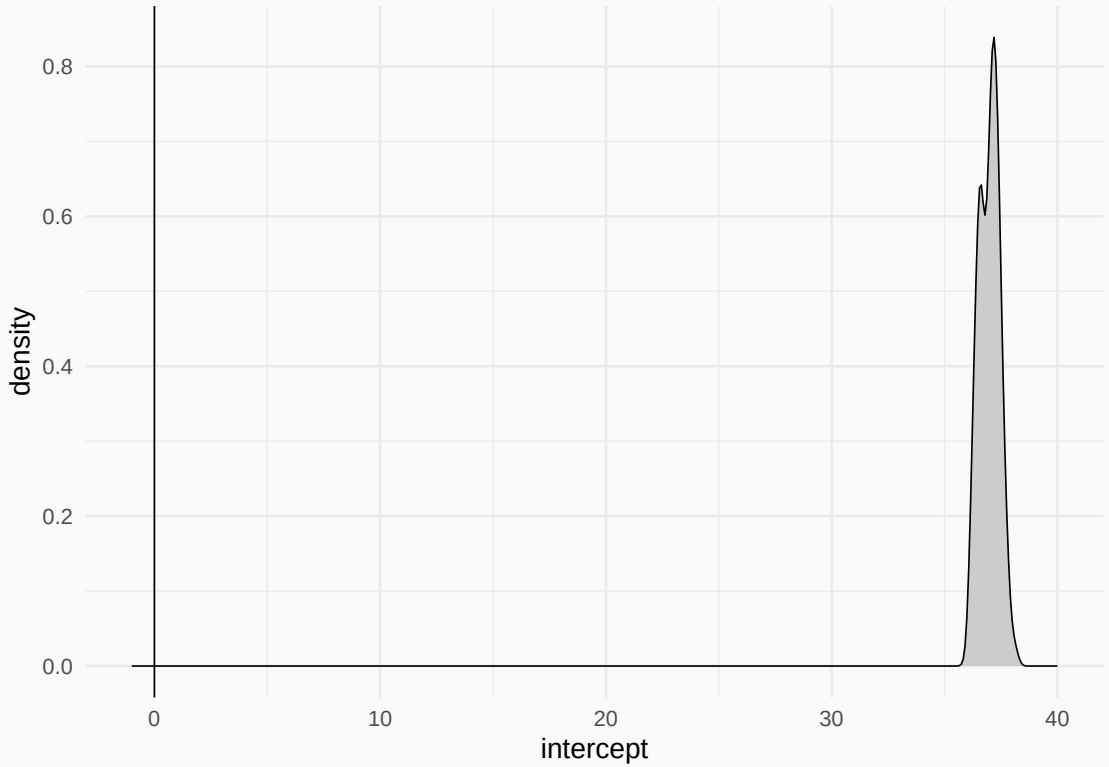
- The effect of sex [male] is statistically non-significant and negative (beta = -0.84, 95% CI [-1.94, 0.26], t(998) = -1.50, p = 0.133; Std. beta = -0.10, 95% CI [-0.22, 0.03])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

Estimated distribution of the intercept parameter

Intercept = Height of females

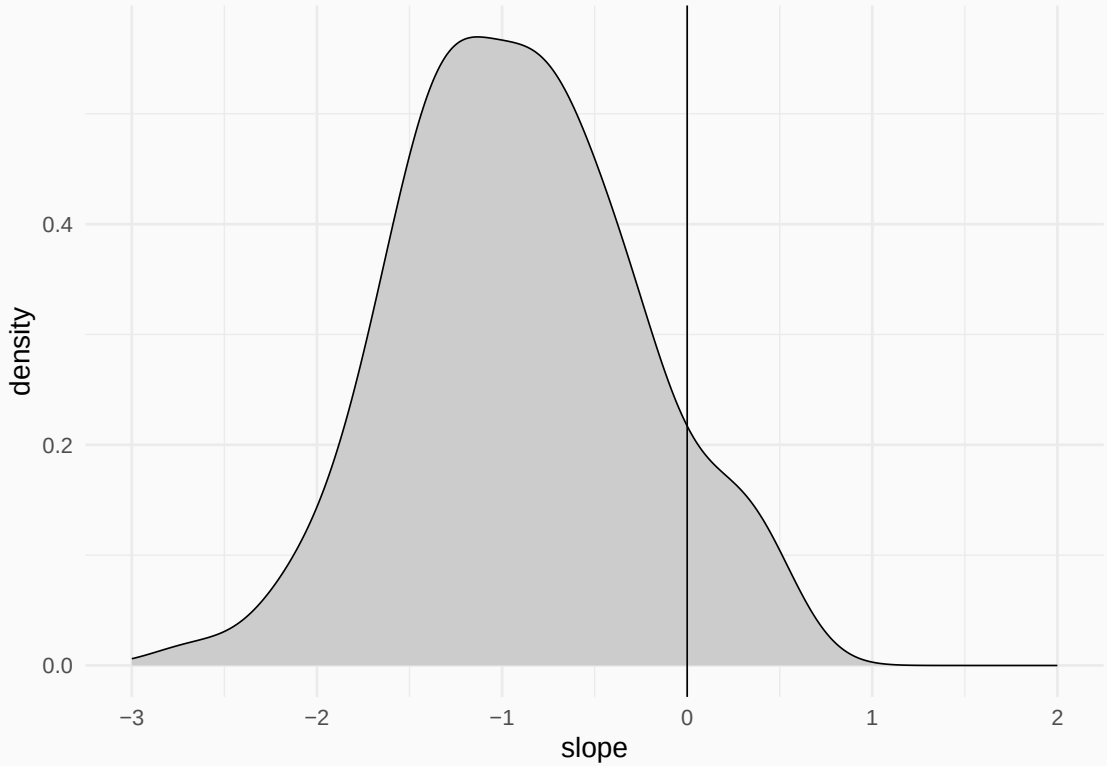
Parameter	Coefficient	SE	95% CI	t(998)	p
(Intercept)	36.93	0.40	[36.15, 37.71]	92.78	< .001



Estimated distribution of the *beta* parameter

beta = **height difference** of males vs females

Parameter	Coefficient	SE	95% CI	t(998)	p
sex [male]	-0.84	0.56	[-1.94, 0.26]	-1.50	0.133



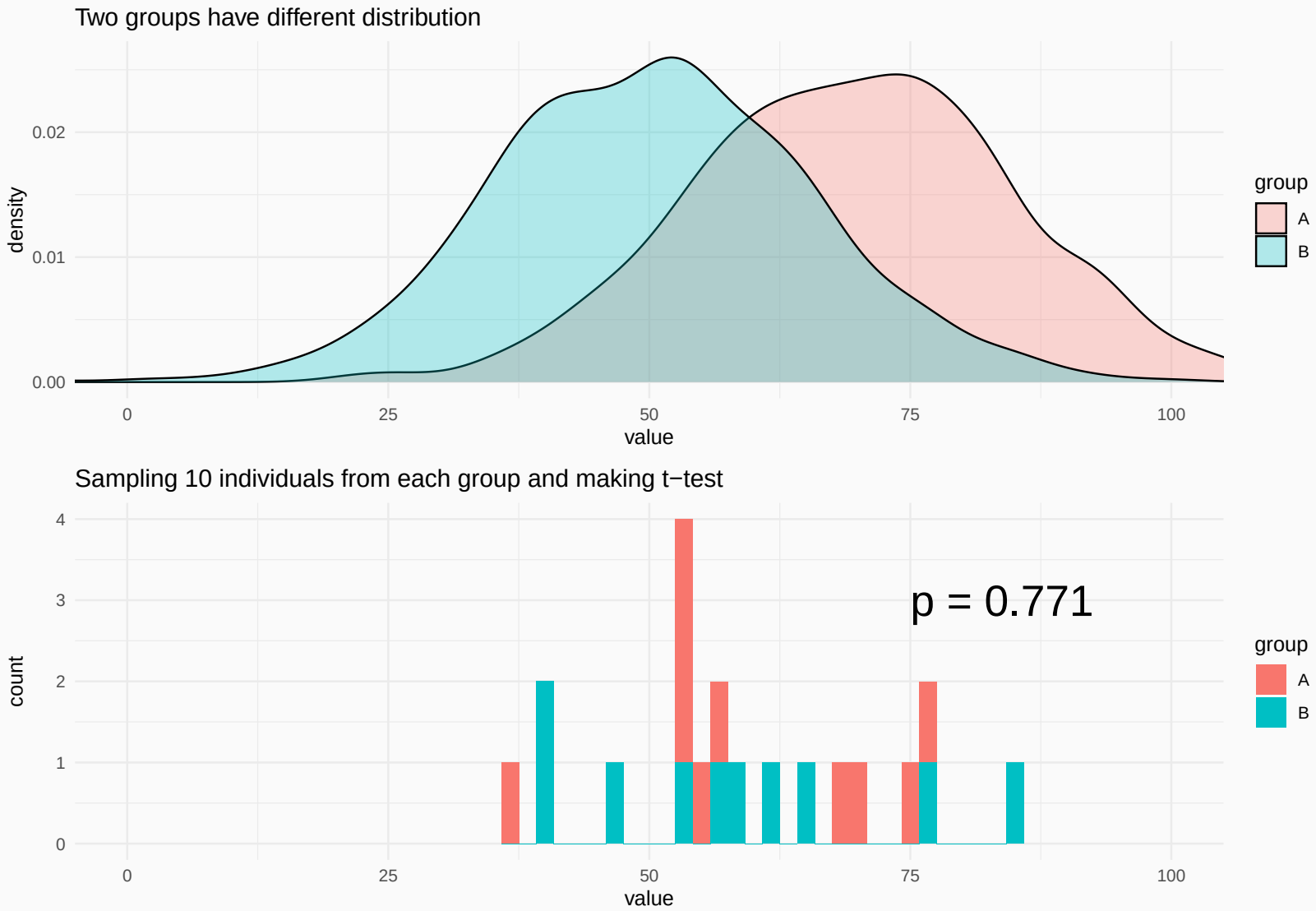
Short digression on p-values

‘Not significant’

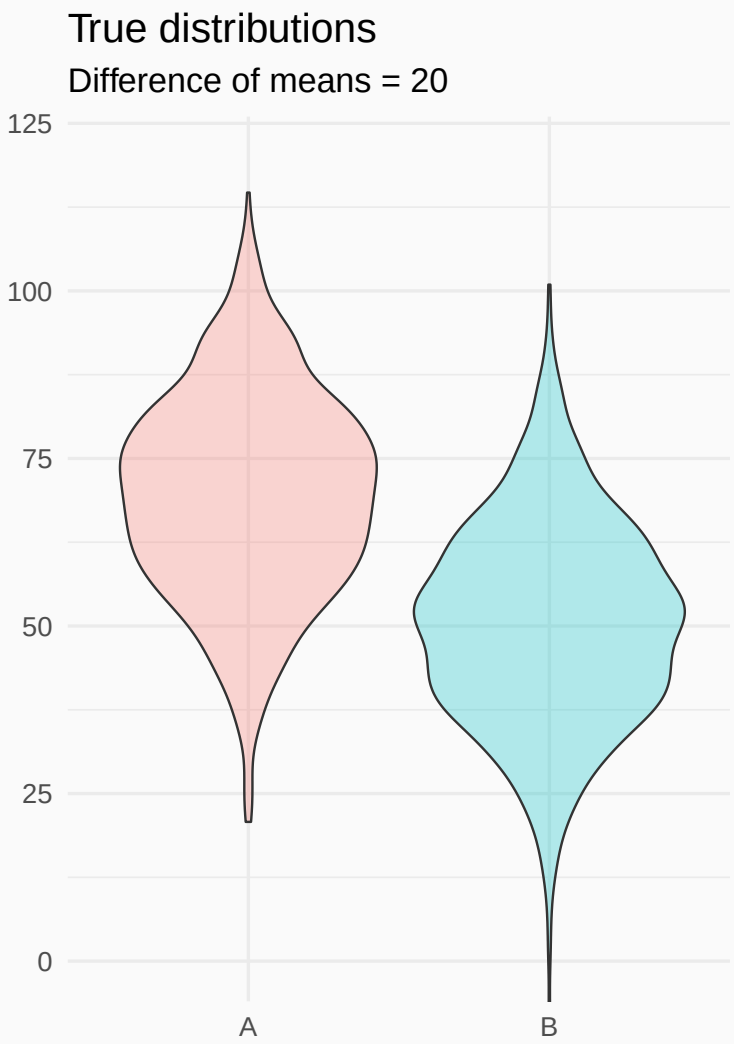
does NOT mean

‘there is no effect’

‘Not significant’ does NOT mean ‘they are equal’



‘Not significant’ does NOT mean ‘there is no effect’



Failure to reject H0 != H0 is true

Absence of evidence != Evidence of absence

p-value > 0.05?

- “We were **unable to find evidence** against the hypothesis that A = B **with the current sample size**” (Harrell)

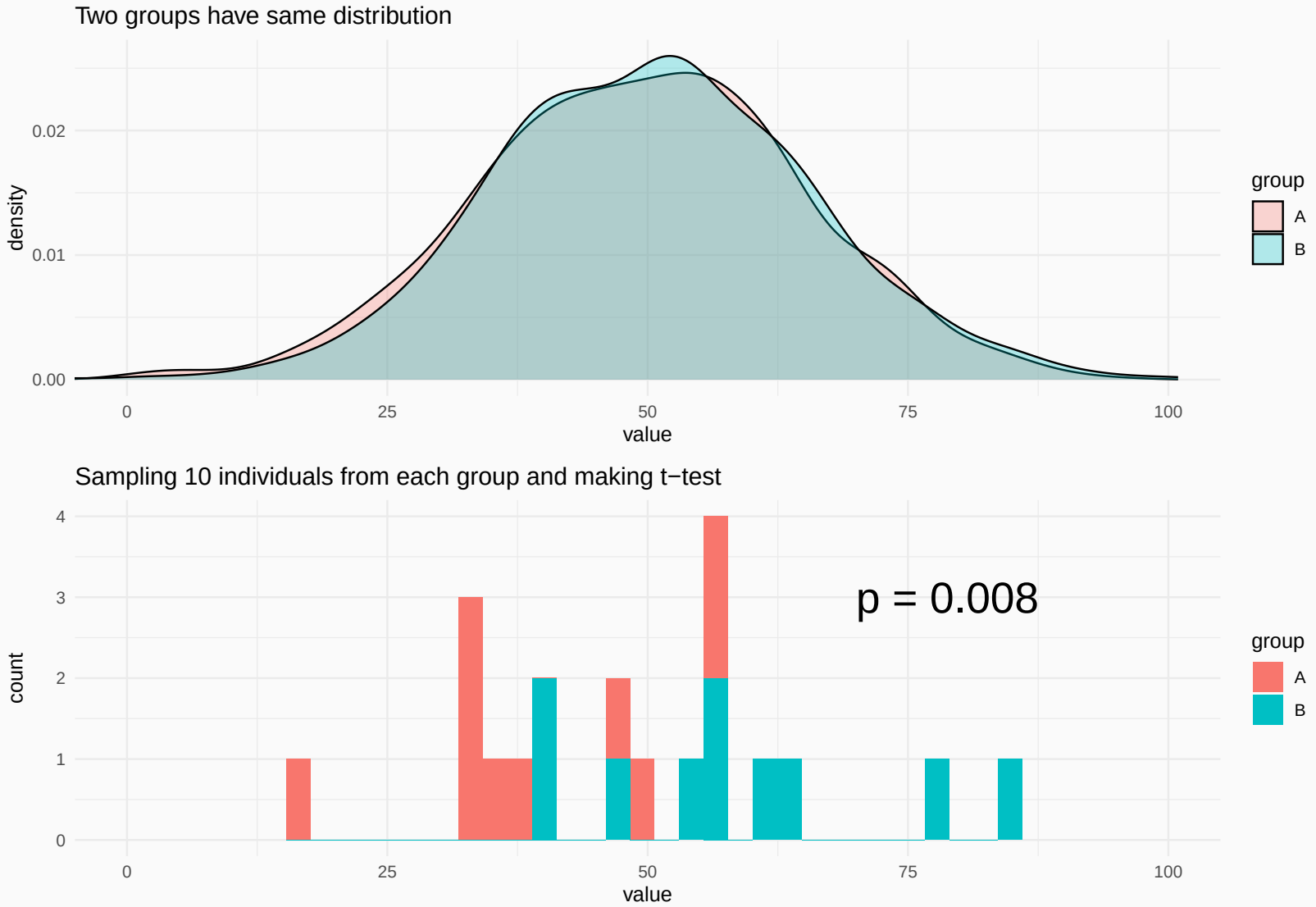
p-value > 0.05?

- "We were **unable to find evidence** against the hypothesis that A = B **with the current sample size**" (Harrell)
- "Differences between groups were **not statistically clear**" (Dushoff et al)

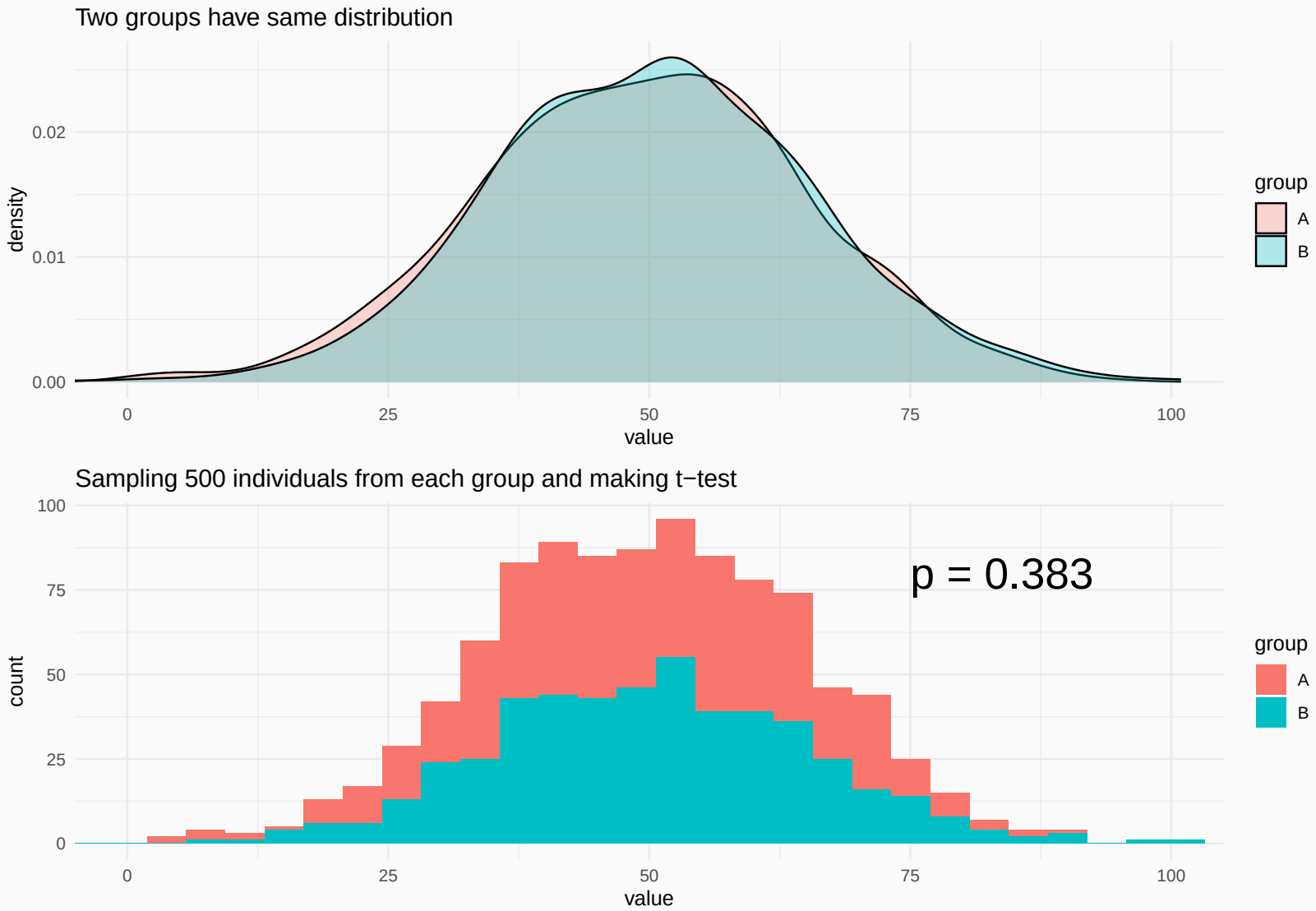
A significant p-value
does NOT mean
we found a true difference

A significant p-value does not mean we found a true difference

Particularly with low sample sizes



If sample size was larger...



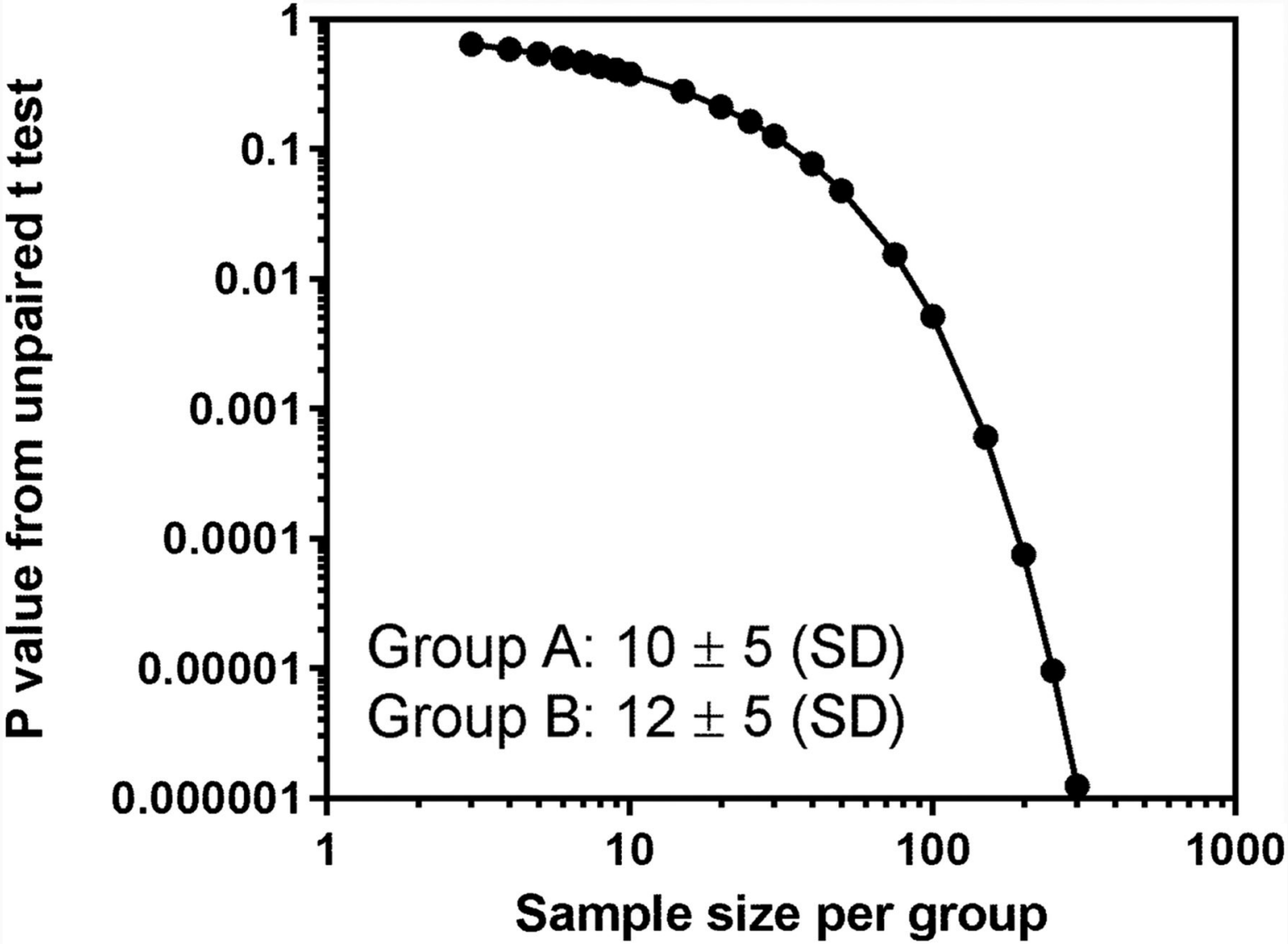
With low sample size (power),

significant p-values

are most likely overestimates

Loken & Gelman 2014, Vasisth et al. 2018

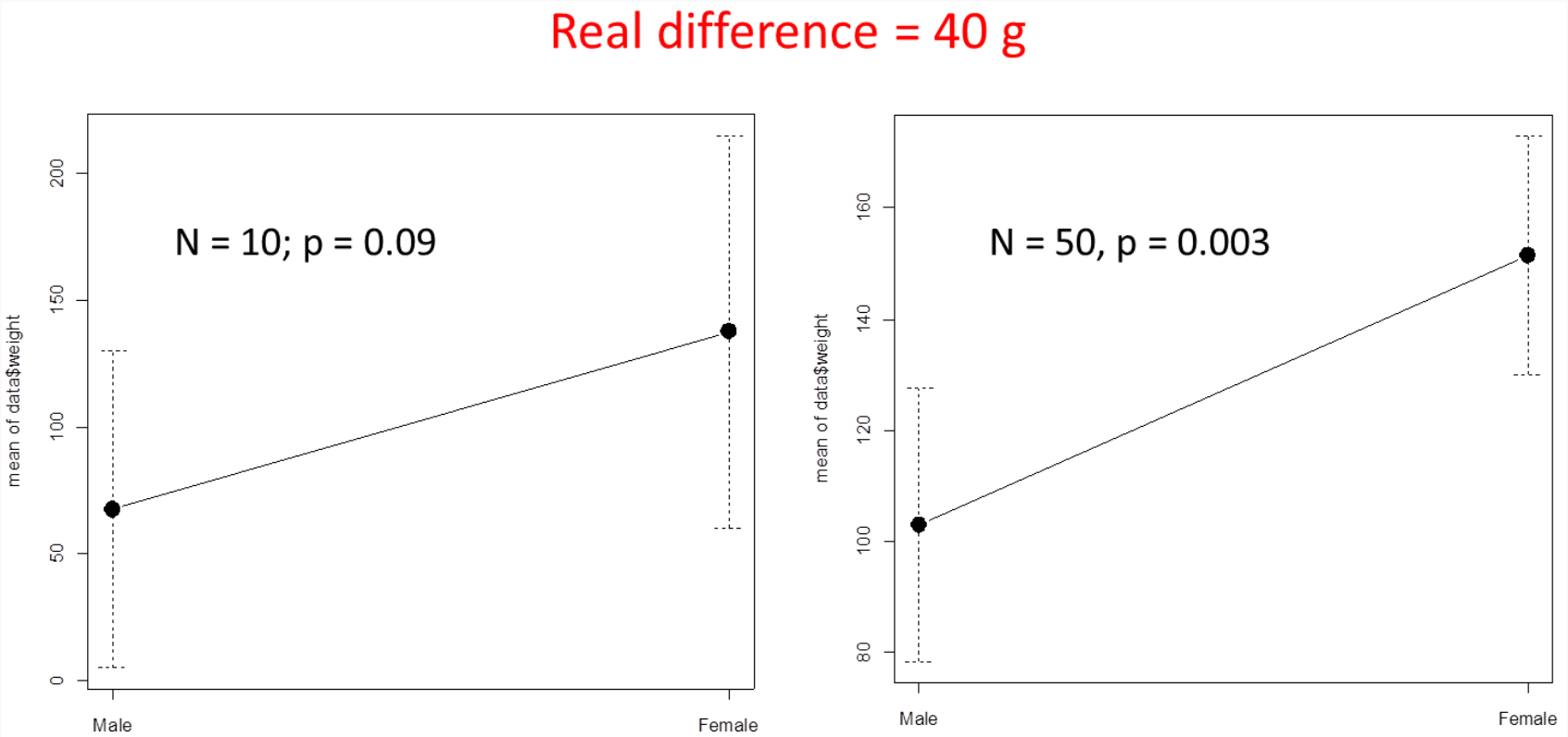
P-value depends on sample size



https://doi.org/10.1002/prp2.93

P-value depends on sample size

Same real difference is detected as **significant or not depending on sample size**



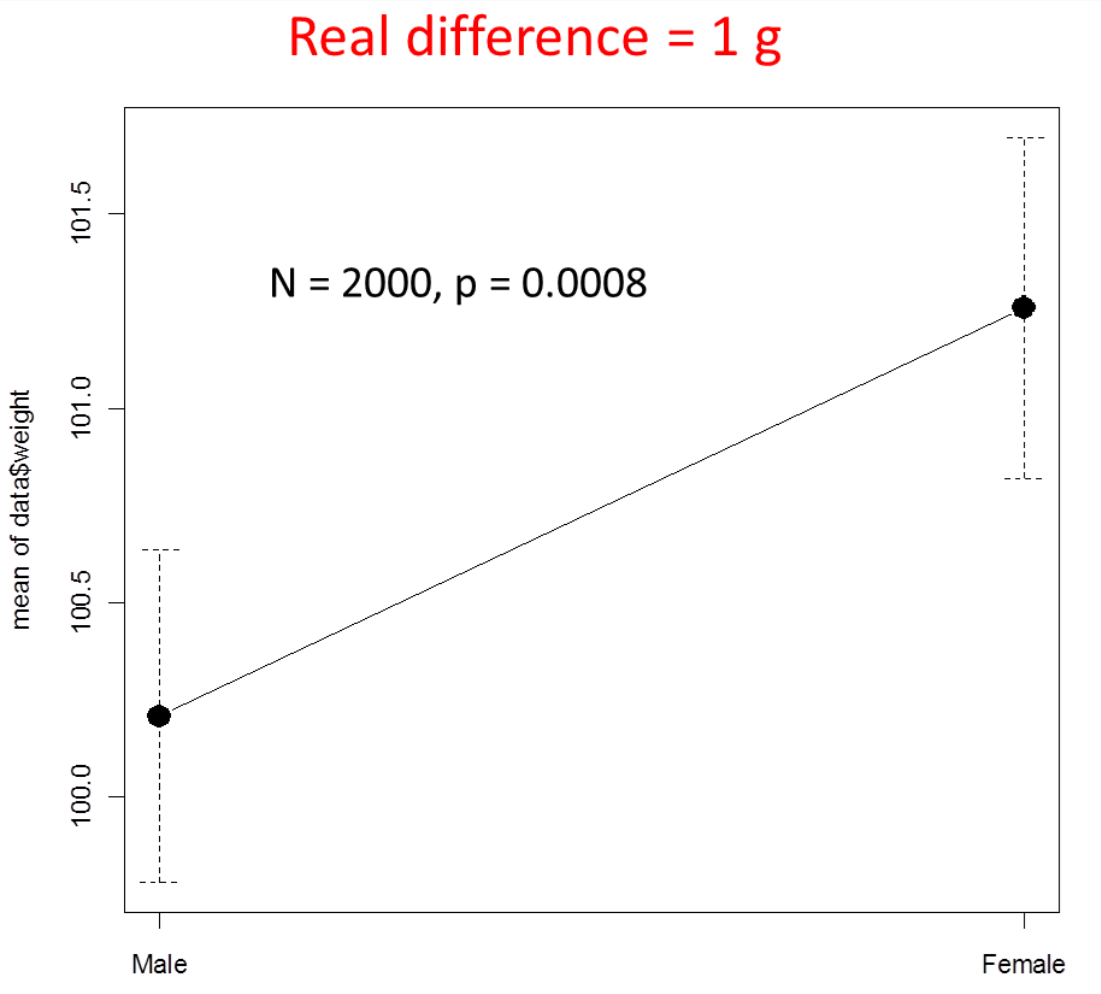
Statistically significant

!=

biologically important

Statistically significant != biologically important

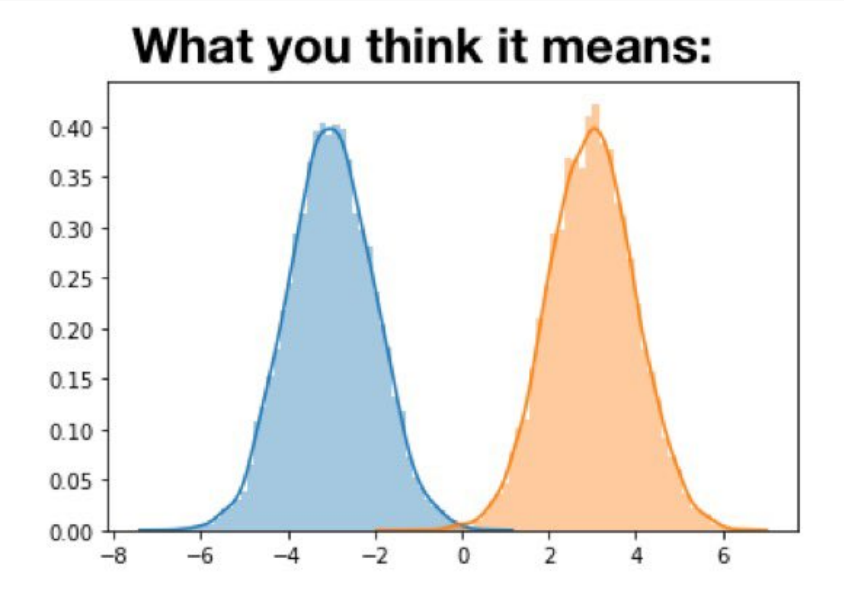
With big sample size, we can find **highly significant but biologically unimportant** differences.

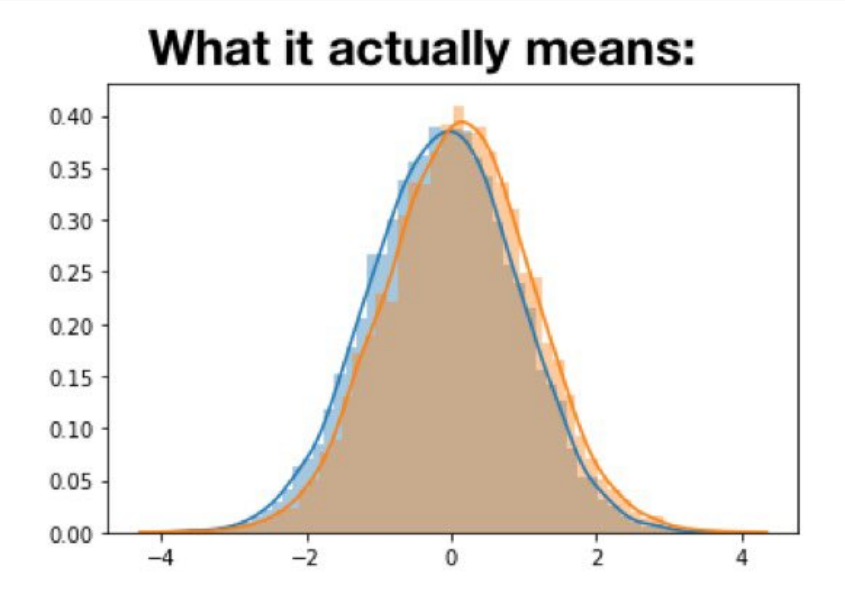


Statistically significant != biologically important

zara weinberg
@weinberz

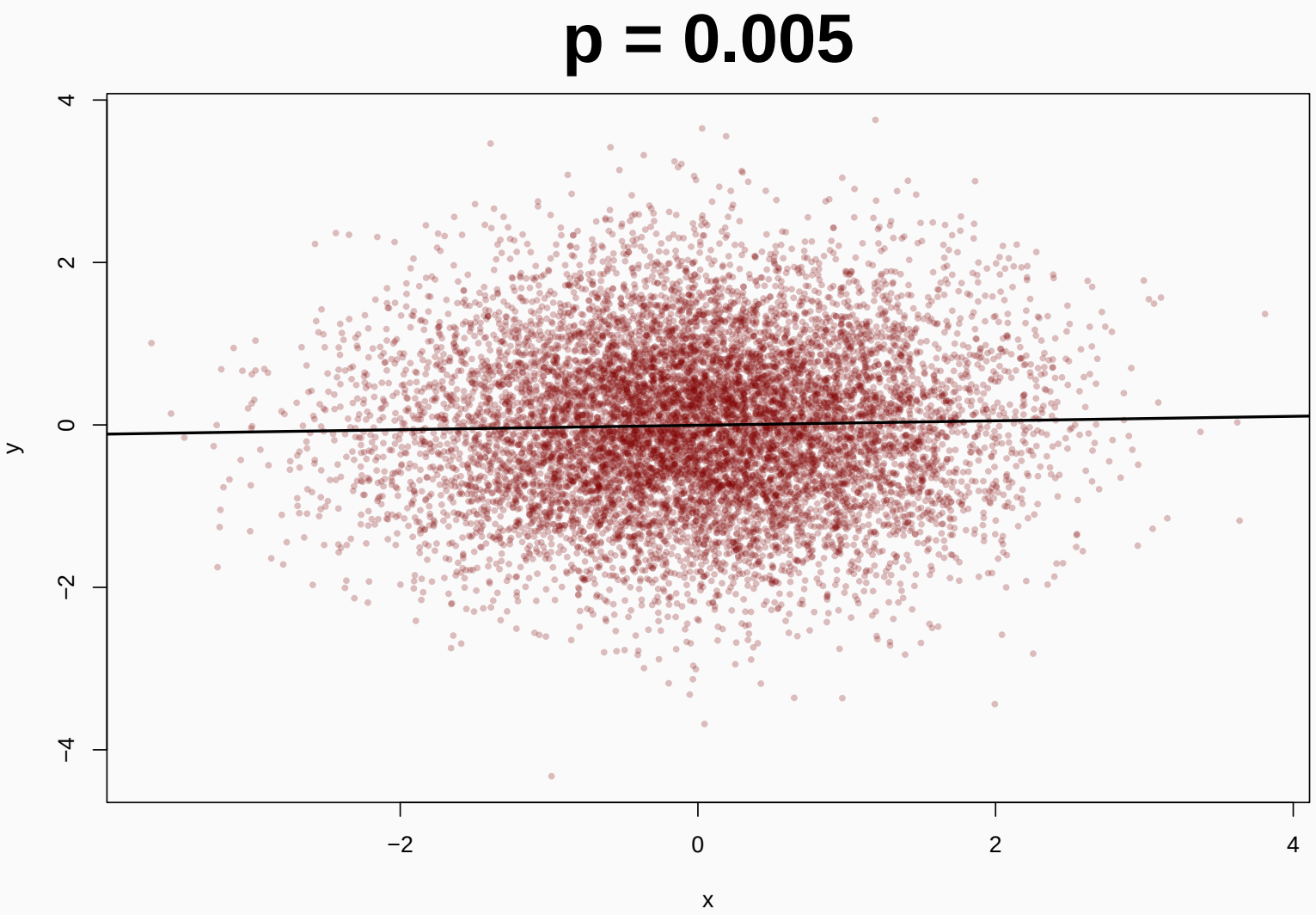
friendly reminder about p < 0.0001:





https://twitter.com/weinberz/status/1422405165236178947?s=20

Statistically significant != biologically important



Statistically significant != biologically important

- Statistically significant = unlikely to be zero

Statistically significant != biologically important

- Statistically significant = unlikely to be zero
- Good read: *significantly misleading*

Statistically significant != biologically important

- Statistically significant = unlikely to be zero
- Good read: *significantly misleading*
- Beyond significant/not significant, look at **effect sizes and their uncertainty**.

ASA statement on p-values

- P-values do not measure the **probability of hypothesis** being true, or the probability that the data were produced by **random chance** alone.

https://doi.org/10.1080/00031305.2016.1154108

See also https://lakens.github.io/statistical_inferences/01-pvalue.html

ASA statement on p-values

- P-values do not measure the **probability of hypothesis** being true, or the probability that the data were produced by **random chance** alone.
- Scientific conclusions or policy decisions should NOT be based only on **whether a p-value passes a specific threshold**.

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- P-value, or statistical significance, does not measure the **size of an effect** or the **importance** of a result.

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ASA statement on p-values

- P-values do not measure the **probability of hypothesis** being true, or the probability that the data were produced by **random chance** alone.
- Scientific conclusions or policy decisions should NOT be based only on **whether a p-value passes a specific threshold**.
- P-value, or statistical significance, does not measure the **size of an effect** or the **importance** of a result.
- By itself, a p-value does NOT provide a good **measure of evidence** regarding a model or hypothesis.

https://doi.org/10.1080/00031305.2016.1154108

See also https://lakens.github.io/statistical_inferences/01-pvalue.html

S-values as alternative to p-values

```
parameters(m2)[2,]
```

```
Parameter   | Coefficient |   SE |         95% CI | t(998) |     p
-------------------------------------------------------------------
sex [male] |       -0.84 | 0.56 | [-1.94, 0.26] |  -1.50 | 0.133
```

```
parameters(m2, s_value = TRUE)[2,]
```

```
Parameter   | Coefficient |   SE |         95% CI | t(998) |    s
-------------------------------------------------------------------
sex [male] |       -0.84 | 0.56 | [-1.94, 0.26] |  -1.50 | 2.91
```

p-value = 0.133 corresponds to *surprise* of obtaining c. 3 heads in a row when tossing a coin

https://marginaleffects.com/bonus/svalues.html

Analysing differences among factor levels

```r
library('easystats')  # modelbased package
estimate_means(m2)
```

```
Estimated Marginal Means

sex    |  Mean |   SE |         95% CI
-----------------------------------------
male   | 36.09 | 0.39 | [35.31, 36.86]
female | 36.93 | 0.40 | [36.15, 37.71]

Marginal means estimated at sex
```

Analysing differences among factor levels

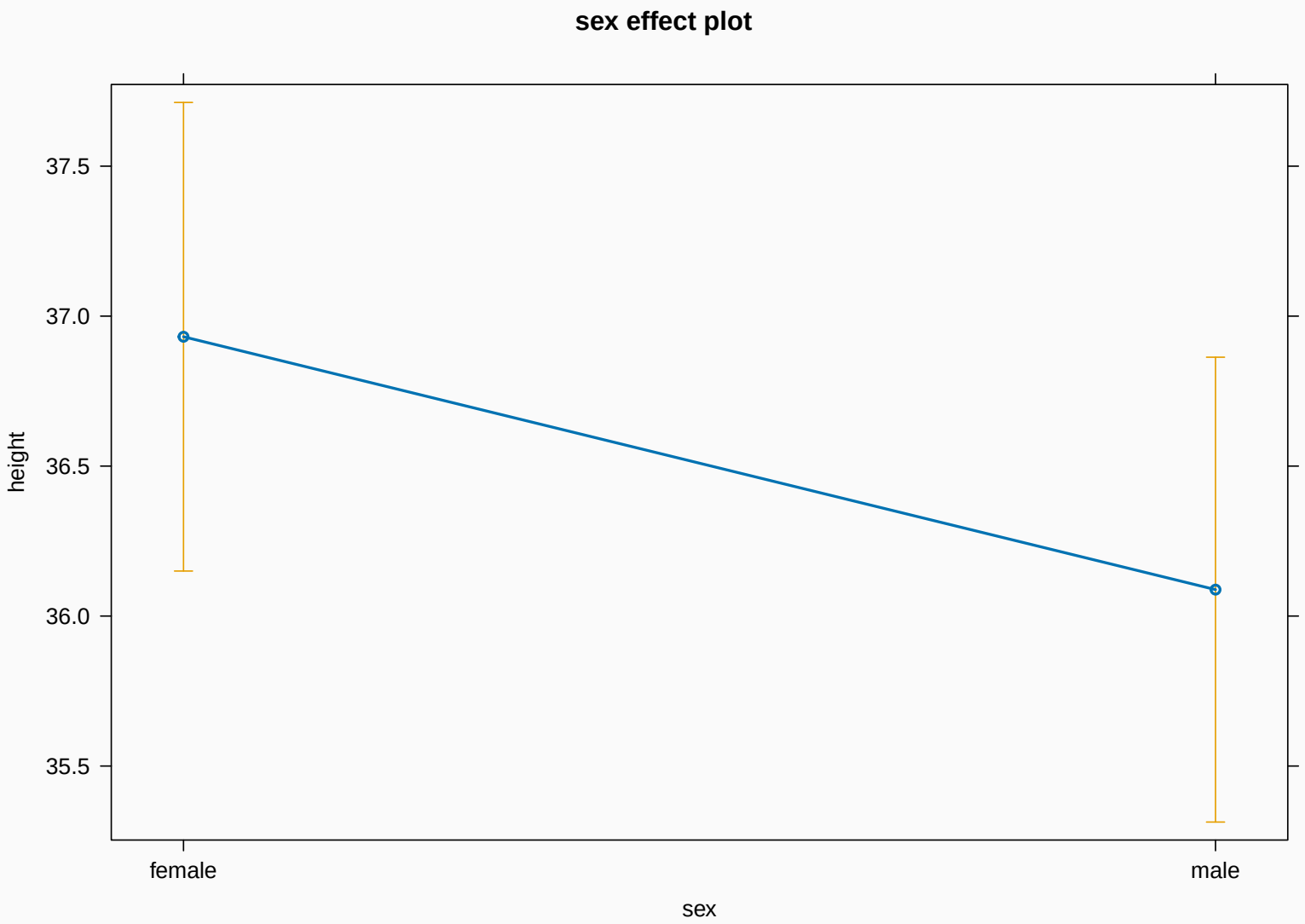
```
estimate_contrasts(m2)
```

```
Marginal Contrasts Analysis

Level1 | Level2 | Difference |        95% CI |   SE | t(998) |     p
-------------------------------------------------------------------
male   | female |      -0.84 | [-1.94, 0.26] | 0.56 |  -1.50 | 0.133

Marginal contrasts estimated at sex
p-value adjustment method: Holm (1979)
```

Visualising the fitted model

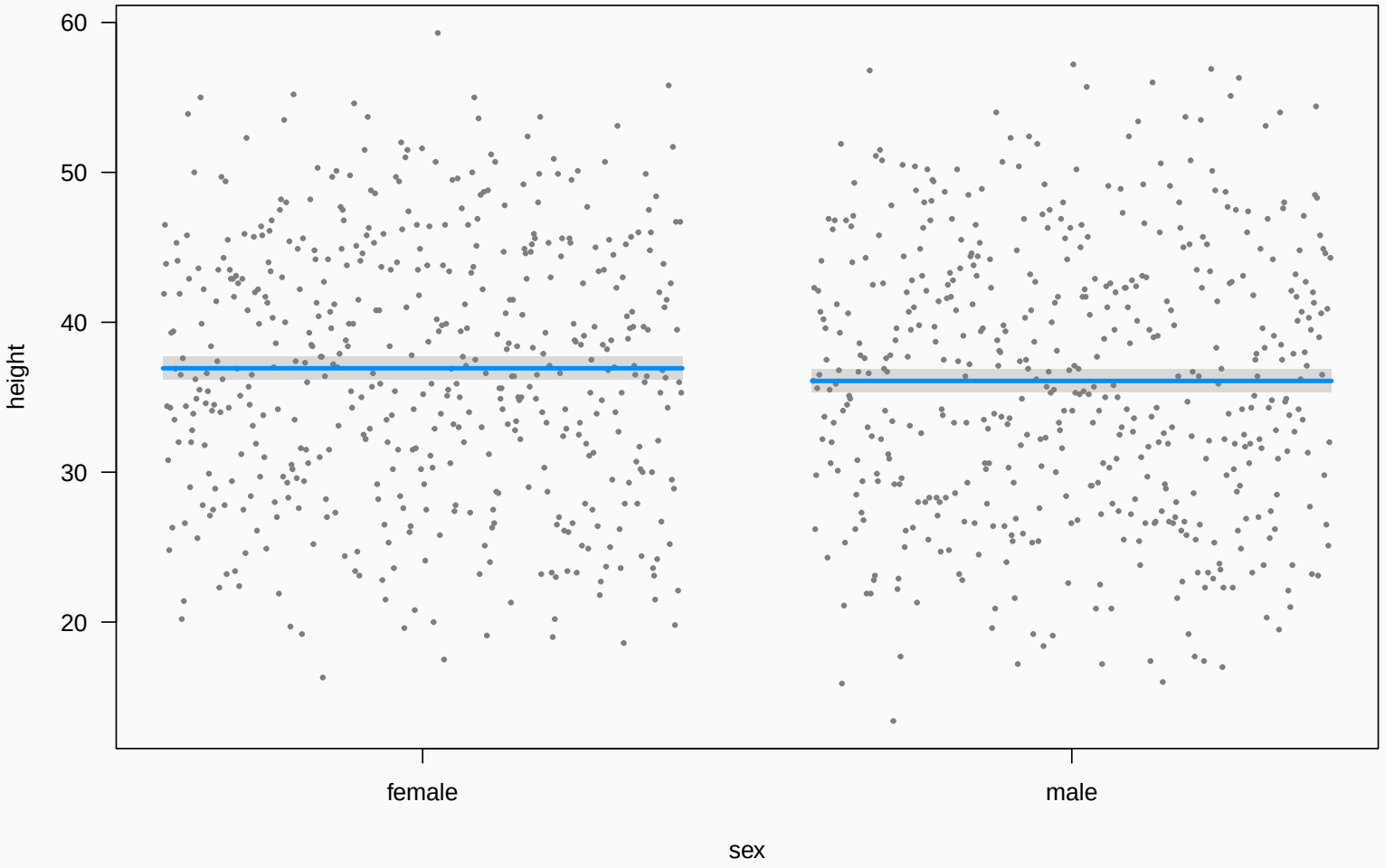
Plot (effects)

```
plot(allEffects(m2))
```



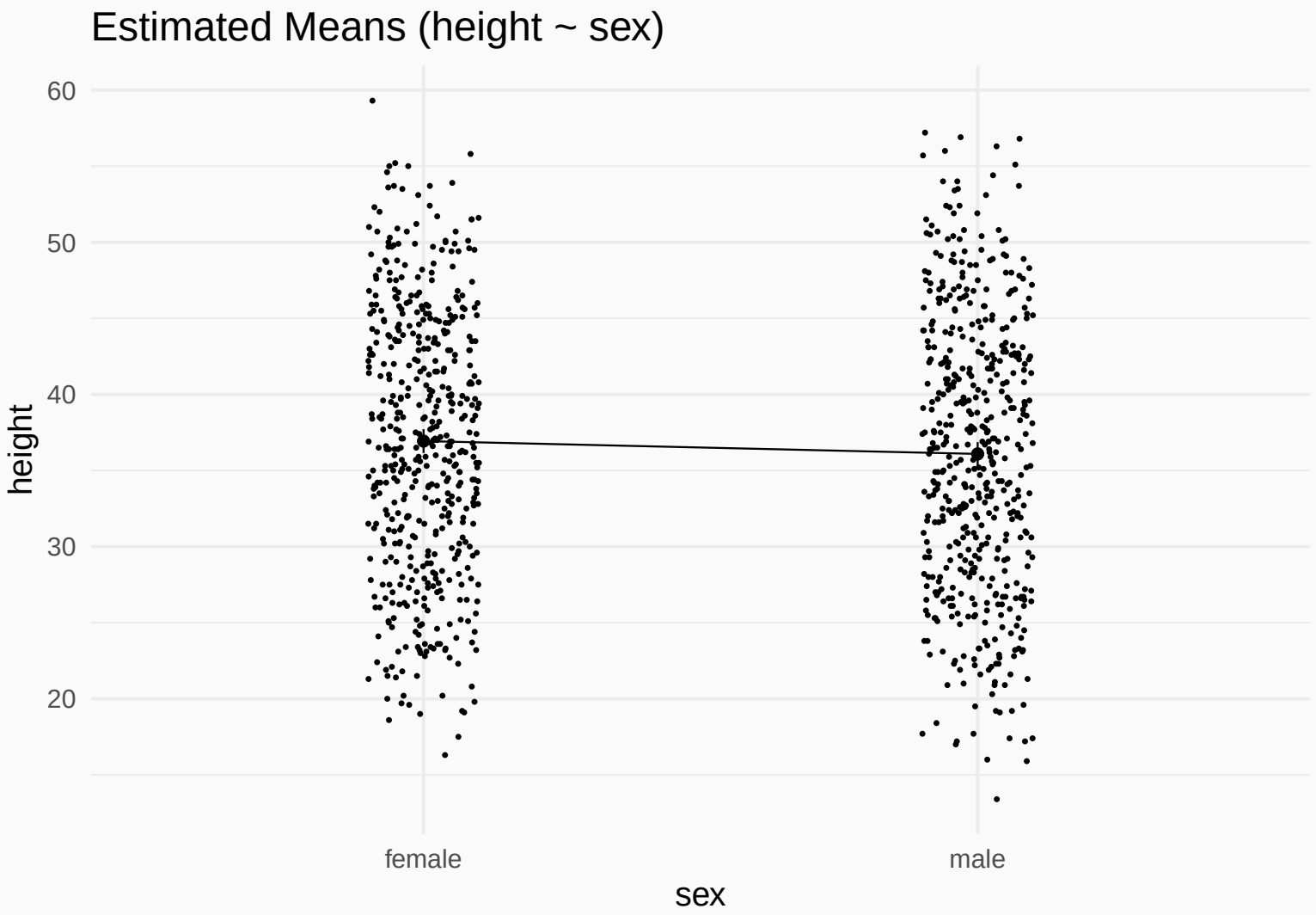
Plot (visreg)

```
visreg(m2)
```



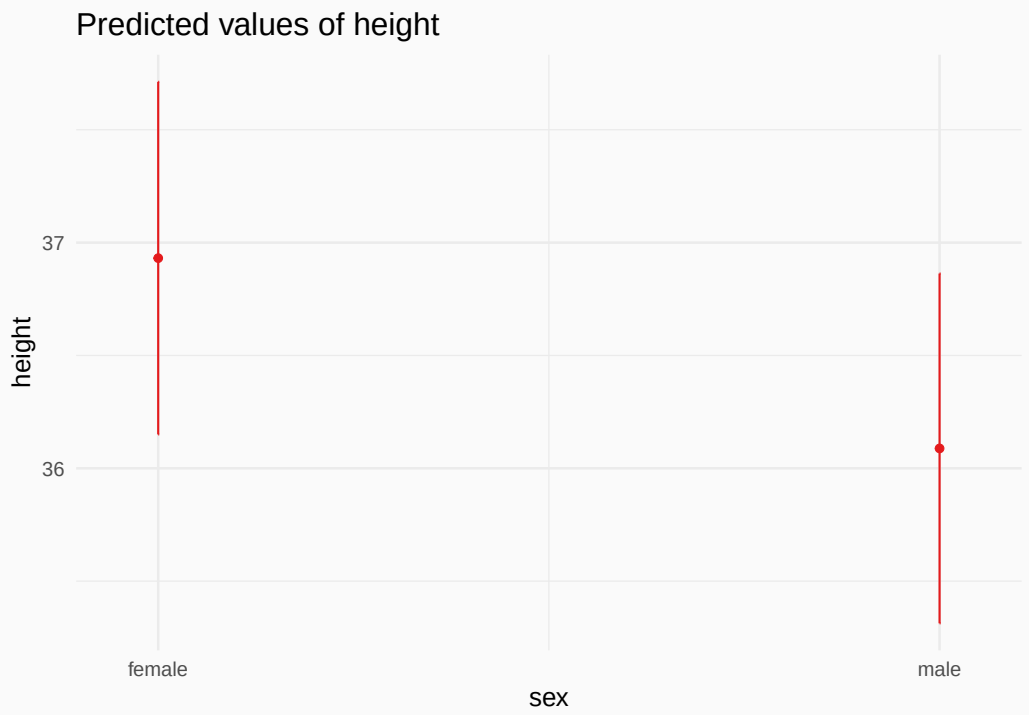
Plot (easystats)

```
plot(estimate_means(m2))
```



Plot model (sjPlot)

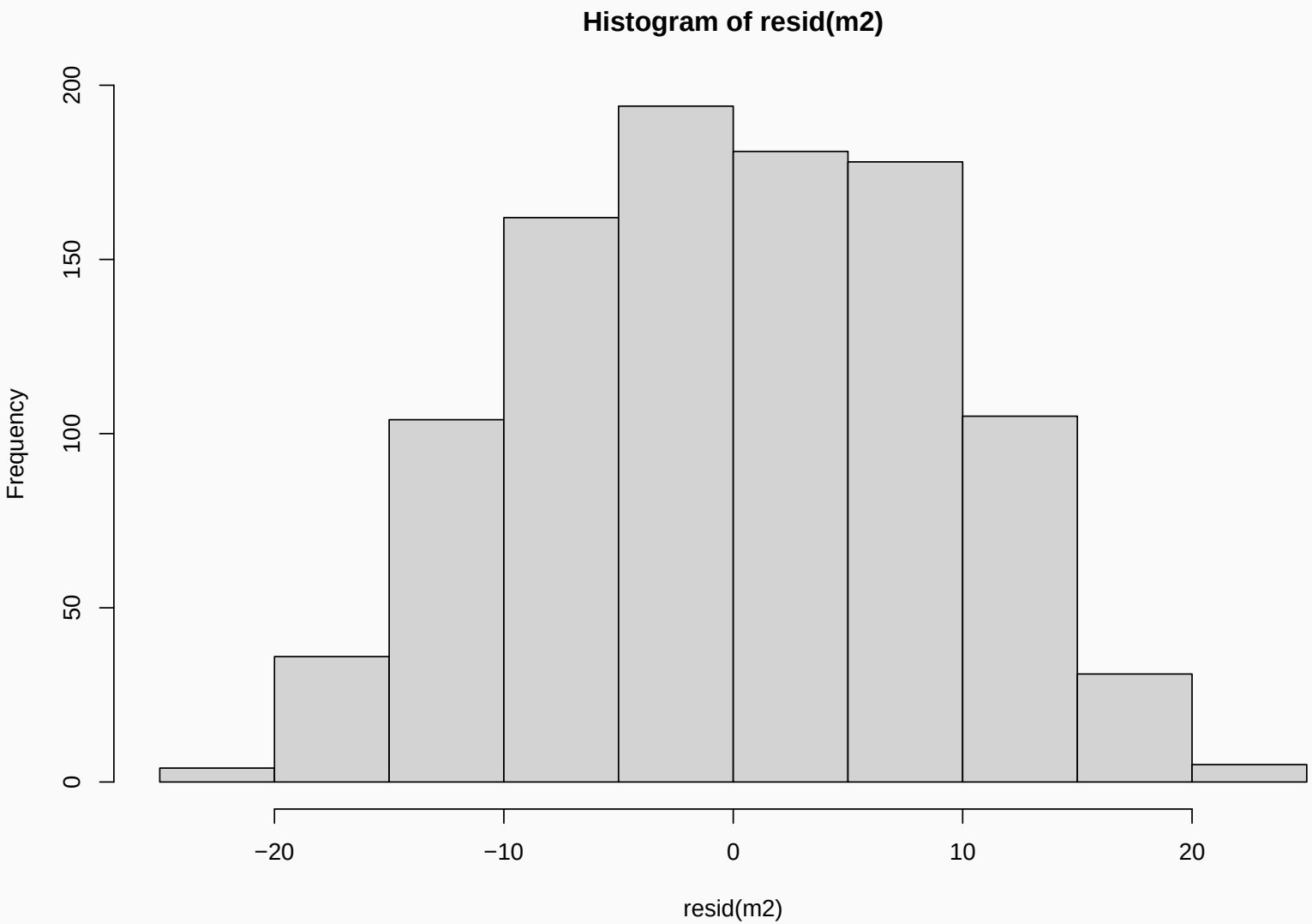
```
library('sjPlot')
plot_model(m2, type = 'eff', terms = 'sex')
```



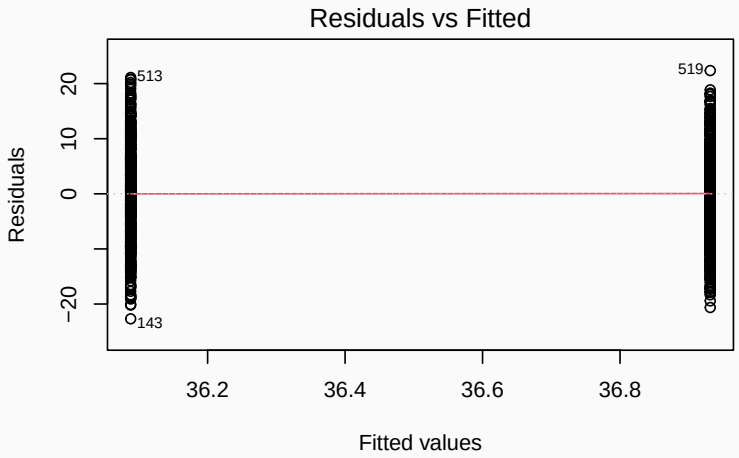
Model checking

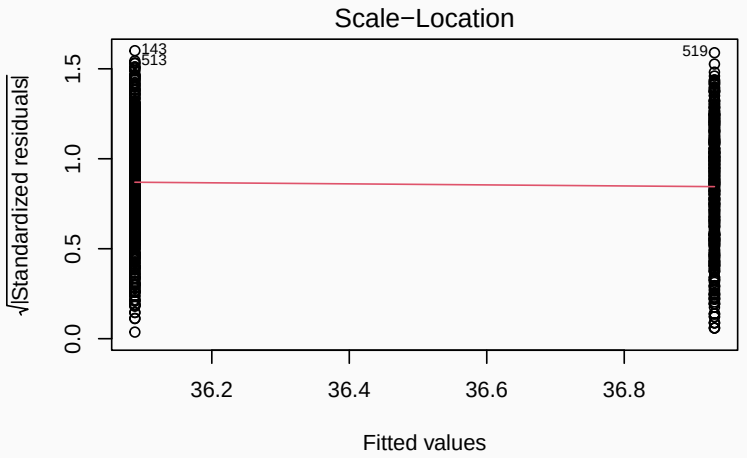
Model checking: residuals

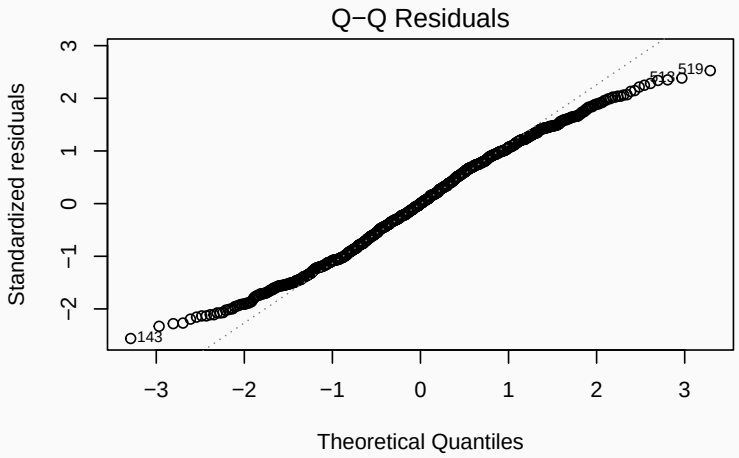
```
hist(resid(m2))
```

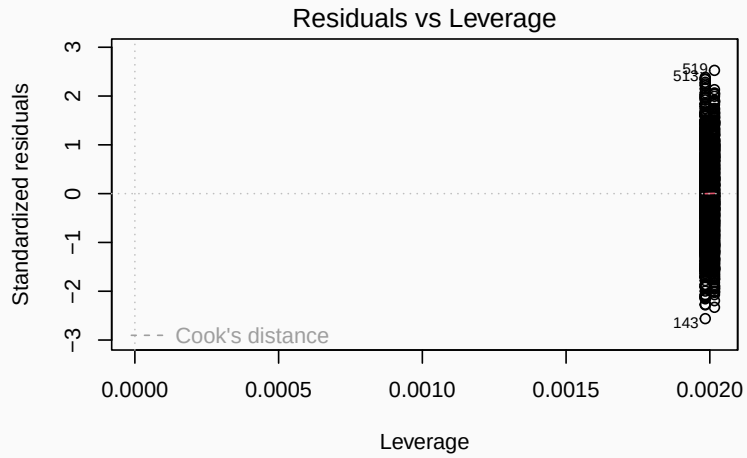


Model checking: residuals



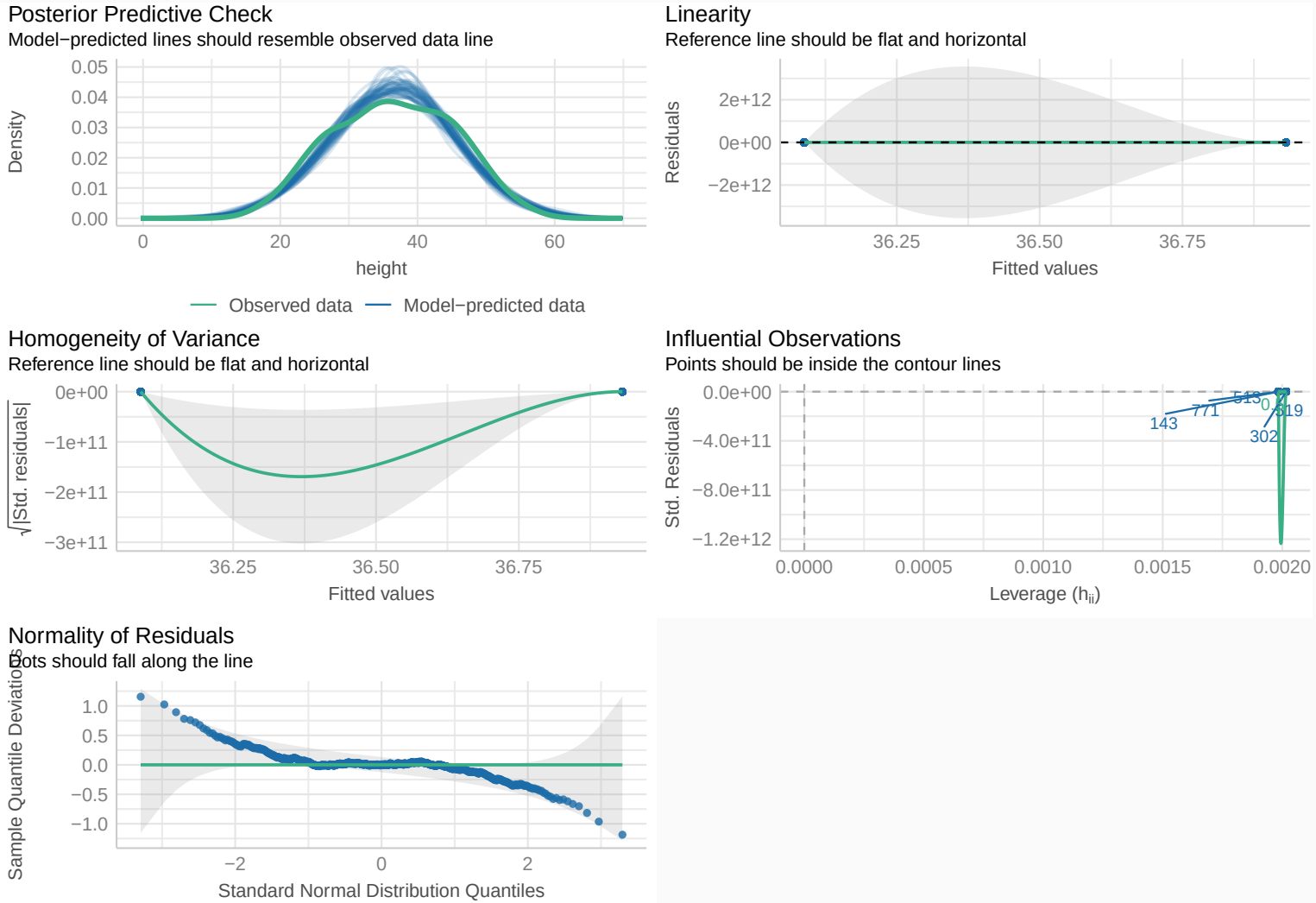






Model checking

```
library('easystats')
check_model(m2)
```



Model dashboard

```
model_dashboard(m2)
```

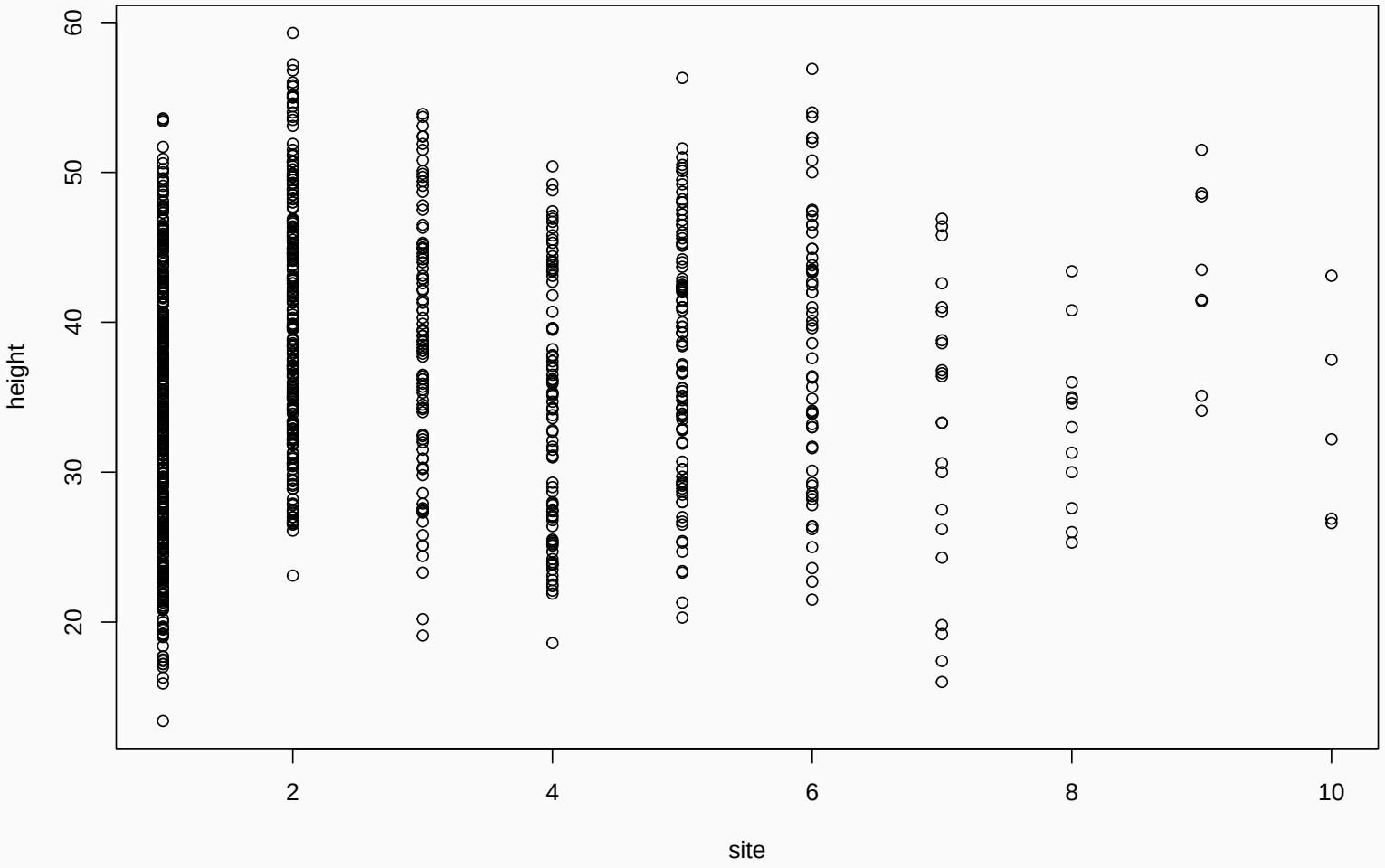
Q: Does height differ among field sites?

Quiz

https://pollev.com/franciscorod726

Plot data first

```
plot(height ~ site, data = trees)
```



Linear model with categorical predictors

```
m3 <- lm(height ~ site, data = trees)
```

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + ... + \varepsilon_i$$

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Model Height ~ site

All right here?

```r
m3 <- lm(height ~ site, data = trees)
```

```
Call:
lm(formula = height ~ site, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-22.4498  -6.7049   0.0709   6.7537  23.0640

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  35.4636     0.4730  74.975  < 2e-16 ***
site          0.3862     0.1413   2.733  0.00639 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.842 on 998 degrees of freedom
Multiple R-squared:  0.007429,  Adjusted R-squared:  0.006435
F-statistic:  7.47 on 1 and 998 DF,  p-value: 0.006385
```

Let's check model structure with `equatiomatic`

```
extract_eq(m3)
```

$$\text{height} = \alpha + \beta_1(\text{site}) + \epsilon \tag{3}$$

site is a factor!

```
trees$site <- as.factor(trees$site)
```

```
trees <- trees |>
  dplyr::mutate(site = as.factor(site))
```

Let's check model structure with `equatiomatic`

```
m3 <- lm(height ~ site, data = trees)

extract_eq(m3)
```

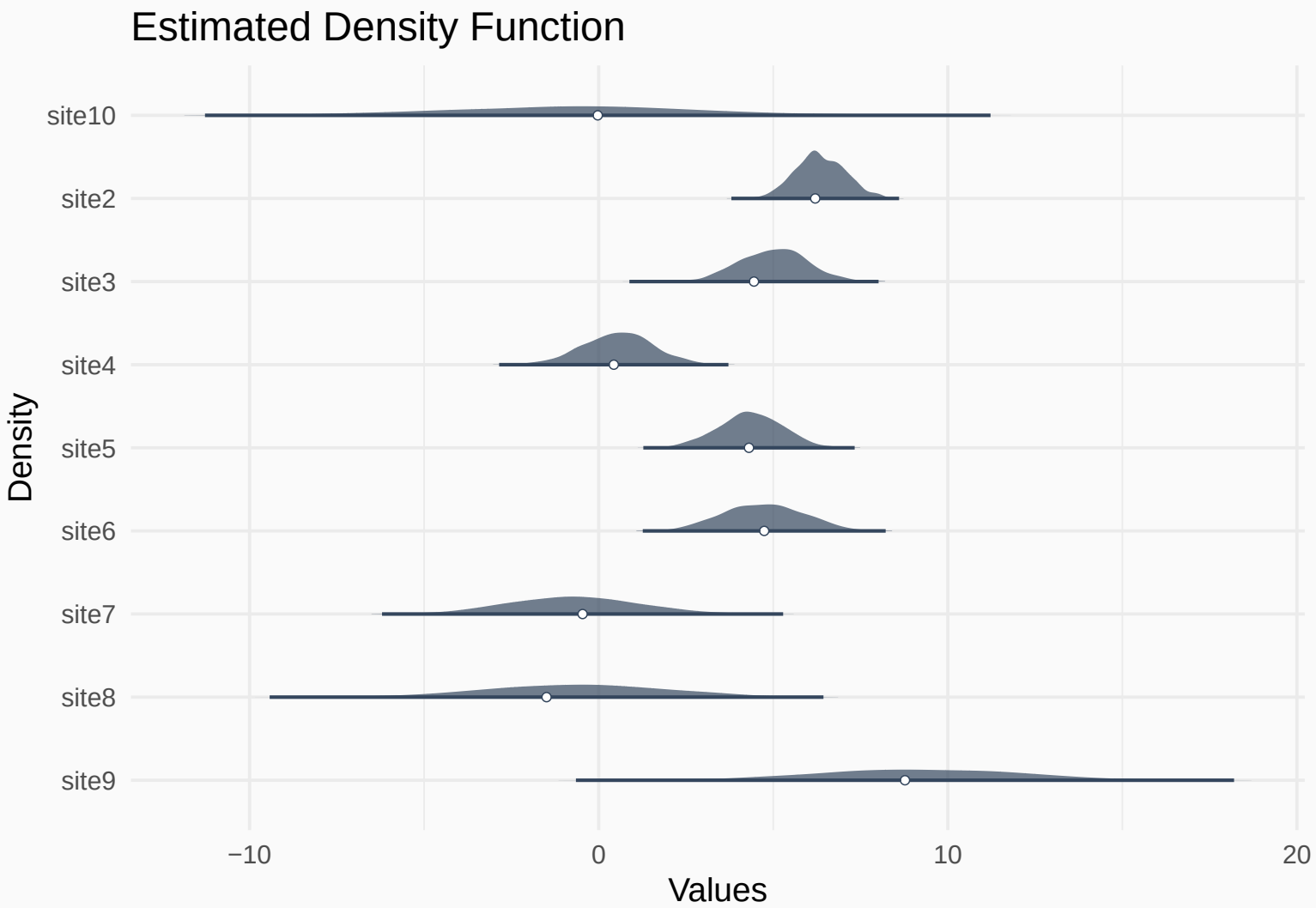
$$\text{height} = \alpha+\beta_1(\text{site}_2)+\beta_2(\text{site}_3)+\beta_3(\text{site}_4)+\beta_4(\text{site}_5)+\beta_5(\text{site}_6)+\beta_6(\text{site}_7)+\beta_7(\text{site}_8)+\beta_8(\text{site} \tag{4}$$

Model Height ~ site

```
Call:
lm(formula = height ~ site, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-20.4416  -6.9004   0.0379   6.3051  19.7584

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  33.8416     0.4266  79.329  < 2e-16 ***
site2         6.3411     0.7126   8.899  < 2e-16 ***
site3         4.9991     0.9828   5.086 4.36e-07 ***
site4         0.5329     0.9872   0.540  0.58949
site5         4.3723     0.9425   4.639 3.97e-06 ***
site6         4.7601     1.1709   4.065 5.18e-05 ***
site7        -0.7416     1.8506  -0.401  0.68871
site8        -0.6832     2.4753  -0.276  0.78258
site9         9.1709     3.0165   3.040  0.00243 **
site10       -0.5816     3.8013  -0.153  0.87843
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.446 on 990 degrees of freedom
Multiple R-squared:  0.1016,    Adjusted R-squared:  0.09344
F-statistic: 12.44 on 9 and 990 DF,  p-value: < 2.2e-16
```

Estimated parameter distributions

```
plot(simulate_parameters(m3), stack = FALSE)
```



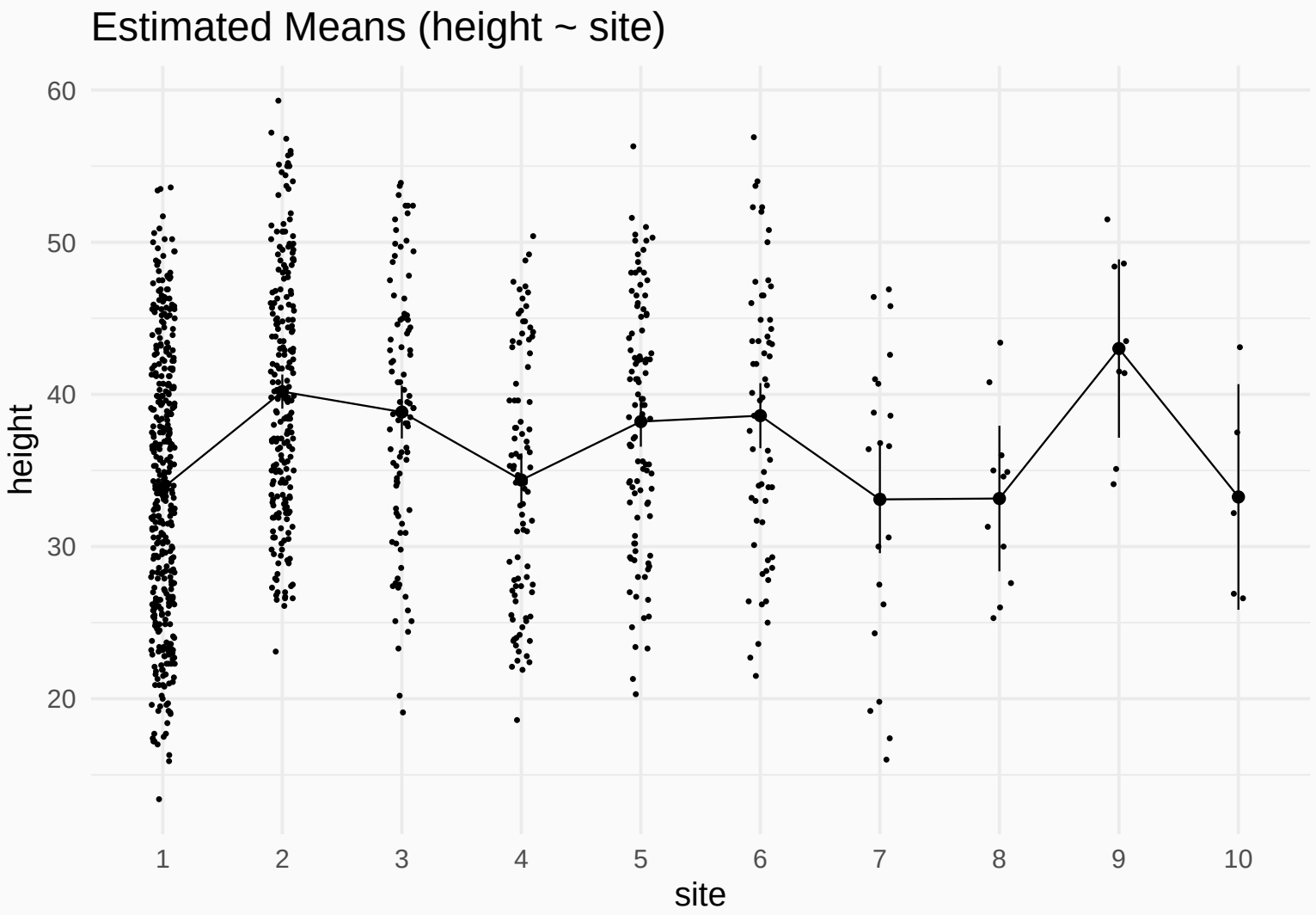
Estimated tree heights for each site

```
estimate_means(m3)
```

```
Estimated Marginal Means

site |  Mean |   SE |         95% CI
-----------------------------------
1    | 33.84 | 0.43 | [33.00, 34.68]
2    | 40.18 | 0.57 | [39.06, 41.30]
3    | 38.84 | 0.89 | [37.10, 40.58]
4    | 34.37 | 0.89 | [32.63, 36.12]
5    | 38.21 | 0.84 | [36.56, 39.86]
6    | 38.60 | 1.09 | [36.46, 40.74]
7    | 33.10 | 1.80 | [29.57, 36.63]
8    | 33.16 | 2.44 | [28.37, 37.94]
9    | 43.01 | 2.99 | [37.15, 48.87]
10   | 33.26 | 3.78 | [25.85, 40.67]
```

Plot estimated tree heights for each site

```
plot(estimate_means(m3))
```



Analysing differences among factor levels

For finer control see **emmeans** package

```
estimate_contrasts(m3)
```

```
Marginal Contrasts Analysis

Level1 | Level2 | Difference |          95% CI |   SE | t(990) |      p
-------------------------------------------------------------------------
site1  | site10 |       0.58 | [-11.85, 13.01] | 3.80 |   0.15 | > .999
site1  |  site2 |      -6.34 | [ -8.67, -4.01] | 0.71 |  -8.90 | < .001
site1  |  site3 |      -5.00 | [ -8.21, -1.78] | 0.98 |  -5.09 | < .001
site1  |  site4 |      -0.53 | [ -3.76,  2.70] | 0.99 |  -0.54 | > .999
site1  |  site5 |      -4.37 | [ -7.45, -1.29] | 0.94 |  -4.64 | < .001
site1  |  site6 |      -4.76 | [ -8.59, -0.93] | 1.17 |  -4.07 | 0.002
site1  |  site7 |       0.74 | [ -5.31,  6.79] | 1.85 |   0.40 | > .999
site1  |  site8 |       0.68 | [ -7.41,  8.78] | 2.48 |   0.28 | > .999
site1  |  site9 |      -9.17 | [-19.04,  0.69] | 3.02 |  -3.04 | 0.090
site2  | site10 |       6.92 | [ -5.57, 19.42] | 3.82 |   1.81 | > .999
site2  |  site3 |       1.34 | [ -2.10,  4.79] | 1.05 |   1.27 | > .999
site2  |  site4 |       5.81 | [  2.35,  9.27] | 1.06 |   5.49 | < .001
site2  |  site5 |       1.97 | [ -1.35,  5.29] | 1.02 |   1.94 | > .999
site2  |  site6 |       1.58 | [ -2.44,  5.61] | 1.23 |   1.28 | > .999
site2  |  site7 |       7.08 | [  0.90, 13.26] | 1.89 |   3.75 | 0.008
site2  |  site8 |       7.02 | [ -1.17, 15.21] | 2.50 |   2.81 | 0.169
site2  |  site9 |      -2.83 | [-12.77,  7.11] | 3.04 |  -0.93 | > .999
site3  | site10 |       5.58 | [ -7.11, 18.27] | 3.88 |   1.44 | > .999
site3  |  site4 |       4.47 | [  0.36,  8.57] | 1.26 |   3.56 | 0.015
site3  |  site5 |       0.63 | [ -3.37,  4.62] | 1.22 |   0.51 | > .999
site3  |  site6 |       0.24 | [ -4.35,  4.83] | 1.40 |   0.17 | > .999
site3  |  site7 |       5.74 | [ -0.82, 12.30] | 2.01 |   2.86 | 0.151
site3  |  site8 |       5.68 | [ -2.80, 14.17] | 2.59 |   2.19 | 0.804
site3  |  site9 |      -4.17 | [-14.36,  6.01] | 3.11 |  -1.34 | > .999
site4  | site10 |       1.11 | [-11.58, 13.81] | 3.88 |   0.29 | > .999
site4  |  site5 |      -3.84 | [ -7.84,  0.16] | 1.22 |  -3.14 | 0.067
site4  |  site6 |      -4.23 | [ -8.83,  0.38] | 1.41 |  -3.00 | 0.099
```

Analysing differences among factor levels

How different are site 2 and site 9?

```
library('marginaleffects')
hypotheses(m3, 'site2 = site9')
```

```
 Estimate Std. Error      z Pr(>|z|)   S 2.5 % 97.5 %
    -2.83       3.04 -0.931    0.352 1.5 -8.79   3.13

Term: site2 = site9
Columns: term, estimate, std.error, statistic, p.value, s.value, co
```

Presenting model results

```
parameters(m3)
```

```
Parameter   | Coefficient |   SE |         95% CI | t(990) |      p
-------------------------------------------------------------------
(Intercept) |       33.84 | 0.43 | [33.00, 34.68] |  79.33 | < .001
site [2]    |        6.34 | 0.71 | [ 4.94,  7.74] |   8.90 | < .001
site [3]    |        5.00 | 0.98 | [ 3.07,  6.93] |   5.09 | < .001
site [4]    |        0.53 | 0.99 | [-1.40,  2.47] |   0.54 | 0.589
site [5]    |        4.37 | 0.94 | [ 2.52,  6.22] |   4.64 | < .001
site [6]    |        4.76 | 1.17 | [ 2.46,  7.06] |   4.07 | < .001
site [7]    |       -0.74 | 1.85 | [-4.37,  2.89] |  -0.40 | 0.689
site [8]    |       -0.68 | 2.48 | [-5.54,  4.17] |  -0.28 | 0.783
site [9]    |        9.17 | 3.02 | [ 3.25, 15.09] |   3.04 | 0.002
site [10]   |       -0.58 | 3.80 | [-8.04,  6.88] |  -0.15 | 0.878
```

Presenting model results

```
estimate_means(m3)
```

```
Estimated Marginal Means

site |  Mean |   SE |         95% CI
-----------------------------------
1    | 33.84 | 0.43 | [33.00, 34.68]
2    | 40.18 | 0.57 | [39.06, 41.30]
3    | 38.84 | 0.89 | [37.10, 40.58]
4    | 34.37 | 0.89 | [32.63, 36.12]
5    | 38.21 | 0.84 | [36.56, 39.86]
6    | 38.60 | 1.09 | [36.46, 40.74]
7    | 33.10 | 1.80 | [29.57, 36.63]
8    | 33.16 | 2.44 | [28.37, 37.94]
9    | 43.01 | 2.99 | [37.15, 48.87]
10   | 33.26 | 3.78 | [25.85, 40.67]

Marginal means estimated at site
```

Presenting model results

```
modelsummary(m3, estimate  = '{estimate} ({std.error})', statistic = NULL,
             fmt = 1, gof_map = NA, coef_rename = paste0('site', 1:10), output = 'markdown')
```

	(1)
site1	33.8 (0.4)
site2	6.3 (0.7)
site3	5.0 (1.0)
site4	0.5 (1.0)
site5	4.4 (0.9)
site6	4.8 (1.2)
site7	-0.7 (1.9)
site8	-0.7 (2.5)
site9	9.2 (3.0)
site10	-0.6 (3.8)

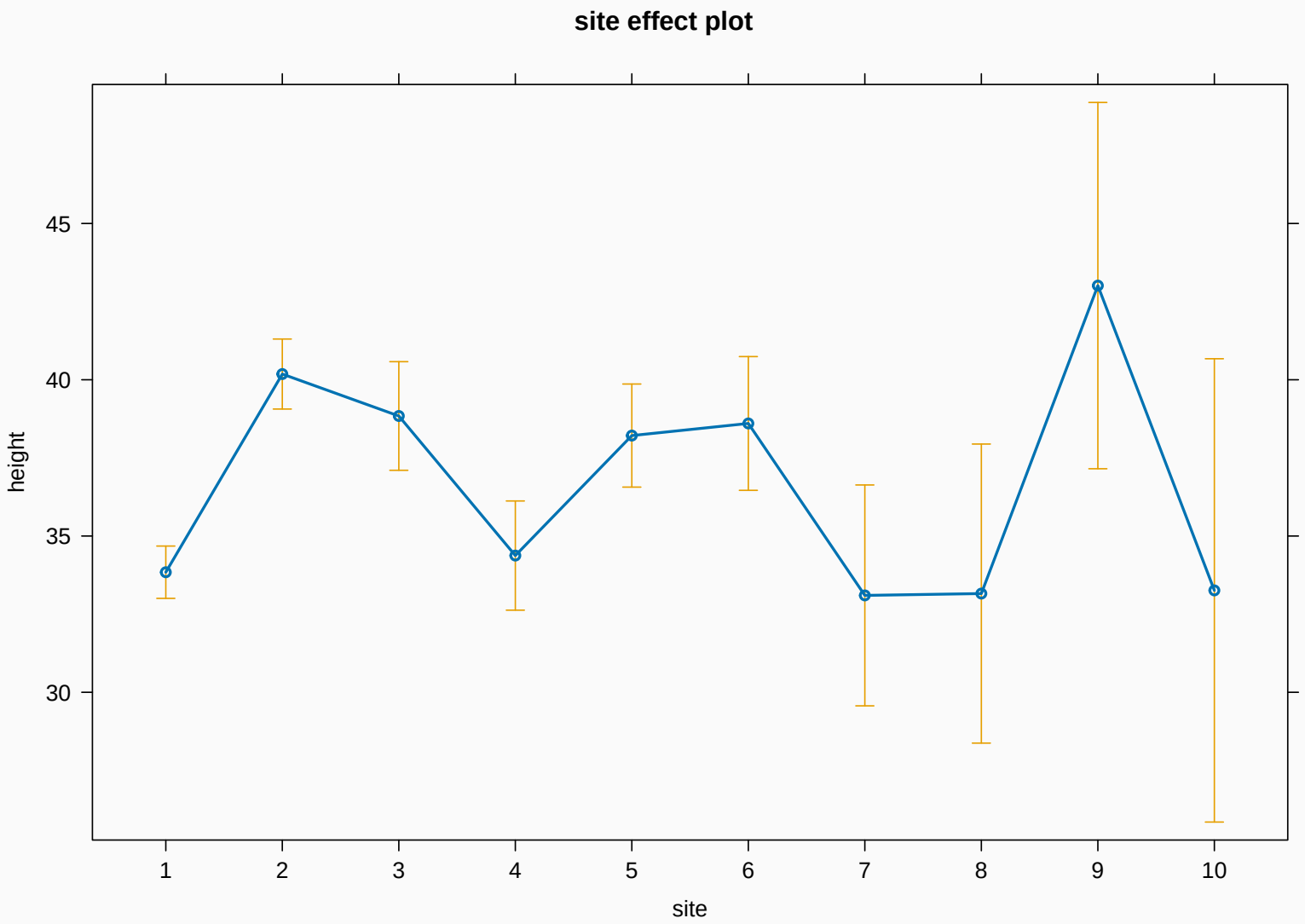
Presenting model results

```
library('gtsummary')
tbl_regression(m3)
```

Characteristic	Beta	95% CI[1]	p-value
site			
1	—	—	
2	6.3	4.9, 7.7	<0.001
3	5.0	3.1, 6.9	<0.001
4	0.53	-1.4, 2.5	0.6
5	4.4	2.5, 6.2	<0.001
6	4.8	2.5, 7.1	<0.001
7	-0.74	-4.4, 2.9	0.7
8	-0.68	-5.5, 4.2	0.8
9	9.2	3.3, 15	0.002
10	-0.58	-8.0, 6.9	0.9

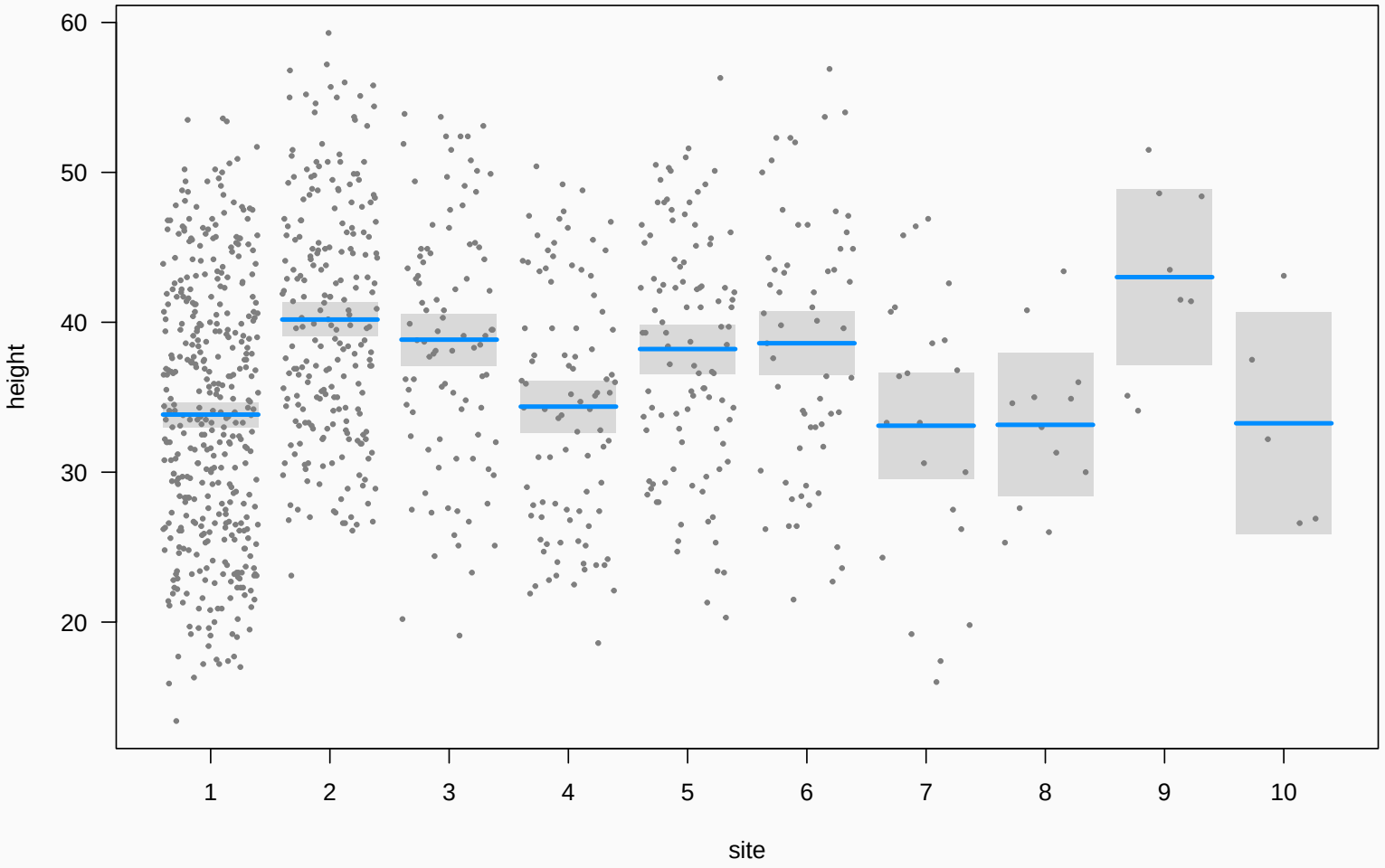
Plot

```
plot(allEffects(m3))
```



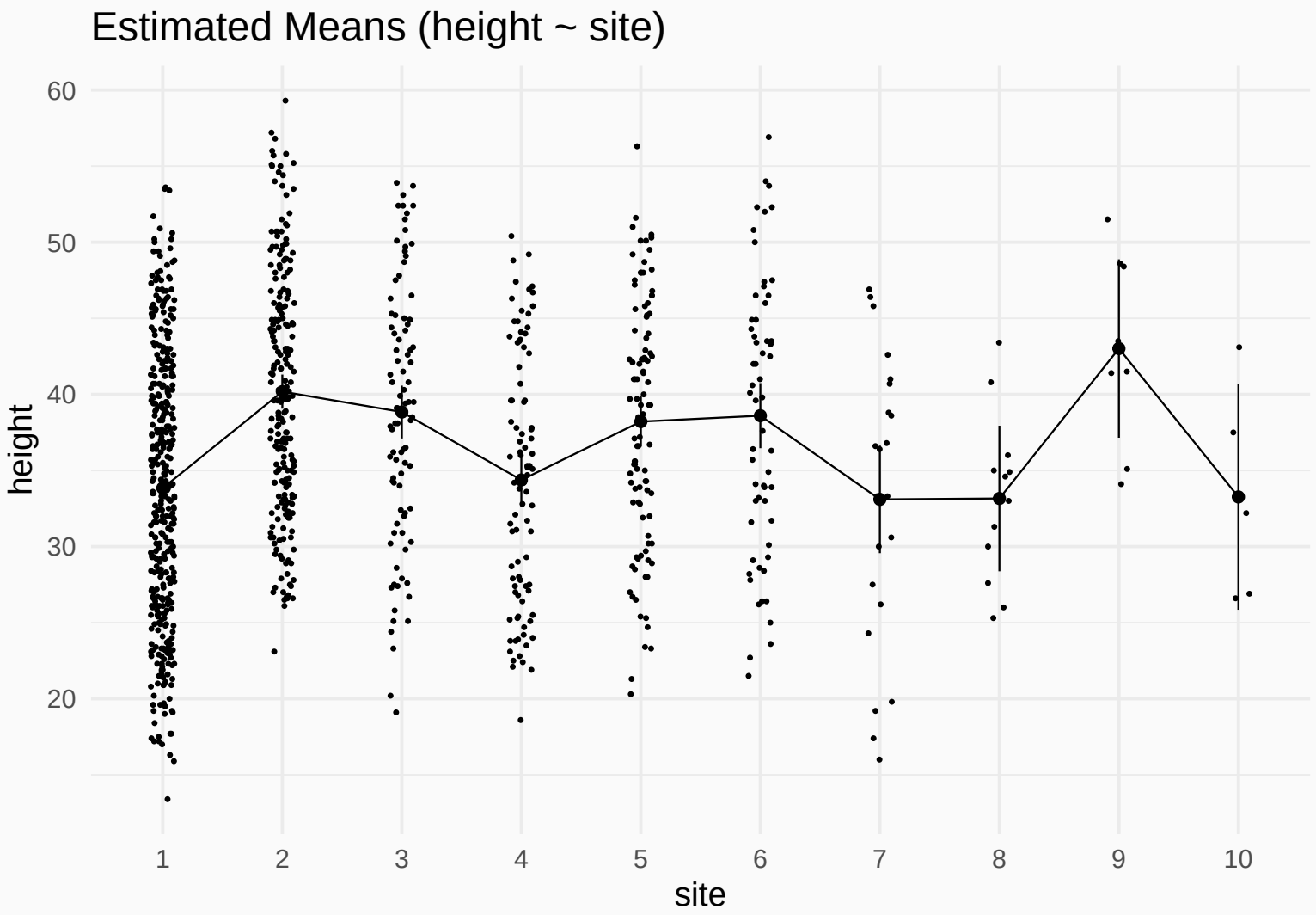
Plot (visreg)

```
visreg(m3)
```



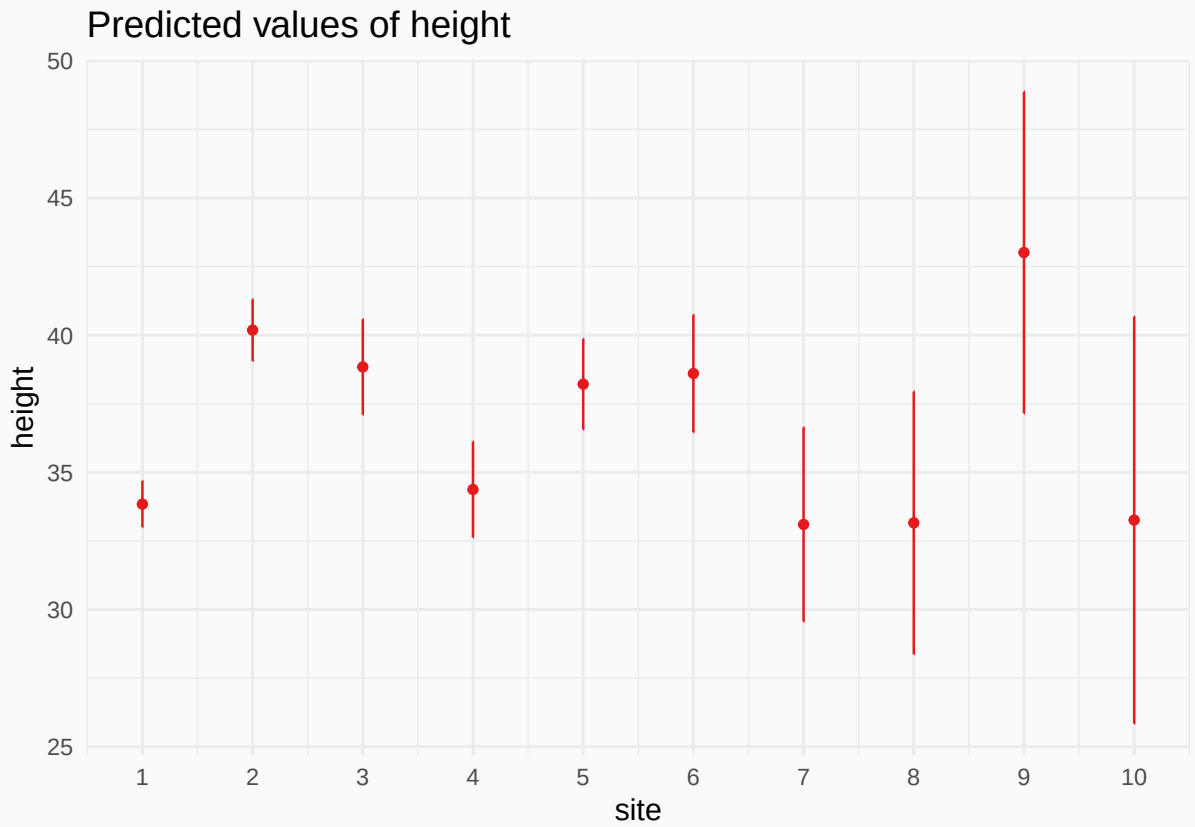
Plot (easystats)

```
plot(estimate_means(m3))
```



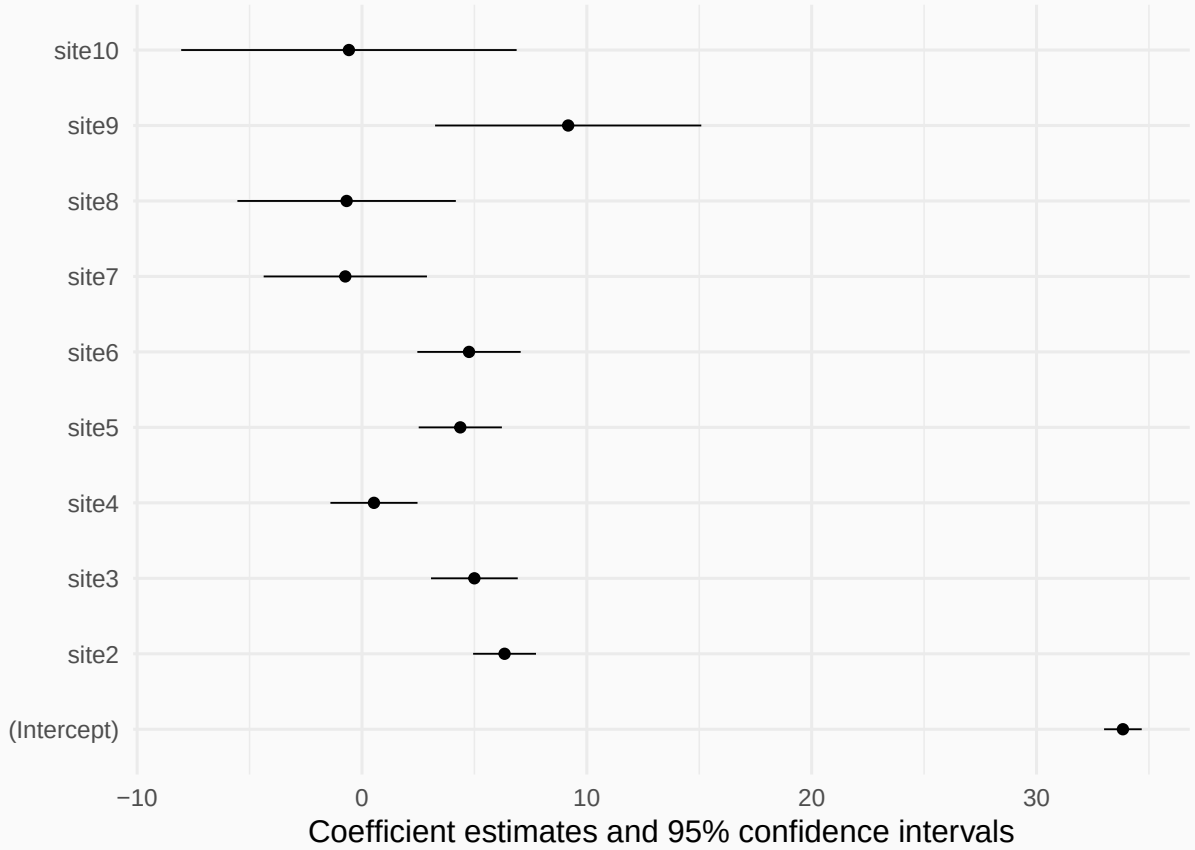
Plot model (sjPlot)

```
plot_model(m3, type = 'eff', terms = 'site')
```



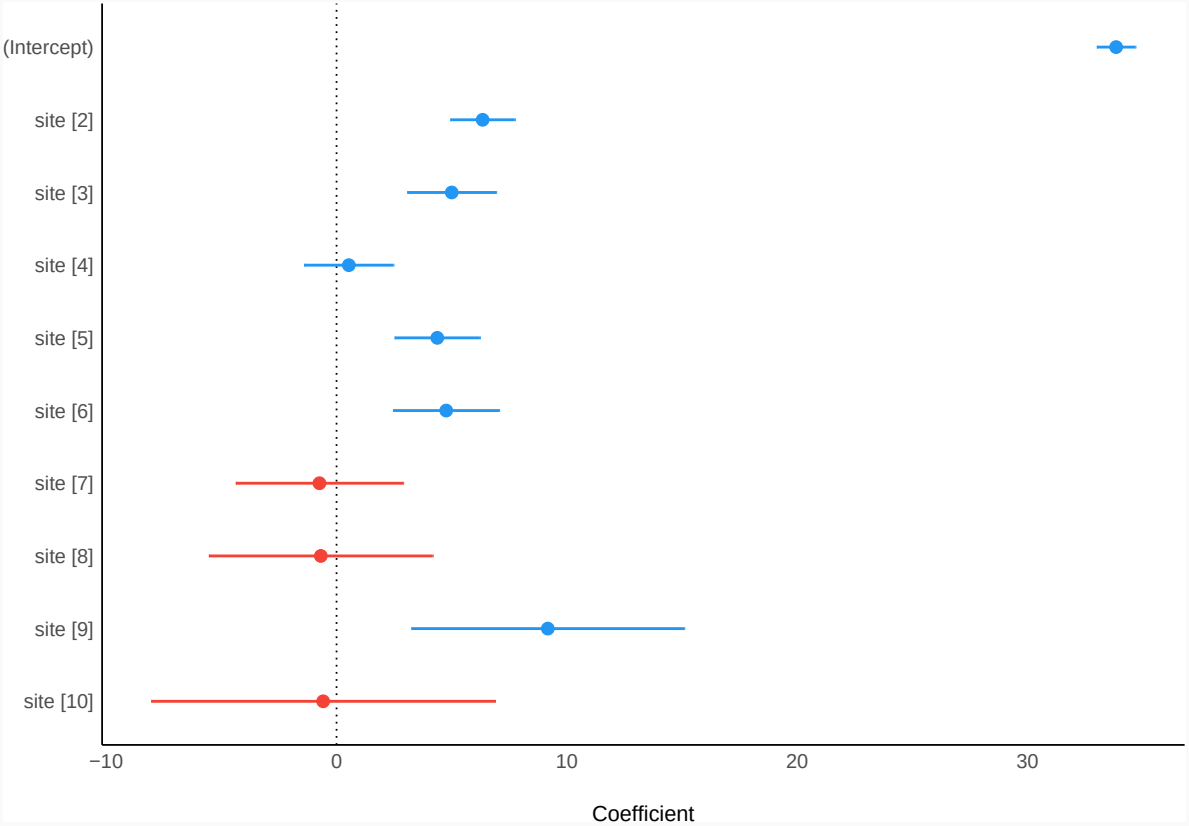
Plot model (modelsummary)

```
modelplot(m3)
```



Plot model (easystats)

```
plot(parameters(m3), show_intercept = TRUE)
```



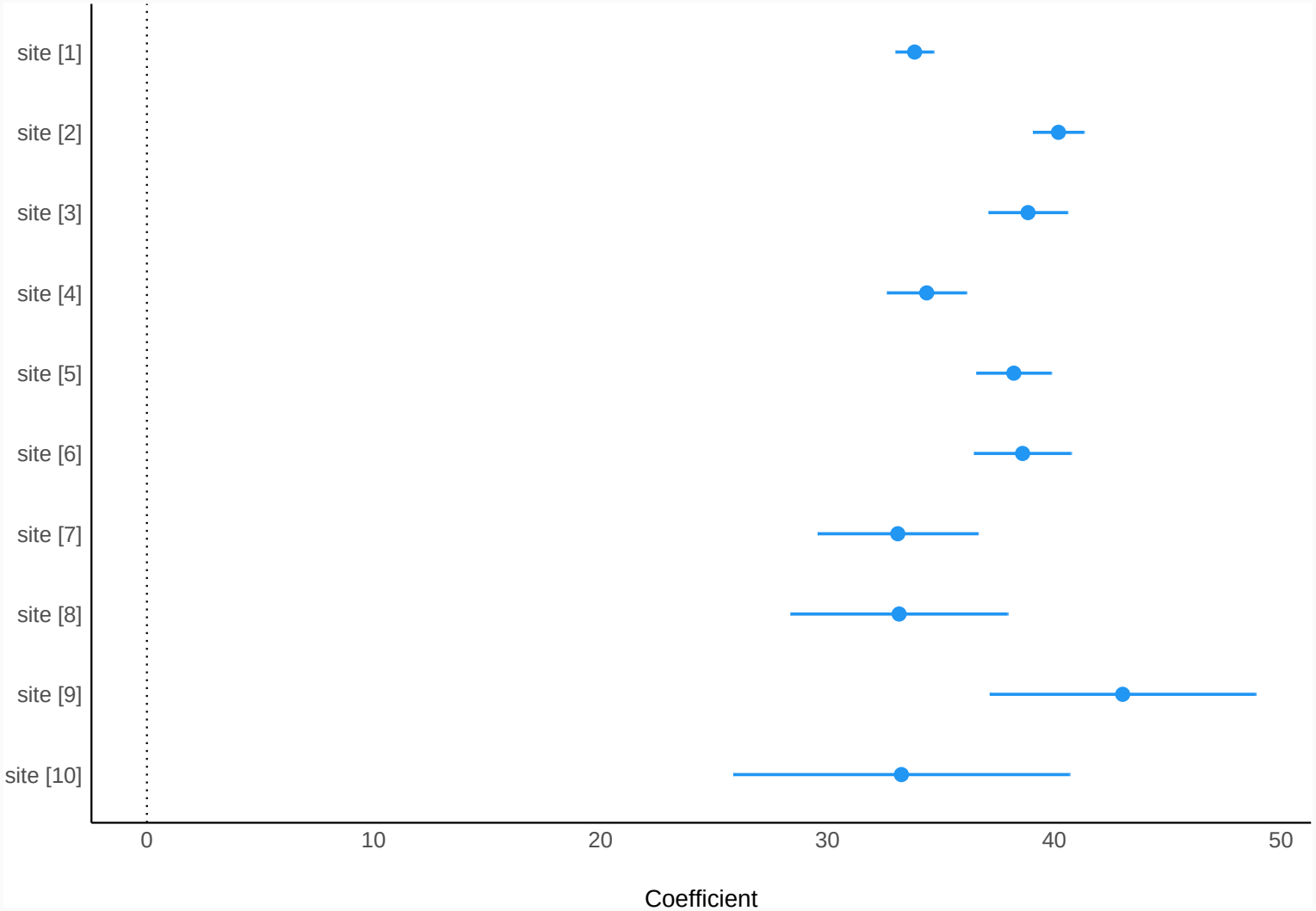
Fit model without intercept

```
m3bis <- lm(height ~ site - 1, data = trees)
```

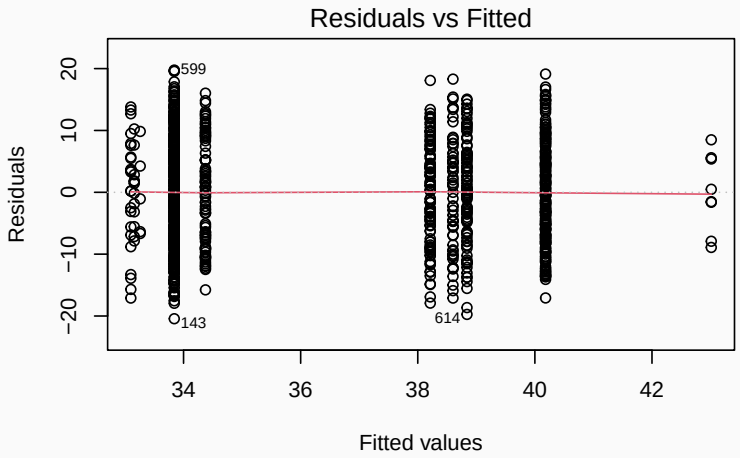
```
Call:
lm(formula = height ~ site - 1, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-20.4416  -6.9004   0.0379   6.3051  19.7584

Coefficients:
       Estimate Std. Error t value Pr(>|t|)
site1   33.8416     0.4266  79.329   <2e-16 ***
site2   40.1826     0.5707  70.404   <2e-16 ***
site3   38.8407     0.8854  43.868   <2e-16 ***
site4   34.3744     0.8903  38.610   <2e-16 ***
site5   38.2139     0.8404  45.469   <2e-16 ***
site6   38.6017     1.0904  35.401   <2e-16 ***
site7   33.1000     1.8007  18.381   <2e-16 ***
site8   33.1583     2.4382  13.599   <2e-16 ***
site9   43.0125     2.9862  14.404   <2e-16 ***
site10  33.2600     3.7773   8.805   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.446 on 990 degrees of freedom
```

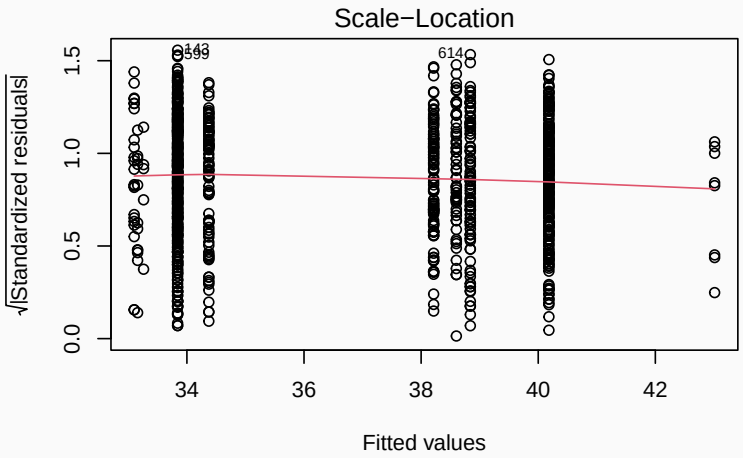
Model without intercept

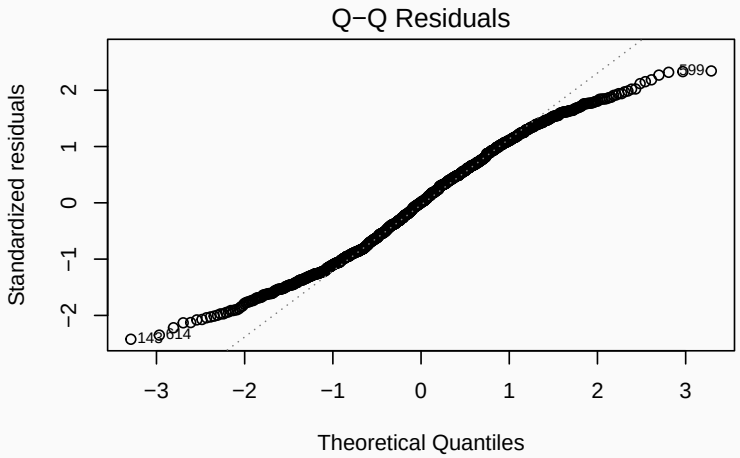
```
plot(parameters(m3bis))
```

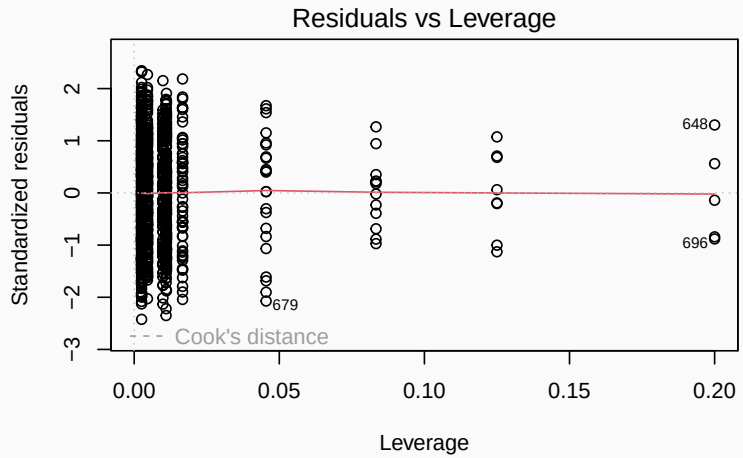


Model checking: residuals



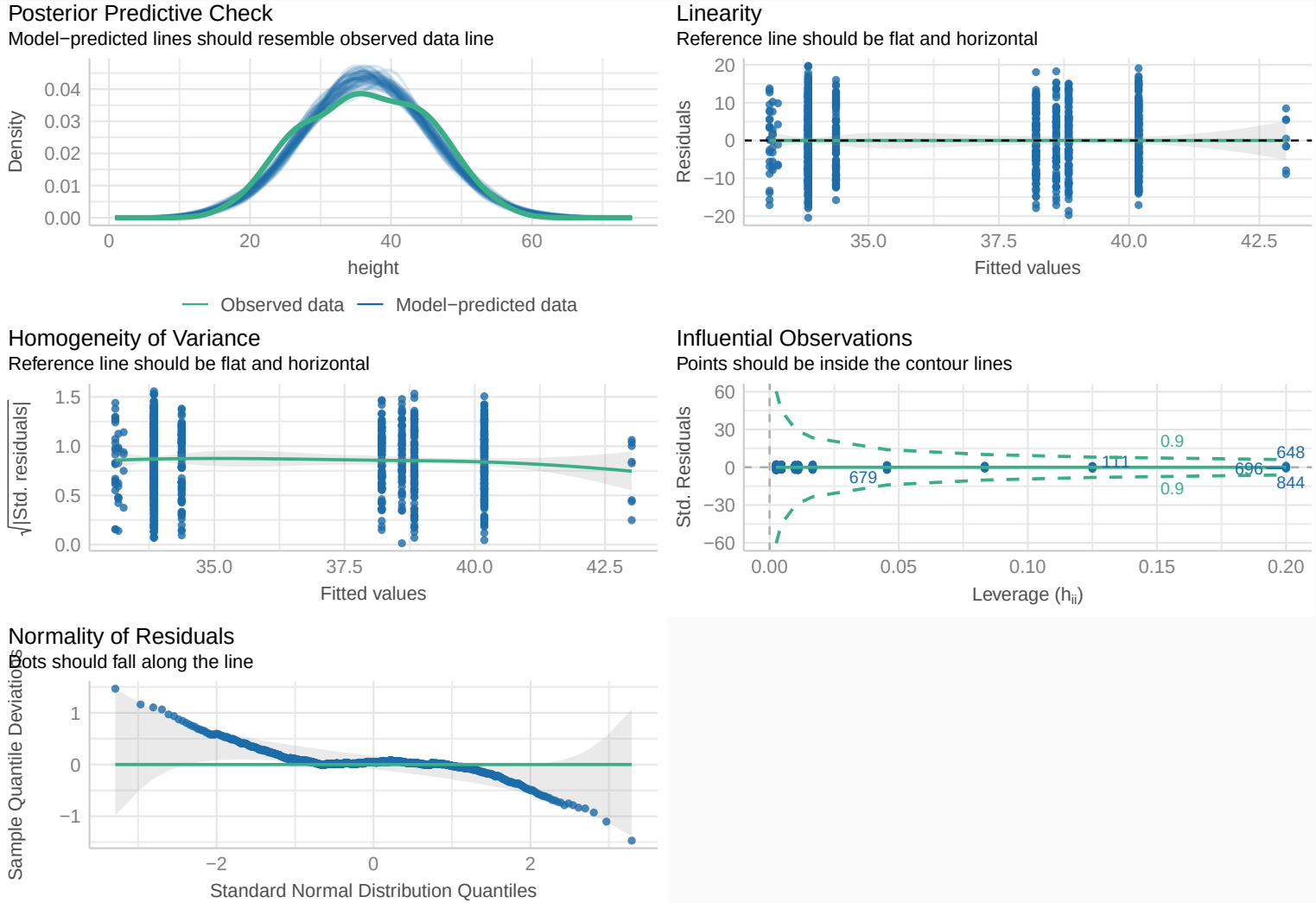






Model checking: residuals

```
check_model(m3)
```



Combining continuous and categorical predictors

Predicting tree height based on dbh and site

```
lm(height ~ site + dbh, data = trees)
```

corresponds to

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + ... + k \cdot DBH_i + \varepsilon_i$$

$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Predicting tree height based on dbh and site

```
Call:
lm(formula = height ~ site + dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-10.1130  -1.9885   0.0582   2.0314  11.3320

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 16.699037   0.260565  64.088  < 2e-16 ***
site2        6.504303   0.256730  25.335  < 2e-16 ***
site3        4.357457   0.354181  12.303  < 2e-16 ***
site4        1.934650   0.356102   5.433 6.98e-08 ***
site5        3.637432   0.339688  10.708  < 2e-16 ***
site6        4.204511   0.421906   9.966  < 2e-16 ***
site7       -0.176193   0.666772  -0.264   0.7916
site8       -5.312648   0.893603  -5.945 3.82e-09 ***
site9        5.437049   1.087766   4.998 6.84e-07 ***
site10       2.263338   1.369986   1.652   0.0988 .
dbh          0.617075   0.007574  81.473  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.043 on 989 degrees of freedom
Multiple R-squared:  0.8835,    Adjusted R-squared:  0.8823
```

Presenting model results

```
parameters(m4)
```

```
Parameter   | Coefficient |       SE |         95% CI | t(989) |      p
-------------------------------------------------------------------------
(Intercept) |       16.70 |     0.26 | [16.19, 17.21] |  64.09 | < .001
site [2]    |        6.50 |     0.26 | [ 6.00,  7.01] |  25.34 | < .001
site [3]    |        4.36 |     0.35 | [ 3.66,  5.05] |  12.30 | < .001
site [4]    |        1.93 |     0.36 | [ 1.24,  2.63] |   5.43 | < .001
site [5]    |        3.64 |     0.34 | [ 2.97,  4.30] |  10.71 | < .001
site [6]    |        4.20 |     0.42 | [ 3.38,  5.03] |   9.97 | < .001
site [7]    |       -0.18 |     0.67 | [-1.48,  1.13] |  -0.26 | 0.792
site [8]    |       -5.31 |     0.89 | [-7.07, -3.56] |  -5.95 | < .001
site [9]    |        5.44 |     1.09 | [ 3.30,  7.57] |   5.00 | < .001
site [10]   |        2.26 |     1.37 | [-0.43,  4.95] |   1.65 | 0.099
dbh         |        0.62 | 7.57e-03 | [ 0.60,  0.63] |  81.47 | < .001
```

Estimated tree heights for each site

```
estimate_means(m4)
```

```
Estimated Marginal Means

site |  Mean |   SE |         95% CI
-----------------------------------
1    | 33.90 | 0.15 | [33.60, 34.21]
2    | 40.41 | 0.21 | [40.01, 40.81]
3    | 38.26 | 0.32 | [37.64, 38.89]
4    | 35.84 | 0.32 | [35.21, 36.47]
5    | 37.54 | 0.30 | [36.95, 38.14]
6    | 38.11 | 0.39 | [37.34, 38.88]
7    | 33.73 | 0.65 | [32.45, 35.00]
8    | 28.59 | 0.88 | [26.86, 30.32]
9    | 39.34 | 1.08 | [37.23, 41.45]
10   | 36.17 | 1.36 | [33.50, 38.84]
```

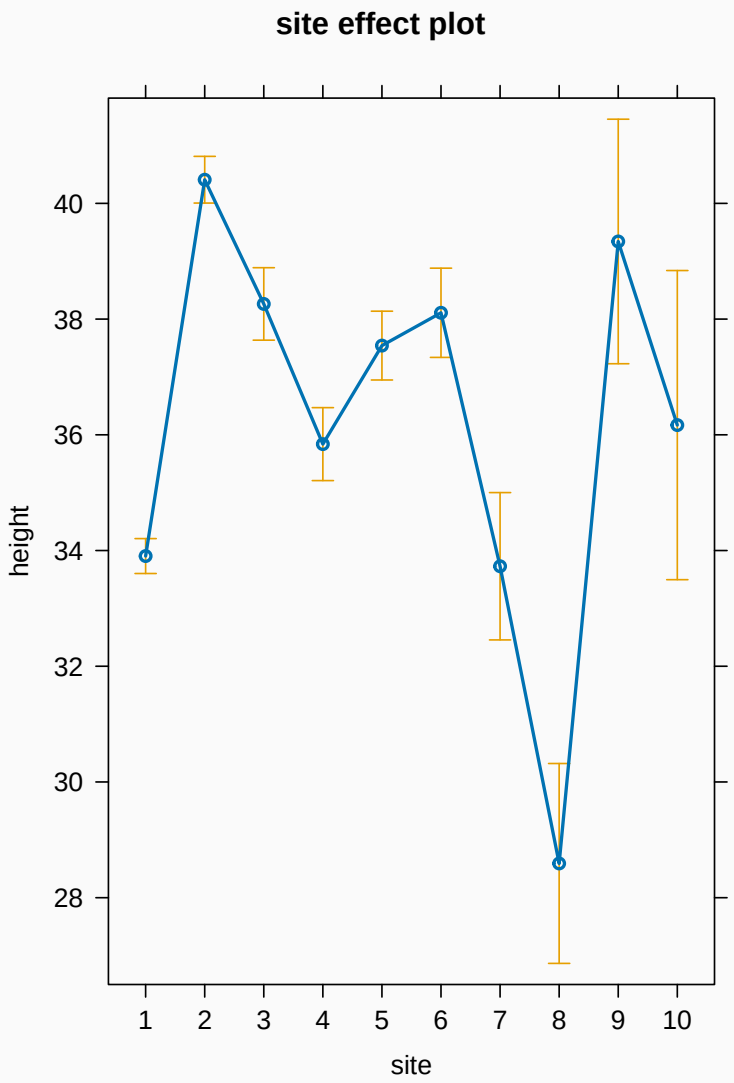
Fit model without intercept

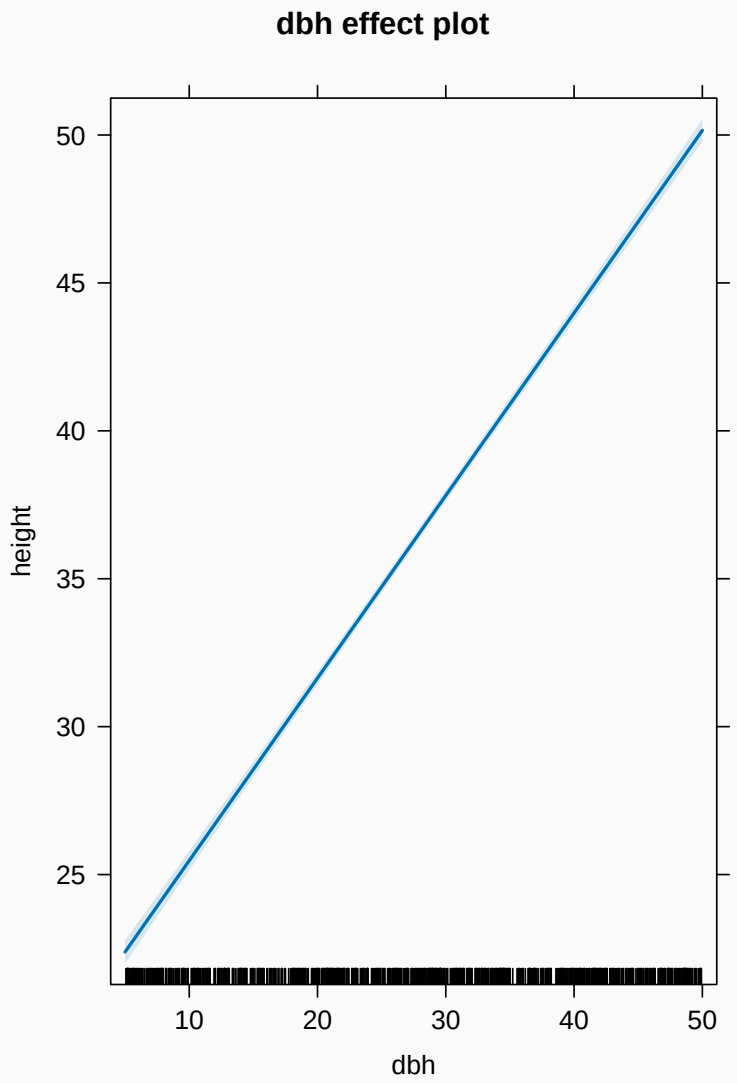
```
m4.noint <- lm(height ~ -1 + site + dbh, data = trees)
```

```
Call:
lm(formula = height ~ -1 + site + dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-10.1130  -1.9885   0.0582   2.0314  11.3320

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
site1  16.699037   0.260565   64.09   <2e-16 ***
site2  23.203340   0.292773   79.25   <2e-16 ***
site3  21.056494   0.386532   54.48   <2e-16 ***
site4  18.633687   0.374456   49.76   <2e-16 ***
site5  20.336469   0.373942   54.38   <2e-16 ***
site6  20.903548   0.448913   46.56   <2e-16 ***
site7  16.522844   0.679936   24.30   <2e-16 ***
site8  11.386389   0.918198   12.40   <2e-16 ***
site9  22.136086   1.105970   20.02   <2e-16 ***
site10 18.962375   1.372158   13.82   <2e-16 ***
dbh     0.617075   0.007574   81.47   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot

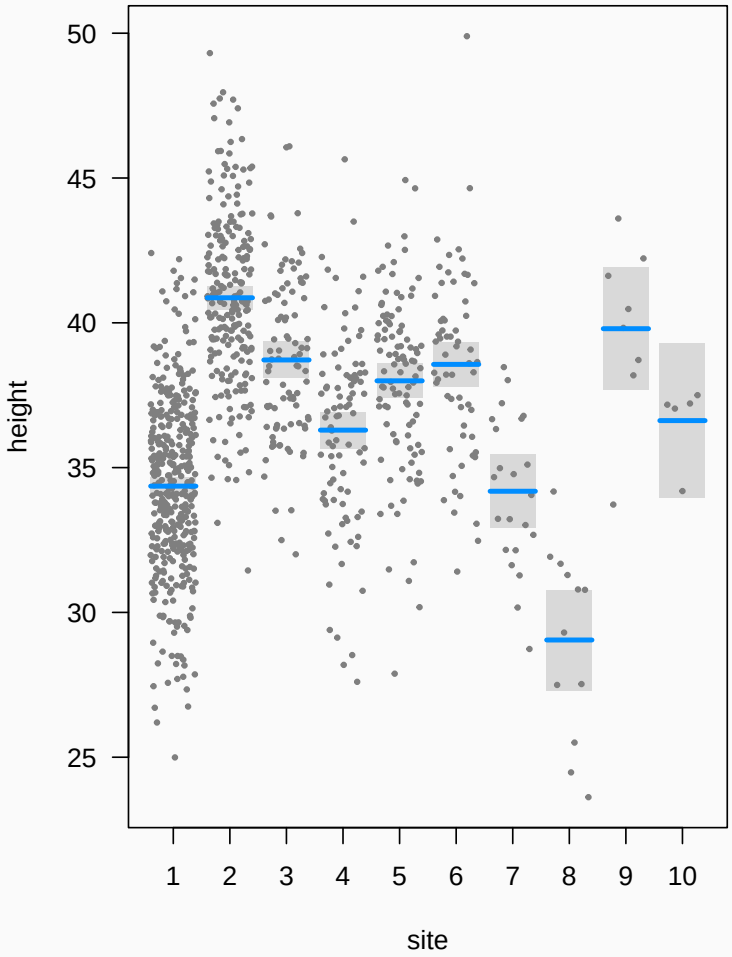
```
plot(allEffects(m4))
```

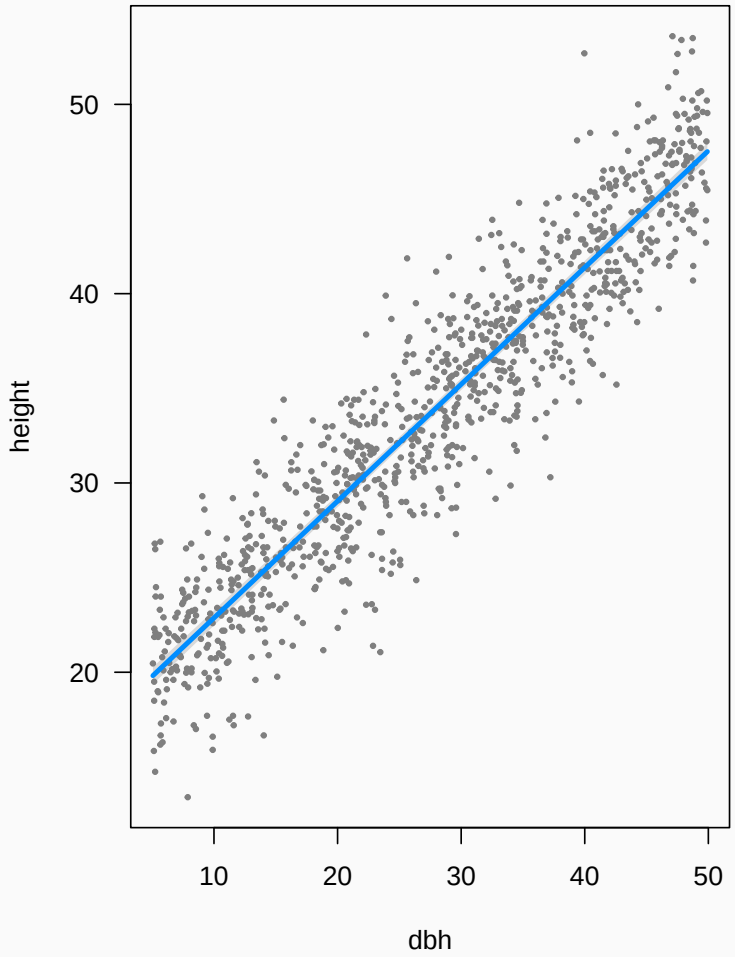




Plot (visreg)

```
visreg(m4)
```

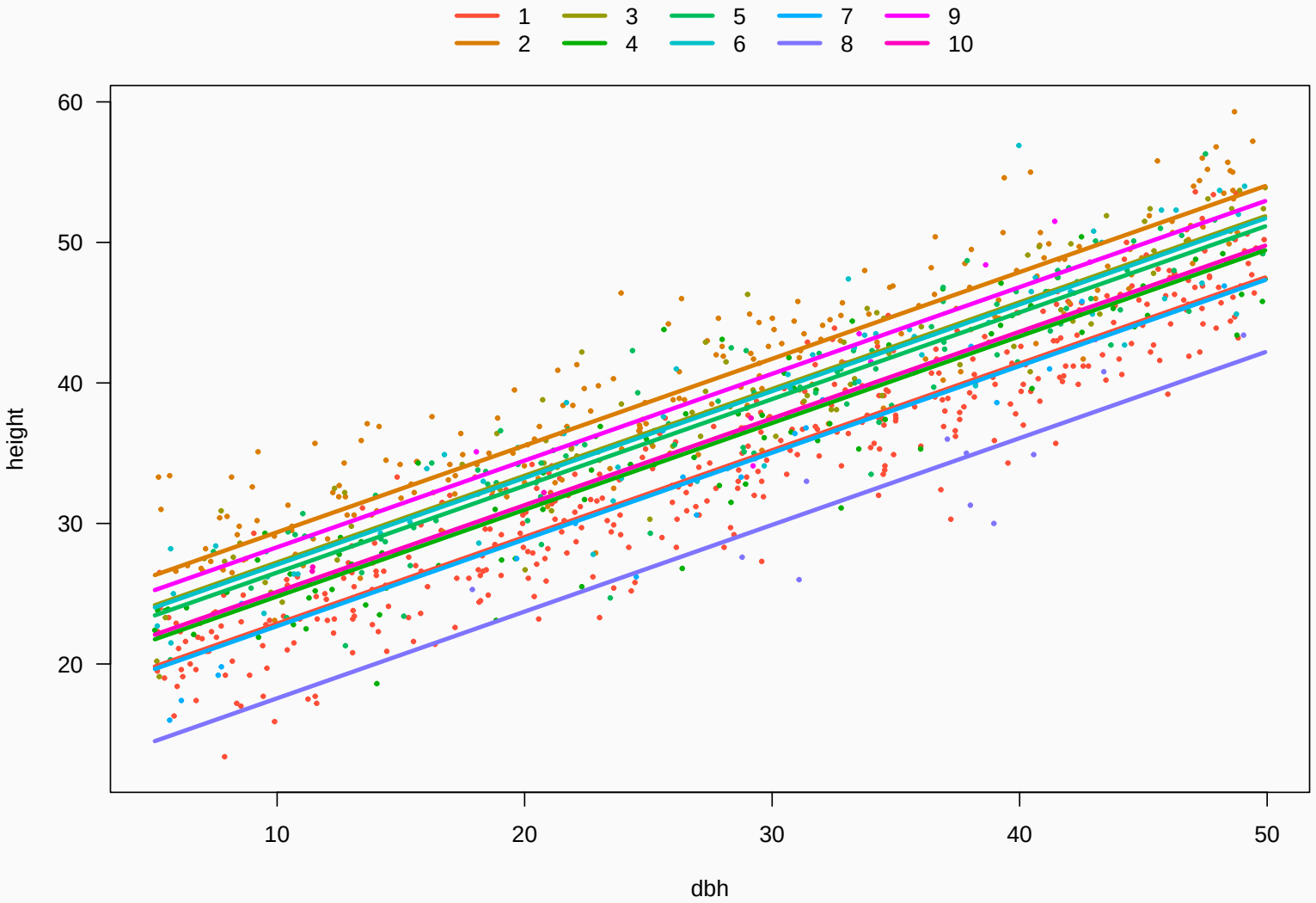





```
null device
          1
```

Plot (visreg)

```
visreg(m4, xvar = 'dbh', by = 'site', overlay = TRUE, band = FALSE)
```

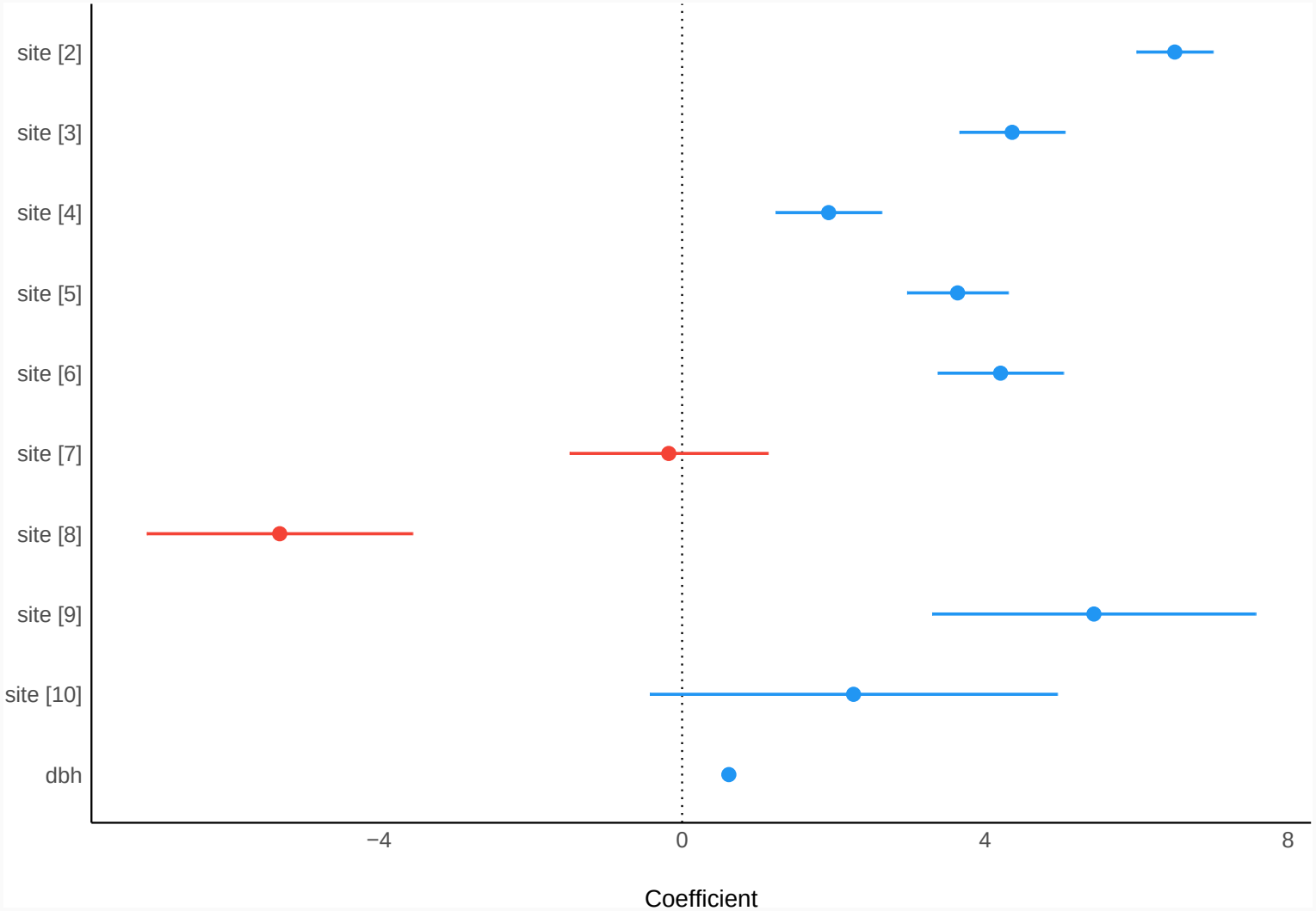


Plot model (sjPlot)

```
plot_model(m4, type = 'eff', terms = 'site')
```

Plot model (easystats)

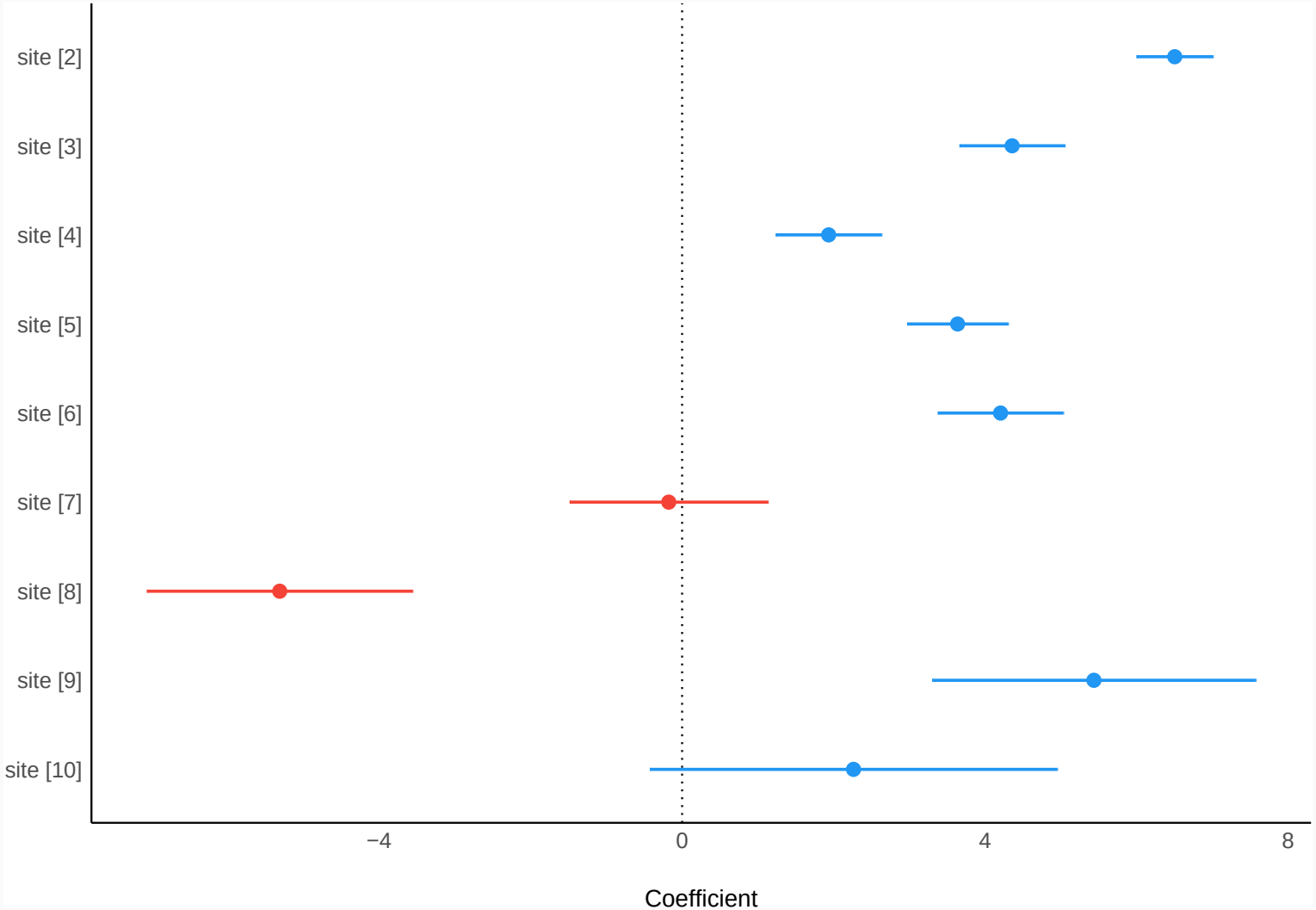
```
plot(parameters(m4))
```



Plot model (easystats)

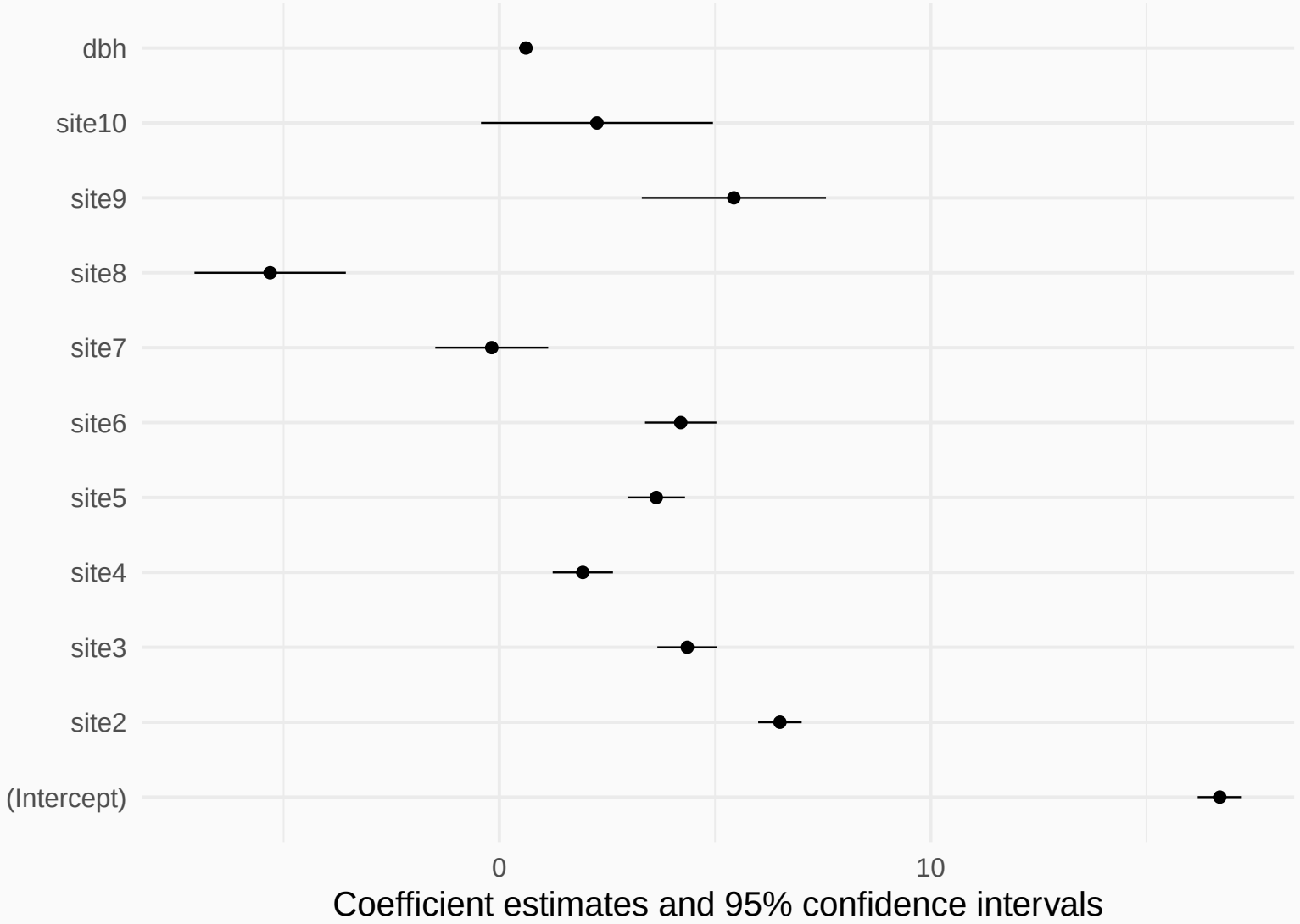
Keeping sites only, dropping 'dbh'

```
plot(parameters(m4, drop = 'dbh'))
```



Plot model (modelsummary)

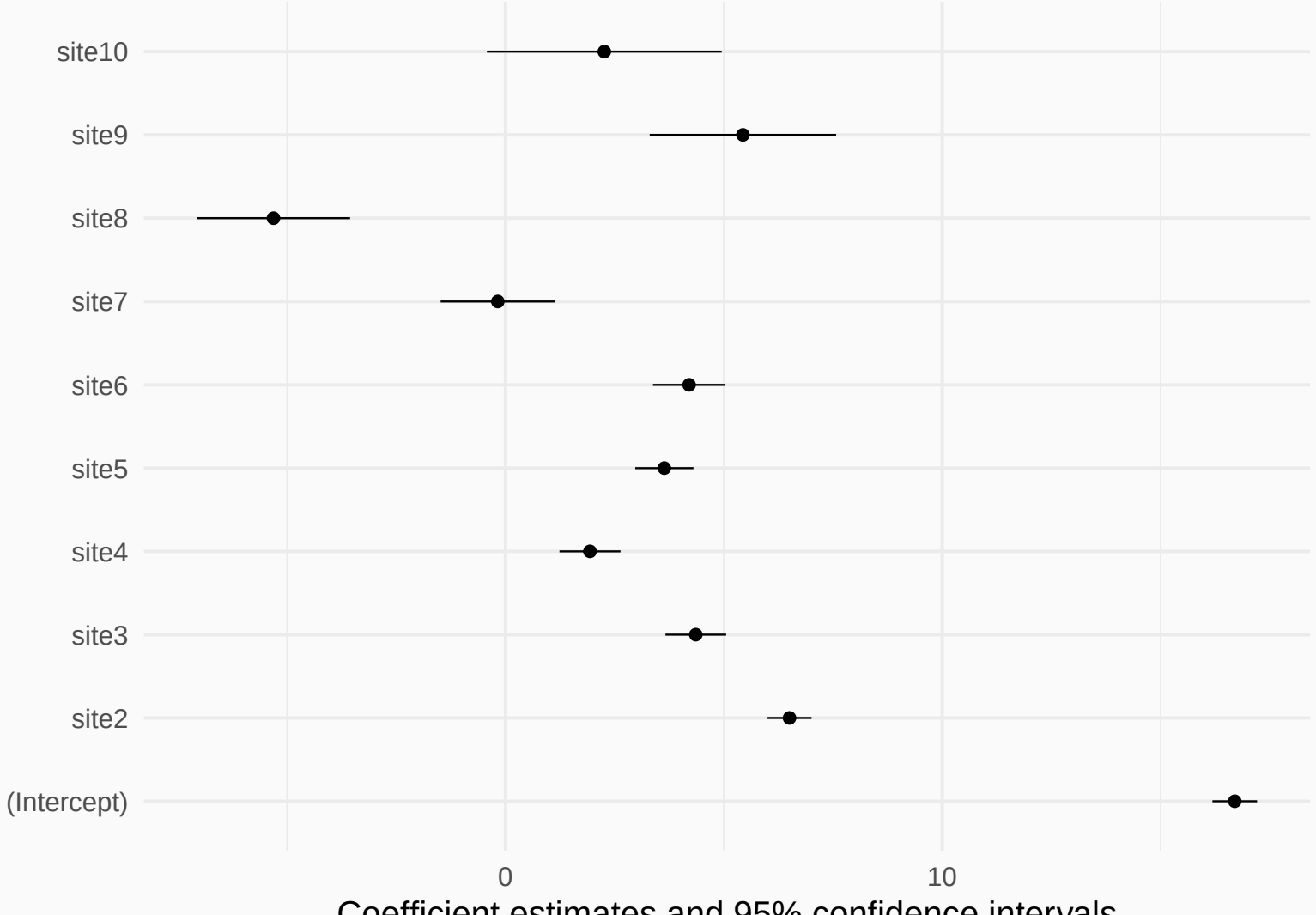
```
modelplot(m4)
```



Plot model (modelsummary)

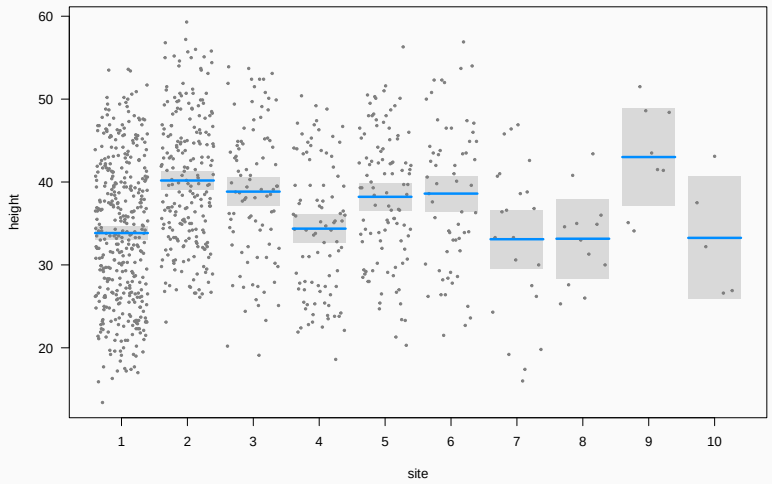
Keeping sites only, dropping 'dbh'

```
modelplot(m4, coef_omit = 'dbh')
```

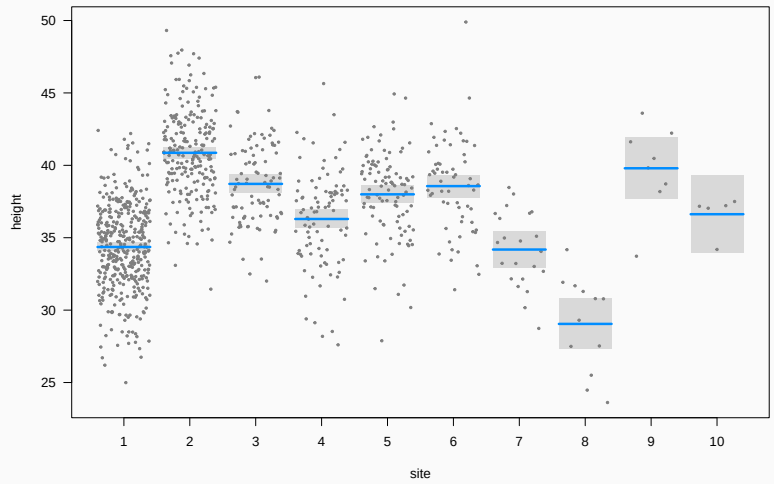


What happened to site 8?

```
visreg(m3)
```

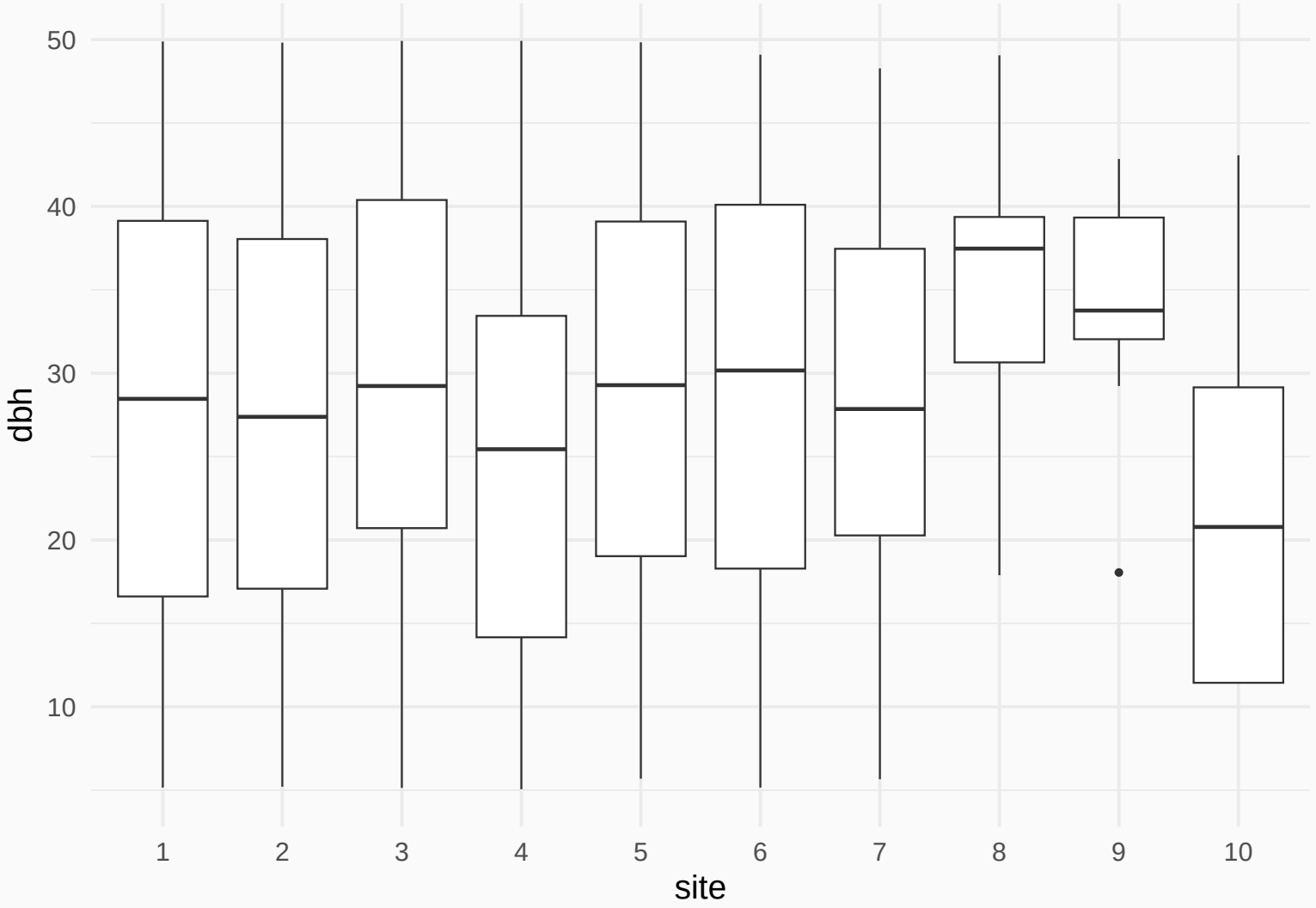



```
visreg(m4, xvar = 'site')
```



What happened to site 8?

site 8 has the largest diameters



What happened to site 8?

DBH

```
aggregate(trees$dbh ~ trees$site, FUN = me
```

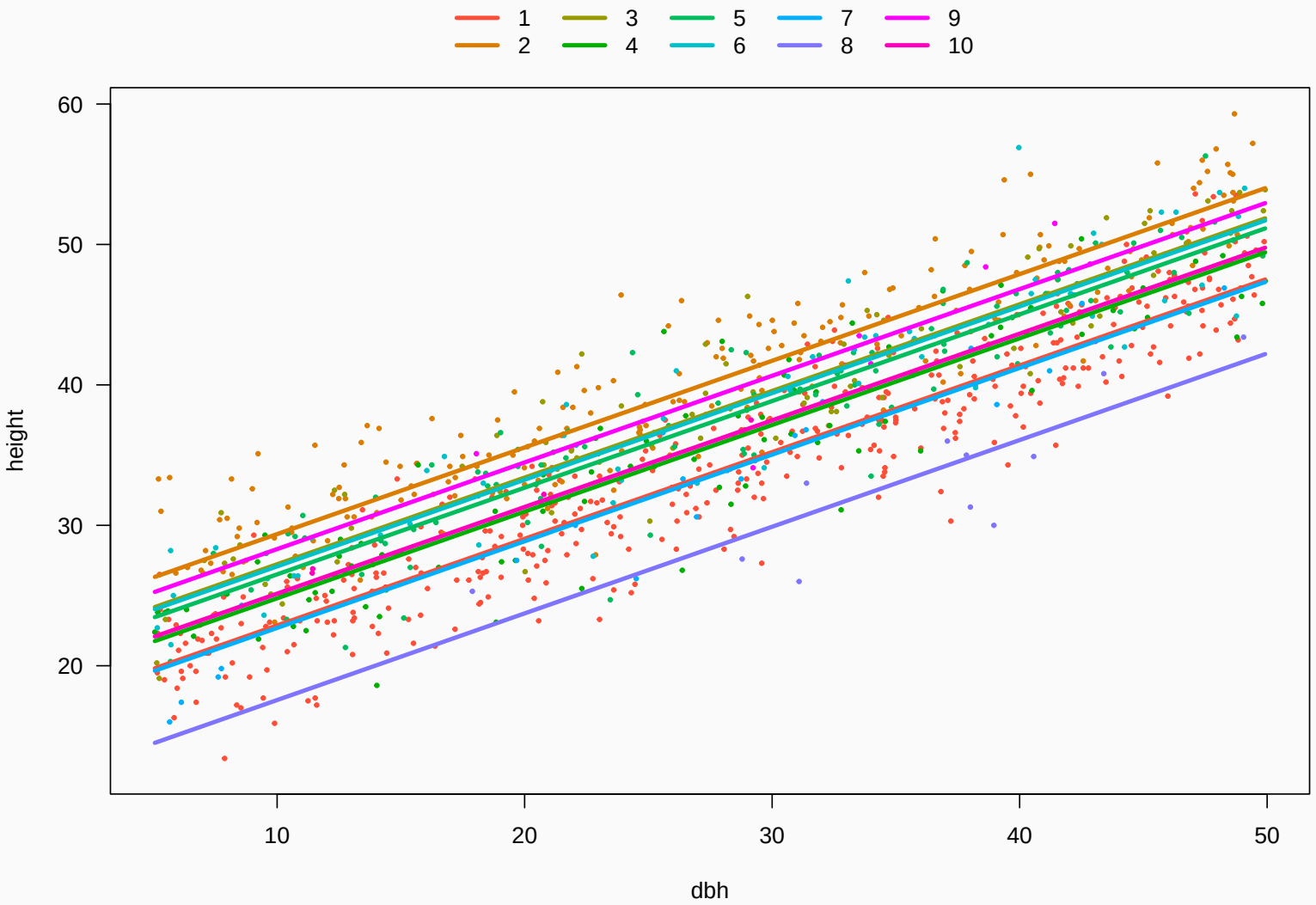
	trees$site	trees$dbh
1	1	27.78033
2	2	27.51580
3	3	28.82011
4	4	25.50867
5	5	28.97119
6	6	28.68067
7	7	26.86409
8	8	35.28250
9	9	33.83125
10	10	23.17000

HEIGHT

```
aggregate(trees$height ~ trees$site, FUN =
```

	trees$site	trees$height
1	1	33.84158
2	2	40.18265
3	3	38.84066
4	4	34.37444
5	5	38.21386
6	6	38.60167
7	7	33.10000
8	8	33.15833
9	9	43.01250
10	10	33.26000

We have fitted model w/ many intercepts and single slope

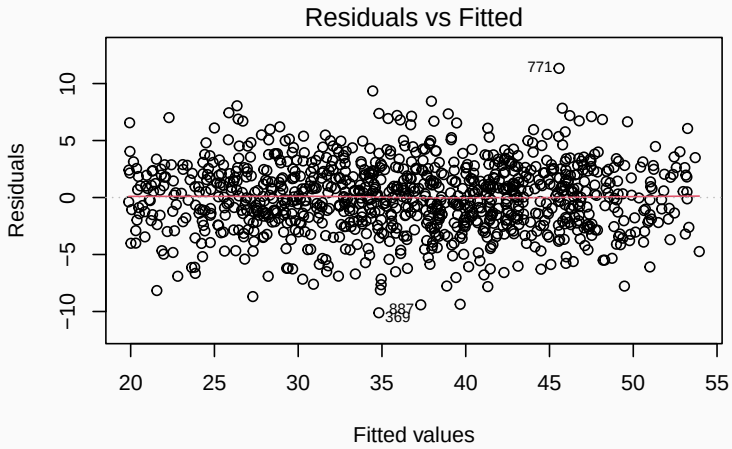


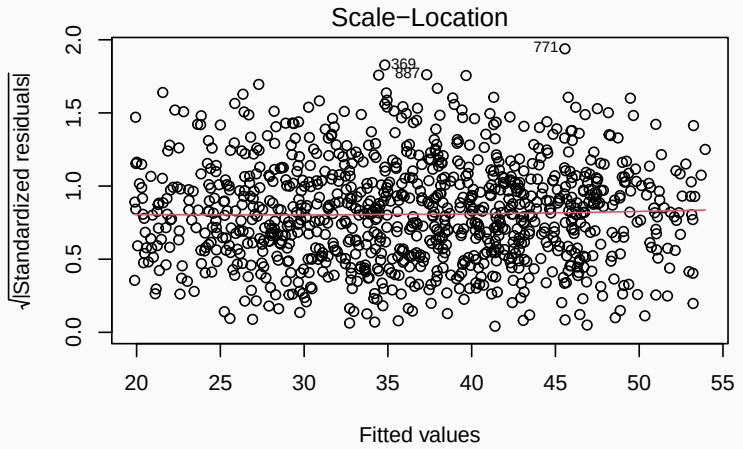
Slope is the same for all sites

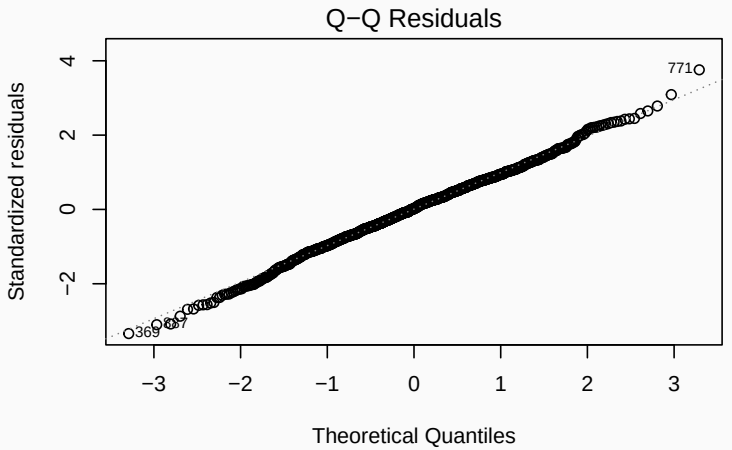
```
parameters(m4, keep = 'dbh')
```

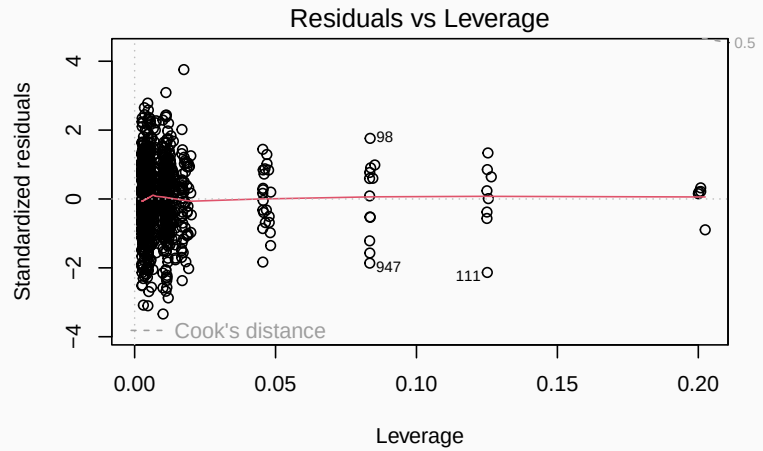
```
Parameter | Coefficient |       SE |       95% CI | t(989) |      p
-------------------------------------------------------------------
dbh       |        0.62 | 7.57e-03 | [0.60, 0.63] |  81.47 | < .001
```

Model checking: residuals



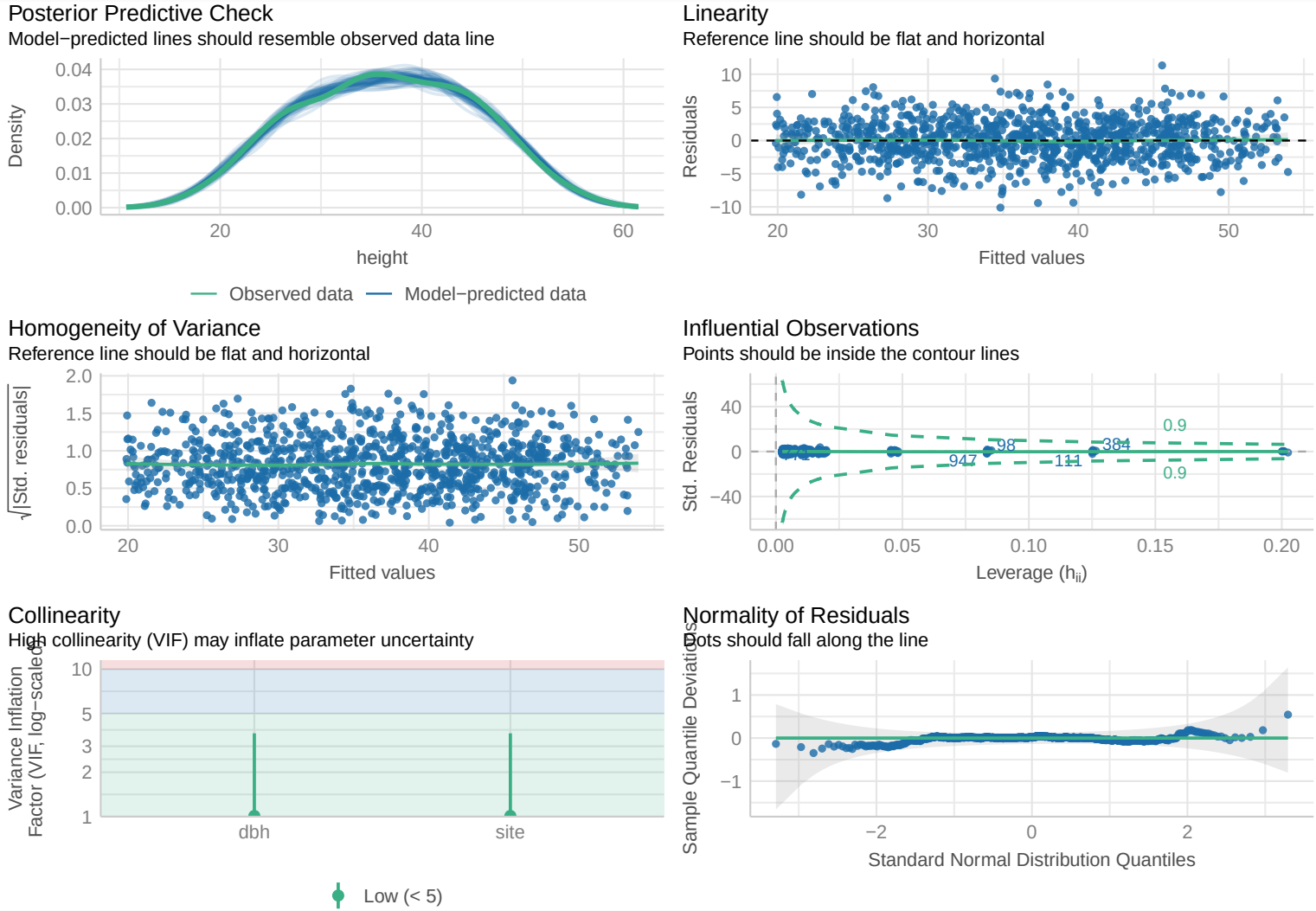






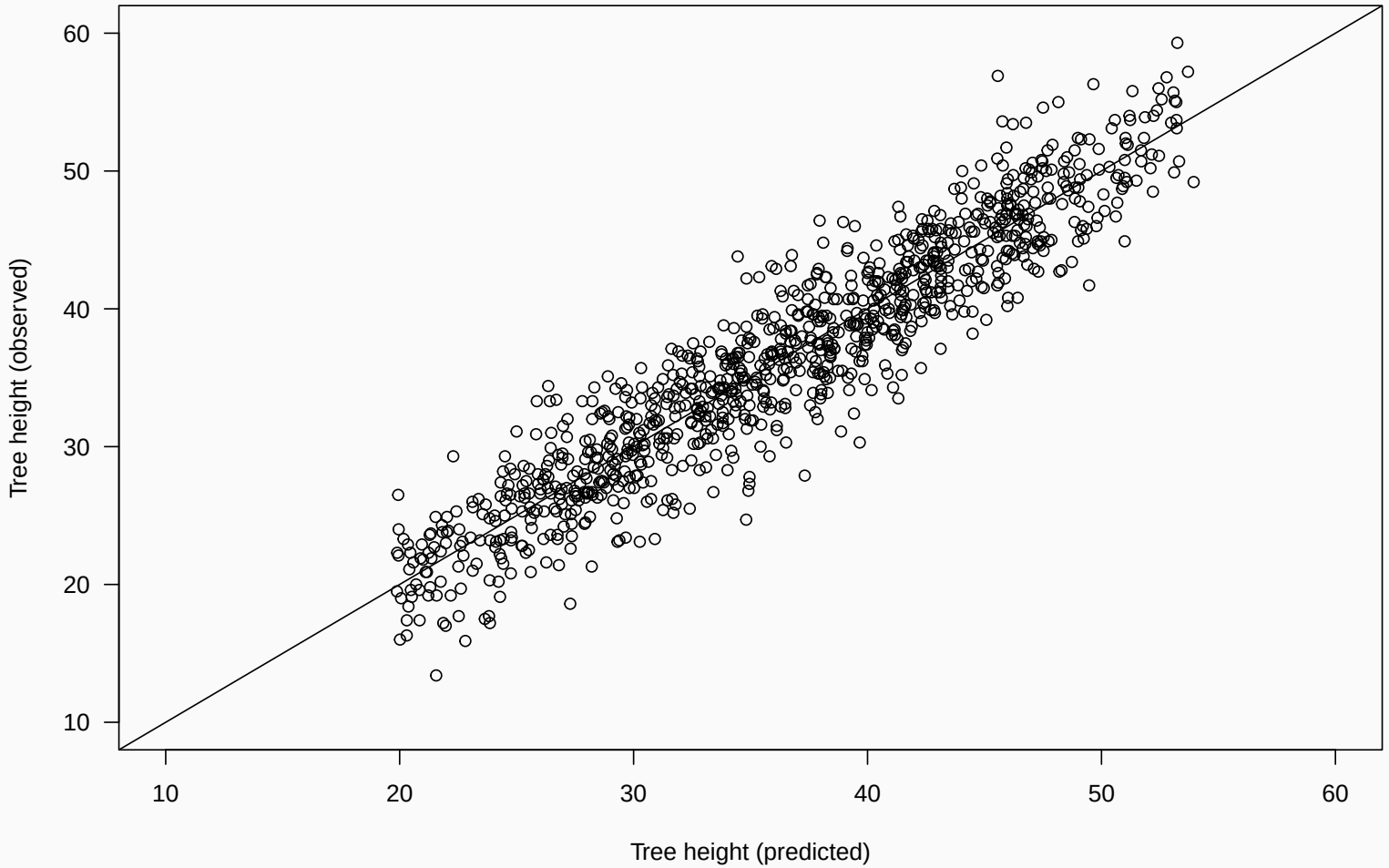
Model checking: residuals

`check_model(m4)`



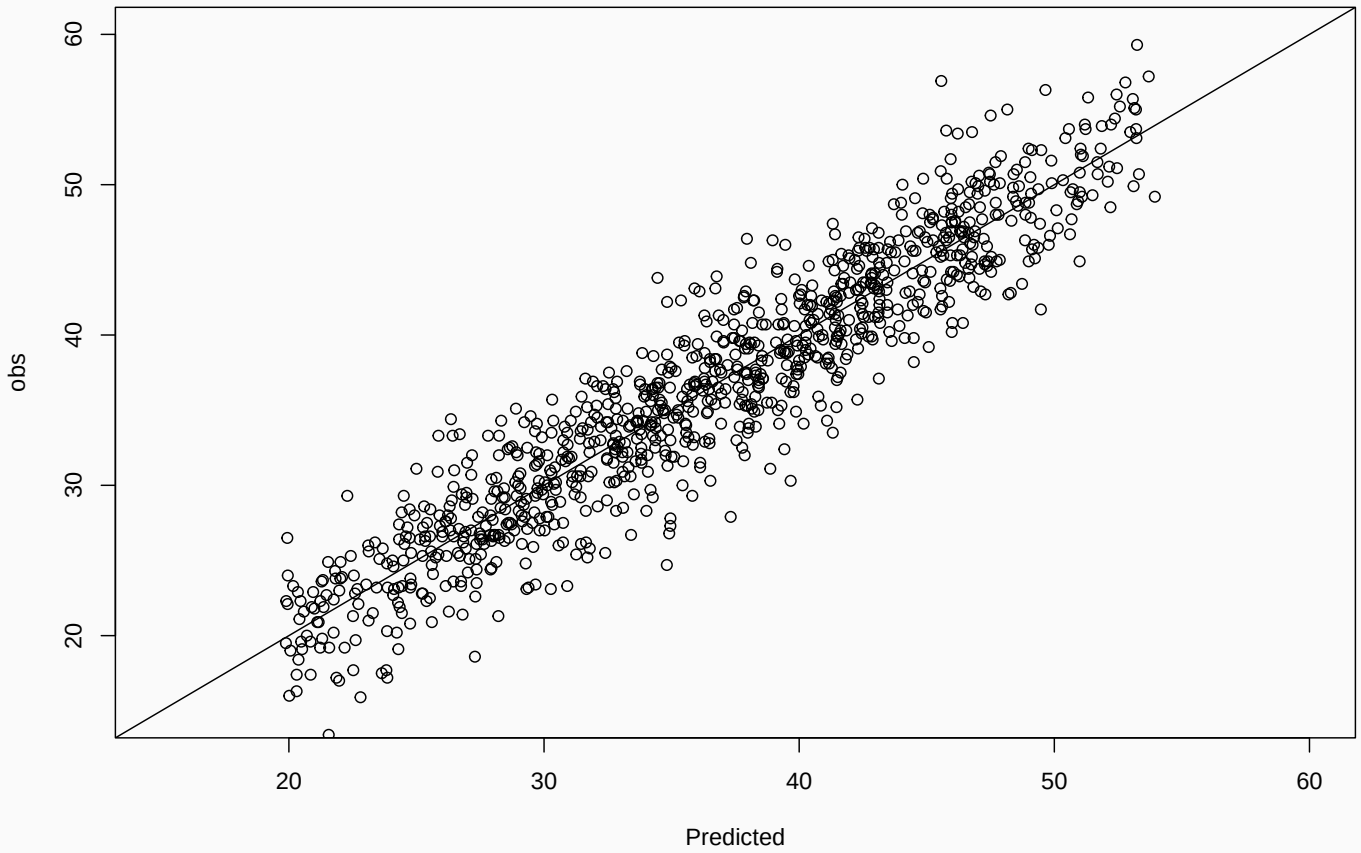
How good is this model? Calibration plot

```
trees$height.pred <- fitted(m4)
plot(trees$height.pred, trees$height, xlab = 'Tree height (predicte
abline(a = 0, b = 1)
```



How good is this model? Calibration plot (easystats)

```
pred <- estimate_expectation(m4)
pred$obs <- trees$height
plot(obs ~ Predicted, data = pred, xlim = c(15, 60), ylim = c(15, 6
abline(a = 0, b = 1)
```

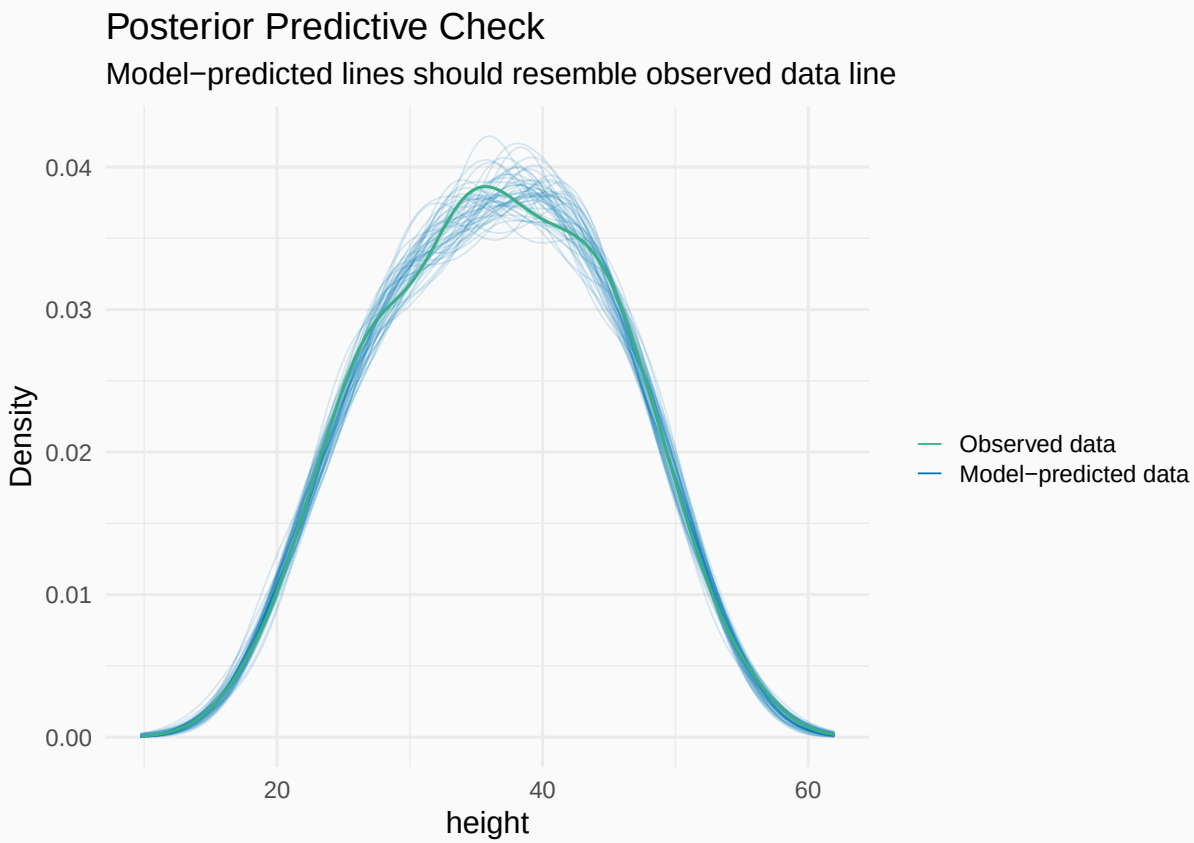


Posterior predictive checking

Simulating response data from fitted model (`yrep`)

and comparing with observed response (`y`)

```
performance::check_predictions(m4)
```



Predicting heights of new trees

Using model for prediction

Expected height of 10-cm diameter tree in each site?

```
trees.10cm <- data.frame(site = as.factor(1:10),
                         dbh = 10)
trees.10cm
```

```
   site dbh
1     1  10
2     2  10
3     3  10
4     4  10
5     5  10
6     6  10
7     7  10
8     8  10
9     9  10
10   10  10
```

Using model for prediction

Confidence interval

```
predict(m4, newdata = trees.10cm, interval = 'confidence')
```

```
        fit      lwr      upr
1  22.86979 22.46878 23.27079
2  29.37409 28.89388 29.85430
3  27.22724 26.54160 27.91289
4  24.80444 24.13410 25.47477
5  26.50722 25.84952 27.16492
6  27.07430 26.25490 27.89370
7  22.69359 21.39601 23.99117
8  17.55714 15.79282 19.32146
9  28.30683 26.16606 30.44761
10 25.13312 22.45540 27.81085
```

Using model for prediction

Prediction interval (accounting for residual variance)

```
predict(m4, newdata = trees.10cm, interval = 'prediction')
```

```
        fit       lwr      upr
1  22.86979 16.88478 28.85480
2  29.37409 23.38325 35.36493
3  27.22724 21.21645 33.23804
4  24.80444 18.79537 30.81350
5  26.50722 20.49955 32.51489
6  27.07430 21.04678 33.10181
7  22.69359 16.58268 28.80451
8  17.55714 11.33039 23.78388
9  28.30683 21.96314 34.65053
10 25.13312 18.58868 31.67757
```

Using model for prediction

Prediction interval (99%)

```
predict(m4, newdata = trees.10cm, interval = 'prediction',
        level = 0.99)
```

```
        fit       lwr      upr
1  22.86979 14.998587 30.74098
2  29.37409 21.495225 37.25295
3  27.22724 19.322133 35.13235
4  24.80444 16.901598 32.70727
5  26.50722 18.606216 34.40822
6  27.07430 19.147195 35.00140
7  22.69359 14.656813 30.73037
8  17.55714  9.368019 25.74626
9  28.30683 19.963913 36.64976
10 25.13312 16.526183 33.74007
```

Predicting heights of new trees (easystats)

Using model for prediction

Expected height of 10-cm diameter tree in each site?

```
trees.10cm <- data.frame(site = as.factor(1:10),
                         dbh = 10)
trees.10cm
```

```
   site dbh
1     1  10
2     2  10
3     3  10
4     4  10
5     5  10
6     6  10
7     7  10
8     8  10
9     9  10
10   10  10
```

Using model for prediction

Expected height of 10-cm DBH trees at each site

```
pred <- estimate_expectation(m4, data = trees.10cm)
```

```
Model-based Expectation

site |   dbh | Predicted |   SE |         95% CI
-----------------------------------------------
1    | 10.00 |     22.87 | 0.20 | [22.47, 23.27]
2    | 10.00 |     29.37 | 0.24 | [28.89, 29.85]
3    | 10.00 |     27.23 | 0.35 | [26.54, 27.91]
4    | 10.00 |     24.80 | 0.34 | [24.13, 25.47]
5    | 10.00 |     26.51 | 0.34 | [25.85, 27.16]
6    | 10.00 |     27.07 | 0.42 | [26.25, 27.89]
7    | 10.00 |     22.69 | 0.66 | [21.40, 23.99]
8    | 10.00 |     17.56 | 0.90 | [15.79, 19.32]
9    | 10.00 |     28.31 | 1.09 | [26.17, 30.45]
10   | 10.00 |     25.13 | 1.36 | [22.46, 27.81]

Variable predicted: height
```

Using model for prediction

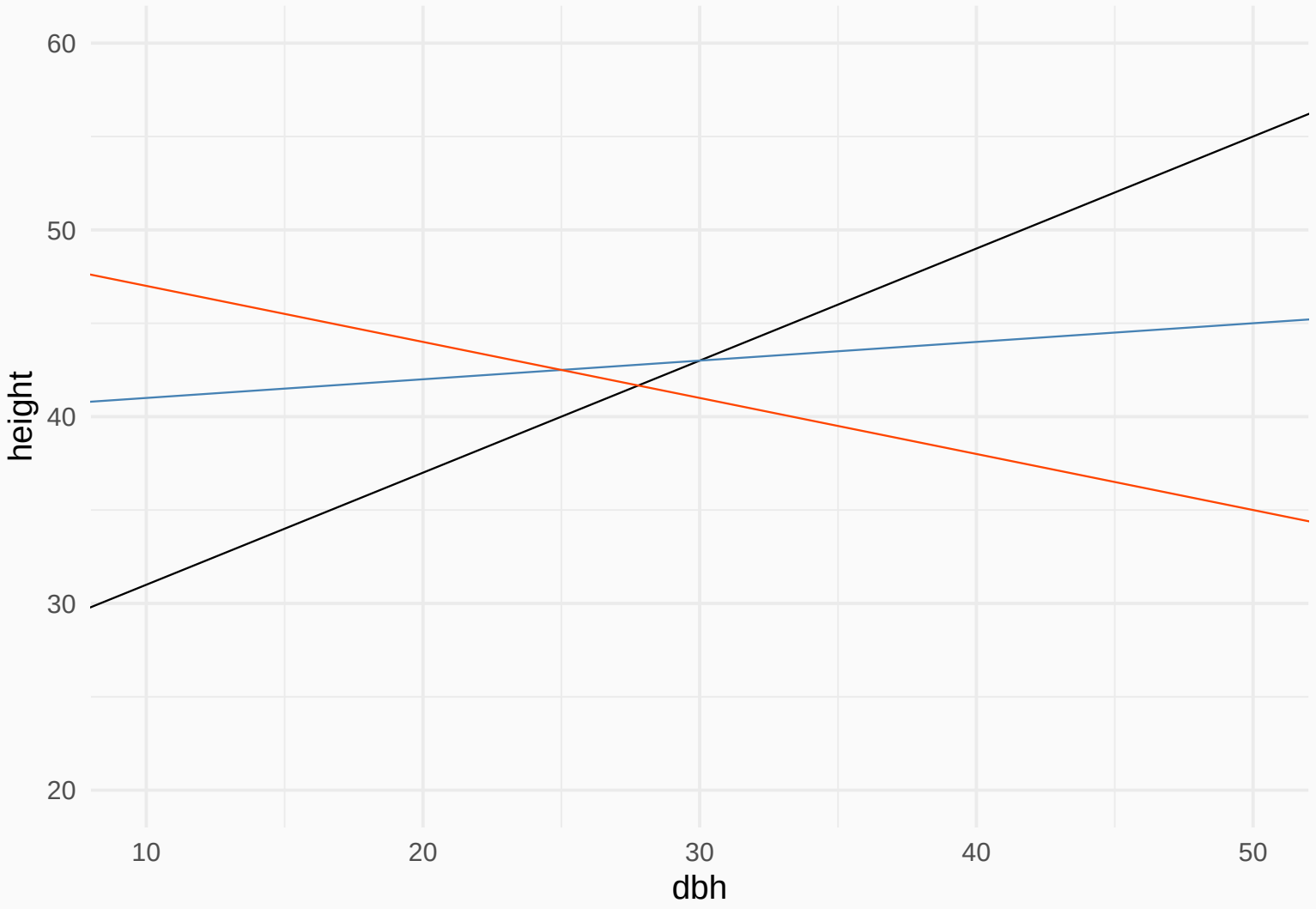
Prediction intervals (accounting for residual variance)

```
pred <- estimate_prediction(m4, data = trees.10cm)
```

```
Model-based Prediction

site |   dbh | Predicted |   SE |         95% CI
-----------------------------------------------
1    | 10.00 |     22.87 | 3.05 | [16.88, 28.85]
2    | 10.00 |     29.37 | 3.05 | [23.38, 35.36]
3    | 10.00 |     27.23 | 3.06 | [21.22, 33.24]
4    | 10.00 |     24.80 | 3.06 | [18.80, 30.81]
5    | 10.00 |     26.51 | 3.06 | [20.50, 32.51]
6    | 10.00 |     27.07 | 3.07 | [21.05, 33.10]
7    | 10.00 |     22.69 | 3.11 | [16.58, 28.80]
8    | 10.00 |     17.56 | 3.17 | [11.33, 23.78]
9    | 10.00 |     28.31 | 3.23 | [21.96, 34.65]
10   | 10.00 |     25.13 | 3.33 | [18.59, 31.68]

Variable predicted: height
```

Q: Does allometric relationship between Height and Diameter vary among sites?

Does allometric relationship between Height and Diameter vary among sites?

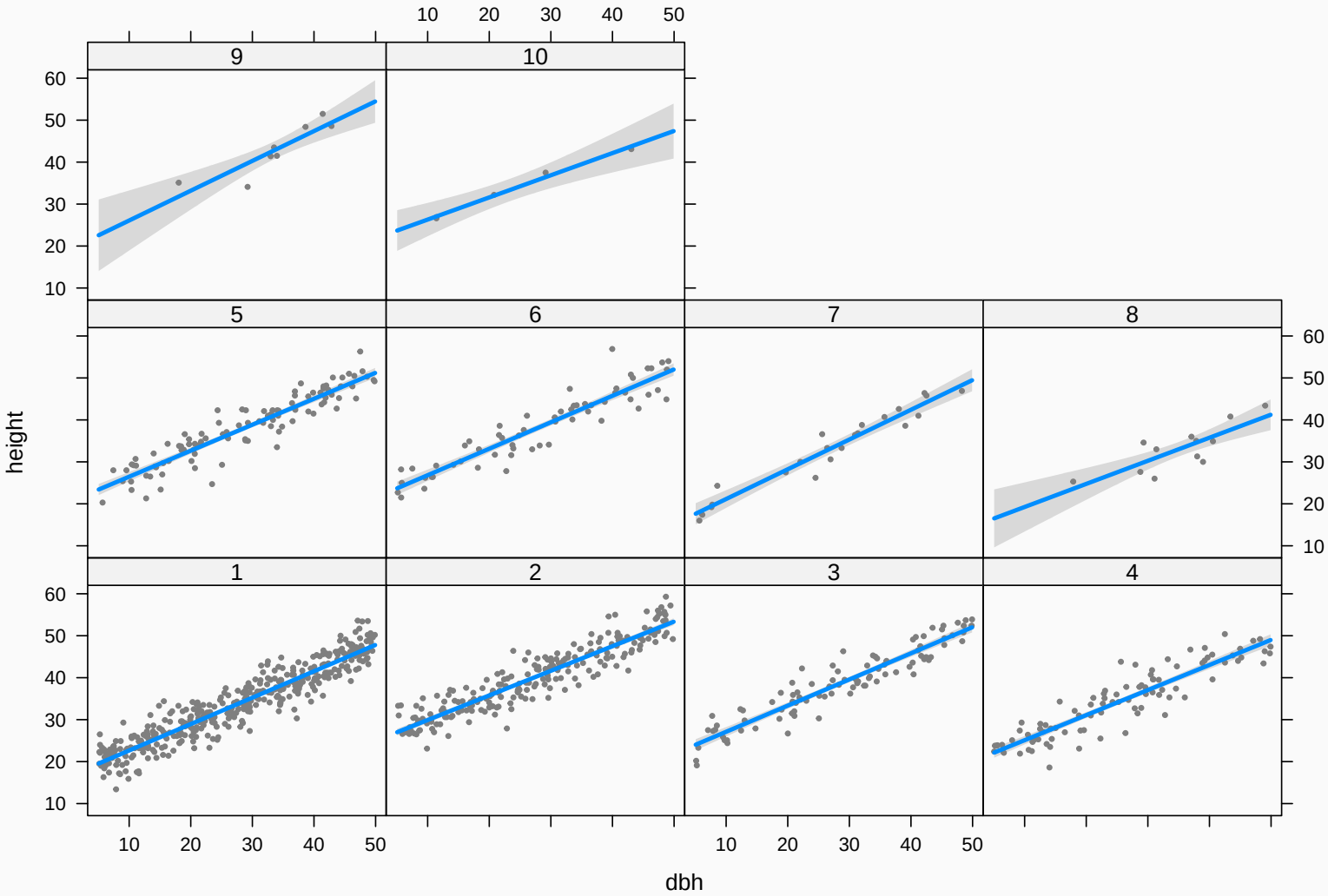


Model with interactions

```
Call:
lm(formula = height ~ site * dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-10.1017  -1.9839   0.0645   2.0486  11.1789

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 16.359437   0.360054  45.436  < 2e-16 ***
site2        7.684781   0.609657  12.605  < 2e-16 ***
site3        4.518568   0.867008   5.212 2.28e-07 ***
site4        2.769336   0.813259   3.405 0.000688 ***
site5        3.917607   0.870983   4.498 7.68e-06 ***
site6        4.155161   1.009379   4.117 4.17e-05 ***
site7       -2.306799   1.551303  -1.487 0.137334
site8       -2.616095   4.090671  -0.640 0.522630
site9        2.621560   5.073794   0.517 0.605492
site10       4.662340   2.991072   1.559 0.119378
dbh          0.629299   0.011722  53.685  < 2e-16 ***
site2:dbh   -0.042784   0.020033  -2.136 0.032950 *
site3:dbh   -0.006031   0.027640  -0.218 0.827312
site4:dbh   -0.031633   0.028225  -1.121 0.262677
site5:dbh   -0.010173   0.027887  -0.365 0.715334
site6:dbh    0.001337   0.032109   0.042 0.966797
site7:dbh    0.079728   0.052056   1.532 0.125951
site8:dbh   -0.079027   0.113386  -0.697 0.485984
site9:dbh    0.081035   0.146649   0.553 0.580679
site10:dbh  -0.101107   0.114520  -0.883 0.377522
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.041 on 980 degrees of freedom
Multiple R-squared:  0.8847,     Adjusted R-squared:  0.8825
```

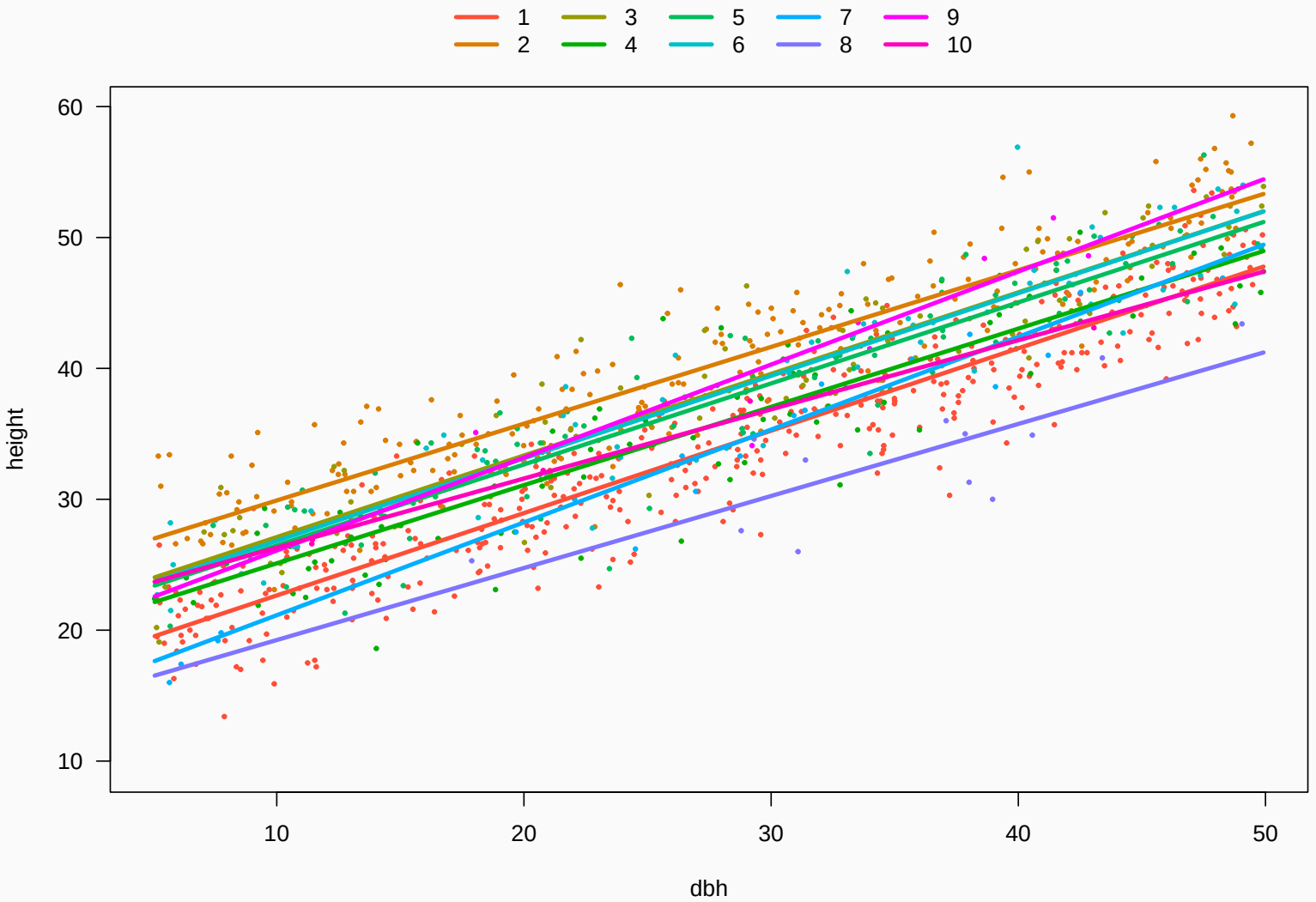
Does slope vary among sites?

```
visreg(m5, xvar = 'dbh', by = 'site')
```



Does slope vary among sites?

```
visreg(m5, xvar = 'dbh', by = 'site', overlay = TRUE, band = FALSE)
```



Does slope vary among sites?

```
library('marginaleffects')
hypotheses(m5, '`site9:dbh` = `site10:dbh`')
```

```
 Estimate Std. Error     z Pr(>|z|)   S  2.5 % 97.5 %
    0.182      0.185 0.983    0.326 1.6 -0.181  0.545

Term: ‘site9:dbh‘ = ‘site10:dbh‘
Columns: term, estimate, std.error, statistic, p.value, s.value, conf.low, conf.high
```

Examining fitted model with {modelStudio}

```
library('modelStudio')
m5.explain <- DALEX::explain(
  m5,
  data = trees,
  y = trees$height)
modelStudio(m5.explain, viewer = 'browser')
```

Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?

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Extra exercises

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- iris: Predict petal length ~ petal width and species
- Penguins data: Body mass ~ Flipper length, Bill length ~ Bill depth, differences across sites...
- racing pigeons: is speed related to sex?

Variable and model selection

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

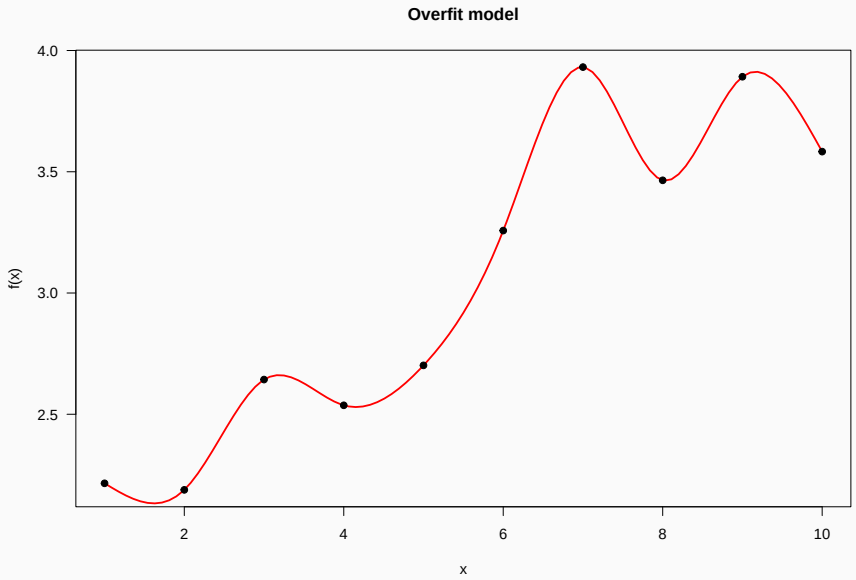
Overfitting and balanced model complexity

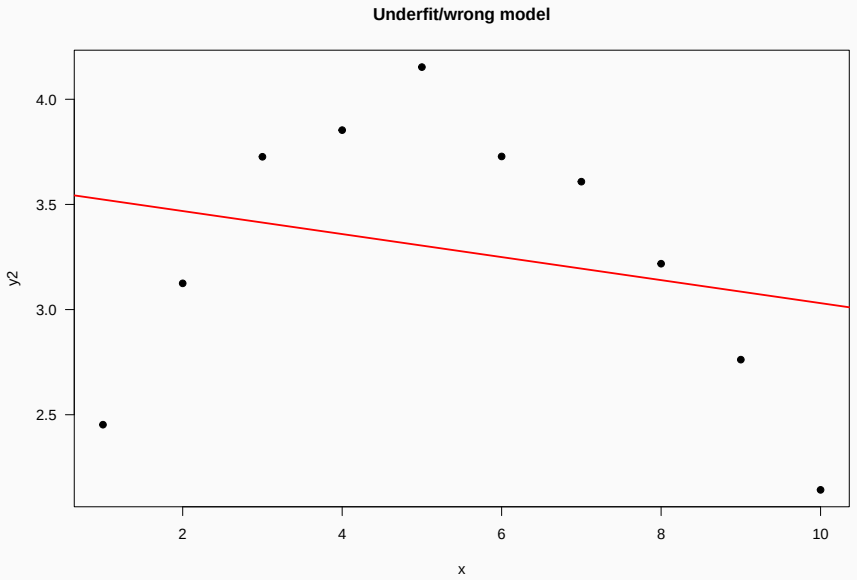
- On one hand, we want to **maximise fit**.

Overfitting and balanced model complexity

- On one hand, we want to **maximise fit**.
- On the other hand, we want to **avoid overfitting** and overly complex models.

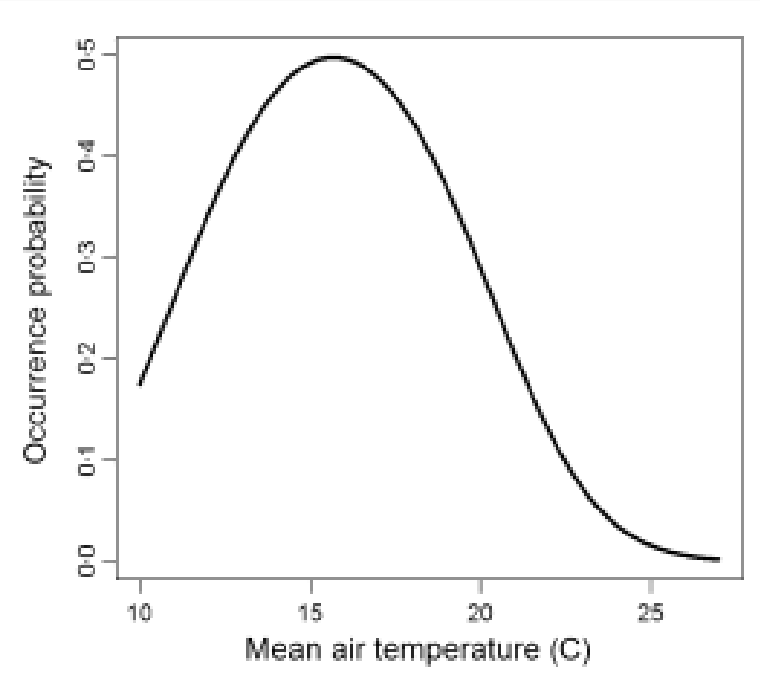
Overfitting and balanced model complexity



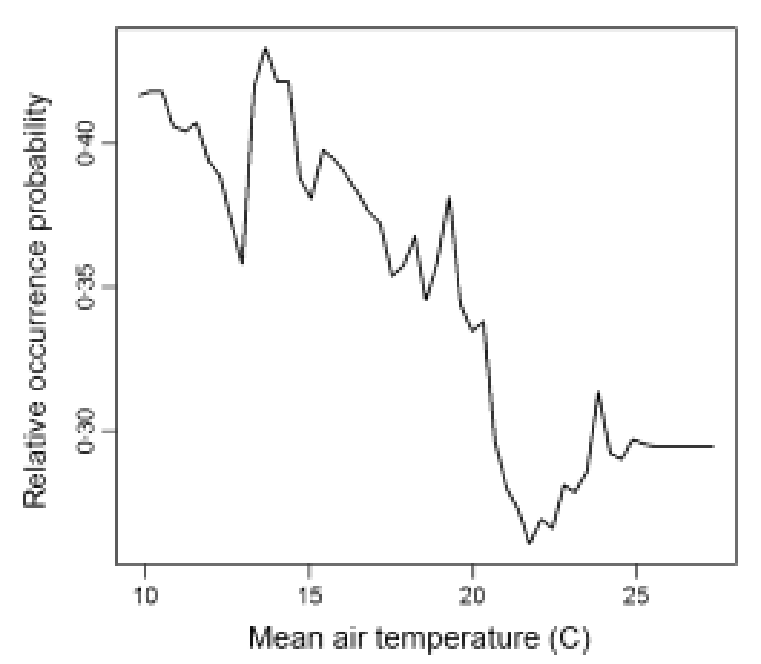


Overfitting and balanced model complexity

GLMM



Random forests



Wenger & Olden (2012)

Overfitted models will work badly on new data

Evaluating models' predictive accuracy

- **Cross-validation** (k-fold, leave one out...)

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- **Information Criteria**:

Evaluating models' predictive accuracy

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  - BIC

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Evaluating models' predictive accuracy

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  - AIC
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Evaluating models' predictive accuracy

- **Cross-validation** (k-fold, leave one out...)
- **Information Criteria**:
  - AIC
  - BIC
  - DIC
  - WAIC...
- All these methods have flaws!

AIC (Akaike Information Criteria)

$$AIC = -2 * LogLikelihood + 2K$$

- First term: **model fit**

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AIC (Akaike Information Criteria)

$$AIC = -2 * LogLikelihood + 2K$$

- First term: **model fit**
- **K = number of parameters** (penalisation for model complexity)
- Lower is better
- AIC biased towards complex models.
- AICc recommended with 'small' sample sizes (n/p < 40). But see Richards 2005

Problems of IC

- No information criteria is panacea: all have problems.

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- They estimate *average* out-of-sample prediction error. But errors can differ substantially within dataset.

Problems of IC

- No information criteria is panacea: all have problems.
- They estimate *average* out-of-sample prediction error. But errors can differ substantially within dataset.
- Sometimes better models rank poorly (e.g. see Gelman et al. 2013). Combine with **thorough model checks**.

So which variables should enter my model?

Choosing predictors

- Choose variables based on **background knowledge**, rather than throwing plenty of them in a fishing expedition.

Choosing predictors

- Choose variables based on **background knowledge**, rather than throwing plenty of them in a fishing expedition.
- Propose single global model or small set (< 10 - 20) of **reasonable** candidate models.

Choosing predictors

- Choose variables based on **background knowledge**, rather than throwing plenty of them in a fishing expedition.
- Propose single global model or small set (< 10 - 20) of **reasonable** candidate models.
- Number of variables **balanced with sample size** (e.g. at least 10 - 30 obs per param)

Choosing predictors

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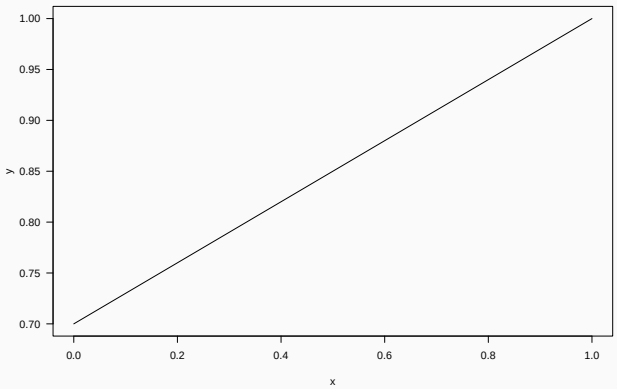
- For predictors with large effects, **consider interactions**.

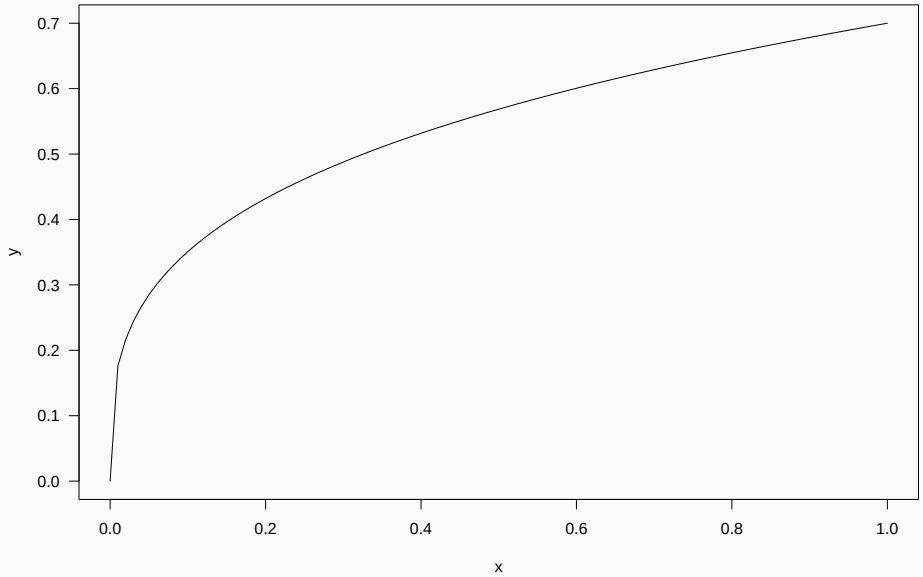
Think about the shape of relationships

y ~ x + z

Really? Not everything has to be linear! Actually, it often is not.

Think about shape of relationship.





Removing predictors

Stepwise regression has many problems

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- This includes `stepAIC` (e.g. Dahlgren 2010; Burnham et al 2011; Hegyi & Garamszegi 2011).

Other common bad practices

- Testing bivariate relationships before building multivariable model

Heinze & Dunkler 2016

Other common bad practices

- Testing bivariate relationships before building multivariable model
- Removing non-significant predictors

Heinze & Dunkler 2016

Removing predictors?

- Always **keep 'core' predictors** (based on previous knowledge)

Heinze et al 2018

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Heinze et al 2018

Removing predictors?

- Always **keep 'core' predictors** (based on previous knowledge)
- If ratio sample size/number of predictors is low (<10 EPP), avoid variable selection (too unstable)
- If performing variable selection, always **assess stability** (bootstrap, etc)

Heinze et al 2018

Summary

1. Choose meaningful variables

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    - Beware collinearity

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4. Always check fitted models thoroughly
5. Always report effect sizes

Model comparison

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Trees dataset

```
trees <- read.csv('data/trees.csv')
head(trees)
```

```
  site   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
3    2 28.03   41.9 female    0
4    5 39.86   46.5 female    0
5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Four models

```
m1 <- lm(height ~ dbh, data = trees)
```

```
m2 <- lm(height ~ sex, data = trees)
```

```
m3 <- lm(height ~ site, data = trees)
```

```
m4 <- lm(height ~ site*dbh, data = trees)
```

Compare model performance

```r
library('performance')
compare_performance(m1, m2, m3, m4)
```

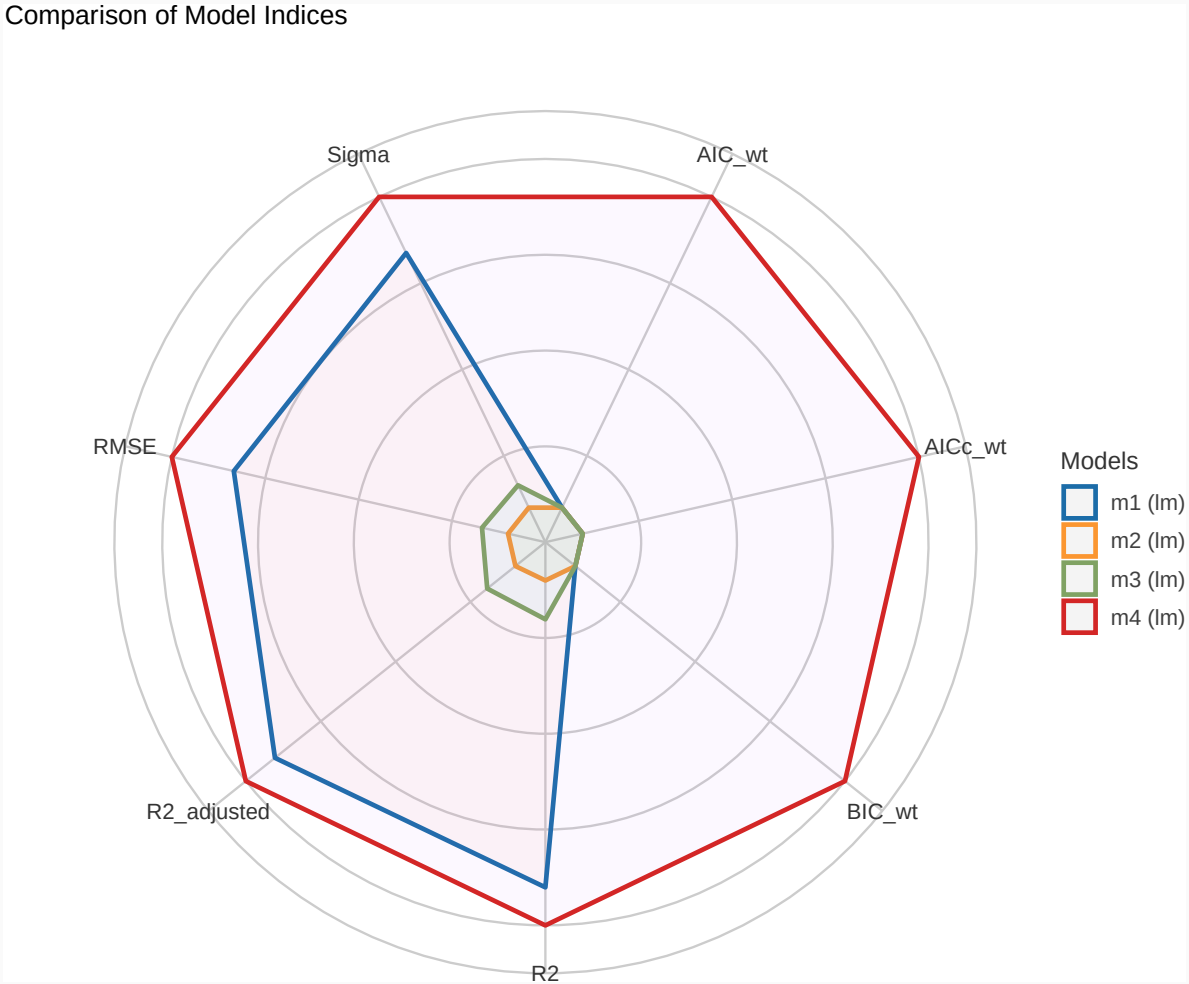
```
# Comparison of Model Performance Indices

Name | Model |  AIC (weights) | AICc (weights) |  BIC (weights) |    R2
-------------------------------------------------------------------------
m1   |    lm | 5660.3 (<.001) | 5660.3 (<.001) | 5675.0 (<.001) | 0.787
m2   |    lm | 7206.1 (<.001) | 7206.2 (<.001) | 7220.9 (<.001) | 0.002
m3   |    lm | 7117.3 (<.001) | 7117.5 (<.001) | 7171.2 (<.001) | 0.102
m4   |    lm | 5084.3 (>.999) | 5085.2 (>.999) | 5187.3 (>.999) | 0.885

Name | R2 (adj.) |  RMSE | Sigma
--------------------------------
m1   |     0.787 | 4.089 | 4.093
m2   |     0.001 | 8.856 | 8.865
m3   |     0.093 | 8.404 | 8.446
m4   |     0.882 | 3.011 | 3.041
```

Compare model performance

```
library('see')
plot(compare_performance(m1, m2, m3, m4))
```



Compare parameters

```
library('parameters')
compare_parameters(m3, m4)
```

```
Parameter       |                   m3 |                        m4
-----------------------------------------------------------------------
(Intercept)     | 33.84 (33.00, 34.68) |     16.36 ( 15.65, 17.07)
site [2]        |  6.34 ( 4.94,  7.74) |      7.68 (  6.49,  8.88)
site [3]        |  5.00 ( 3.07,  6.93) |      4.52 (  2.82,  6.22)
site [4]        |  0.53 (-1.40,  2.47) |      2.77 (  1.17,  4.37)
site [5]        |  4.37 ( 2.52,  6.22) |      3.92 (  2.21,  5.63)
site [6]        |  4.76 ( 2.46,  7.06) |      4.16 (  2.17,  6.14)
site [7]        | -0.74 (-4.37,  2.89) |     -2.31 ( -5.35,  0.74)
site [8]        | -0.68 (-5.54,  4.17) |     -2.62 (-10.64,  5.41)
site [9]        |  9.17 ( 3.25, 15.09) |      2.62 ( -7.34, 12.58)
site [10]       | -0.58 (-8.04,  6.88) |      4.66 ( -1.21, 10.53)
site [3] × dbh  |                      | -6.03e-03 ( -0.06,  0.05)
site [4] × dbh  |                      |     -0.03 ( -0.09,  0.02)
dbh             |                      |      0.63 (  0.61,  0.65)
site [2] × dbh  |                      |     -0.04 ( -0.08,  0.00)
site [7] × dbh  |                      |      0.08 ( -0.02,  0.18)
site [8] × dbh  |                      |     -0.08 ( -0.30,  0.14)
site [5] × dbh  |                      |     -0.01 ( -0.06,  0.04)
site [6] × dbh  |                      |  1.34e-03 ( -0.06,  0.06)
site [9] × dbh  |                      |      0.08 ( -0.21,  0.37)
site [10] × dbh |                      |     -0.10 ( -0.33,  0.12)
-----------------------------------------------------------------------
```

Compare parameters

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library('parameters')
plot(compare_parameters(m3, m4))
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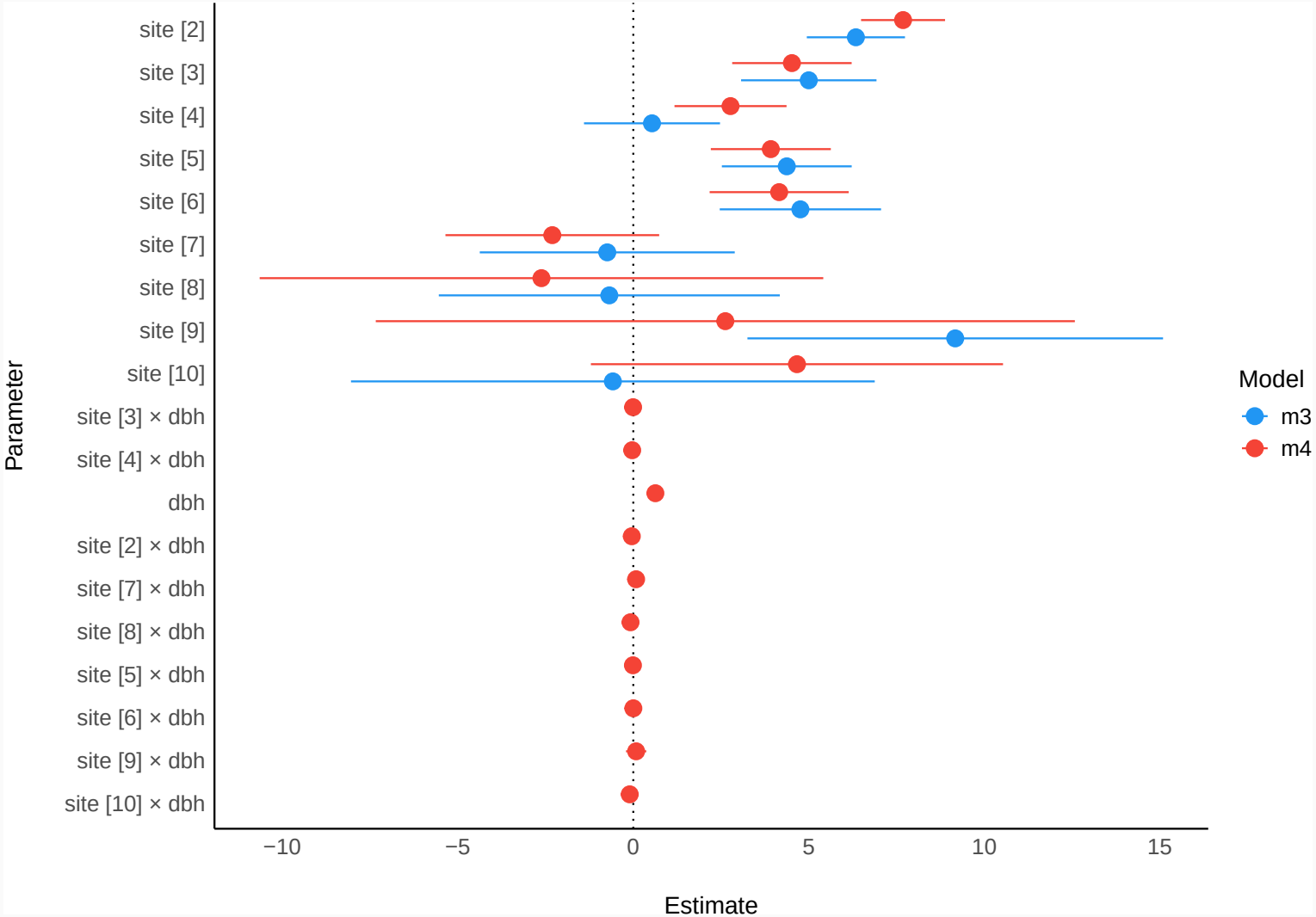


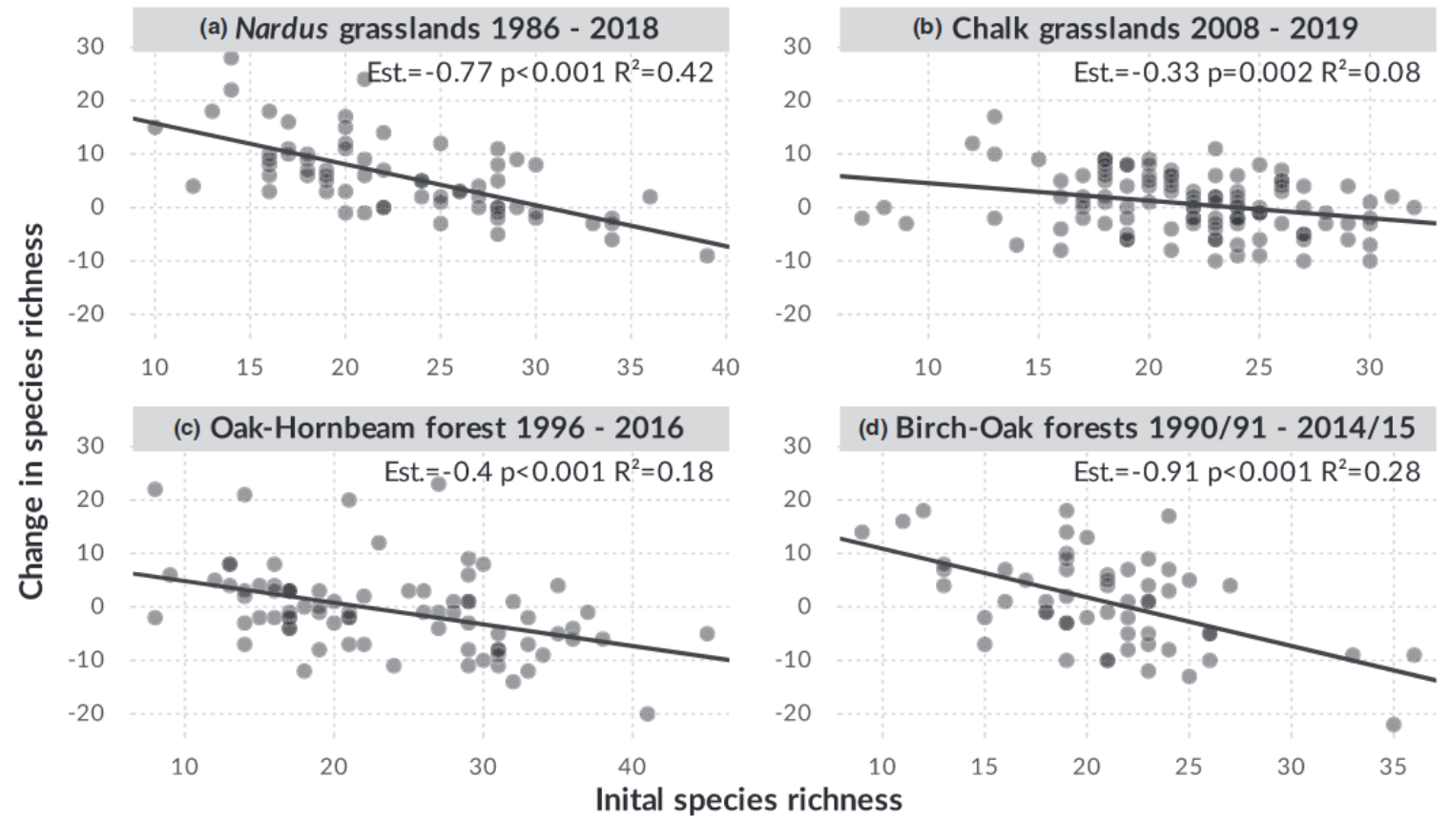
Regression to the mean

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

The most biodiverse sites are losing more species

WHY??



Mazalla & Diekmann 2022

Most biodiverse sites are losing more species. Why?

- Stronger competition

Most biodiverse sites are losing more species. Why?

- Stronger competition
- Humans destroying most species-rich sites

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Most biodiverse sites are losing more species. Why?

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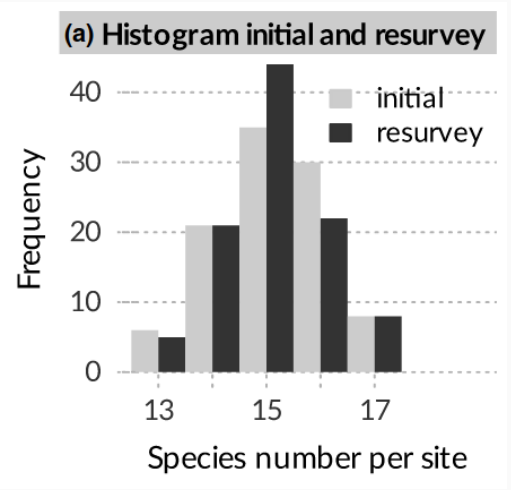
- No ecological cause, but stochastic variation (**regression to the mean**)

A simulation for 100 sites

- Simulate initial number of species:



A simulation for 100 sites

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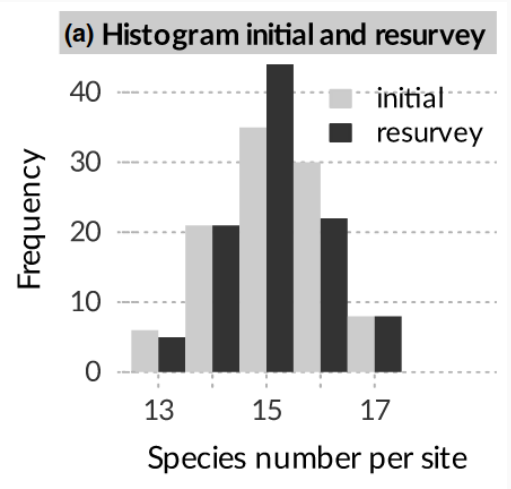

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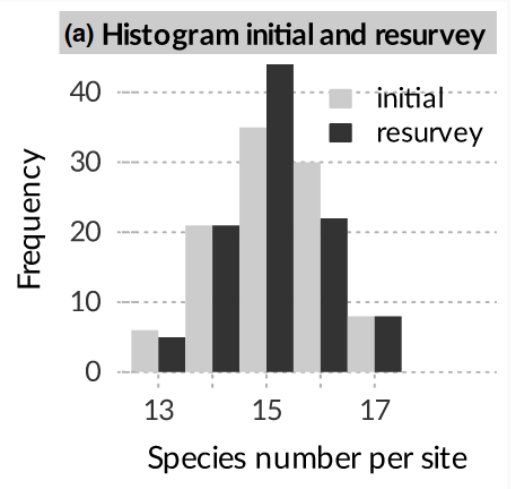

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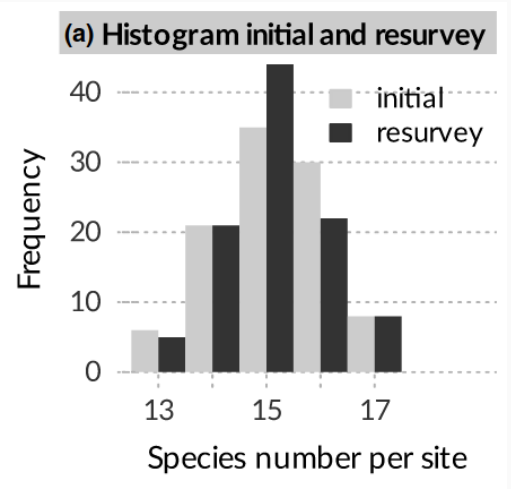

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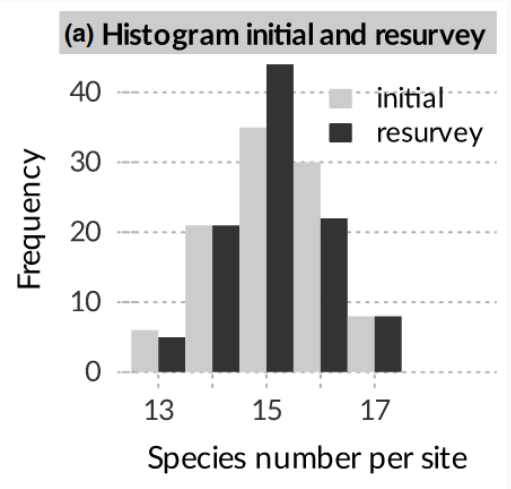

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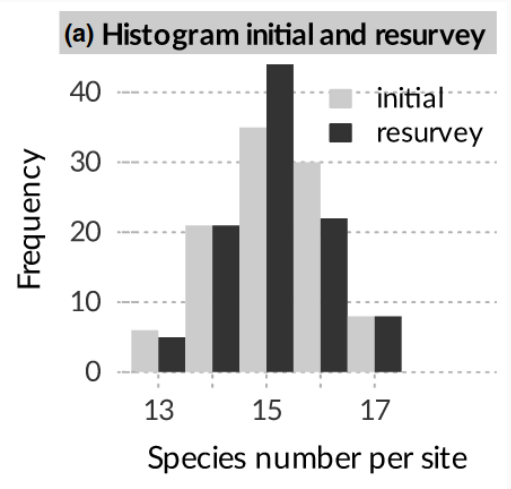
- (only stochastic variation)

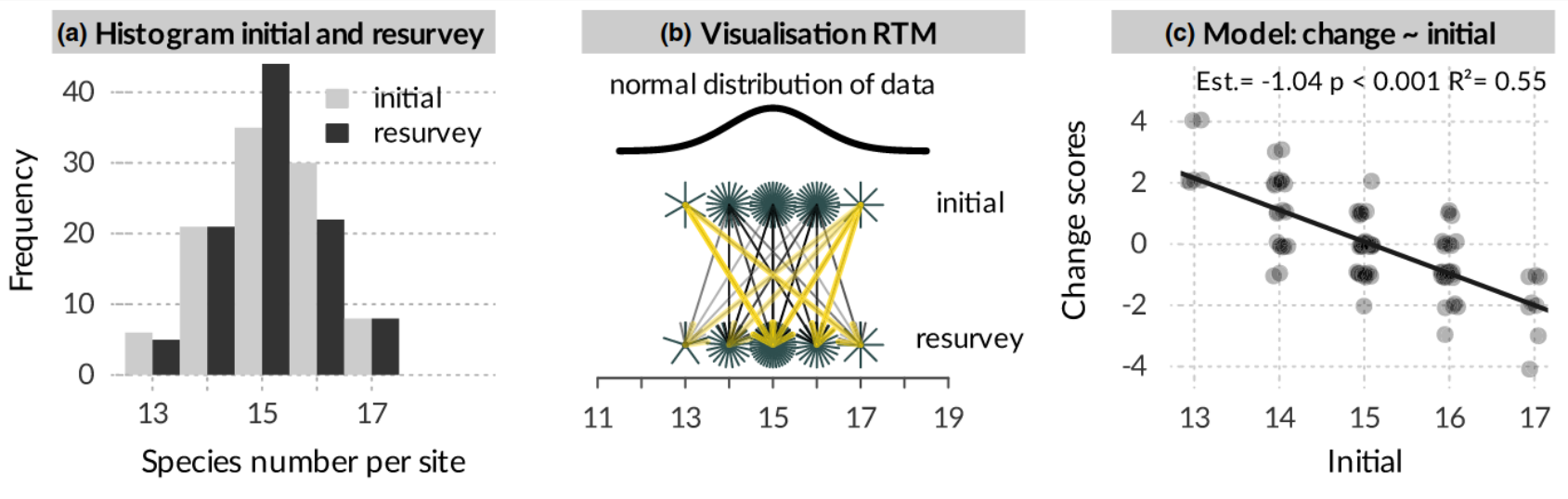


Regression to the mean

Species-rich sites lose more species

Species-poor sites gain more species

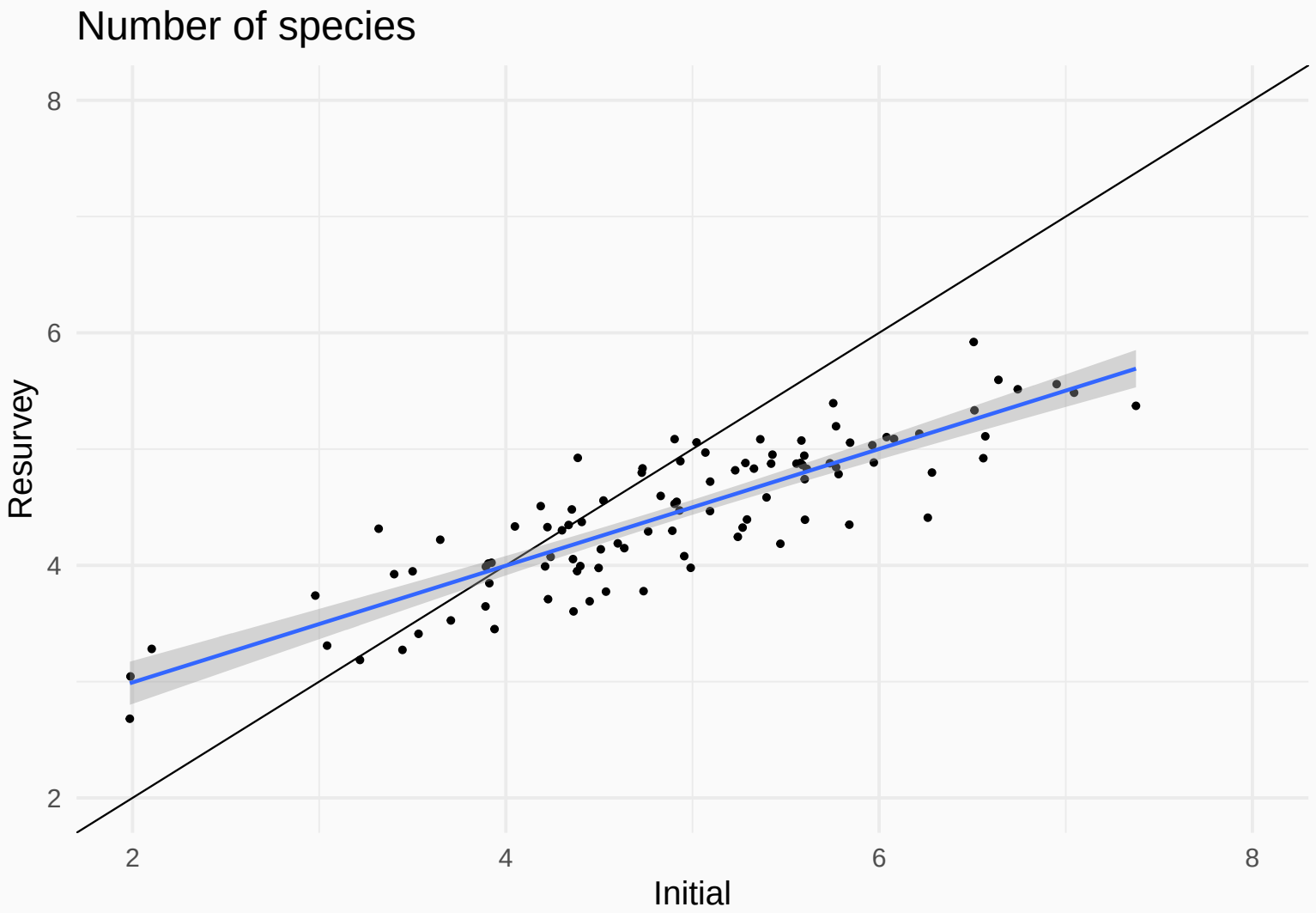
Negative trend against baseline



Mazalla & Diekmann 2022

Whenever two sets of measurements are not perfectly correlated

there will be regression towards the mean



What to do?

- Model outcome ~ baseline

What to do?

- Model outcome ~ baseline
- If modelling Change, include baseline as predictor

To learn more

- Mazalla & Diekmann 2022

To learn more

- Mazalla & Diekmann 2022
- Kelly & Price 2005

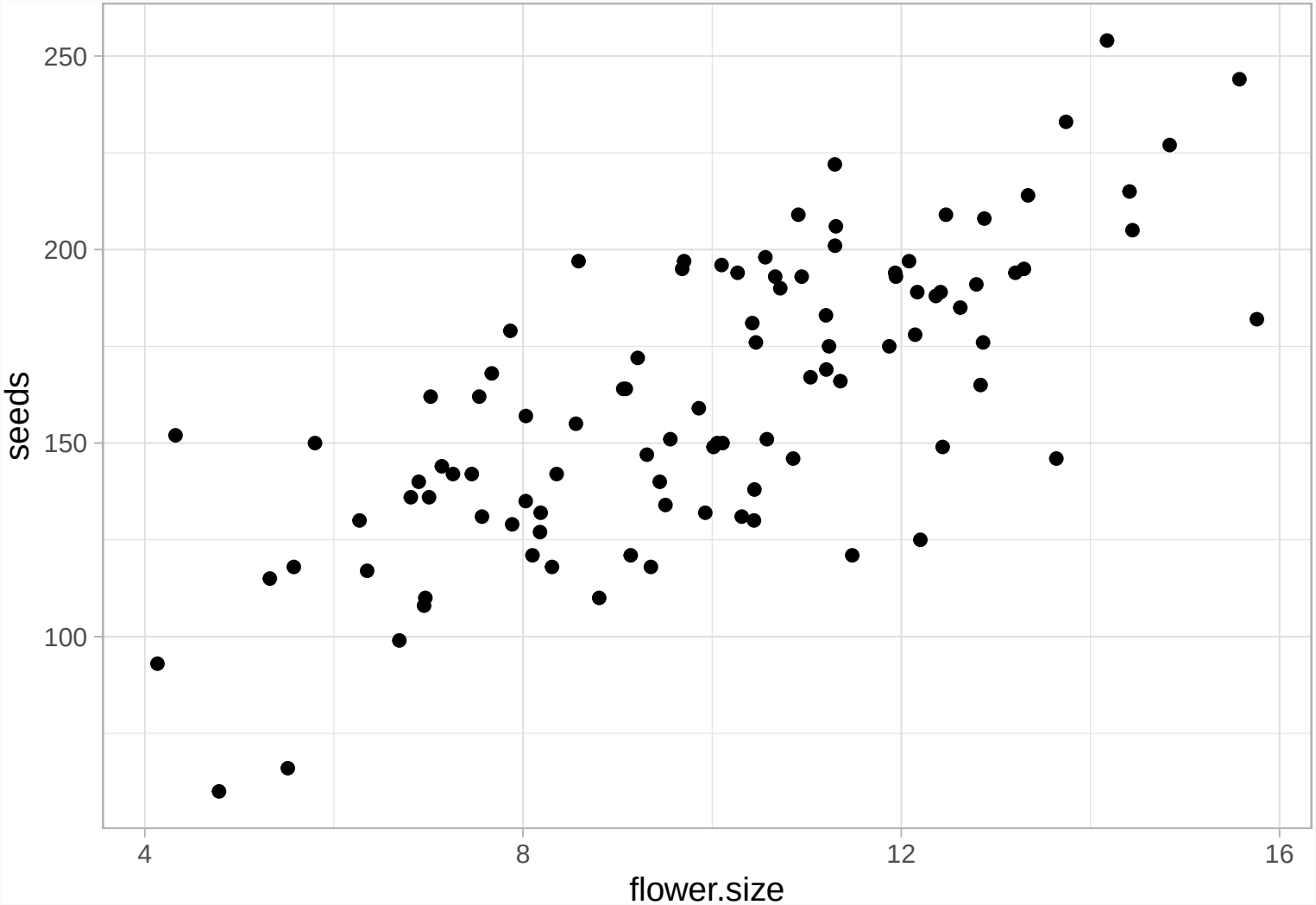
From causal salads to causal inference

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Self-learnt stuff ahead

Larger flowers produce more seeds



Larger flowers produce more seeds

```
lm(seeds ~ flower.size)
```

Variable	*Beta*	*SE*	*p.value*
(Intercept)	57	10.1	<0.001
flower.size	**11**	**0.978**	**<0.001**

Does flower size

really **cause**

increased seed production?

Shall we select plants with large flowers

to increase seed production?

Shall we select plants with large flowers

to increase seed production?

We tried but didn’t get the expected benefits

Maybe **large plants** (e.g. growing on better soil)

have **large flowers** AND produce **more seeds**?

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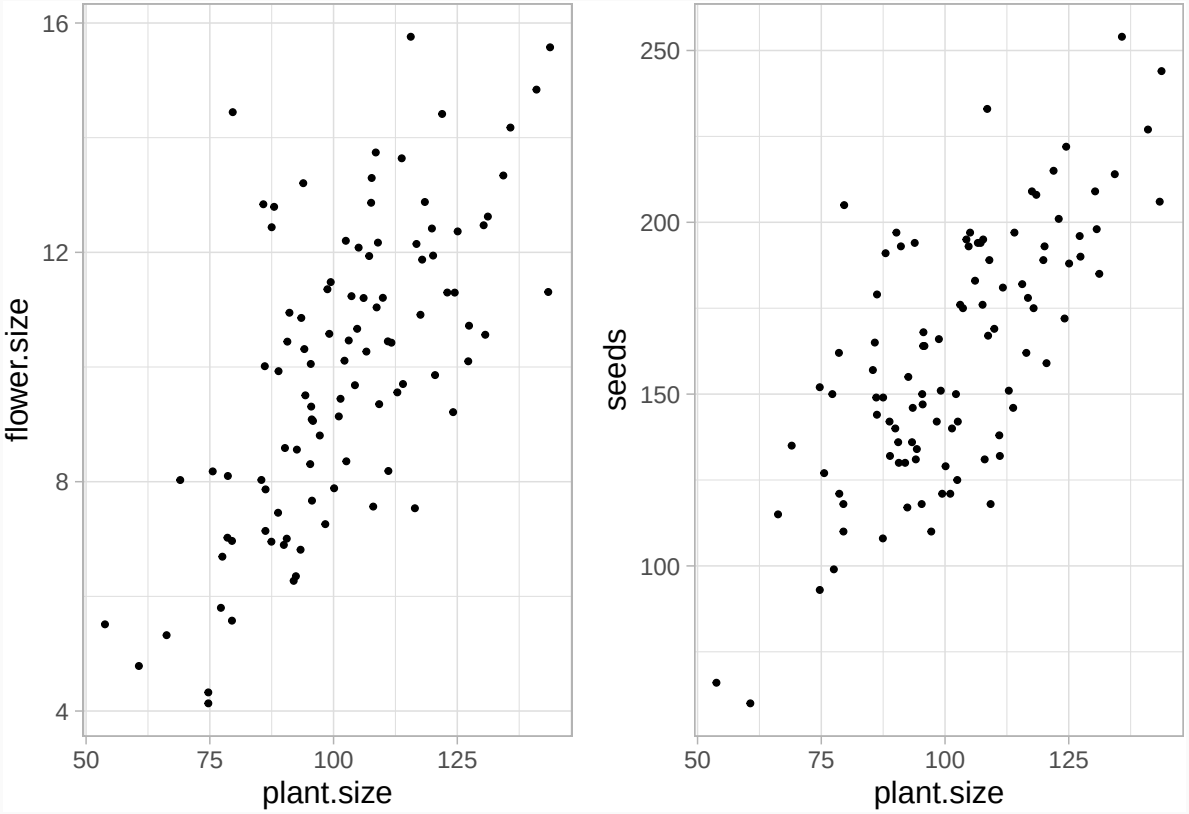
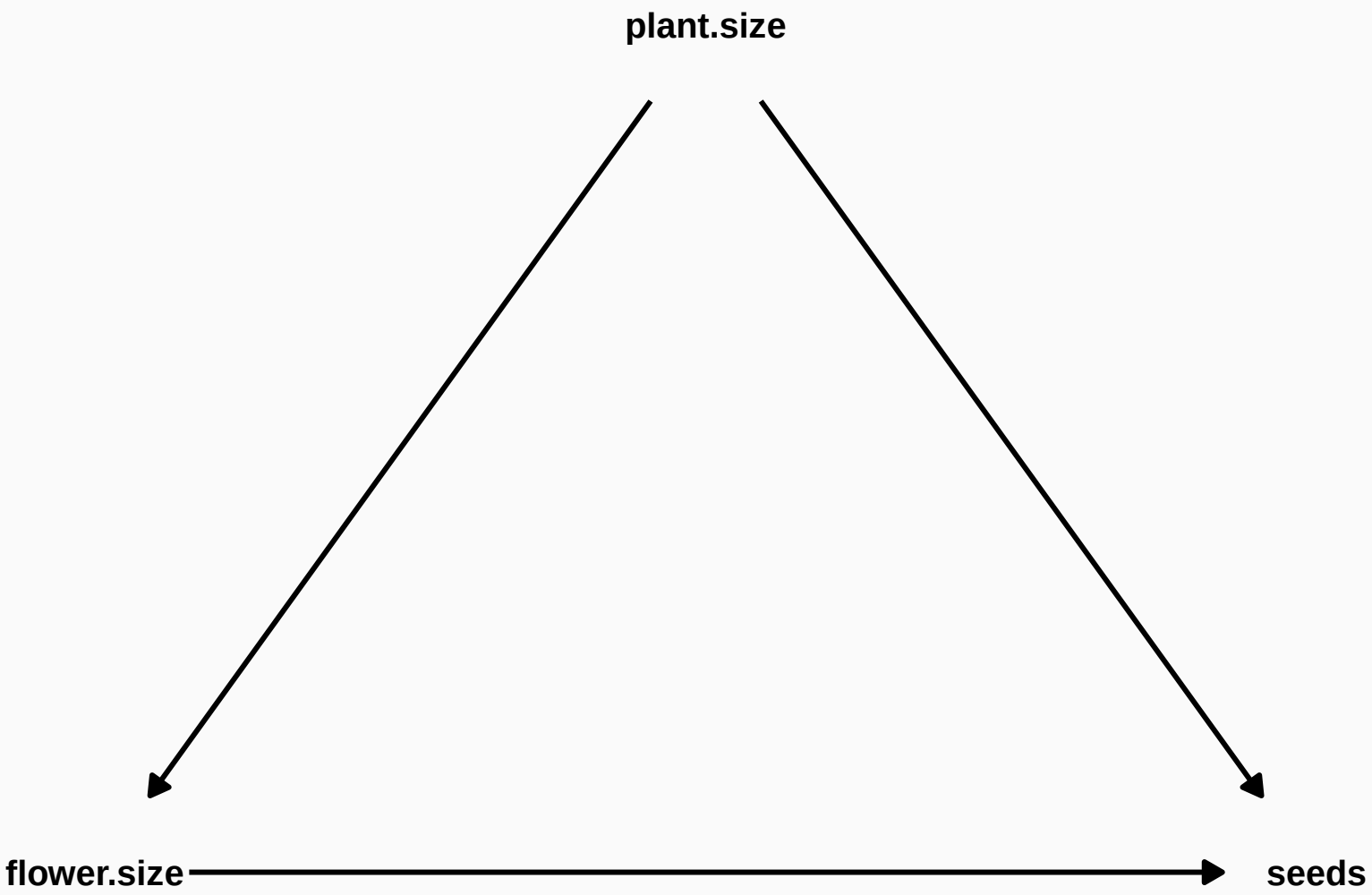


Maybe plant size is a **CONFOUNDER**?



Adjusting for plant size (confounding)

```
lm(seeds ~ flower.size + plant.size)
```

Variable	*Beta*	*SE*	*p.value*
(Intercept)	12	12.9	0.4
flower.size	**6.6**	**1.18**	**<0.001**
plant.size	0.82	0.168	<0.001

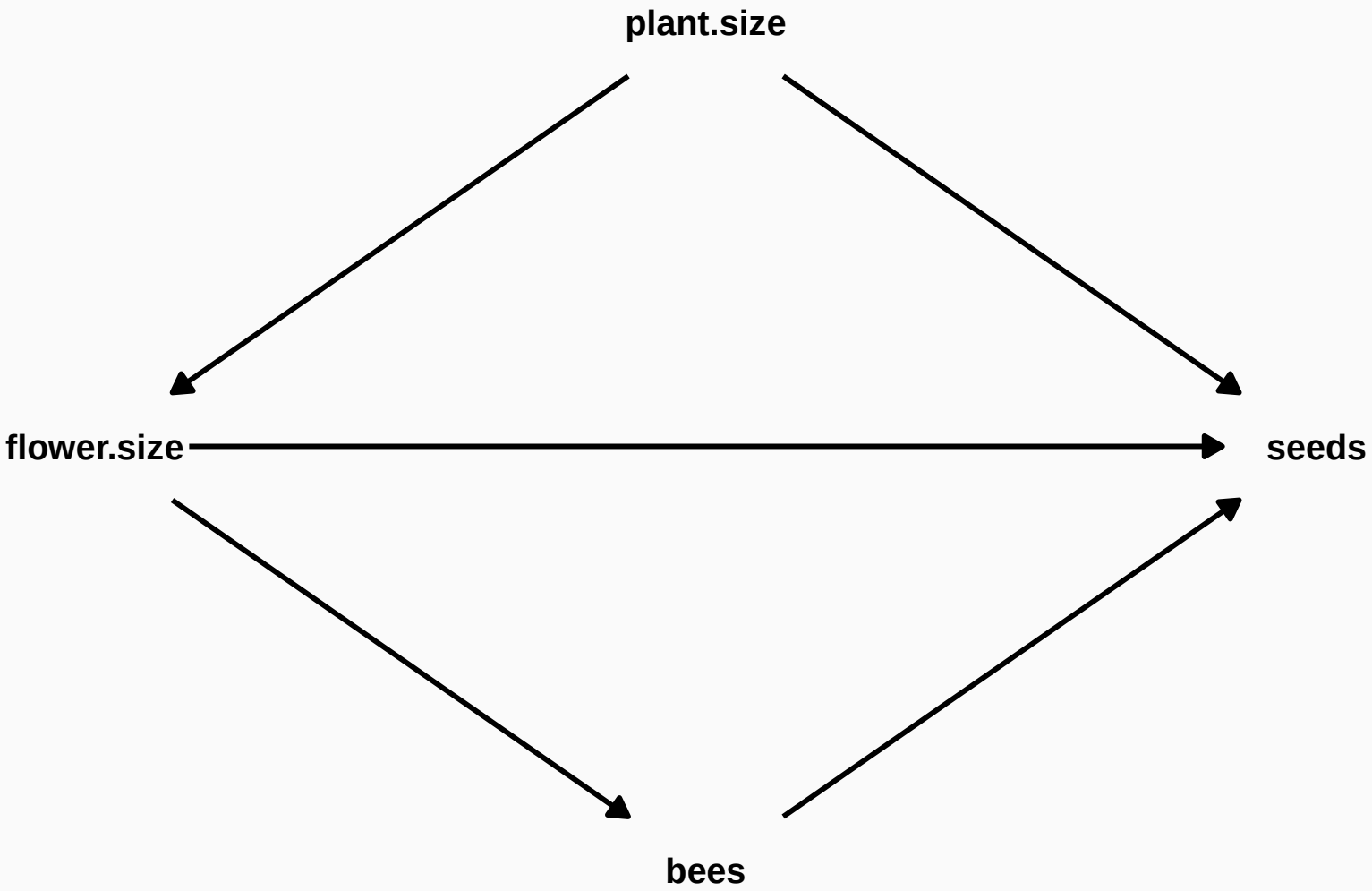
Including pollinators (bees)

Including pollinators (bees)

```
lm(seeds ~ flower.size + plant.size + bees)
```

Variable	*Beta*	*SE*	*p.value*
(Intercept)	5.2	12.1	0.7
flower.size	**2.1**	**1.56**	**0.2**
plant.size	0.90	0.157	<0.001
bees	8.8	2.14	<0.001

Pollinators are a **MEDIATOR**



Including beetles

(pollen & seed predators)

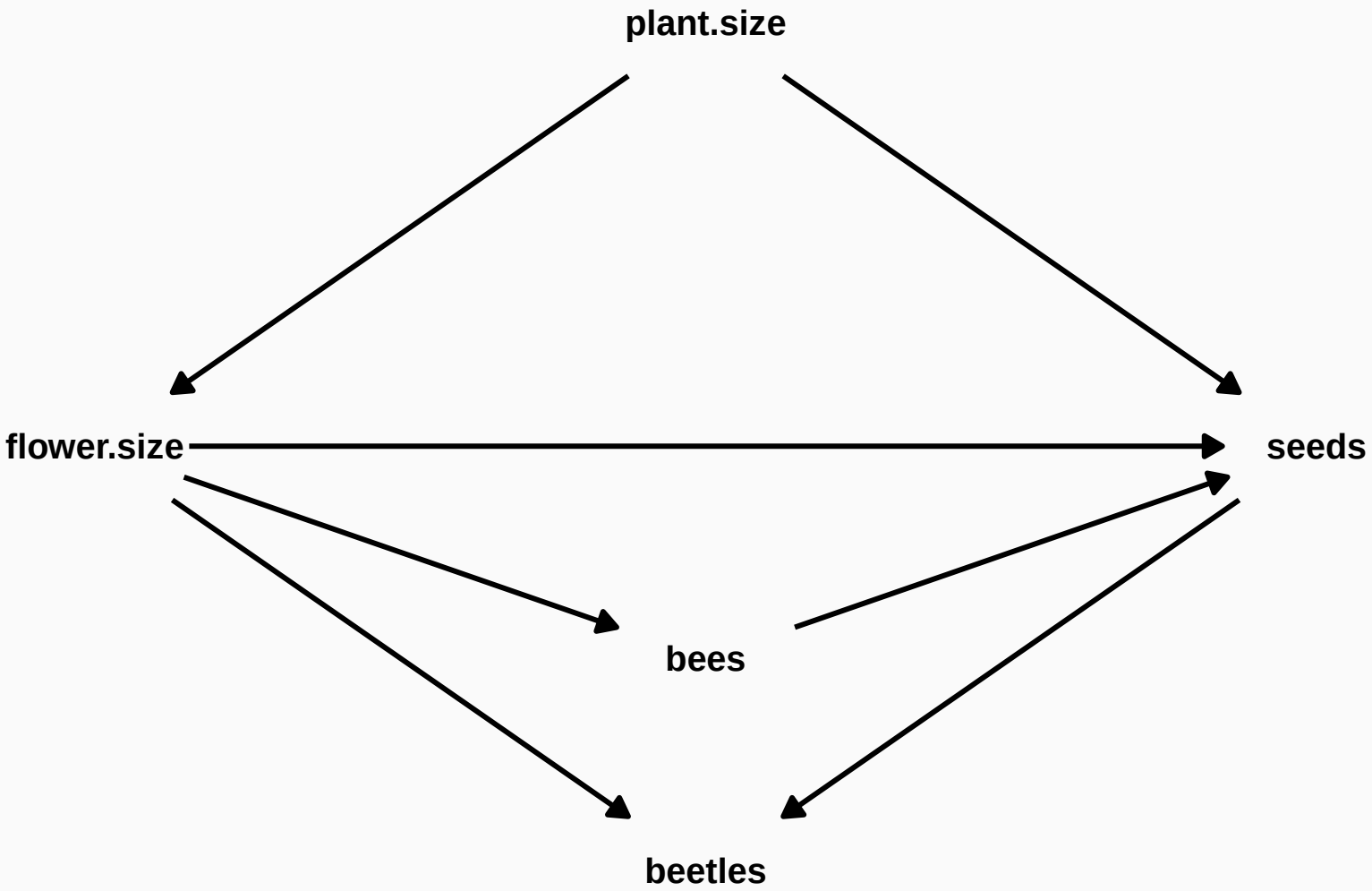
Including beetles (pollen & seed predators)

```
lm(seeds ~ flower.size + plant.size + bees +
beetles)
```

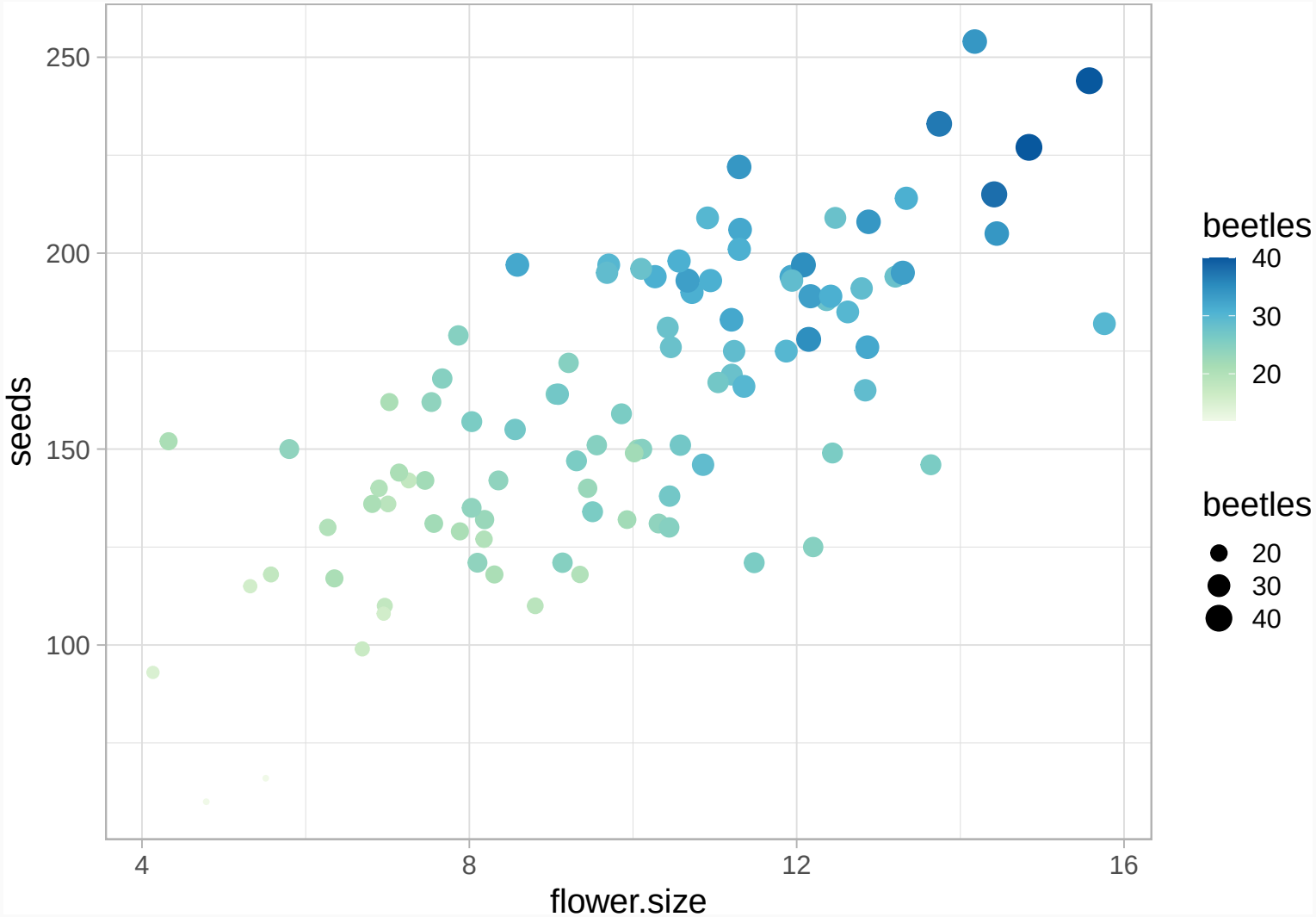
Variable	*Beta*	*SE*	*p.value*
(Intercept)	-11	8.67	0.2
flower.size	**-3.8**	**1.25**	**0.003**
plant.size	0.47	0.118	<0.001
bees	4.8	1.56	0.003
beetles	5.2	0.529	<0.001

Now flower.size has negative coefficient!!

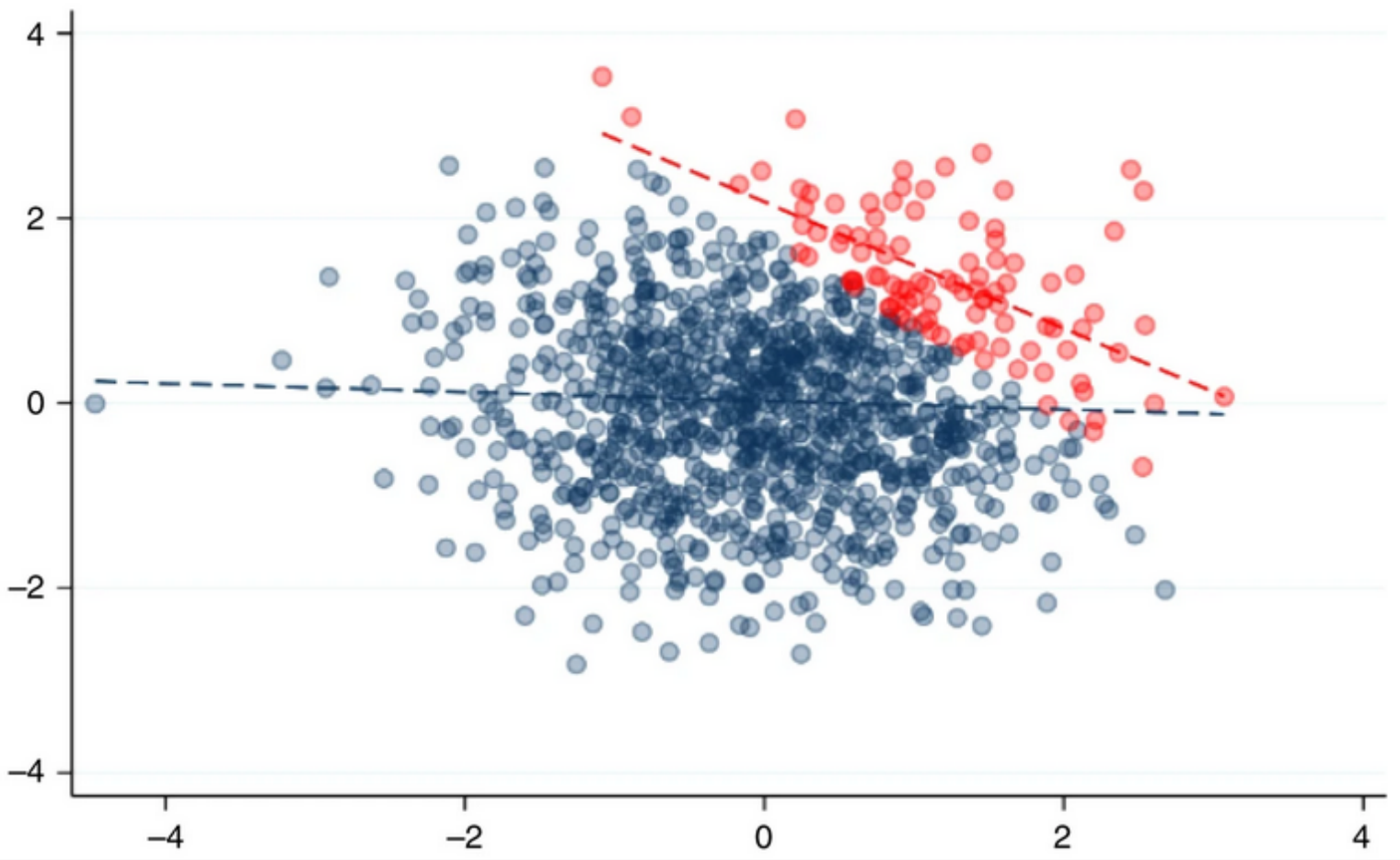
Beetles are a **COLLIDER**



Colliders induce non-causal negative relation between treatment (*flower.size*) and outcome (*seeds*)



Colliders induce non-causal negative relation between treatment and outcome

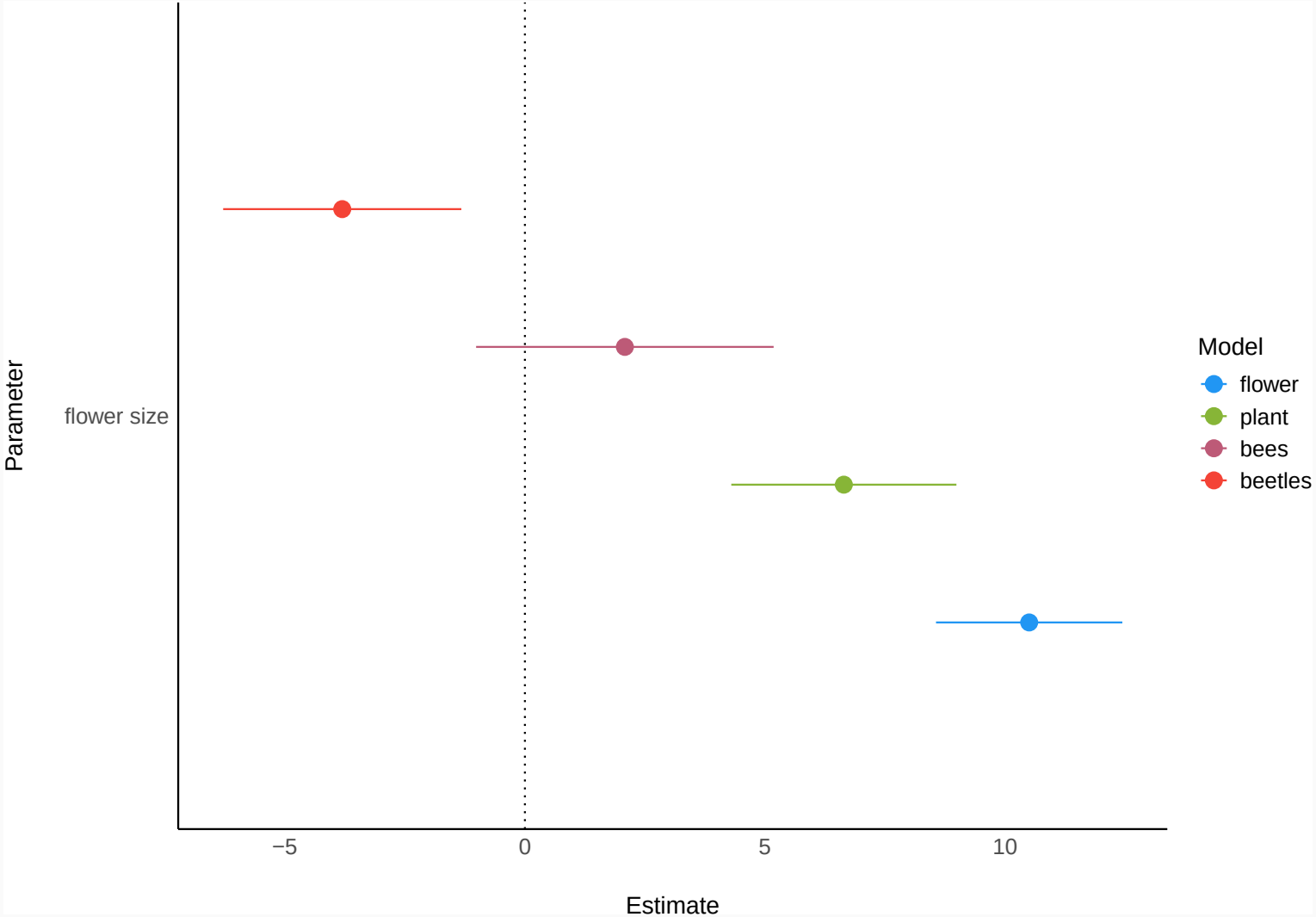


Griffith et al 2020

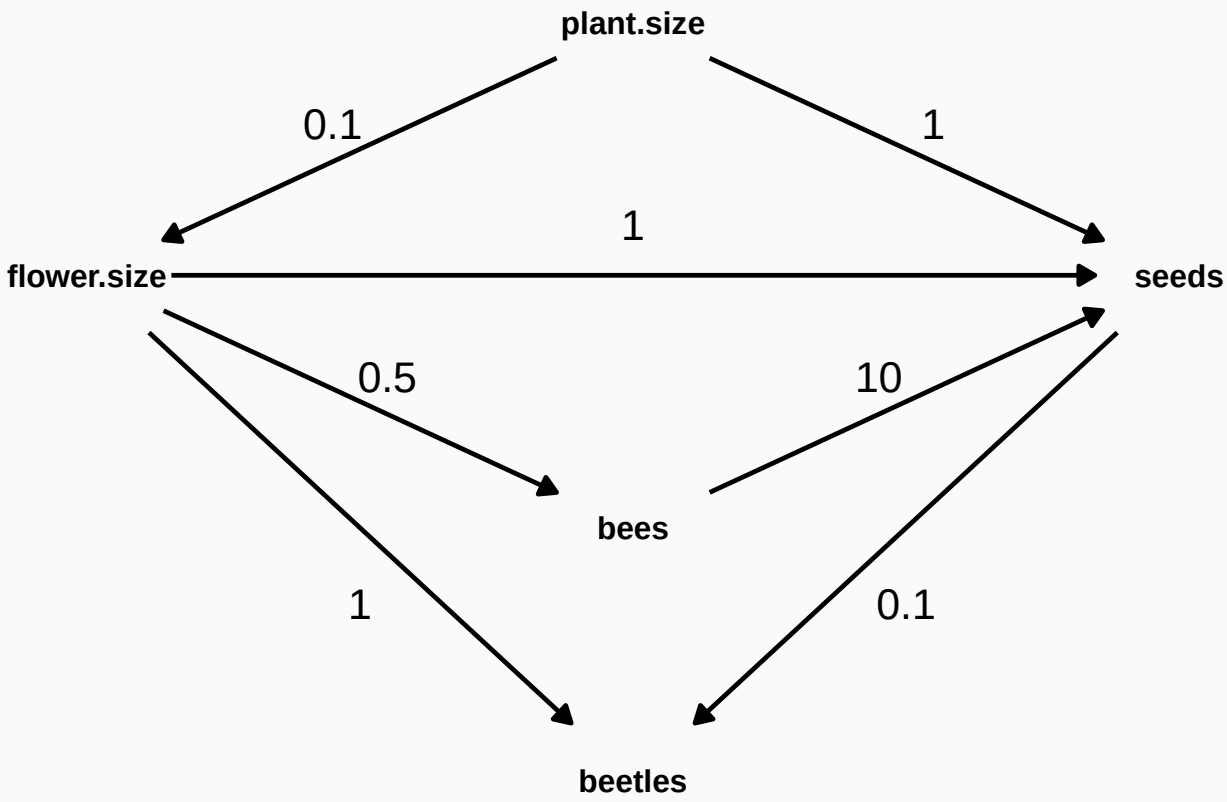
Recapitulating...

What is the real causal effect of flower size?

What is the real causal effect of flower size?

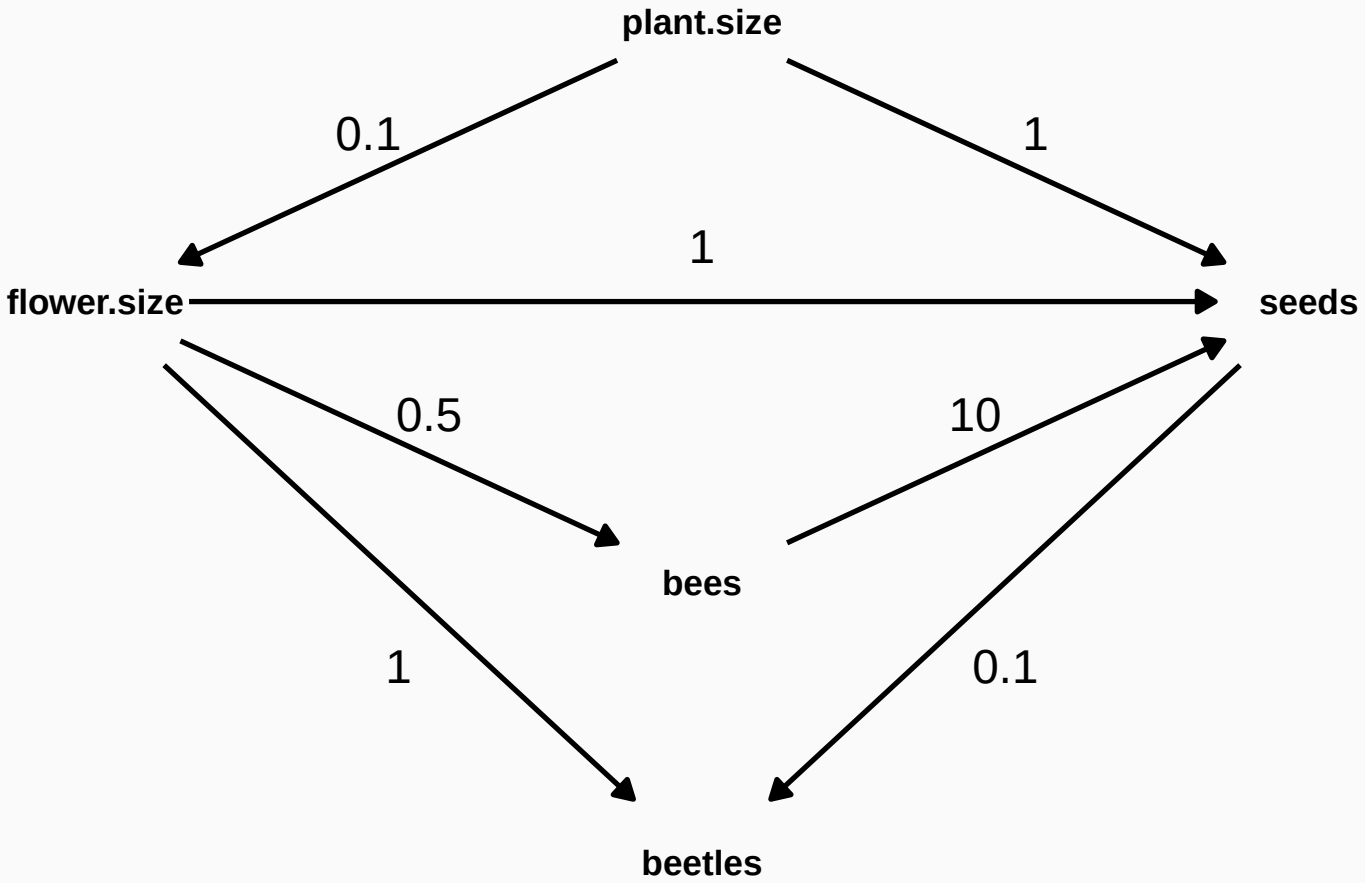


What is the real causal effect of flower size?



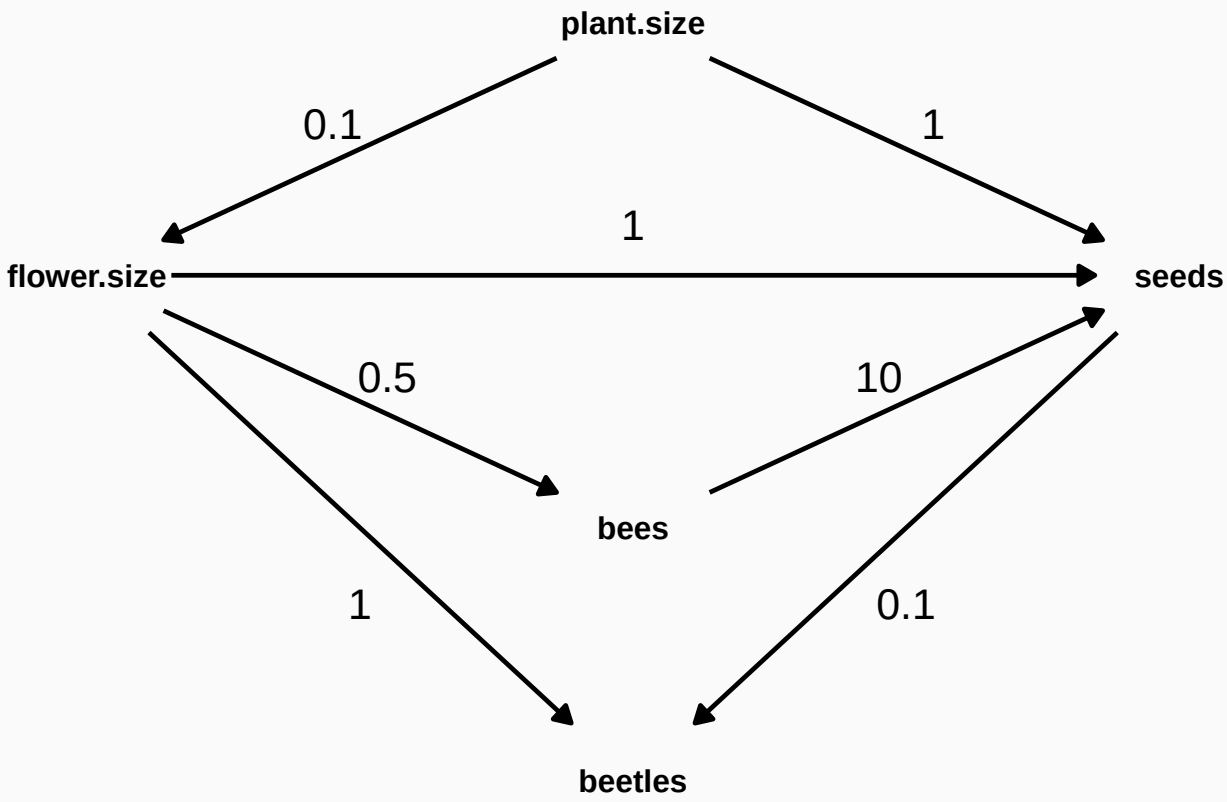
Variable	*Beta*	*SE*	*p.value*
(Intercept)	-11	8.67	0.2
flower.size	**-3.8**	**1.25**	**0.003**
plant.size	0.47	0.118	<0.001
bees	4.8	1.56	0.003
beetles	5.2	0.529	<0.001

What is the real causal effect of flower size?



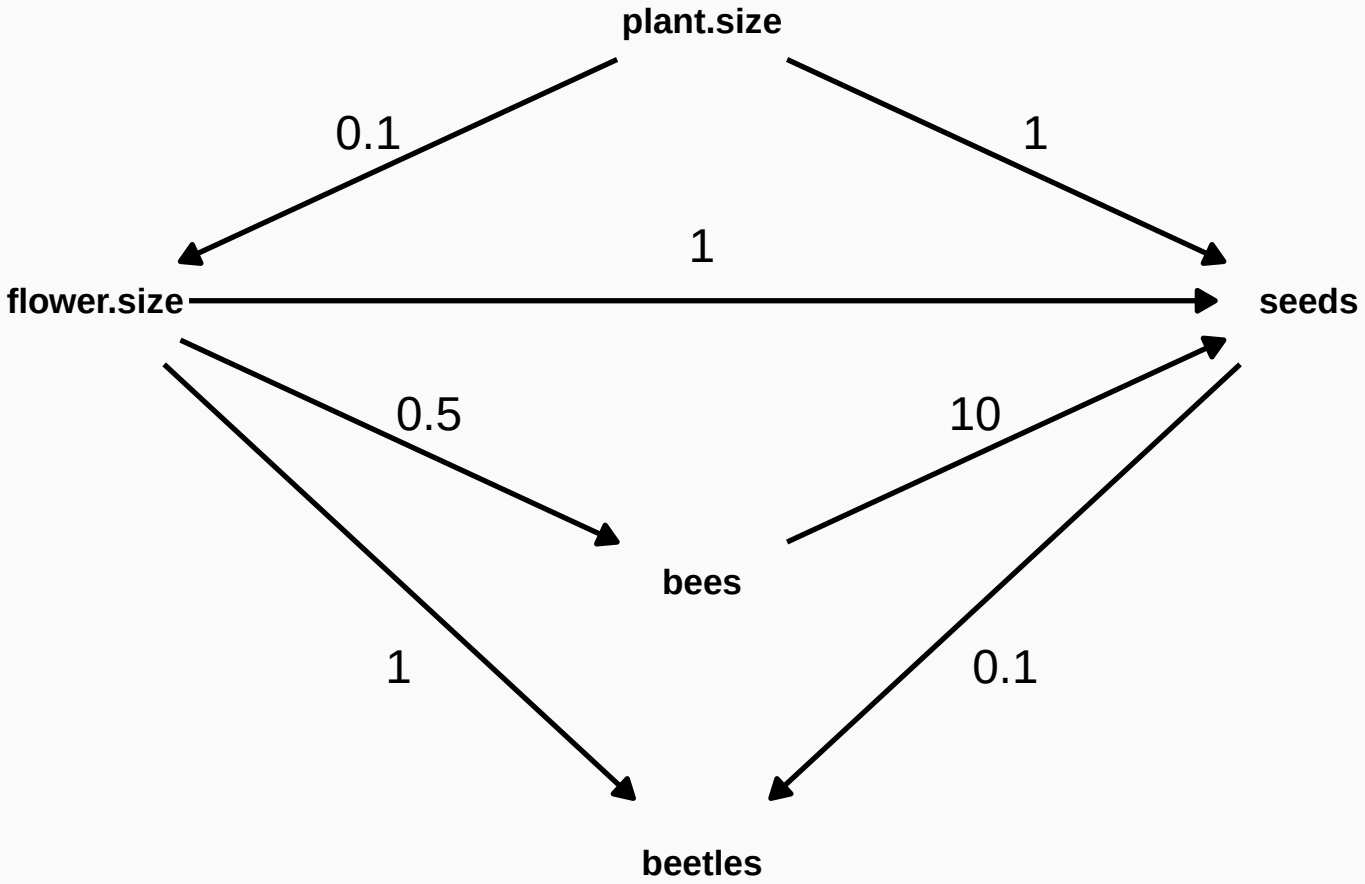
Avoid **COLLIDERS** -> collider/selection bias

What is the real causal effect of flower size?



Variable	*Beta*	*SE*	*p.value*
(Intercept)	5.2	12.1	0.7
flower.size	**2.1**	**1.56**	**0.2**
plant.size	0.90	0.157	<0.001
bees	8.8	2.14	<0.001

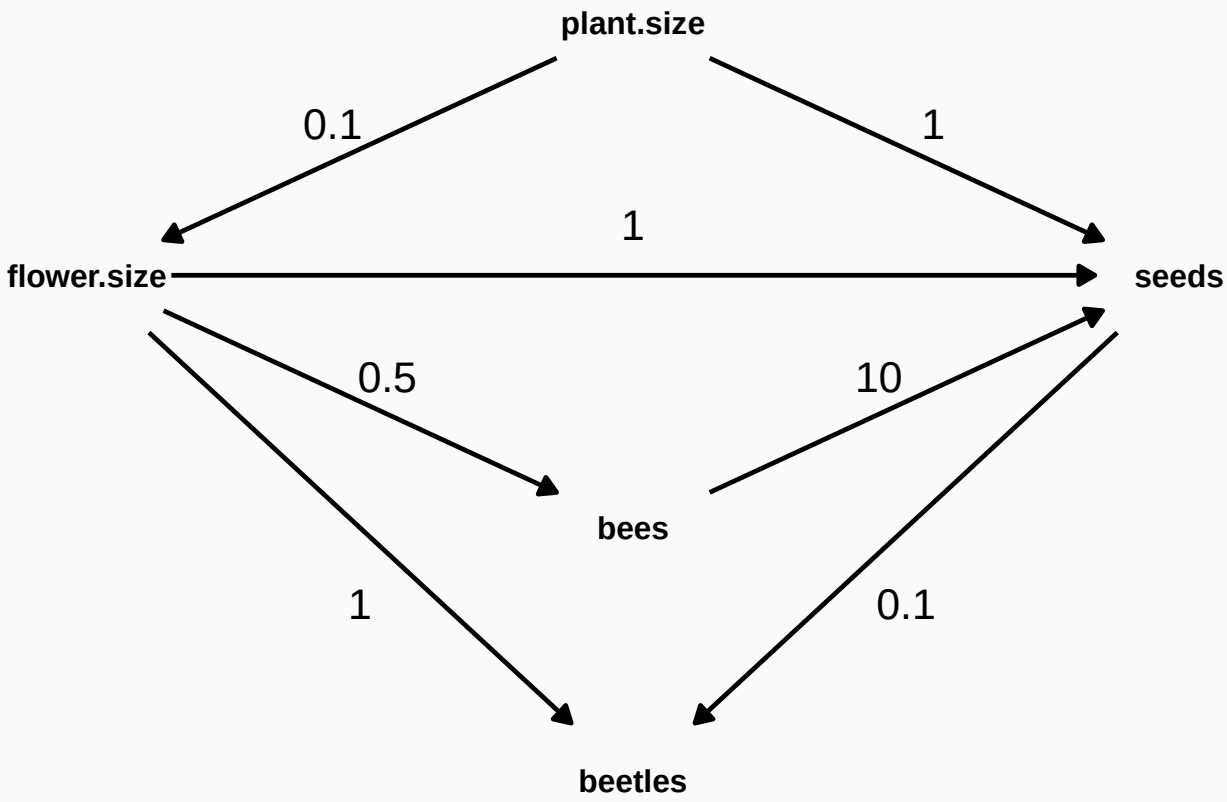
What is the real causal effect of flower size?



MEDIATORS split **total effect** into **direct** and **indirect** effects

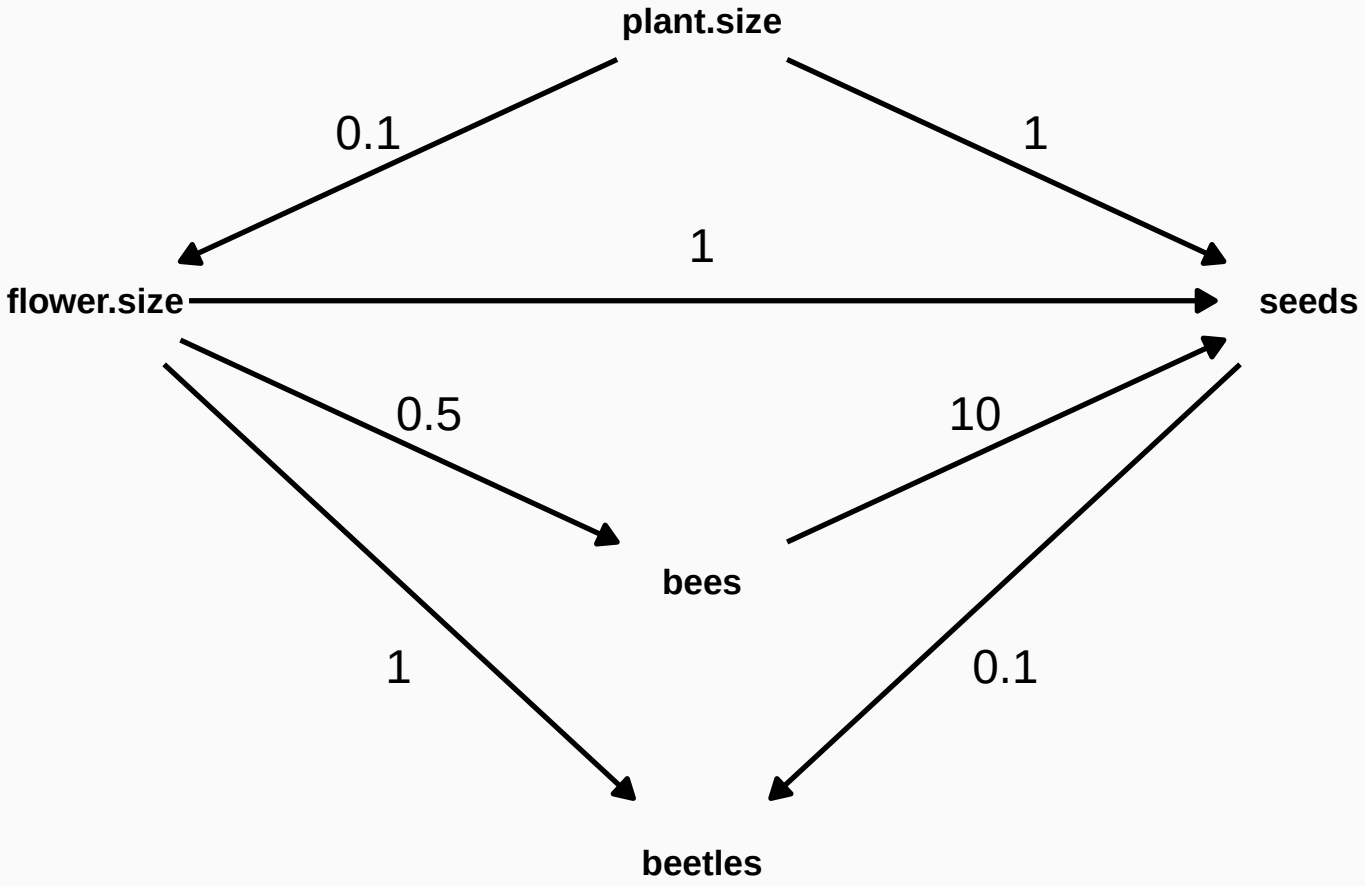
(overcontrol bias)

What is the real causal effect of flower size?



Variable	*Beta*	*SE*	*p.value*
(Intercept)	12	12.9	0.4
flower.size	**6.6**	**1.18**	**<0.001**
plant.size	0.82	0.168	<0.001

What is the real causal effect of flower size?

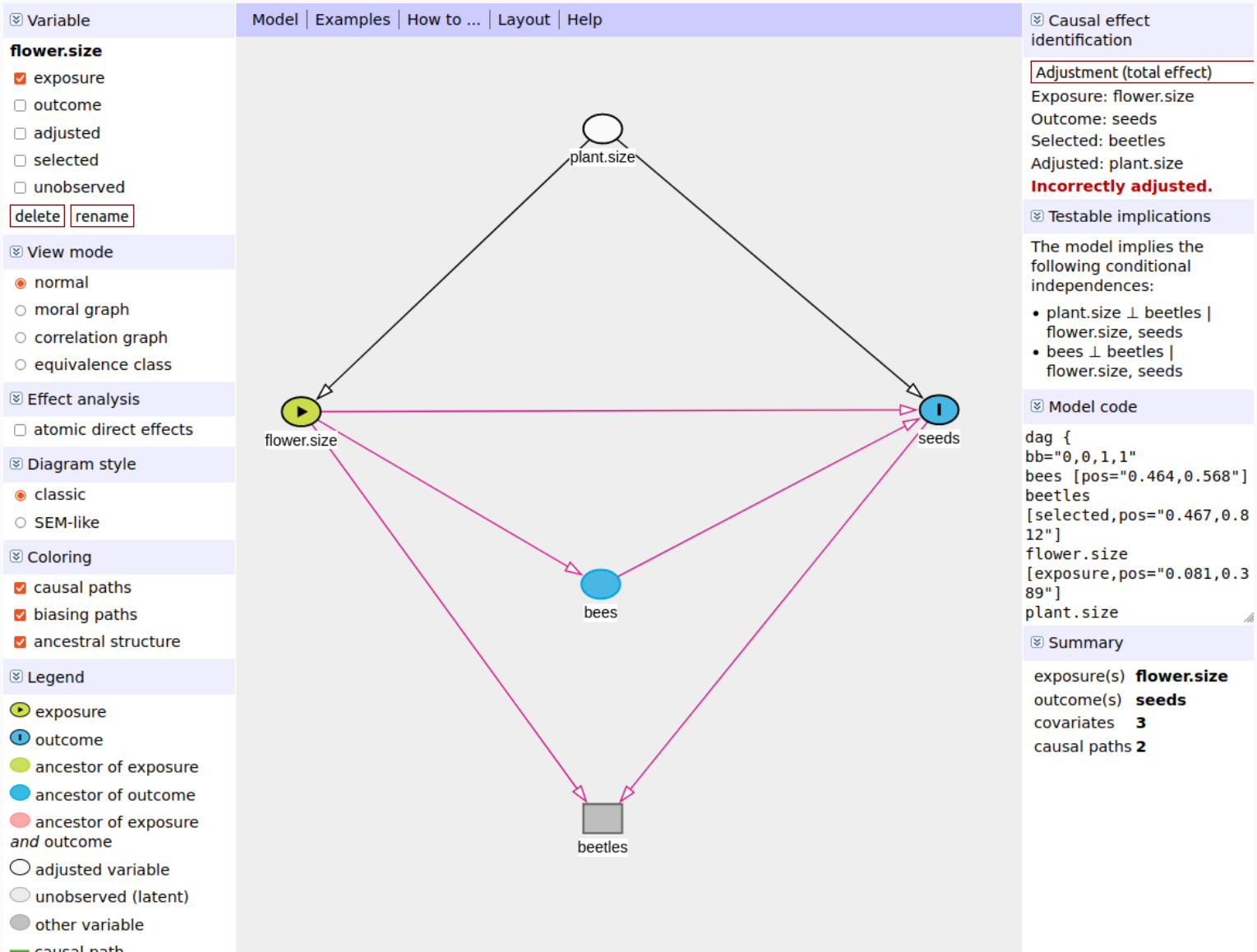


Include **CONFOUNDERS** to avoid **‘omitted variable bias’**

(use **backdoor criterion**)

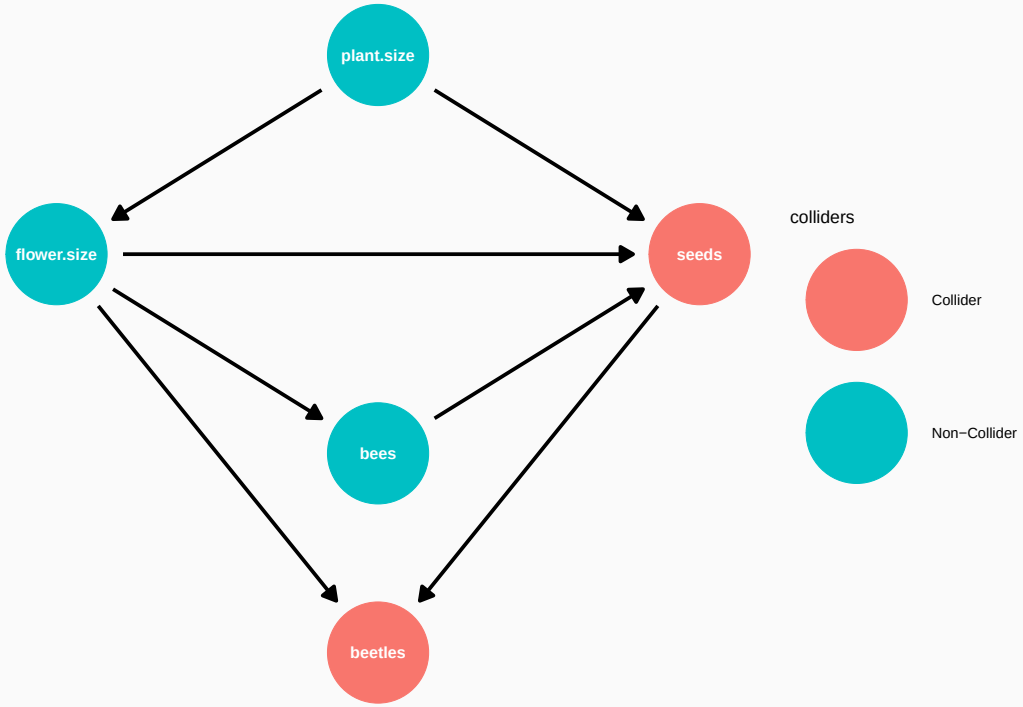
Tools to identify correct causal structure

https://daggity.net



Tools to identify correct causal structure

```
dagify(
  seeds ~ plant.size + flower.size + bees,
  flower.size ~ plant.size,
  bees ~ flower.size,
  beetles ~ flower.size + seeds,
  coords = coords
) |>
  ggdag_collider(size = 2) + theme_dag_blank()
```



Tools to identify correct causal structure

```r
library(easystats)
dag <- check_dag(
  seeds ~ flower.size + plant.size + bees,
  flower.size ~ plant.size,
  bees ~ flower.size,
  beetles ~ flower.size + seeds,
  outcome = "seeds",
  exposure = "flower.size",
  adjusted = c("plant.size", "bees", "beetles")
  )
dag
```

```
# Check for correct adjustment sets
- Outcome: seeds
- Exposure: flower.size
- Adjustments: bees, beetles and plant.size
- Collider: beetles

Identification of direct and total effects

Incorrectly adjusted!
Your model adjusts for a potential collider. To estimate the direct and total effect, do not adjust for 'beetle
```

Causal salads

Causal salads

You put everything into a regression equation, toss with some creative story-telling, and hope the reviewers eat it

R. McElreath

{Jerry Pank}

Causal salads

Throwing predictor variables into a statistical model

hoping this will improve the analysis is a dreadful idea

Jan Vanhove

Predictive criteria don’t help for causal inference

Predictive criteria don't help to choose correct causal model

Making good predictions doesn't require accurate causal model

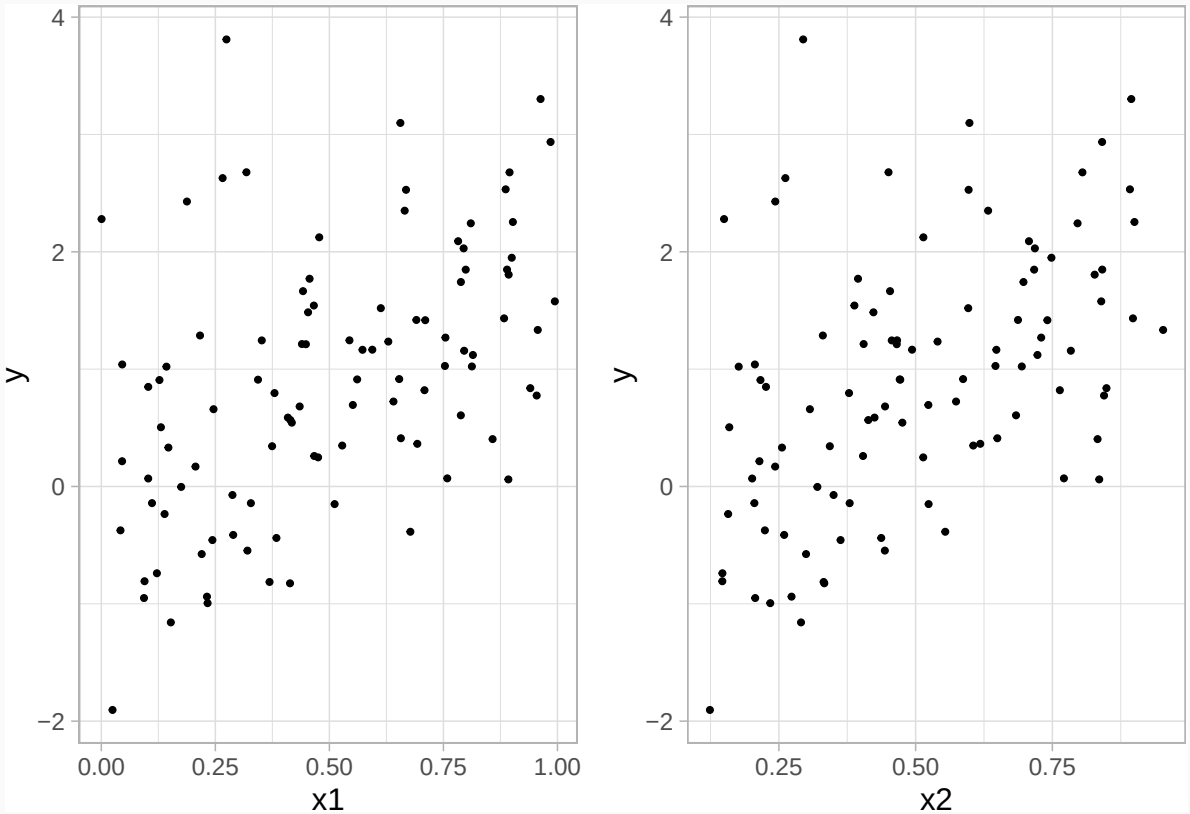
Model	AIC	R2
m.flower	933.3	0.5
m.flower.plant	913.2	0.6
m.flower.plant.bees	899.1	0.7
m.flower.plant.bees.beetles	829.9	0.8

'Best model' (based on AIC or R2) not good for causal inference

Simpler (best) model provides biased causal estimates

Simulate response depending on two correlated variables (Hartig 2022)

```
x1 = runif(100)
x2 = 0.8*x1 + 0.2*runif(100)
y = x1 + x2 + rnorm(100)
```



Simpler (best) model provides biased causal estimates

Simulate response depending on two correlated variables (Hartig 2022)

```
fullmodel = lm(y ~ x1 + x2)
```

```
Call:
lm(formula = y ~ x1 + x2)

Residuals:
    Min      1Q  Median      3Q     Max
-1.8994 -0.6821 -0.1086  0.5749  3.3663

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.1408     0.2862  -0.492    0.624
x1            1.2158     1.5037   0.809    0.421
x2            0.8518     1.8674   0.456    0.649

Residual standard error: 0.9765 on 97 degrees of freedom
Multiple R-squared:  0.237, Adjusted R-squared:  0.2212
F-statistic: 15.06 on 2 and 97 DF,  p-value: 2.009e-06
```

Simpler (best) model provides biased causal estimates

```r
simplemodel = MASS::stepAIC(fullmodel, trace = 0)
```

```
Call:
lm(formula = y ~ x1)

Residuals:
    Min      1Q  Median      3Q     Max
-1.9047 -0.6292 -0.1019  0.6077  3.3394

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.04633    0.19670  -0.236    0.814
x1           1.88350    0.34295   5.492 3.13e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9725 on 98 degrees of freedom
Multiple R-squared:  0.2353,    Adjusted R-squared:  0.2275
F-statistic: 30.16 on 1 and 98 DF,  p-value: 3.134e-07
```

Automated model selection (dredge)

Simulating data with 10 random predictors

```
dat <- data.frame(y = rnorm(100),
                  x = matrix(runif(1000), ncol = 10))
```

y	x.1	x.2	x.3	x.4	x.5	x.6	x.7	x.8	x.9	x.10
-0.1	0.6	0.6	0.3	0.8	0.2	0.0	0.4	0.4	0.3	0.2
0.8	0.4	0.4	0.9	0.2	0.5	0.1	0.6	0.2	0.0	0.0
-0.5	0.0	0.3	0.4	0.3	0.1	0.1	0.9	0.9	0.5	0.8
-0.6	0.7	0.7	0.4	0.5	0.2	0.7	0.7	0.8	0.5	0.3
0.7	0.0	0.6	0.9	0.1	0.2	0.4	0.8	0.6	0.6	0.1
-0.1	0.4	0.2	0.9	0.4	0.6	0.5	0.9	0.1	0.8	0.8

Automated model selection

Running `MuMIn::dredge` with 10 random predictors

```
full.model <- lm(y ~ ., data = dat)
dd <- MuMIn::dredge(full.model)
```

Best model:

Parameter	Coefficient	SE	p
(Intercept)	-1.50	0.36	0.00
x.2	0.78	0.36	0.03
x.5	0.59	0.32	0.07
x.6	0.61	0.35	0.09
x.9	0.87	0.34	0.01

Extract from `dredge` help

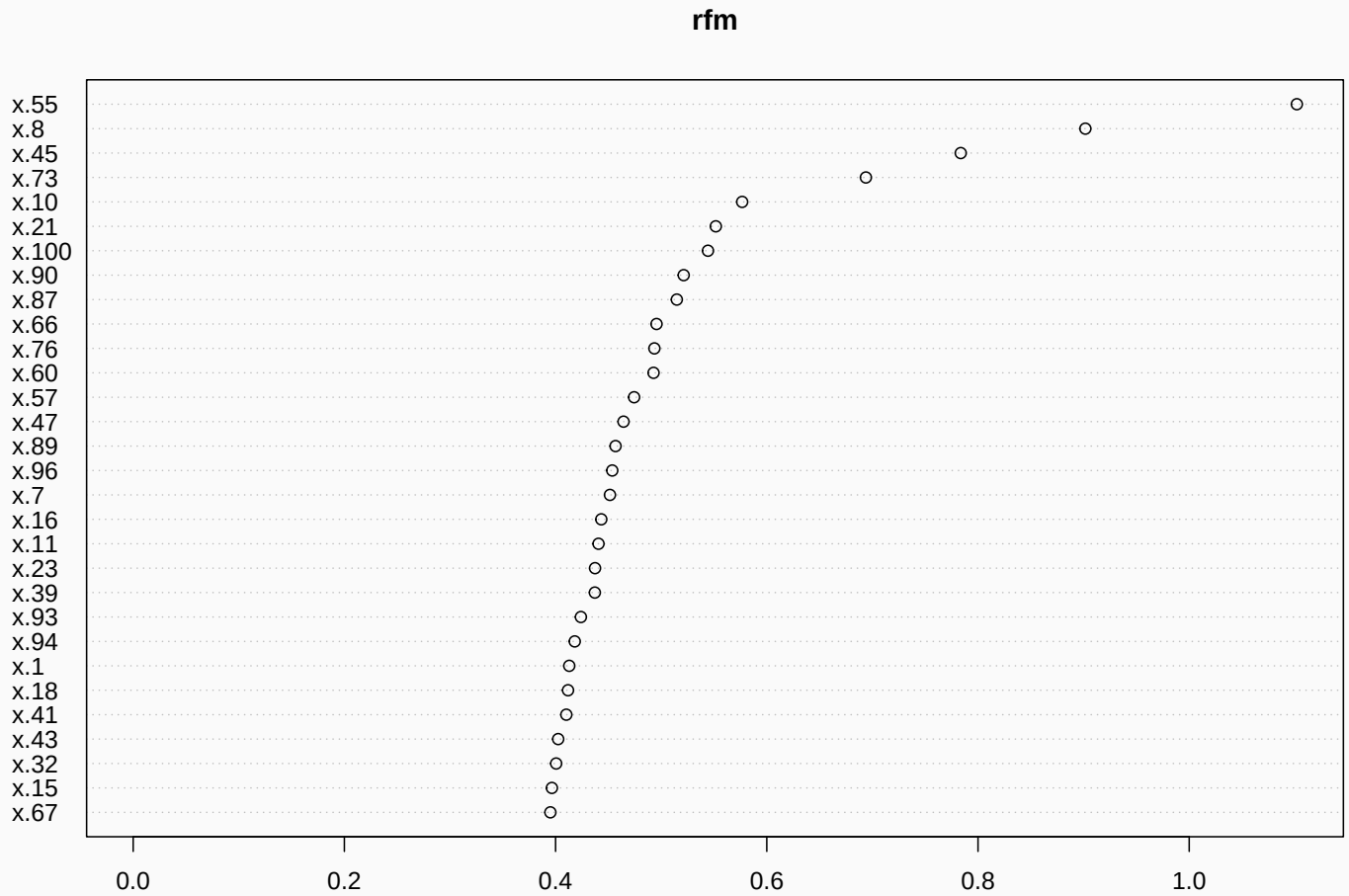
"Let the computer find out" is a poor strategy and usually reflects the fact that the researcher did not bother to think clearly about the problem of interest and its scientific setting

Burnham and Anderson 2002

Variable importance in machine learning

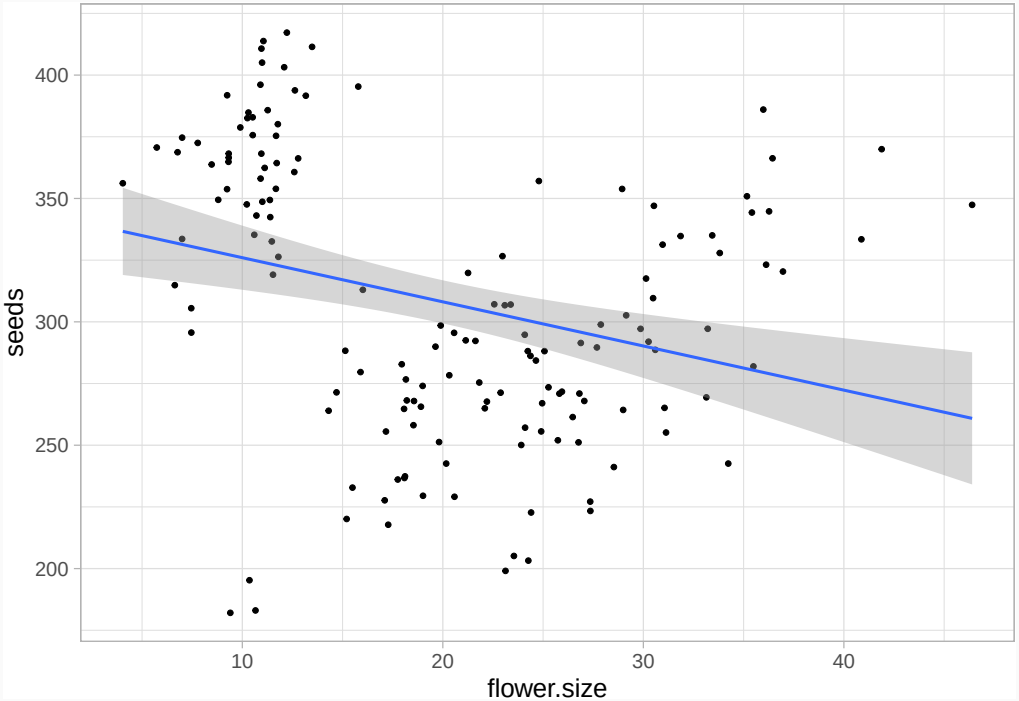
Random forest on **100 random predictors**

```
dat <- data.frame(x = matrix(runif(50000), ncol = 100), y = runif(500))
rfm <- randomForest::randomForest(y ~ ., data = dat)
varImpPlot(rfm)
```



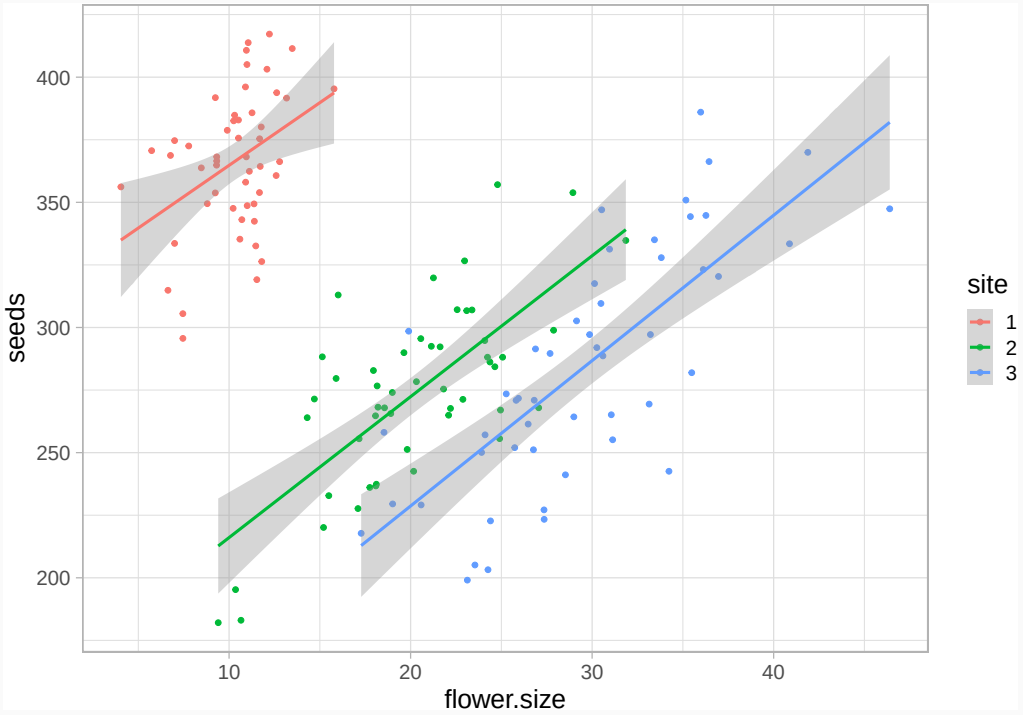
Simpson's paradox as a causal problem

Simpson's paradox



Variable	*Beta*	*SE*	*p.value*
(Intercept)	344	10.7	<0.001
flower.size	**-1.8**	**0.486**	**<0.001**

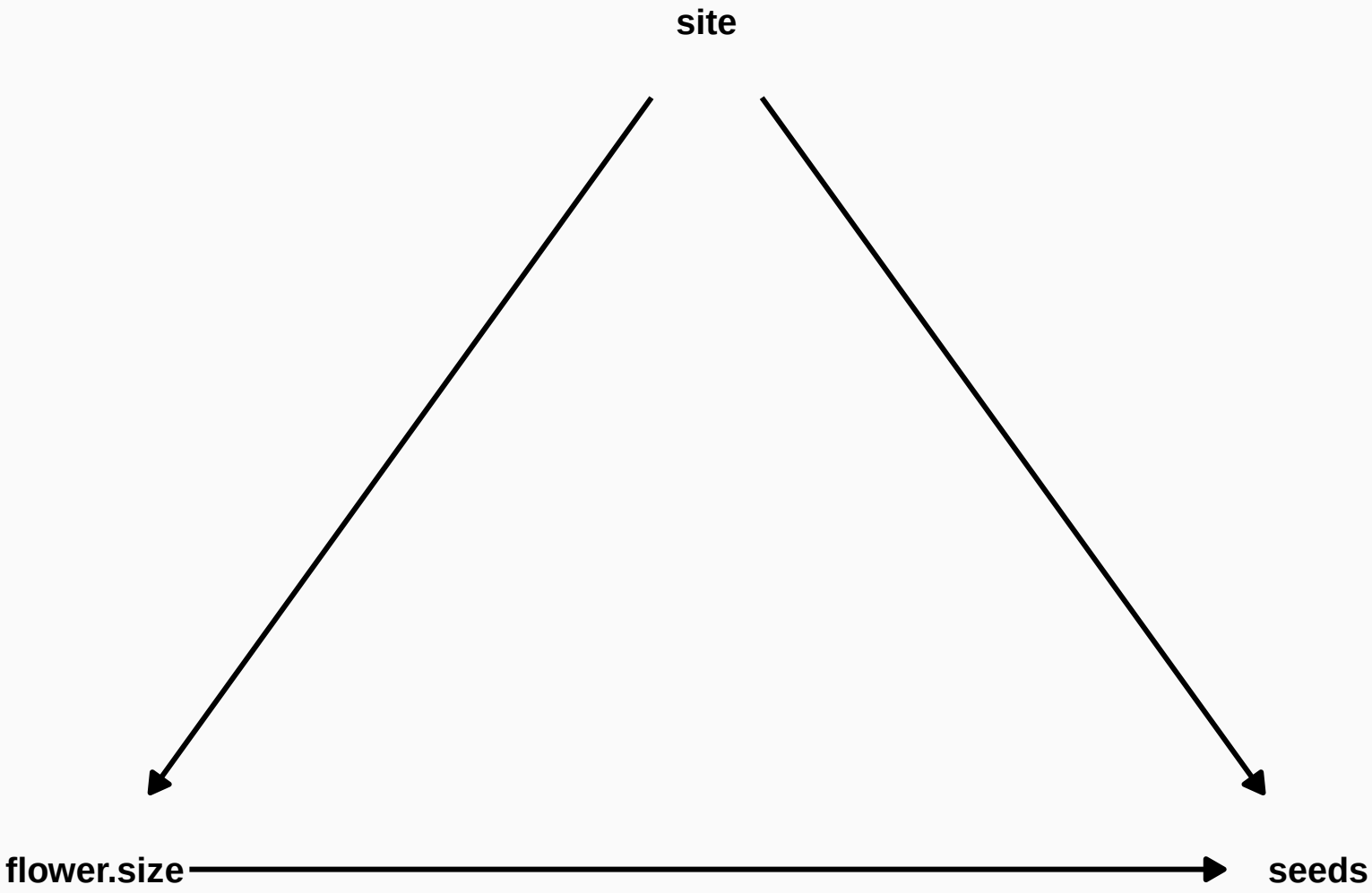
Simpson's paradox



Variable	*Beta*	*SE*	*p.value*
(Intercept)	308	6.50	<0.001
flower.size	**5.7**	**0.500**	**<0.001**
site			
1	—	—	
2	-149	7.50	<0.001
3	-192	11.1	<0.001

Simpson's paradox

Site is a confounder!



From causal salads to causal inference

Causal interpretation requires

external knowledge

To estimate causal effects accurately we require more information than can be gleaned from statistical tools alone

D'Agostino et al

Causal interpretation requires

external knowledge

To estimate causal effects accurately we require more information than can be gleaned from statistical tools alone

D'Agostino et al

No amount of data reliably turns salad into sense

R. McElreath

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand
- Control for **confounders**

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand
- Control for **confounders**
- Avoid conditioning on **post-treatment variables**

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand
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- Avoid conditioning on **post-treatment variables**
    - Treatment -> Covariate -> Outcome

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand
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    - Treatment -> Covariate -> Outcome
- Beware of **collider bias**

From causal salad to causal inference

- Draw the **causal graph** (DAG) beforehand
- Control for **confounders**
- Avoid conditioning on **post-treatment variables**
    - Treatment -> Covariate -> Outcome
- Beware of **collider bias**
- **Predictive criteria** not fit for causal inference

To learn more

Suchinta Arif's papers

McElreath's workshop on causal inference

Byrnes & Dee 2024

`https://www.r-causal.org`

`https://theeffectbook.net`

Extras

Collider bias

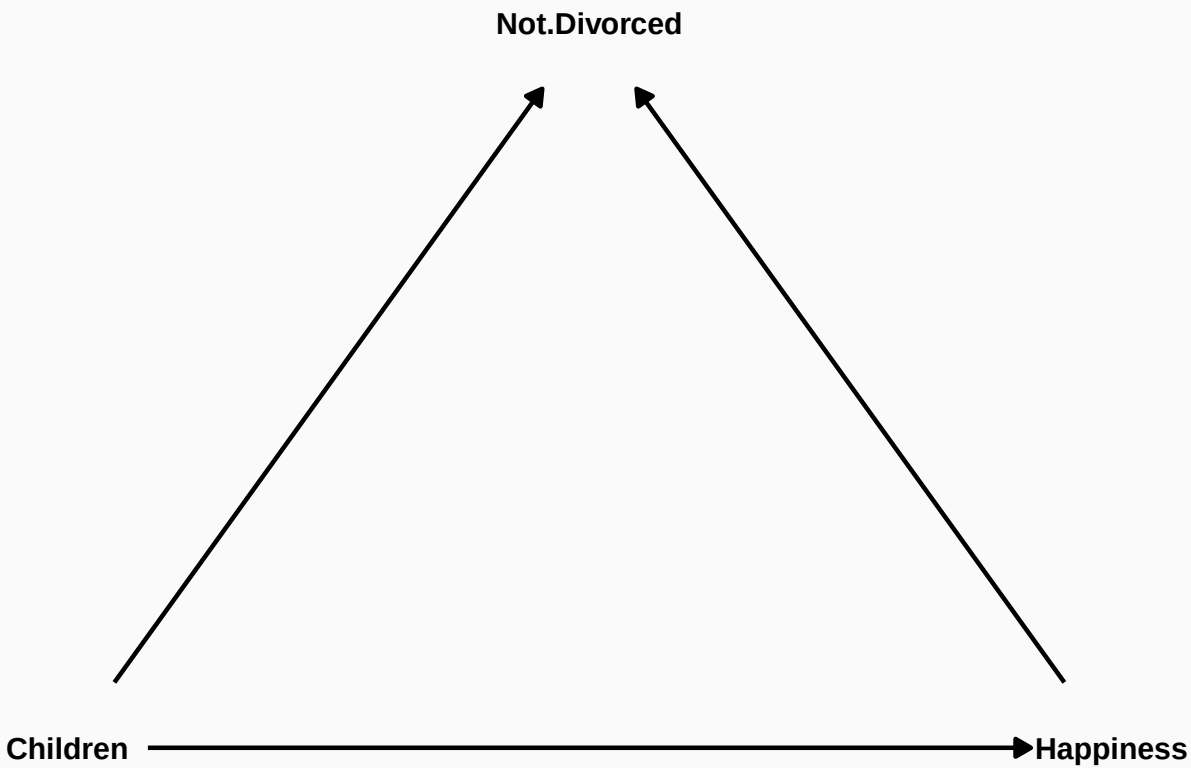
Number of children is significant negative predictor of marital satisfaction

The more children, the more unhappy couples are

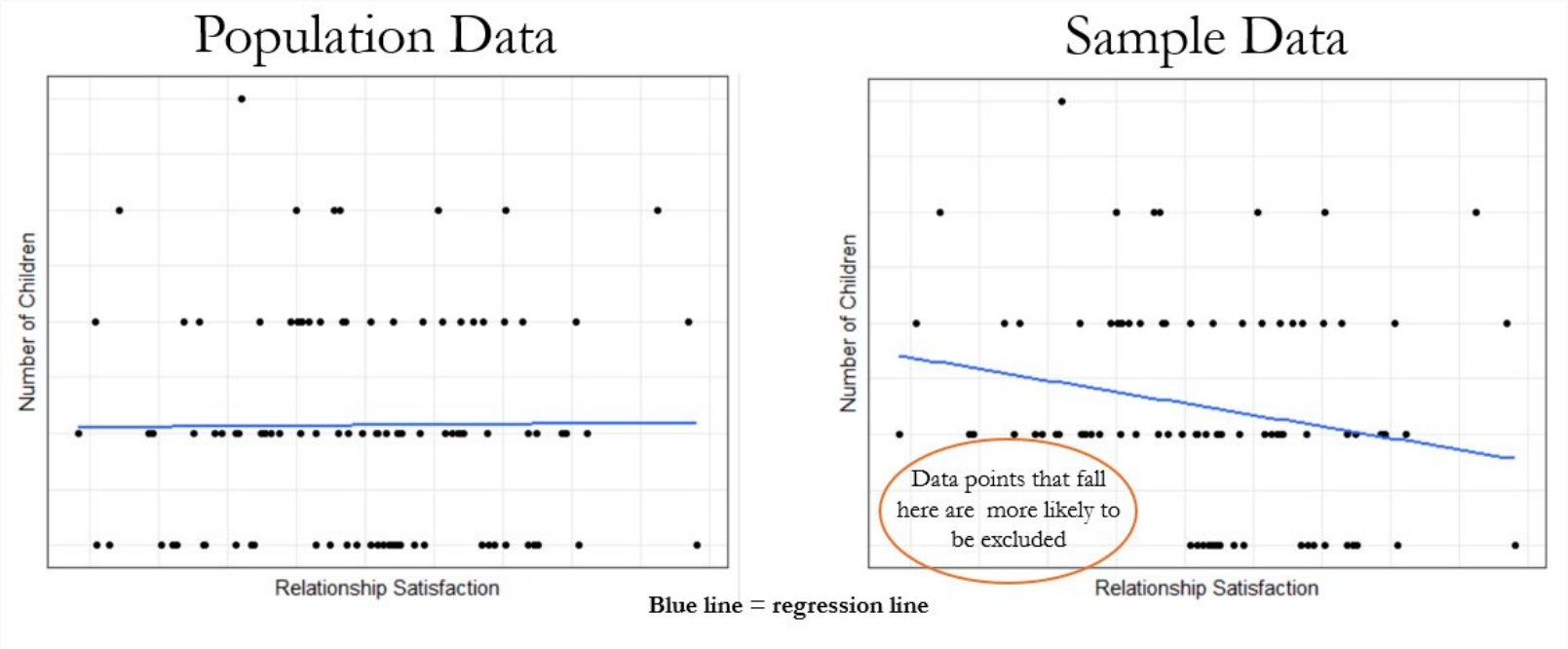
There is collider/selection bias

Selection bias: data only include married couples (not divorced)

And couples with children or happy are less likely to get divorced



Collider induces negative correlation between number of children and happiness



@ AnnaWysocki3

Generalised Linear Models

Logistic regression

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Q: Survival of passengers on the Titanic ~ Class

Read `titanic_long.csv` dataset and fit linear model (survival ~ class).

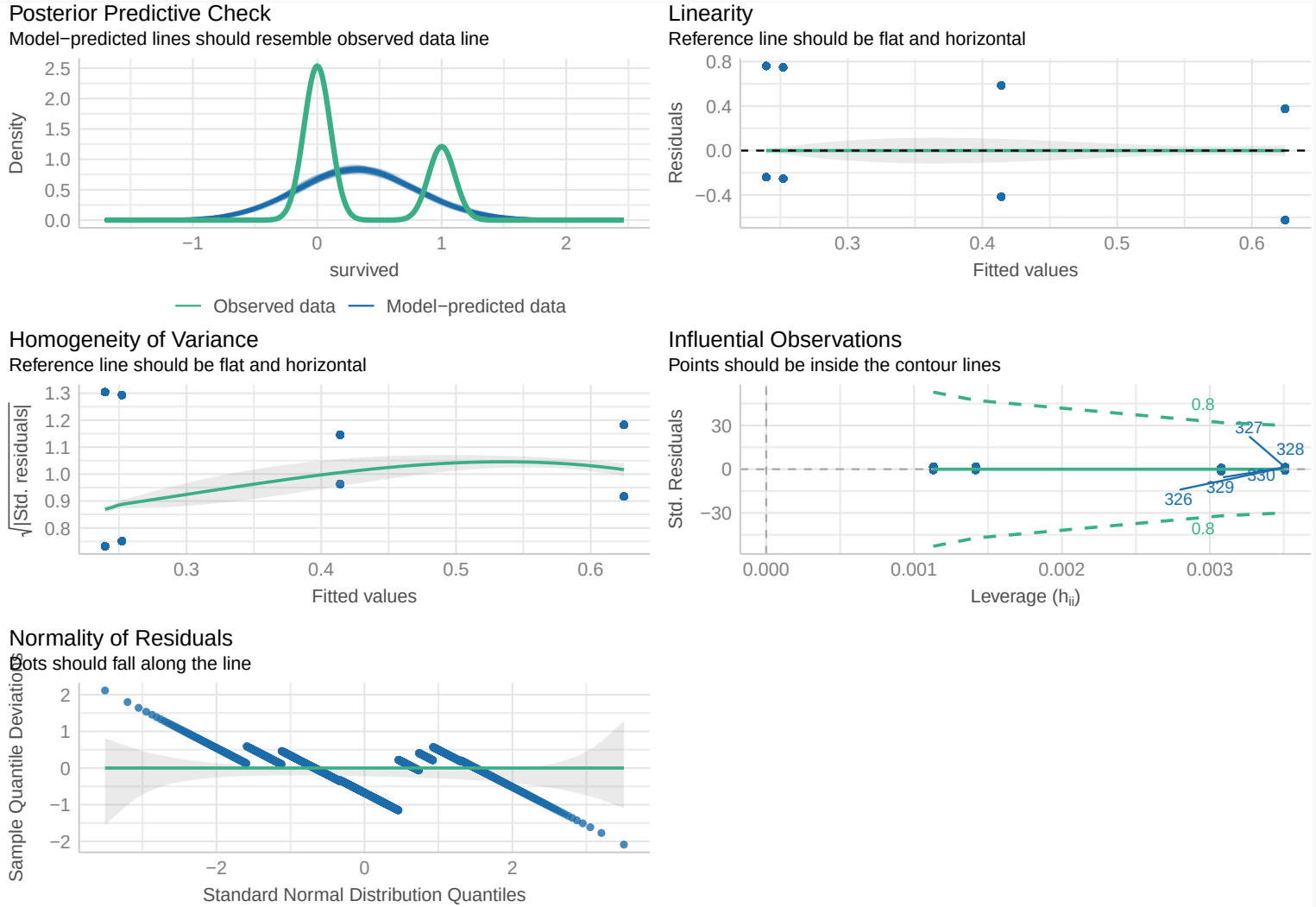
```
  class   age  sex survived
1 first adult male        1
2 first adult male        1
3 first adult male        1
4 first adult male        1
5 first adult male        1
6 first adult male        1
```

Quiz: Did passenger class influence survival?

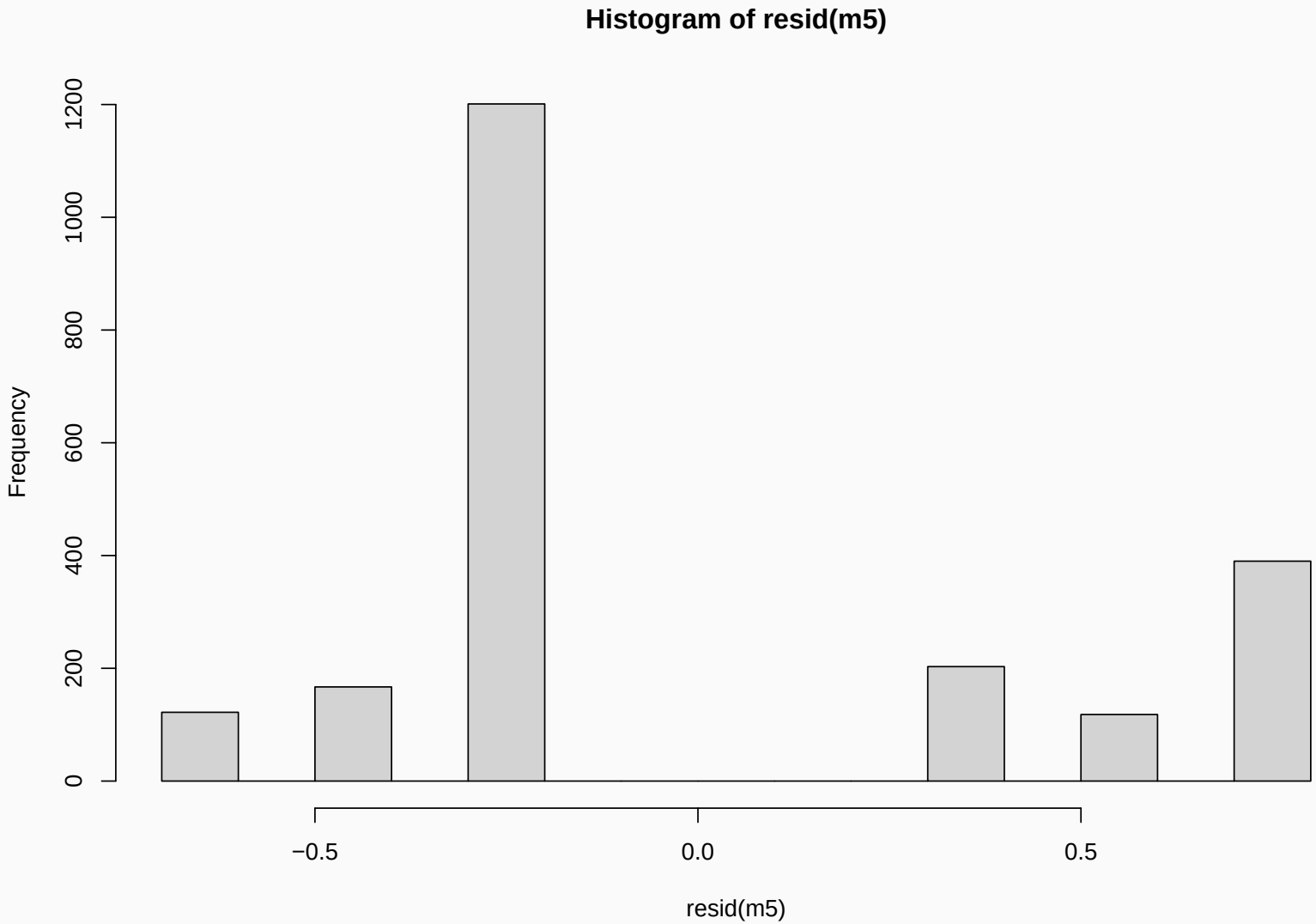
https://pollev.com/franciscorod726

Let’s check linear model:

```
m5 <- lm(survived ~ class, data = titanic)
library('easystats')
check_model(m5)
```



Weird residuals!



What if your residuals are clearly non-normal or variance not constant (heteroscedasticity)?

- Binary variables (0/1)

What if your residuals are clearly non-normal or variance not constant (heteroscedasticity)?

- Binary variables (0/1)
- Counts (0, 1, 2, 3, ...)

What if your residuals are clearly non-normal or variance not constant (heteroscedasticity)?

- Binary variables (0/1)
- Counts (0, 1, 2, 3, ...)
- Categories ('small', 'medium', 'large'...)

What if your residuals are clearly non-normal or variance not constant (heteroscedasticity)?

- Binary variables (0/1)
- Counts (0, 1, 2, 3, ...)
- Categories ('small', 'medium', 'large'...)

- **Generalised Linear Models to the rescue!**

Generalised Linear Models

1. **Response variable** - distribution `family`

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

3. **Link function**

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

3. **Link function**
    - Gaussian: identity

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

3. **Link function**
    - Gaussian: identity
    - Binomial: logit, probit

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

3. **Link function**
    - Gaussian: identity
    - Binomial: logit, probit
    - Poisson: log...

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc

2. **Predictors** (continuous or categorical)

3. **Link function**
    - Gaussian: identity
    - Binomial: logit, probit
    - Poisson: log...
    - See `family`.

The modelling process

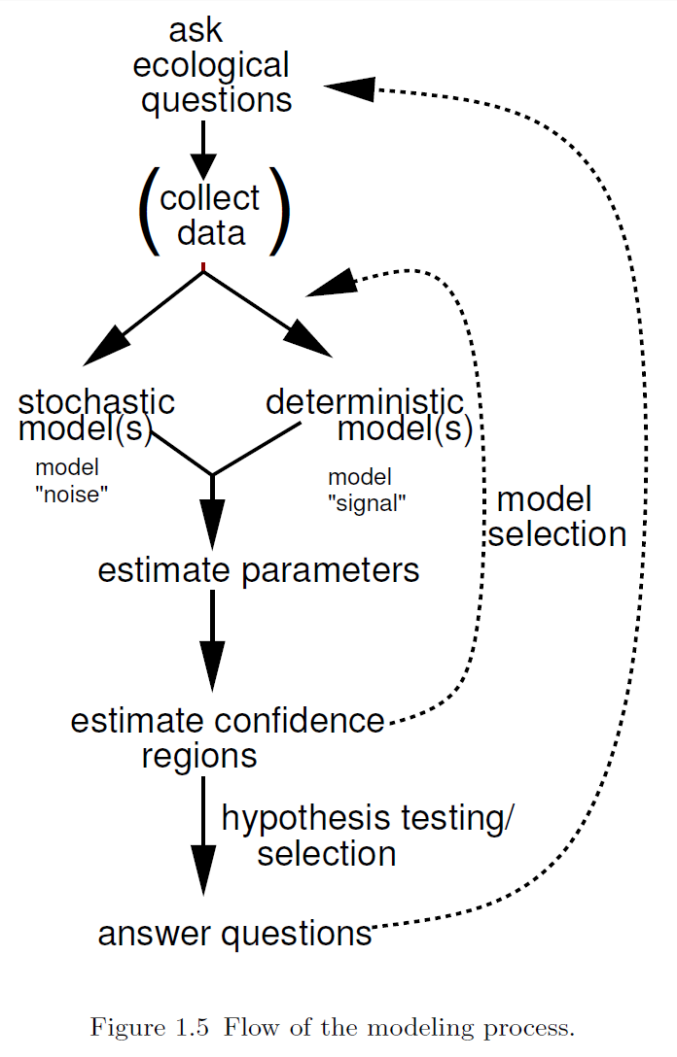


Figure 1.5 Flow of the modeling process.

Bolker 2008

Bernouilli - Binomial distribution (Logistic regression)

Response variable: **`Yes/No`** (e.g. survival, sex, presence/absence)

Canonical link function: **`logit`** (*log odds*), but others possible (see **`family`**)

$$logit(p) = \log\left(\frac{p}{1-p}\right)$$

Then

$$logit(P(alive)) = a + bx$$

$$P(alive) = invlogit(a + bx) = \frac{e^{a+bx}}{1 + e^{a+bx}}$$

Where is the variance?

In a Gaussian GLM

$$y \sim Normal(\mu, \sigma)$$

In a Binomial GLM

$$y \sim Binomial(n, p)$$

n = number of trials

p = probability of success

$$Var(y) = np(1 - p)$$

(maximum variance when **p** around 0.5)

Back to survival of Titanic passengers

How many survived in each class?

```
table(titanic$class, titanic$survived)
```

```
          0   1
  crew   673 212
  first  122 203
  second 167 118
  third  528 178
```

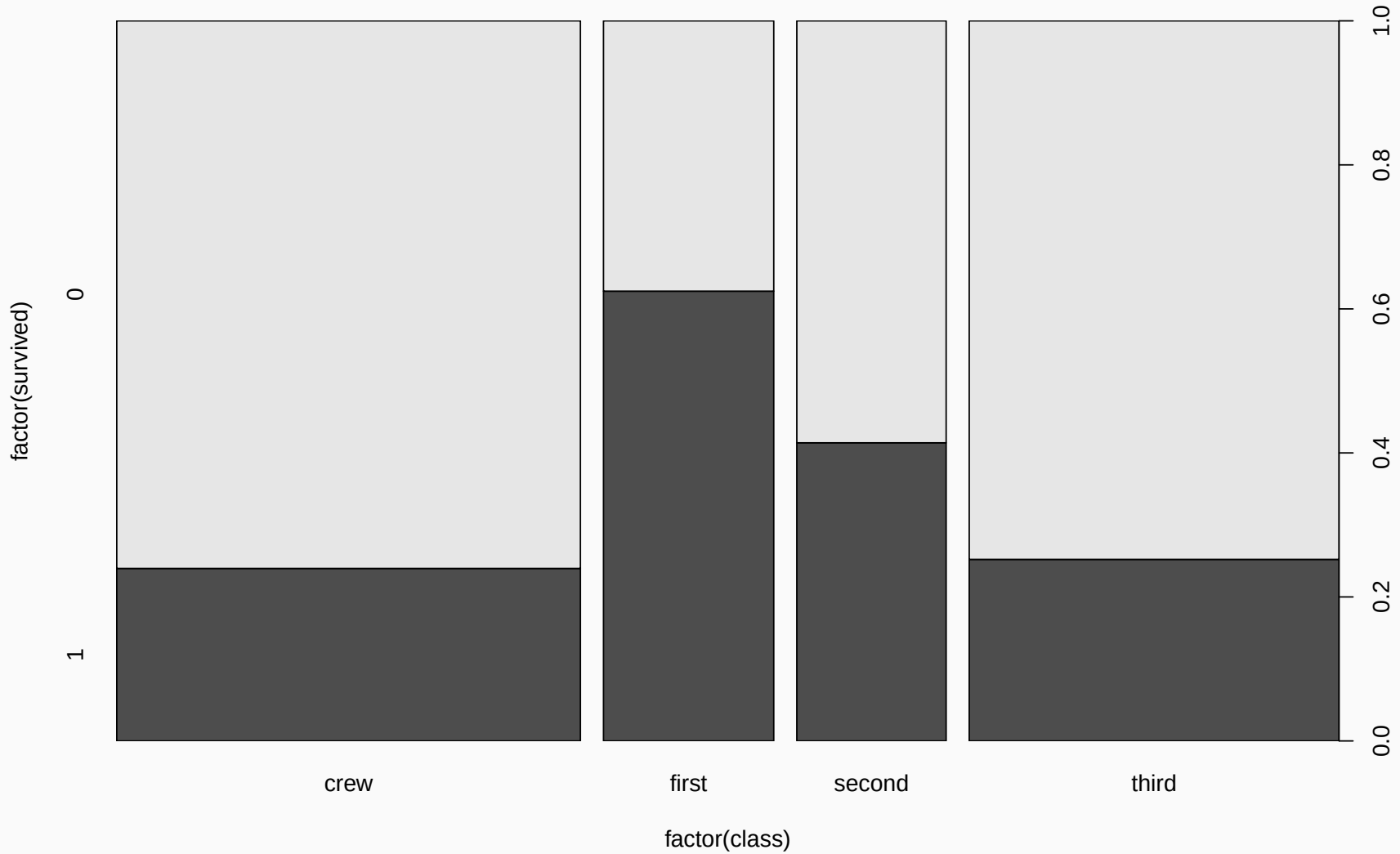
How many survived in each class? (*dplyr*)

```
titanic |>
  group_by(class, survived) |>
  summarise(count = n())
```

```
# A tibble: 8 x 3
# Groups:   class [4]
  class  survived count
  <chr>     <int> <int>
1 crew          0   673
2 crew          1   212
3 first         0   122
4 first         1   203
5 second        0   167
6 second        1   118
7 third         0   528
8 third         1   178
```

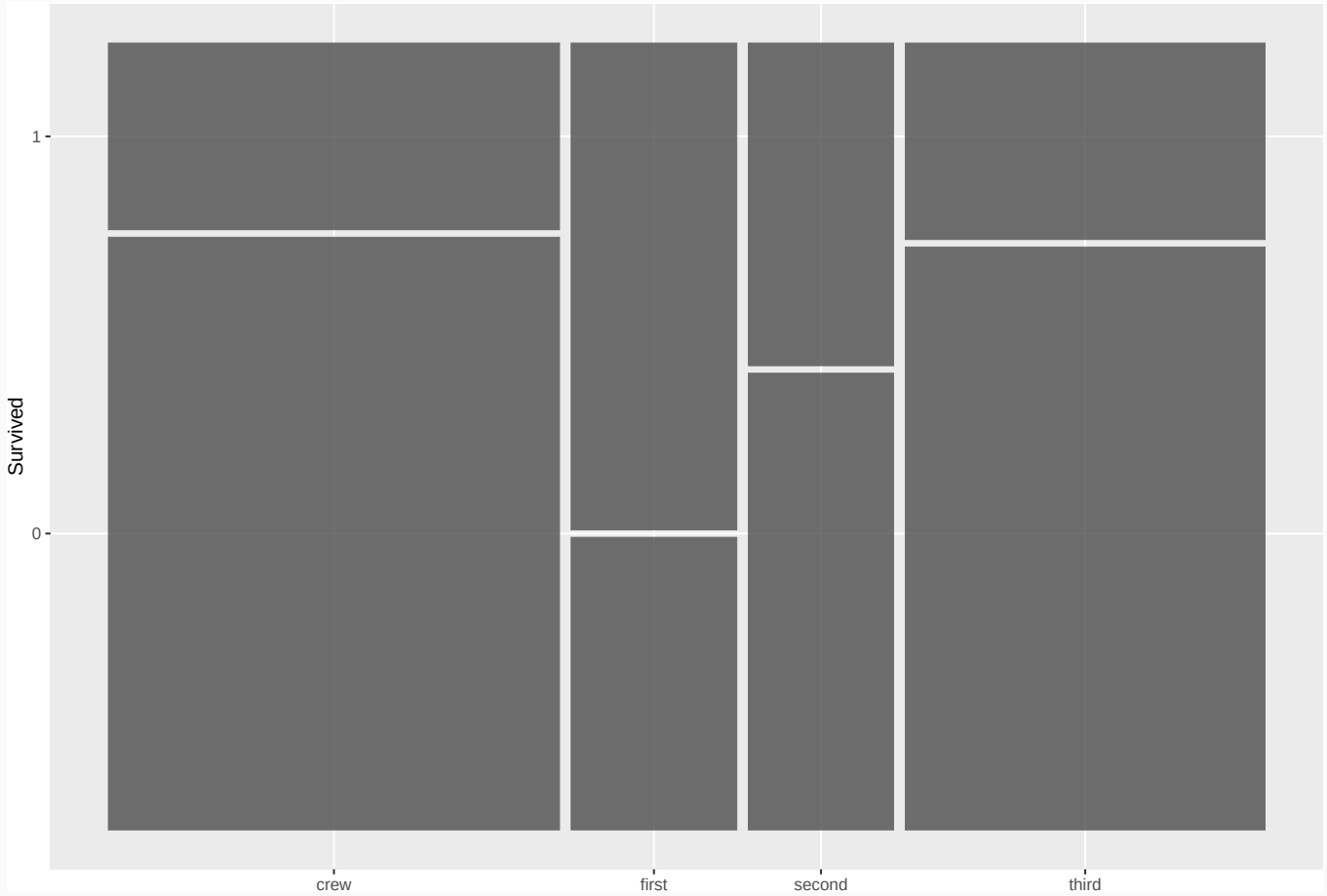
Data visualisation (mosaic plot)

```
plot(factor(survived) ~ factor(class), data = titanic)
```



Mosaic plots (ggplot2)

```
library('ggmosaic')
ggplot(titanic) +
  geom_mosaic(aes(x = product(survived, class))) +
  labs(x = '', y = 'Survived')
```



Fitting GLMs in R: `glm`

```
tit.glm <- glm(survived ~ class,
               data = titanic,
               family = binomial)
```

which corresponds to

$$logit\big(P(survival)_i\big) = a + b \cdot class_i$$

$$logit\big(P(survival)_i\big) = a + b_{first} + c_{second} + d_{third}$$

Interpreting binomial GLM

```r
tit.glm <- glm(survived ~ class, data = titanic, family = binomial)
```

```
Call:
glm(formula = survived ~ class, family = binomial, data = titanic)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.15516    0.07876 -14.667  < 2e-16 ***
classfirst   1.66434    0.13902  11.972  < 2e-16 ***
classsecond  0.80785    0.14375   5.620 1.91e-08 ***
classthird   0.06785    0.11711   0.579    0.562
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2769.5  on 2200  degrees of freedom
Residual deviance: 2588.6  on 2197  degrees of freedom
AIC: 2596.6

Number of Fisher Scoring iterations: 4
```

Binomial GLM estimates are in `logit` scale!

We need to **back-transform** (apply *inverse logit*):

- Manually: `plogis`

Binomial GLM estimates are in `logit` scale!

We need to **back-transform** (apply *inverse logit*):

- Manually: `plogis`
- Automatically: `easystats`, etc.

Interpreting logistic regression output (easystats)

```r
library('easystats')   # 'modelbased' pkg
estimate_means(tit.glm)
```

```
Estimated Marginal Means

class  | Probability |   SE |       95% CI
-----------------------------------------
first  |        0.62 | 0.03 | [0.57, 0.68]
second |        0.41 | 0.03 | [0.36, 0.47]
third  |        0.25 | 0.02 | [0.22, 0.29]
crew   |        0.24 | 0.01 | [0.21, 0.27]

Marginal means estimated at class
```

Analysing differences among factor levels (class)

```
estimate_contrasts(tit.glm)
```

```
Marginal Contrasts Analysis

Level1 | Level2 | Difference |        95% CI |   SE |  df |     z |      p
-------------------------------------------------------------------------
first  |   crew |       1.66 | [ 1.30, 2.03] | 0.14 | Inf | 11.97 | < .001
first  | second |       0.86 | [ 0.42, 1.29] | 0.17 | Inf |  5.16 | < .001
first  |  third |       1.60 | [ 1.22, 1.98] | 0.14 | Inf | 11.11 | < .001
second |   crew |       0.81 | [ 0.43, 1.19] | 0.14 | Inf |  5.62 | < .001
second |  third |       0.74 | [ 0.35, 1.13] | 0.15 | Inf |  4.99 | < .001
third  |   crew |       0.07 | [-0.24, 0.38] | 0.12 | Inf |  0.58 | 0.562

Marginal contrasts estimated at class
p-value adjustment method: Holm (1979)
```

Pseudo R-squared for GLMs

```
library('easystats')   # 'performance' pkg
r2(tit.glm)
```

```
# R2 for Logistic Regression
  Tjur's R2: 0.087
```

But there are caveats (e.g. see here and here)

Presenting model results

```
kable(xtable::xtable(tit.glm), digits = 2)
```

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-1.16	0.08	-14.67	0.00
classfirst	1.66	0.14	11.97	0.00
classsecond	0.81	0.14	5.62	0.00
classthird	0.07	0.12	0.58	0.56

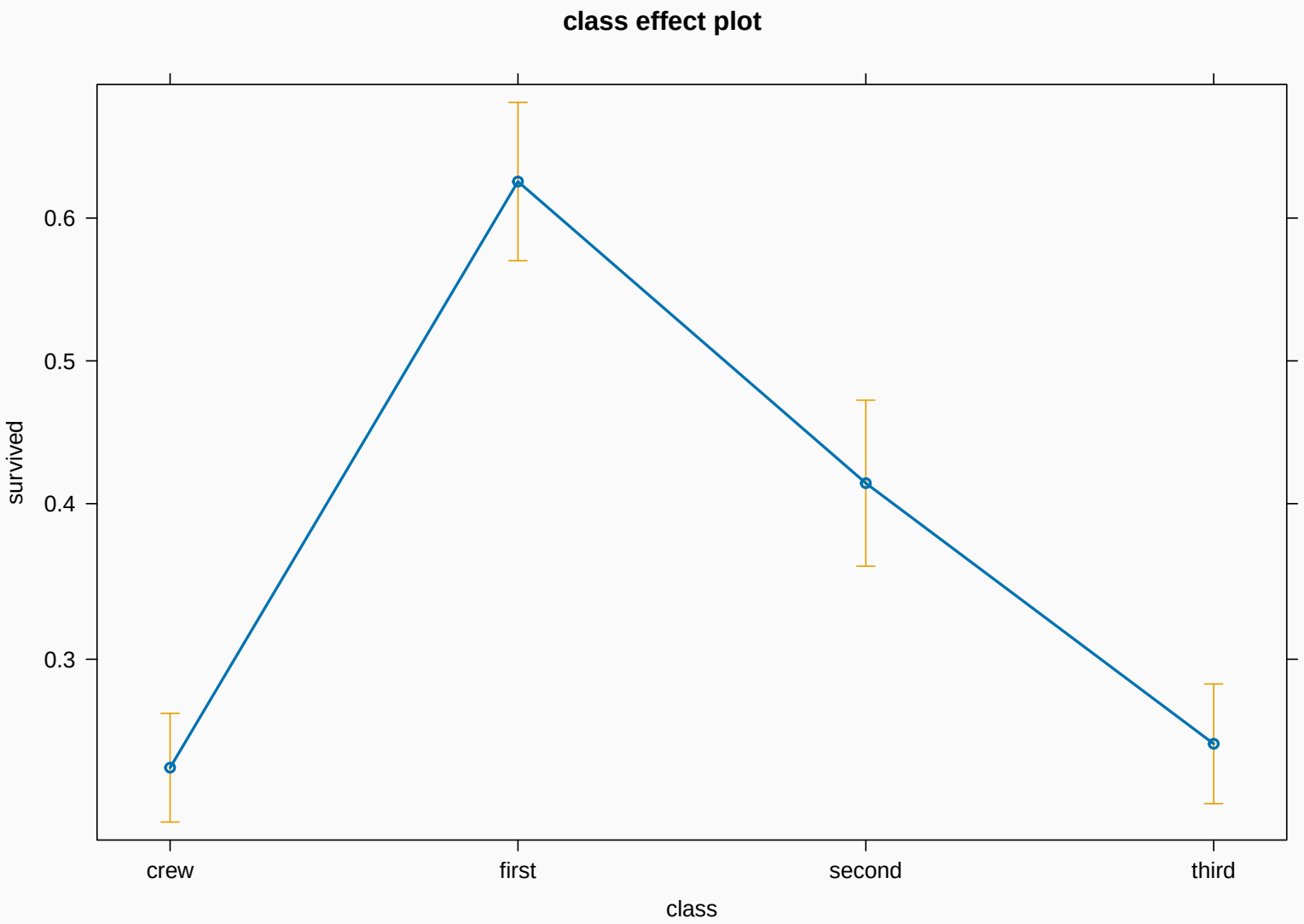
Presenting model results

```
library('modelsummary')
modelsummary(tit.glm, output = 'markdown')
```

	(1)
(Intercept)	-
	1.155
	(0.079)
classfirst	1.664
	(0.139)
classsecond	0.808
	(0.144)
classthird	0.068
	(0.117)
Num.Obs.	2201
AIC	2596.6
BIC	2619.3
Log.Lik.	-

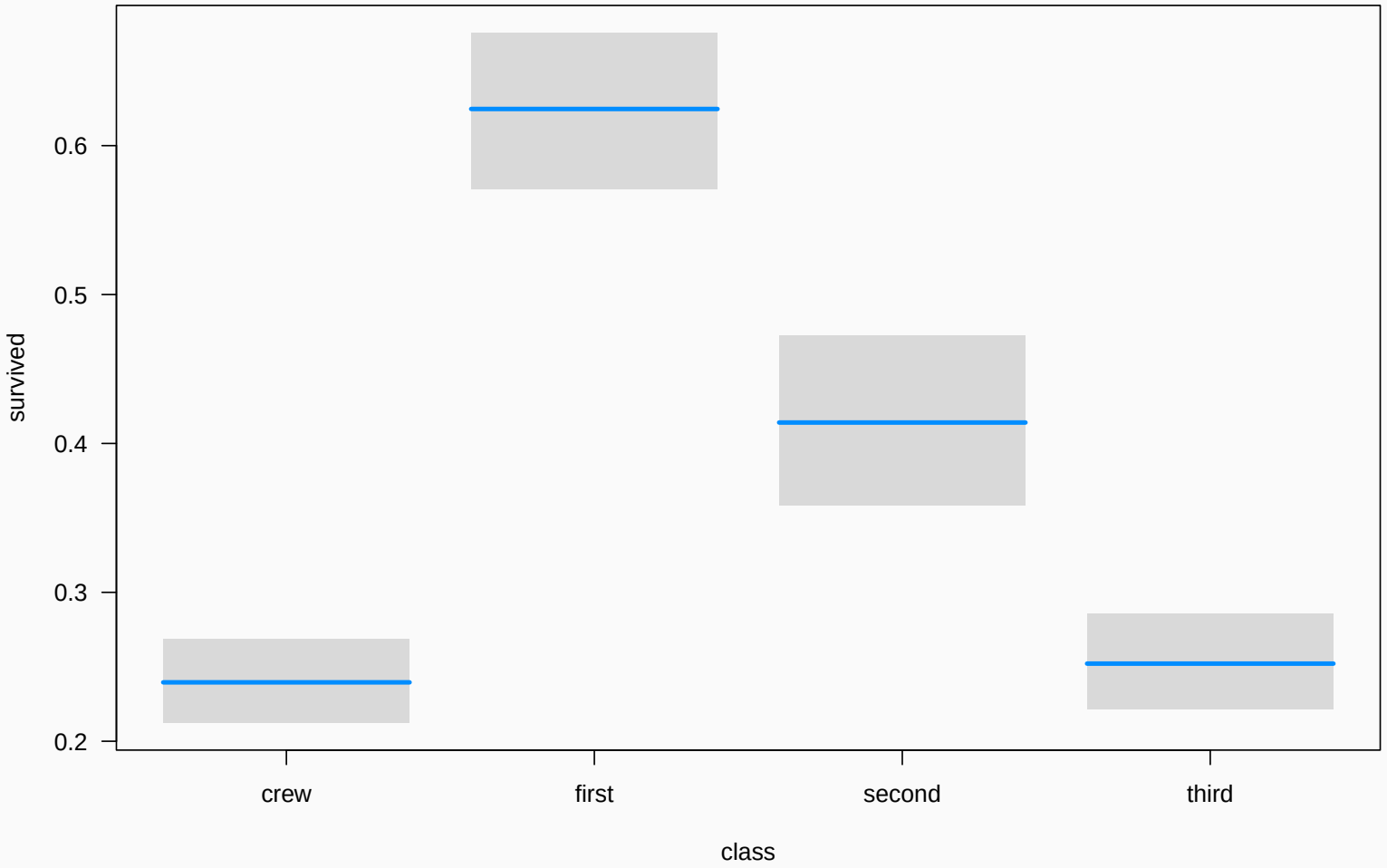
Visualising model: `effects` package

```
plot(allEffects(tit.glm))
```



Visualising model: `visreg` package

```
visreg(tit.glm, scale = 'response', rug = FALSE)
```

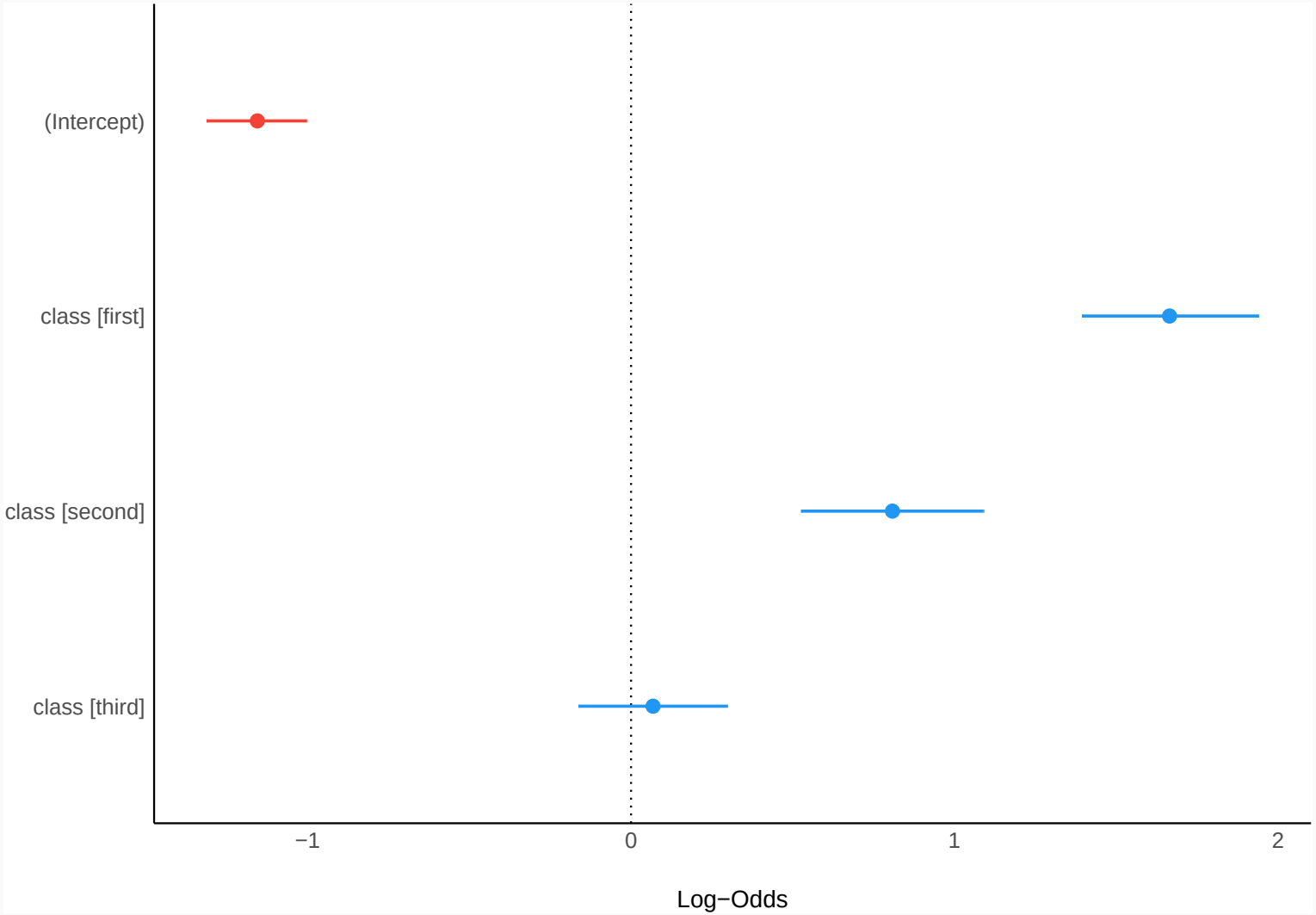


Visualising model: `sjPlot` package

```
sjPlot::plot_model(tit.glm, type = 'eff', terms = 'class')
```

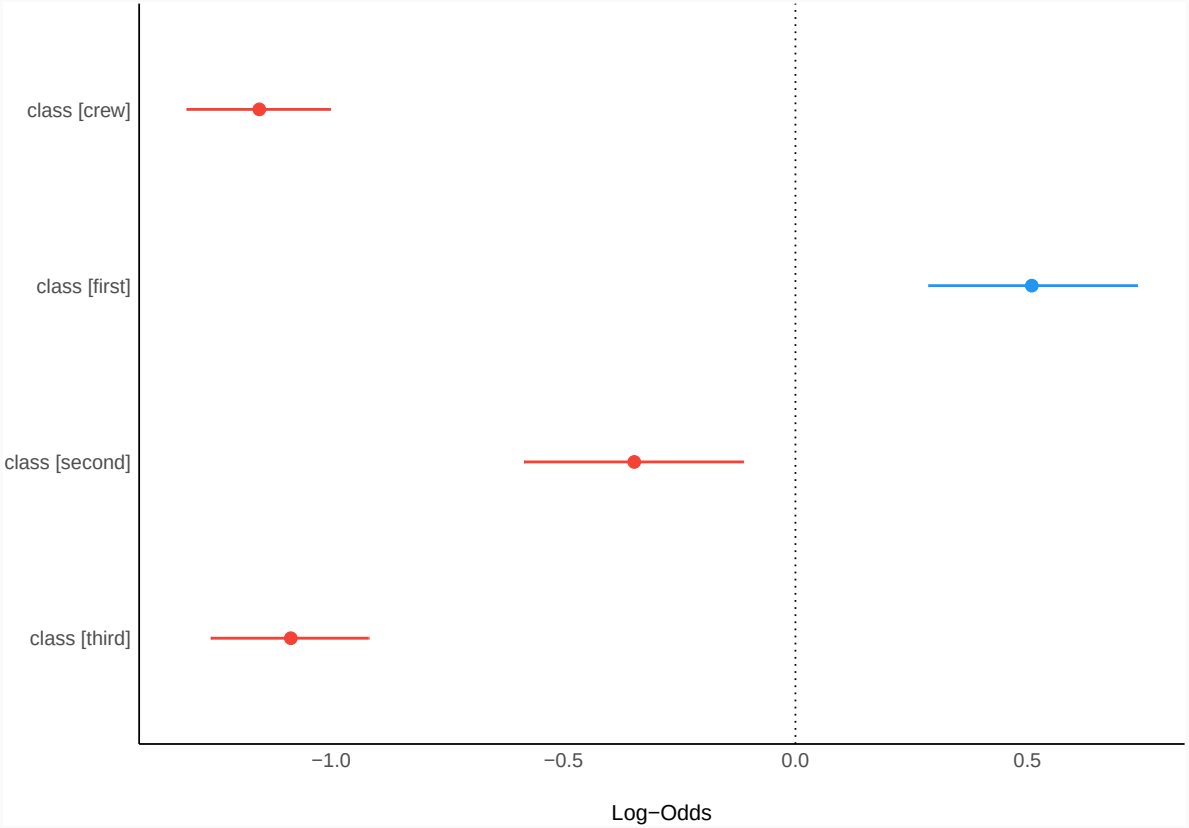
Visualising model: `easystats` (`see` package)

```
plot(parameters(tit.glm), show_intercept = TRUE)
```



Model without intercept

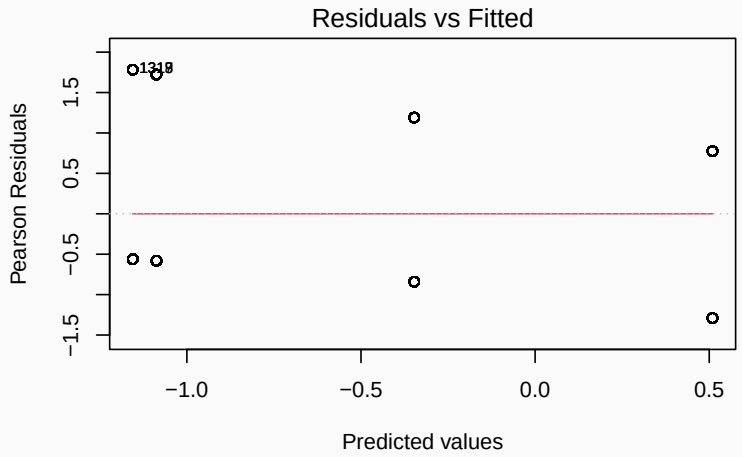
```
no.intercept <- glm(survived ~ class - 1, family = binomial, data =
plot(parameters(no.intercept))
```

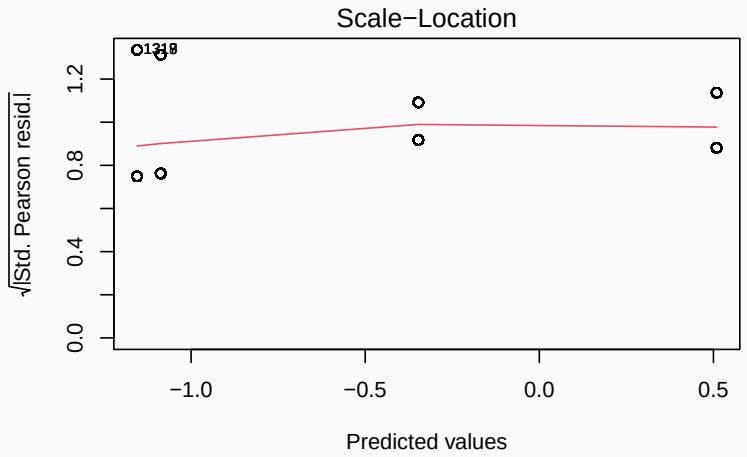


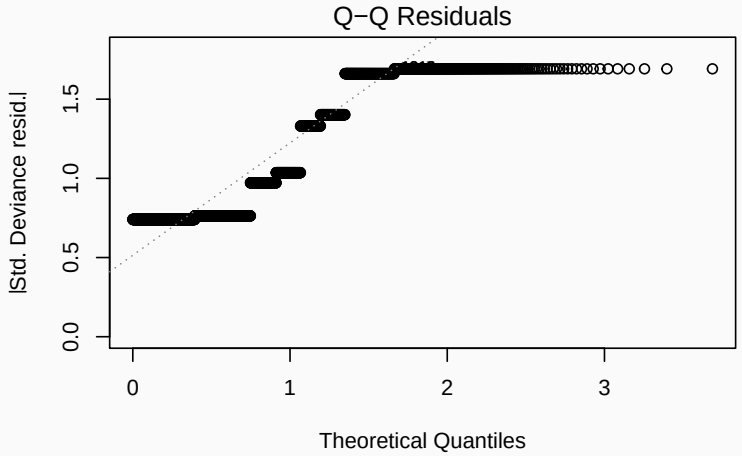
Model checking

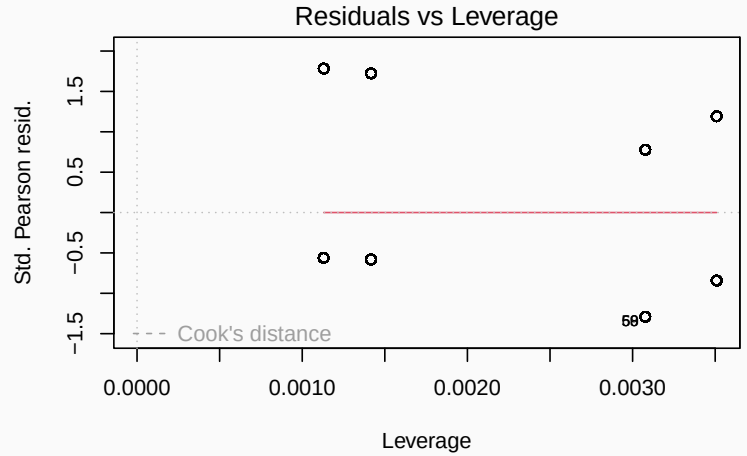
`plot(model)` not very useful with binomial GLM

```
plot(tit.glm)
```





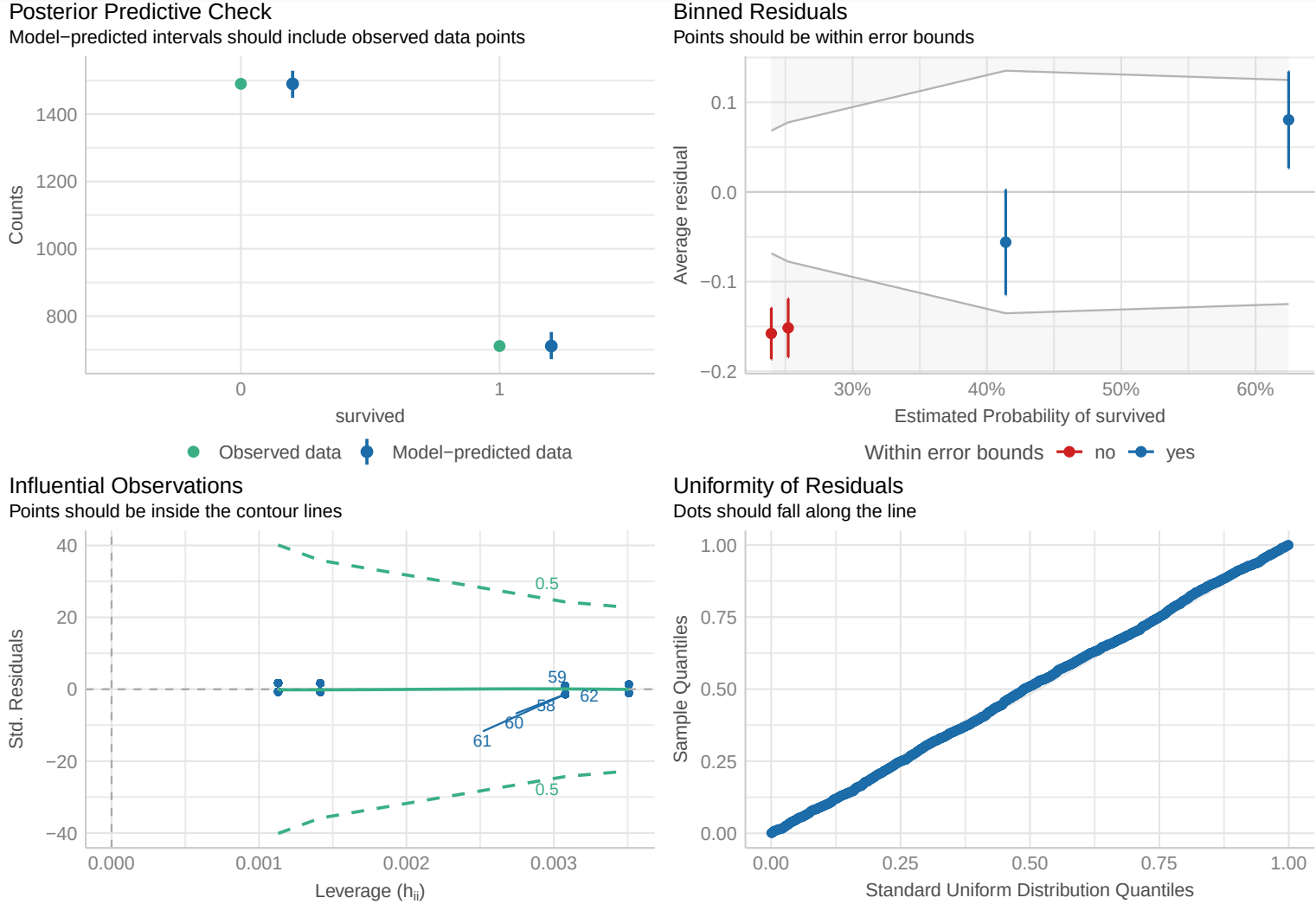





```
null device
          1
```

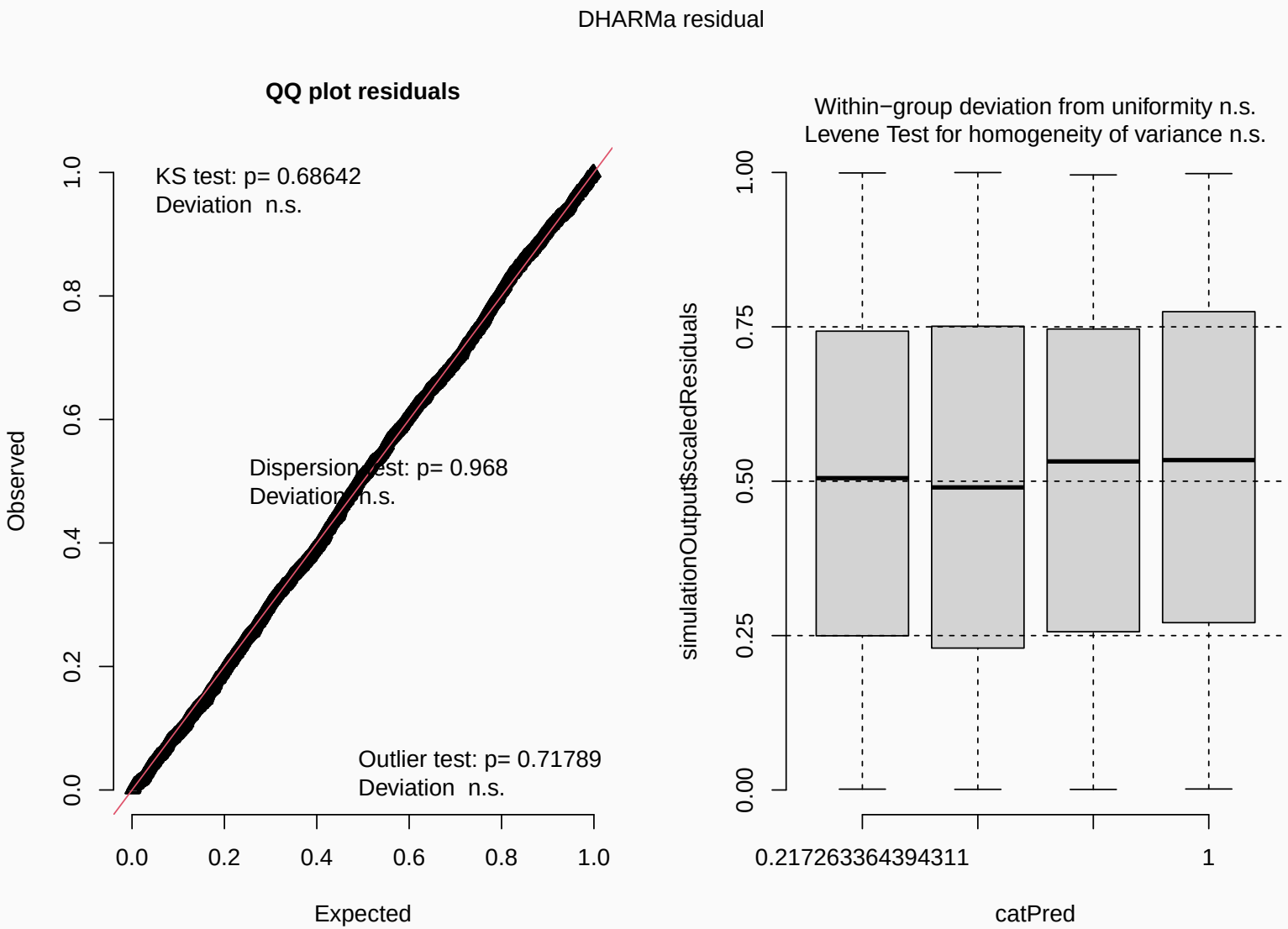
check_model (easystats)

```
check_model(tit.glm)
```



Residual diagnostics with DHARMa

```
library('DHARMa')
simulateResiduals(tit.glm, plot = TRUE)
```

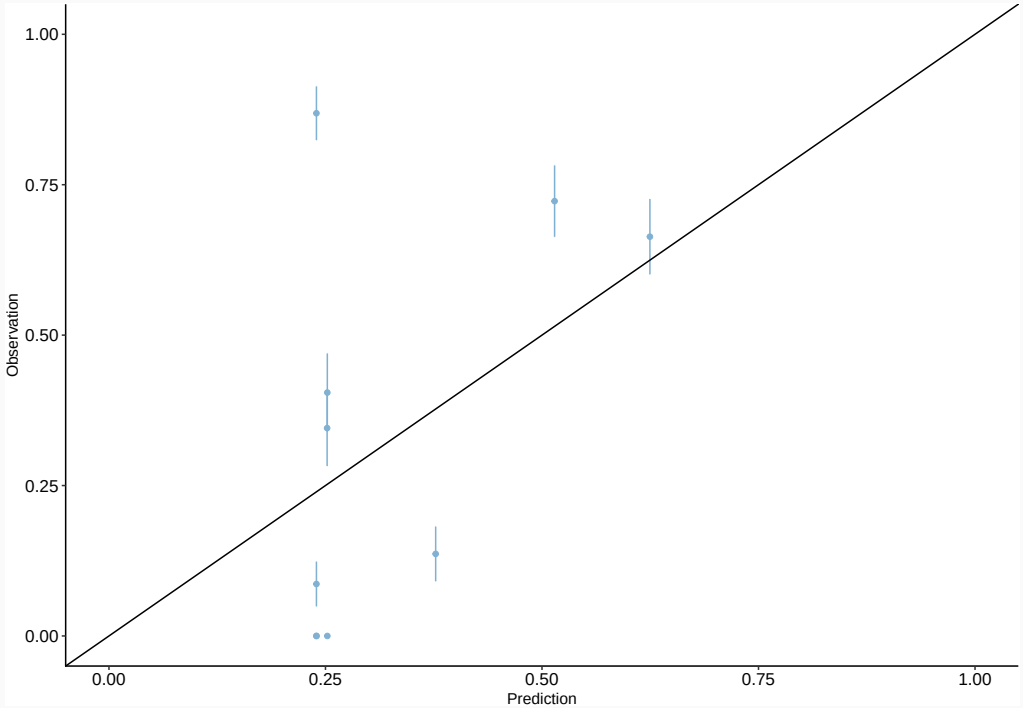


Calibration plot

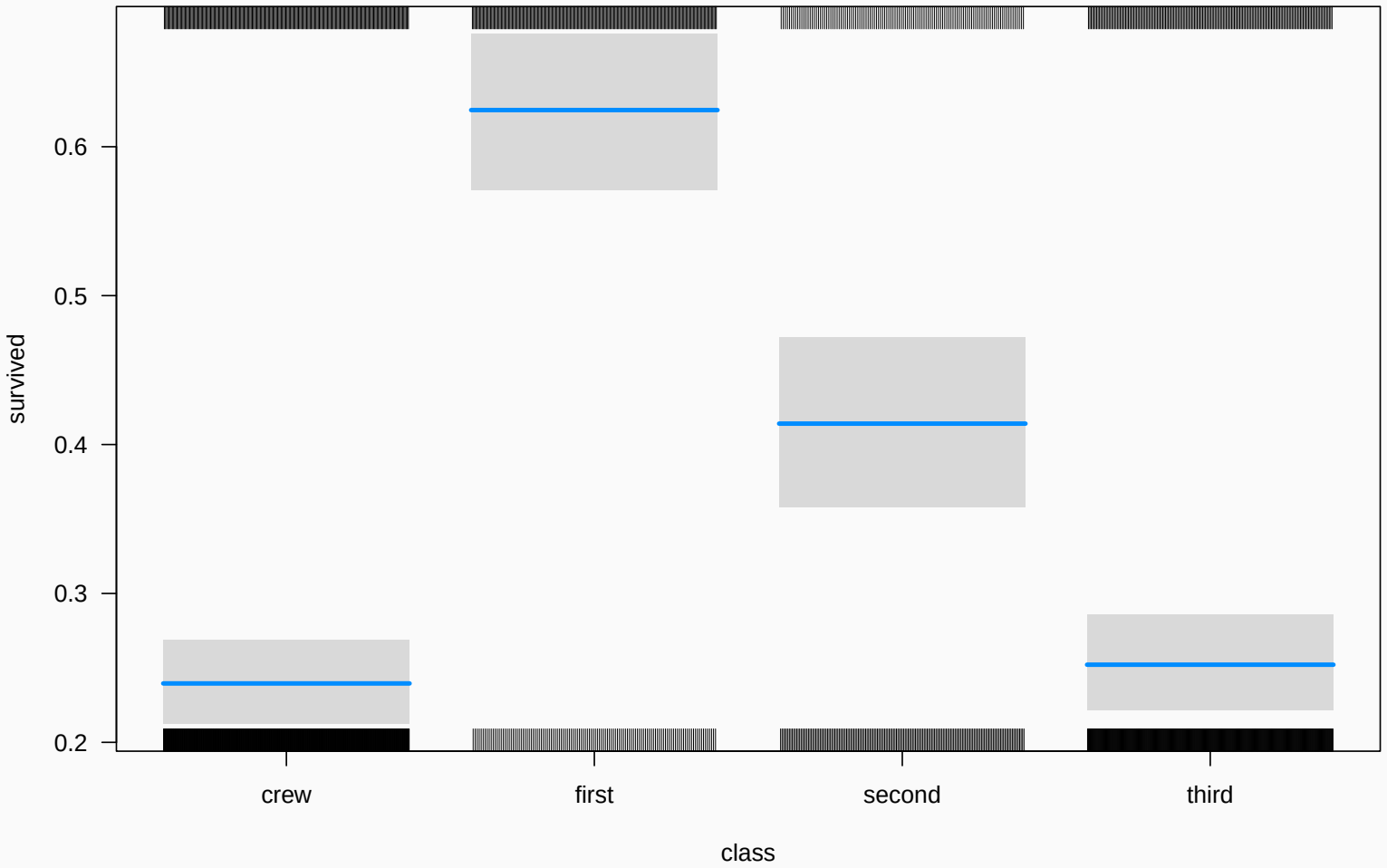
Compares predicted vs observed probabilities (grouped by quantiles)

```
library('predtools')
titanic$surv.pred <- predict(tit.glm, type = 'response')
calibration_plot(data = titanic, obs = 'survived', pred = 'surv.pred',
                 x_lim = c(0,1), y_lim = c(0,1))
```

```
$calibration_plot
```



Passenger class was important, but lots of unexplained variation



The goal is not to test whether the model's assumptions are 'true', because all models are false.

Rather, the goal is to assess exactly **how the model fails to describe the data**, as a path towards **model comprehension, revision, and improvement**.

Richard McElreath. *Statistical Rethinking*

Recapitulating

1. Visualise data

Recapitulating

1. **Visualise data**

2. **Fit model**: `glm`. Don't forget to specify `family`!

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5. **Plot model**: `visreg`, ...

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3. **Examine model**: `summary`

4. **Back-transform parameters** from *logit* into probability scale (`estimate_means`)

5. **Plot model**: `visreg`, ...

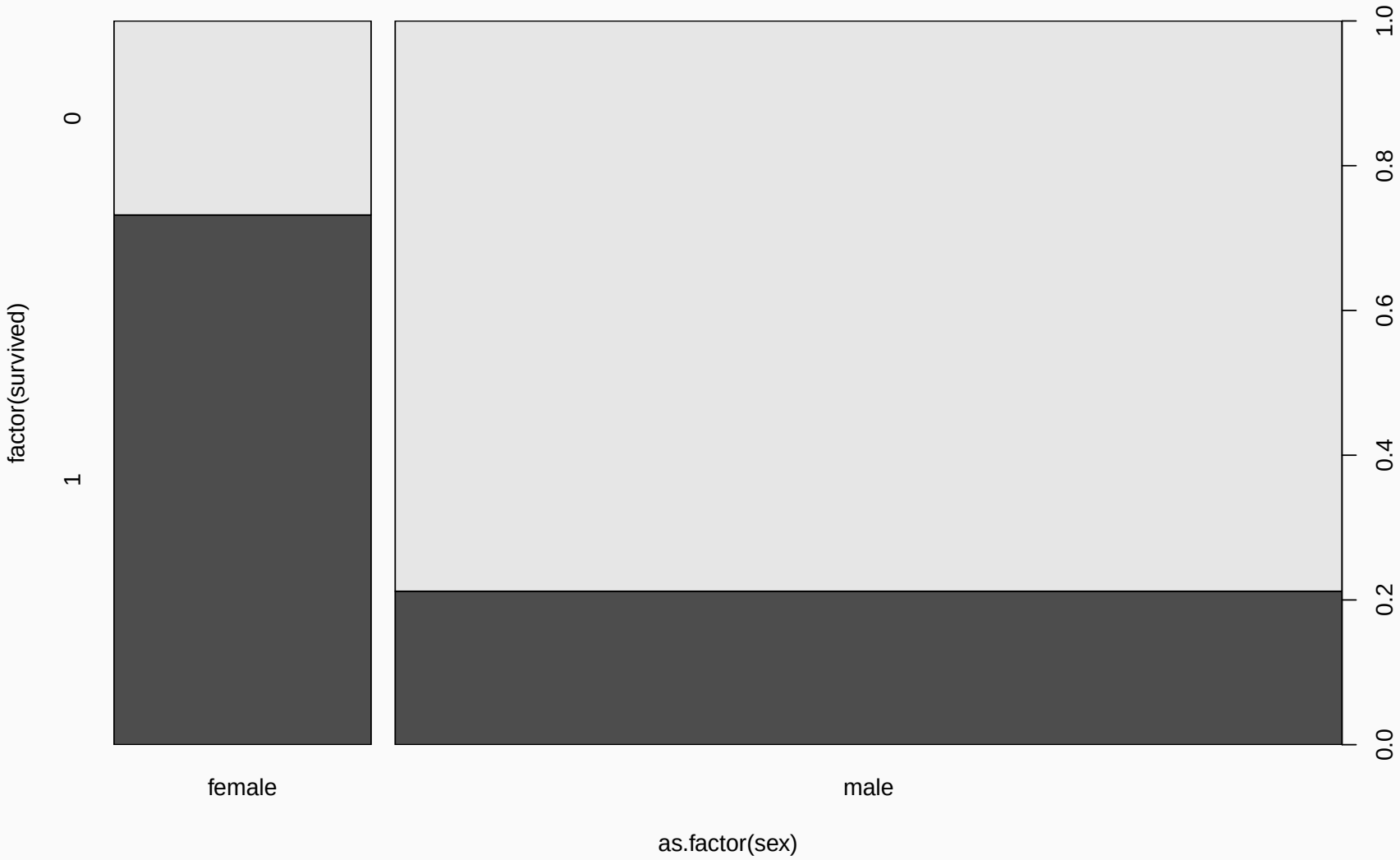
6. **Check model**: `check_model`, `DHARMa::simulateResiduals`, `calibration_plot`

Q: Did men have higher survival than women?

Quiz

https://pollev.com/franciscorod726

First, visualise data



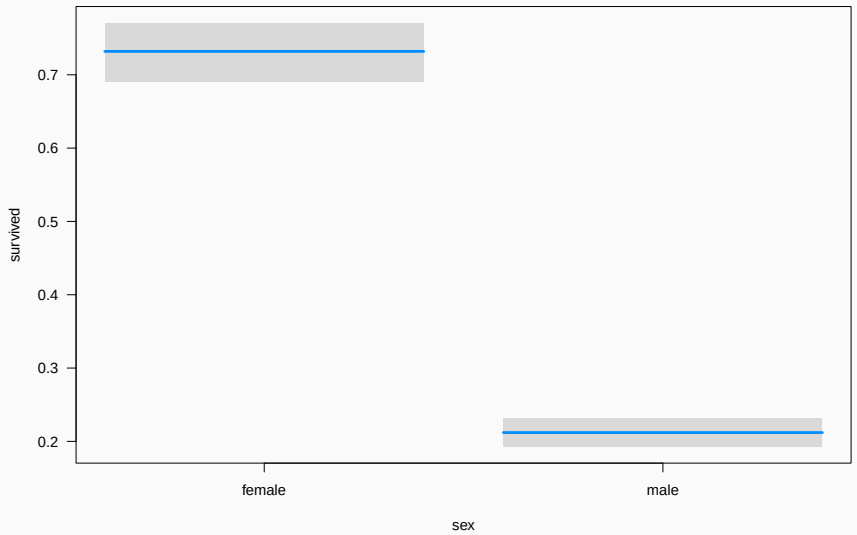
Fit model

```
Call:
glm(formula = survived ~ sex, family = binomial, data = titanic)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.0044     0.1041   9.645   <2e-16 ***
sexmale      -2.3172     0.1196 -19.376   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2769.5  on 2200  degrees of freedom
Residual deviance: 2335.0  on 2199  degrees of freedom
AIC: 2339

Number of Fisher Scoring iterations: 4
```

Model interpretation

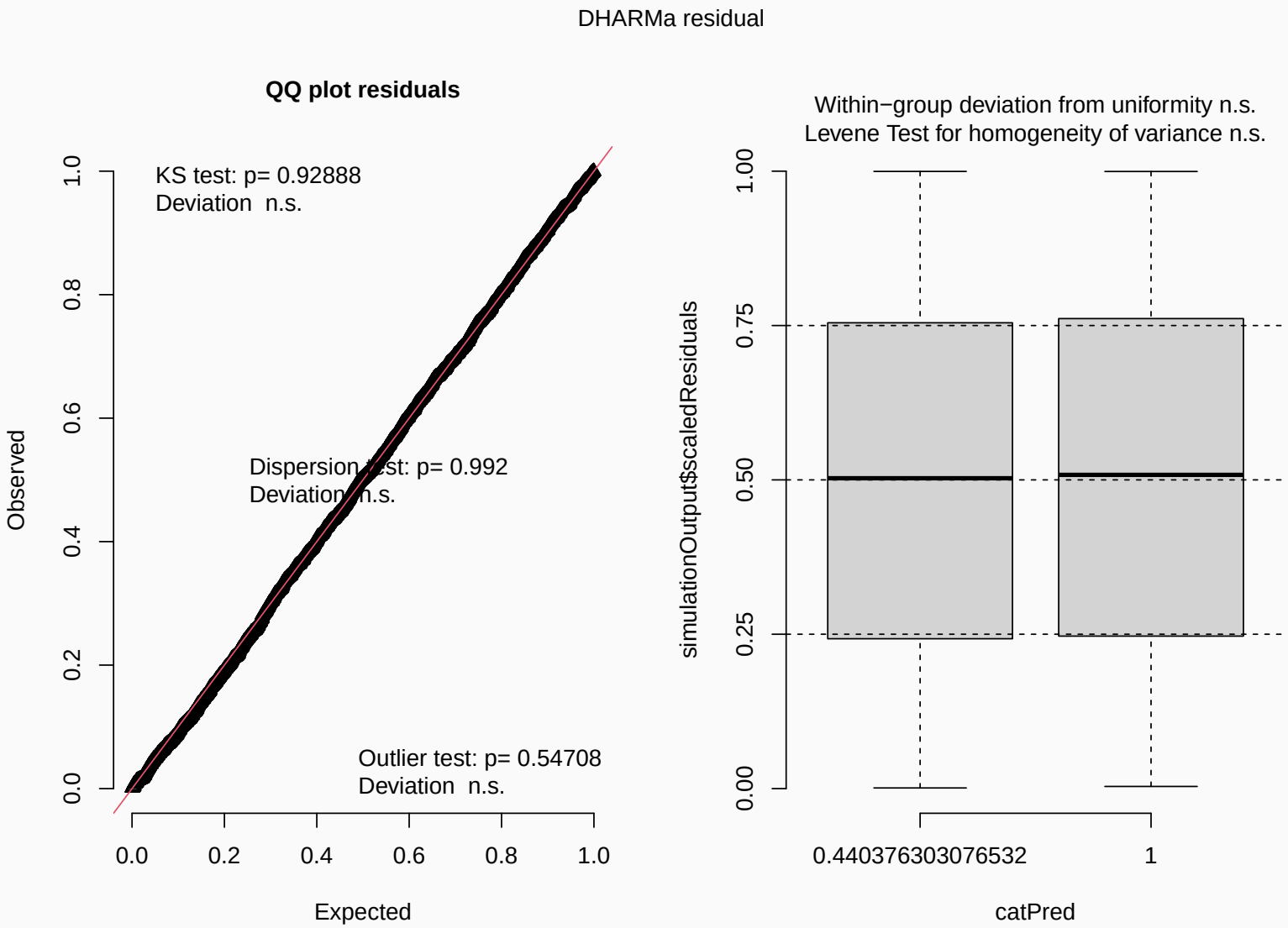
```
estimate_means(tit.sex)
```

```
Estimated Marginal Means

sex    | Probability |       SE |       95% CI
-------------------------------------------------
male   |        0.21 | 9.82e-03 | [0.19, 0.23]
female |        0.73 |     0.02 | [0.69, 0.77]

Marginal means estimated at sex
```



Model checking

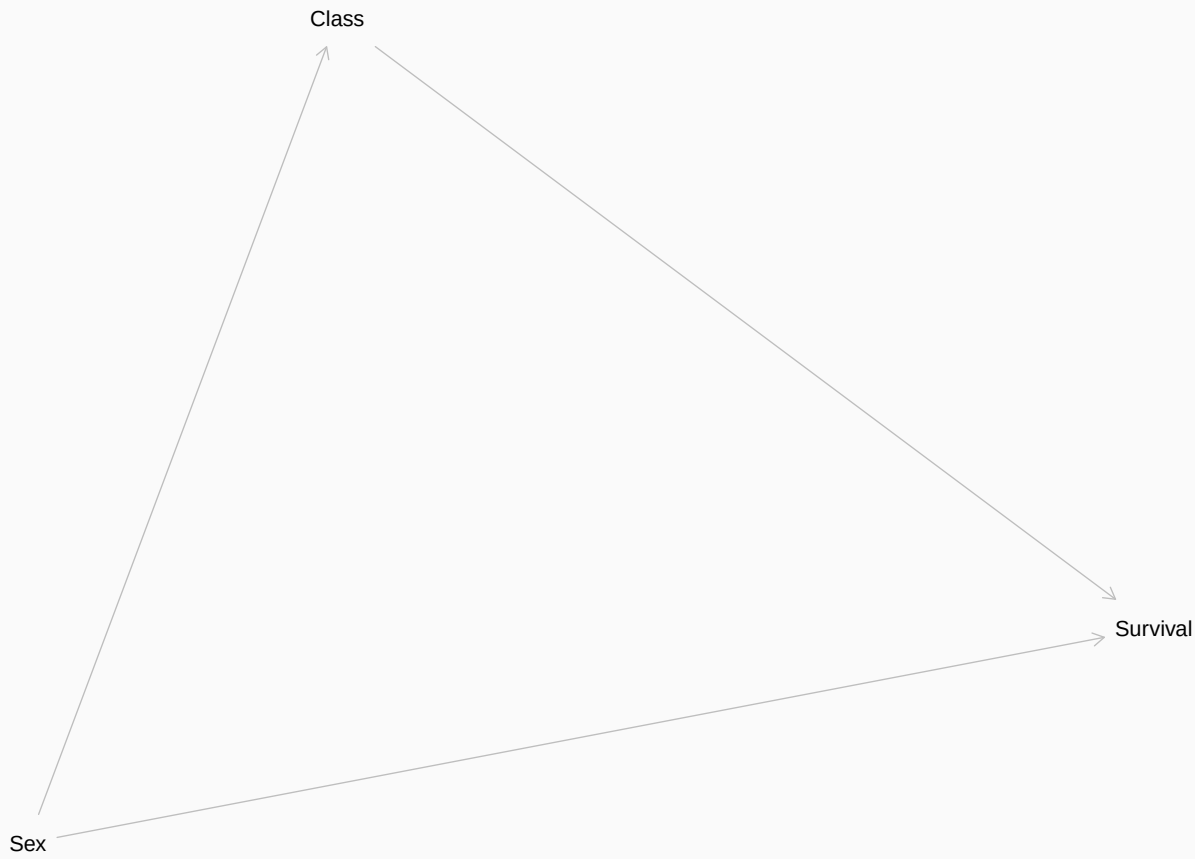
```
simulateResiduals(tit.sex, plot = TRUE)
```



Q: Did women have higher survival because they travelled more in first class?

Did women have higher survival because they travelled more in first class?

Sex is a confounder



Let’s look at the data

```
table(titanic$class, titanic$survived, titanic$sex)
```

```
, ,  = female


          0   1
  crew    3  20
  first   4 141
  second 13  93
  third 106  90

, ,  = male


          0   1
  crew  670 192
  first 118  62
  second 154  25
  third 422  88
```

Quiz

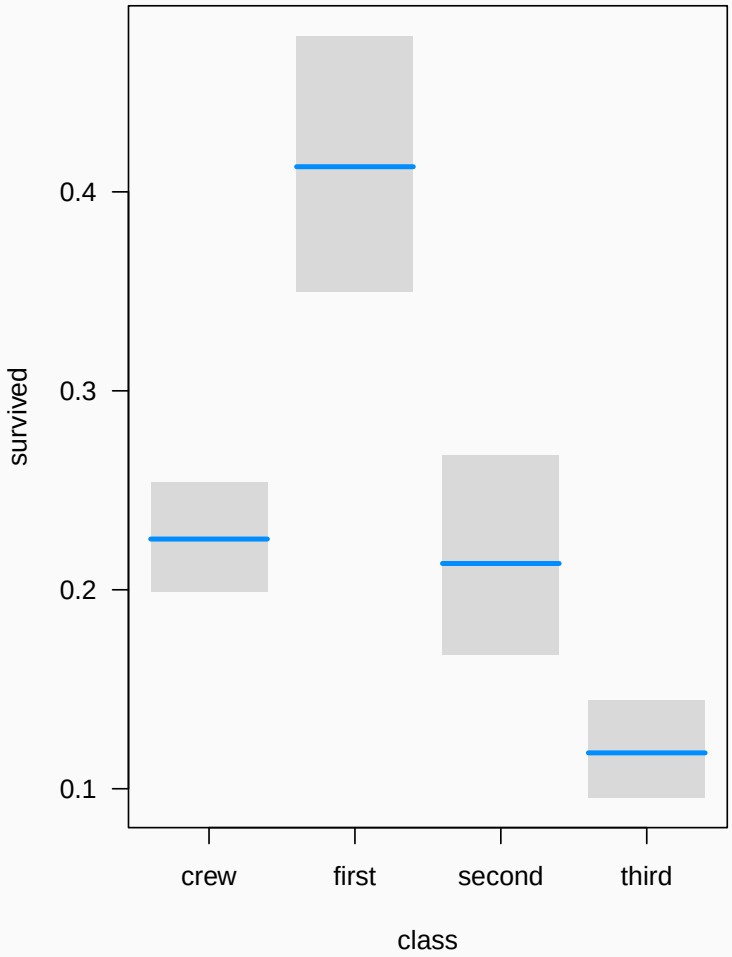
https://pollev.com/franciscorod726

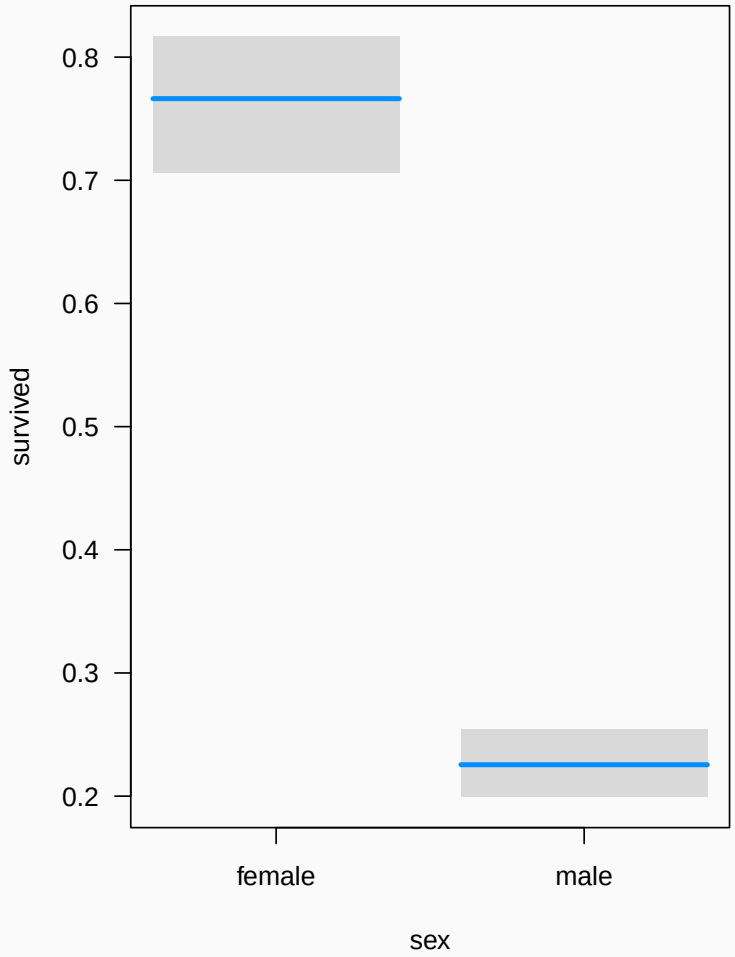
Fit additive model with both factors

```
Call:
glm(formula = survived ~ class + sex, family = binomial, data = titanic)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.18740    0.15747   7.541 4.68e-14 ***
classfirst   0.88081    0.15697   5.611 2.01e-08 ***
classsecond -0.07178    0.17093  -0.420    0.675
classthird  -0.77742    0.14231  -5.463 4.69e-08 ***
sexmale     -2.42133    0.13909 -17.408  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2769.5  on 2200  degrees of freedom
Residual deviance: 2228.9  on 2196  degrees of freedom
AIC: 2238.9

Number of Fisher Scoring iterations: 4
```

Plot additive model

```
visreg(tit.sex.class.add, scale = 'response', rug = FALSE)
```






```
null device
          1
```

Fit model with the interaction of both factors

```
Call:
glm(formula = survived ~ class * sex, family = binomial, data = titanic)

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)         1.89712    0.61914   3.064  0.00218 **
classfirst          1.66535    0.80026   2.081  0.03743 *
classsecond         0.07053    0.68630   0.103  0.91815
classthird         -2.06075    0.63551  -3.243  0.00118 **
sexmale            -3.14690    0.62453  -5.039 4.68e-07 ***
classfirst:sexmale -1.05911    0.81959  -1.292  0.19627
classsecond:sexmale -0.63882    0.72402  -0.882  0.37760
classthird:sexmale  1.74286    0.65139   2.676  0.00746 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2769.5  on 2200  degrees of freedom
Residual deviance: 2163.7  on 2193  degrees of freedom
AIC: 2179.7
```

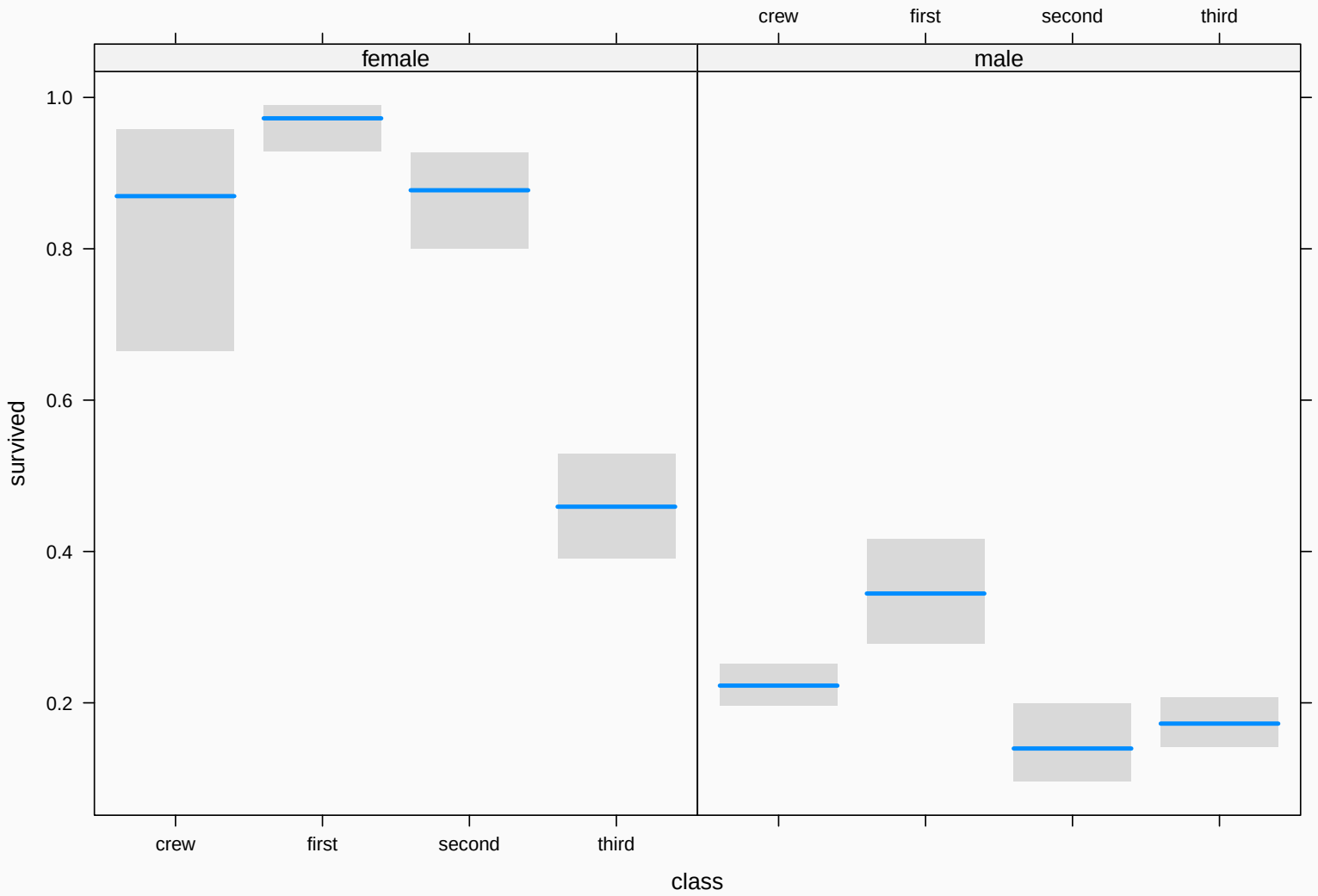
Women had higher survival than men, even within the same class

```
estimate_means(tit.sex.class.int)
```

```
Estimated Marginal Means

class  |    sex | Probability |   SE |       95% CI
-----------------------------------------------------
first  |   male |        0.34 | 0.04 | [0.28, 0.42]
second |   male |        0.14 | 0.03 | [0.10, 0.20]
third  |   male |        0.17 | 0.02 | [0.14, 0.21]
crew   |   male |        0.22 | 0.01 | [0.20, 0.25]
first  | female |        0.97 | 0.01 | [0.93, 0.99]
second | female |        0.88 | 0.03 | [0.80, 0.93]
third  | female |        0.46 | 0.04 | [0.39, 0.53]
crew   | female |        0.87 | 0.07 | [0.66, 0.96]

Marginal means estimated at class
```

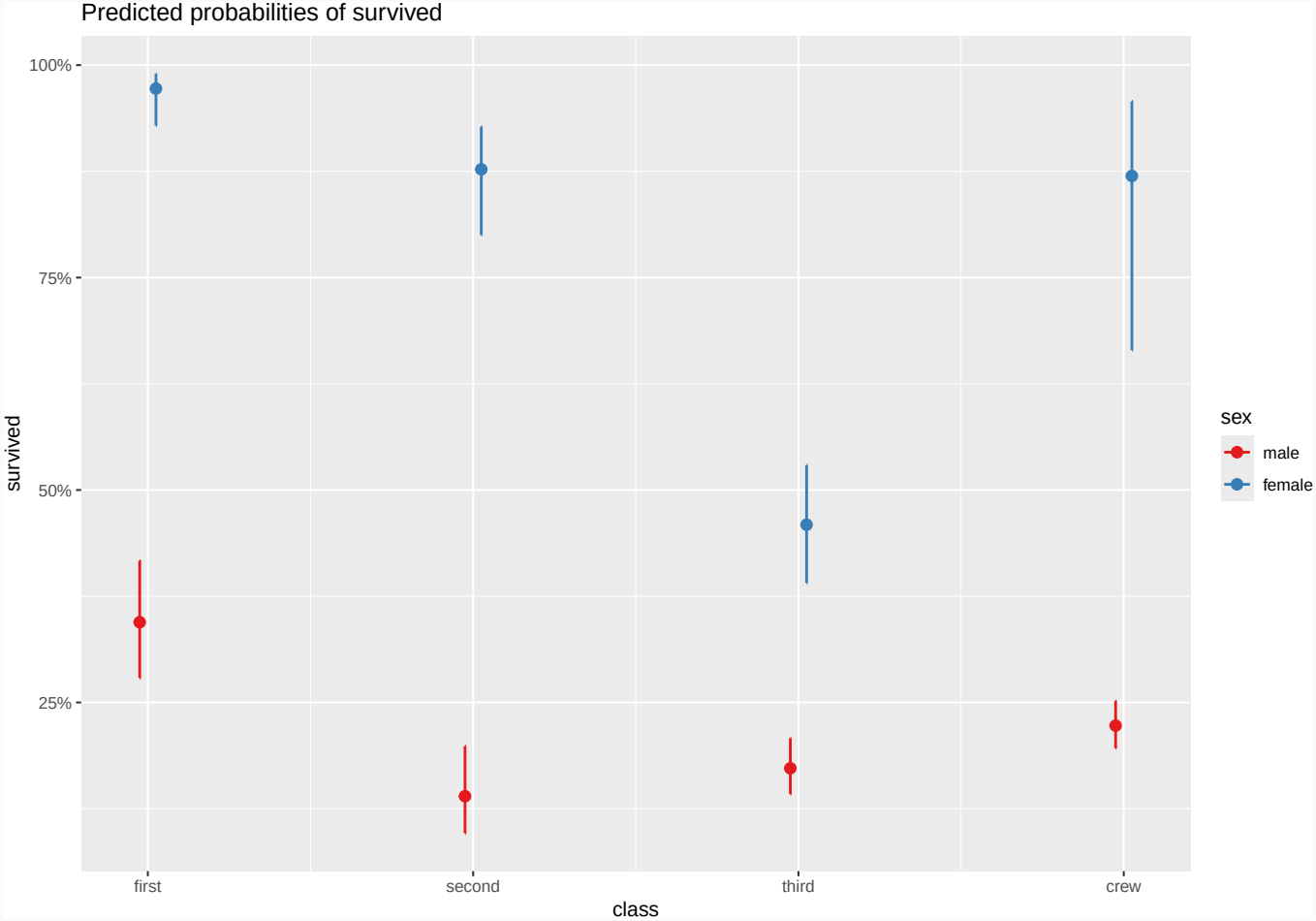
Women had higher survival than men, even within the same class

```
visreg(tit.sex.class.int, by = 'sex', xvar = 'class', scale = 'response', rug = FAL
```



Visualising model (`sjPlot`)

```
library('sjPlot')
plot_model(tit.sex.class.int, type = 'int')
```



Comparing models

```
library('easystats')   # 'performance' pkg
compare_performance(tit.sex.class.add, tit.sex.class.int)
```

```
# Comparison of Model Performance Indices

Name              | Model |  AIC (weights) | AICc (weights) |  BIC (weights)
-------------------------------------------------------------------------------
tit.sex.class.add |   glm | 2238.9 (<.001) | 2238.9 (<.001) | 2267.4 (<.001)
tit.sex.class.int |   glm | 2179.7 (>.999) | 2179.8 (>.999) | 2225.3 (>.999)

Name              | Tjur's R2 |  RMSE | Sigma | Log_loss | Score_log
-----------------------------------------------------------------------
tit.sex.class.add |     0.248 | 0.405 | 1.000 |    0.506 |      -Inf
tit.sex.class.int |     0.271 | 0.399 | 1.000 |    0.492 |      -Inf

Name              | Score_spherical |   PCP
-----------------------------------------
tit.sex.class.add |           0.004 | 0.671
tit.sex.class.int |           0.002 | 0.681
```

Comparing parameters

```
compare_parameters(tit.sex.class.add, tit.sex.class.int)
```

Parameter	tit.sex.class.add	tit.sex.class.int
(Intercept)	1.19 (0.88, 1.50)	1.90 (0.68, 3.11)
class [first]	0.88 (0.57, 1.19)	1.67 (0.10, 3.23)
class [second]	-0.07 (-0.41, 0.26)	0.07 (-1.27, 1.42)
class [third]	-0.78 (-1.06, -0.50)	-2.06 (-3.31, -0.82)
sex [male]	-2.42 (-2.69, -2.15)	-3.15 (-4.37, -1.92)
class [first] × sex [male]		-1.06 (-2.67, 0.55)
class [second] × sex [male]		-0.64 (-2.06, 0.78)
class [third] × sex [male]		1.74 (0.47, 3.02)
Observations	2201	2201

Extra exercises:

Is survival related to age?

Are age effects dependent on sex?

Logistic regression for proportion data

Read Titanic data in different format

Read `titanic_prop.csv` data.

```
  X Class    Sex   Age  No Yes
1 1   1st Female Adult   4 140
2 2   1st Female Child   0   1
3 3   1st   Male Adult 118  57
4 4   1st   Male Child   0   5
5 5   2nd Female Adult  13  80
6 6   2nd Female Child   0  13
```

These are the same data, but summarized (see `Freq` variable).

Use `cbind(n.success, n.failures)` as response

```
prop.glm <- glm(cbind(Yes, No) ~ Class, data = tit.prop, family = binomial)
```

```
Call:
glm(formula = cbind(Yes, No) ~ Class, family = binomial, data = tit.prop)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.5092     0.1146   4.445 8.79e-06 ***
Class2nd     -0.8565     0.1661  -5.157 2.51e-07 ***
Class3rd     -1.5965     0.1436 -11.114  < 2e-16 ***
ClassCrew    -1.6643     0.1390 -11.972  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 671.96  on 13  degrees of freedom
Residual deviance: 491.06  on 10  degrees of freedom
AIC: 545.68

Number of Fisher Scoring iterations: 4
```

Survival probability by class

```
estimate_means(prop.glm)
```

```
Estimated Marginal Means

Class | Probability |   SE |       95% CI
-----------------------------------------
1st   |        0.62 | 0.03 | [0.57, 0.68]
2nd   |        0.41 | 0.03 | [0.36, 0.47]
3rd   |        0.25 | 0.02 | [0.22, 0.29]
Crew  |        0.24 | 0.01 | [0.21, 0.27]

Marginal means estimated at Class
```

Logistic regression with continuous predictors

Example dataset: GDP and infant mortality

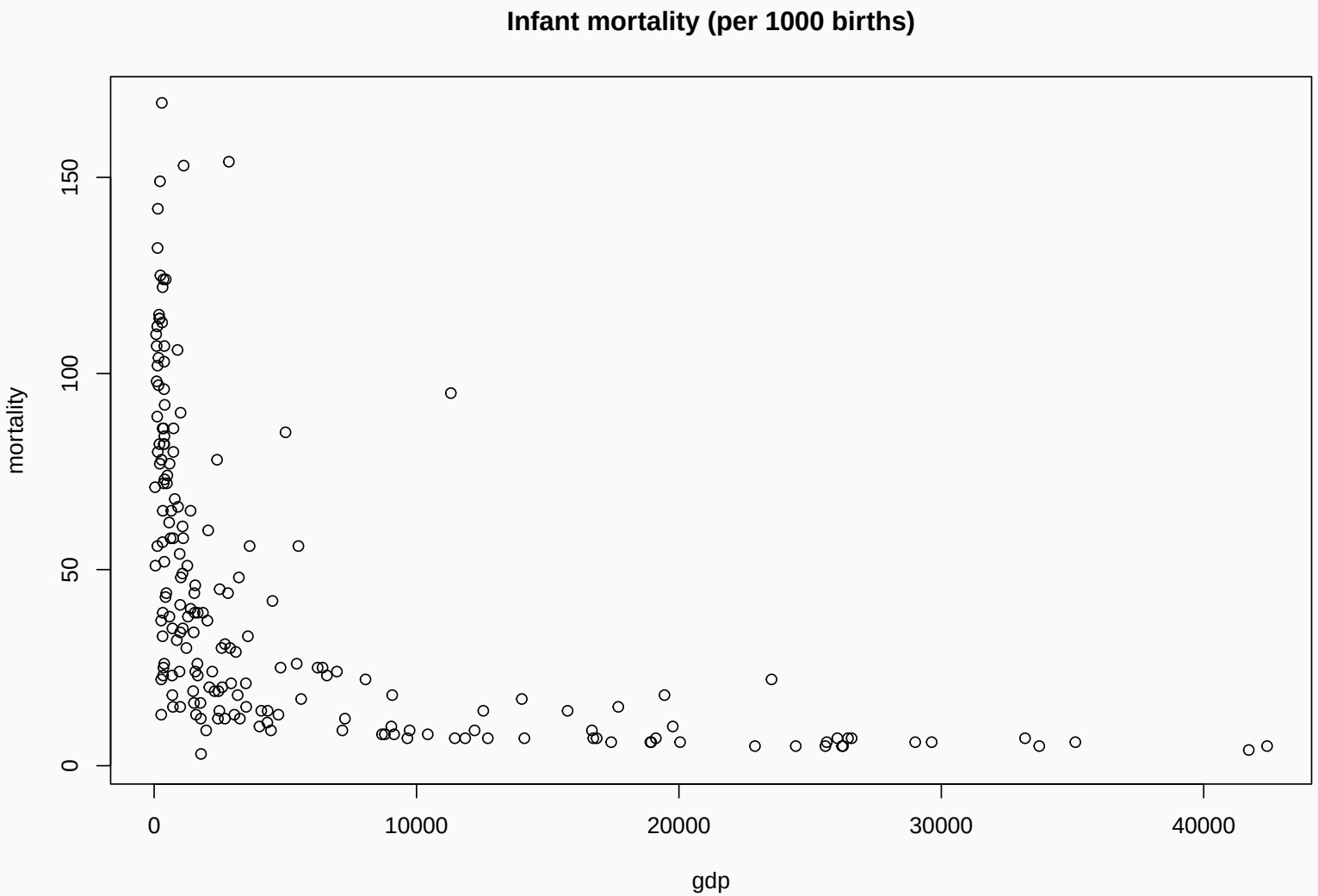
Read `UN_GDP_infantmortality.csv`.

```
   country             mortality           gdp        
 Length:207         Min.   :  2.00   Min.   :   36  
 Class :character   1st Qu.: 12.00   1st Qu.:  442  
 Mode  :character   Median : 30.00   Median : 1779  
                    Mean   : 43.48   Mean   : 6262  
                    3rd Qu.: 66.00   3rd Qu.: 7272  
                    Max.   :169.00   Max.   :42416  
                    NA's   :6        NA's   :10     
```

Q: Is infant mortality related to GDP?

https://pollev.com/franciscorod726

Visualising data



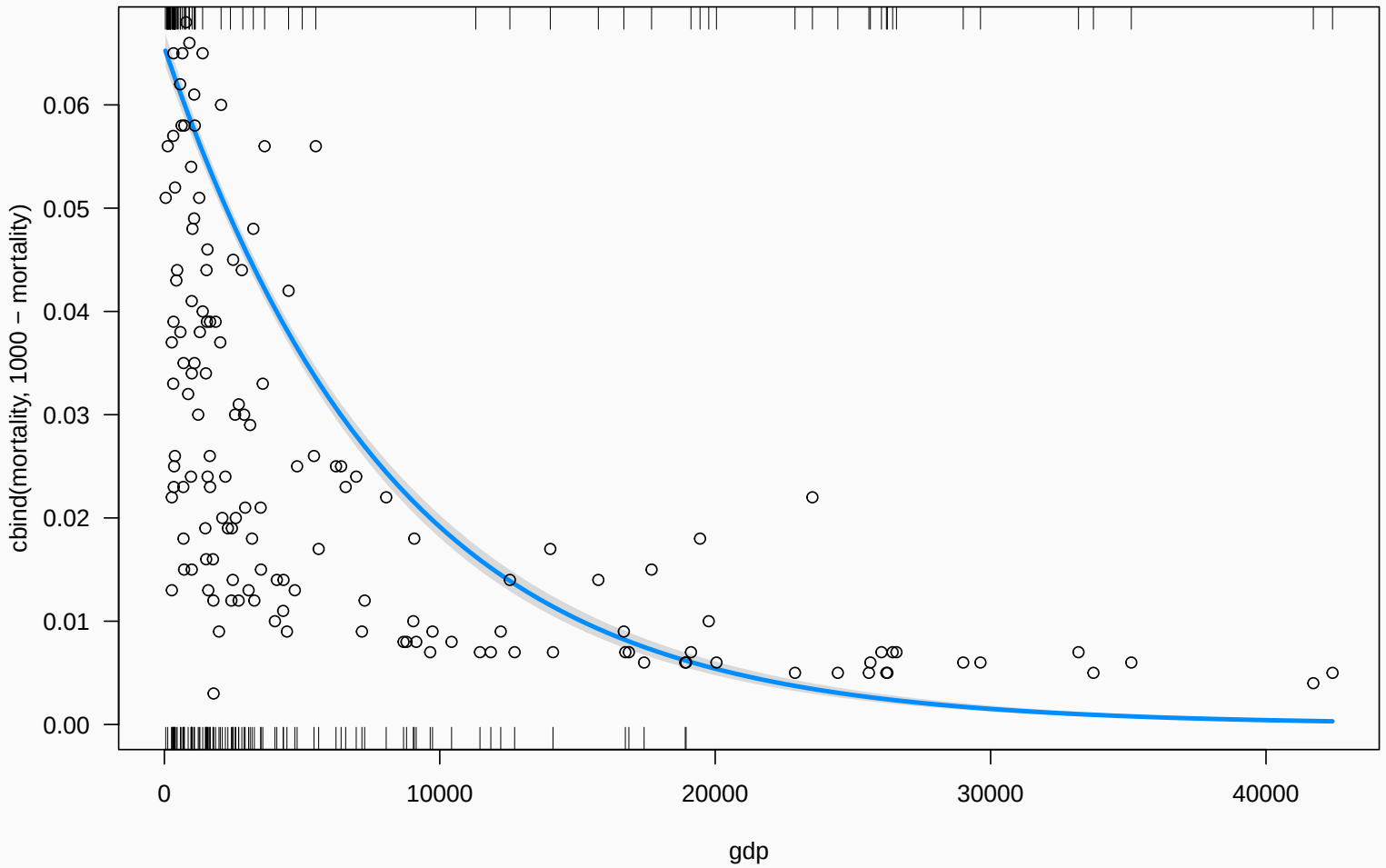
Fit model

```
gdp.glm <- glm(cbind(mortality, 1000 - mortality) ~ gdp,
               data = gdp, family = binomial)
```

```
Call:
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family = binomial,
    data = gdp)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.657e+00  1.311e-02 -202.76   <2e-16 ***
gdp         -1.279e-04  3.458e-06  -36.98   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 6430.2  on 192  degrees of freedom
Residual deviance: 3530.2  on 191  degrees of freedom
  (14 observations deleted due to missingness)
AIC: 4525.8
```

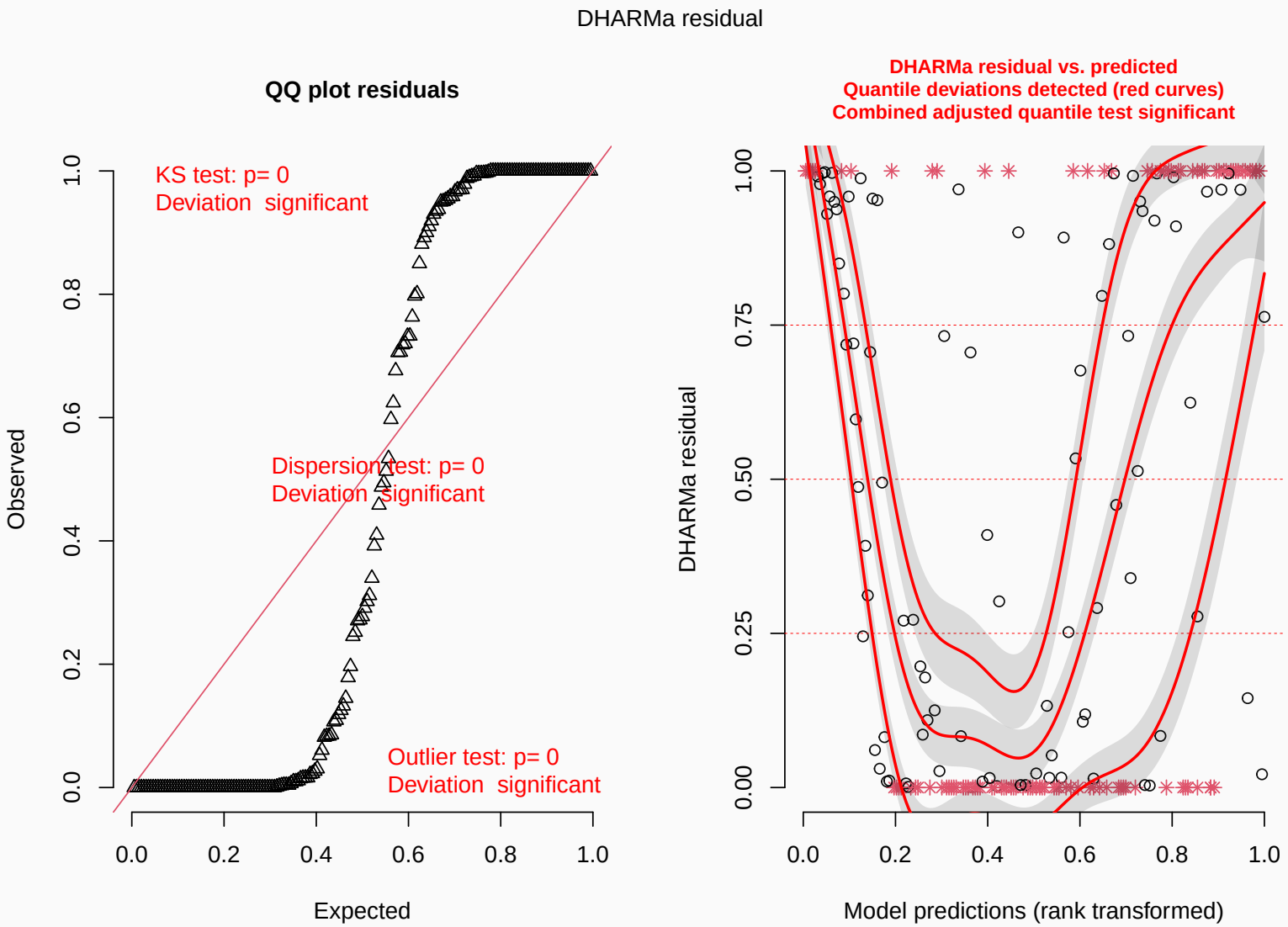
Plot model using visreg:

```
visreg(gdp.glm, scale = 'response')
points(mortality/1000 ~ gdp, data = gdp)
```



Residuals diagnostics with DHARMa

```
simulateResiduals(gdp.glm, plot = TRUE)
```



Overdispersion

Overdispersion:

more variation in the data than assumed by statistical model

$$Var(y) = np(1-p)$$

Testing for overdispersion (DHARMa)

```
simres <- simulateResiduals(gdp.glm, refit = TRUE)
testDispersion(simres, plot = FALSE)
```

```
    DHARMa nonparametric dispersion test via mean deviance residual
    vs. simulated-refitted

data:  simres
dispersion = 21, p-value < 2.2e-16
alternative hypothesis: two.sided
```

Testing for overdispersion (easystats)

```
check_overdispersion(gdp.glm)
```

```
# Overdispersion test

 dispersion ratio =   2.933
          p-value = < 0.001
```

`quasibinomial` allows us to model overdispersed binomial data

Overdispersion in logistic regression with proportion data

```
gdp.overdisp <- glm(cbind(mortality, 1000 - mortality) ~ gdp,
                    data = gdp, family = quasibinomial)
```

```
Call:
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family = quasibinomial,
    data = gdp)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.657e+00  5.977e-02 -44.465  < 2e-16 ***
gdp         -1.279e-04  1.577e-05  -8.111 5.96e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 20.7947)

    Null deviance: 6430.2  on 192  degrees of freedom
Residual deviance: 3530.2  on 191  degrees of freedom
  (14 observations deleted due to missingness)
AIC: NA
```

Mean estimates do not change after accounting for overdispersion

But standard errors (uncertainty) do!

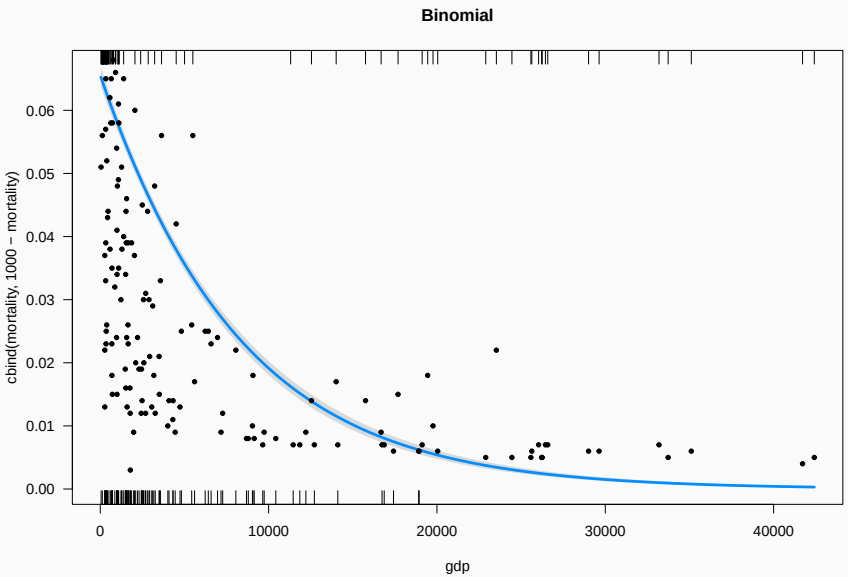
```
parameters(gdp.overdisp)
```

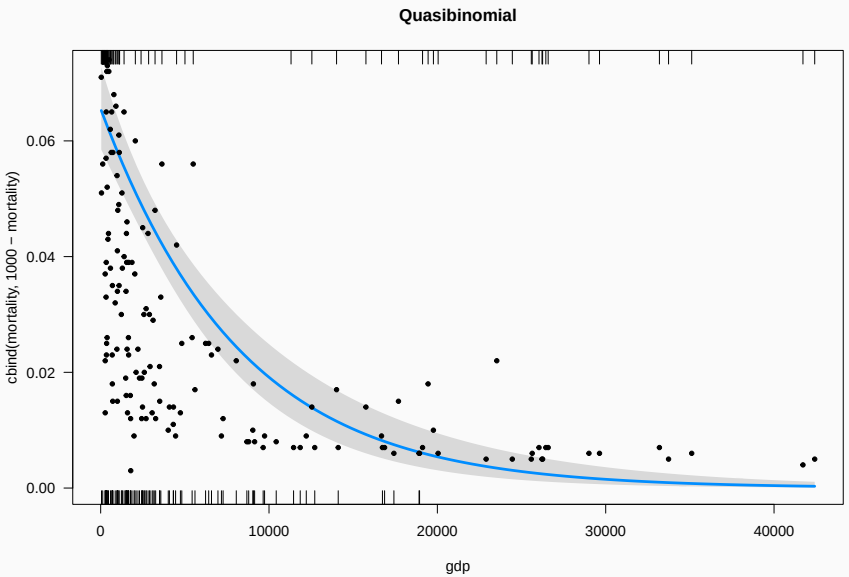
```
Parameter   |  Log-Odds |       SE |         95% CI | t(191) |      p
-------------------------------------------------------------------
(Intercept) |     -2.66 |     0.06 | [-2.78, -2.54] | -44.46 | < .001
gdp         | -1.28e-04 | 1.58e-05 | [ 0.00,  0.00] |  -8.11 | < .001
```

```
parameters(gdp.glm)
```

```
Parameter   |  Log-Odds |       SE |         95% CI |       z |      p
-------------------------------------------------------------------
(Intercept) |     -2.66 |     0.01 | [-2.68, -2.63] | -202.76 | < .001
gdp         | -1.28e-04 | 3.46e-06 | [ 0.00,  0.00] |  -36.99 | < .001
```

But standard errors (uncertainty) do!

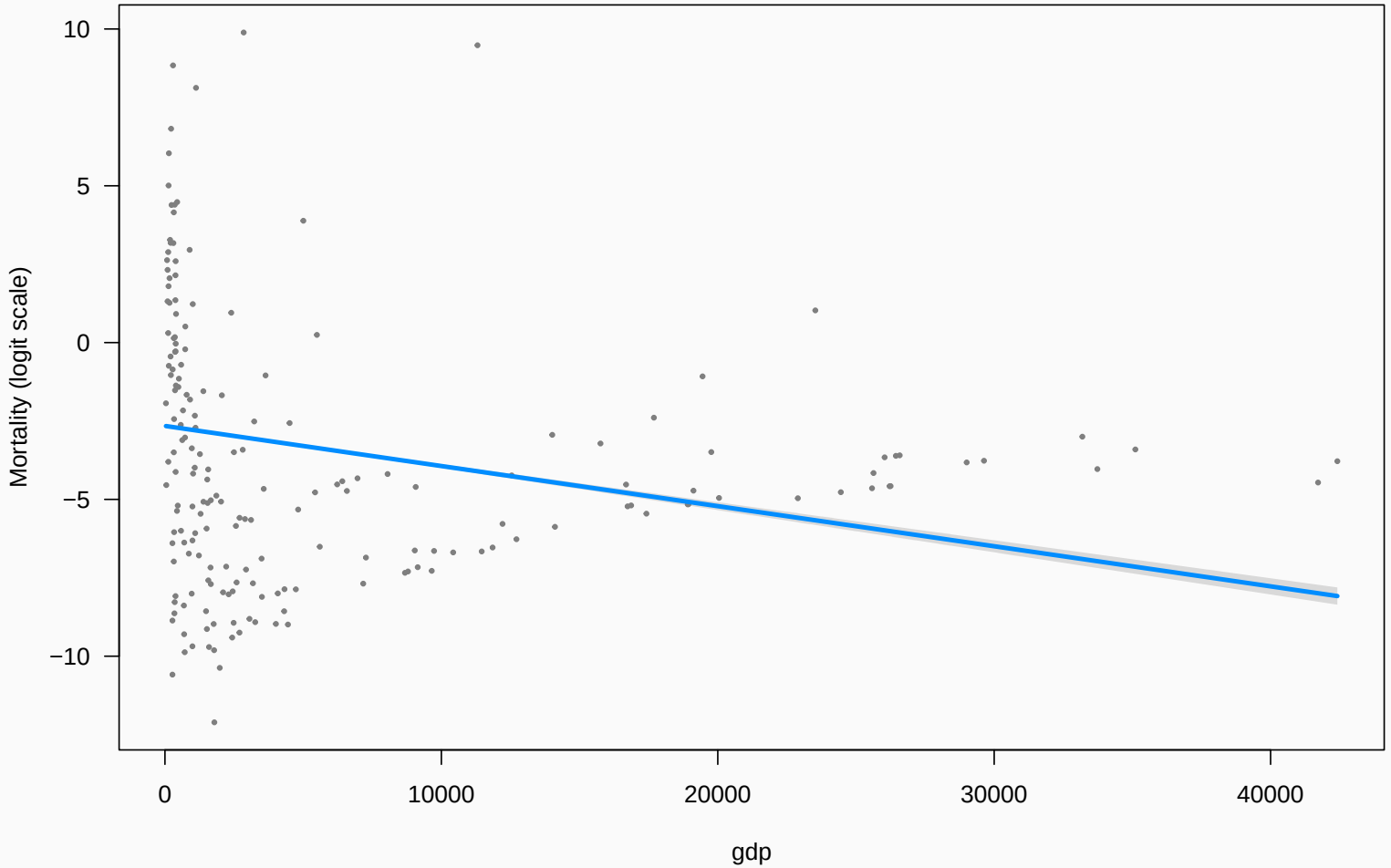




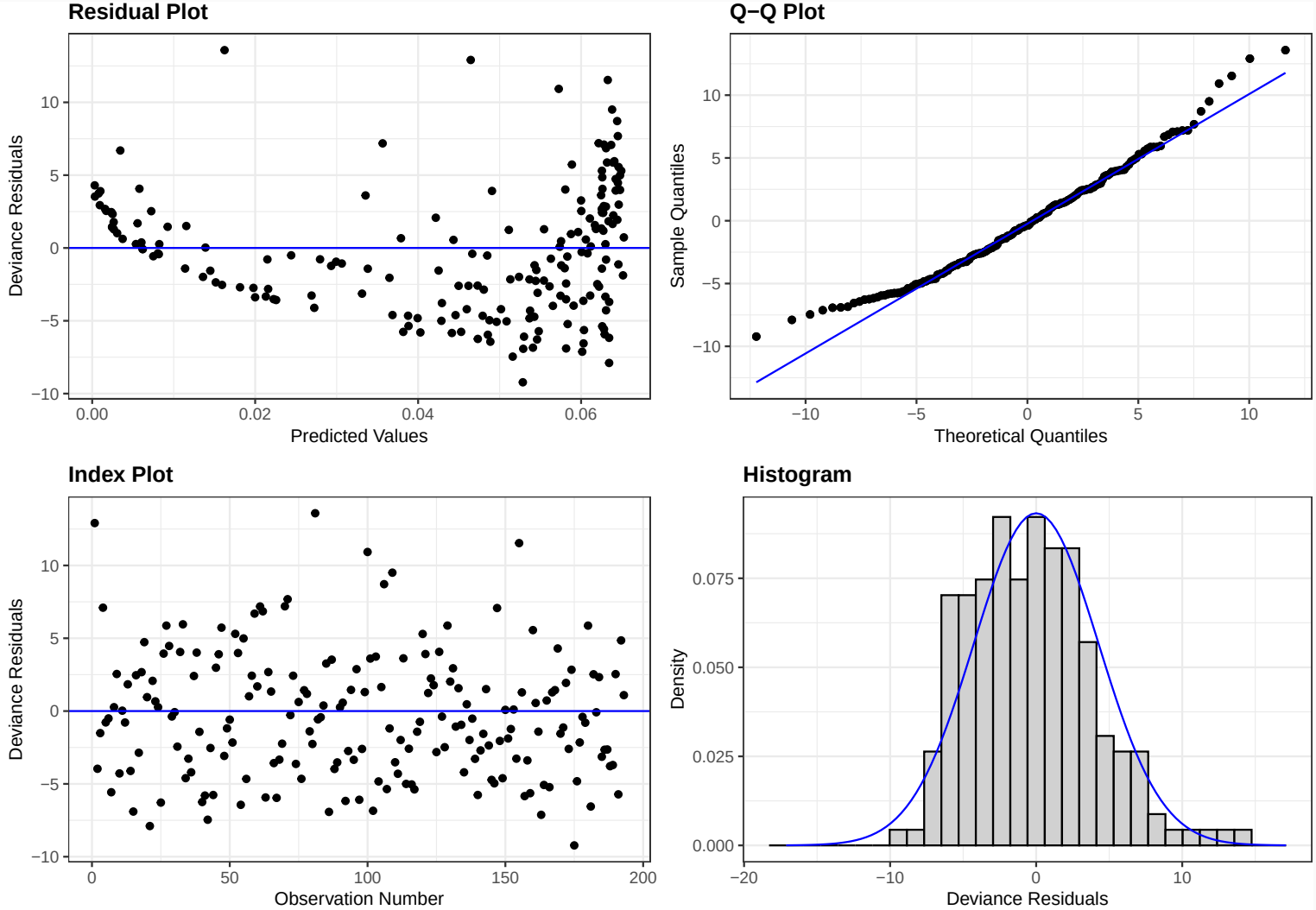
Think about the shape of relationships

Think about the shape of relationships

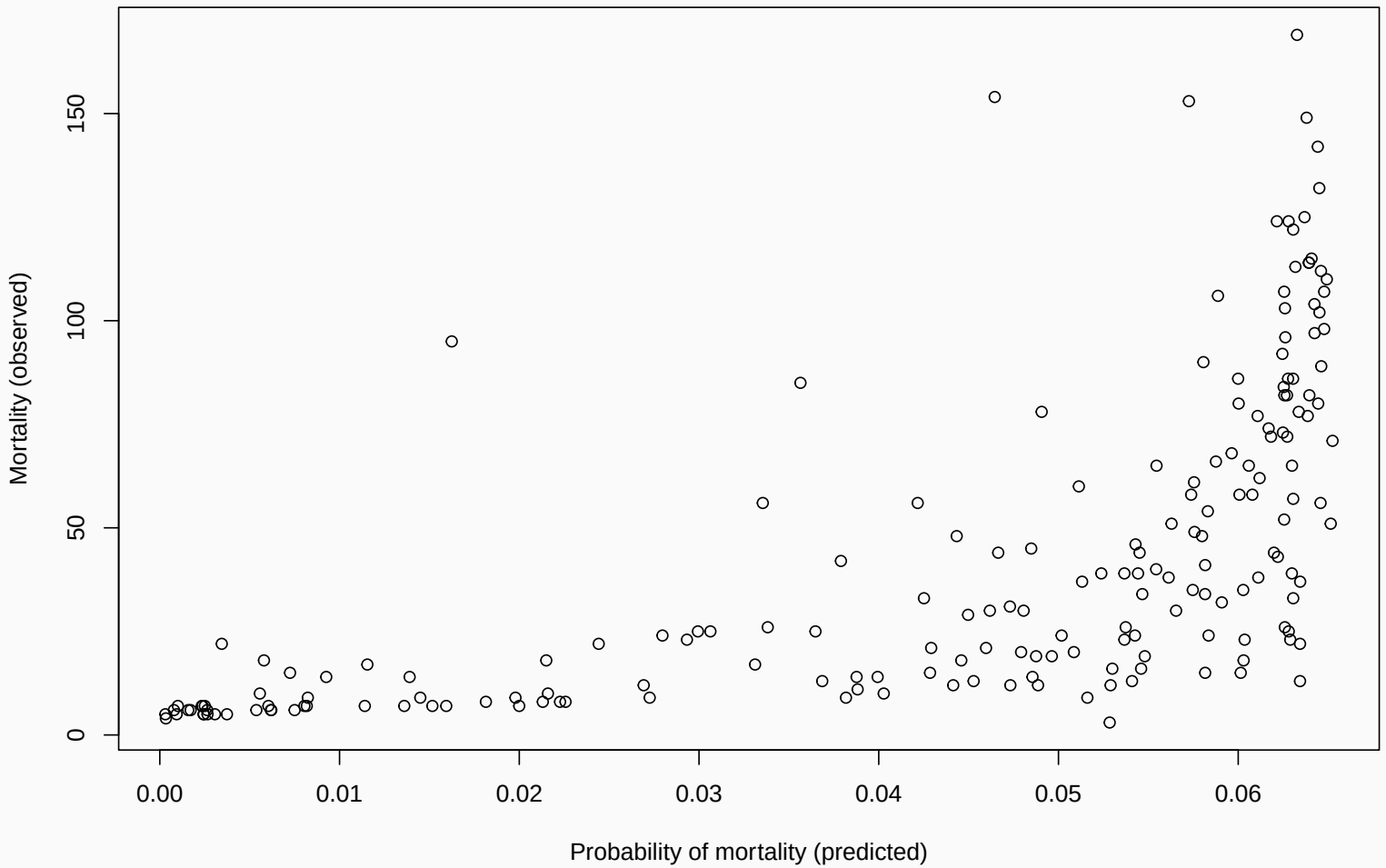
Not everything has to be linear...



Residuals show non-linear pattern

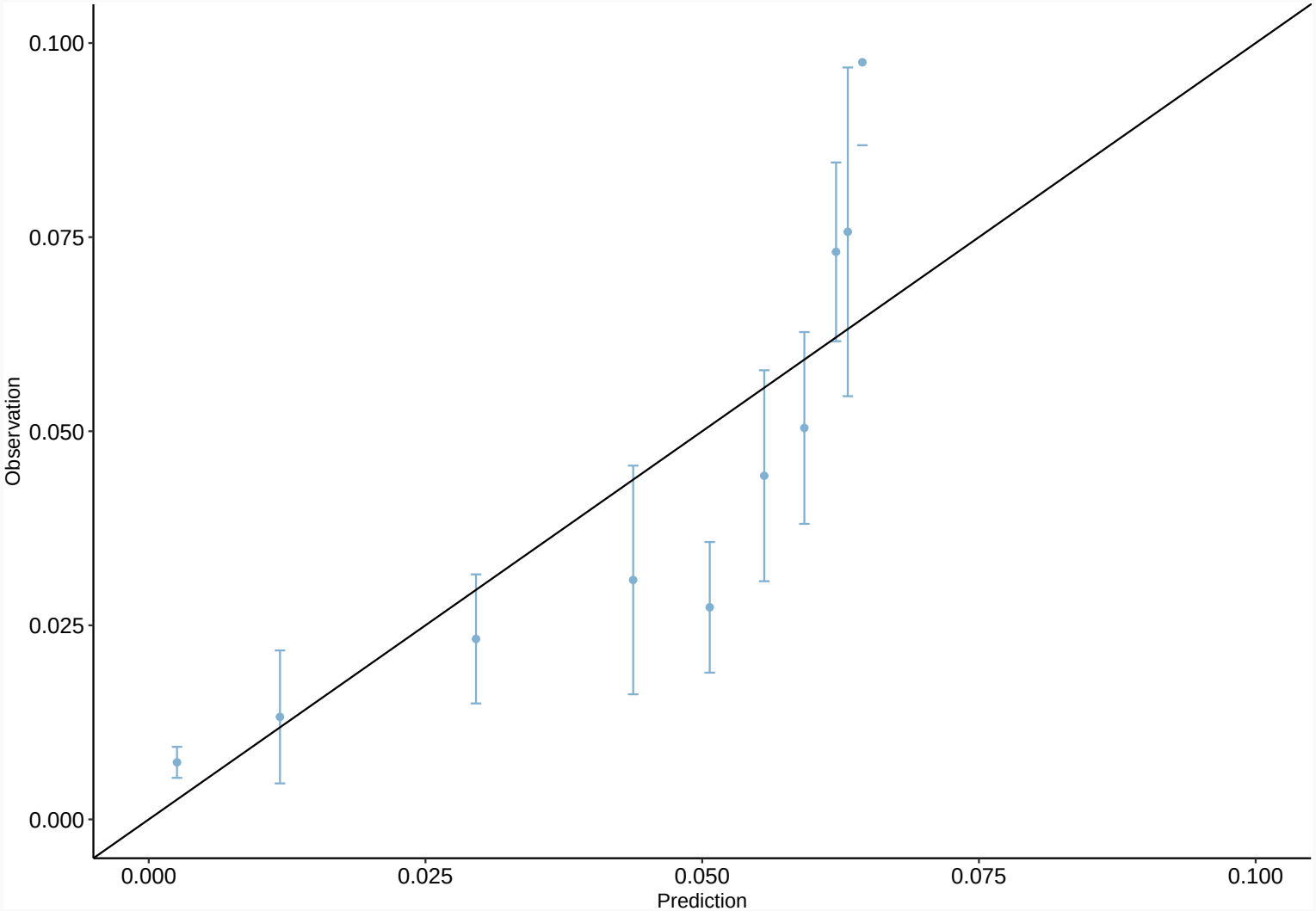


Calibration plot shows non-linear pattern

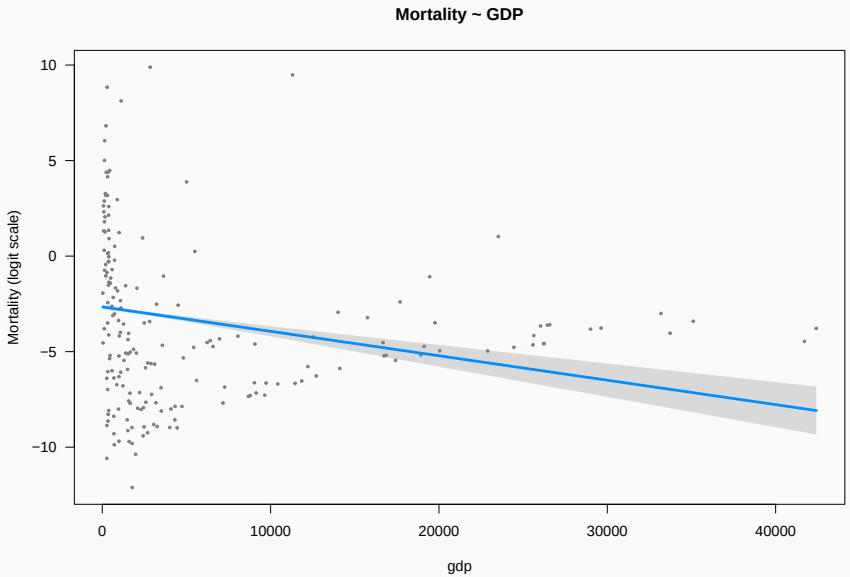


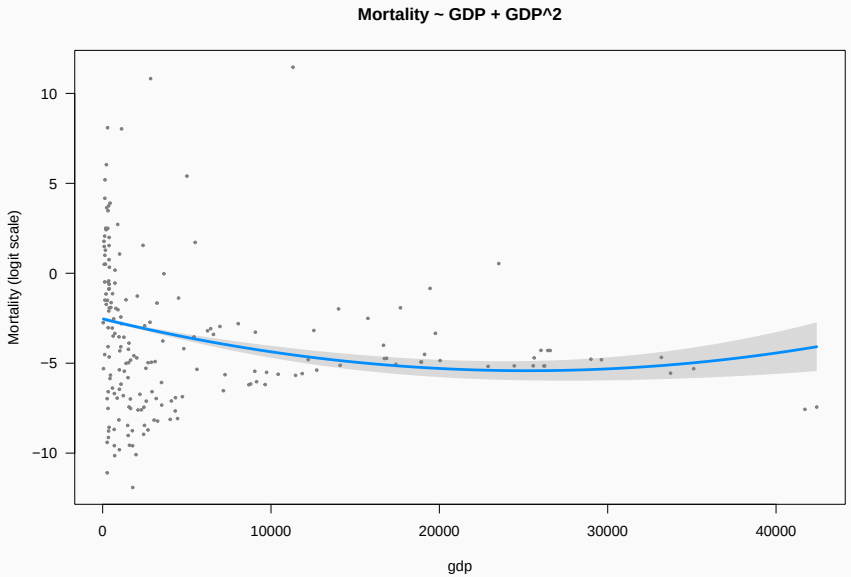
Calibration plot shows non-linear pattern

```
$calibration_plot
```

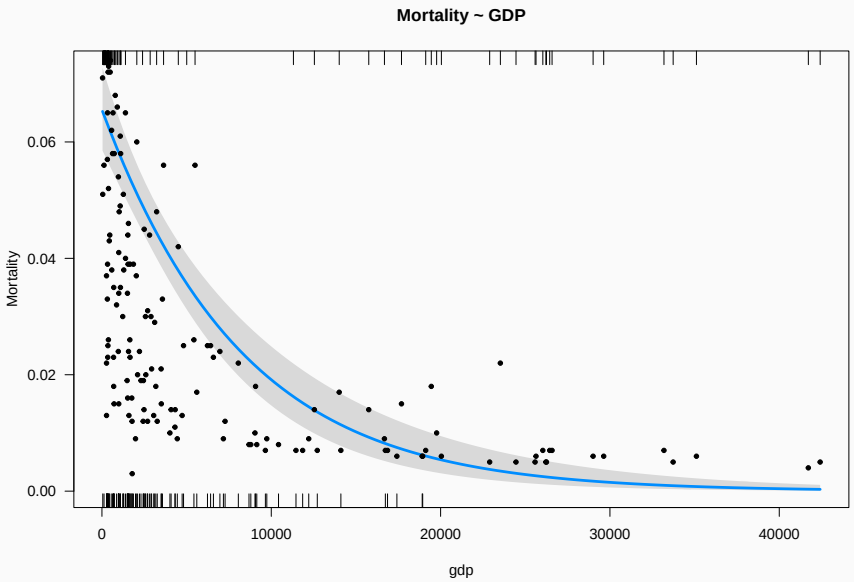


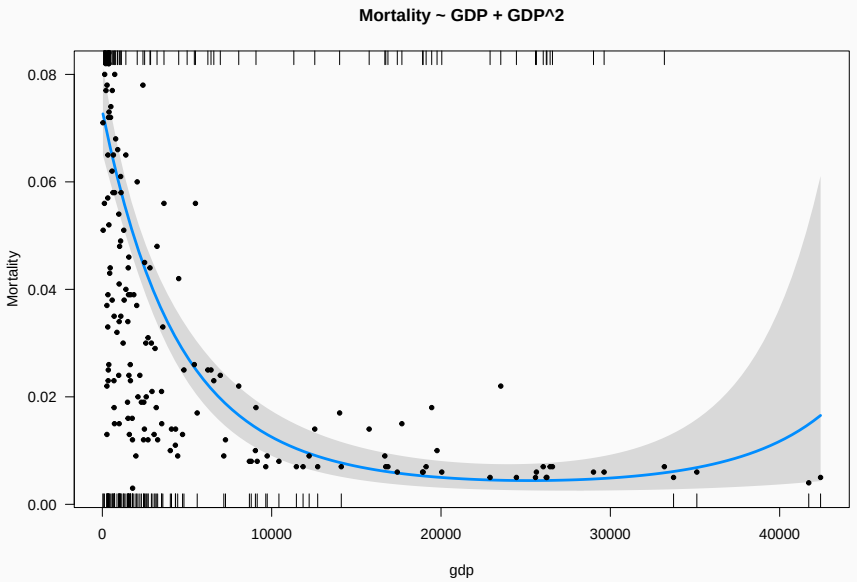
Trying polynomial predictor (GDP + GDP^2)



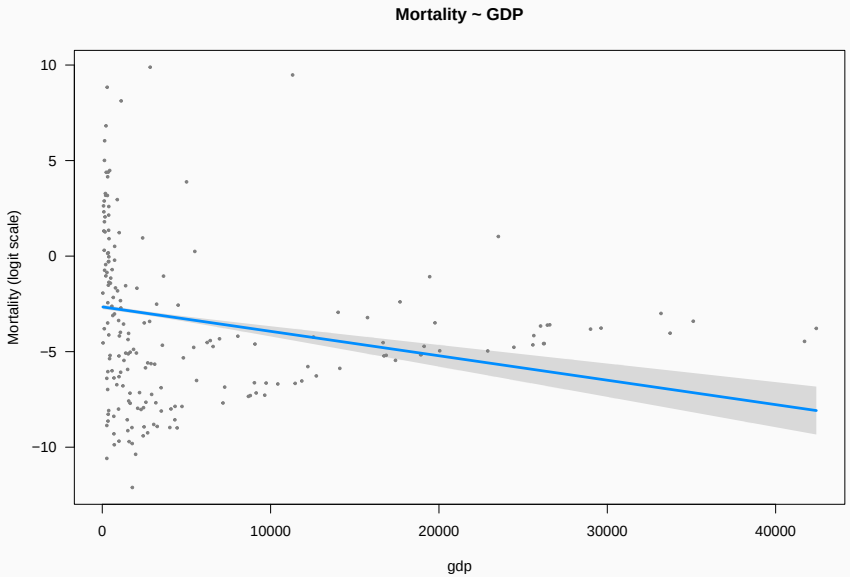


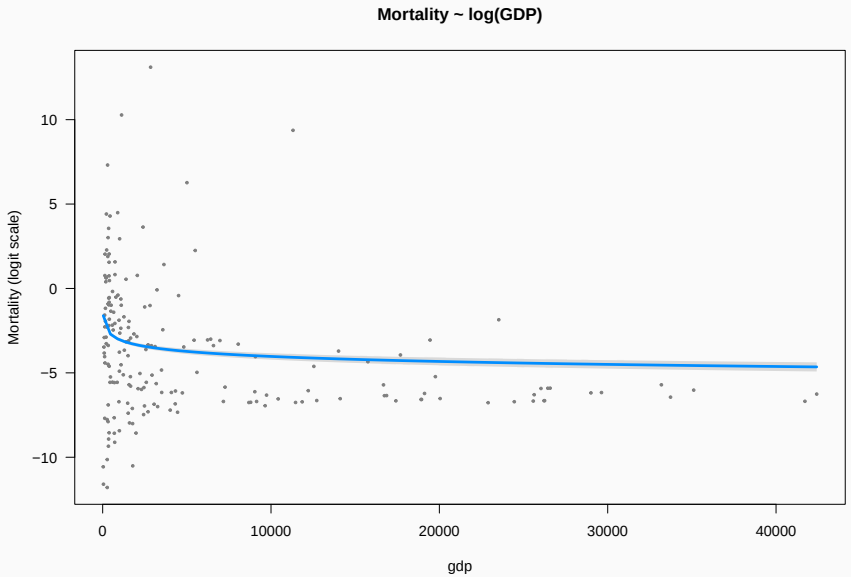
Think about the shape of relationships



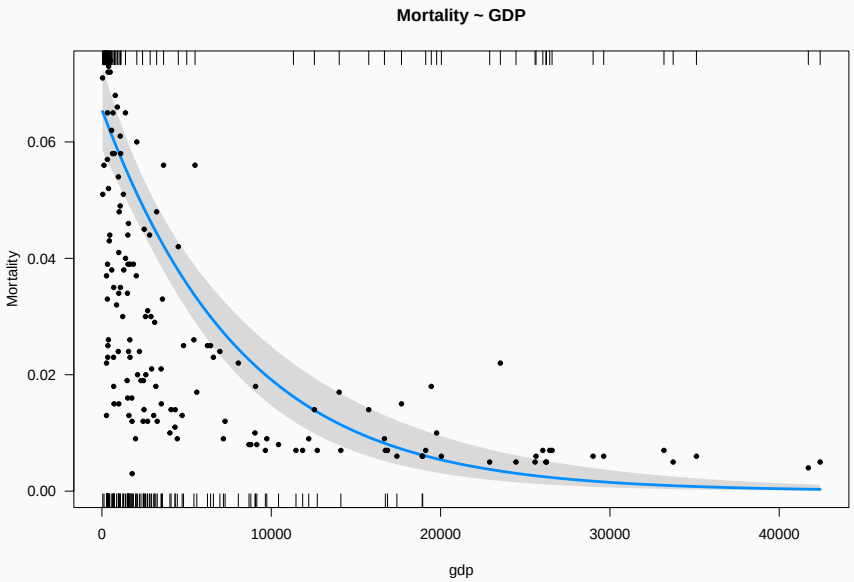


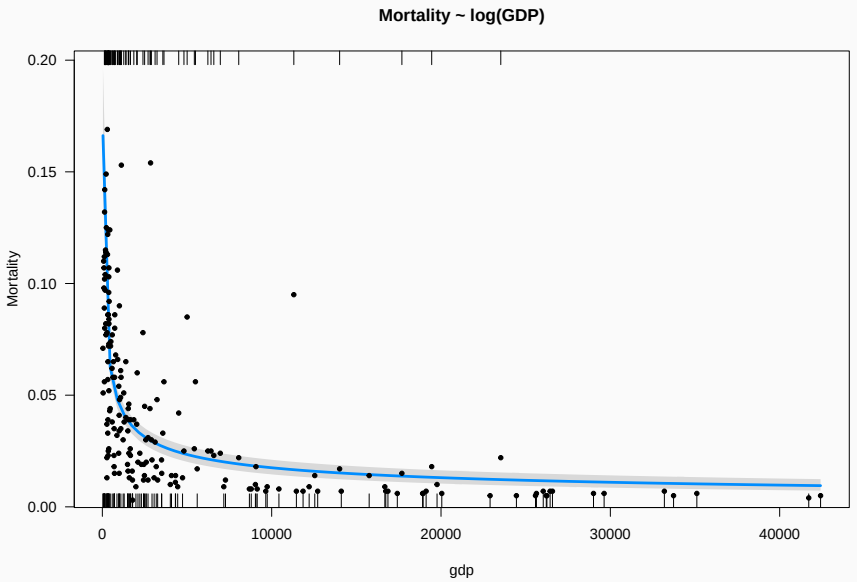
Trying log(GDP)





Trying log(GDP)





More examples

- `moth.csv`: Probability of moth predation on trunk trees depending on morph (light/dark) and distance to Liverpool (Bishop 1972)

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- `seedset.csv`: Comparing seed set among plants (Data from Harder et al. 2011)

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- `moth.csv`: Probability of moth predation on trunk trees depending on morph (light/dark) and distance to Liverpool (Bishop 1972)
- `seedset.csv`: Comparing seed set among plants (Data from Harder et al. 2011)
- `soccer.csv`: Probability of scoring penalty depending on goalkeeper's team being ahead, behind or tied (Roskes et al 2011)

Moth predation

The industrial revolution and evolution of dark morphs

The data

```
moth <- read.csv('data/moth.csv')
```

```
  MORPH DISTANCE PLACED REMOVED
1 light      0.0     56      17
2  dark      0.0     56      14
3 light      7.2     80      28
4  dark      7.2     80      20
5 light     24.1     52      18
6  dark     24.1     52      22
```

Creating new variable: REMAIN

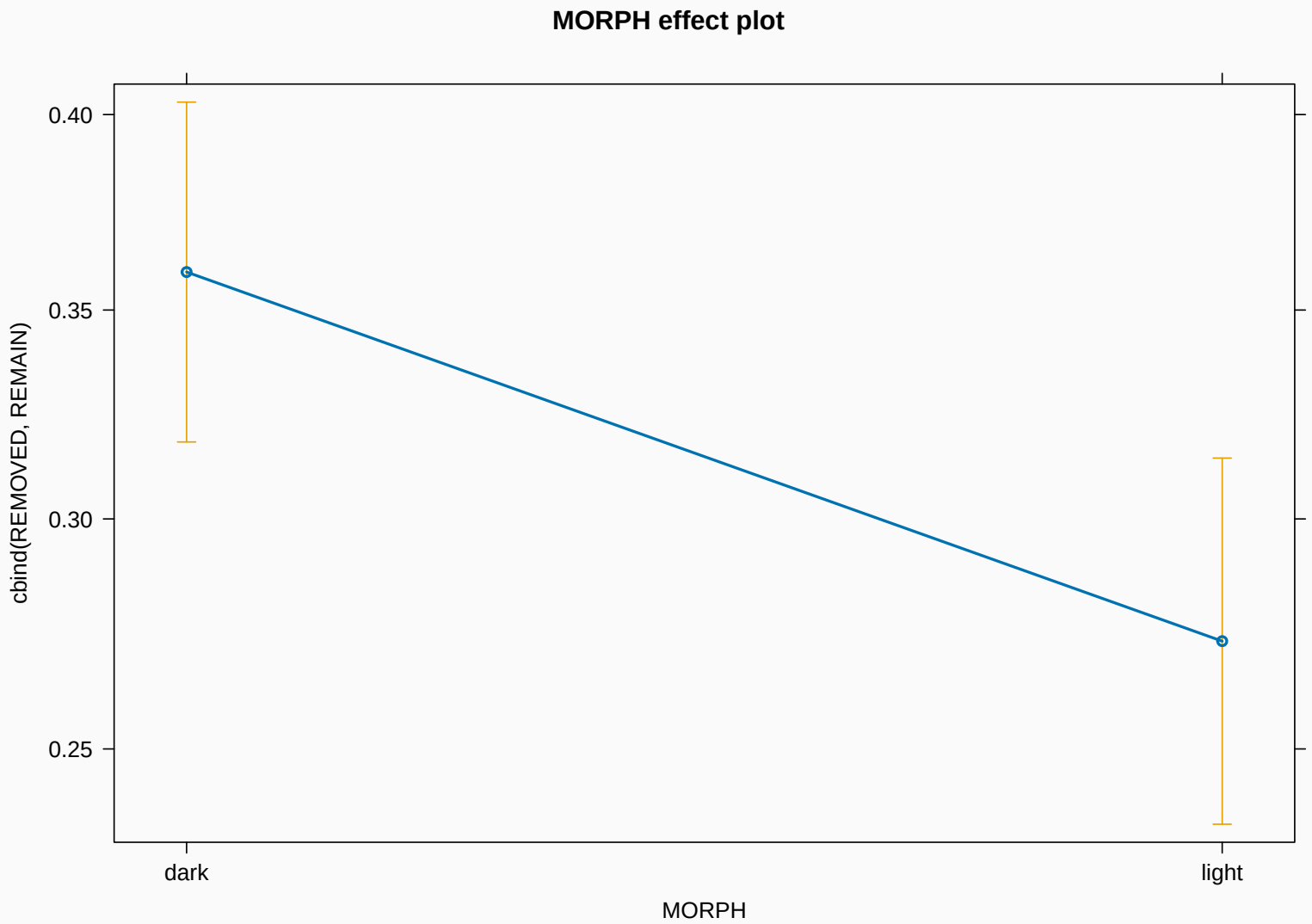
```
moth$REMAIN <- moth$PLACED - moth$REMOVED
```

```
  MORPH DISTANCE PLACED REMOVED REMAIN
1 light      0.0     56      17     39
2  dark      0.0     56      14     42
3 light      7.2     80      28     52
4  dark      7.2     80      20     60
5 light     24.1     52      18     34
6  dark     24.1     52      22     30
```

Did some morph have higher predation overall?

```
Call:
glm(formula = cbind(REMOVED, REMAIN) ~ MORPH, family = binomial,
    data = moth)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.57752    0.09473  -6.097 1.08e-09 ***
MORPHlight  -0.40331    0.13925  -2.896  0.00377 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 35.385  on 13  degrees of freedom
Residual deviance: 26.936  on 12  degrees of freedom
AIC: 93.61

Number of Fisher Scoring iterations: 4
```

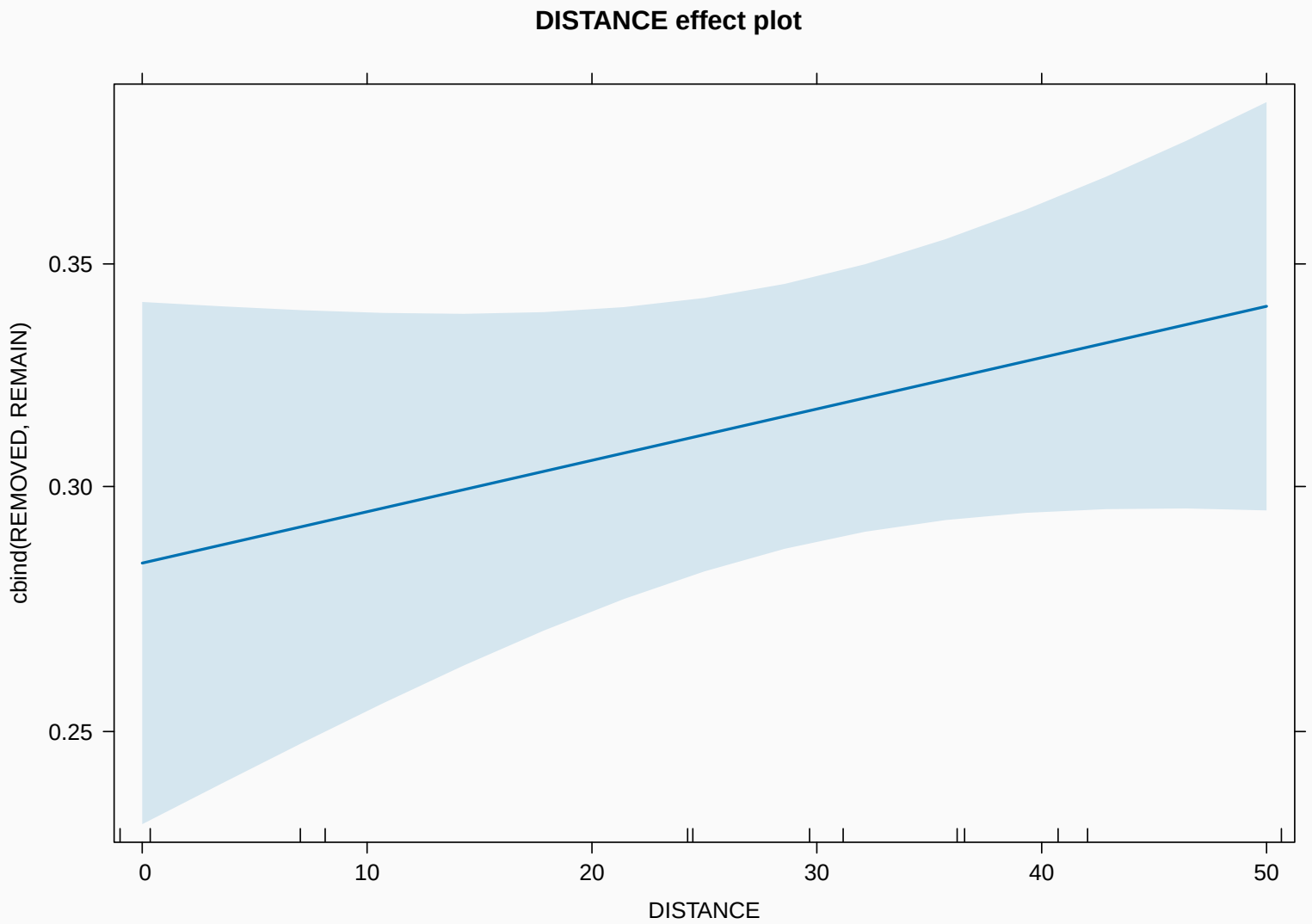
Did some morph have higher predation overall?



Did predation increase farther from city centre?

```
Call:
glm(formula = cbind(REMOVED, REMAIN) ~ DISTANCE, family = binomial,
    data = moth)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.925861   0.136634  -6.776 1.23e-11 ***
DISTANCE     0.005268   0.003984   1.322    0.186
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 35.385  on 13  degrees of freedom
Residual deviance: 33.626  on 12  degrees of freedom
AIC: 100.3

Number of Fisher Scoring iterations: 4
```

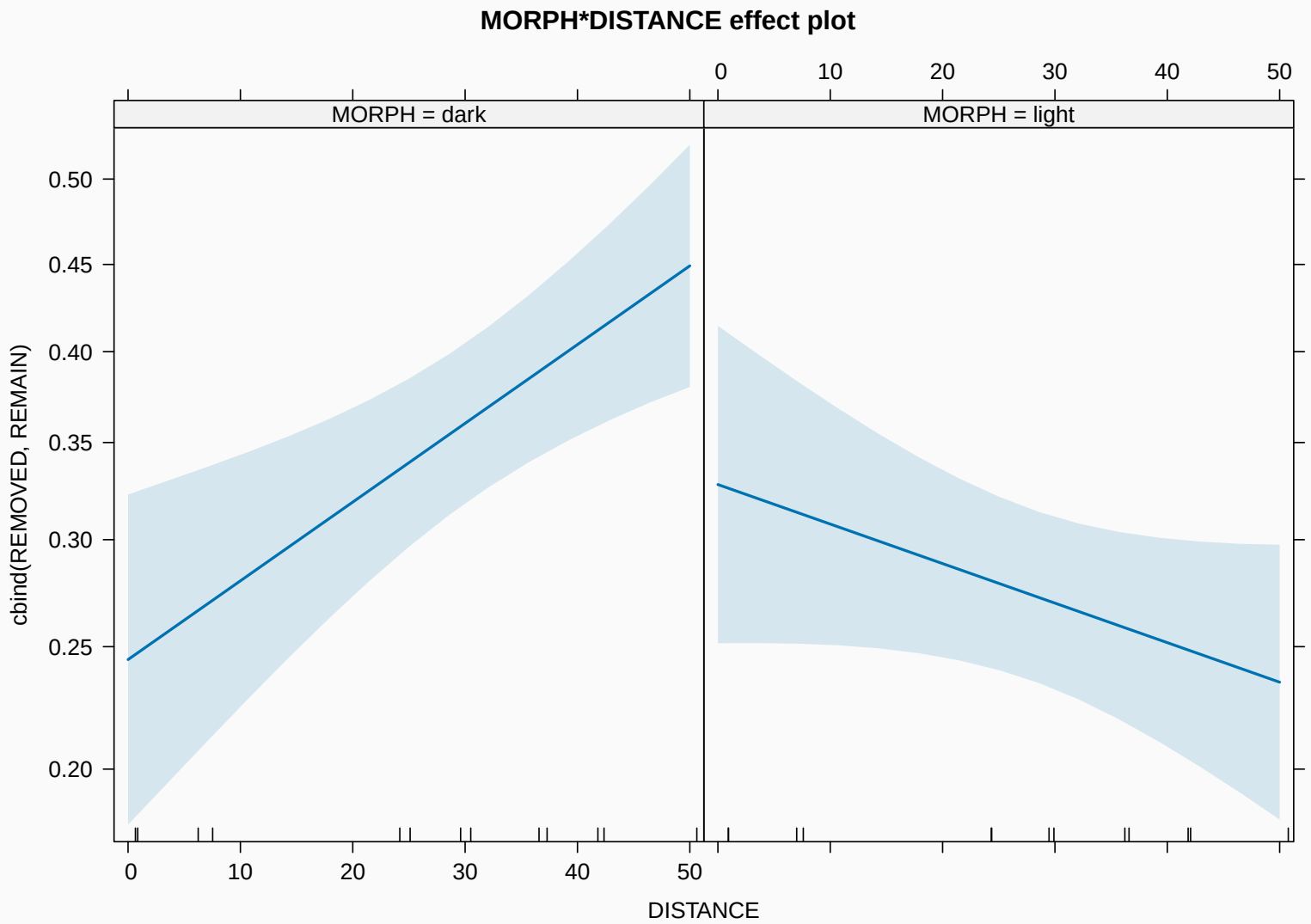
Did predation increase farther from city centre?



Did dark morph have lower predation in city & light have lower predation in countryside?

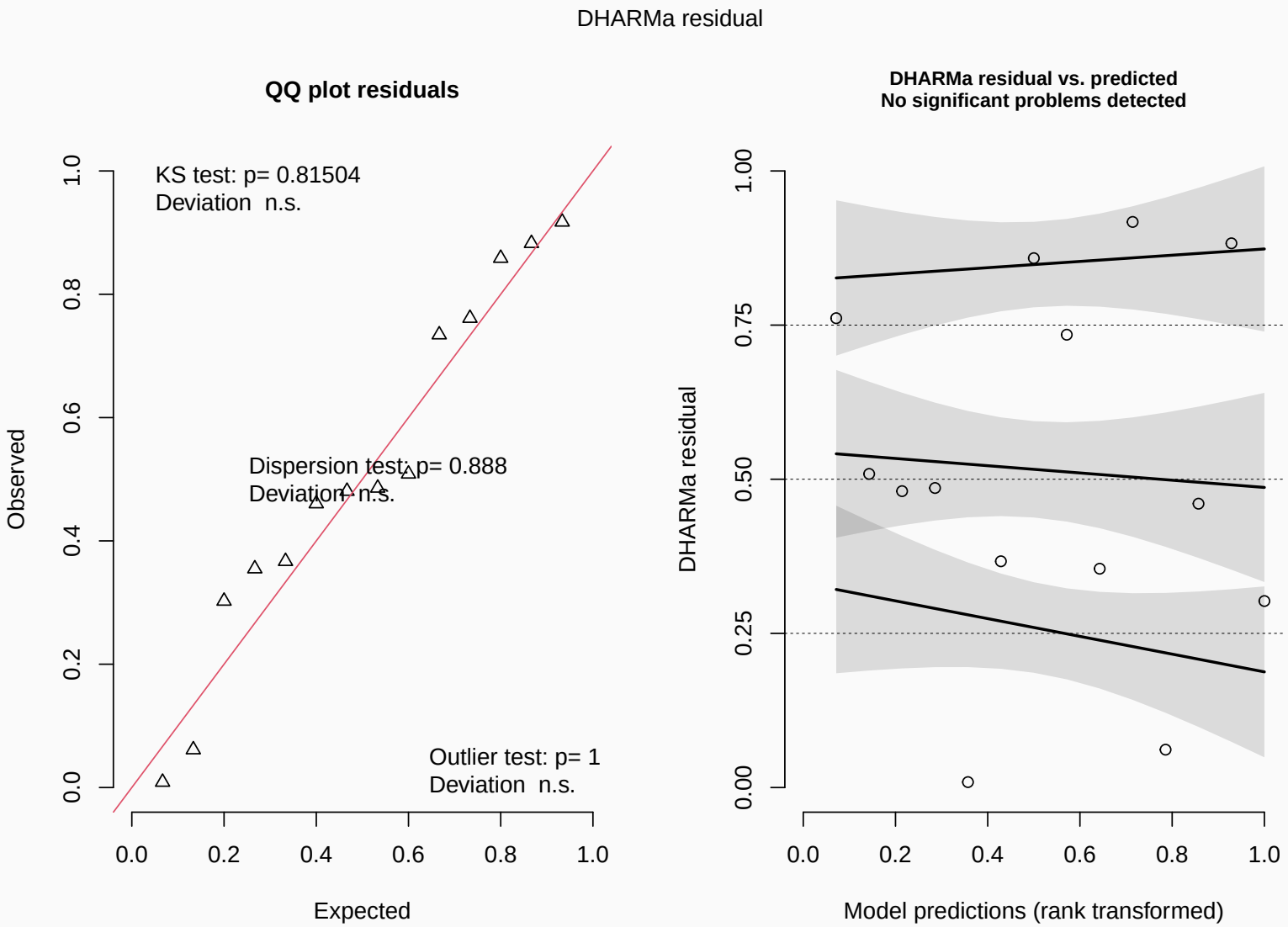
```
Call:
glm(formula = cbind(REMOVED, REMAIN) ~ MORPH * DISTANCE, family = binomial,
    data = moth)

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)         -1.128987   0.197906  -5.705 1.17e-08 ***
MORPHlight           0.411257   0.274490   1.498 0.134066
DISTANCE             0.018502   0.005645   3.277 0.001048 **
MORPHlight:DISTANCE -0.027789   0.008085  -3.437 0.000588 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 35.385  on 13  degrees of freedom
Residual deviance: 13.230  on 10  degrees of freedom
AIC: 83.904
```

Did dark morph have lower predation in city & light have lower predation in countryside?



Model check

```
simulateResiduals(pred.int, plot = TRUE)
```



Seed set among plants

Seed set among plants

Seed set among plants

```
# A tibble: 6 x 6
  species    plant pcmass fertilized seeds ovulecnt
  <chr>      <dbl>  <dbl>      <dbl> <dbl>    <dbl>
1 ferruginea     2  0            70    52      330
2 ferruginea     2  0.2         321   188      461
3 ferruginea     2  0.485       351   278      435
4 ferruginea     2  0.737       386   301      430
5 ferruginea     2  1           367   342      419
6 ferruginea     3  0           185    39      470
```

Questions:

https://pollev.com/franciscorod726

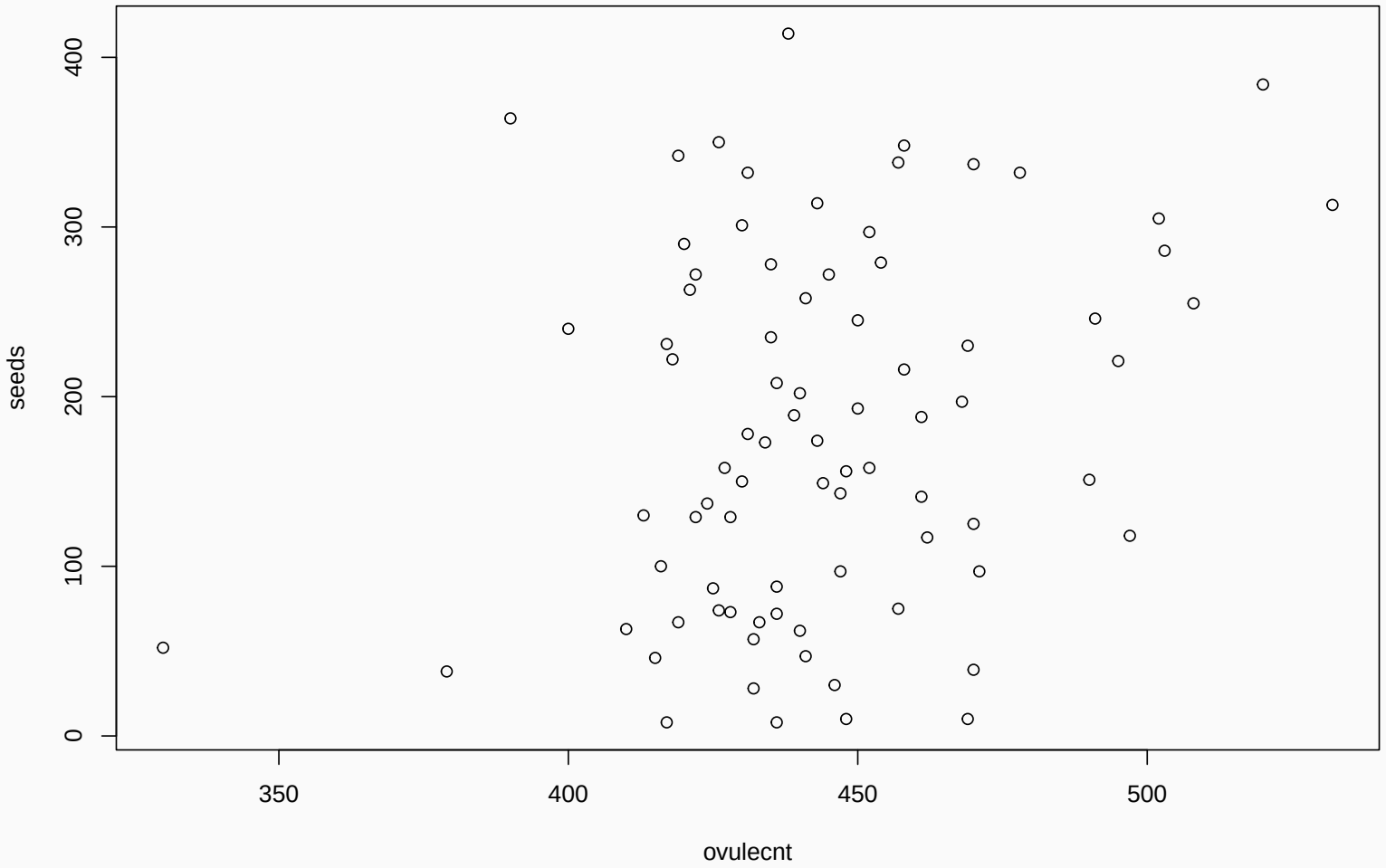
- Is seed set related to proportion of outcross pollen (pcmass)?

Questions:

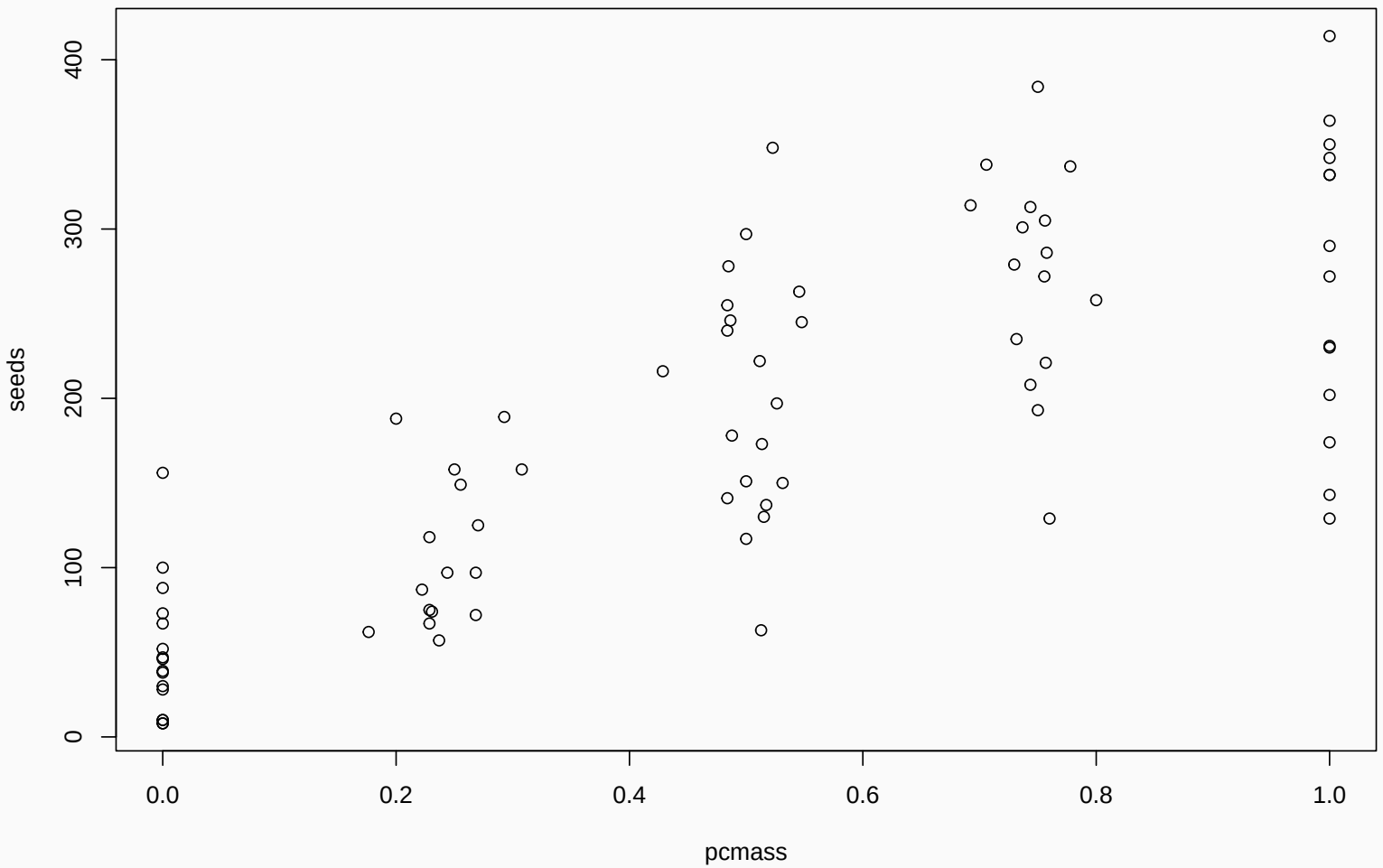
https://pollev.com/franciscorod726

- Is seed set related to proportion of outcross pollen (pcmass)?
- Which plant had lower seed set?

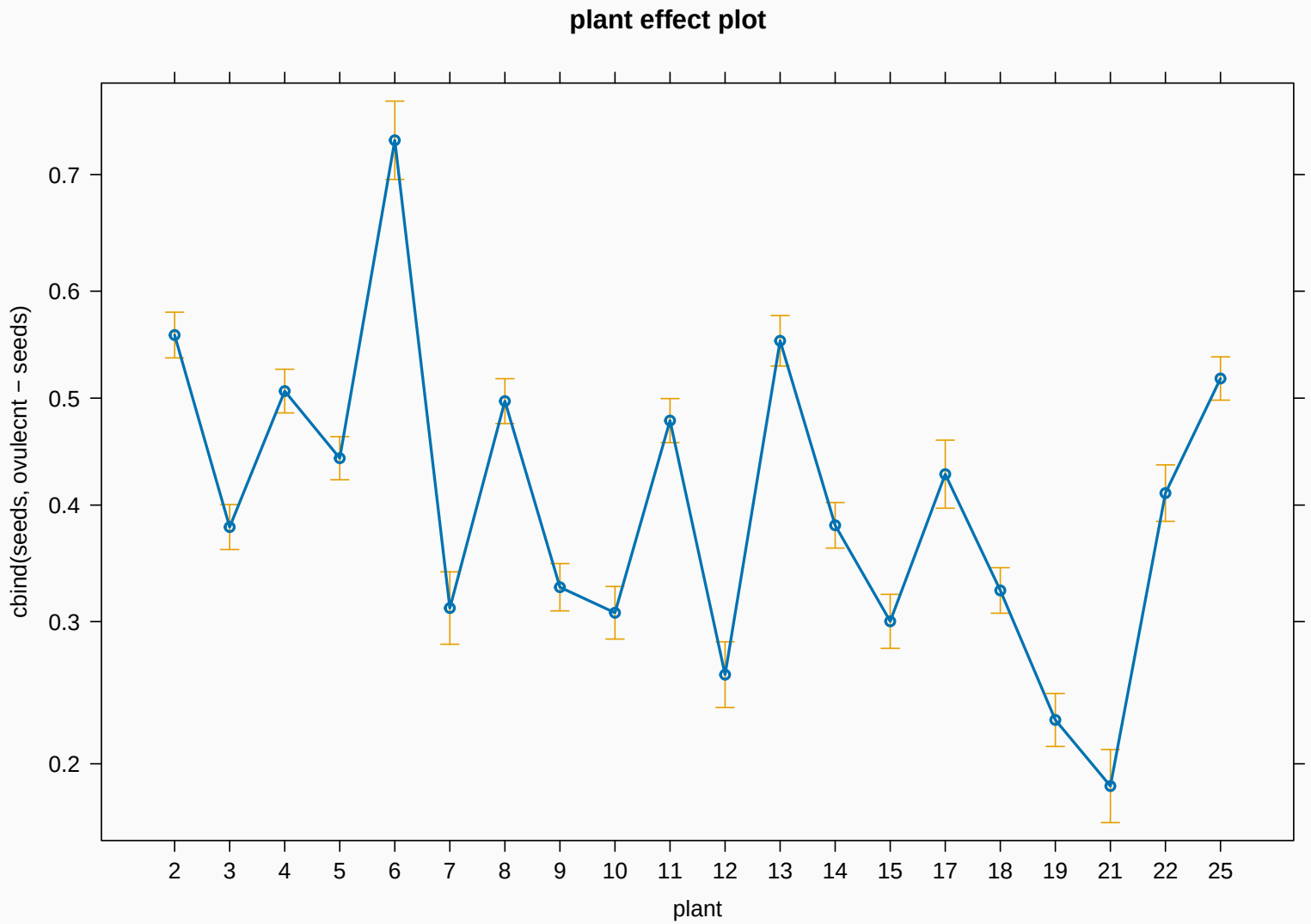
Number of seeds vs Number of ovules



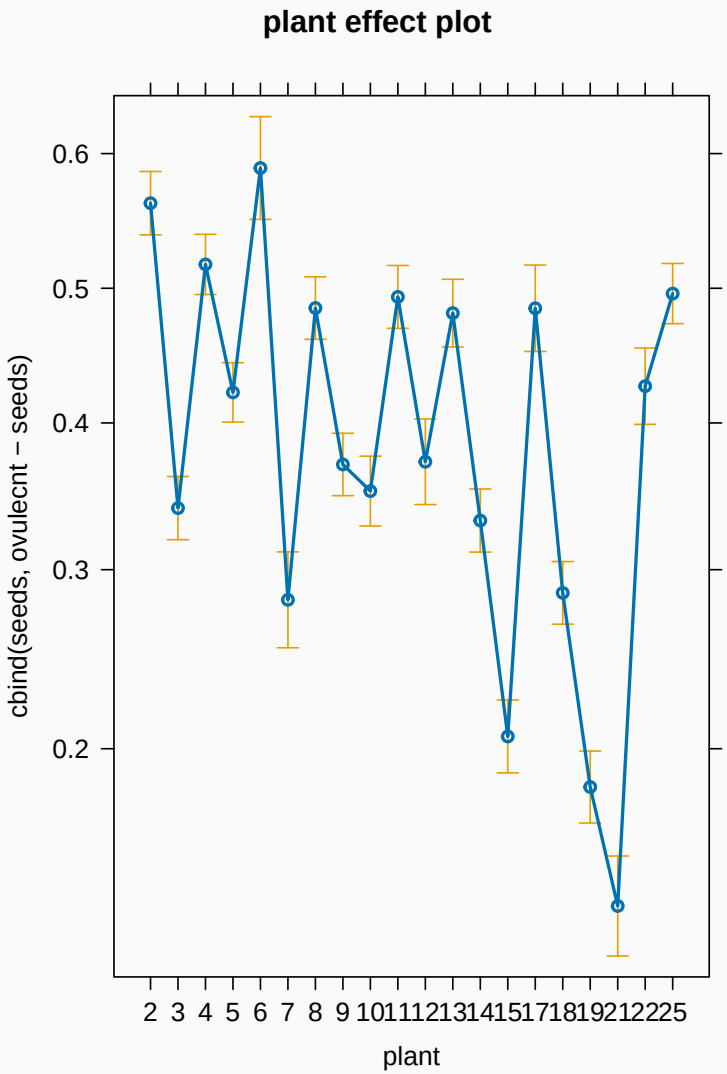
Number of seeds vs Proportion outcross pollen

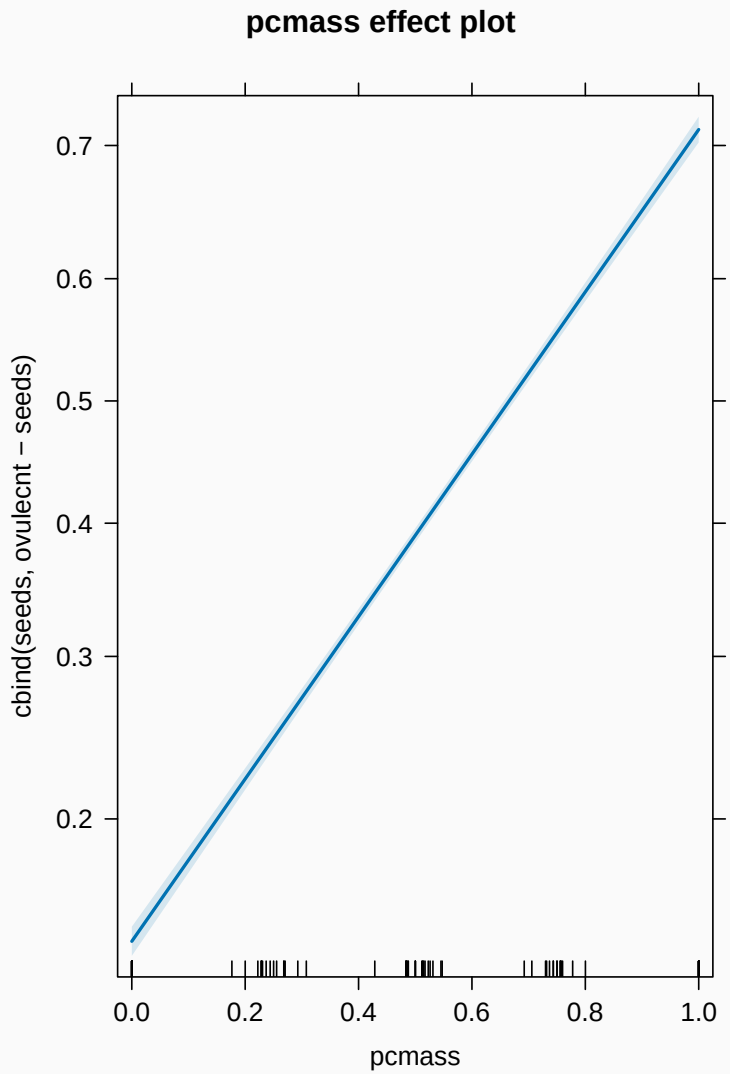


Seed set across plants



Seed set ~ outcross pollen





Probability of scoring penalty

Data on penalty shots

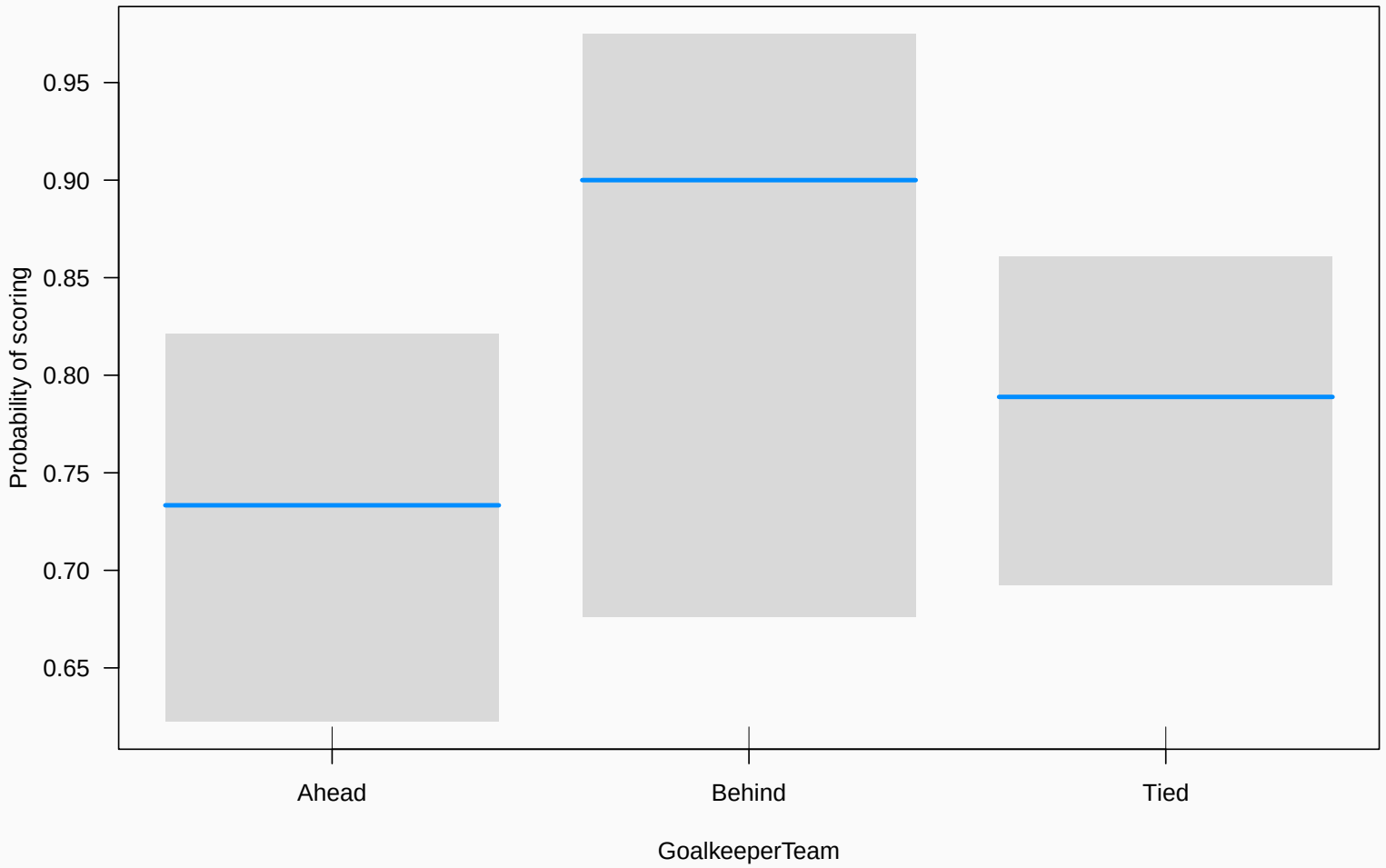
```
soccer <- read.csv('data/soccer.csv')
soccer
```

```
  GoalkeeperTeam Nshots Scored
1         Behind     20     18
2           Tied     90     71
3          Ahead     75     55
```

Does probability of scoring penalty depends on match situation?

https://pollev.com/franciscorod726

Probability of scoring depending on match situation



GLM for count data

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Types of response variable

- **Gaussian**: lm

Types of response variable

- **Gaussian**: lm
- **Binary**: glm (family `binomial / quasibinomial`)

Types of response variable

- **Gaussian**: lm
- **Binary**: glm (family `binomial / quasibinomial`)
- **Counts**: glm (family `poisson / quasipoisson`)

Poisson regression

- Response variable: Counts (0, 1, 2, 3...) - discrete
- Link function: `log`

Then

$$log(N) = a + bx$$
$$N = e^{a+bx}$$

Example dataset: Seedling counts in quadrats

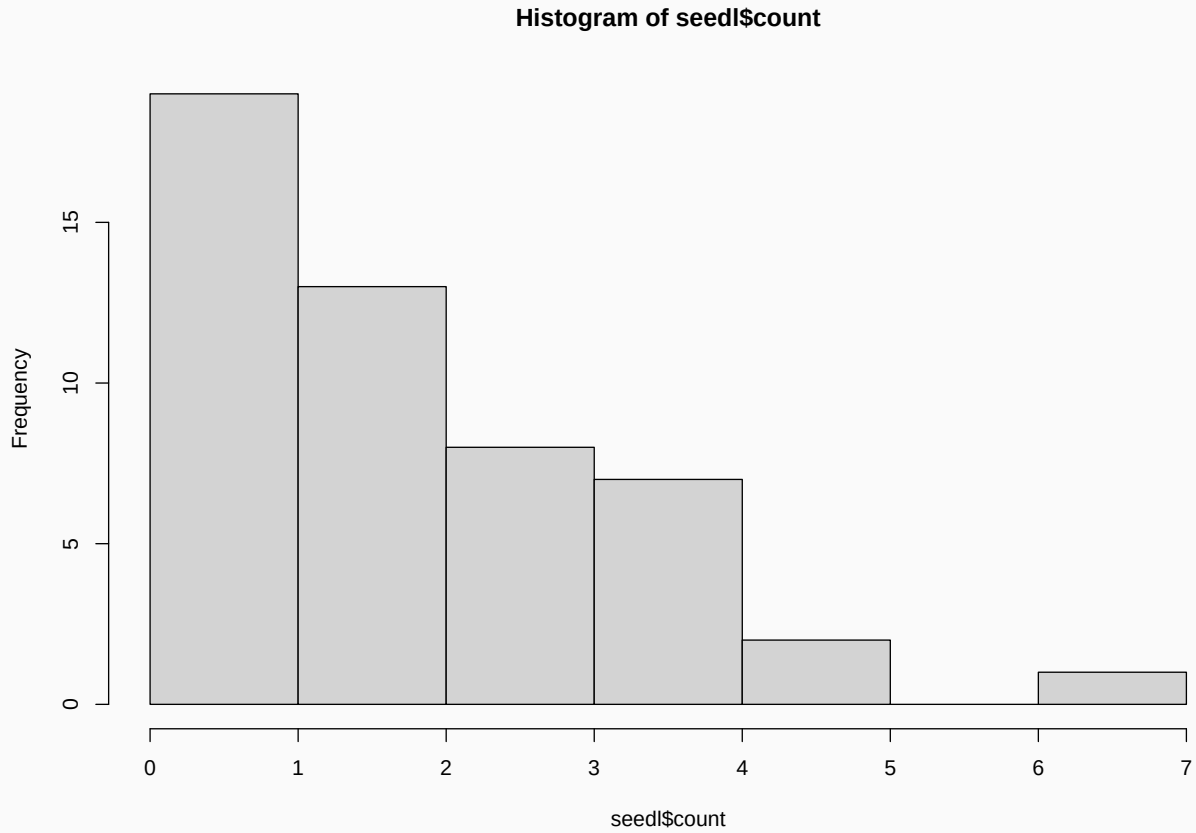
```
seedl <- read.csv('data/seedlings.csv')
```

```
     sample          count           light             area       
 Min.   : 1.00   Min.   :0.00   Min.   : 2.571   Min.   :0.25  
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:26.879   1st Qu.:0.25  
 Median :25.50   Median :2.00   Median :47.493   Median :0.50  
 Mean   :25.50   Mean   :2.14   Mean   :47.959   Mean   :0.62  
 3rd Qu.:37.75   3rd Qu.:3.00   3rd Qu.:67.522   3rd Qu.:1.00  
 Max.   :50.00   Max.   :7.00   Max.   :99.135   Max.   :1.00  
```

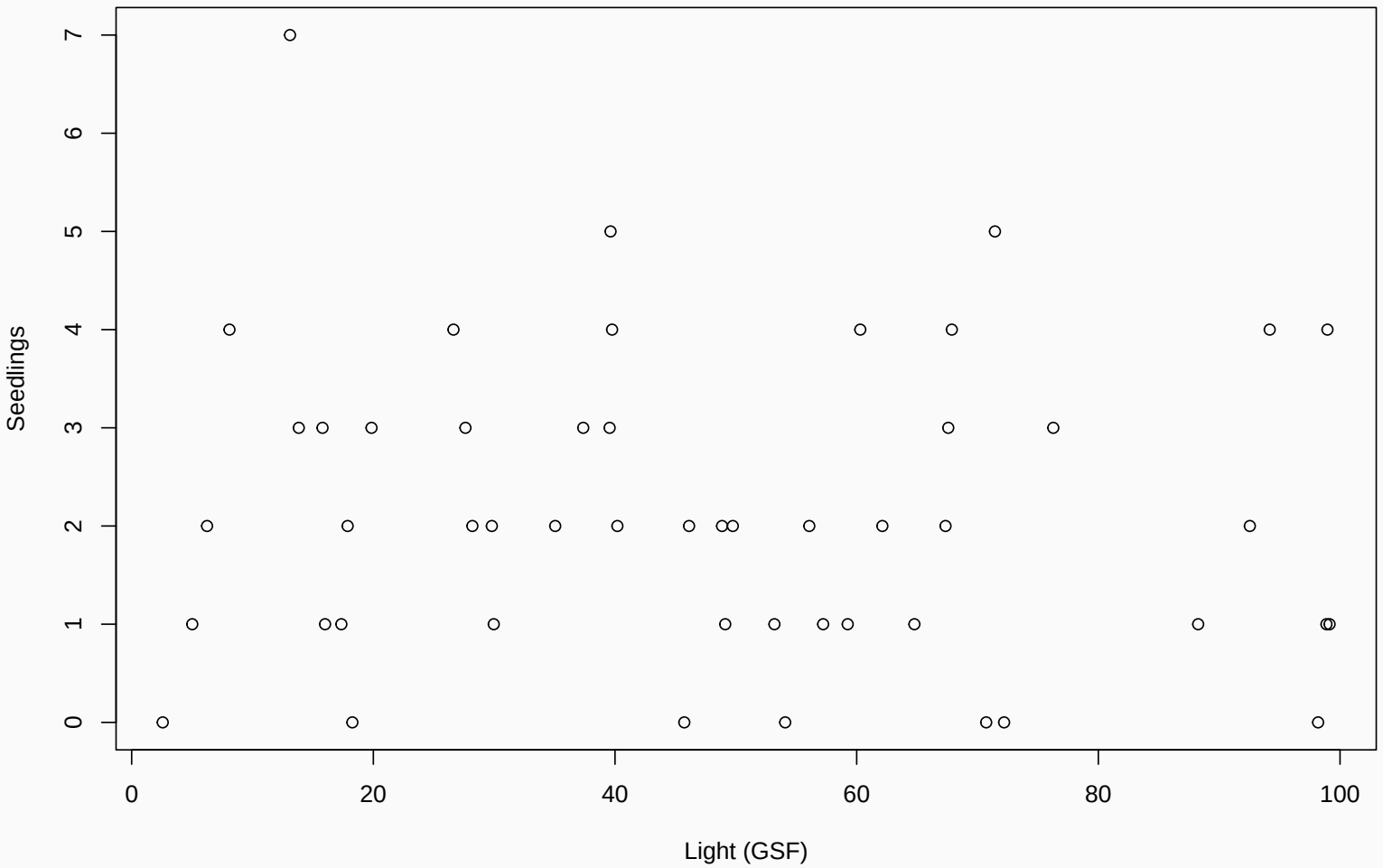
Exploring the data

```
table(seedl$count)
```

```
 0  1  2  3  4  5  7
 7 12 13  8  7  2  1
```



Relationship between Nseedlings and light?



Poisson regression

```
seedl.glm <- glm(count ~ light,
                 data = seedl,
                 family = poisson)
```

which corresponds to

```
equatiomatic::extract_eq(seedl.glm)
```

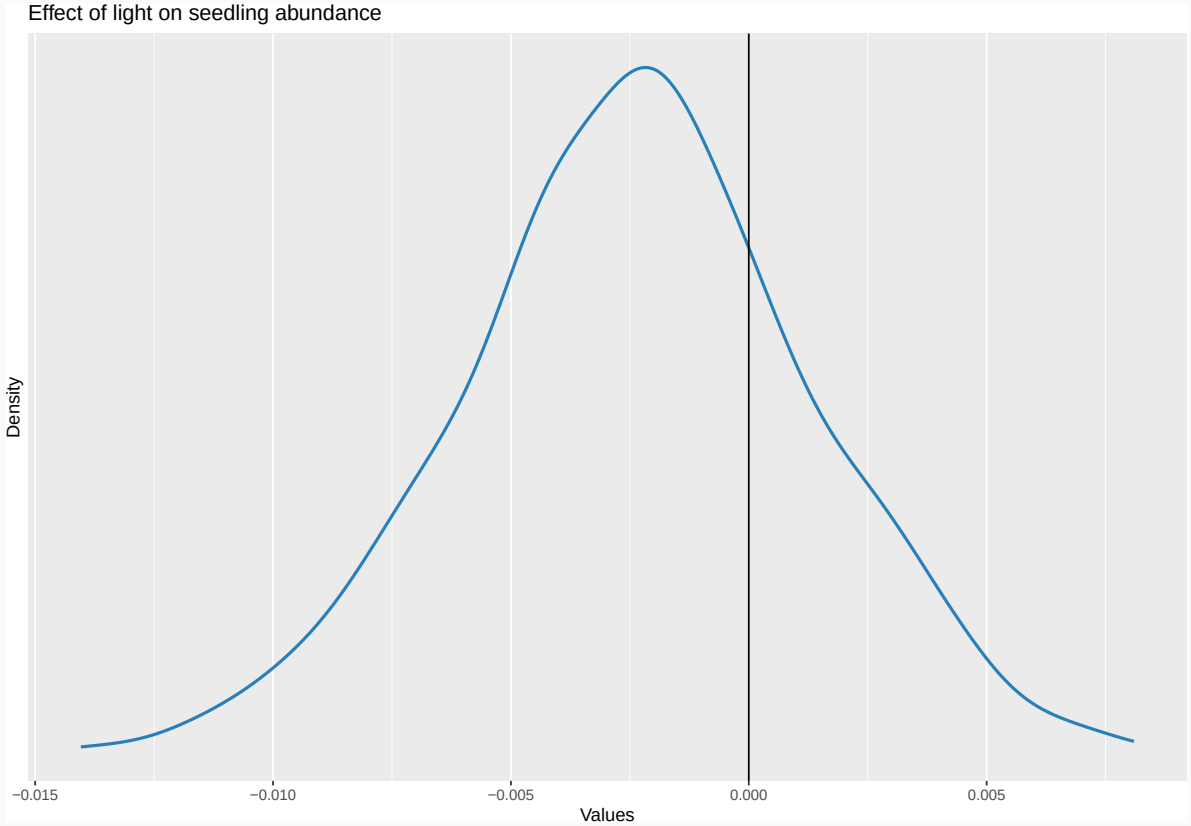
$$\log(E(\text{count})) = \alpha + \beta_1(\text{light}) \tag{1}$$

Interpreting Poisson GLM

```
Call:
glm(formula = count ~ light, family = poisson, data = seedl)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.881805   0.188892   4.668 3.04e-06 ***
light       -0.002576   0.003528  -0.730    0.465
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 63.029  on 49  degrees of freedom
Residual deviance: 62.492  on 48  degrees of freedom
AIC: 182.03

Number of Fisher Scoring iterations: 5
```

Estimated distribution of the slope parameter

```
library('parameters')
plot(simulate_parameters(seedl.glm)) +
  geom_vline(xintercept = 0) +
  ggtitle('Effect of light on seedling abundance')
```



Parameter estimates are in log scale!

Parameter estimates (log scale):

```
coef(seedl.glm)[1]
```

```
(Intercept)
   0.881805
```

We need to back-transform: apply the inverse of the logarithm

```
exp(coef(seedl.glm)[1])
```

```
(Intercept)
   2.415255
```

Using easystats

```
library('easystats')
parameters(seedl.glm)
```

```
Parameter   |  Log-Mean |       SE |         95% CI |     z |      p
-------------------------------------------------------------------
(Intercept) |      0.88 |     0.19 | [ 0.50, 1.24] |  4.67 | < .001
light       | -2.58e-03 | 3.53e-03 | [-0.01, 0.00] | -0.73 | 0.465
```

```
parameters(seedl.glm, exponentiate = TRUE)
```

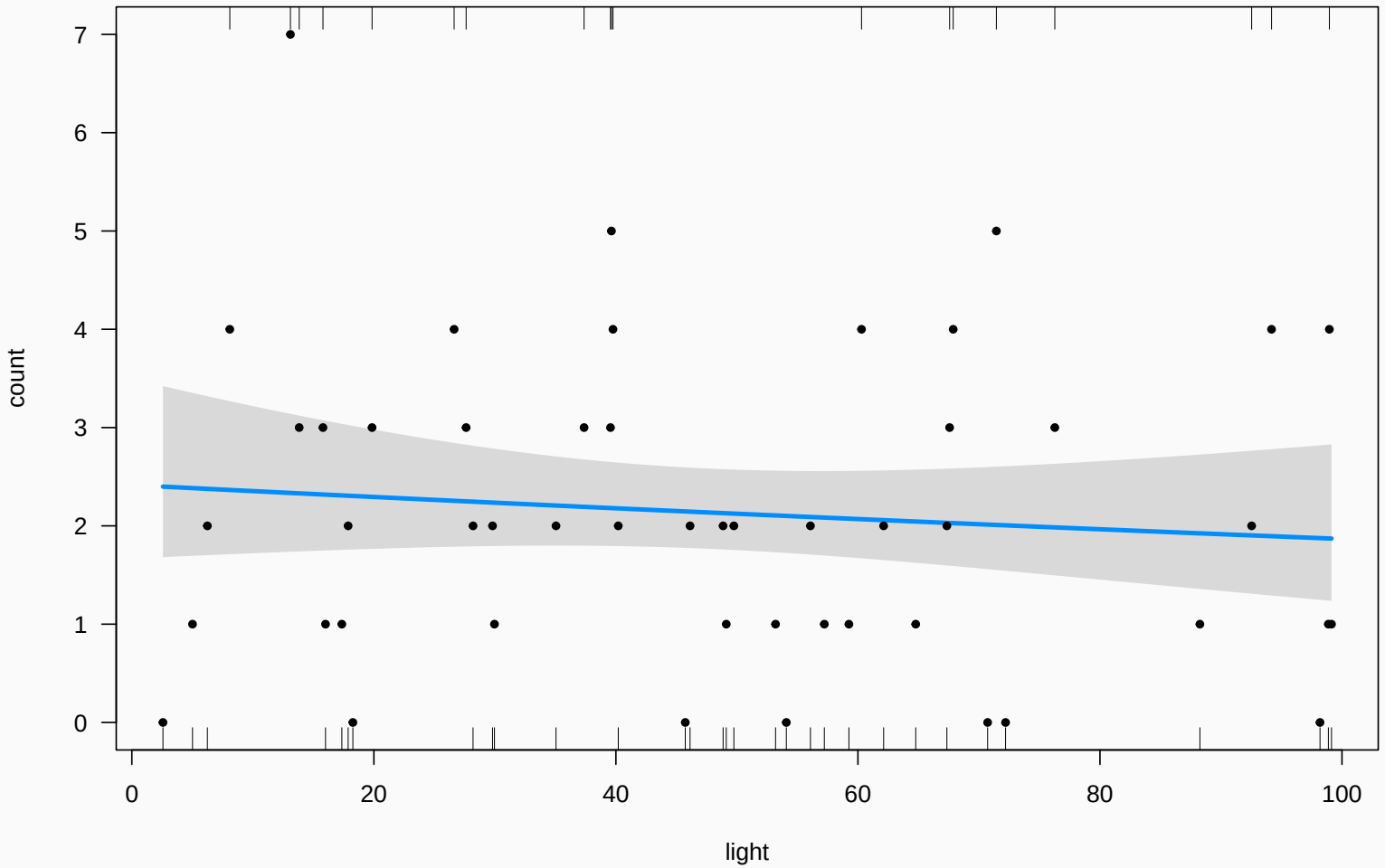
```
Parameter   |  IRR |       SE |        95% CI |     z |      p
-----------------------------------------------------------------
(Intercept) | 2.42 |     0.46 | [1.65, 3.46] |  4.67 | < .001
light       | 1.00 | 3.52e-03 | [0.99, 1.00] | -0.73 | 0.465
```

How Nseedlings decrease with light

```
Model-based Expectation

light | Predicted |   SE |       95% CI
-------------------------------------
2.57  |      2.40 | 0.43 | [1.68, 3.42]
13.30 |      2.33 | 0.35 | [1.74, 3.13]
24.03 |      2.27 | 0.28 | [1.78, 2.89]
34.76 |      2.21 | 0.23 | [1.80, 2.71]
45.49 |      2.15 | 0.21 | [1.78, 2.60]
56.22 |      2.09 | 0.22 | [1.71, 2.56]
66.95 |      2.03 | 0.25 | [1.60, 2.58]
77.68 |      1.98 | 0.29 | [1.48, 2.64]
88.41 |      1.92 | 0.34 | [1.36, 2.73]
99.13 |      1.87 | 0.39 | [1.24, 2.83]

Variable predicted: count
Predictors modulated: light
```

Visualising how Nseedlings decrease with light

```
visreg(seedl.glm, scale = 'response', ylim = c(0, 7))
points(count ~ light, data = seedl, pch = 20)
```



Low R-squared

```
library('performance')
r2(seedl.glm)
```

```
# R2 for Generalized Linear Regression
  Nagelkerke's R2: 0.015
```

Describing the model results

```
library('report')
report(seedl.glm)
```

We fitted a poisson model (estimated using ML) to predict count with light (formula: count ~ light). The model's explanatory power is very weak (Nagelkerke's R2 = 0.01). The model's intercept, corresponding to light = 0, is at 0.88 (95% CI [0.50, 1.24], p < .001). Within this model:

- The effect of light is statistically non-significant and negative (beta = -2.58e-03, 95% CI [-9.57e-03, 4.28e-03], p = 0.465; Std. beta = -0.07, 95% CI [-0.27, 0.12])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald z-distribution approximation.

Model checking

Assumptions of Poisson regression

- Linearity (log response ~ predictors)

Assumptions of Poisson regression

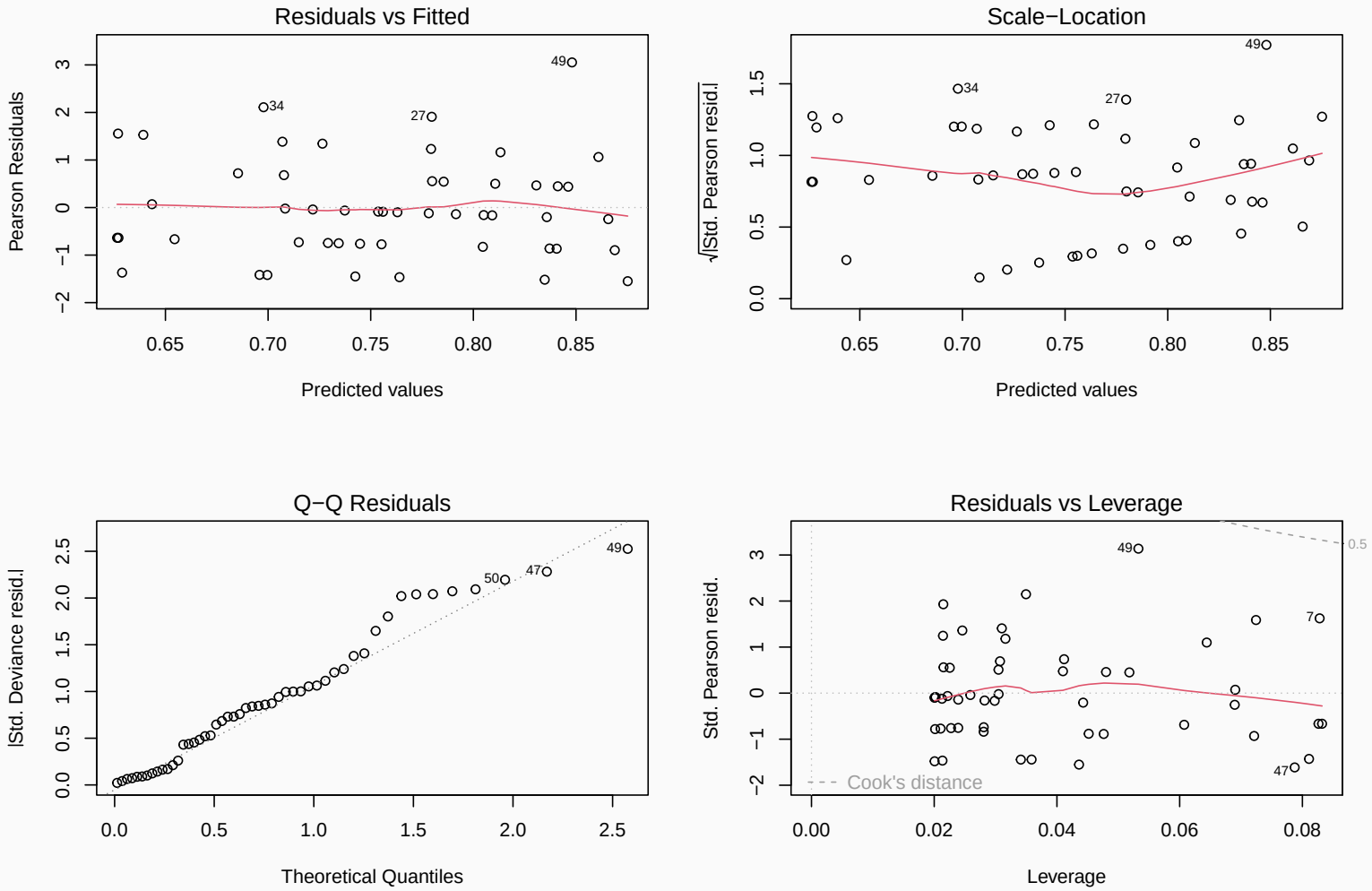
- Linearity (log response ~ predictors)
- Observations are independent

Assumptions of Poisson regression

- Linearity (log response ~ predictors)
- Observations are independent
- Mean = Variance

Checking Poisson GLM

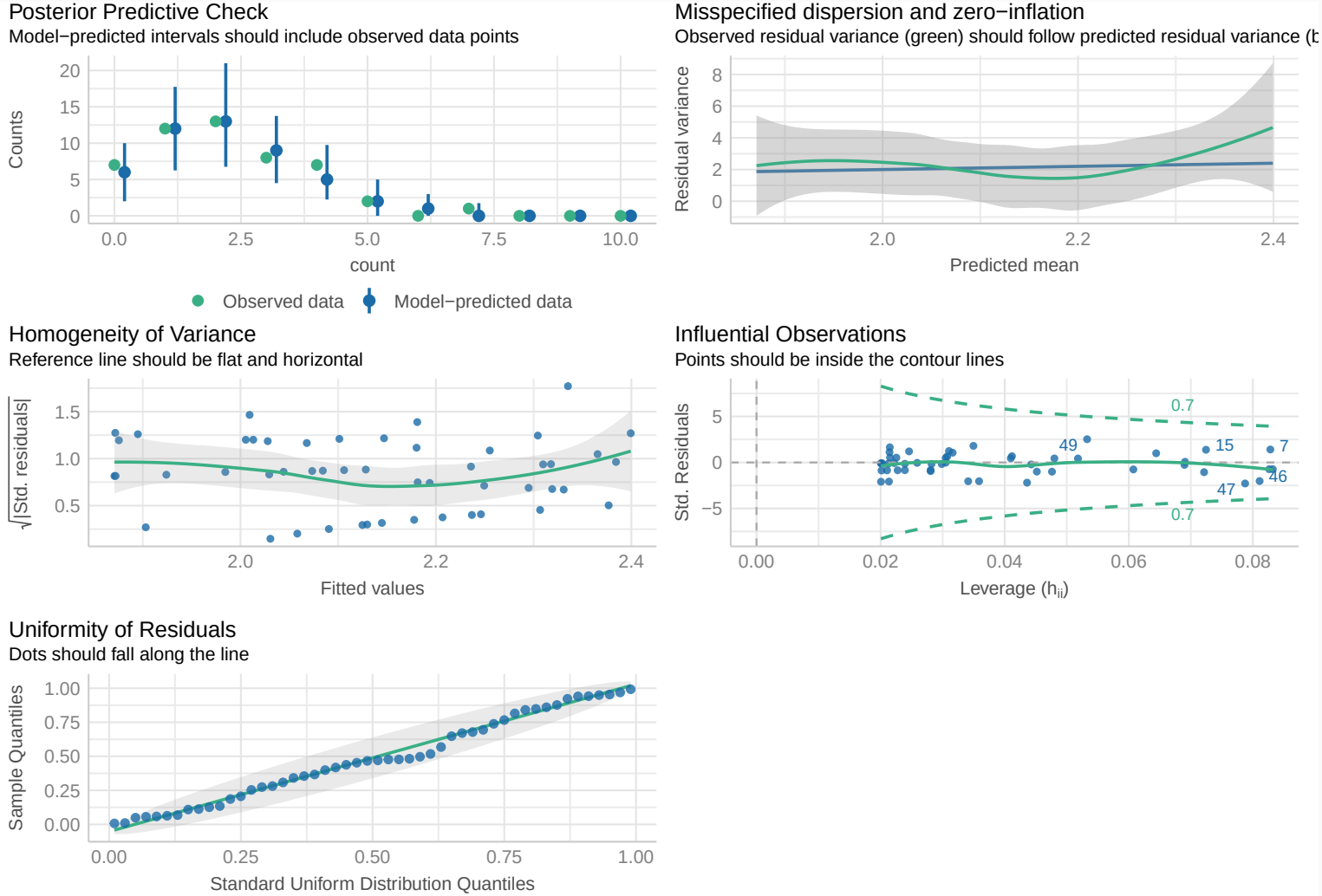
```
plot(seedl.glm)
```




```
null device
          1
```

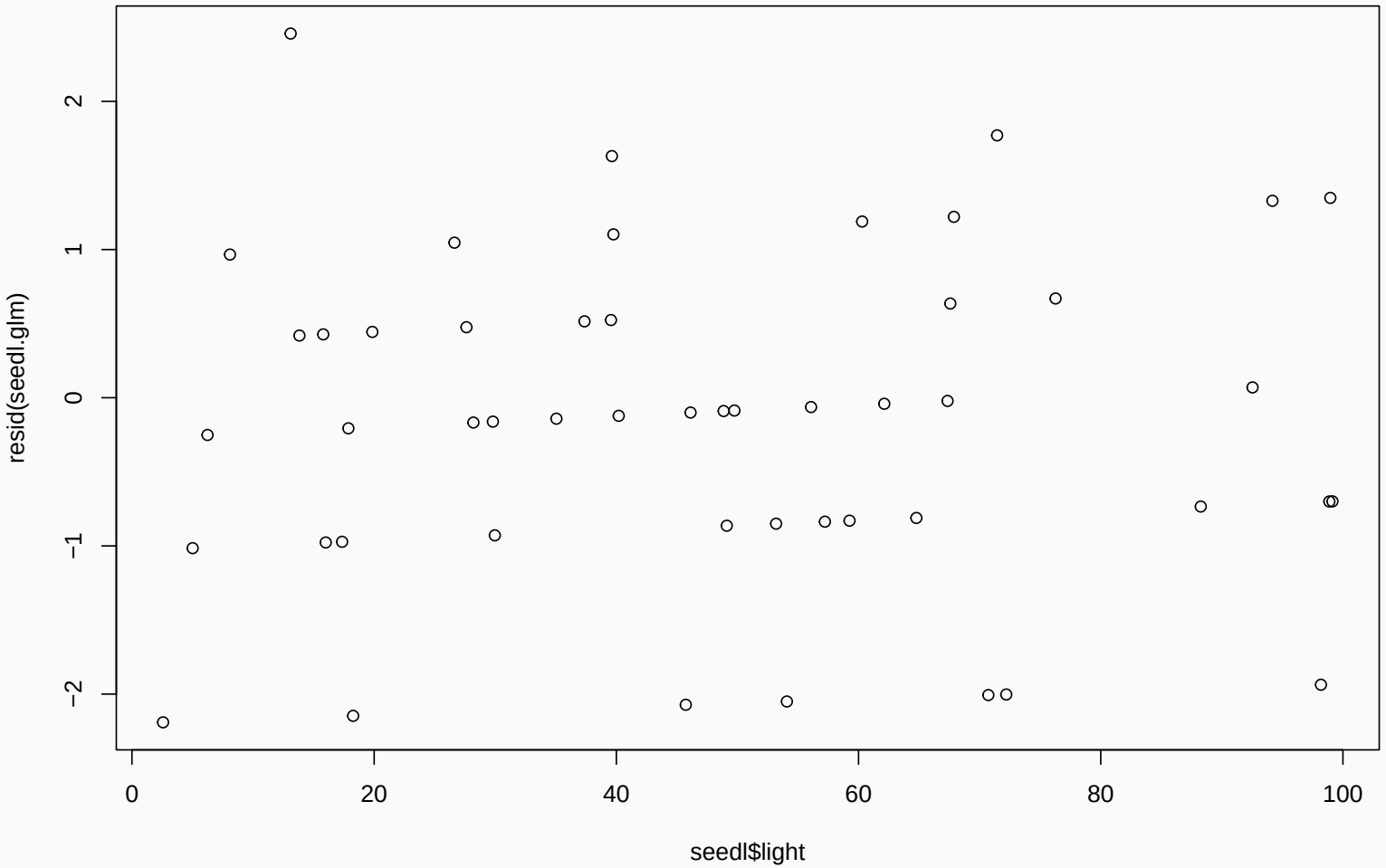
Checking Poisson GLM

```
check_model(seedl.glm)
```



Is there pattern of residuals along predictor?

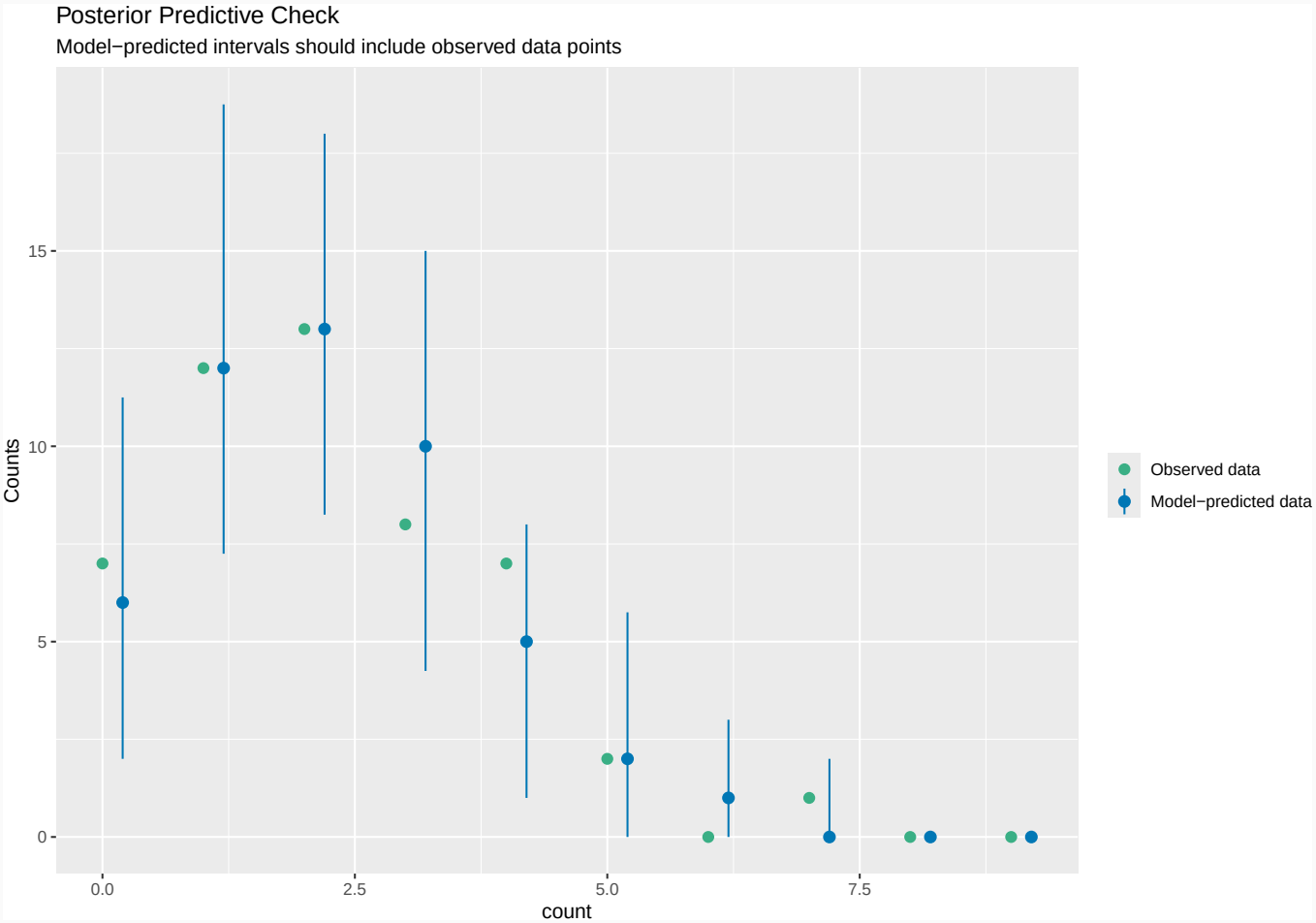
```
plot(seedl$light, resid(seedl.glm))
```



Posterior predictive checking

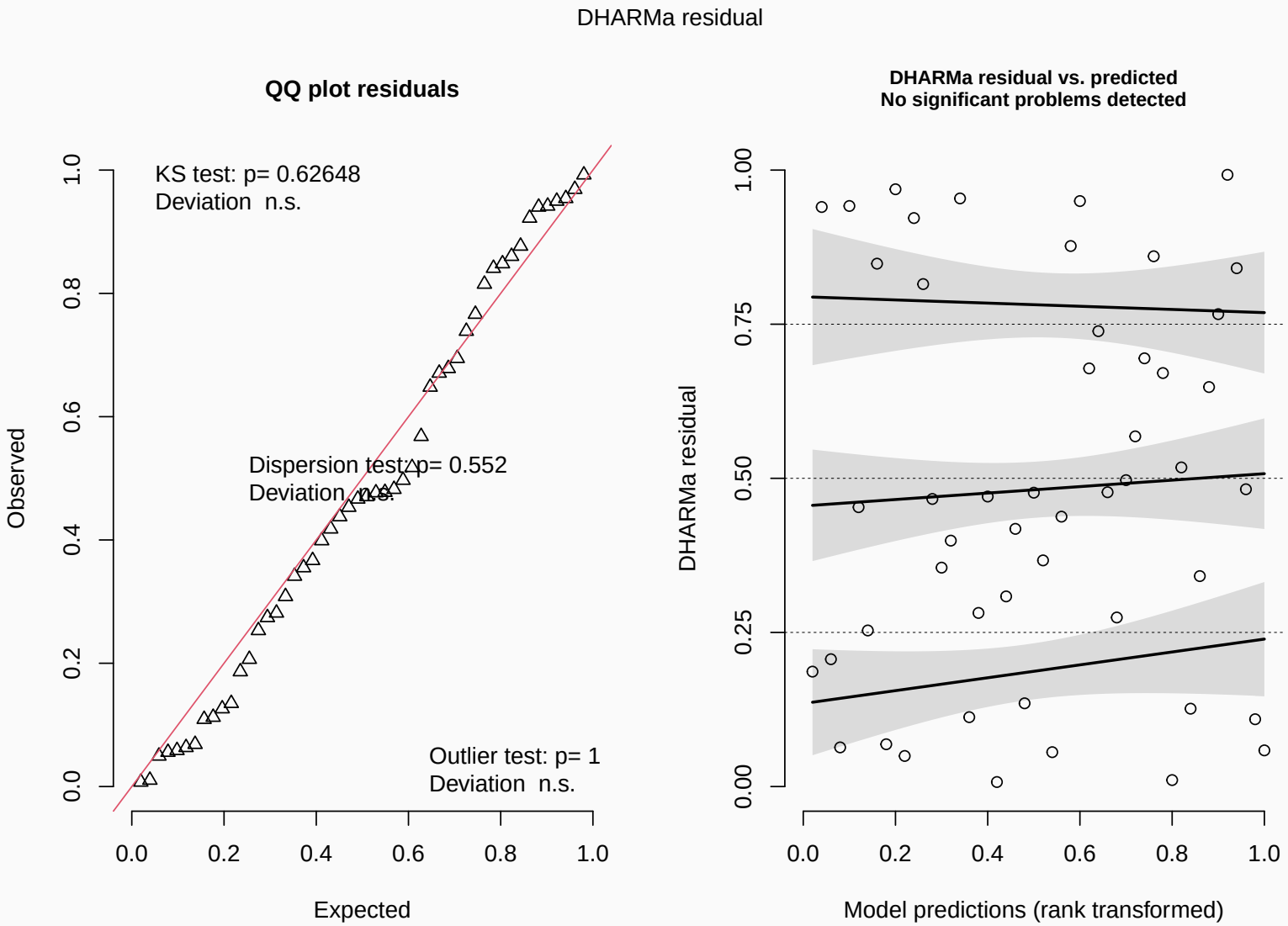
Simulate data from fitted model (`yrep`) and compare with observed data (`y`)

```
check_predictions(seedl.glm)
```



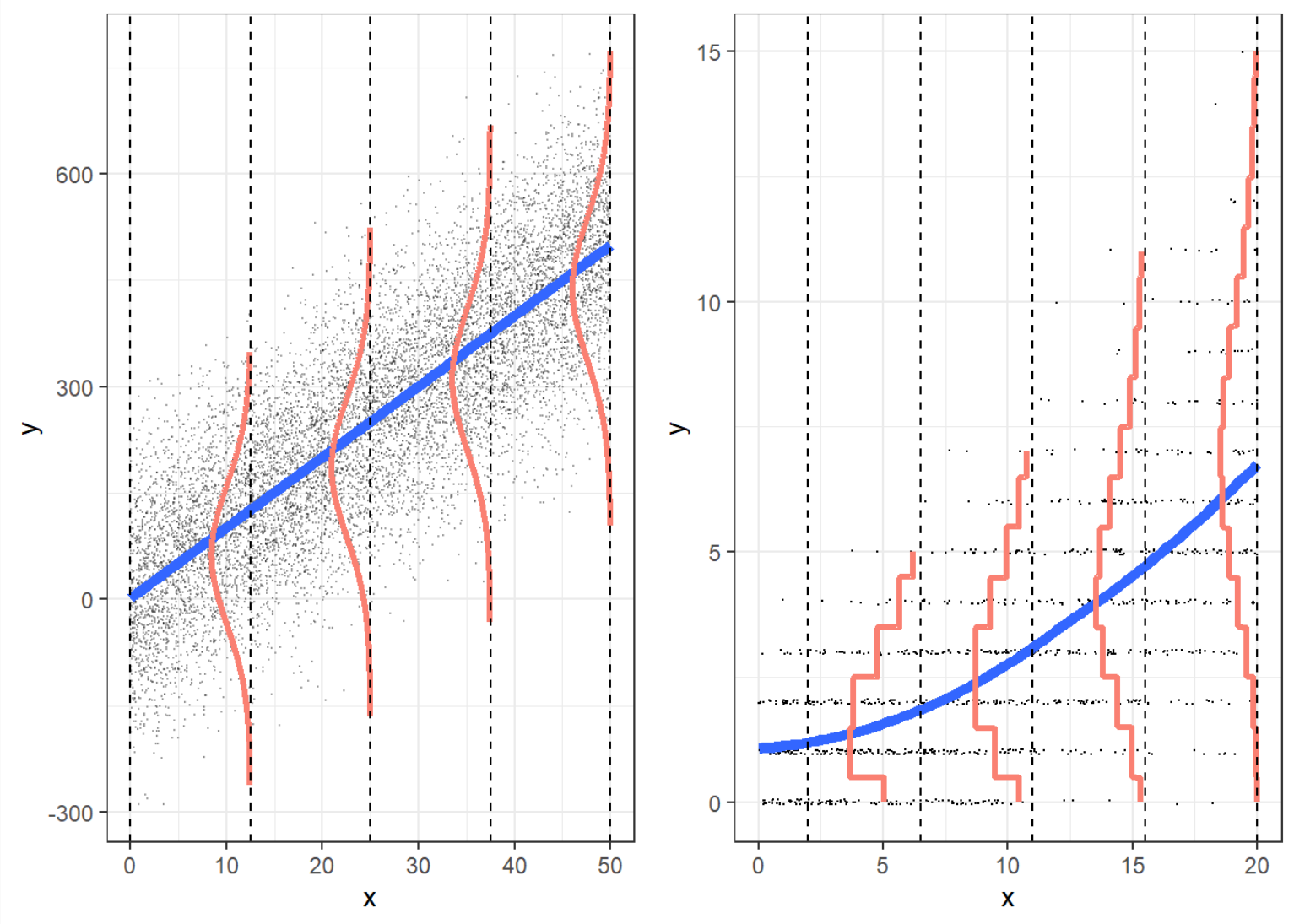
Residuals diagnostics with DHARMa

```
simulateResiduals(seedl.glm, plot = TRUE)
```



Overdispersion

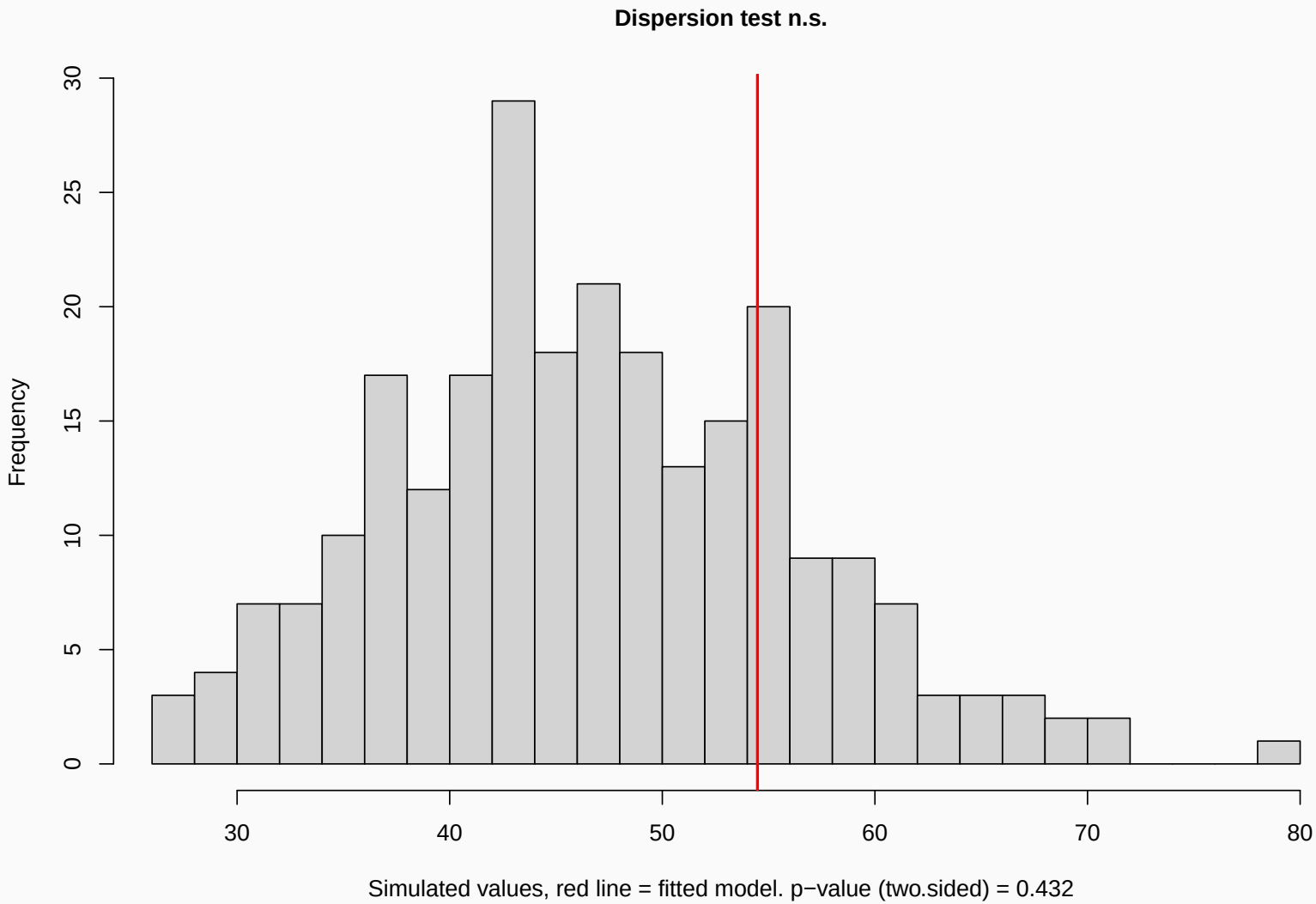
Poisson GLM assumes mean = variance



Roback & Legler 2021

Always check overdispersion with count data

```
simres <- simulateResiduals(seedl.glm, refit = TRUE)
testDispersion(simres)
```



Accounting for overdispersion in count data

- Use family `quasipoisson`

Accounting for overdispersion in count data

- Use family `quasipoisson`
- Use negative binomial distribution (`MASS::glm.nb`)

Accounting for overdispersion in count data

- Use family `quasipoisson`
- Use negative binomial distribution (`MASS::glm.nb`)
- Include observation-level random effect (e.g. see Harrison 2014)

Accounting for overdispersion with family `quasipoisson`

```
Call:
glm(formula = count ~ light, family = quasipoisson, data = seedl)

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.881805   0.201230   4.382 6.37e-05 ***
light       -0.002576   0.003758  -0.685    0.496
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 1.134907)

    Null deviance: 63.029  on 49  degrees of freedom
Residual deviance: 62.492  on 48  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Mean estimates do not change after accounting for overdispersion

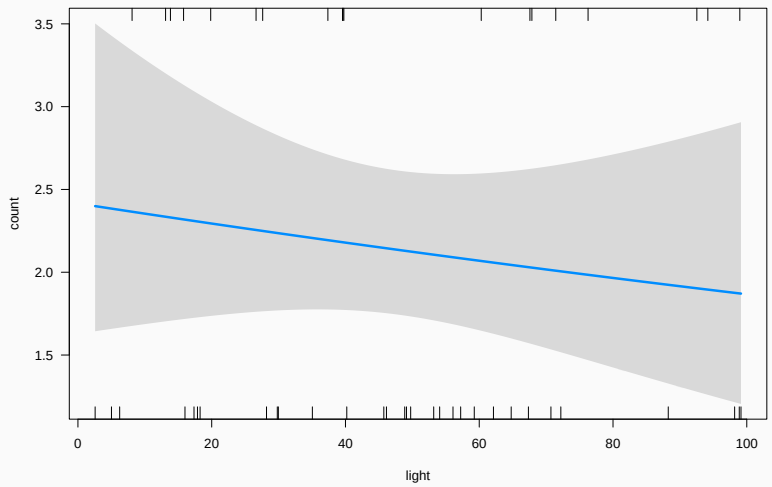
```
parameters(seedl.overdisp)
```

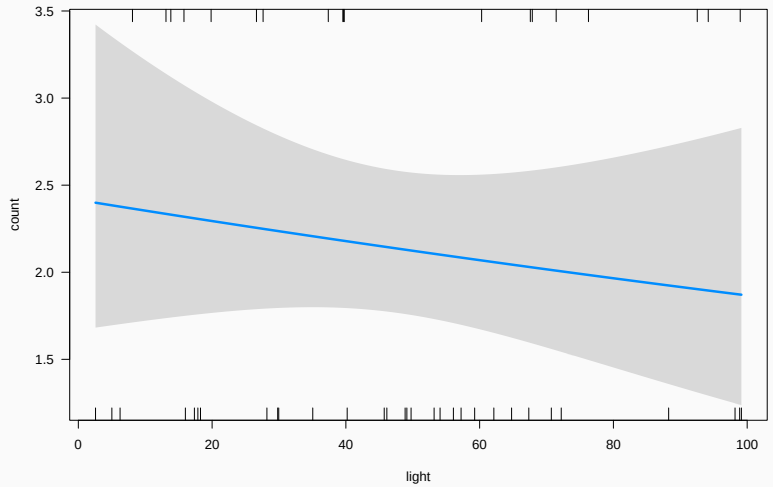
```
Parameter   |  Log-Mean |       SE |         95% CI | t(48) |      p
-------------------------------------------------------------------
(Intercept) |      0.88 |     0.20 | [ 0.47, 1.26] |  4.38 | < .001
light       | -2.58e-03 | 3.76e-03 | [-0.01, 0.00] | -0.69 | 0.493
```

```
parameters(seedl.glm)
```

```
Parameter   |  Log-Mean |       SE |         95% CI |     z |      p
-------------------------------------------------------------------
(Intercept) |      0.88 |     0.19 | [ 0.50, 1.24] |  4.67 | < .001
light       | -2.58e-03 | 3.53e-03 | [-0.01, 0.00] | -0.73 | 0.465
```

But standard errors may change





Accounting for overdispersion using negative binomial

```r
library('MASS')
seedl.nb <- glm.nb(count ~ light, data = seedl)
```

```
Call:
glm.nb(formula = count ~ light, data = seedl, init.theta = 22.23419419,
    link = log)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.881996   0.198213   4.450  8.6e-06 ***
light       -0.002580   0.003691  -0.699    0.485
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(22.2342) family taken to be 1)

    Null deviance: 58.247  on 49  degrees of freedom
Residual deviance: 57.756  on 48  degrees of freedom
AIC: 183.83

Number of Fisher Scoring iterations: 1
```

Comparing Poisson and Negative Binomial

```
compare_models(seedl.glm, seedl.nb)
```

```
Parameter    |               seedl.glm |                seedl.nb
-------------------------------------------------------------------
(Intercept)  |      0.88 ( 0.51, 1.25) |      0.88 ( 0.49, 1.27)
light        | -2.58e-03 (-0.01, 0.00) | -2.58e-03 (-0.01, 0.00)
-------------------------------------------------------------------
Observations |                      50 |                      50
```

```
compare_performance(seedl.glm, seedl.nb)
```

```
# Comparison of Model Performance Indices

Name      |  Model | AIC (weights) | AICc (weights) | BIC (weights)
-------------------------------------------------------------------
seedl.glm |    glm | 182.0 (0.710) |  182.3 (0.737) | 185.9 (0.864)
seedl.nb  | negbin | 183.8 (0.290) |  184.3 (0.263) | 189.6 (0.136)

Name      | Nagelkerke's R2 |  RMSE | Sigma | Score_log | Score_spherical
-------------------------------------------------------------------------
seedl.glm |           0.015 | 1.529 | 1.000 |    -1.780 |           0.131
seedl.nb  |           0.014 | 1.529 | 1.000 |    -1.821 |           0.133
```

What if survey plots have different area?

Shall we *standardise* counts dividing by sampling plot area?

Model would be: count/area ~ light

	sample	count	light	area
1	1	0	70.71854	0.50
2	2	1	88.26021	0.25
3	3	2	67.35133	0.50
4	4	3	67.57850	1.00
5	5	4	26.63098	0.25
6	6	3	15.79433	1.00

Avoid regression of ratios

J. R. Statist. Soc. A (1993)
156, *Part* 3, *pp.* 379–392

Spurious Correlation and the Fallacy of the Ratio Standard Revisited

By RICHARD A. KRONMAL†

https://doi.org/10.2307/2983064

Use `offset` to account for variable sampling effort

```
seedl.offset <- glm(count ~ light,
                    offset = log(area),
                    data = seedl,
                    family = poisson)
```

Note estimates now referred to area units!

```
Call:
glm(formula = count ~ light, family = poisson, data = seedl,
    offset = log(area))

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.513185   0.183245   8.258   <2e-16 ***
light       -0.005674   0.003384  -1.677   0.0936 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 95.199  on 49  degrees of freedom
Residual deviance: 92.354  on 48  degrees of freedom
AIC: 211.9
```

Note estimates now referred to area units!

```
exp(coef(seedl.offset)[1])
```

```
(Intercept)
   4.541173
```

Prediction

Predicting number of seedlings given light

```
new.lights <- data.frame(light = c(10, 90))
predict(seedl.glm, newdata = new.lights, type = 'response', se.fit
```

```
$fit
       1        2
2.353841 1.915533

$se.fit
        1         2
0.3756992 0.3502446

$residual.scale
[1] 1
```

Prediction (easystats)

```
new.lights <- data.frame(light = c(10, 90))
estimate_expectation(seedl.glm, data = new.lights)
```

```
Model-based Expectation

light | Predicted |   SE |       95% CI
---------------------------------------
10.00 |      2.35 | 0.38 | [1.72, 3.22]
90.00 |      1.92 | 0.35 | [1.34, 2.74]

Variable predicted: count
```

```
estimate_prediction(seedl.glm, data = new.lights)
```

```
Model-based Prediction

light | Predicted |       95% CI
-------------------------------
10.00 |      2.35 | [0.00, 6.00]
90.00 |      1.92 | [0.00, 5.00]

Variable predicted: count
```

Poisson GLM: more examples

- Infant mortality ~ GDP

Poisson GLM: more examples

- Infant mortality ~ GDP
- Number of cones consumed by squirrels (data)

Poisson GLM: more examples

- Infant mortality ~ GDP
- Number of cones consumed by squirrels (data)
- Elephant matings (Poole 1989)

Modelling zero-inflated (and overdispersed) count data

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

How many eggs in nests?

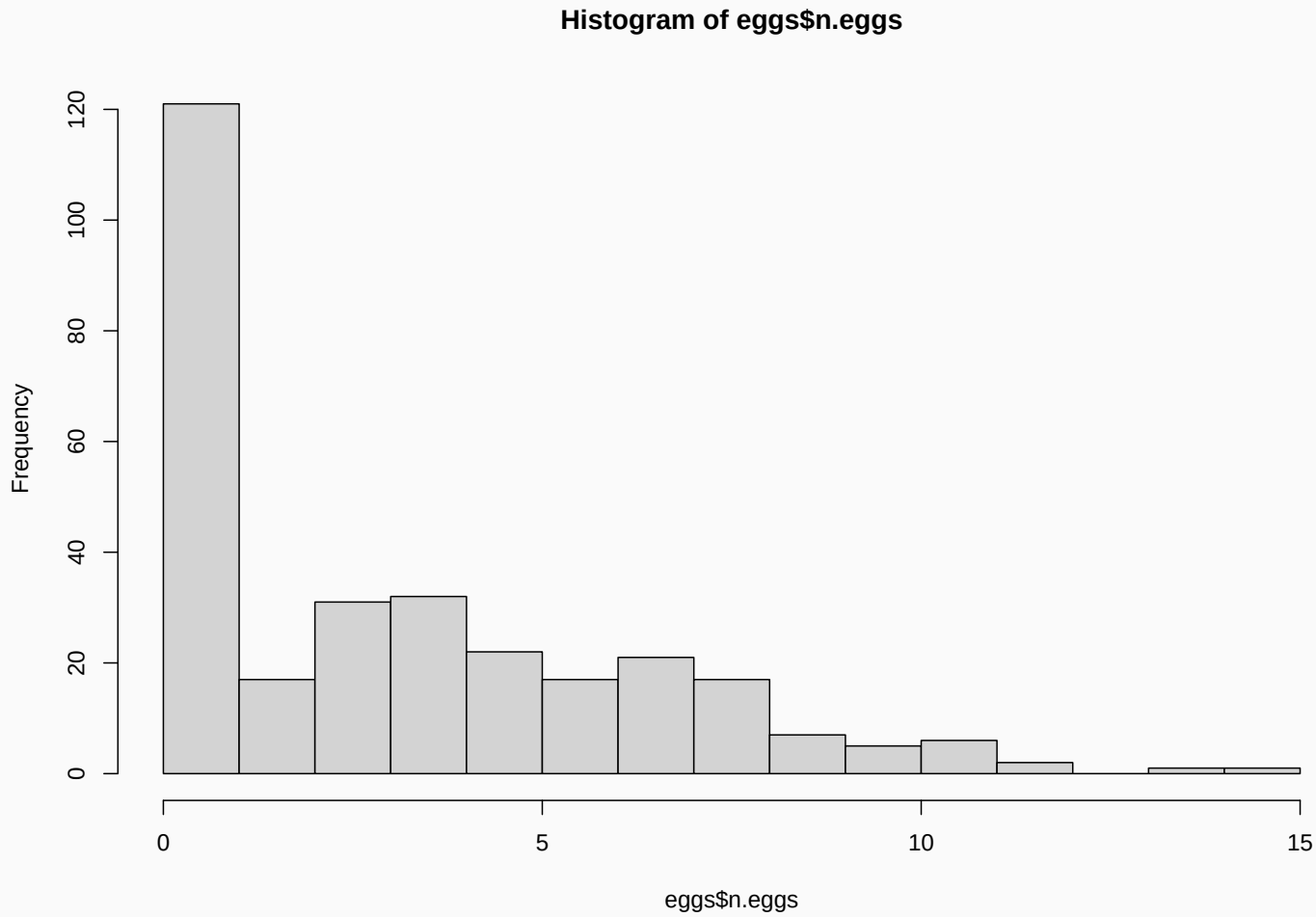
```
eggs <- read.csv('data/eggs.csv')
```

diameter	old	n.eggs
14	no	4
8	yes	0
7	yes	0

`diameter`: nest diameter (cm)

`old`: does nest look old/abandoned?

How many eggs in nests?



Many zeros does not mean you need a zero-inflated model!

Check model afterwards

How many eggs in nests?

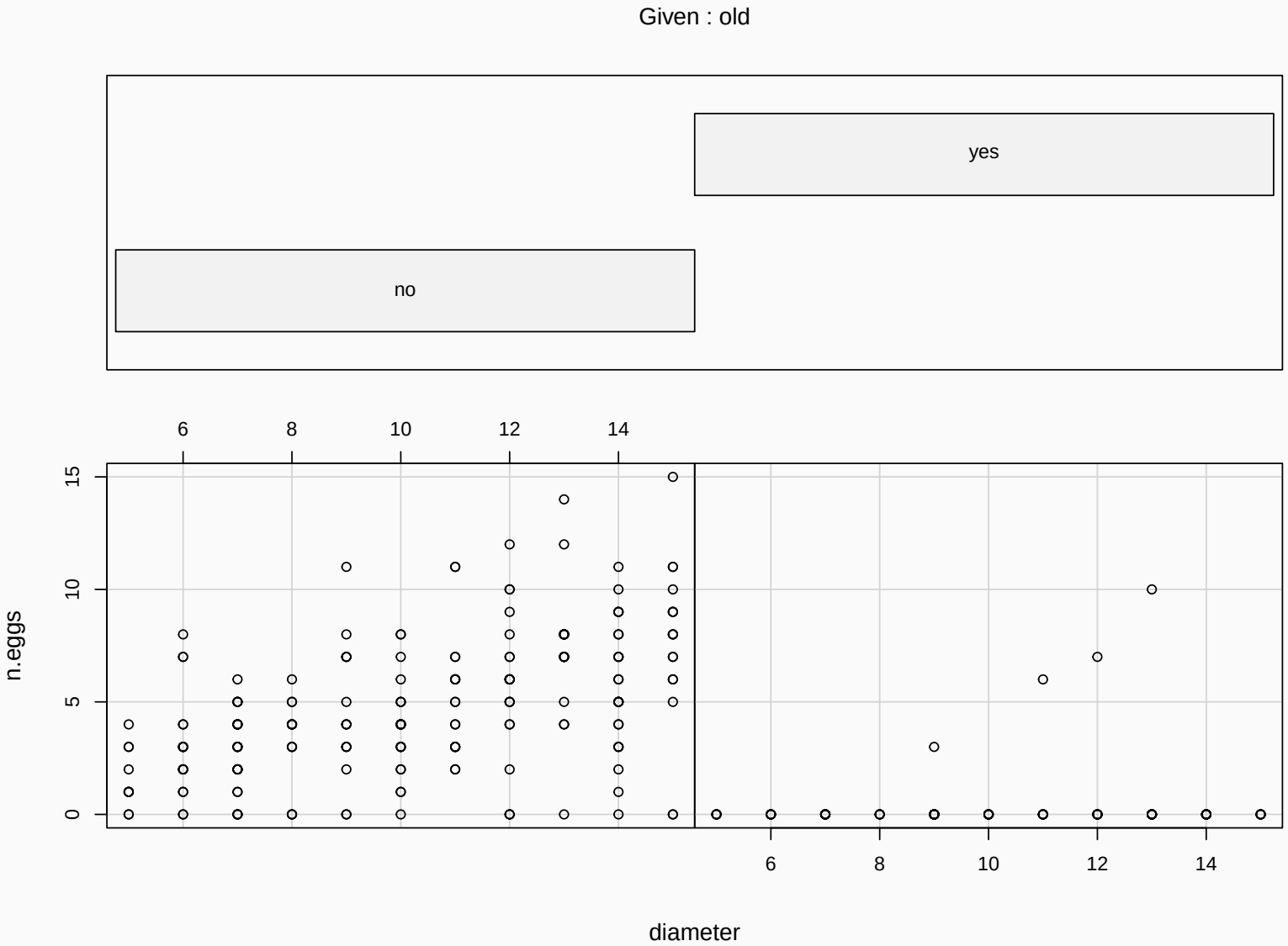
- Nests may be occupied or not

How many eggs in nests?

- Nests may be occupied or not
- Occupied nests may not have eggs (too soon, predation, etc)

Number of eggs ~ nest diameter * old appearance

```
coplot(n.eggs ~ diameter | old, data = eggs)
```



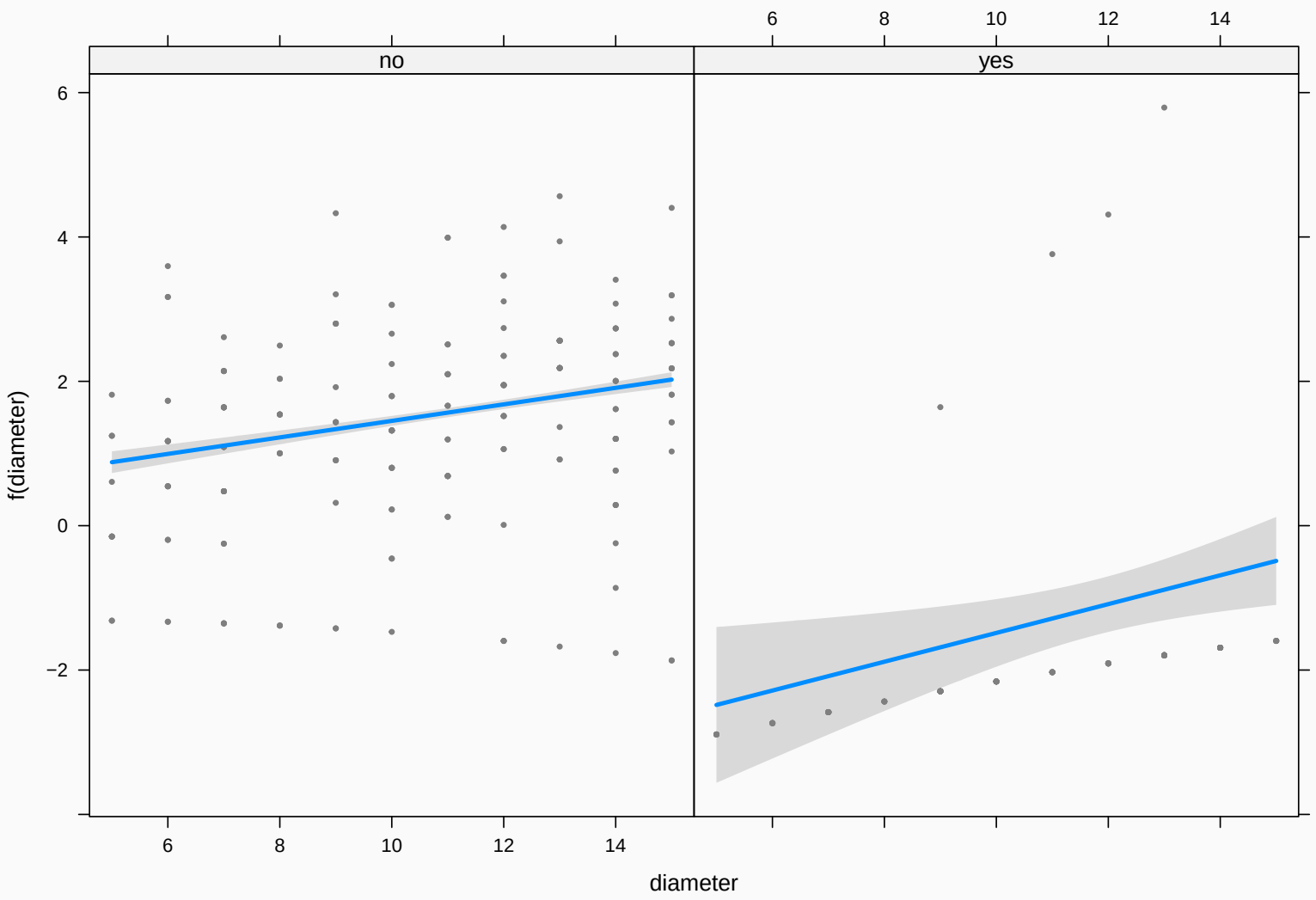
Trying Poisson GLM

```
eggs.poi <- glm(n.eggs ~ old * diameter,
                data = eggs,
                family = poisson)
```

Trying Poisson GLM

```
Call:
glm(formula = n.eggs ~ old * diameter, family = poisson, data = eggs)

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)     0.30773    0.12883   2.389   0.0169 *
oldyes         -3.78879    0.92230  -4.108 3.99e-05 ***
diameter        0.11441    0.01105  10.354  < 2e-16 ***
oldyes:diameter  0.08513    0.07634   1.115   0.2648
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1184.57  on 299  degrees of freedom
Residual deviance:  526.97  on 296  degrees of freedom
AIC: 1176.7

Number of Fisher Scoring iterations: 7
```

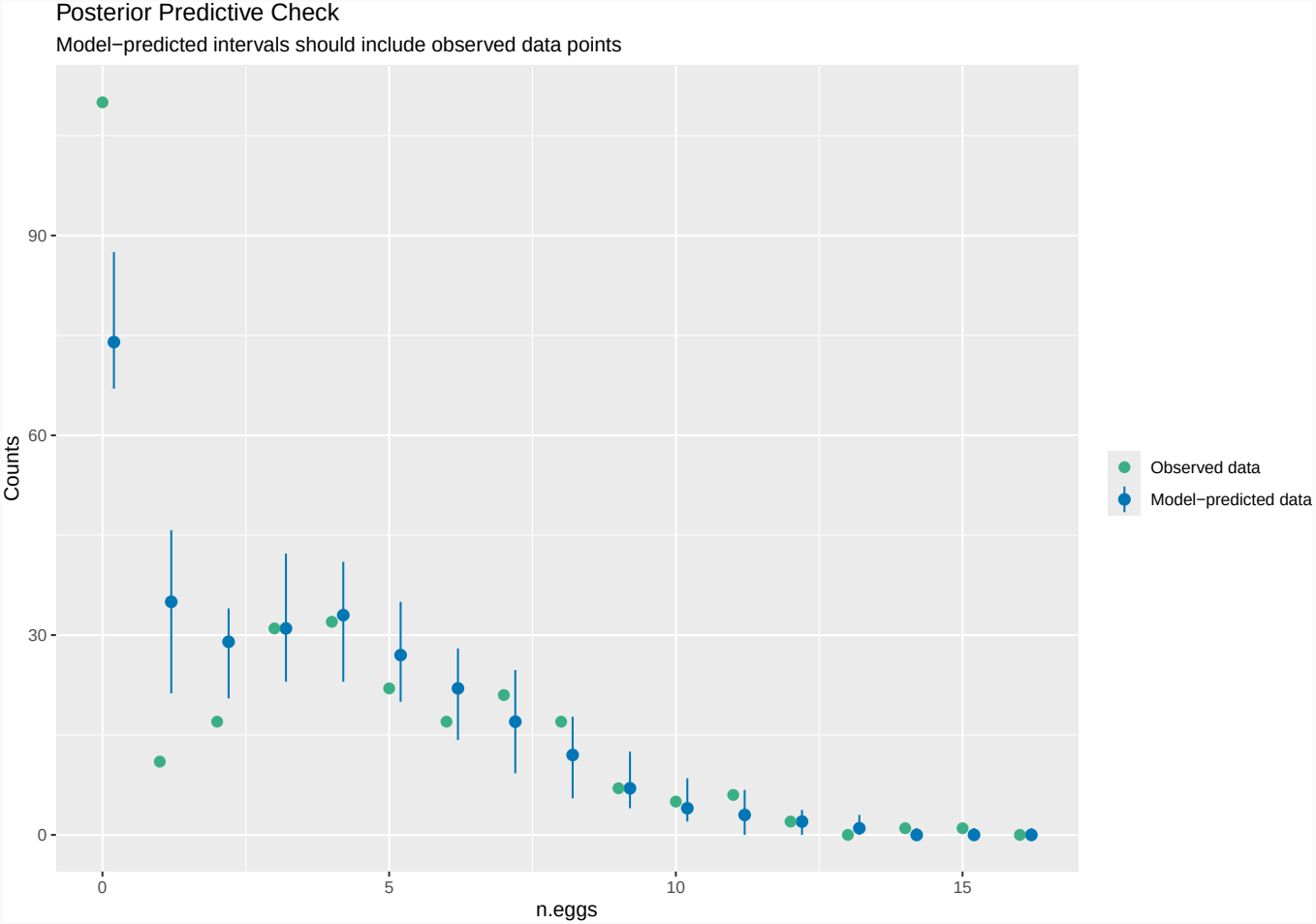
Visualising the fitted Poisson GLM



Checking Poisson GLM

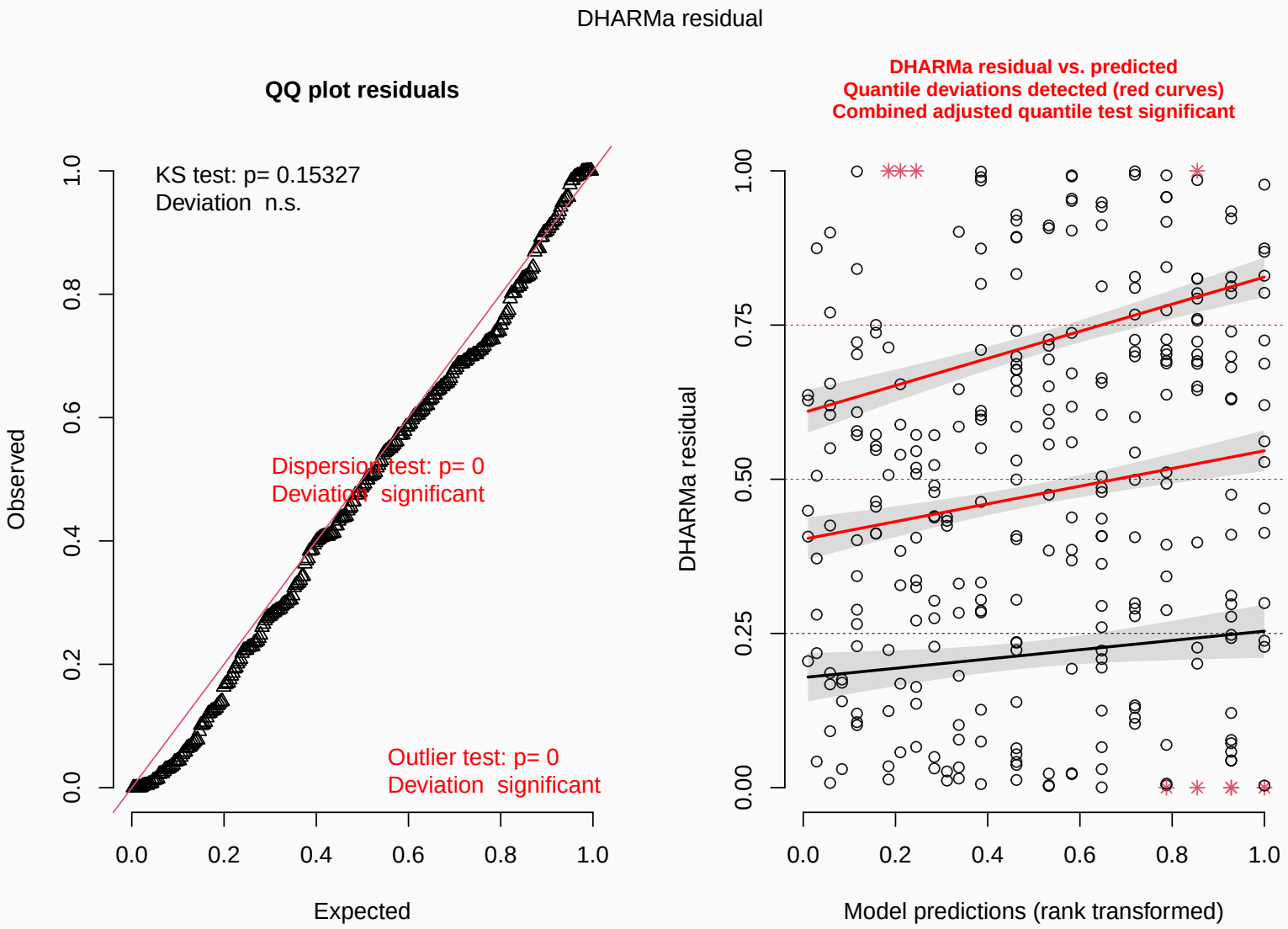
Simulate data from fitted model (**yrep**) and compare with observed data (**y**)

```
library('easystats')
check_predictions(eggs.poi)
```



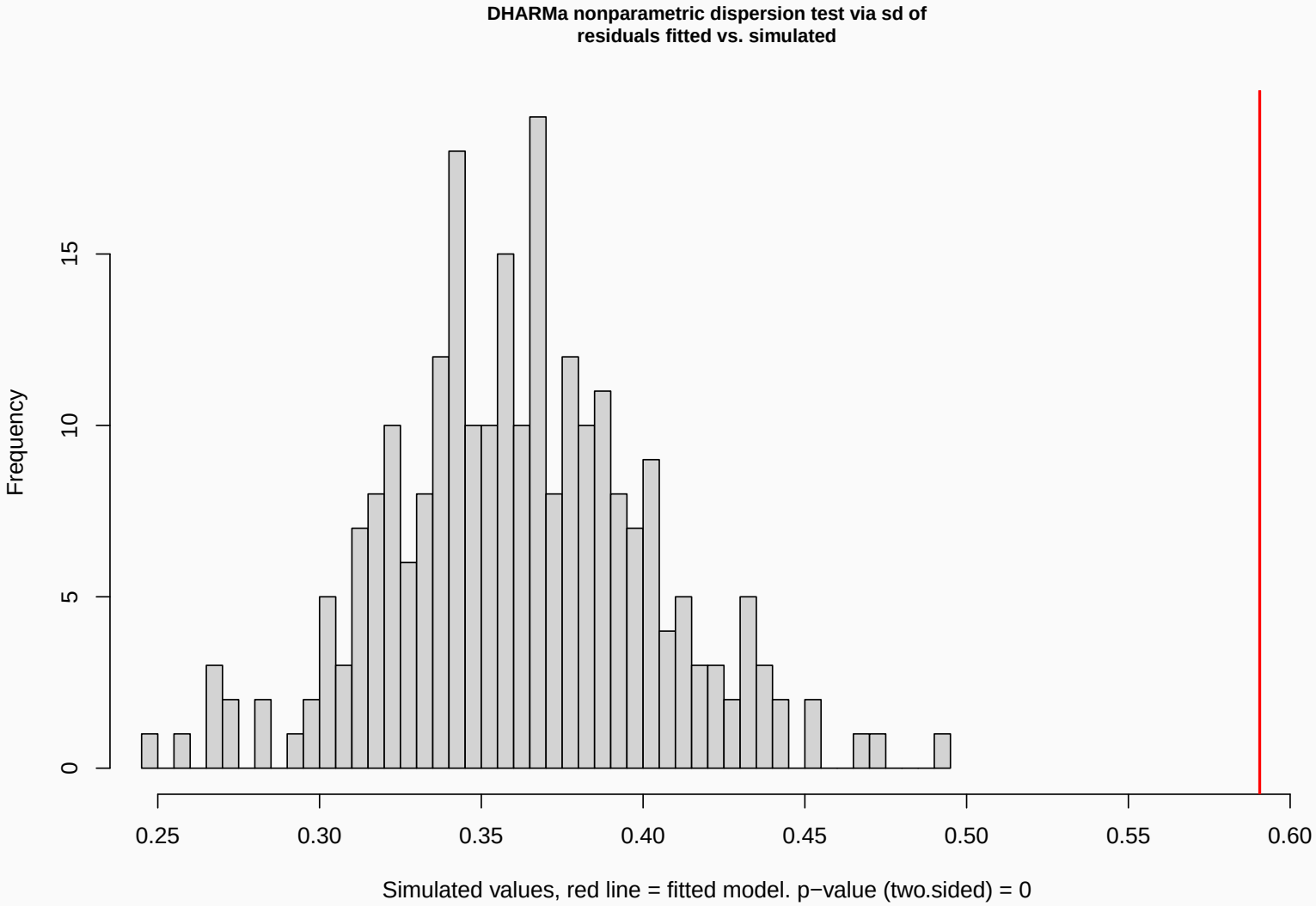
Checking Poisson GLM with DHARMa

```
library('DHARMa')
eggs.poi.res <- simulateResiduals(eggs.poi, plot = TRUE)
```



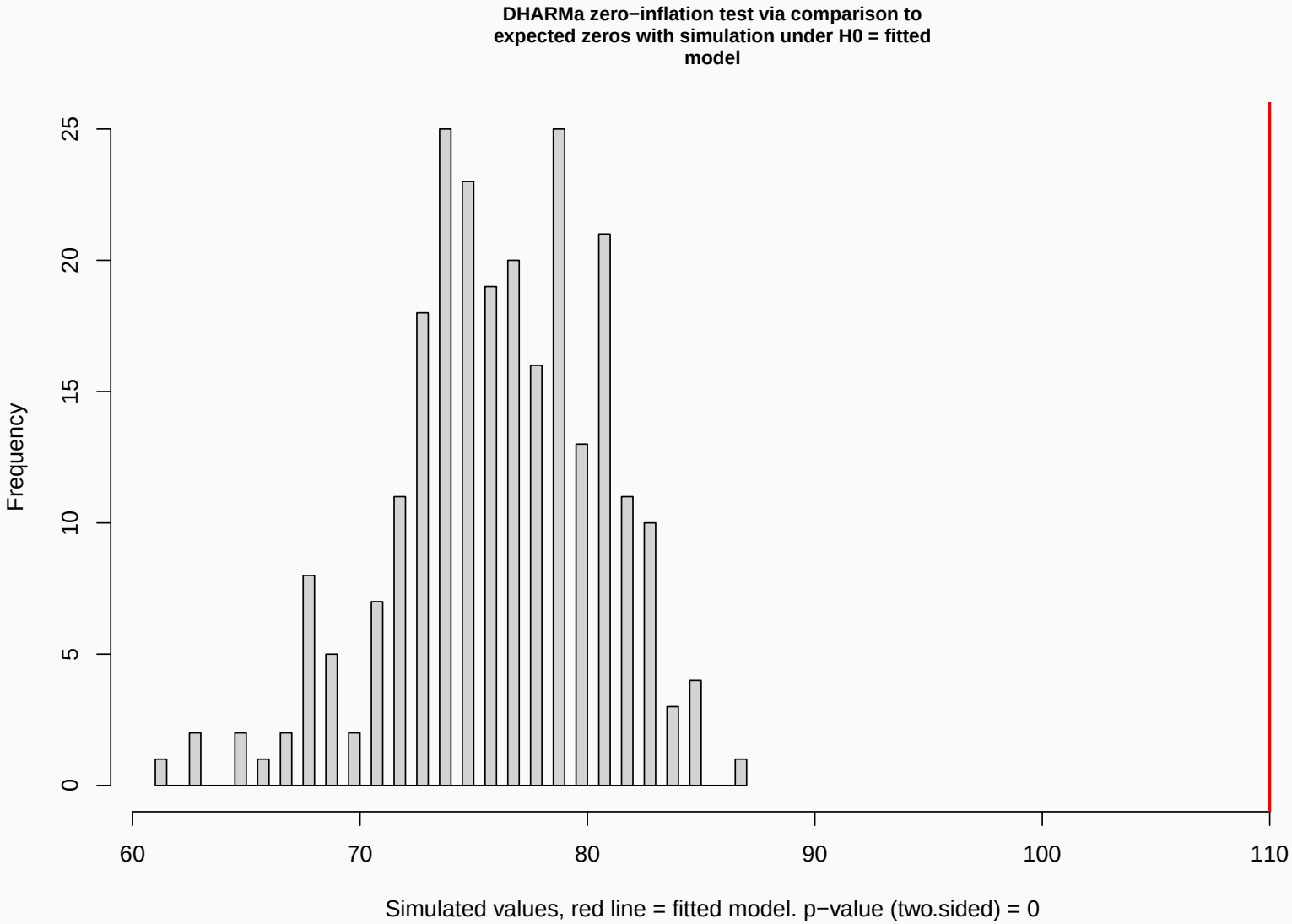
Checking overdispersion

```
testDispersion(eggs.poi.res)
```



Checking zero inflation

```
testZeroInflation(eggs.poi.res)
```



Accounting for zero-inflation

Zero-inflated Poisson/Negative Binomial

Mixture model:

1. Model probability of 0 (`Binomial`)

Zero-inflated Poisson/Negative Binomial

Mixture model:

1. Model probability of 0 (`Binomial`)
2. Model counts (including 0) (`Poisson/Negative Binomial`)

Modelling egg number as Zero-Inflated Poisson (ZIP)

Nests may be occupied or not:

Probability nest not occupied ~ old *(Binomial)*

For occupied nests:

Number of eggs ~ Nest diameter *(Poisson)*

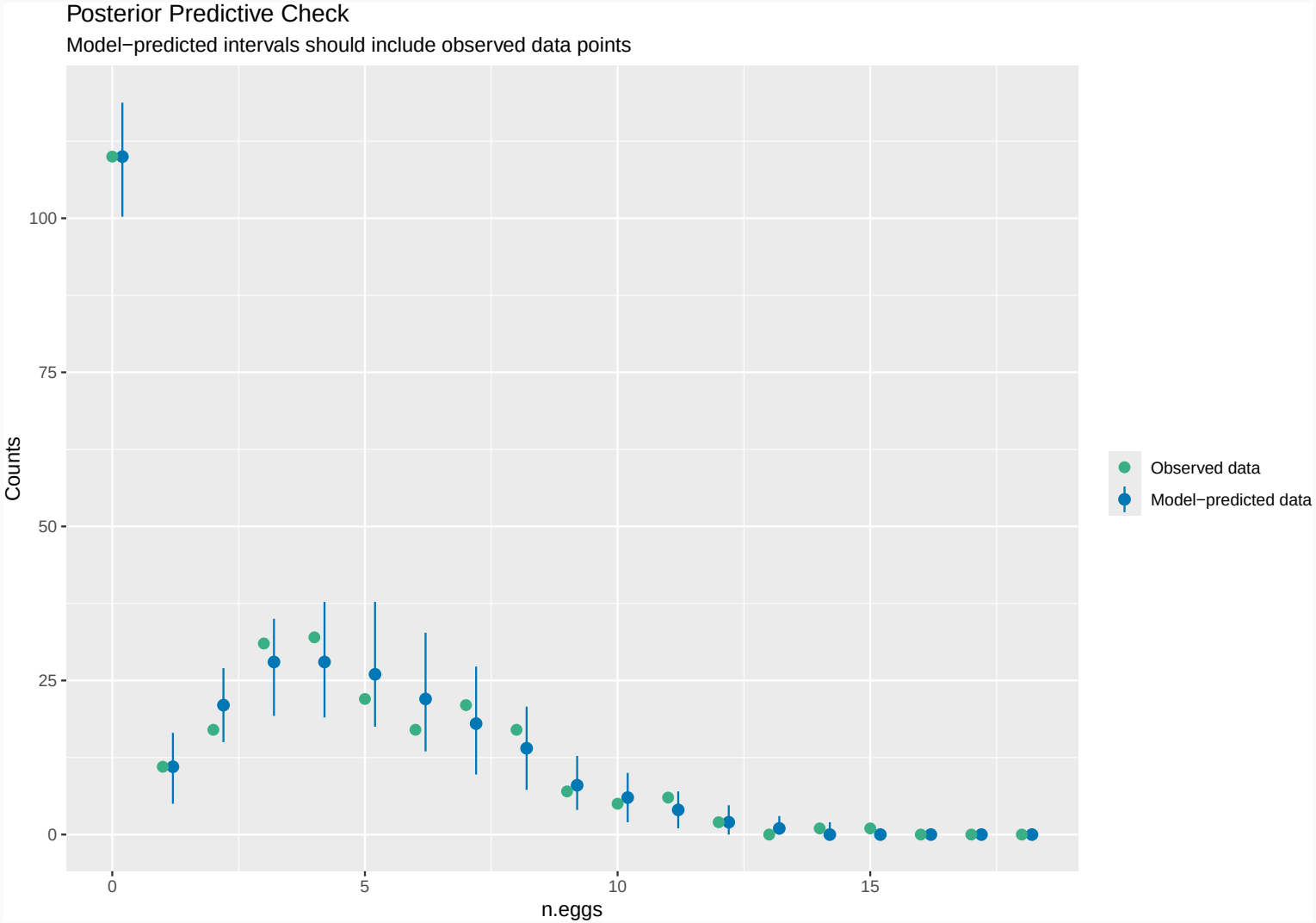
```
library('glmmTMB')
eggs.zip <- glmmTMB(n.eggs ~ diameter,
                    family = 'poisson',
                    ziformula = ~ old,
                    data = eggs)
```

Modelling egg number as Zero-Inflated Poisson

```
 Family: poisson  ( log )
Formula:          n.eggs ~ diameter
Zero inflation:          ~old
Data: eggs

     AIC      BIC   logLik deviance df.resid
   993.8   1008.6   -492.9    985.8      296


Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.41622    0.13619   3.056  0.00224 **
diameter     0.11248    0.01155   9.737  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4054     0.2803  -8.582   <2e-16 ***
oldyes        5.4897     0.5830   9.416   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

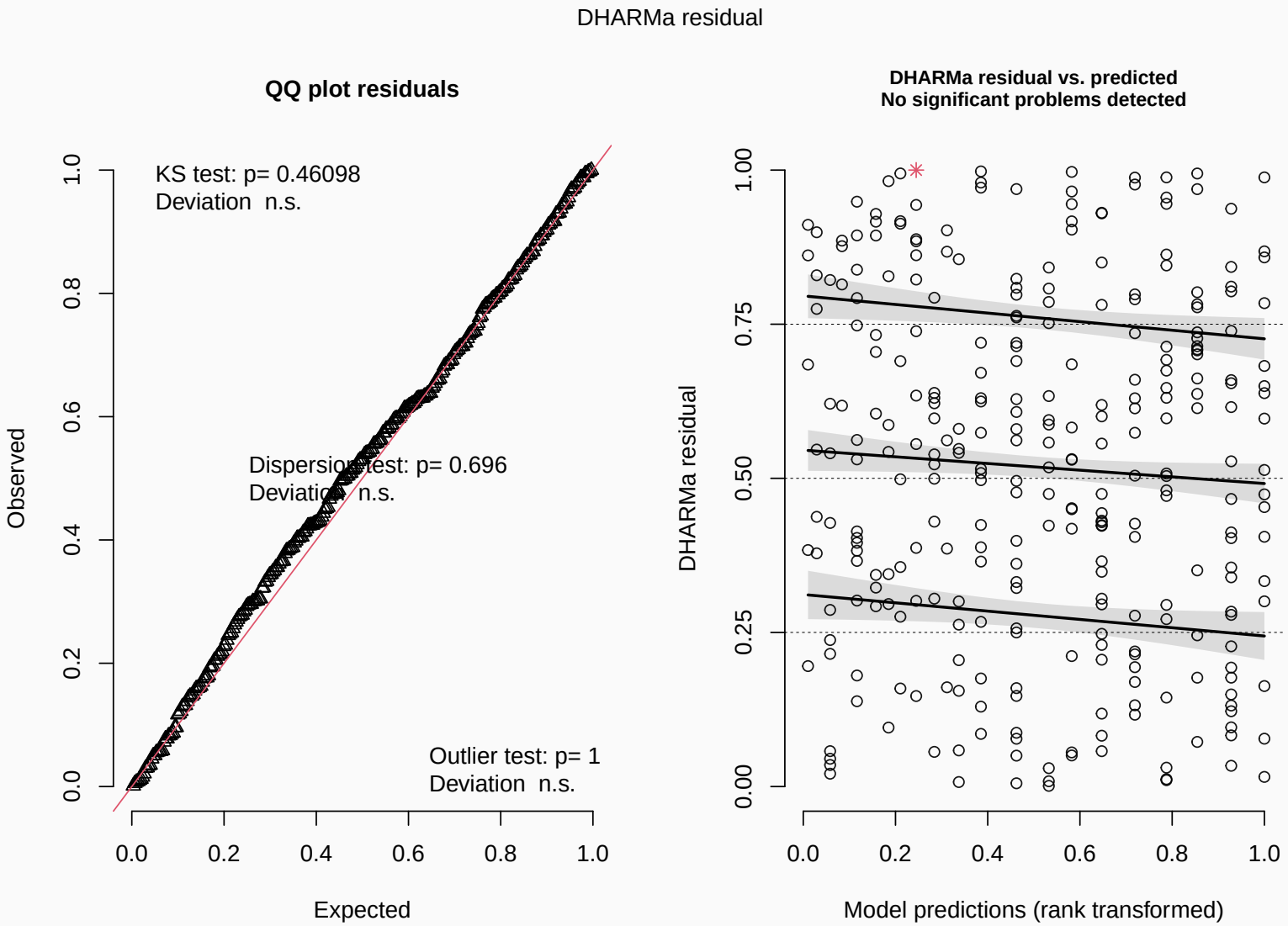
Checking ZIP model

```
check_predictions(eggs.zip)
```



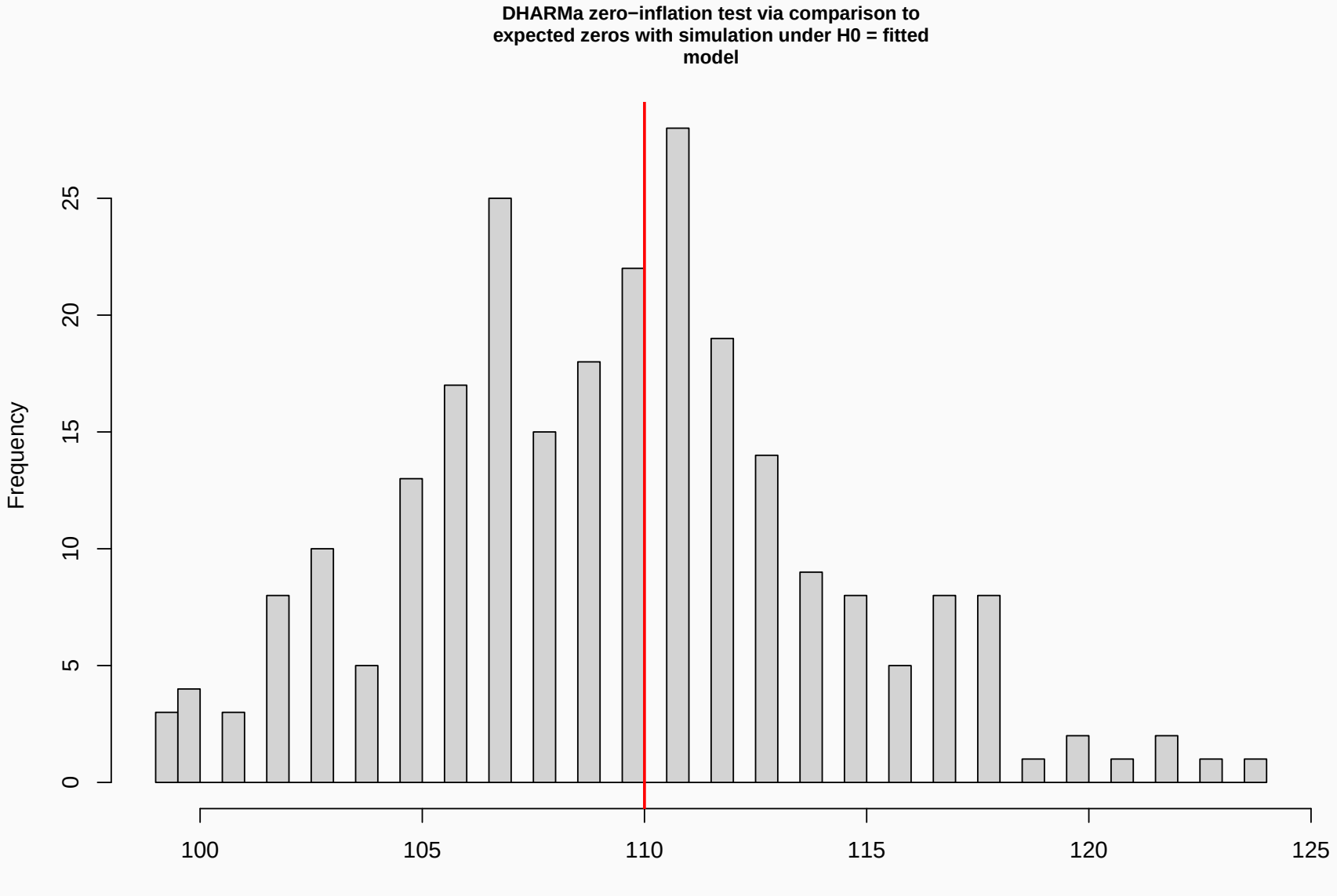
Checking ZIP model with DHARMa

```
eggs.zip.res <- simulateResiduals(eggs.zip, plot = TRUE)
```



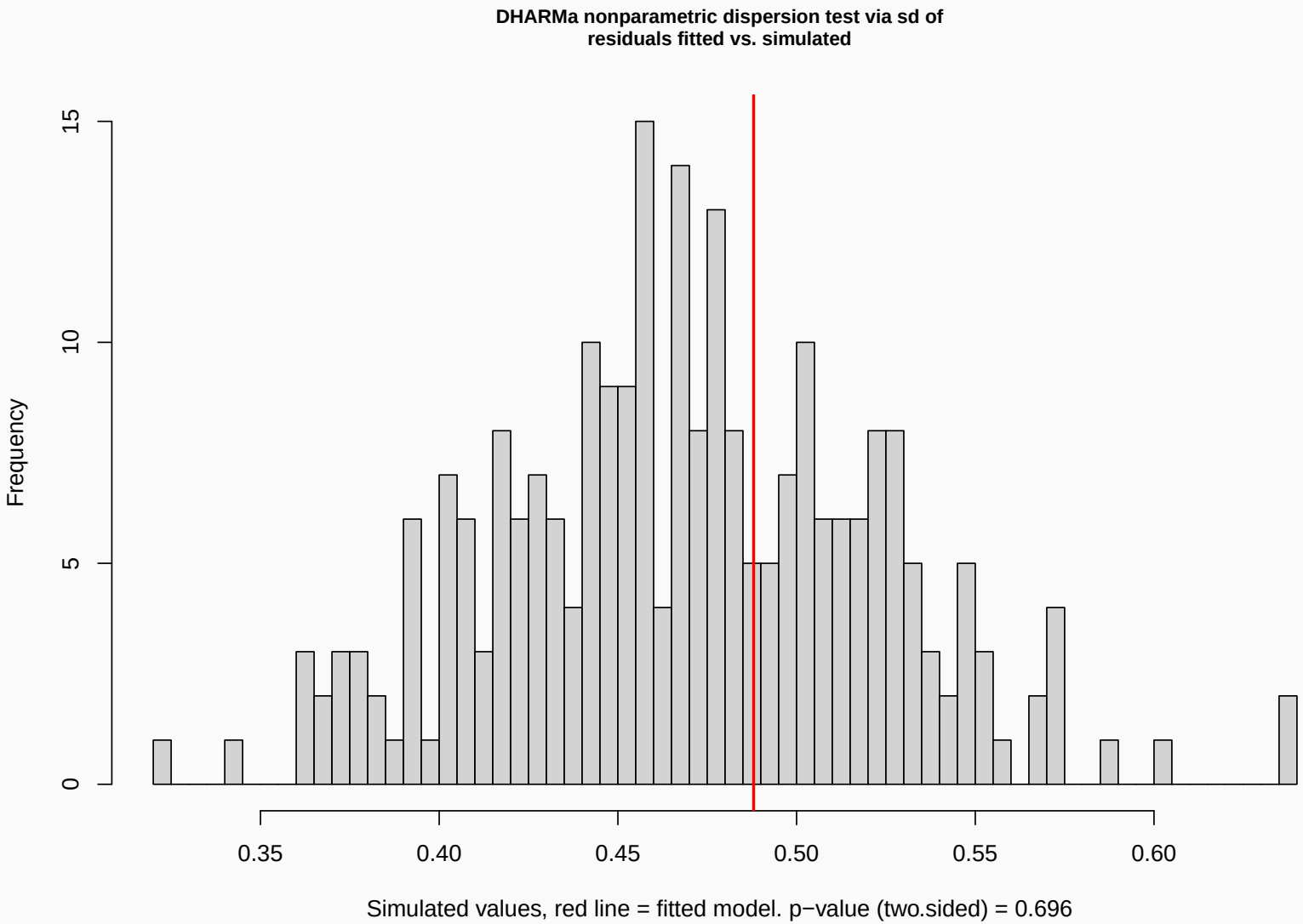
Checking ZIP model with DHARMa

```
testZeroInflation(eggs.zip.res)
```



Checking ZIP model with DHARMa

```
testDispersion(eggs.zip.res)
```



Modelling egg number as Zero-Inflated Negative Binomial (ZINB)

(If there were overdispersion with Poisson)

```
eggs.zinb <- glmmTMB(n.eggs ~ diameter,
                     family = 'nbinom2',
                     ziformula = ~ old,
                     data = eggs)
```

Modelling egg number as ZINB

```
 Family: nbinom2  ( log )
Formula:          n.eggs ~ diameter
Zero inflation:          ~old
Data: eggs

     AIC      BIC   logLik deviance df.resid
   995.7   1014.2   -492.8    985.7      295


Dispersion parameter for nbinom2 family ():  143

Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.4118     0.1389   2.964  0.00304 **
diameter      0.1128     0.0118   9.561  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4160     0.2846  -8.489   <2e-16 ***
oldyes        5.4995     0.5850   9.401   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comparing models

```
library('parameters')
compare_models(eggs.poi, eggs.zip, eggs.zinb)
```

Parameter	eggs.poi	eggs.zip	eggs.zinb
(Intercept)	0.31 (0.06, 0.56)	0.42 (0.15, 0.68)	0.41 (0.14, 0.68)
diameter	0.11 (0.09, 0.14)	0.11 (0.09, 0.14)	0.11 (0.09, 0.14)
old [yes]	-3.79 (-5.60, -1.98)		
old [yes] × diameter	0.09 (-0.06, 0.23)		
Observations	300	300	300

Comparing models

```r
library('performance')
compare_performance(eggs.poi, eggs.zip, eggs.zinb)
```

```
# Comparison of Model Performance Indices

Name      |   Model |  AIC (weights) | AICc (weights) |  BIC (weights) |  RMSE
-------------------------------------------------------------------------------
eggs.poi  |     glm | 1176.7 (<.001) | 1176.8 (<.001) | 1191.5 (<.001) | 2.324
eggs.zip  | glmmTMB |  993.8 (0.719) |  993.9 (0.726) | 1008.6 (0.942) | 2.324
eggs.zinb | glmmTMB |  995.7 (0.281) |  995.9 (0.274) | 1014.2 (0.058) | 2.324

Name      |   Sigma |    R2 | R2 (adj.) | Score_log | Score_spherical | Nagelkerke'
-------------------------------------------------------------------------------------
eggs.poi  |   1.000 |       |           |    -1.948 |           0.042 |           0
eggs.zip  |   1.000 | 0.118 |     0.112 |    -1.643 |           0.040 |
eggs.zinb | 143.279 | 0.118 |     0.112 |           |                 |
```

Accounting for zero-inflation with hurdle models

Tracking measles outbreak

Counting number of hives/person

Many people not sick (0 hives)

Those sick, have many hives (>1)

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero

Hurdle:

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

1. Binomial model: probability of non-zero

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

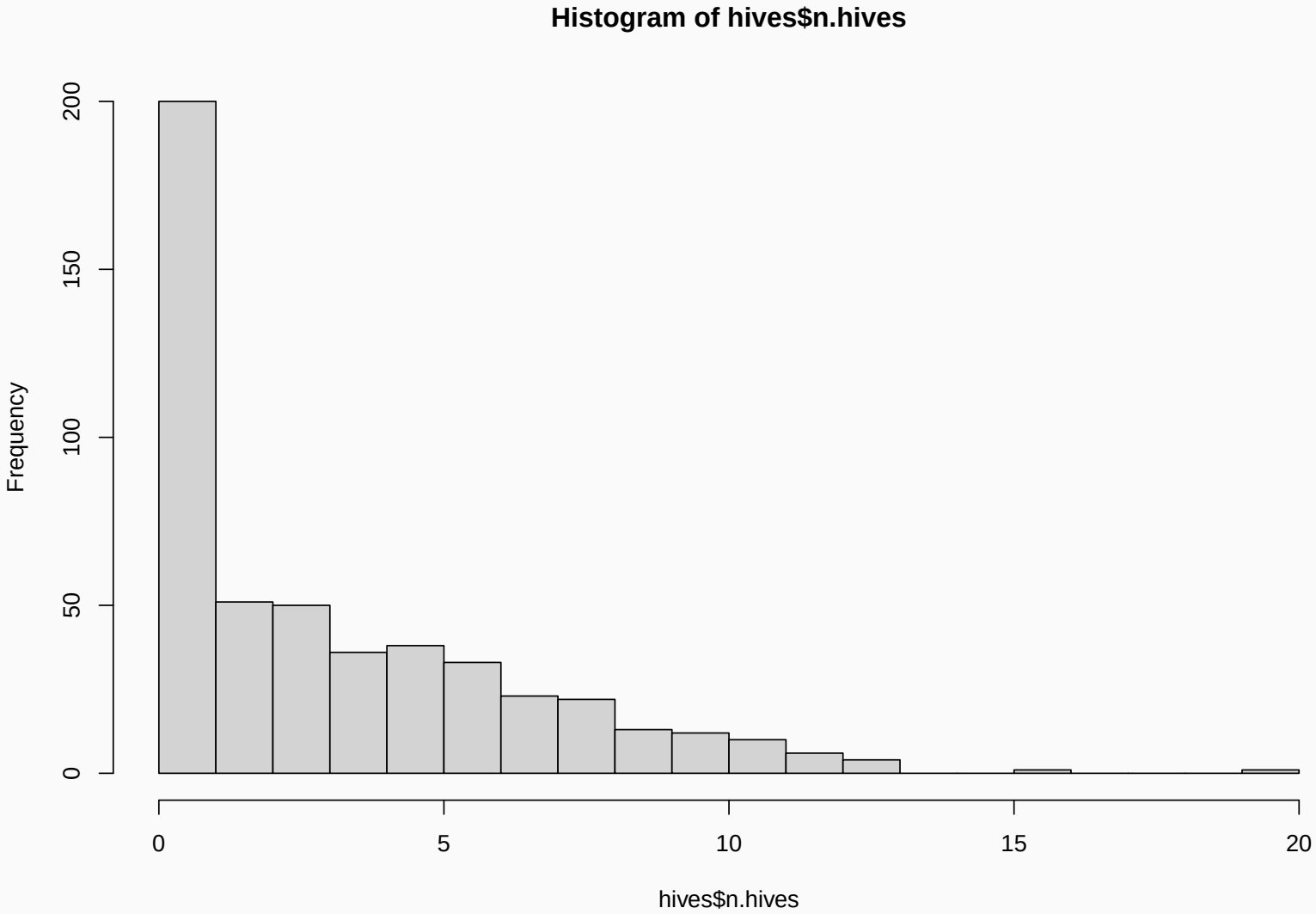
1. Binomial model: probability of non-zero
2. Count model truncated at 1

How many hives per skin area?

```
hives <- read.csv('data/hives.csv')
```

```
      age          vaccinated       area.cm2         n.hives      
 Min.   : 1.0   Min.   :0.000   Min.   : 5.000   Min.   : 0.000  
 1st Qu.:23.0   1st Qu.:0.000   1st Qu.: 6.000   1st Qu.: 0.000  
 Median :45.0   Median :1.000   Median : 8.000   Median : 2.000  
 Mean   :44.7   Mean   :0.648   Mean   : 7.482   Mean   : 3.256  
 3rd Qu.:65.0   3rd Qu.:1.000   3rd Qu.: 9.000   3rd Qu.: 5.250  
 Max.   :90.0   Max.   :1.000   Max.   :10.000   Max.   :20.000  
```

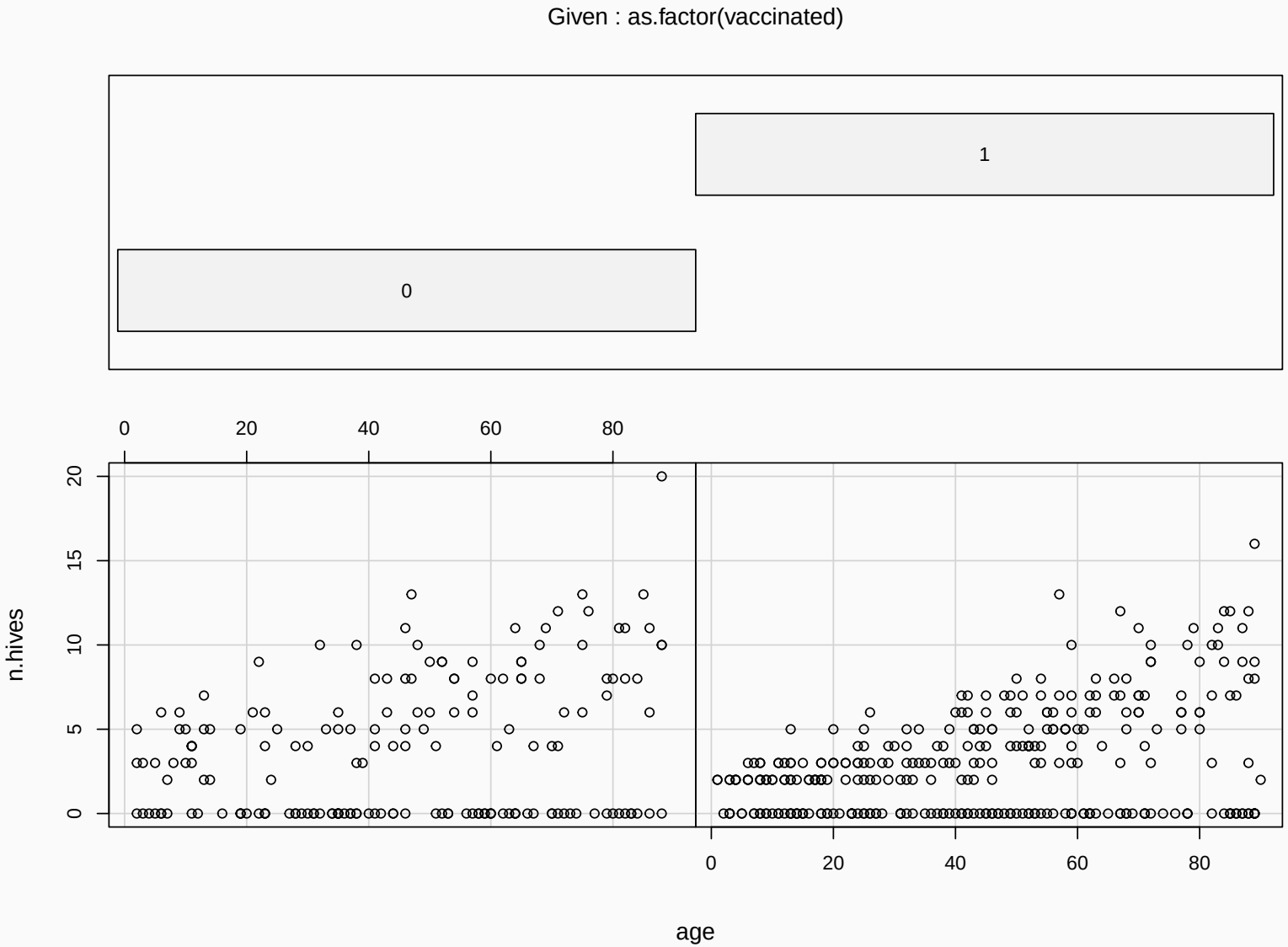
Many people with 0 hives



(that does not mean we need zero-inflated model!)

Number of hives ~ age * vaccinated

```
coplot(n.hives ~ age | as.factor(vaccinated), data = hives)
```



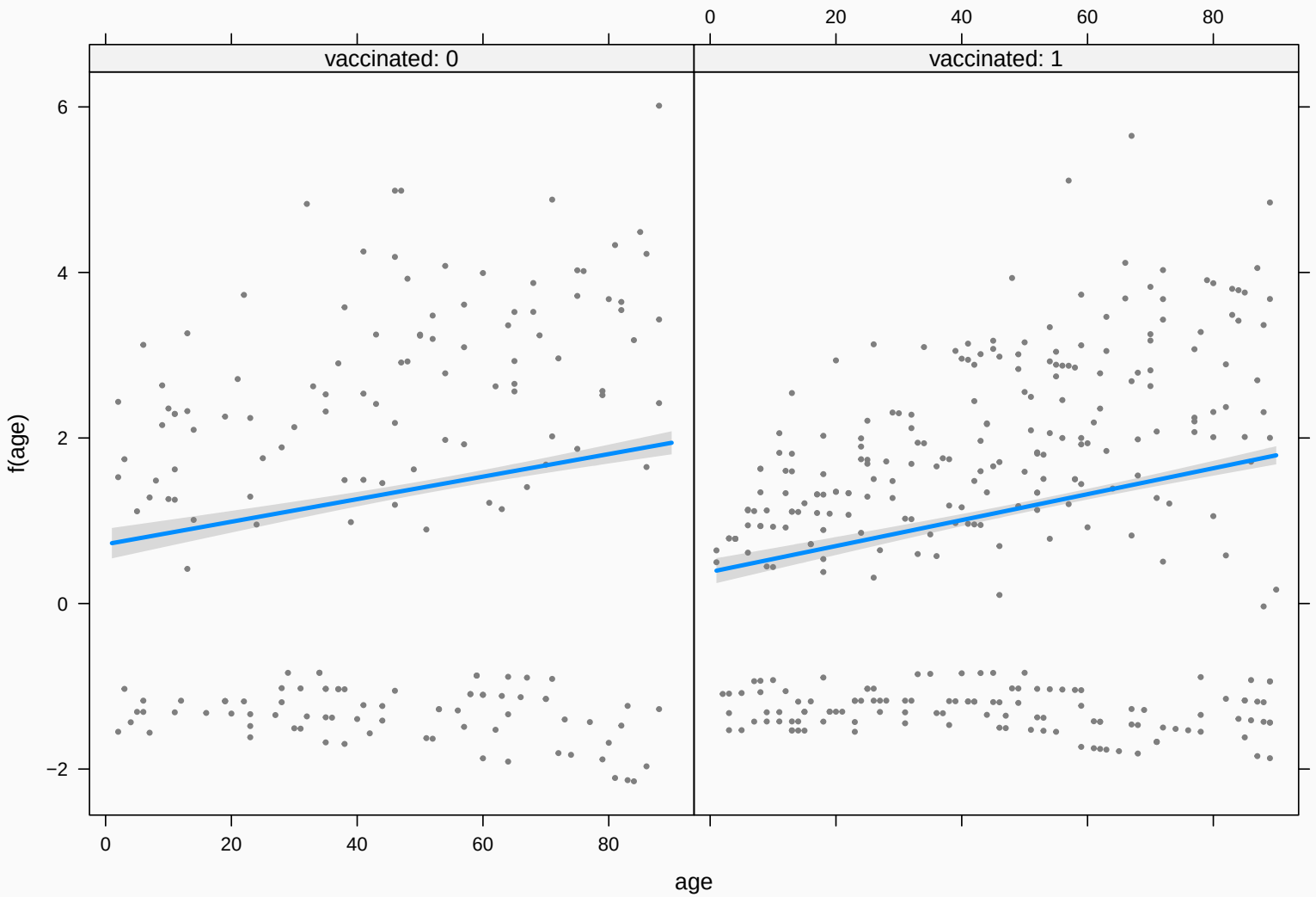
Trying Poisson GLM

```
hives.poi <- glm(n.hives ~ vaccinated * age,
                 offset = log(area.cm2),
                 data = hives,
                 family = poisson)
```

Trying Poisson GLM

```
Call:
glm(formula = n.hives ~ vaccinated * age, family = poisson, data = hives,
    offset = log(area.cm2))

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)    -1.363696   0.095097 -14.340  < 2e-16 ***
vaccinated     -0.334184   0.122887  -2.719  0.00654 **
age             0.013626   0.001623   8.395  < 2e-16 ***
vaccinated:age  0.002034   0.002075   0.980  0.32708
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2137.0  on 499  degrees of freedom
Residual deviance: 1891.7  on 496  degrees of freedom
AIC: 2925.6

Number of Fisher Scoring iterations: 5
```

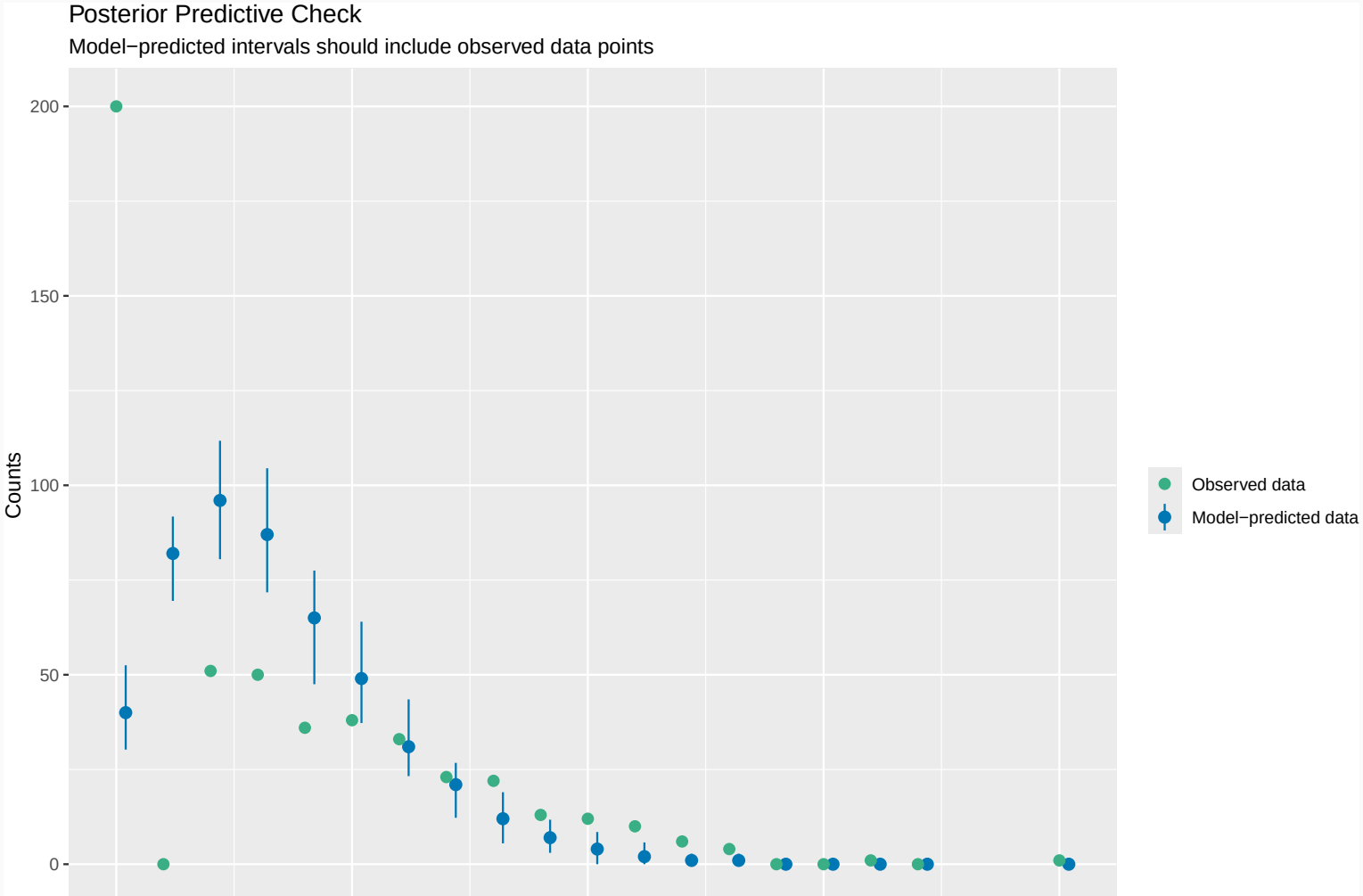
Visualising fitted Poisson GLM



Checking Poisson GLM

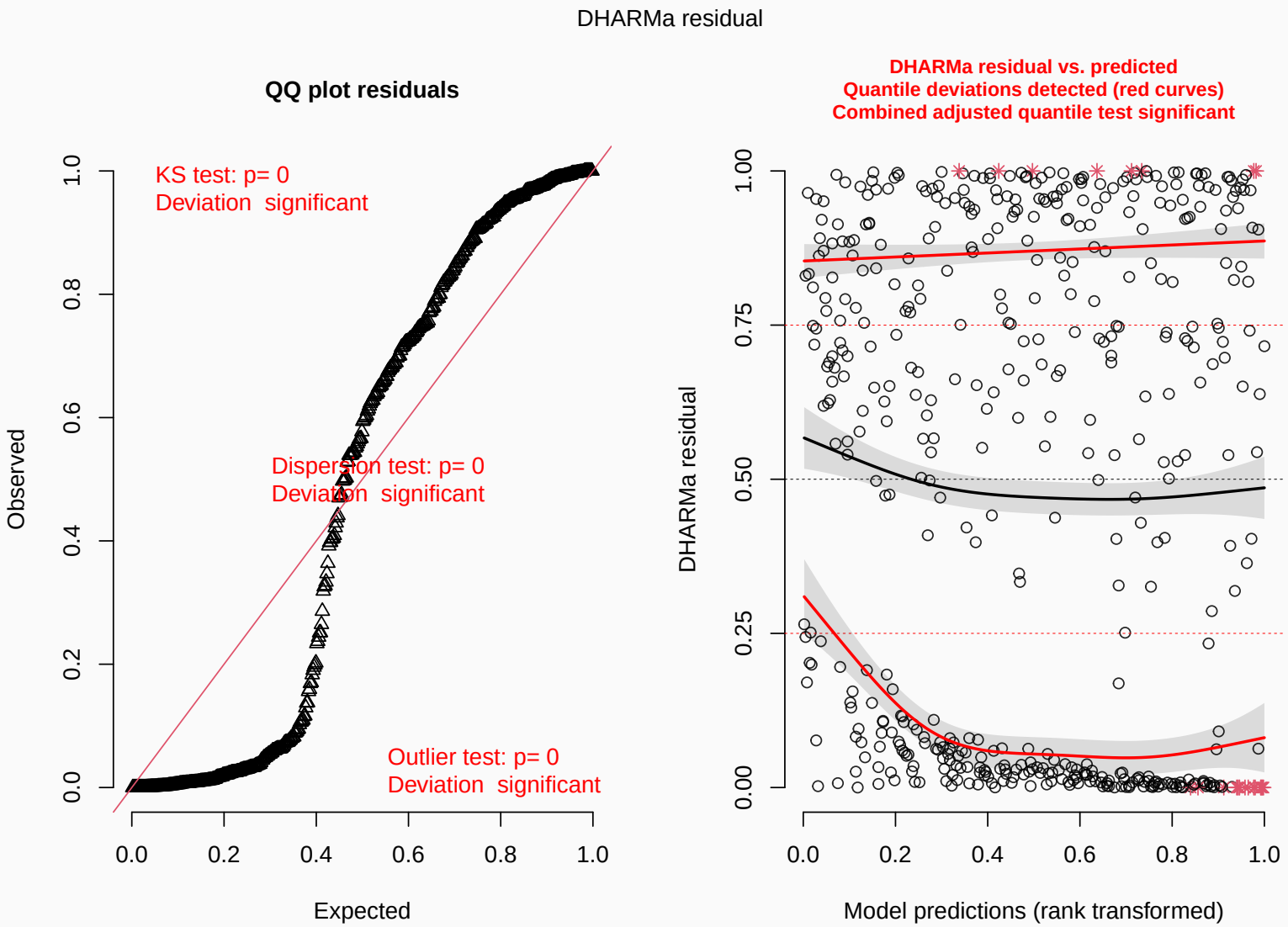
```
check_predictions(hives.poi)
```

```
Warning: Maximum value of original data is not included in the
  replicated data.
  Model may not capture the variation of the data.
```



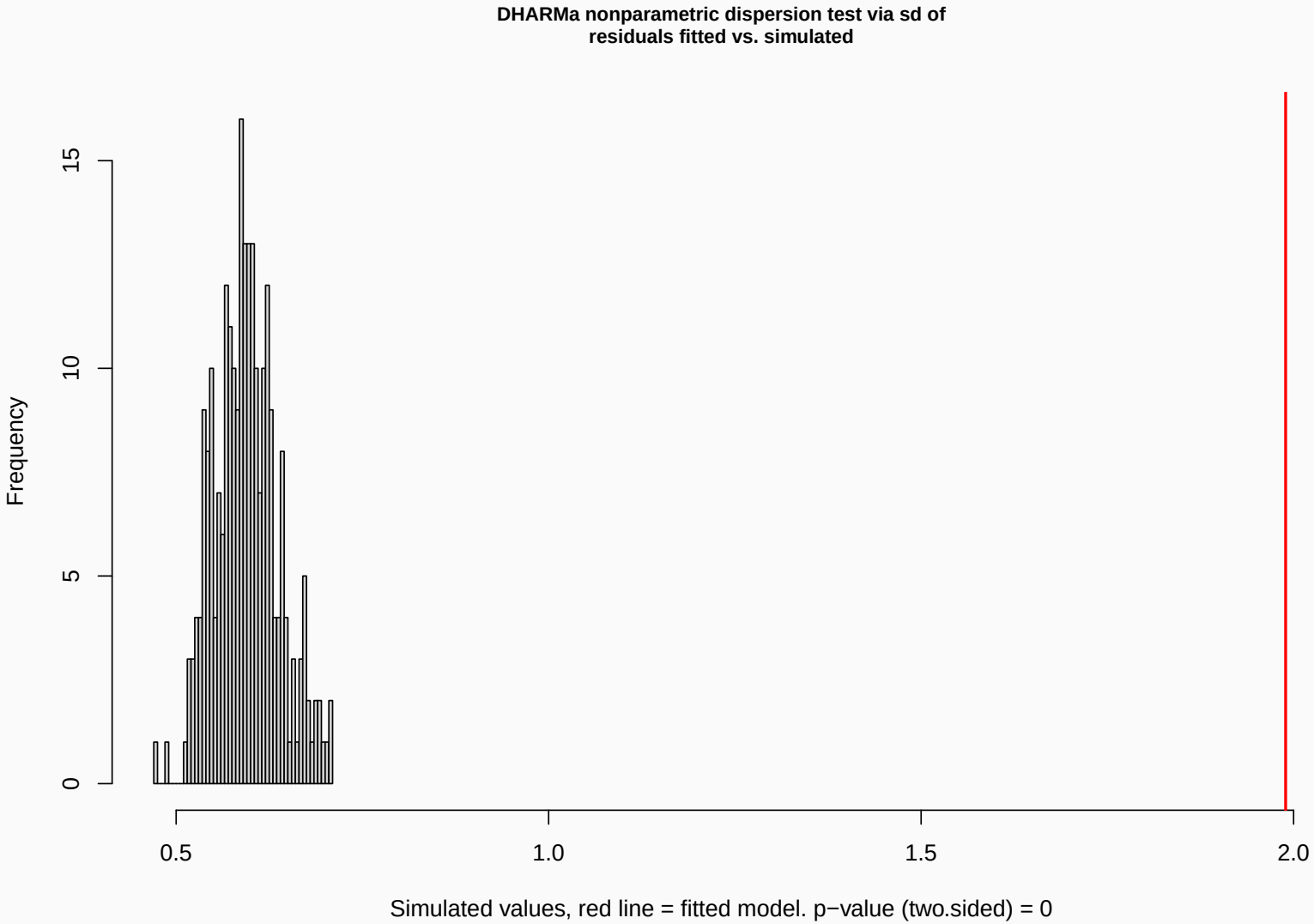
Checking Poisson GLM

```
hives.poi.res <- simulateResiduals(hives.poi, plot = TRUE)
```



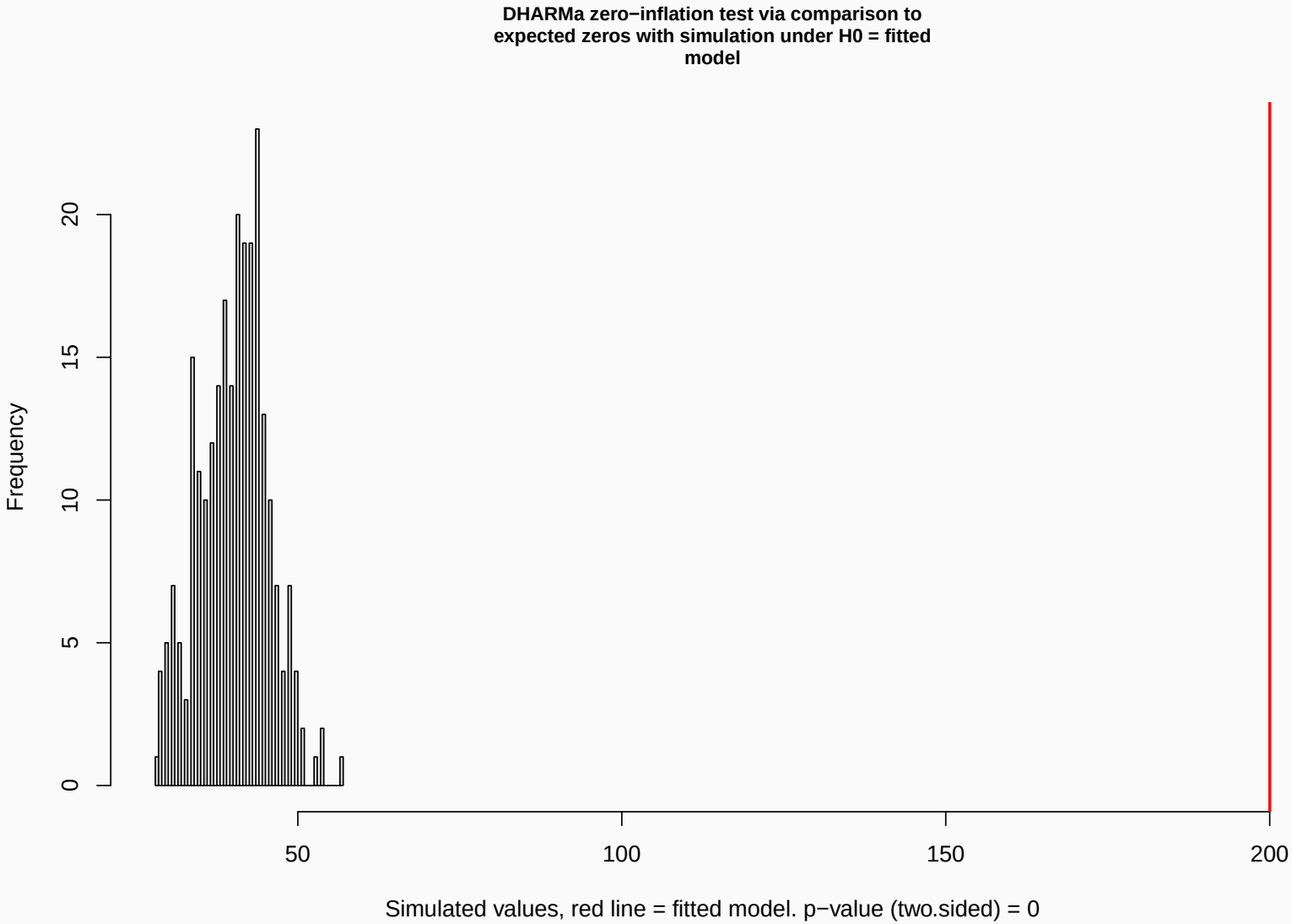
Checking overdispersion

```
testDispersion(hives.poi.res)
```



Checking zero inflation

```
testZeroInflation(hives.poi.res)
```



Accounting for zero-inflation with hurdle model

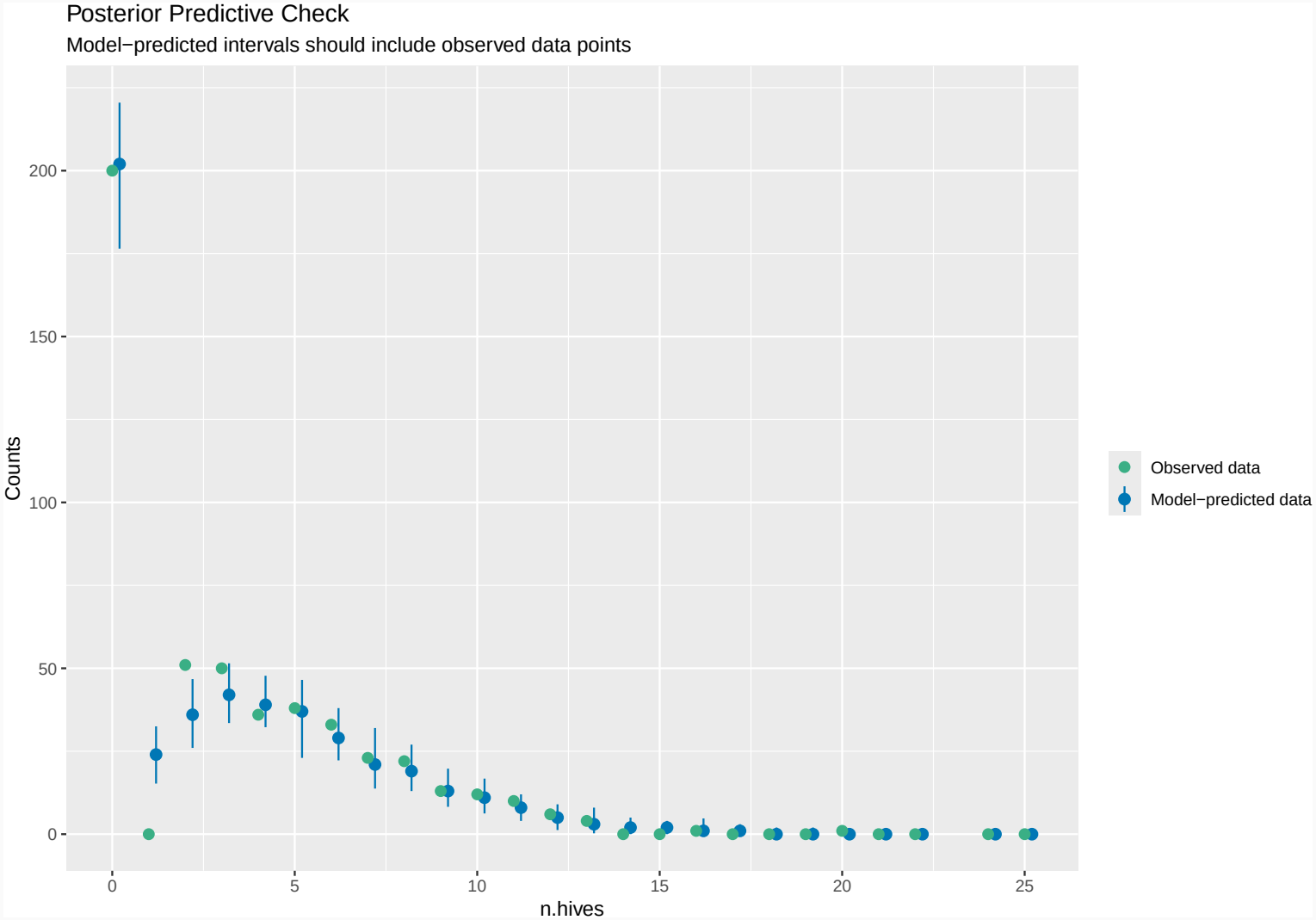
```
hives.hur <- glmmTMB(n.hives ~ vaccinated + age,
                     family = truncated_poisson,
                     ziformula = ~ 1,
                     offset = log(area.cm2),
                     data = hives)
```

Accounting for zero-inflation with hurdle model

```
 Family: truncated_poisson  ( log )
Formula:          n.hives ~ vaccinated + age
Zero inflation:           ~1
Data: hives
 Offset: log(area.cm2)

     AIC      BIC   logLik deviance df.resid
  1932.1   1949.0   -962.1   1924.1      496


Conditional model:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.853885   0.070755 -12.068  < 2e-16 ***
vaccinated  -0.365664   0.051532  -7.096 1.29e-12 ***
age          0.014860   0.001065  13.955  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.40547    0.09129  -4.442 8.93e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

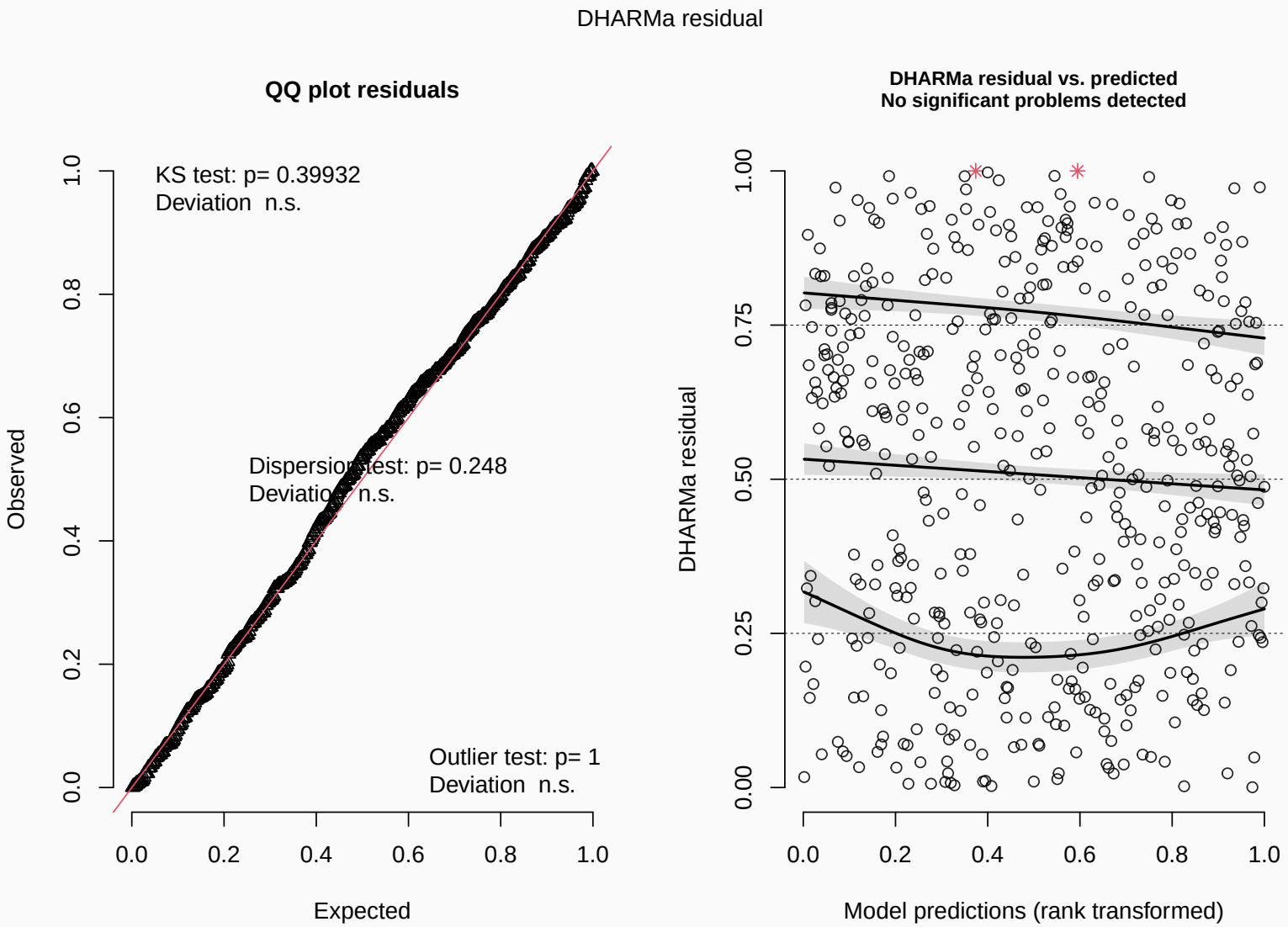
Checking hurdle model

```
check_predictions(hives.hur)
```



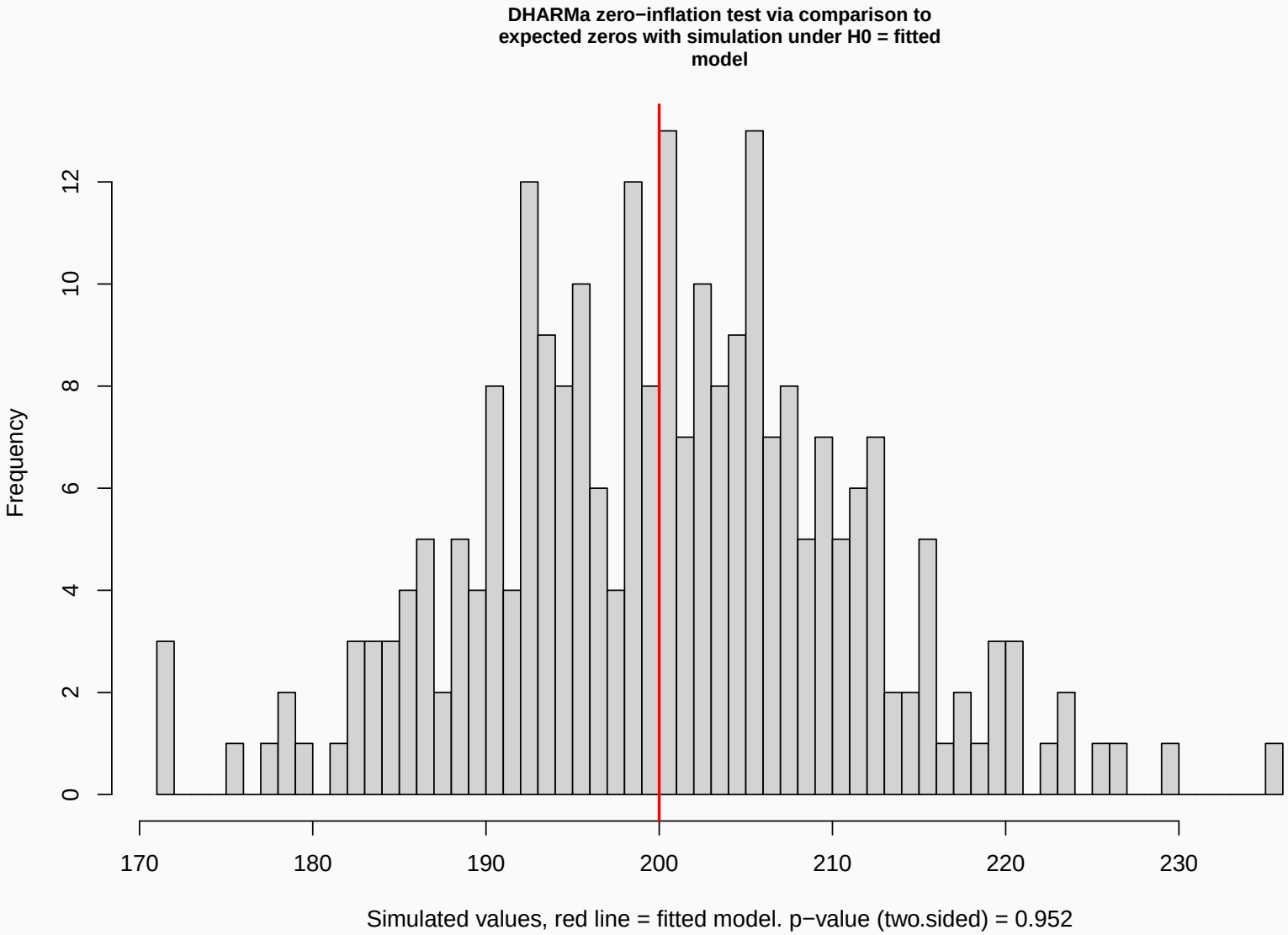
Checking hurdle model with DHARMa

```
hives.hur.res <- simulateResiduals(hives.hur, plot = TRUE)
```



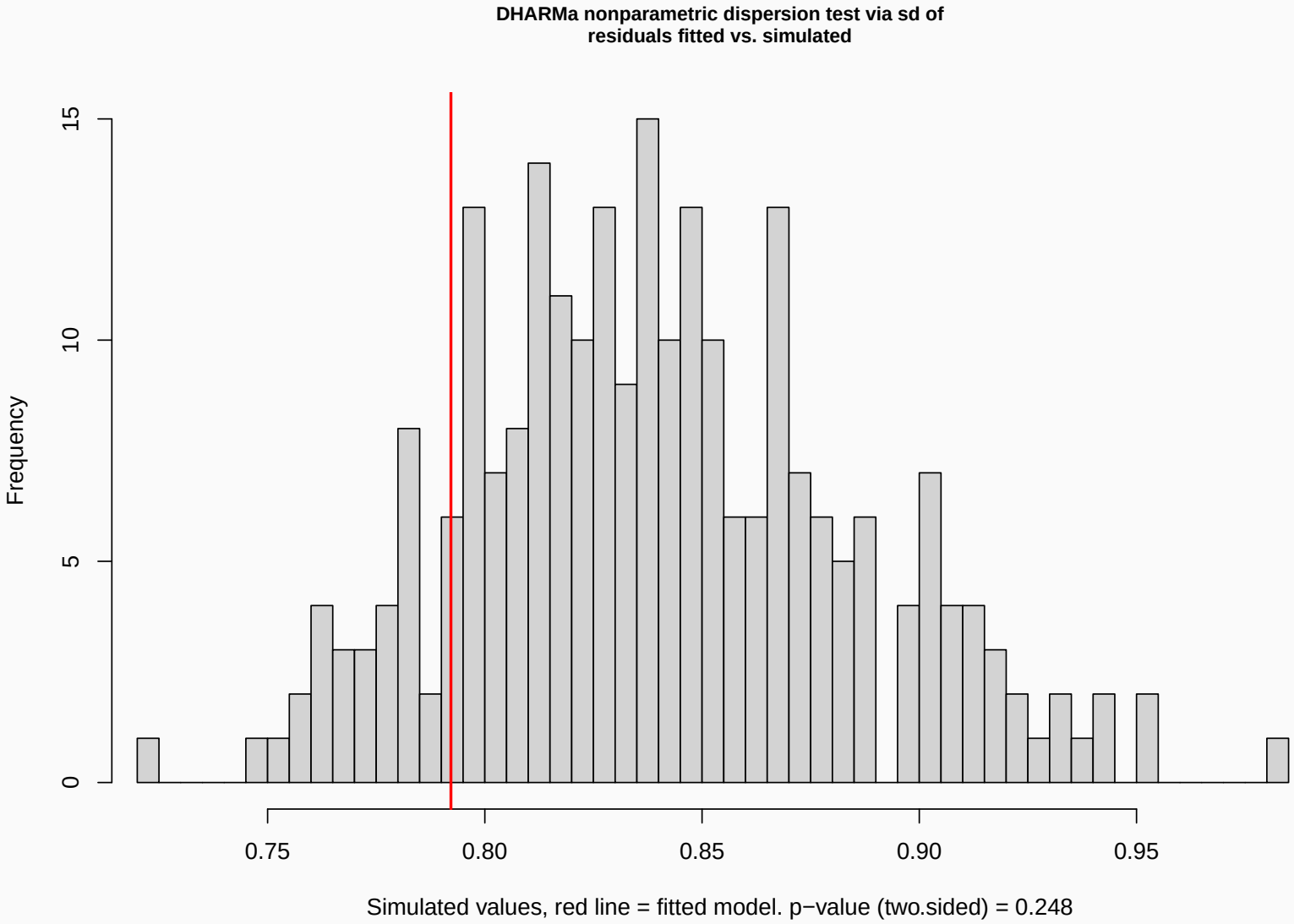
Checking zero inflation

```
testZeroInflation(hives.hur.res)
```



Checking overdispersion

```
testDispersion(hives.hur.res)
```



Comparing models

```
compare_models(hives.poi, hives.hur)
```

Parameter	hives.poi	hives.hur
(Intercept)	-1.36 (-1.55, -1.18)	-0.85 (-0.99, -0.72)
vaccinated	-0.33 (-0.58, -0.09)	-0.37 (-0.47, -0.26)
age	0.01 (0.01, 0.02)	0.01 (0.01, 0.02)
vaccinated × age	2.03e-03 (0.00, 0.01)	
Observations	500	500

Comparing models

```
compare_performance(hives.poi, hives.hur)
```

```
# Comparison of Model Performance Indices

Name      |   Model |  AIC (weights) | AICc (weights) |  BIC (weights) |  RMSE
-------------------------------------------------------------------------------
hives.poi |     glm | 2925.6 (<.001) | 2925.7 (<.001) | 2942.5 (<.001) | 3.299
hives.hur | glmmTMB | 1932.1 (>.999) | 1932.2 (>.999) | 1949.0 (>.999) | 3.310

Name      | Sigma | Score_log | Score_spherical | Nagelkerke's R2 |    R2 | R2 (adj
-------------------------------------------------------------------------------
hives.poi | 1.000 |    -2.918 |           0.034 |           0.393 |       |
hives.hur | 1.000 |    -2.246 |           0.035 |                 | 0.498 |     0.4
```

Mixed / Multilevel Models

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Example dataset: trees

- Data on 1000 trees from 10 sites.

```
head(trees)
```

```
  site   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
3    2 28.03   41.9 female    0
4    5 39.86   46.5 female    0
5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Example dataset: trees

- Data on 1000 trees from 10 sites.
- Trees per site: 4 - 392.

```
head(trees)
```

```
  site   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
3    2 28.03   41.9 female    0
4    5 39.86   46.5 female    0
5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Q: What's the relationship between tree diameter and height?

A simple linear model

```r
lm.simple <- lm(height ~ dbh, data = trees)
```

```
Call:
lm(formula = height ~ dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-13.3270  -2.8978   0.1057   2.7924  12.9511

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 19.33920    0.31064   62.26   <2e-16 ***
dbh          0.61570    0.01013   60.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remember our model structure

$$y_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta x_i$$

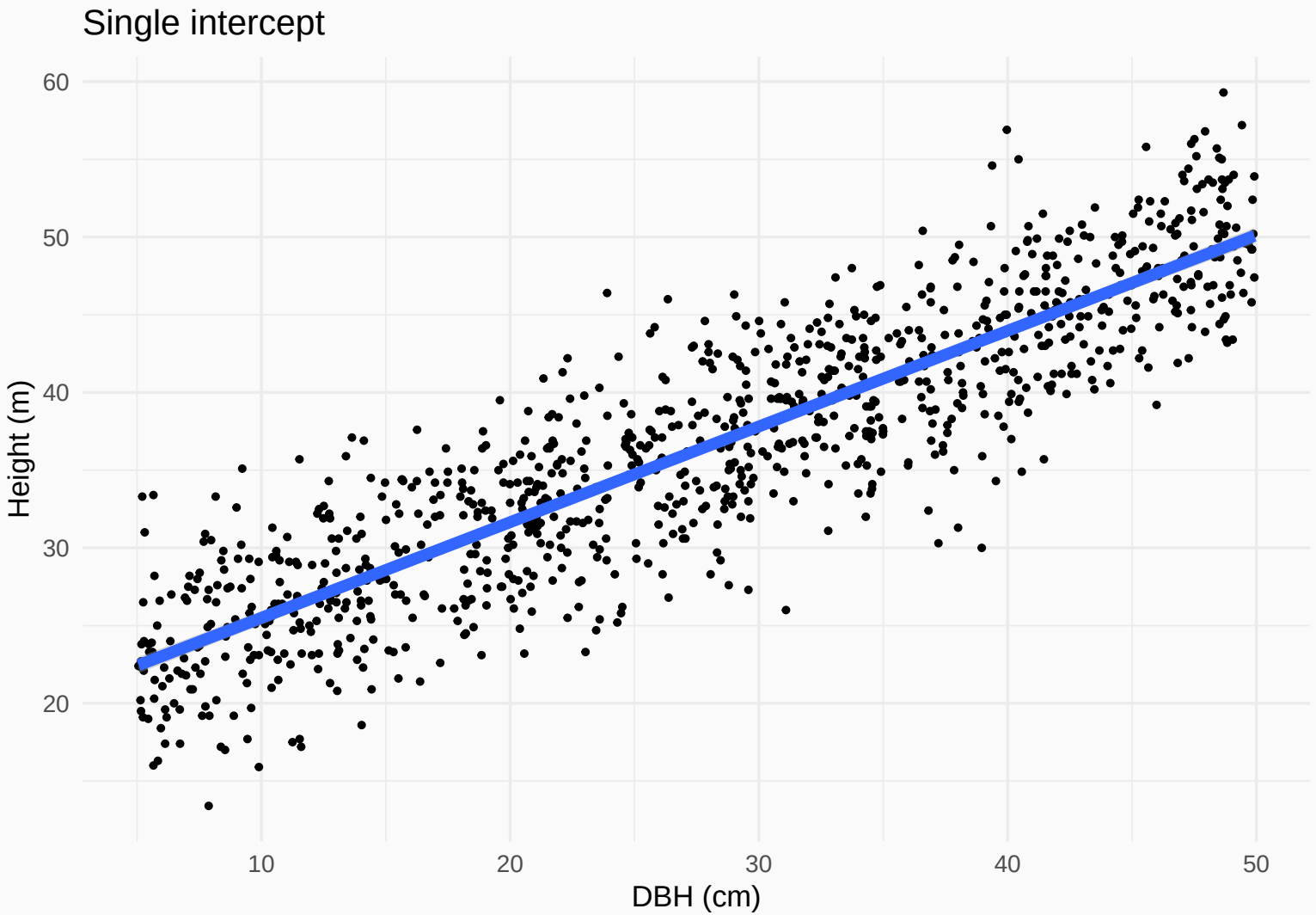
In this case:

$$Height_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta DBH_i$$

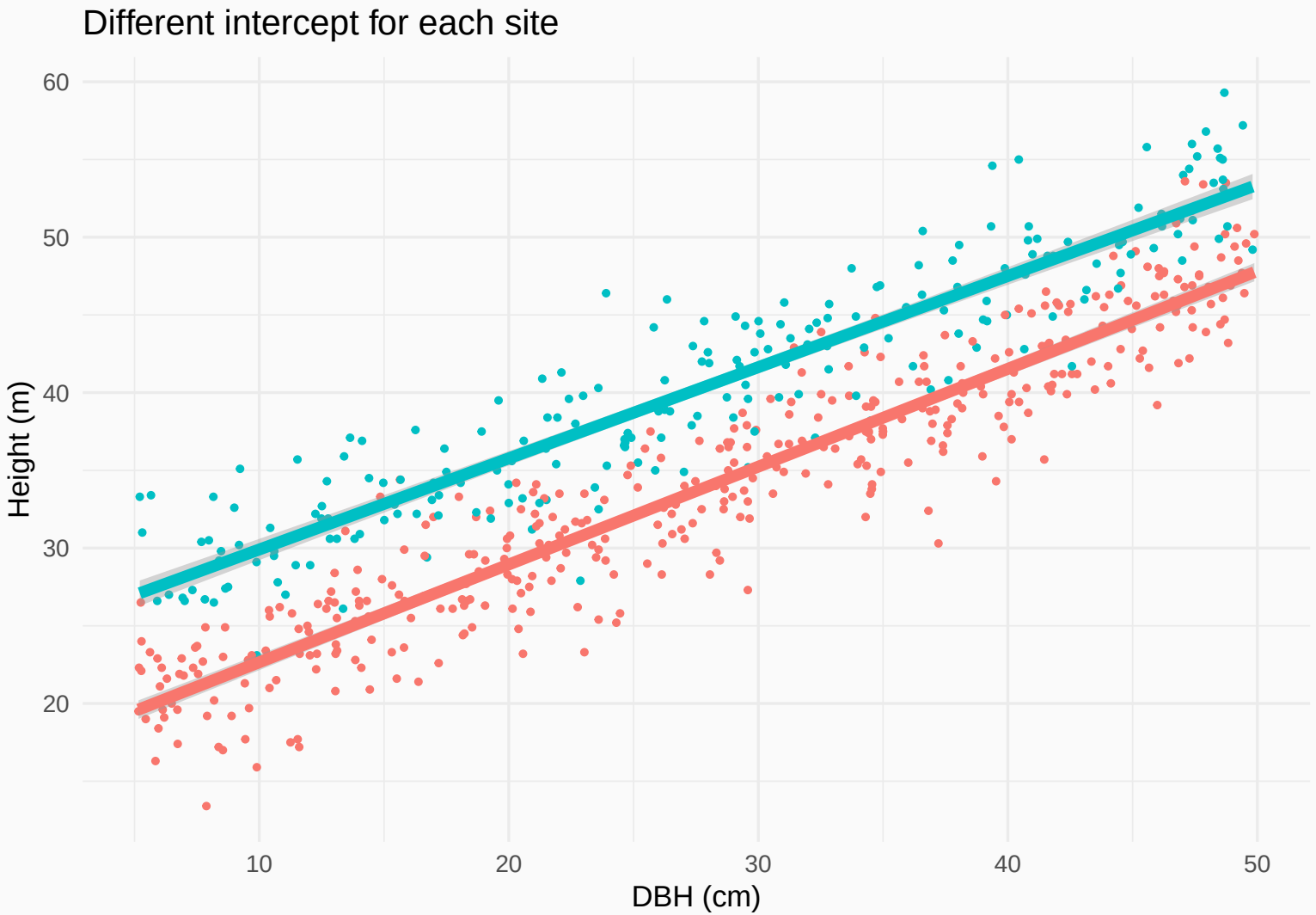
α: expected height when DBH = 0

β: how much height increases with every unit increase of DBH

There is only one intercept



What if allometry varies among sites?

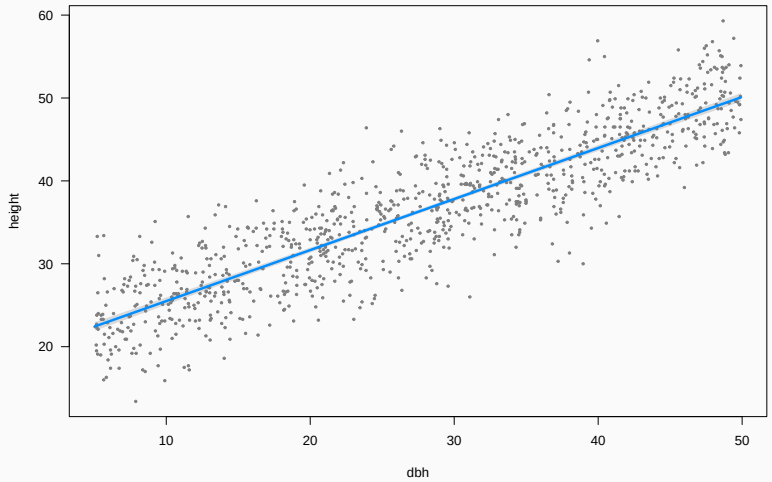


Fitting a varying intercepts model with `lm`

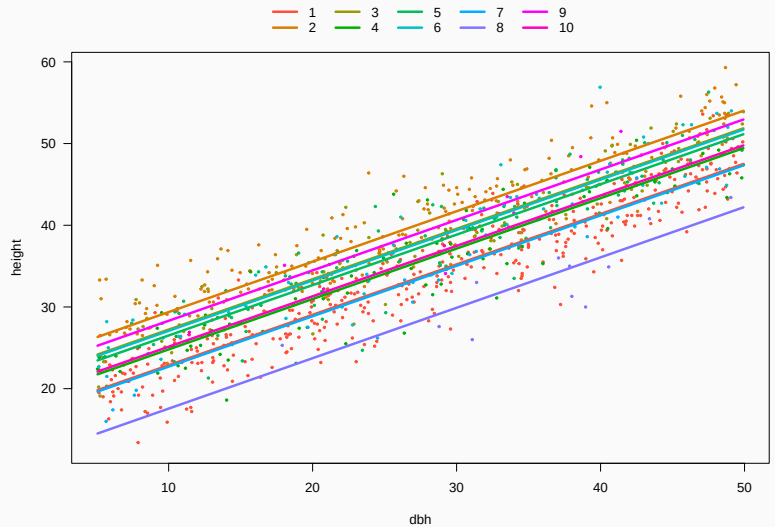
```
Call:
lm(formula = height ~ site + dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-10.1130  -1.9885   0.0582   2.0314  11.3320

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 16.699037   0.260565  64.088  < 2e-16 ***
site2        6.504303   0.256730  25.335  < 2e-16 ***
site3        4.357457   0.354181  12.303  < 2e-16 ***
site4        1.934650   0.356102   5.433 6.98e-08 ***
site5        3.637432   0.339688  10.708  < 2e-16 ***
site6        4.204511   0.421906   9.966  < 2e-16 ***
site7       -0.176193   0.666772  -0.264   0.7916
site8       -5.312648   0.893603  -5.945 3.82e-09 ***
site9        5.437049   1.087766   4.998 6.84e-07 ***
site10       2.263338   1.369986   1.652   0.0988 .
dbh          0.617075   0.007574  81.473  < 2e-16 ***
---
```

Single vs varying intercept

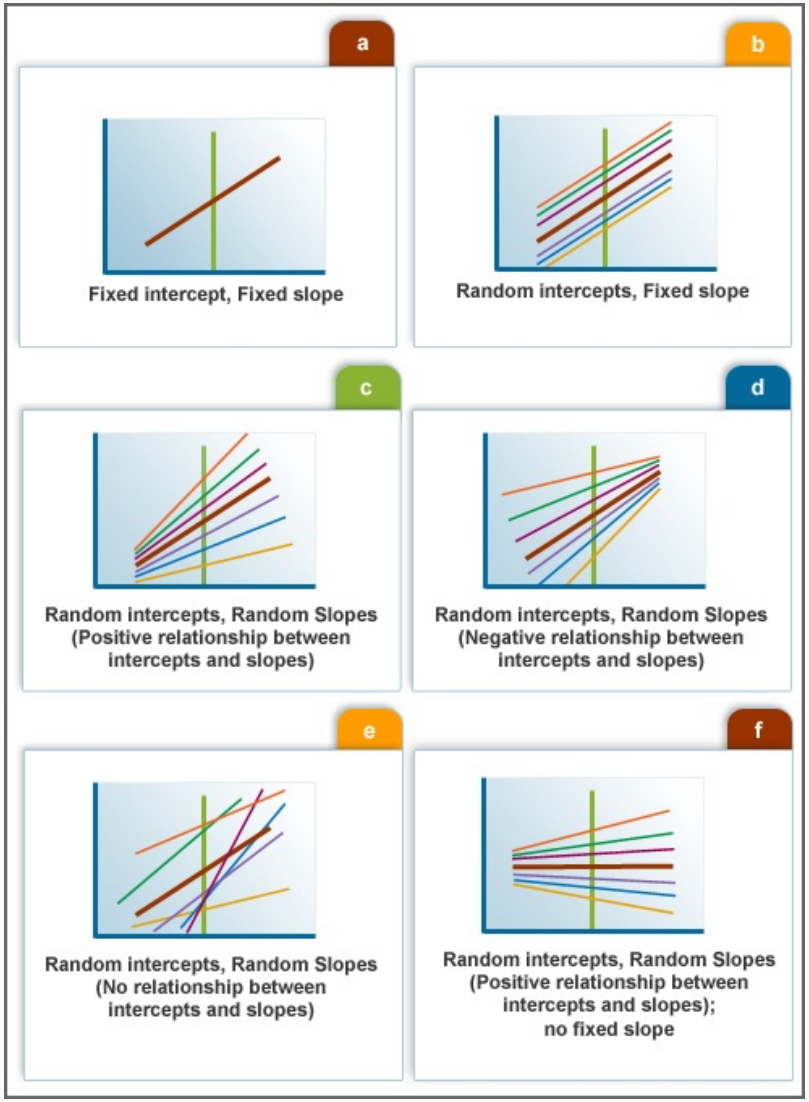
Single intercept



Different intercept for each site



Mixed models enable us to account for variability



www.esourceresearch.org/

Mixed model with varying intercepts

$$y_i = a + \alpha_j + b \cdot x_i + \varepsilon_i$$
$$\alpha_j \sim N\left(0, \tau^2\right)$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

In our example:

$$Height_i = a + site_j + b \cdot DBH_i + \varepsilon_i$$
$$site_j \sim N\left(0, \tau^2\right)$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$

Mixed models estimate **varying parameters**

(intercepts and/or slopes)

with pooling among levels

(rather than considering them fully independent)

Hence there's gradient between

- **complete pooling**: Single overall intercept.

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- **complete pooling**: Single overall intercept.
    - `lm (height ~ dbh)`

Hence there's gradient between

- **complete pooling**: Single overall intercept.
    - `lm (height ~ dbh)`

- **no pooling**: One *independent* intercept for each site.

Hence there's gradient between

- **complete pooling**: Single overall intercept.
    - `lm (height ~ dbh)`

- **no pooling**: One *independent* intercept for each site.
    - `lm (height ~ dbh + site)`

Hence there's gradient between

- **complete pooling**: Single overall intercept.
    - `lm (height ~ dbh)`

- **no pooling**: One *independent* intercept for each site.
    - `lm (height ~ dbh + site)`

- **partial pooling**: Inter-related intercepts.

Hence there's gradient between

- **complete pooling**: Single overall intercept.
    - `lm (height ~ dbh)`
- **no pooling**: One *independent* intercept for each site.
    - `lm (height ~ dbh + site)`
- **partial pooling**: Inter-related intercepts.
    - `lmer(height ~ dbh + (1 | site))`

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

Random vs Fixed effects?

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2. Effects are fixed if they are interesting in themselves; random if interest in the underlying population.

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3. Fixed when sample exhausts the population; random when the sample is small part of the population.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

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4. Random effect if it's assumed to be a realized value of random variable.

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Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.
2. Effects are fixed if they are interesting in themselves; random if interest in the underlying population.
3. Fixed when sample exhausts the population; random when the sample is small part of the population.
4. Random effect if it's assumed to be a realized value of random variable.
5. Fixed effects estimated using least squares or maximum likelihood; random effects estimated with shrinkage.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

What is a random effect, really?

- Varies by group

Random effects are estimated with *partial pooling* (shrinkage, regularisation), while fixed effects are not (infinite variance).

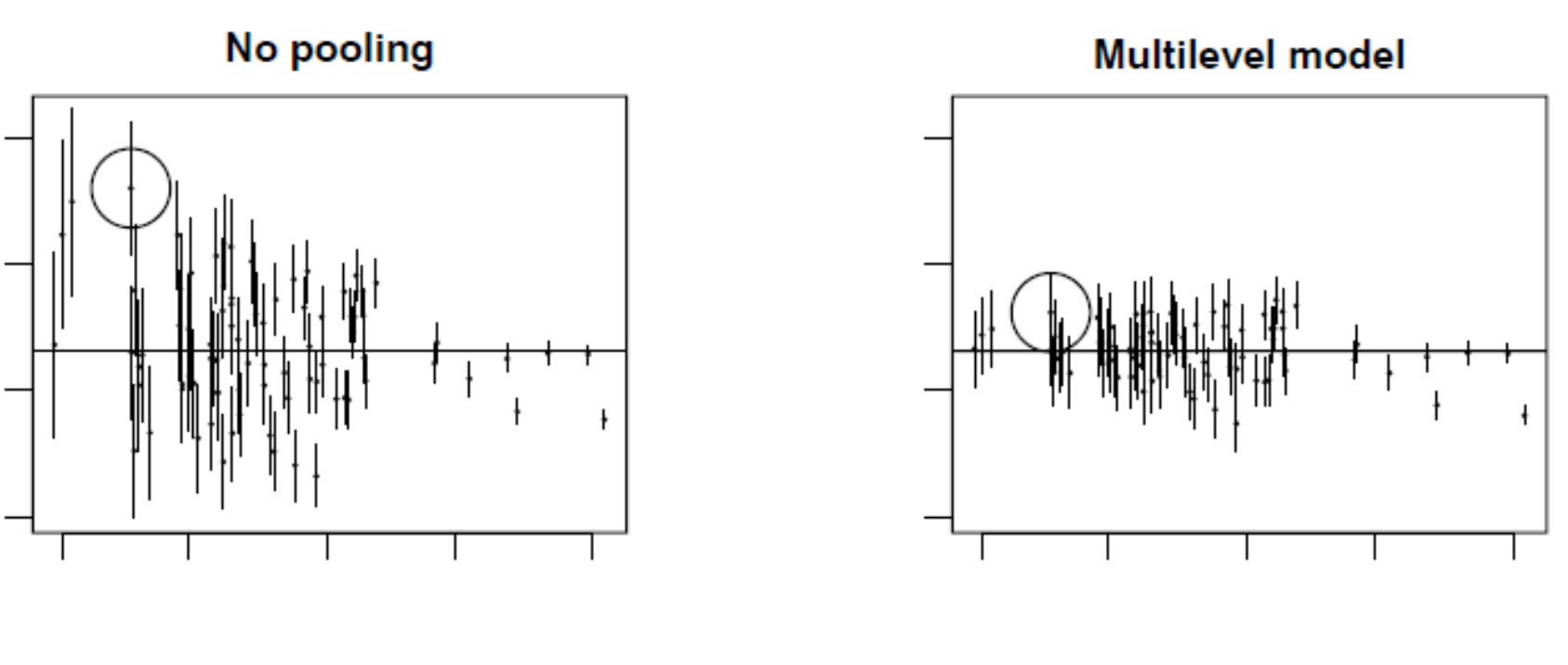
What is a random effect, really?

- Varies by group
- Variation estimated with **probability model**

Random effects are estimated with *partial pooling* (shrinkage, regularisation), while fixed effects are not (infinite variance).

Shrinkage improves parameter estimation

Especially for groups with low sample size



From Gelman & Hill p. 253

Fitting mixed/multilevel models

```
library('glmmTMB')
mixed <- glmmTMB(height ~ dbh + (1|site), data = trees)
```

```
 Family: gaussian  ( identity )
Formula:          height ~ dbh + (1 | site)
Data: trees

     AIC      BIC   logLik deviance df.resid
  5110.3   5129.9  -2551.1   5102.3      996

Random effects:

Conditional model:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 10.007   3.163
 Residual              9.252   3.042
Number of obs: 1000, groups:  site, 10

Dispersion estimate for gaussian family (sigma^2): 9.25

Conditional model:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 19.014671   1.045018   18.20   <2e-16 ***
dbh          0.616911   0.007569   81.51   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fitting mixed/multilevel models

```
library('lme4')
mixed <- lmer(height ~ dbh + (1|site), data = trees)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 | site)
   Data: trees

REML criterion at convergence: 5108.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.3199 -0.6607  0.0227  0.6716  3.7328

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 11.195   3.346
 Residual              9.261   3.043
Number of obs: 1000, groups:  site, 10

Fixed effects:
             Estimate Std. Error t value
(Intercept) 19.011468   1.100444   17.28
dbh          0.616927   0.007572   81.47

Correlation of Fixed Effects:
    (Intr)
dbh -0.197
```

Statistical model structure

```
library(equatiomatic)
equatiomatic::extract_eq(mixed)
```

$$
\begin{aligned}
\text{height}_i &\sim N\left(\alpha_{j[i]} + \beta_1(\text{dbh}), \sigma^2\right) \\
\alpha_j &\sim N\left(\mu_{\alpha_j}, \sigma^2_{\alpha_j}\right), \text{for site j = 1, . . . ,J}
\end{aligned}
\tag{1}
$$

Retrieve model coefficients

```
coef(mixed)
```

```
$site
   (Intercept)       dbh
1     16.70800 0.6169271
2     23.19162 0.6169271
3     21.04229 0.6169271
4     18.64086 0.6169271
5     20.32995 0.6169271
6     20.88200 0.6169271
7     16.61686 0.6169271
8     11.88302 0.6169271
9     21.84779 0.6169271
10    18.97228 0.6169271

attr(,"class")
[1] "coef.mer"
```

Compare site effects between mixed and lm

	lm	mixed
site1	16.7	16.7
site2	23.2	23.2
site3	21.1	21.0
site4	18.6	18.6
site5	20.3	20.3
site6	20.9	20.9
site7	16.5	16.6
site8	11.4	11.9
site9	22.1	21.8
site10	19.0	19.0

Broom: model estimates in tidy form

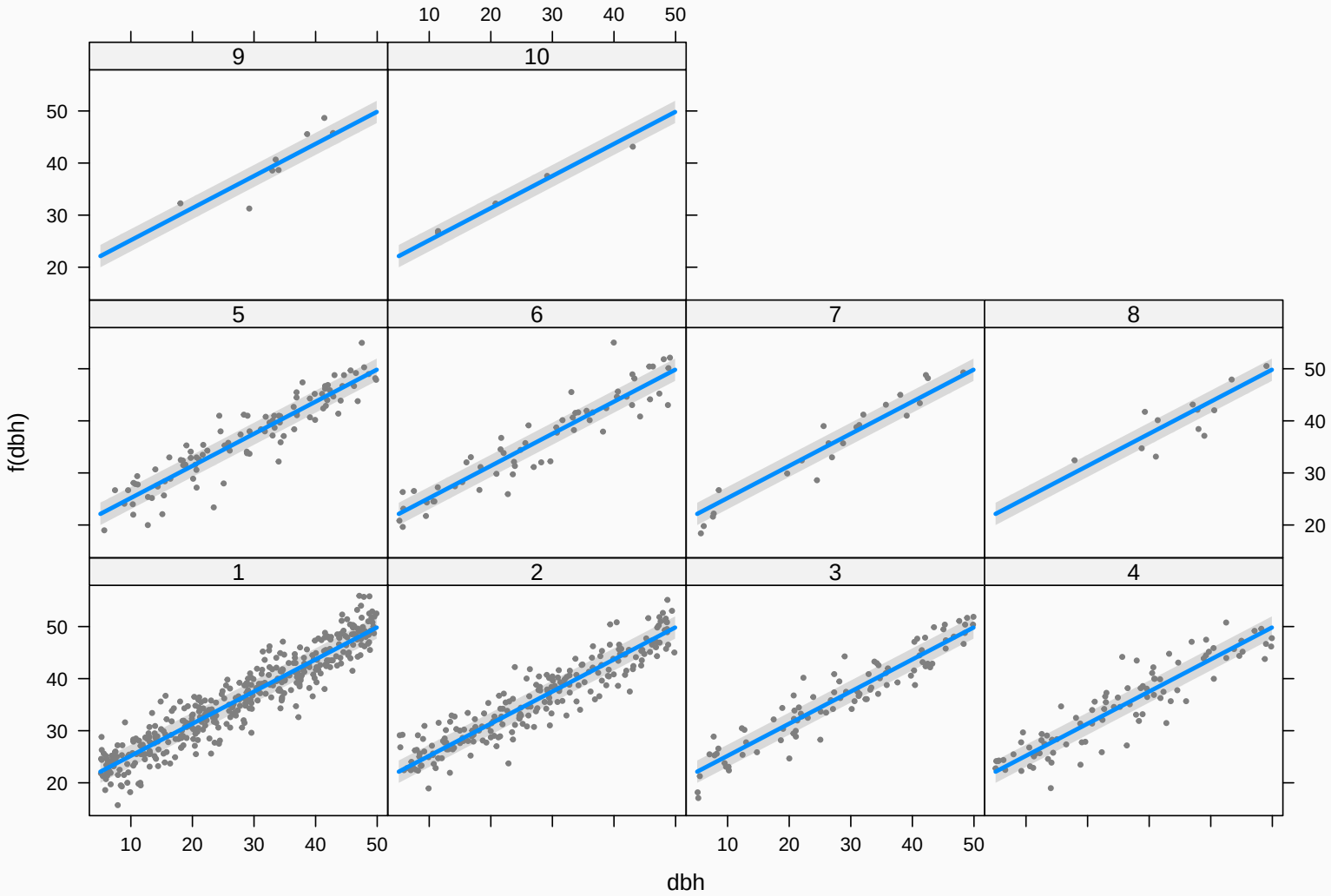
```
library(broom.mixed)
tidy(mixed)
```

```
# A tibble: 4 x 6
  effect   group    term             estimate std.error statistic
  <chr>    <chr>    <chr>               <dbl>     <dbl>     <dbl>
1 fixed    <NA>     (Intercept)       19.0     1.10         17.3
2 fixed    <NA>     dbh                0.617   0.00757      81.5
3 ran_pars site     sd__(Intercept)    3.35    NA            NA
4 ran_pars Residual sd__Observation    3.04    NA            NA
```

See also broom.mixed

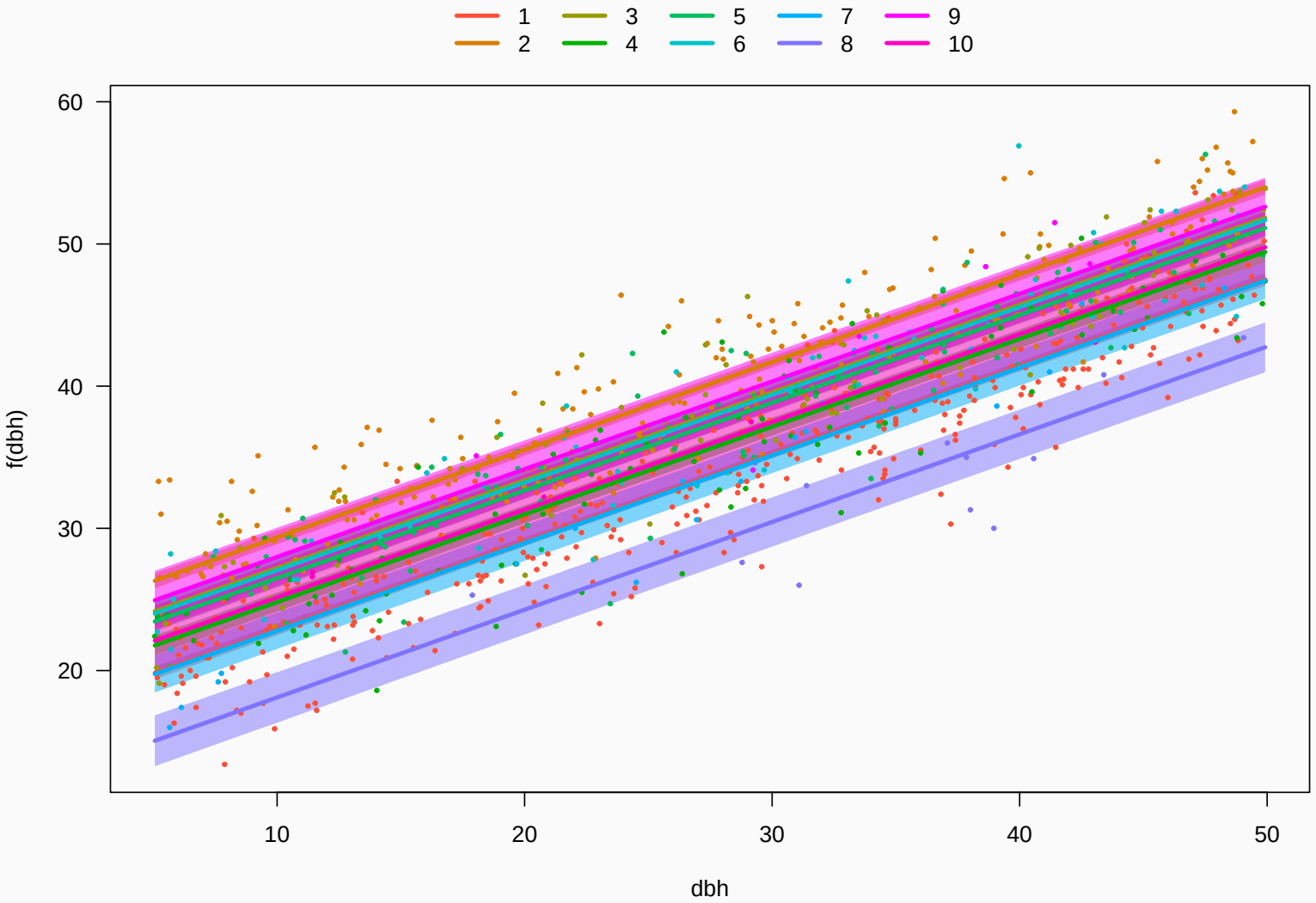
Visualising model: `visreg`

```
visreg(mixed, xvar = 'dbh', by = 'site')
```



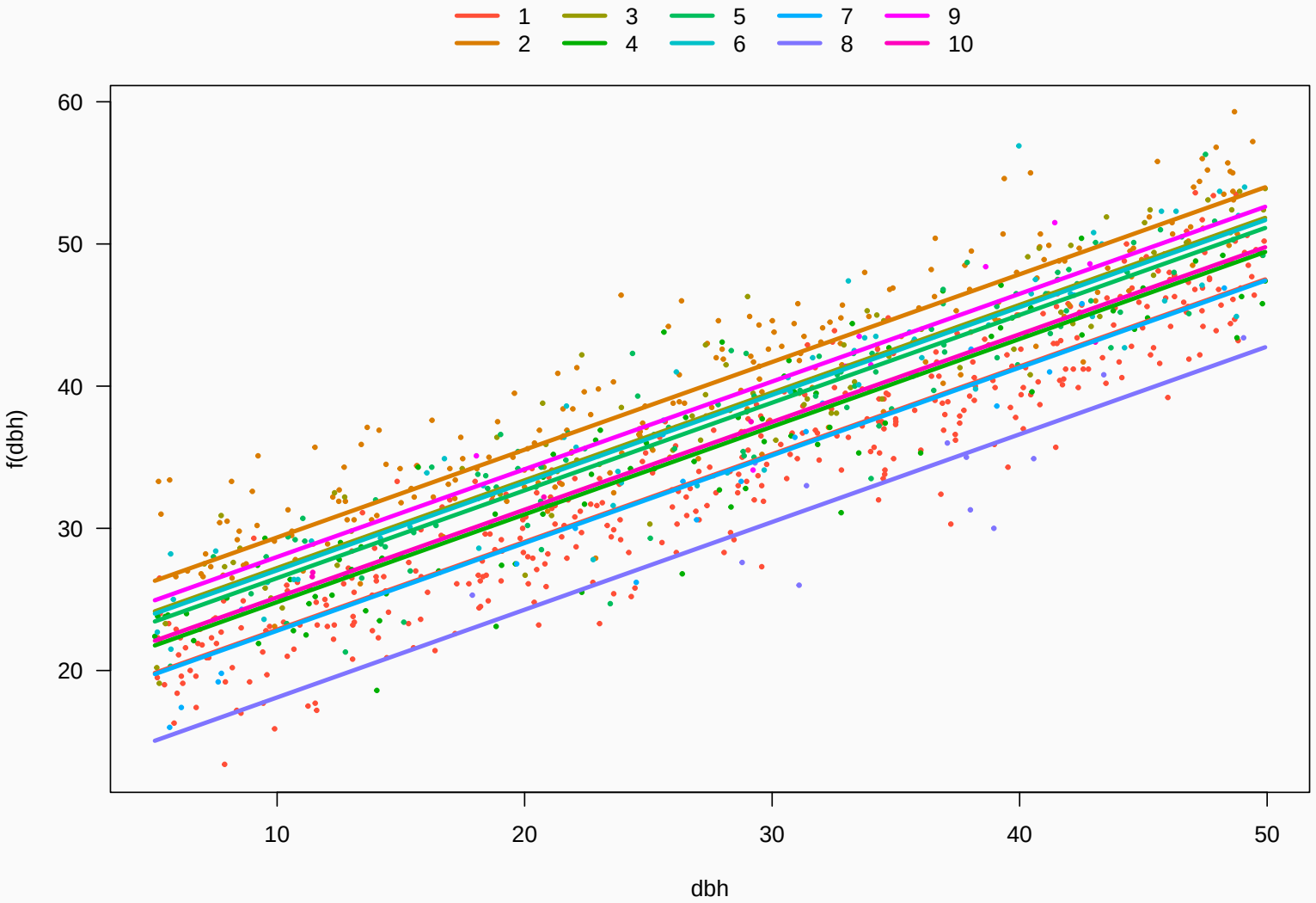
Visualising model

```
visreg(mixed, xvar = 'dbh', by = 'site', overlay = TRUE)
```



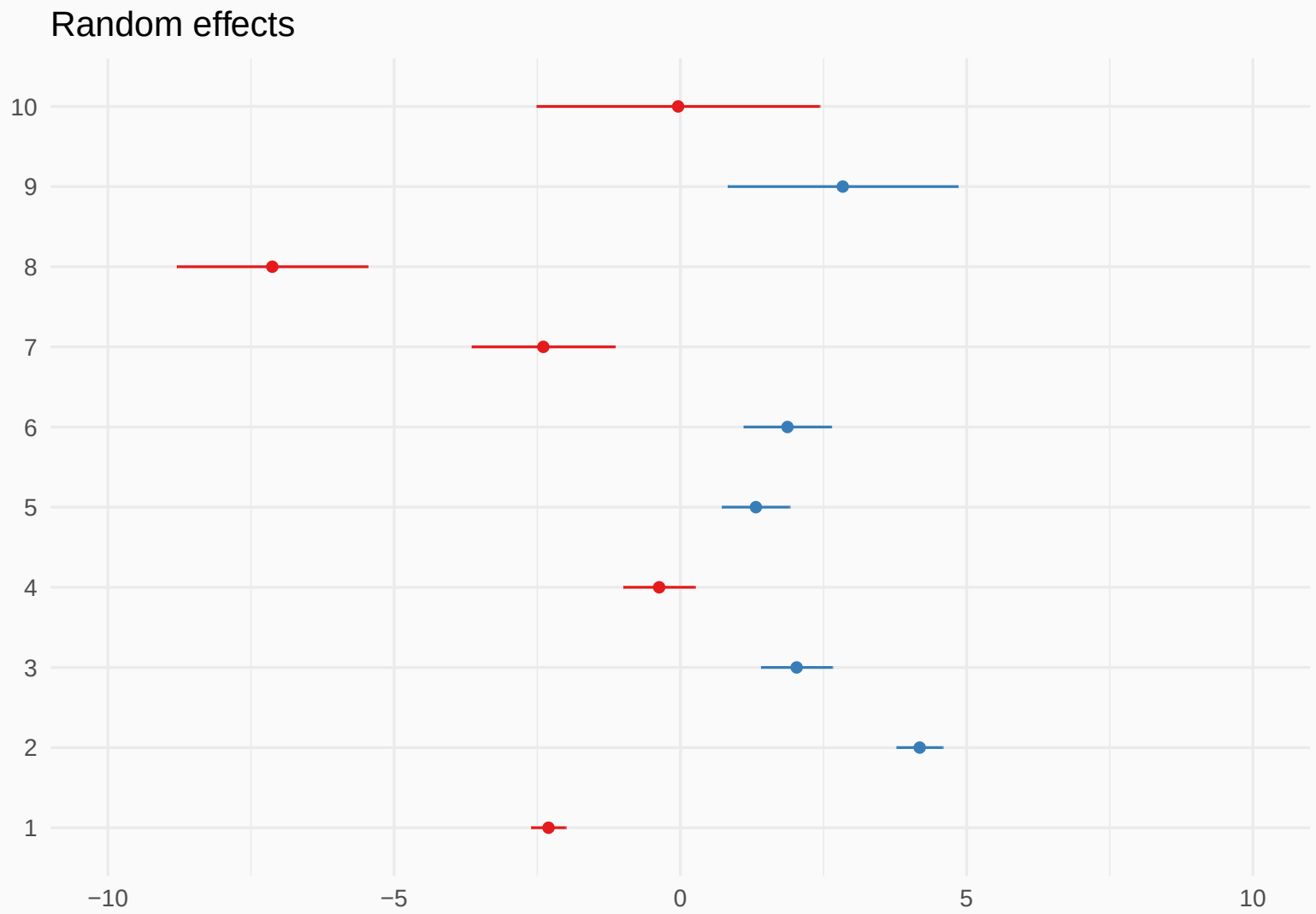
Visualising model

```
visreg(mixed, xvar = 'dbh', by = 'site', overlay = TRUE, band = FAL
```



Visualising model: `sjPlot`

```
sjPlot::plot_model(mixed, type = 're')
```

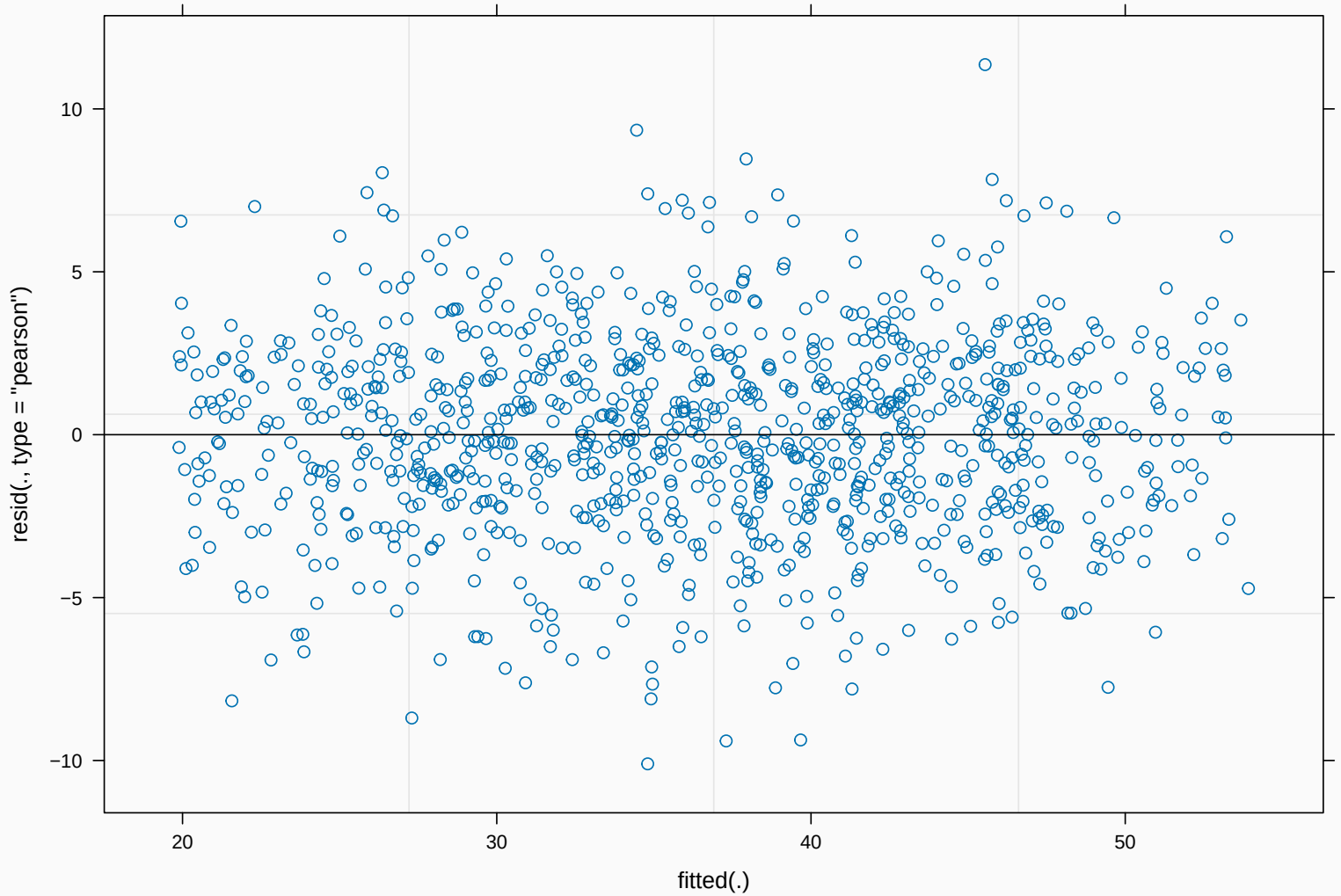


Using merTools to understand fitted model

```
library('merTools')
shinyMer(mixed)
```

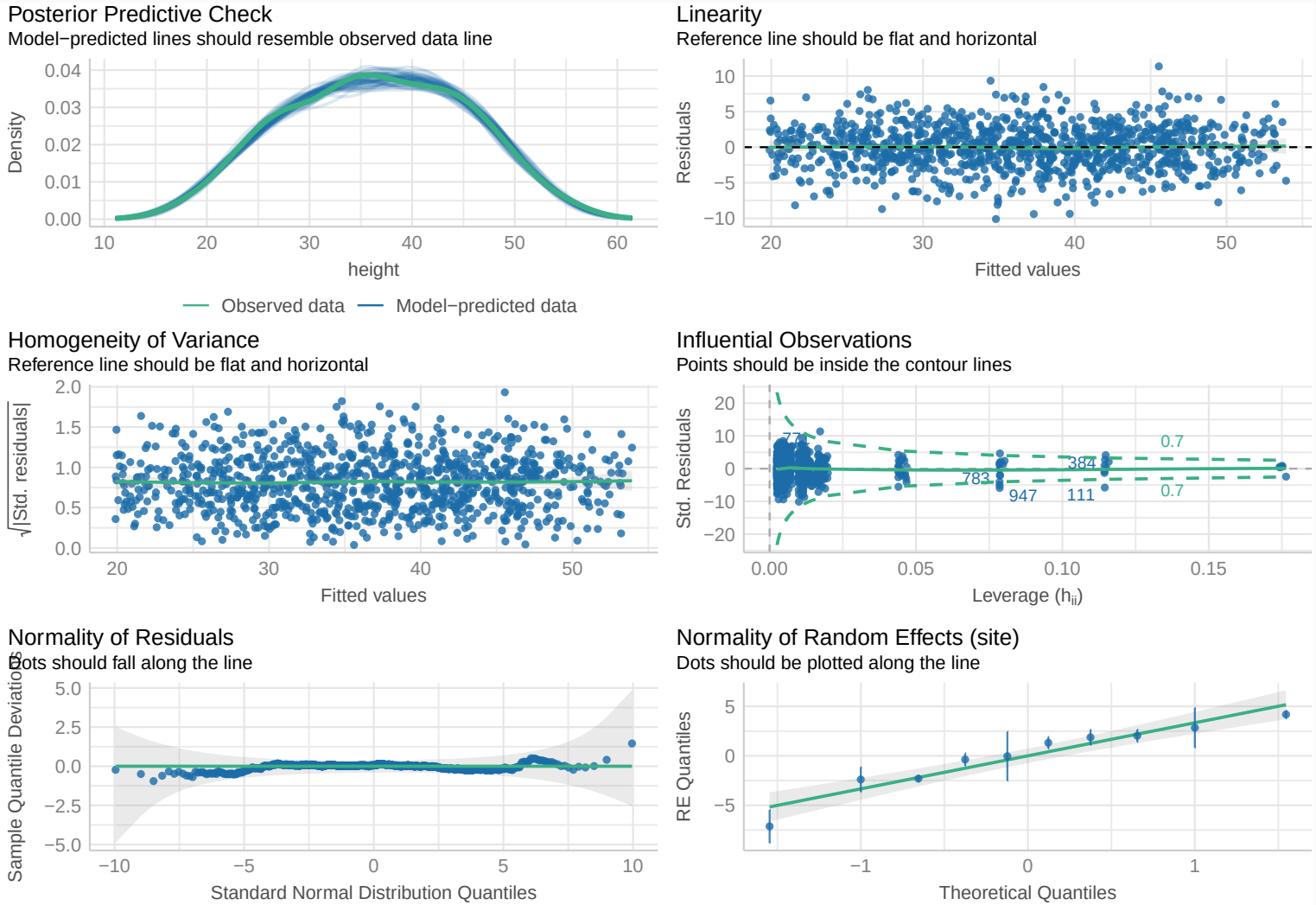
Checking residuals

```
plot(mixed)
```



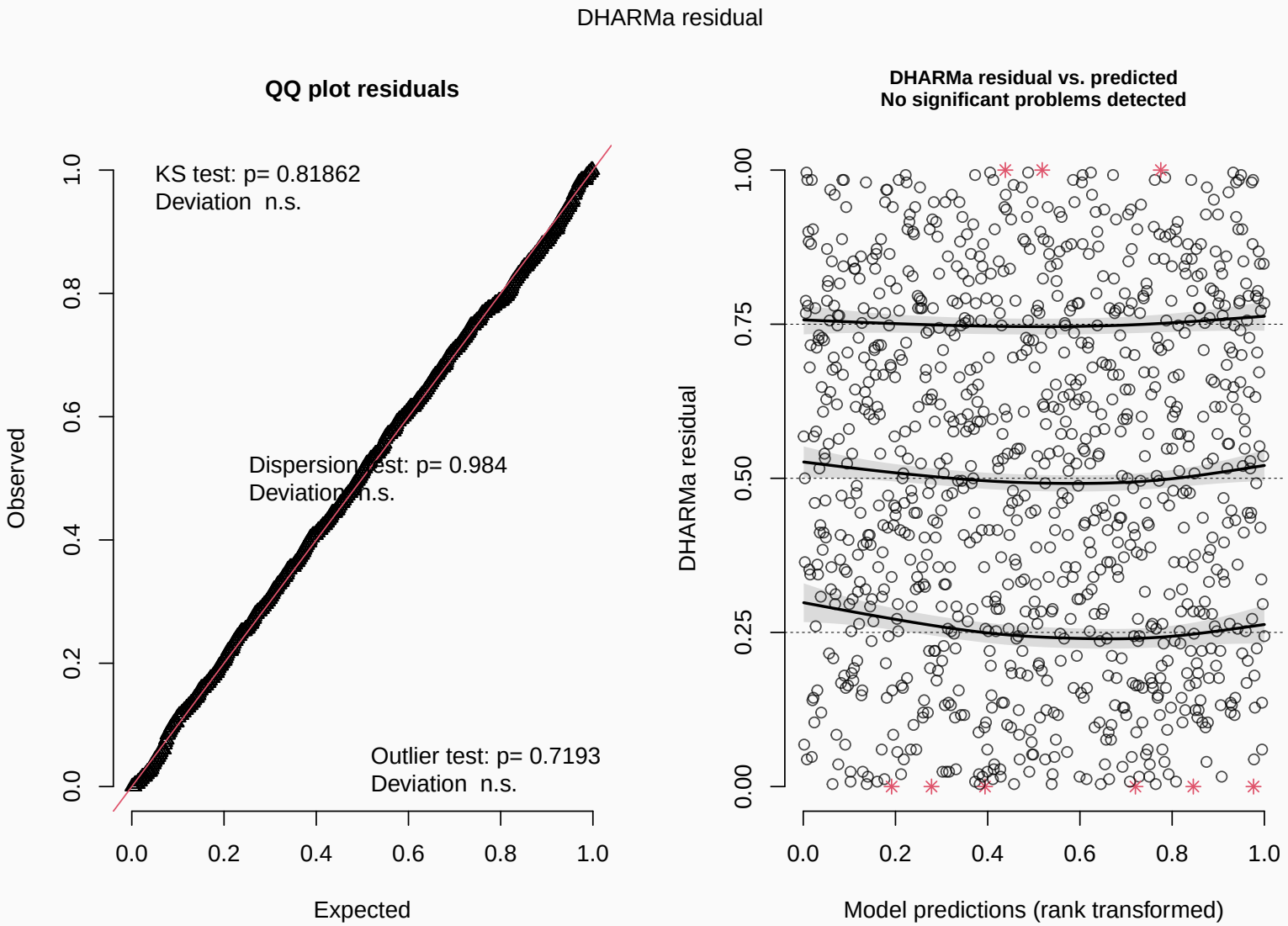
Checking residuals

```
library('performance')
check_model(mixed)
```



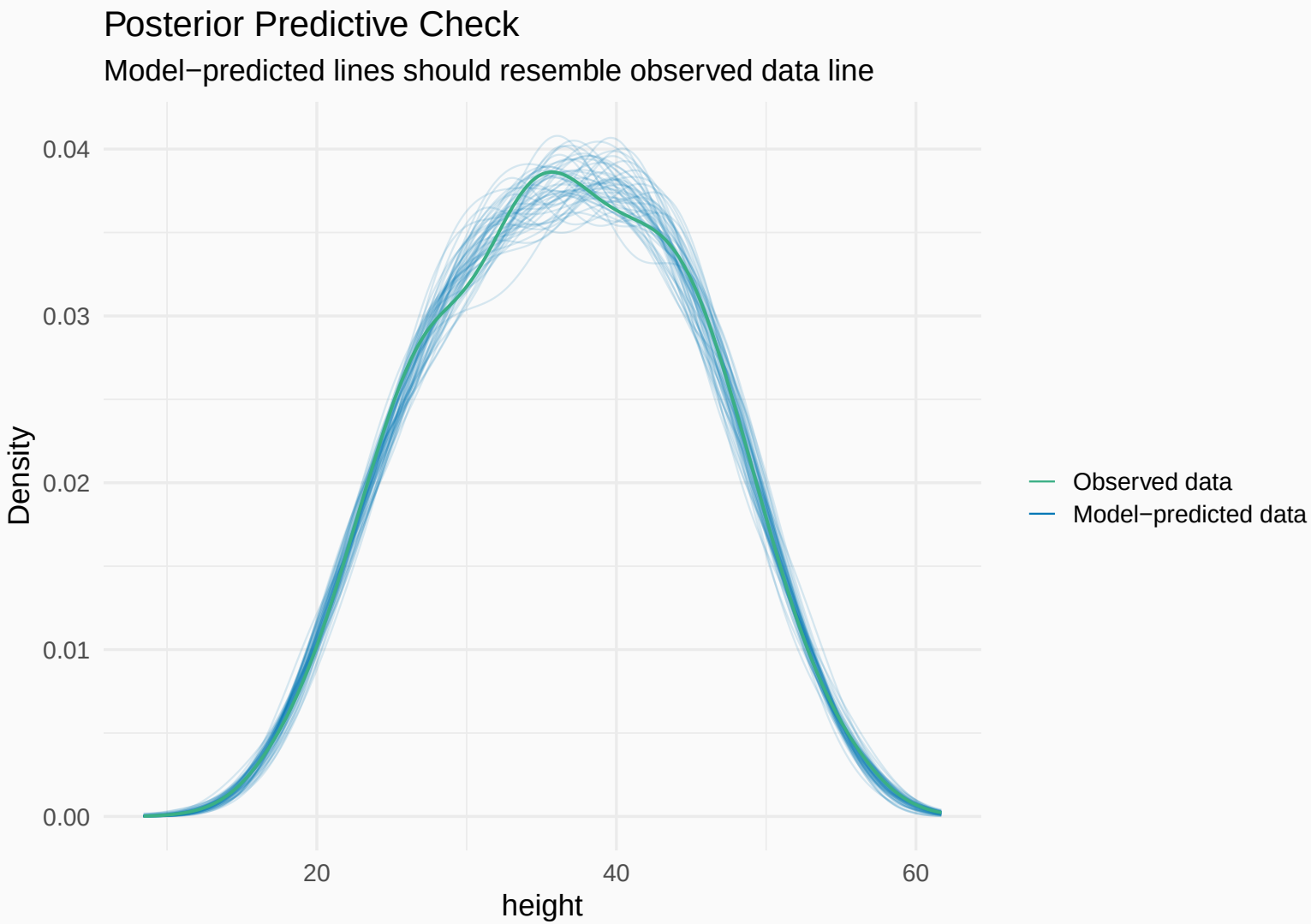
Checking residuals (DHARMa)

```
DHARMa::simulateResiduals(mixed, plot = TRUE, re.form = NULL)
```



Model checking with simulated data

```
check_predictions(mixed)
```



R-squared for GLMMs

Many approaches! Somewhat polemic (e.g. see this).

Nakagawa & Schielzeth propose **marginal** (considering fixed effects only) and **conditional** R^2 (including random effects too):

```
r2(mixed)
```

```
# R2 for Mixed Models

  Conditional R2: 0.888
     Marginal R2: 0.753
```

Growing the hierarchy: adding site-level predictors

Model with group-level predictors

We had:

$$
\begin{aligned}
y_i &= a + \alpha_j + b \cdot x_i + \varepsilon_i \\
\alpha_j &\sim N(0, \tau^2) \\
\varepsilon_i &\sim N(0, \sigma^2)
\end{aligned}
$$

Now

$$
\begin{aligned}
y_i &= a + \alpha_j + b \cdot x_i + \varepsilon_i \\
\alpha_j &\sim N(\mu_j, \tau^2) \\
\mu_j &= \delta \cdot \mathit{Predictor}_j \\
\varepsilon_i &\sim N(0, \sigma^2)
\end{aligned}
$$

Are height differences among sites related to temperature?

$$
\begin{aligned}
Height_i &= site_j + b \cdot DBH_i + \varepsilon_i \\
site_j &\sim N(\mu_j, \tau^2) \\
\mu_j &= a + \delta \cdot Temperature_j \\
\varepsilon_i &\sim N(0, \sigma^2)
\end{aligned}
$$

Are height differences among sites related to temperature?

```
sitedata <- read.csv('data/sitedata.csv')
sitedata
```

```
   site temp
1     1 15.1
2     2 22.0
3     3 20.1
4     4 20.4
5     5 20.0
6     6 20.1
7     7 17.5
8     8 14.6
9     9 19.2
10   10 16.0
```

Merging trees and site data

```
trees.full <- merge(trees, sitedata, by = 'site')
head(trees.full)
```

```
  site   dbh height    sex dead temp
1    1 21.05   32.2   male    0 15.1
2    1 46.63   45.9 female    0 15.1
3    1 43.86   45.5   male    0 15.1
4    1 29.03   35.5   male    0 15.1
5    1  6.02   21.1   male    0 15.1
6    1 40.82   38.7   male    0 15.1
```

Fit multilevel model

```
group.pred <- lmer(height ~ dbh + (1 | site) + temp, data = trees.full)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 | site) + temp
   Data: trees.full

REML criterion at convergence: 5098.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.3247 -0.6517  0.0192  0.6663  3.7268

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 3.158    1.777
 Residual             9.266    3.044
Number of obs: 1000, groups:  site, 10

Fixed effects:
             Estimate Std. Error t value
(Intercept) -1.730910   4.671330  -0.371
dbh          0.616894   0.007571  81.484
temp         1.115104   0.248000   4.496

Correlation of Fixed Effects:
     (Intr) dbh
dbh  -0.055
temp -0.991  0.008
```

Too strong correlation of parameters!

Centre (and scale) continuous variables

```
mean(sitedata$temp)
```

```
[1] 18.5
```

```
trees.full$temp.c <- trees.full$temp - 18
```

Temperatures now referred as deviations from 18 ºC (close to average)

Fit multilevel model

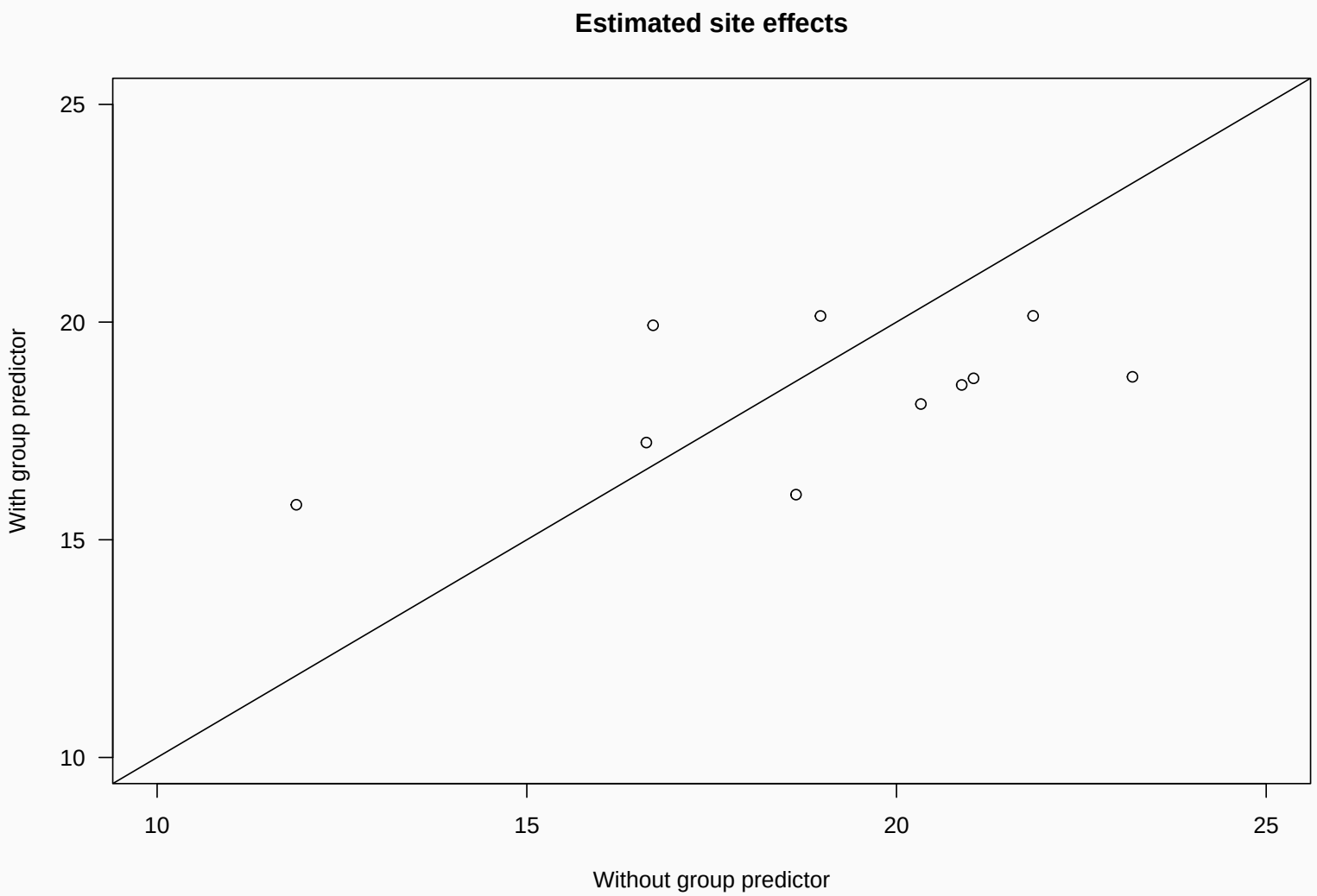
```
group.pred <- lmer(height ~ dbh + (1 | site) + temp.c, data = trees.full)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 | site) + temp.c
   Data: trees.full

REML criterion at convergence: 5098.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.3247 -0.6517  0.0192  0.6663  3.7268

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 3.158    1.777
 Residual             9.266    3.044
Number of obs: 1000, groups:  site, 10

Fixed effects:
             Estimate Std. Error t value
(Intercept) 18.340954   0.655054  27.999
dbh          0.616894   0.007571  81.484
temp.c       1.115104   0.248000   4.496

Correlation of Fixed Effects:
       (Intr) dbh
```

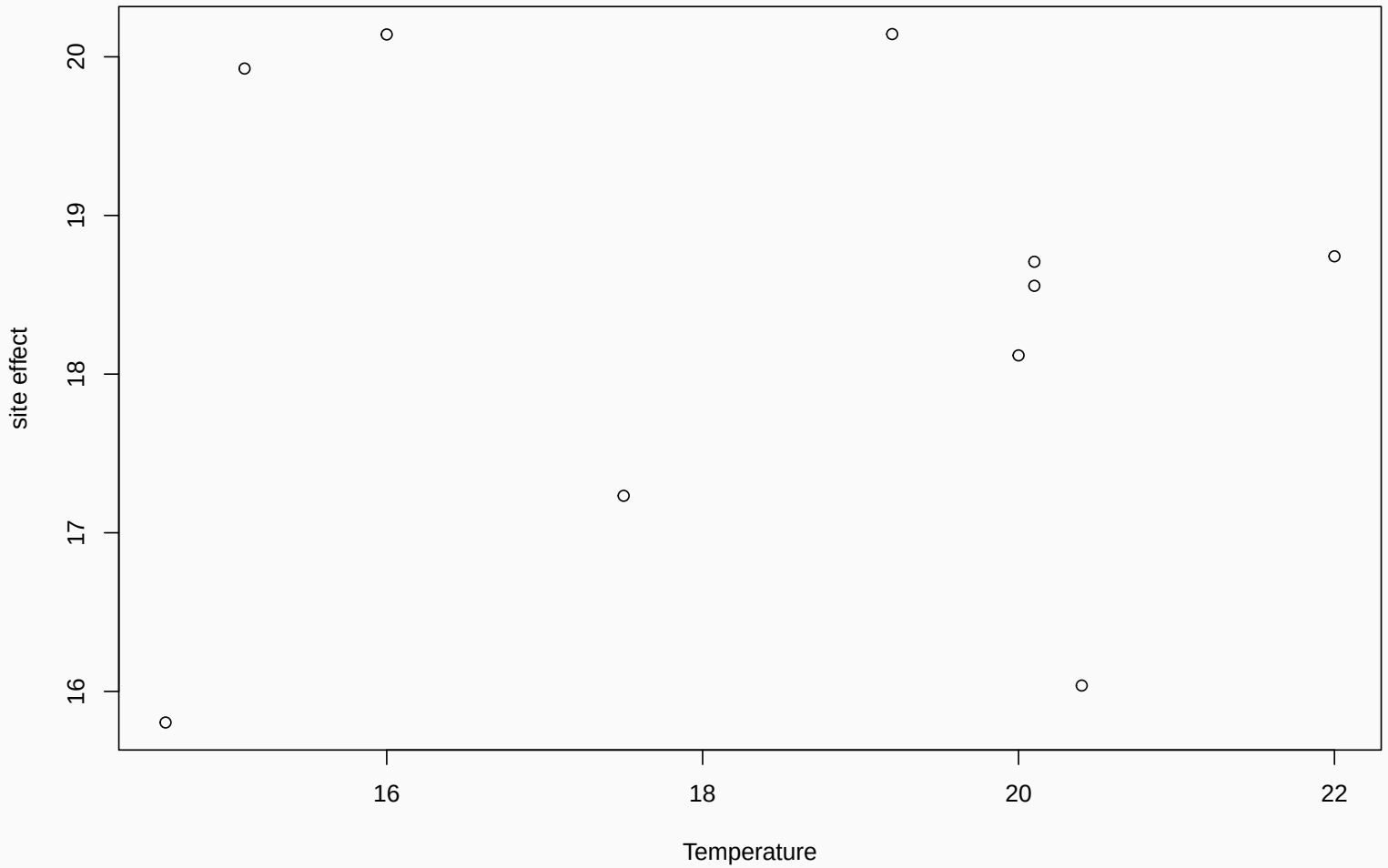
Examine model with merTools

```
shinyMer(group.pred)
```

Comparing site effects with and without group predictor



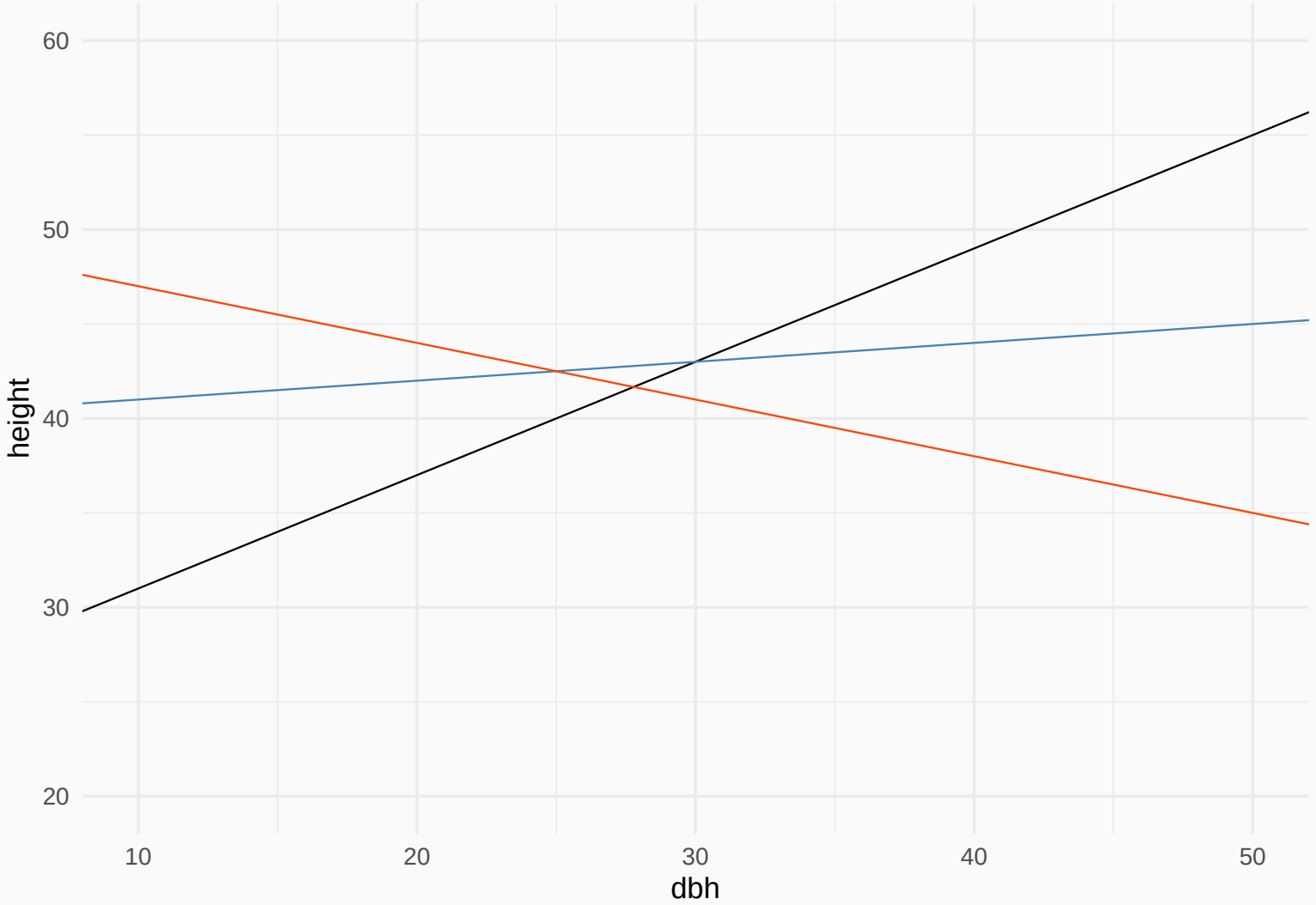
Are site effects related to temperature?



Varying intercepts and slopes

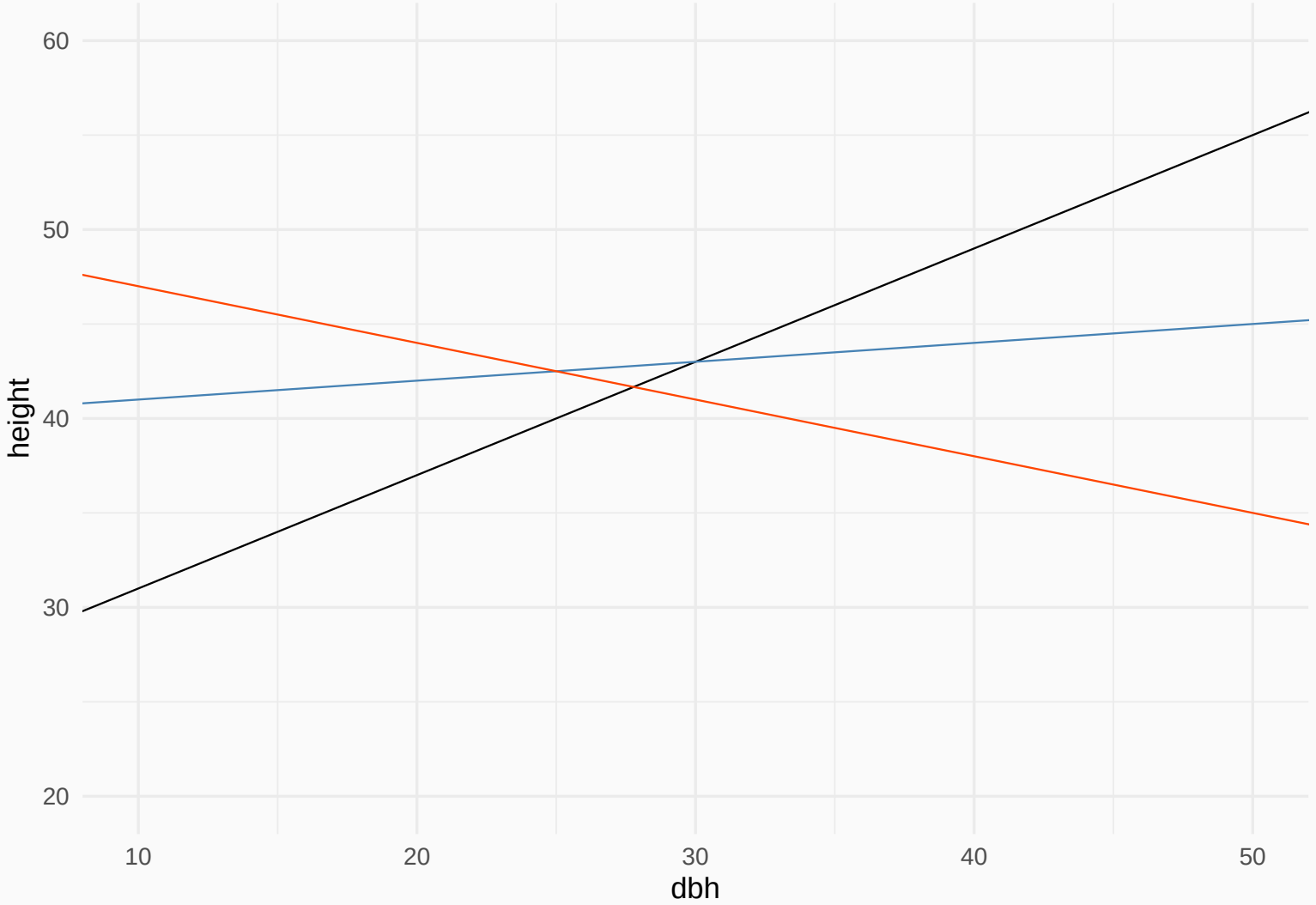
Varying intercepts and slopes

- There is overall difference in height among sites (different intercepts)



Varying intercepts and slopes

- There is overall difference in height among sites (different intercepts)
- Relationship between DBH and Height varies among sites (different slopes)



Varying intercepts and slopes

```
mixed.slopes <- lmer(height ~ dbh + (1 + dbh | site), data=trees)
equatiomatic::extract_eq(mixed.slopes)
```

$$\begin{aligned}
\text{height}_i &\sim N\left(\alpha_{j[i]} + \beta_{1j[i]}(\text{dbh}), \sigma^2\right) \\
\begin{pmatrix} \alpha_j \\ \beta_{1j} \end{pmatrix} &\sim N\left(\begin{pmatrix} \mu_{\alpha_j} \\ \mu_{\beta_{1j}} \end{pmatrix}, \begin{pmatrix} \sigma^2_{\alpha_j} & \rho_{\alpha_j\beta_{1j}} \\ \rho_{\beta_{1j}\alpha_j} & \sigma^2_{\beta_{1j}} \end{pmatrix}\right), \text{for site j = 1, . . . ,J}
\end{aligned} \tag{2}$$

Varying intercepts and slopes

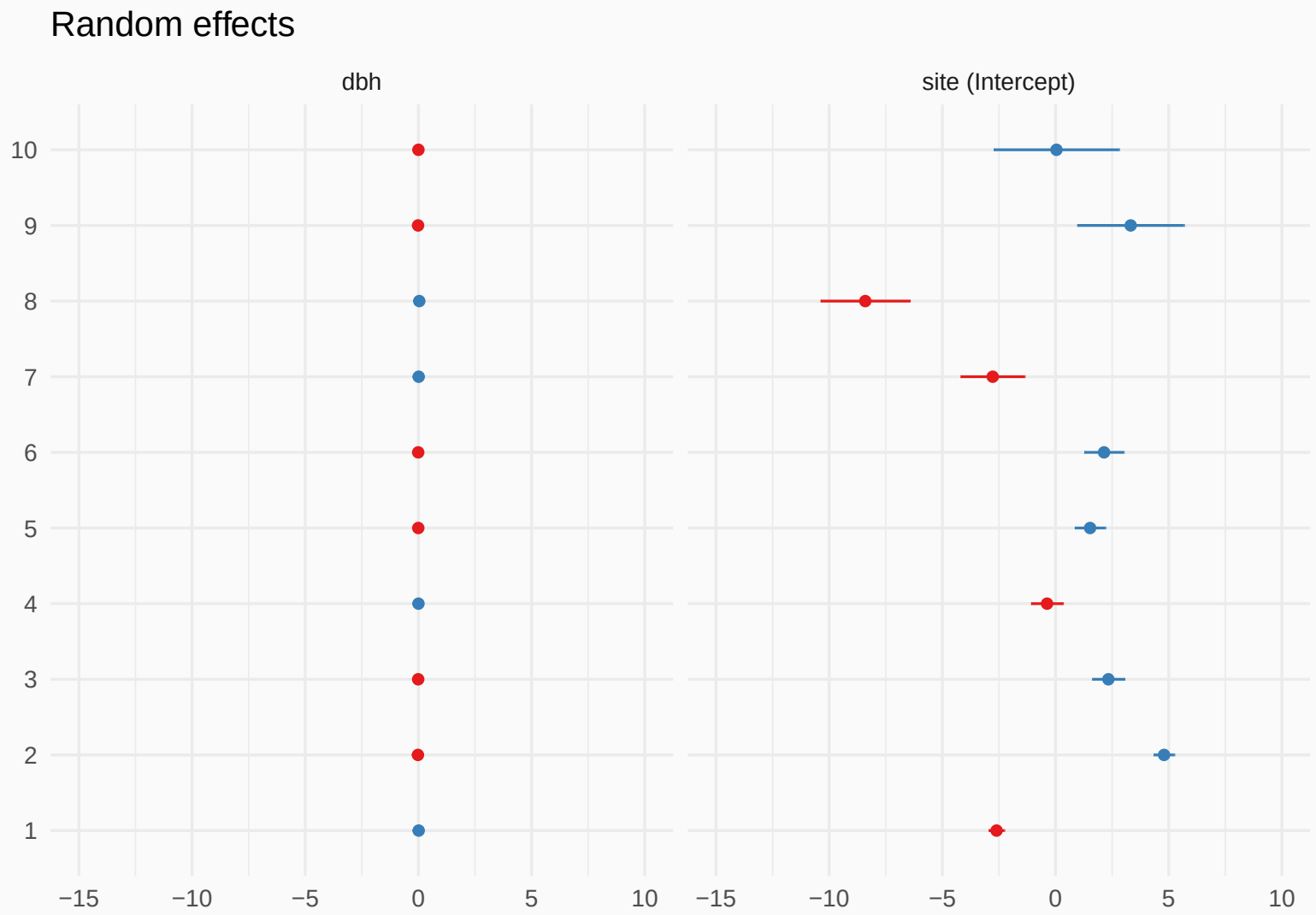
```
Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 + dbh | site)
   Data: trees

REML criterion at convergence: 5105.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.3342 -0.6599  0.0375  0.6916  3.7756

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 site     (Intercept) 1.566e+01 3.95671
          dbh         3.087e-04 0.01757  -1.00
 Residual             9.226e+00 3.03744
Number of obs: 1000, groups:  site, 10

Fixed effects:
            Estimate Std. Error t value
(Intercept) 18.95272    1.29190   14.67
dbh          0.61837    0.00946   65.37
```

Varying intercepts and slopes

```
$site
   (Intercept)       dbh
1     16.34655 0.6299443
2     23.74733 0.5970814
3     21.28802 0.6080019
4     18.57844 0.6200337
5     20.47961 0.6115916
6     21.09608 0.6088542
7     16.17675 0.6306983
8     10.54681 0.6556978
9     22.27301 0.6036281
10    18.99463 0.6181856

attr(,"class")
[1] "coef.mer"
```

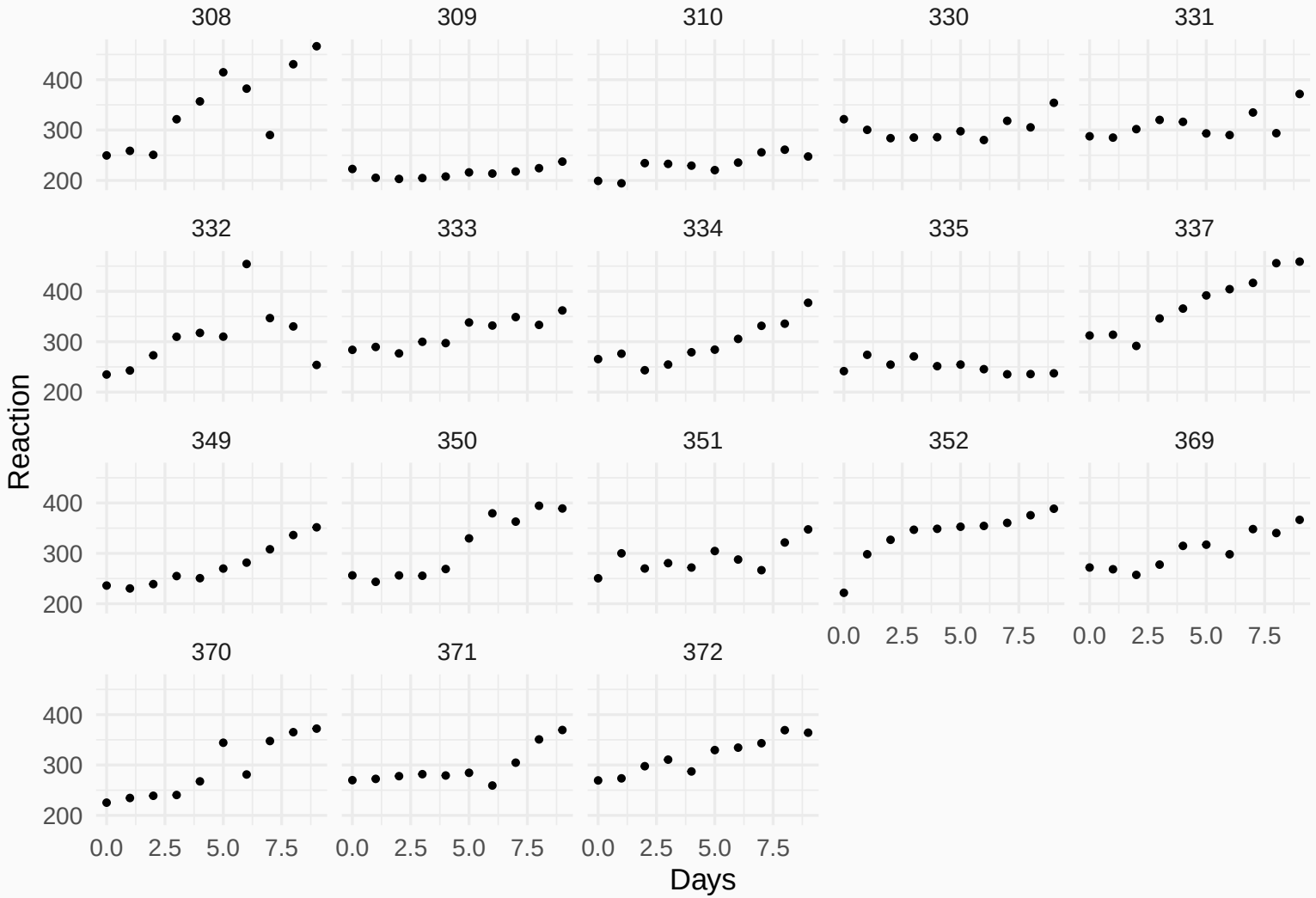
Visualising model: `sjPlot`

```
plot_model(mixed.slopes, type = 're')
```



More examples

sleepstudy (repeated measures)



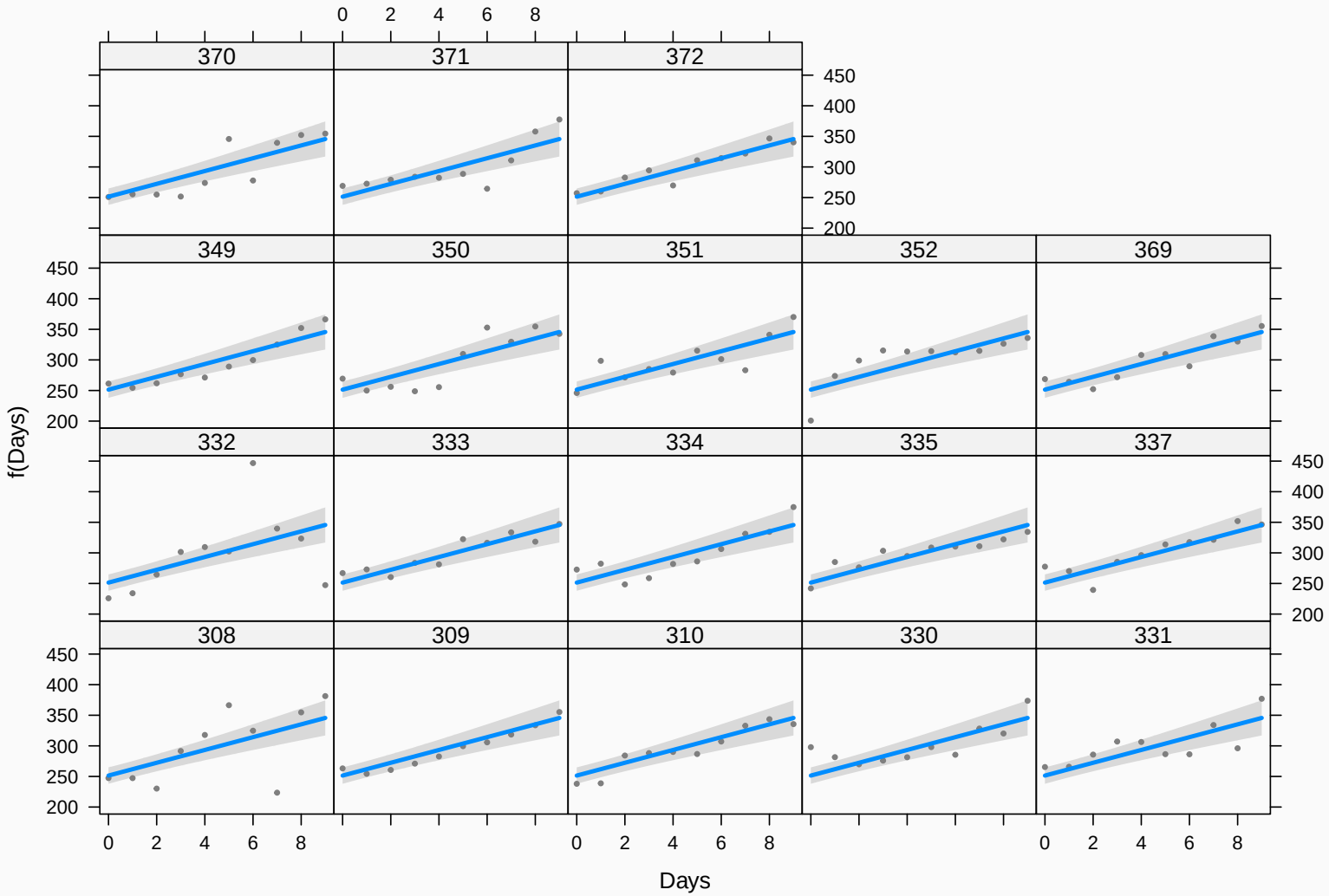
Varying intercepts and slopes (lme4)

```
sleep <- lmer(Reaction ~ Days + (1+Days|Subject), data = sleepstudy)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: Reaction ~ Days + (1 + Days | Subject)
   Data: sleepstudy

REML criterion at convergence: 1743.6

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.9536 -0.4634  0.0231  0.4634  5.1793

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Subject  (Intercept) 612.10   24.741
          Days         35.07    5.922   0.07
 Residual             654.94   25.592
Number of obs: 180, groups:  Subject, 18

Fixed effects:
            Estimate Std. Error t value
(Intercept)  251.405      6.825  36.838
Days          10.467      1.546   6.771

Correlation of Fixed Effects:
     (Intr)
```

Varying intercepts and slopes (lme4)

```
visreg(sleep, xvar = 'Days', by = 'Subject')
```



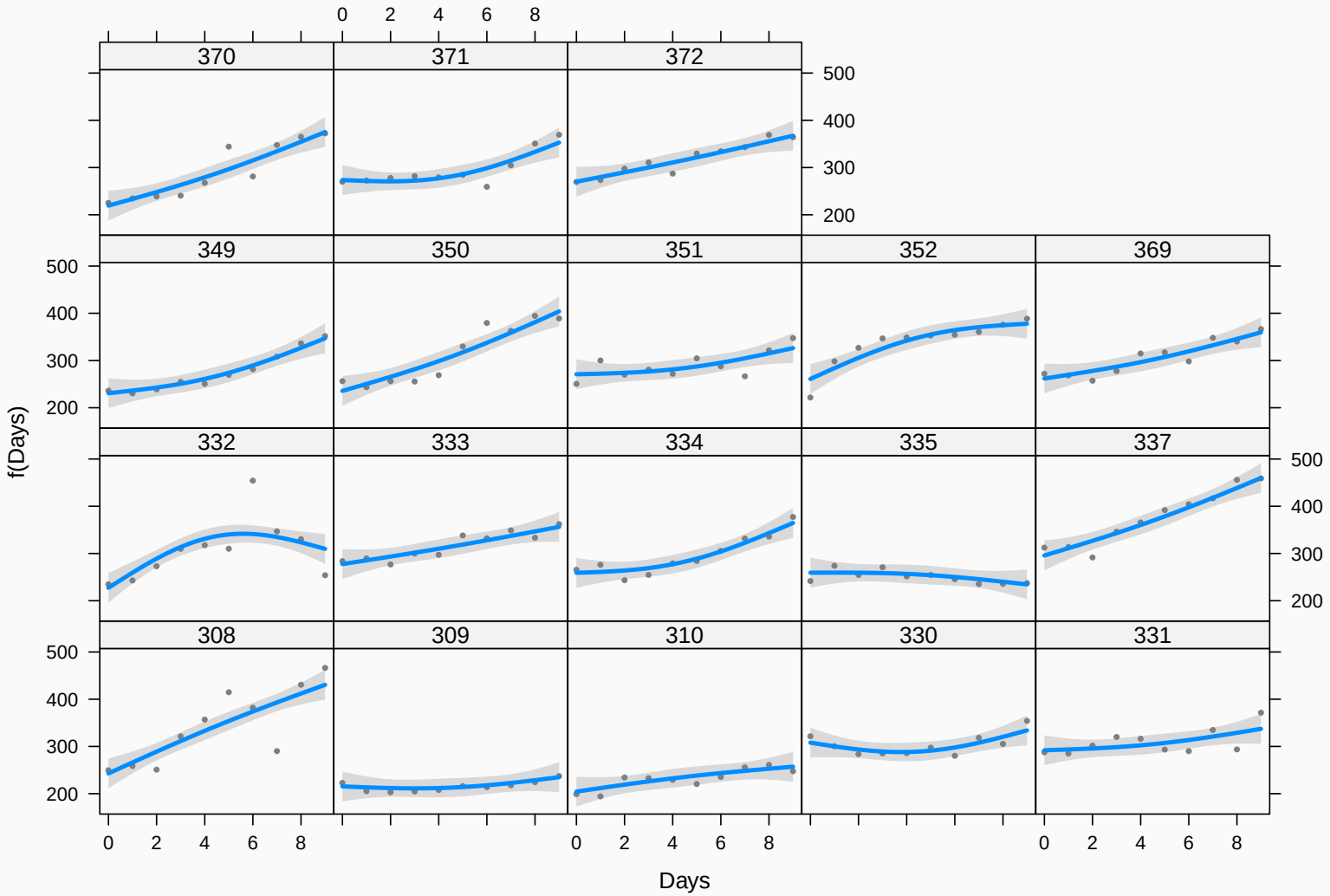
Fitting multilevel models (GAMM) with mgcv

```
sgamm <- mgcv::gam(Reaction ~ s(Days, Subject, k = 3, bs = 'fs'),
                   data = sleepstudy, method = 'REML')
```

```
Family: gaussian
Link function: identity

Formula:
Reaction ~ s(Days, Subject, k = 3, bs = "fs")

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   298.51       9.05   32.98   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
                  edf Ref.df     F p-value
s(Days,Subject) 45.67     53 17.11  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.835   Deviance explained = 87.7%
-REML = 883.64  Scale est. = 523.2     n = 180
```

Fitting multilevel models (GAMM) with mgcv

```
visreg(sgamm, xvar = 'Days', by = 'Subject')
```



Hierarchical generalized additive models: an introduction with mgcv

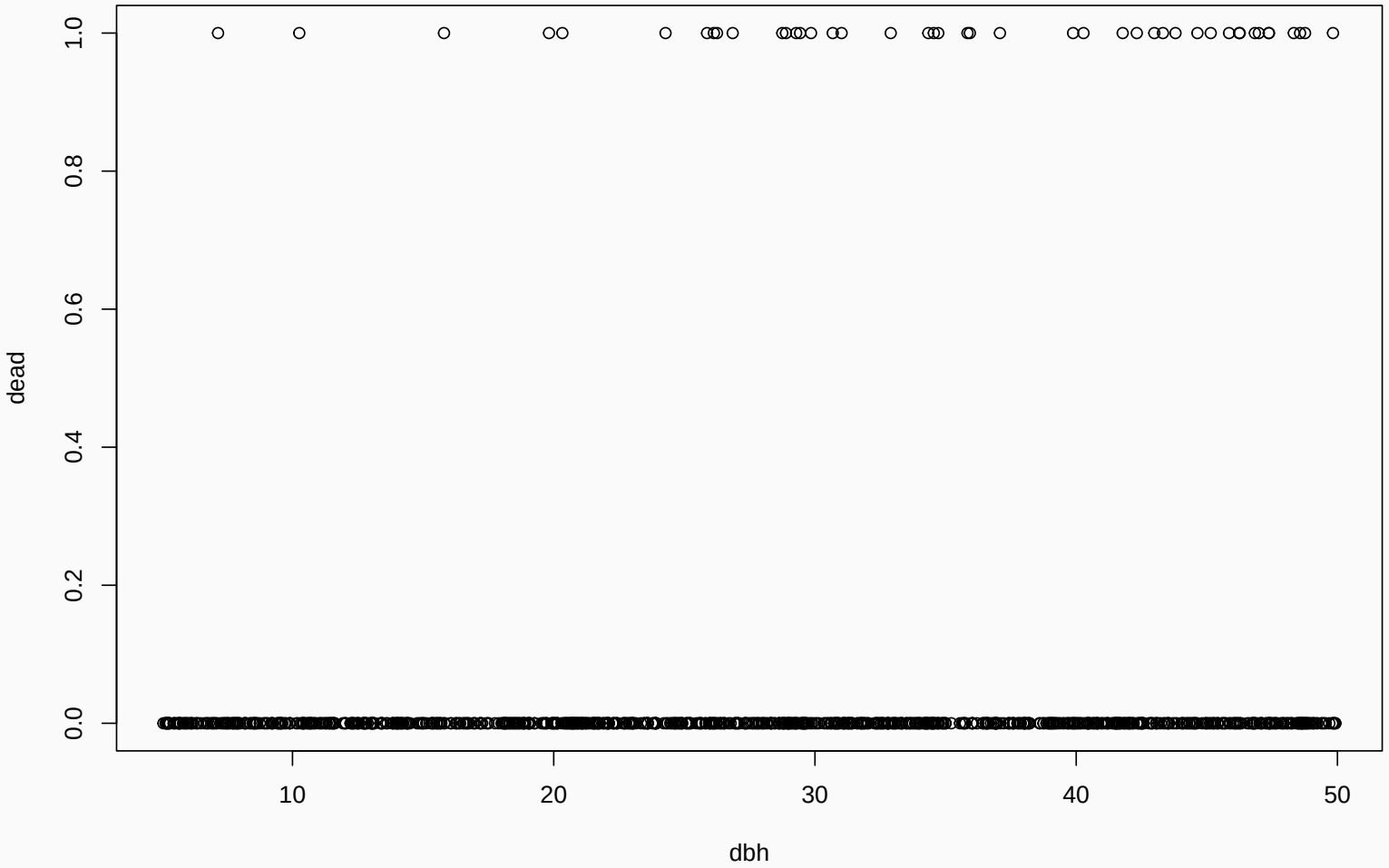
Eric J Pedersen [Corresp., 1, 2], David L. Miller [3, 4], Gavin L. Simpson [5], Noam Ross [6]

https://doi.org/10.7287/peerj.preprints.27320v1

Multilevel logistic regression

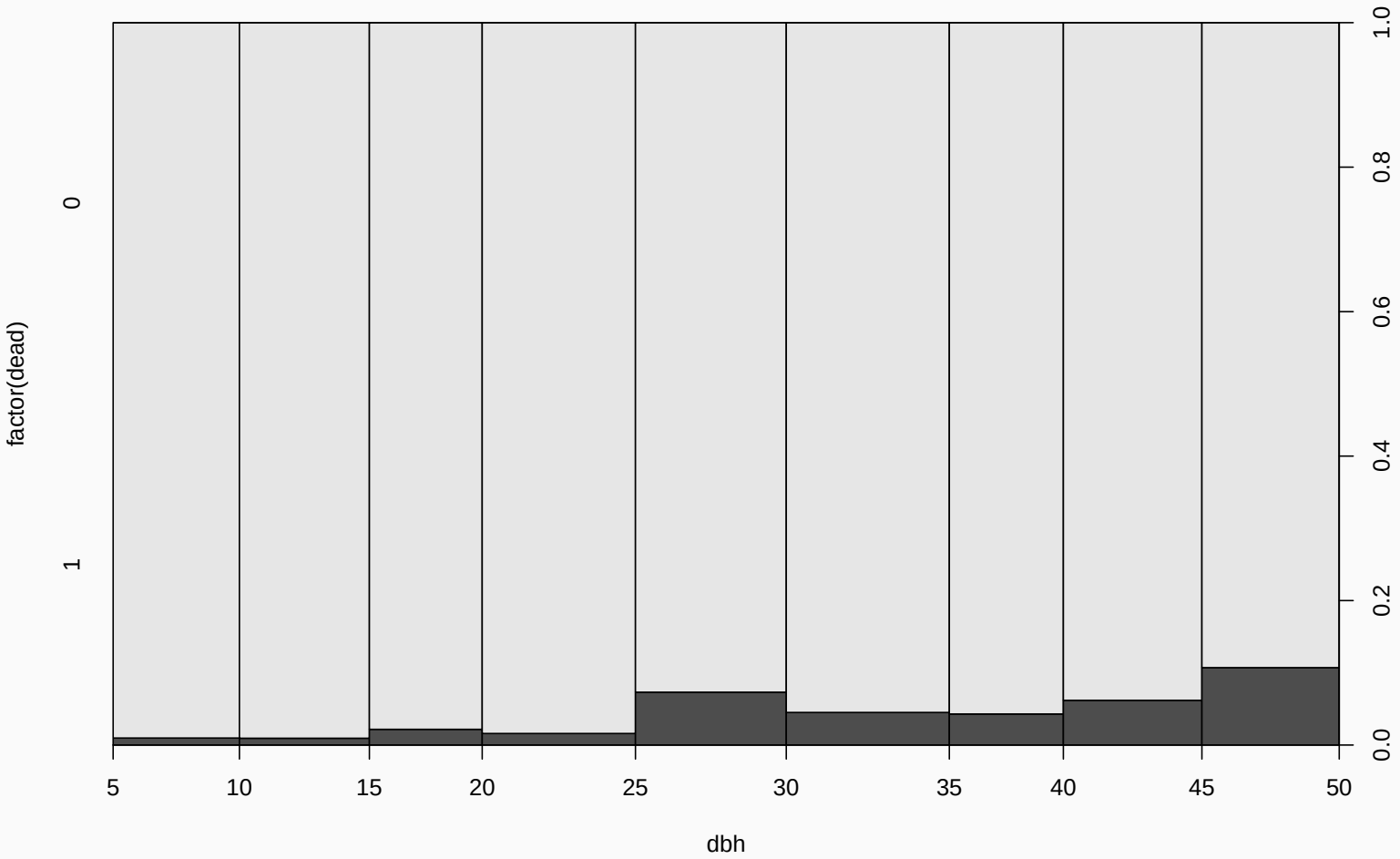
Q: Relationship between tree size and mortality

```
plot(dead ~ dbh, data = trees)
```



Q: Relationship between tree size and mortality

```
plot(factor(dead) ~ dbh, data = trees)
```



Fit simple logistic regression

```
simple.logis <- glm(dead ~ dbh, data = trees, family=binomial)
```

```
Call:
glm(formula = dead ~ dbh, family = binomial, data = trees)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.77874    0.50902  -9.388  < 2e-16 ***
dbh          0.05365    0.01377   3.895 9.82e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 360.91  on 999  degrees of freedom
Residual deviance: 343.69  on 998  degrees of freedom
AIC: 347.69

Number of Fisher Scoring iterations: 6
```

Logistic regression with *independent* site effects

```
logis2 <- glm(dead ~ dbh + site, data = trees, family=binomial)
```

```
Call:
glm(formula = dead ~ dbh + site, family = binomial, data = trees)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   -4.80123    0.54985  -8.732   <2e-16 ***
dbh            0.05371    0.01381   3.889   0.0001 ***
site2         -0.29692    0.46073  -0.644   0.5193
site3          0.21275    0.52799   0.403   0.6870
site4          0.39841    0.53025   0.751   0.4524
site5         -0.42557    0.64018  -0.665   0.5062
site6          0.66861    0.53656   1.246   0.2127
site7          0.11862    1.06211   0.112   0.9111
site8          0.43899    1.08058   0.406   0.6846
site9        -13.63389  840.90382  -0.016   0.9871
site10       -13.17148 1042.21823  -0.013   0.9899
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 360.91  on 999  degrees of freedom
Residual deviance: 338.58  on 989  degrees of freedom
```

Fit multilevel logistic regression

```
mixed.logis <- glmer(dead ~ dbh + (1|site), data=trees, family = binomial)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: dead ~ dbh + (1 | site)
   Data: trees

     AIC      BIC   logLik deviance df.resid
   349.7    364.4   -171.8    343.7      997

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.3498 -0.2528 -0.1888 -0.1370  9.0031

Random effects:
 Groups Name        Variance Std.Dev.
 site   (Intercept) 0        0
Number of obs: 1000, groups:  site, 10

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.77874    0.50904  -9.388  < 2e-16 ***
dbh          0.05365    0.01377   3.895 9.83e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

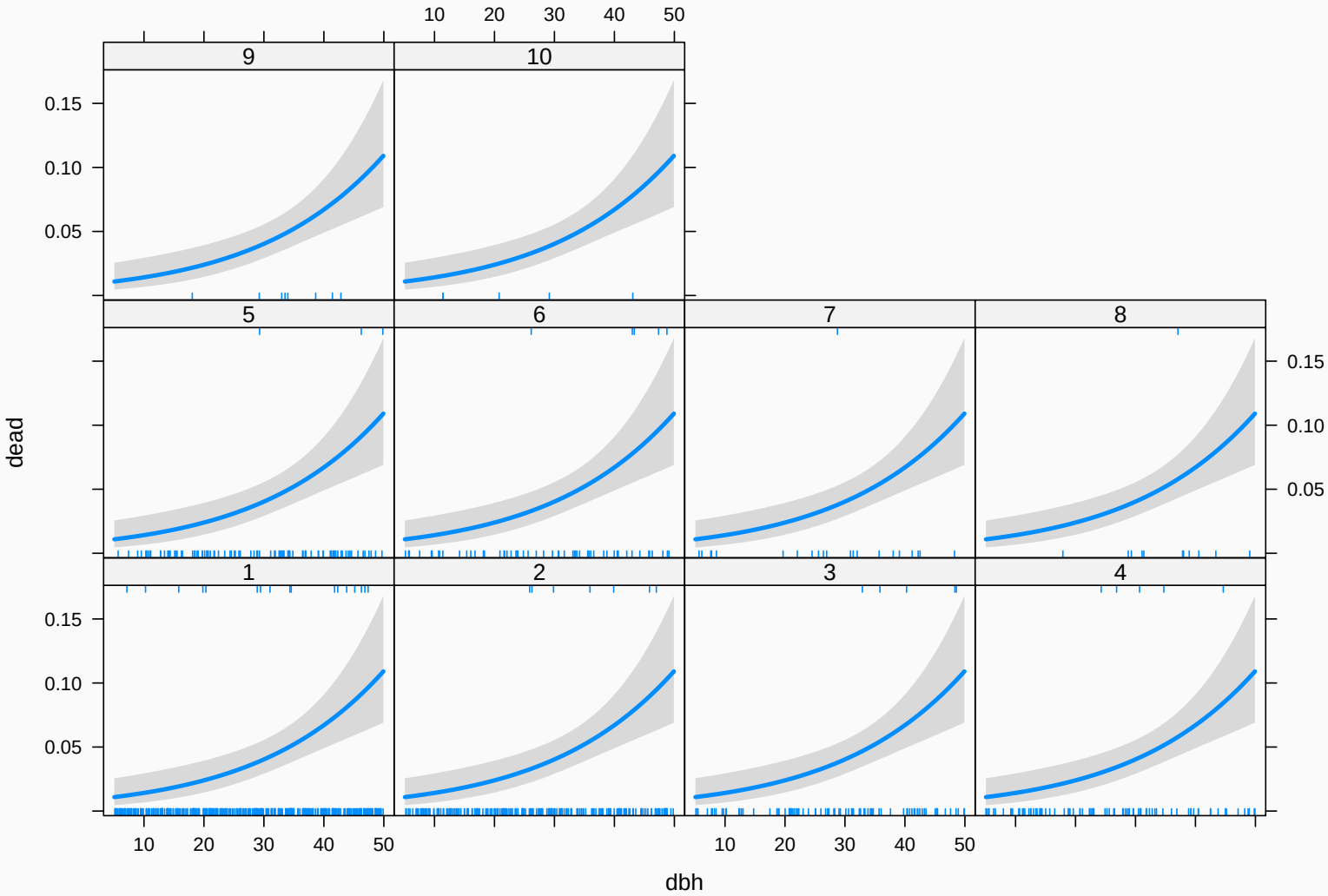
Retrieve model coefficients

```
coef(mixed.logis)
```

```
$site
   (Intercept)        dbh
1    -4.778744 0.05364989
2    -4.778744 0.05364989
3    -4.778744 0.05364989
4    -4.778744 0.05364989
5    -4.778744 0.05364989
6    -4.778744 0.05364989
7    -4.778744 0.05364989
8    -4.778744 0.05364989
9    -4.778744 0.05364989
10   -4.778744 0.05364989

attr(,"class")
[1] "coef.mer"
```

Visualising model: `visreg`

```
visreg(mixed.logis, xvar = 'dbh', by = 'site', scale = 'response')
```



Visualising model: `sjPlot`

```
# plot_model(mixed.logis, type = 'eff', show.ci = TRUE)
```

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- Accommodate **variation** in treatment effects
- More **efficient inference** of regression parameters
- Using all the data to perform inferences for groups with **small sample size**
- Allow predictions for **unobserved groups**

Formula syntax for different models

- Varying intercepts

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- Varying intercepts and slopes, 2 groups (crossed)
  - `y ~ x + (1 + x | group1) + (1 + x | group2)`

To read more about GLMM

https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

http://mfviz.com/hierarchical-models/

https://www.jstor.org/stable/23736938

https://m-clark.github.io/mixed-models-with-R/

https://www.middleprofessor.com/files/applied-biostatistics_bookdown/_book/lmm

https://bookdown.org/roback/bookdown-BeyondMLR/

https://www.learn-mlms.com/

https://doi.org/10.7717/peerj.4794

https://doi.org/10.7717/peerj.9522

Exercises

- Starlings: body mass growth depending on nest type

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- Mixed_binom: Species presence/absence ~ environment

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- Starlings: body mass growth depending on nest type
- Mixed_binom: Species presence/absence ~ environment
- Mixed_count: Species counts ~ environment

Generalised Additive Models

Francisco Rodríguez-Sánchez

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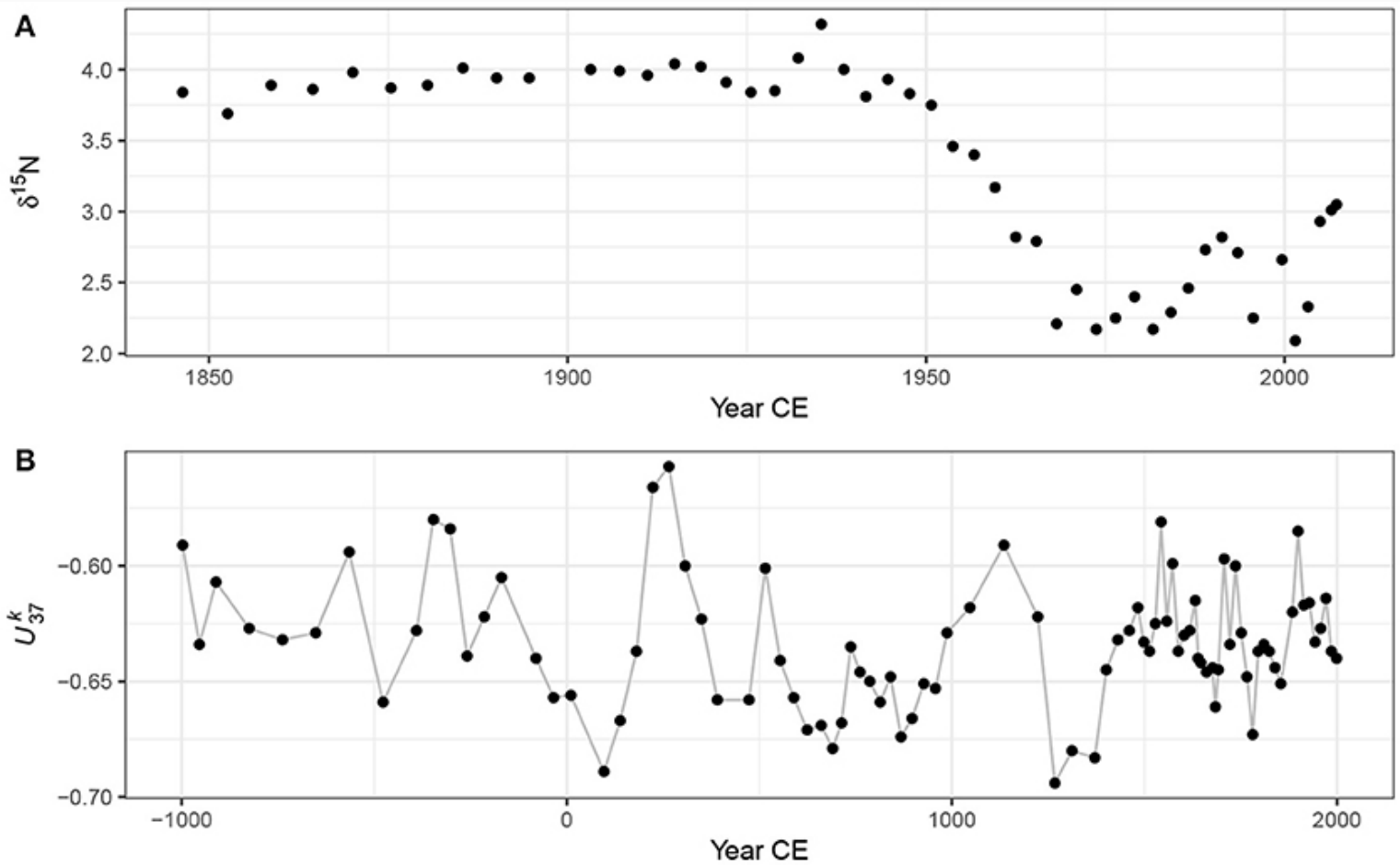
How do we model these time series?



Simpson 2018

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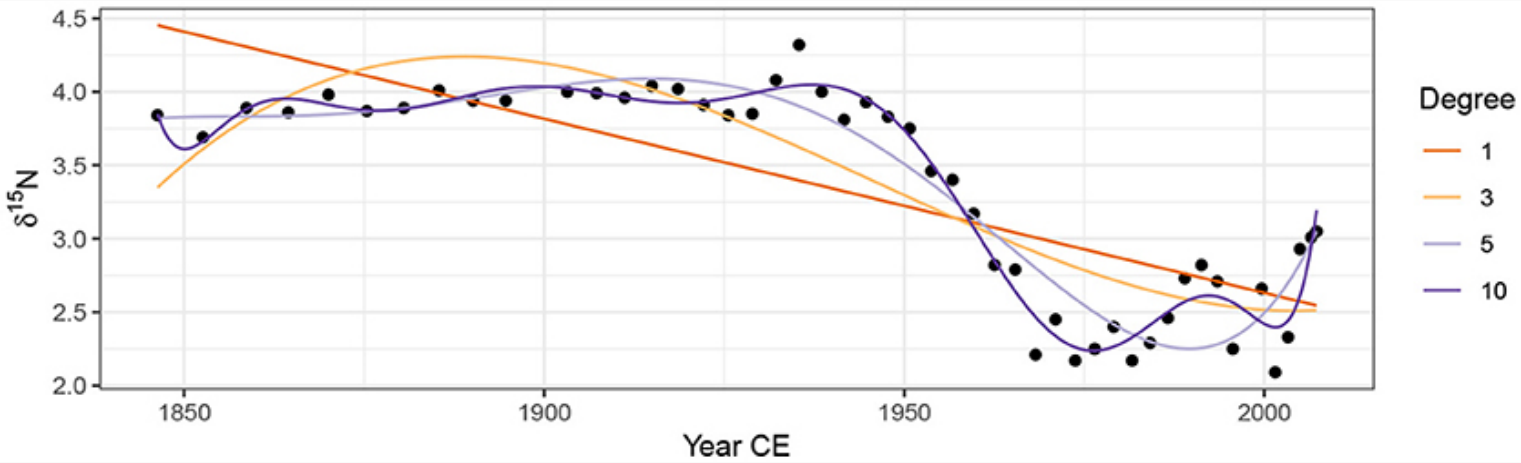


Simpson 2018

GAMs allow us to model non-linear relationships using smooths

Generalised Linear Model (GLM):

$$y = a + bx$$

Generalised Additive Model (GAM):

$$y = a + s(x)$$

```
isotopes <- readRDS('data/isotope.rds')
```

```
  Depth   d13C  TotalC d15N TotalN DryWeight     Year
1   0.2 -27.57  806.49 3.05  64.21        8.2 2007.254
2   0.4 -27.67  949.33 3.01  73.26        7.6 2006.510
3   0.8 -27.63 1305.52 2.93  93.25       11.6 2004.941
4   1.2 -27.62 1136.04 2.33  86.09        9.6 2003.269
5   1.6 -27.48 1028.27 2.09  93.80       10.9 2001.496
6   2.0 -27.39  809.91 2.66  79.98        9.9 1999.626
```

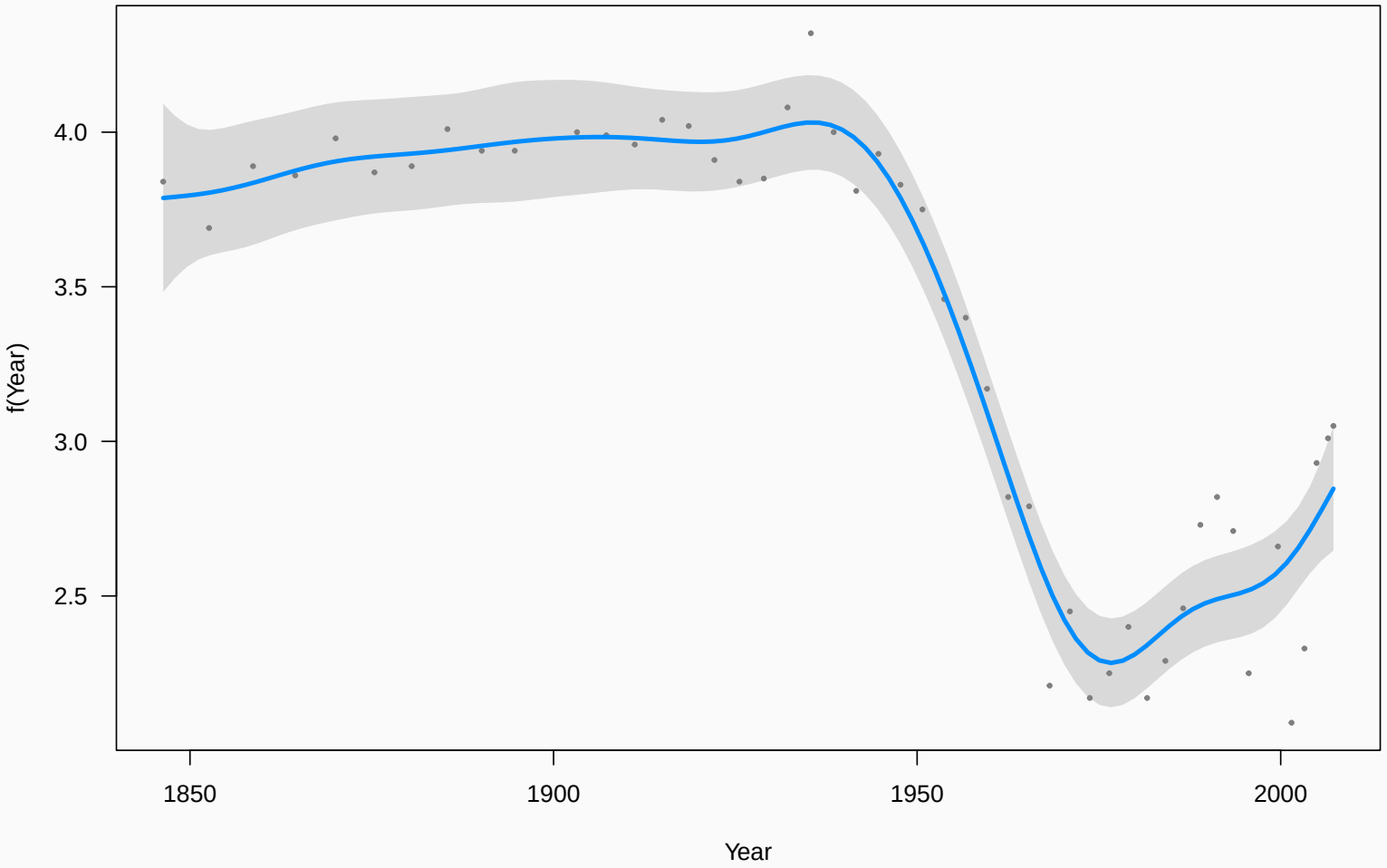
Modelling non-linear time series with GAM

```r
library('mgcv')
m <- gam(d15N ~ s(Year, k = 15), data = isotopes, method = 'REML')
```

```
Family: gaussian
Link function: identity

Formula:
d15N ~ s(Year, k = 15)

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.30958    0.02622   126.2   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
          edf Ref.df     F p-value
s(Year) 9.282  11.07 61.33  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.935   Deviance explained = 94.8%
-REML = 3.9734  Scale est. = 0.03299   n = 48
```

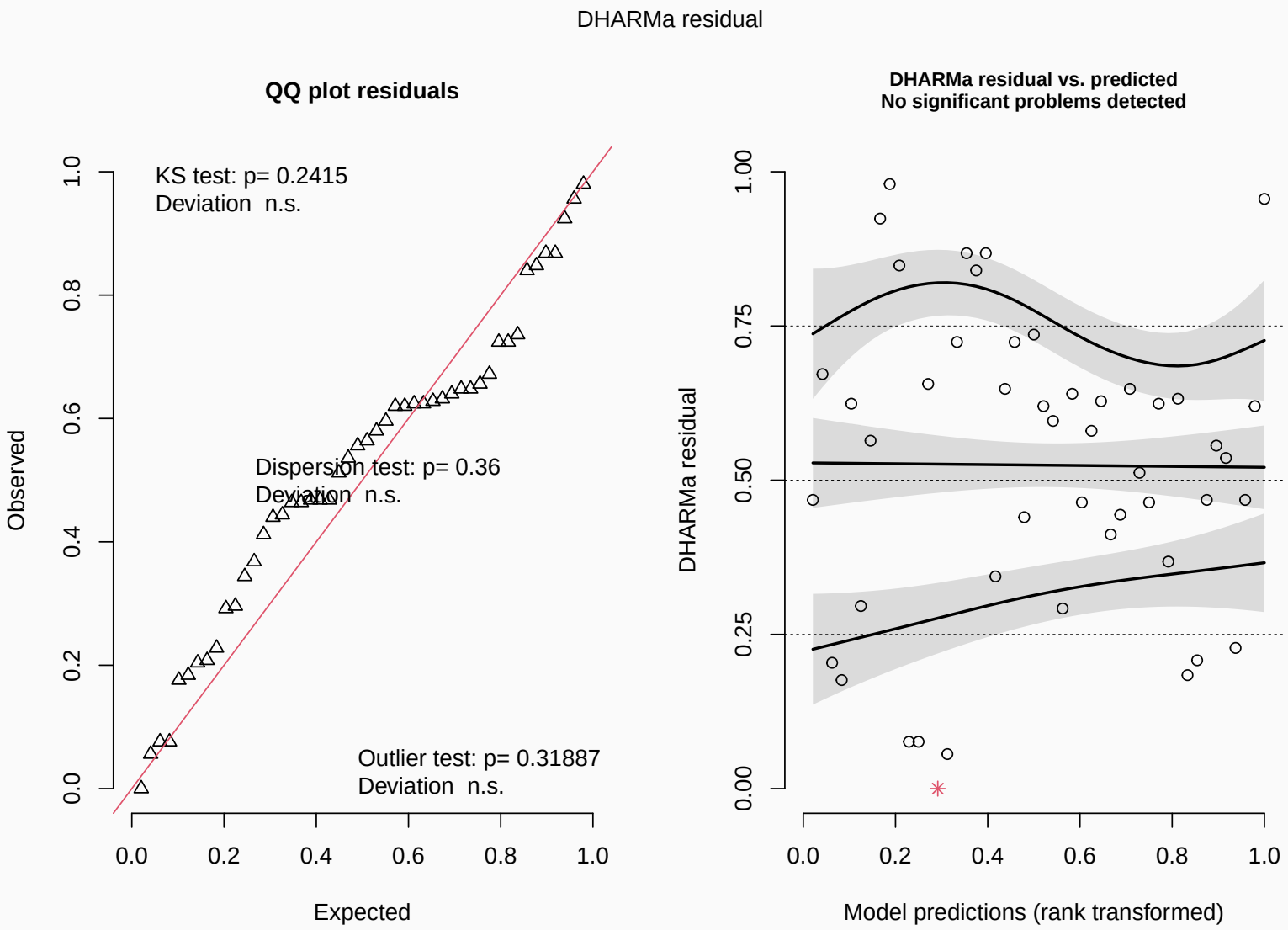
Visualising fitted GAM

```
visreg(m)
```



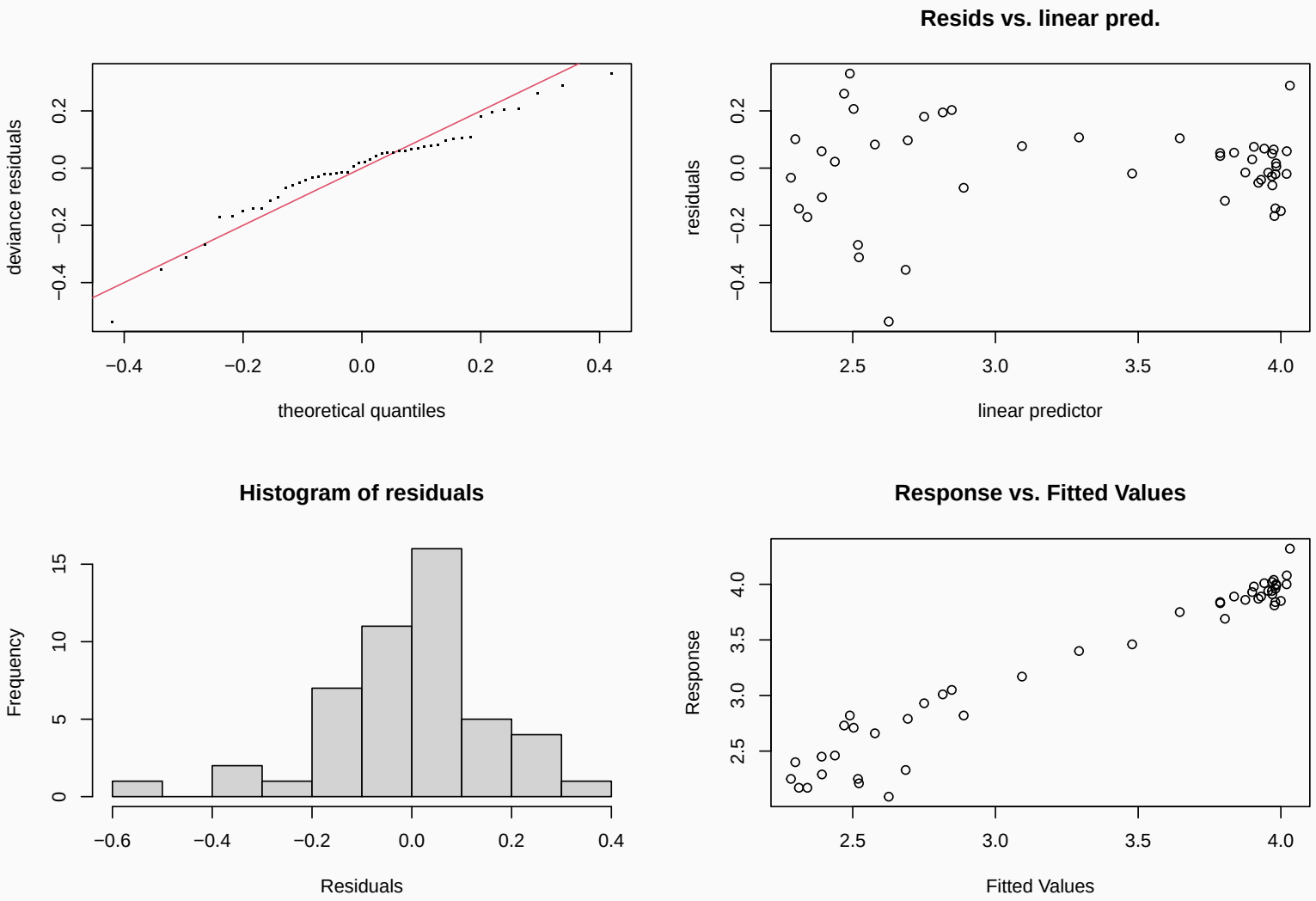
Checking fitted GAM

```
library('DHARMa')
simulateResiduals(m, plot = TRUE)
```



Checking fitted GAM

```
gam.check(m)
```



Including temporal autocorrelation

```
mod <- gamm(d15N ~ s(Year, k = 15), data = isotopes,
            correlation = corCAR1(form = ~ Year), method = 'REML')
```

```
Family: gaussian
Link function: identity

Formula:
d15N ~ s(Year, k = 15)

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.30909    0.03489   94.84   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
          edf Ref.df     F p-value
s(Year) 7.954  7.954 47.44  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Modelling infant mortality

Modelling infant mortality

```
mort <- read.csv('data/UN_GDP_infantmortality.csv')
```

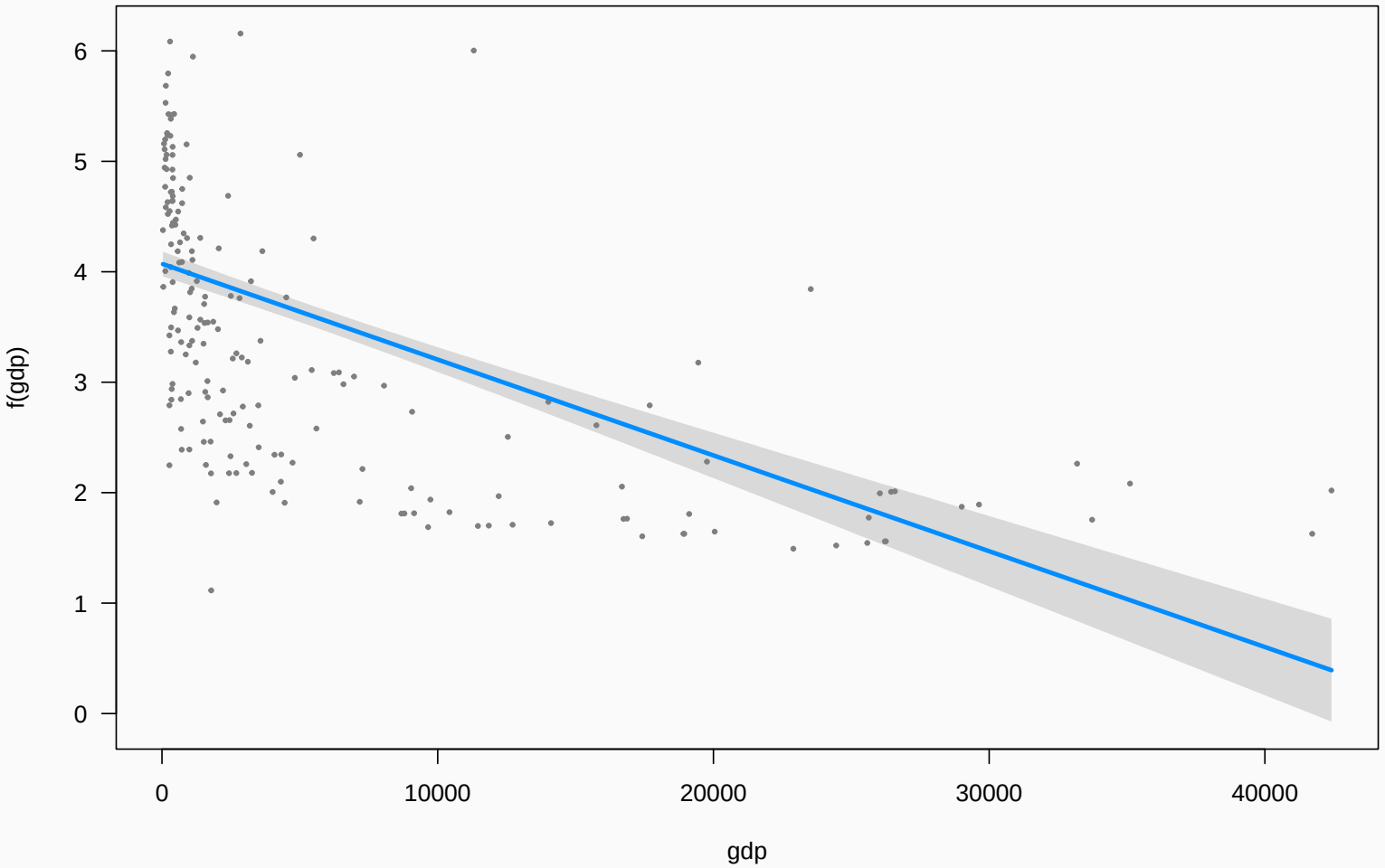
```
          country infant.mortality  gdp
1     Afghanistan               154 2848
2         Albania                32  863
3         Algeria                44 1531
4 American.Samoa                11   NA
5         Andorra                NA   NA
6          Angola               124  355
```

Modelling infant mortality with a GLM

```r
library('MASS')
mort.glm <- glm.nb(infant.mortality ~ gdp, data = mort)
```

```
Call:
glm.nb(formula = infant.mortality ~ gdp, data = mort, init.theta = 2.460991808,
    link = log)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.072e+00  5.727e-02   71.11   <2e-16 ***
gdp         -8.675e-05  6.221e-06  -13.95   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(2.461) family taken to be 1)

    Null deviance: 385.83  on 192  degrees of freedom
Residual deviance: 202.51  on 191  degrees of freedom
  (14 observations deleted due to missingness)
AIC: 1715
```

Modelling infant mortality with a GLM

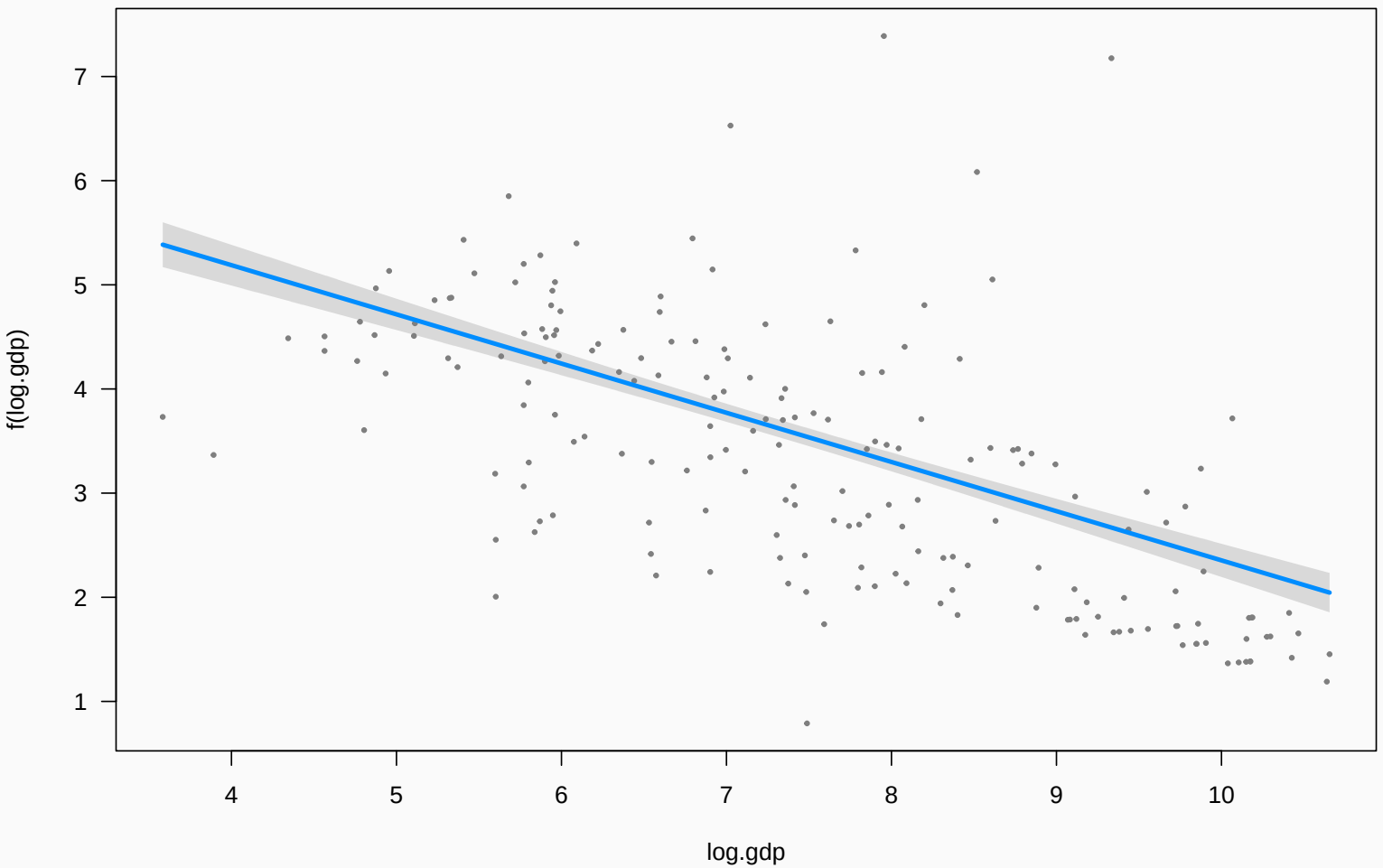


Modelling infant mortality with a GLM (log.gdp)

```r
mort$log.gdp <- log(mort$gdp)
mort.glm.log <- glm.nb(infant.mortality ~ log.gdp, data = mort)
```

```
Call:
glm.nb(formula = infant.mortality ~ log.gdp, data = mort, init.theta = 3.119314453,
    link = log)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  7.07818    0.20045   35.31   <2e-16 ***
log.gdp     -0.47238    0.02647  -17.85   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(3.1193) family taken to be 1)

    Null deviance: 478.54  on 192  degrees of freedom
Residual deviance: 198.03  on 191  degrees of freedom
  (14 observations deleted due to missingness)
AIC: 1667.7
```

Modelling infant mortality with a GLM (log.gdp)

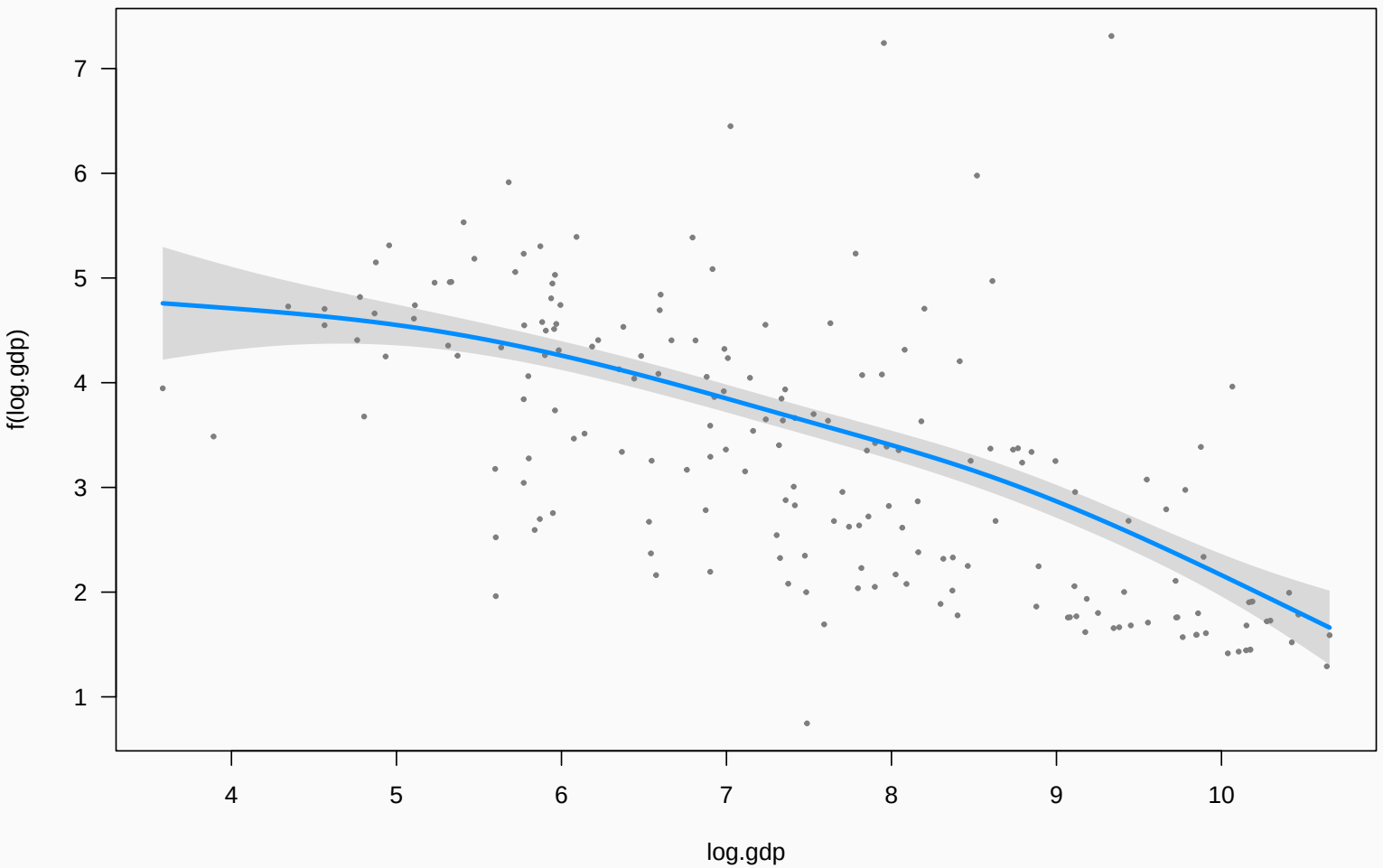


Modelling infant mortality with a GAM

```r
library('mgcv')
mort.gam <- gam(infant.mortality ~ s(log.gdp), family = nb, data = mort)
```

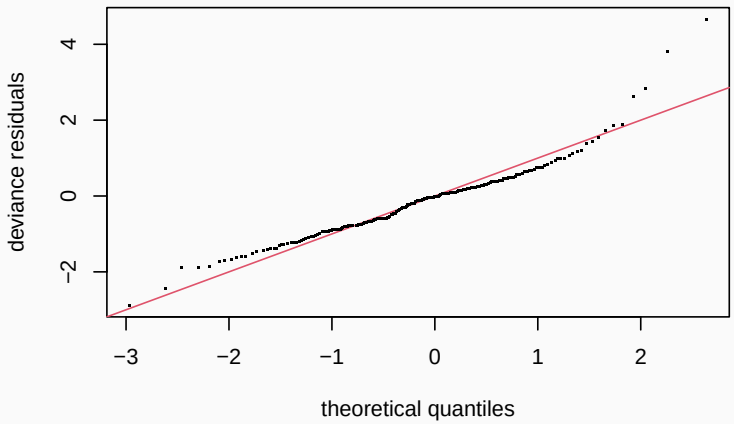
```
Family: Negative Binomial(3.251)
Link function: log

Formula:
infant.mortality ~ s(log.gdp)

Parametric coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.51137    0.04257   82.49   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
             edf Ref.df Chi.sq p-value
s(log.gdp) 3.134  3.937  329.9  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

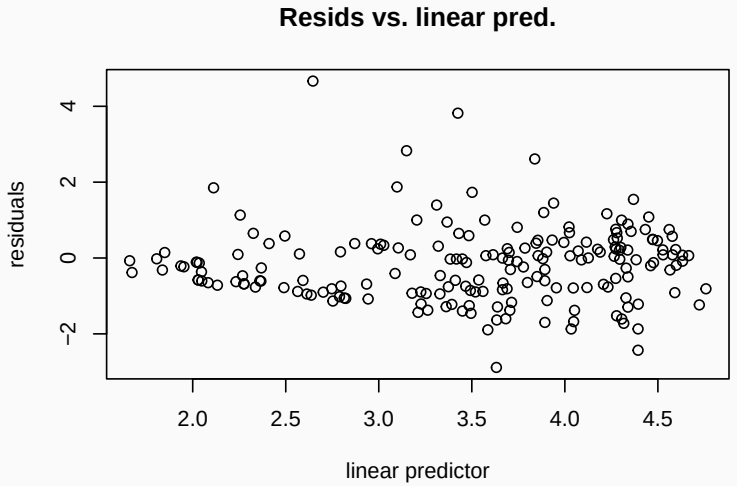
Modelling infant mortality with a GAM

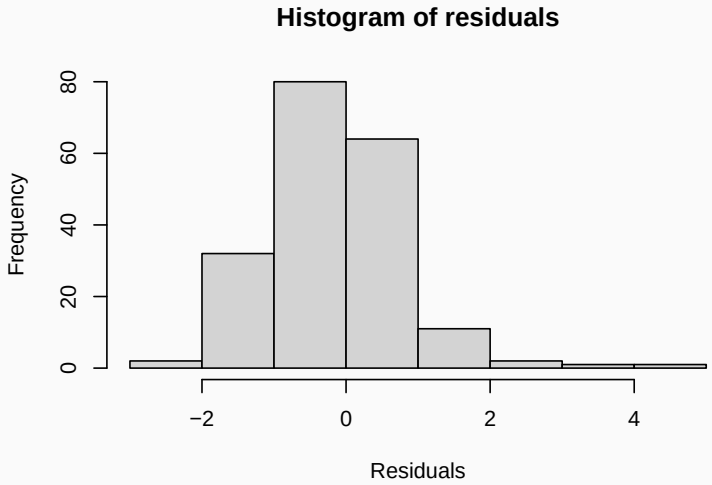


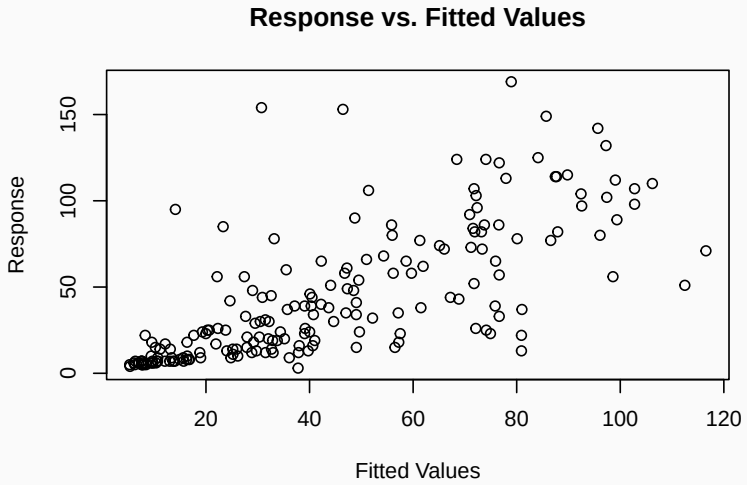
Checking GAM

```
gam.check(mort.gam)
```









Comparing models

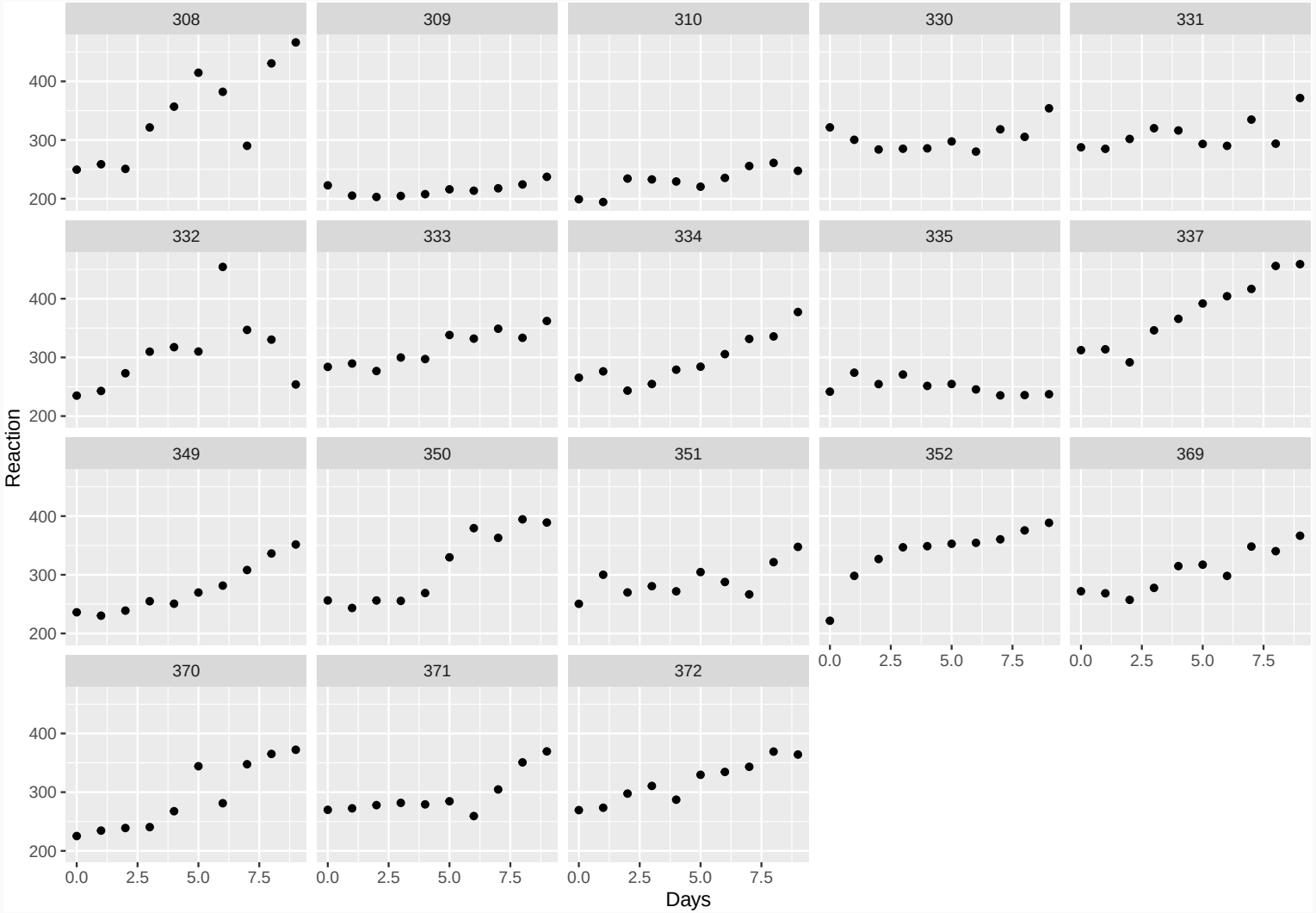
```r
library('easystats')
compare_performance(mort.glm, mort.glm.log, mort.gam)
```

```
# Comparison of Model Performance Indices

Name         |  Model |  AIC (weights) | AICc (weights) |  BIC (weights)
-------------------------------------------------------------------------
mort.glm     | negbin | 1715.0 (<.001) | 1715.1 (<.001) | 1724.7 (<.001)
mort.glm.log | negbin | 1667.7 (0.035) | 1667.9 (0.041) | 1677.5 (0.816)
mort.gam     |    gam | 1661.1 (0.965) | 1661.6 (0.959) | 1680.5 (0.184)

Name         |   RMSE | Sigma | Score_log | Score_spherical | Nagelkerke's R2 |    R2
-------------------------------------------------------------------------------------
mort.glm     | 31.089 | 1.000 |    -4.437 |           0.048 |           0.709 |
mort.glm.log | 30.034 | 1.000 |    -4.356 |           0.053 |           0.836 |
mort.gam     | 26.249 | 1.000 |    -4.296 |           0.049 |                 | 0.526
```

Generalised Additive Mixed Models (GAMM)

Reaction time with sleep deprivation

```
library('lme4')
data('sleepstudy')
```



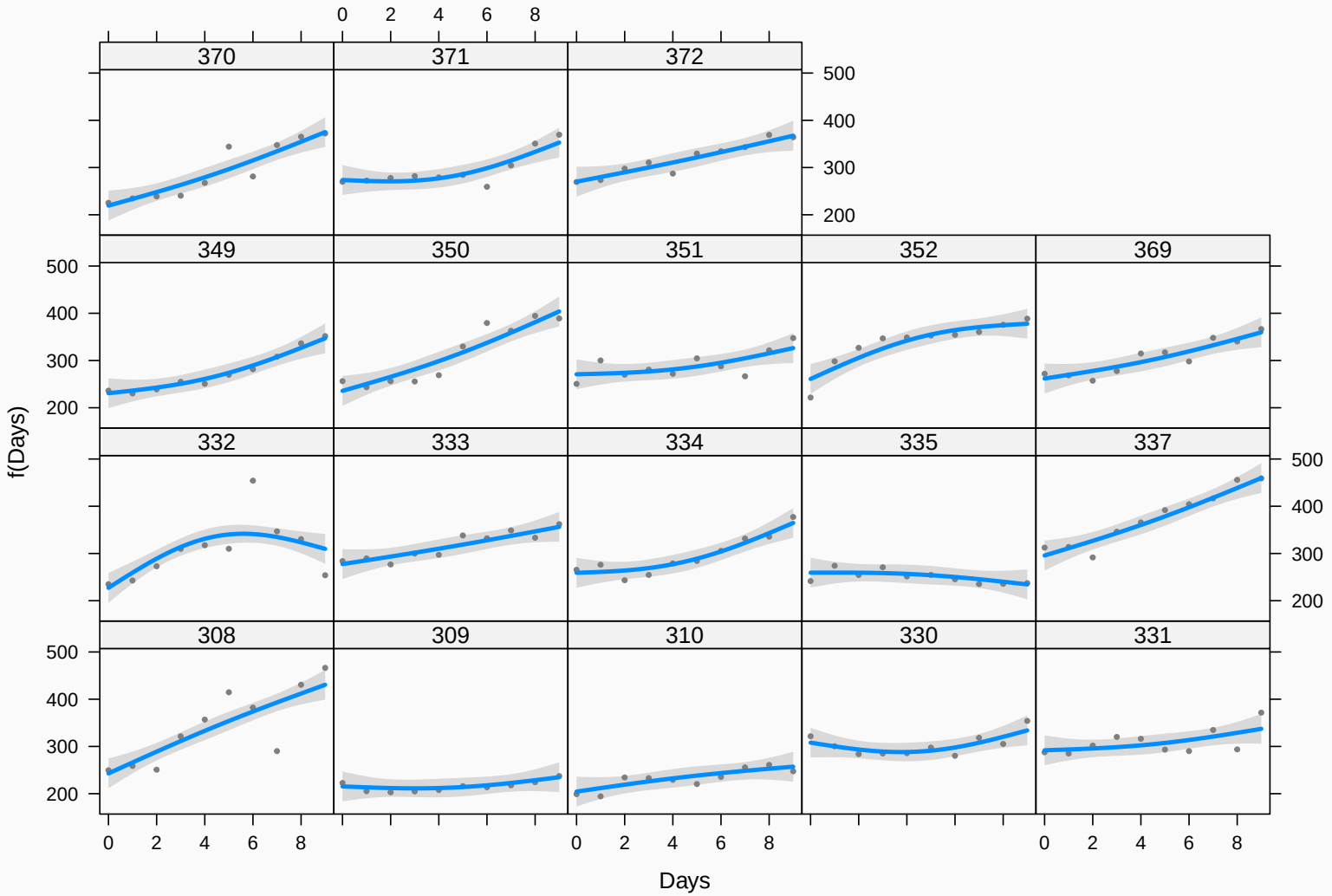
Modelling reaction time with sleep deprivation (GAMM)

```
sgamm <- gam(Reaction ~ s(Days, Subject, k = 3, bs = 'fs'),
                  data = sleepstudy, method = 'REML')
```

```
Family: gaussian
Link function: identity

Formula:
Reaction ~ s(Days, Subject, k = 3, bs = "fs")

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   298.51       9.05   32.98   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
                  edf Ref.df     F p-value
s(Days,Subject) 45.67     53 17.11  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.835   Deviance explained = 87.7%
-REML = 883.64  Scale est. = 523.2     n = 180
```

Modelling reaction time with sleep deprivation (GAMM)

```
visreg(sgamm, xvar = 'Days', by = 'Subject')
```



An introduction to Bayesian modelling with brms and Stan

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

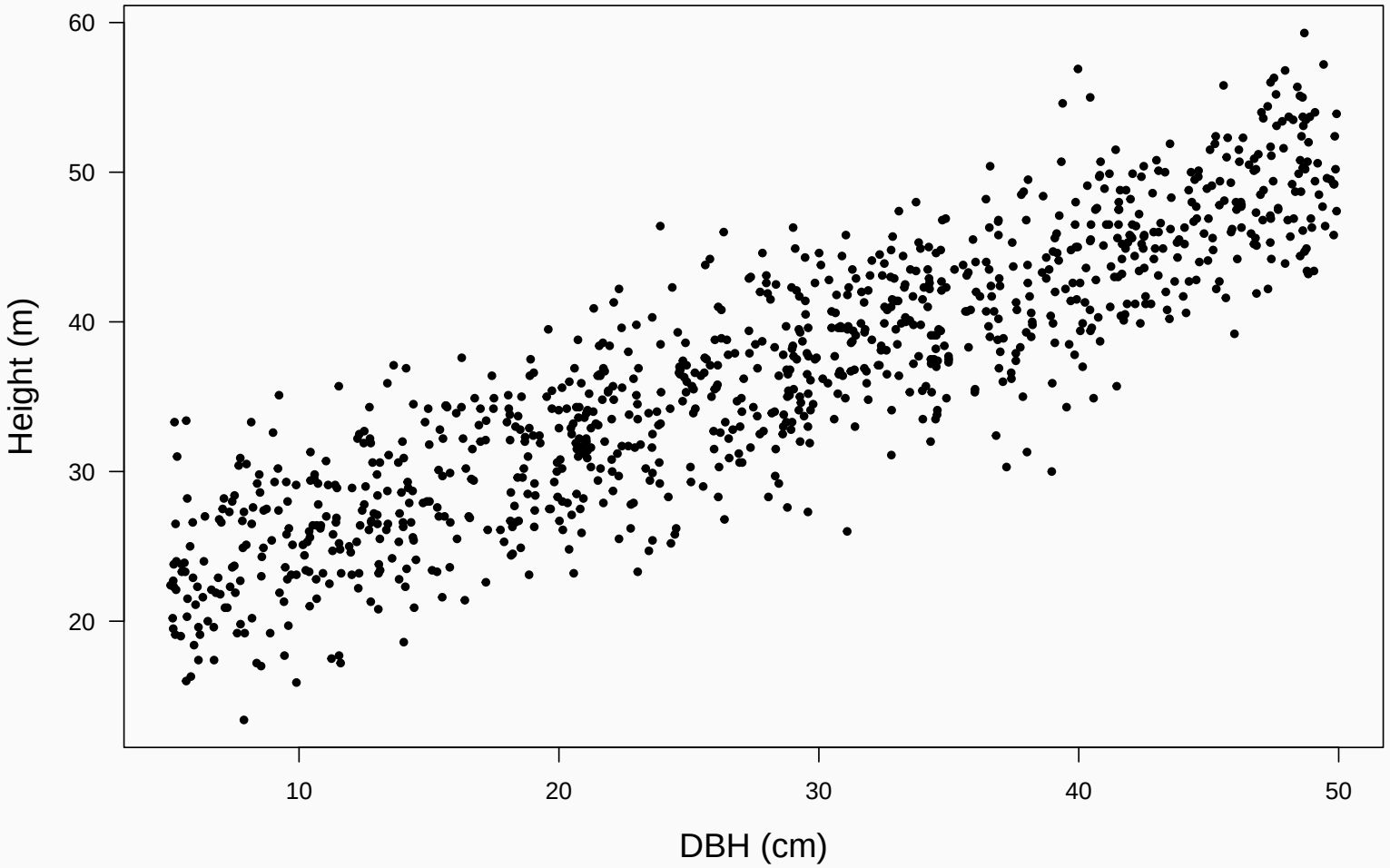
Our dataset: tree heights and DBH

- One species
- 10 plots
- 1000 trees
- Number of trees per plot ranging from 4 to 392

```
trees <- read.csv('data/trees.csv')
```

```
      site           dbh              height     
 Min.   : 1.0   Min.   : 5.06   Min.   :13.40  
 1st Qu.: 1.0   1st Qu.:17.69   1st Qu.:29.68  
 Median : 2.0   Median :28.62   Median :36.55  
 Mean   : 2.7   Mean   :27.88   Mean   :36.51  
 3rd Qu.: 4.0   3rd Qu.:38.97   3rd Qu.:43.33  
 Max.   :10.0   Max.   :49.92   Max.   :59.30  
```

What's the relationship between DBH and height?



First step: linear regression (lm)

```r
simple.lm <- lm(height ~ dbh, data = trees)
```

```
Call:
lm(formula = height ~ dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max
-13.3270  -2.8978   0.1057   2.7924  12.9511

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 19.33920    0.31064   62.26   <2e-16 ***
dbh          0.61570    0.01013   60.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.093 on 998 degrees of freedom
Multiple R-squared:  0.7874,    Adjusted R-squared:  0.7871
F-statistic:  3695 on 1 and 998 DF,  p-value: < 2.2e-16
```

Center continuous variables

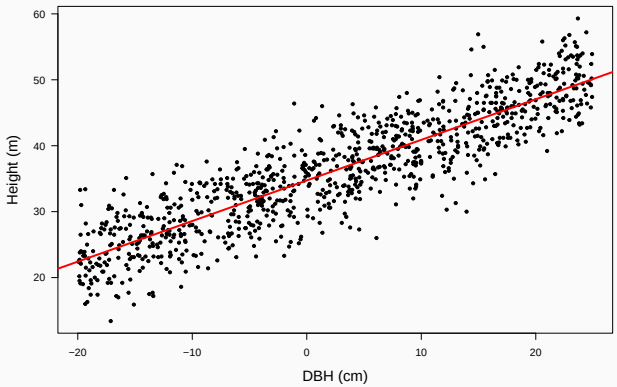
```
summary(trees$dbh)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   5.06   17.69   28.62   27.88   38.97   49.92
```

```
trees$dbh.c <- trees$dbh - 25
```

So, all parameters will be referred to a 25 cm DBH tree.

Linear regression with centred DBH



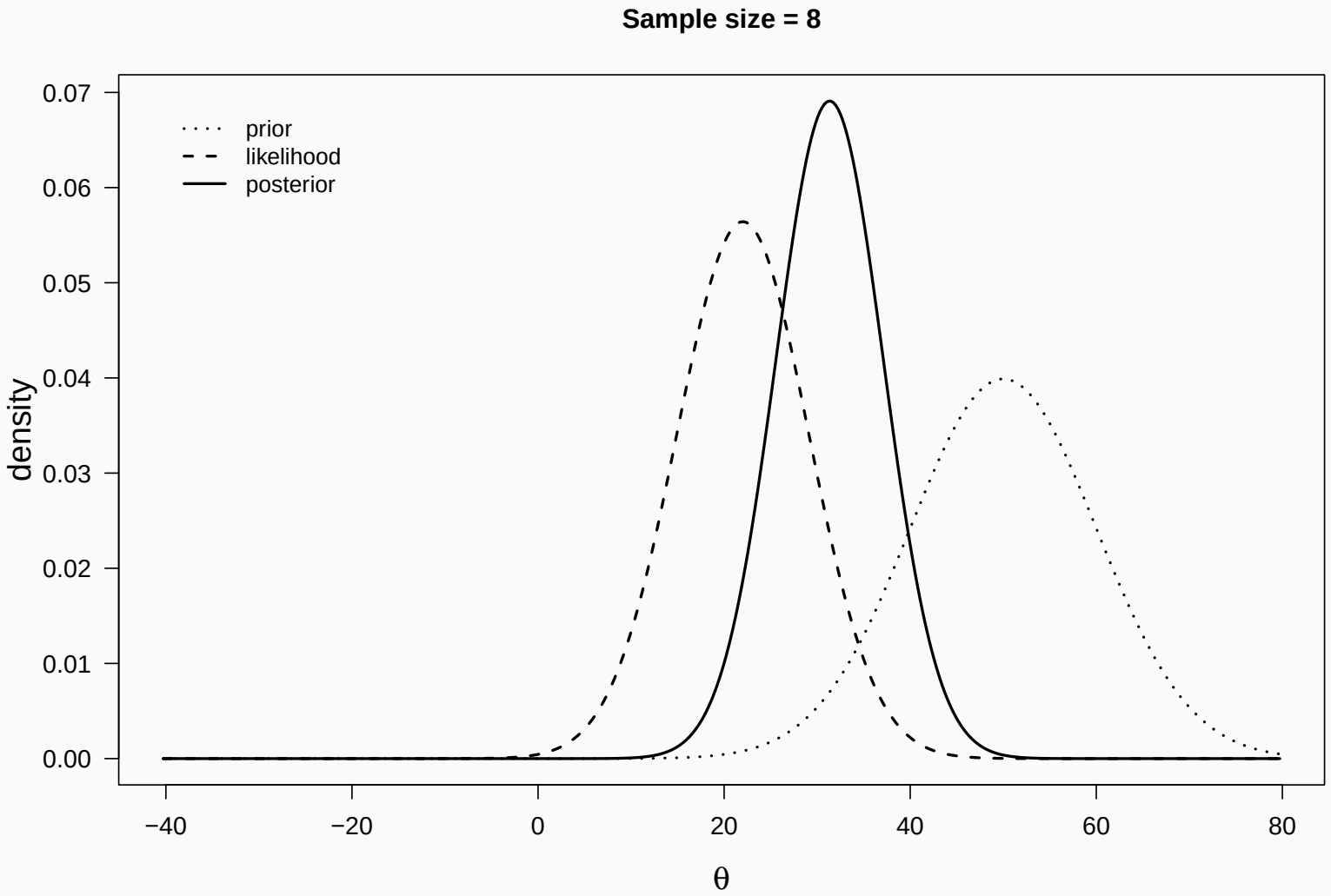

```
lm(formula = height ~ dbh.c, data = trees
            coef.est coef.se
(Intercept) 34.73     0.13
dbh.c        0.62     0.01
---
n = 1000, k = 2
residual sd = 4.09, R-Squared = 0.79
```

Let’s make it Bayesian

Bayesian inference: prior, posterior, and likelihood

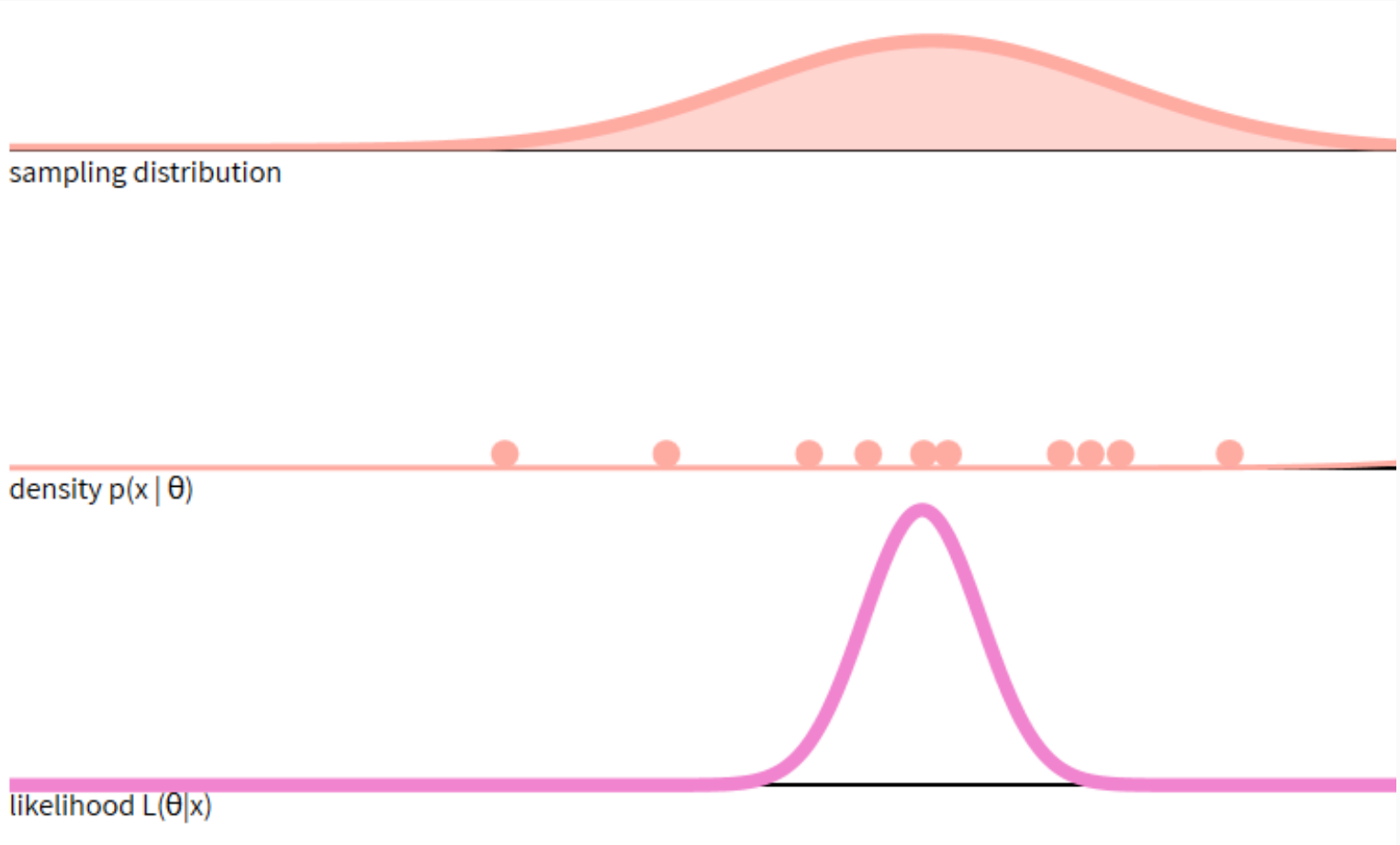
$$P(Unknown|Data) \propto P(Data|Unknown) \times P(Unknown)$$

$$Posterior \propto Likelihood \times Prior$$



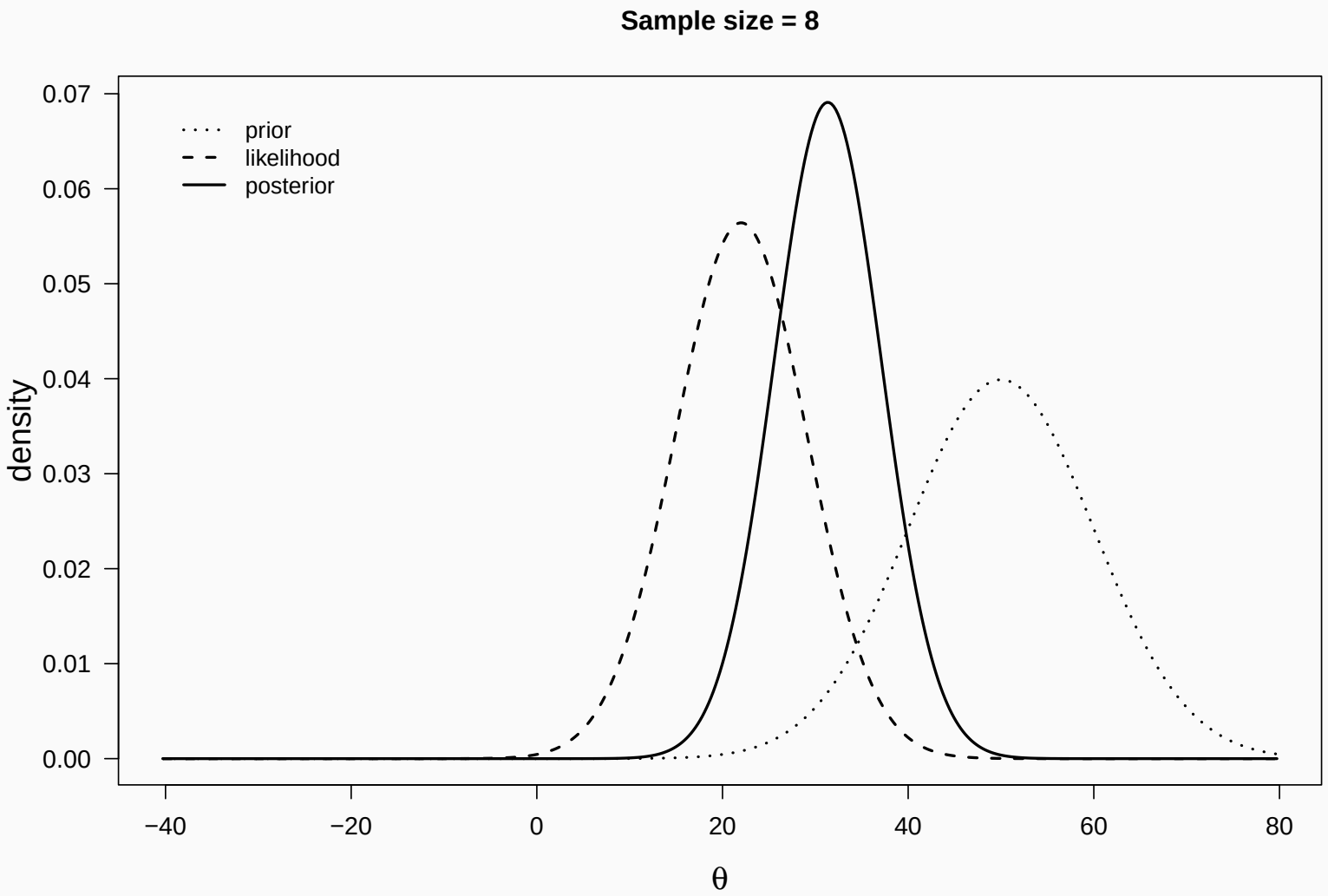
What is the likelihood?

$$L(\theta|x) = P(x|\theta)$$

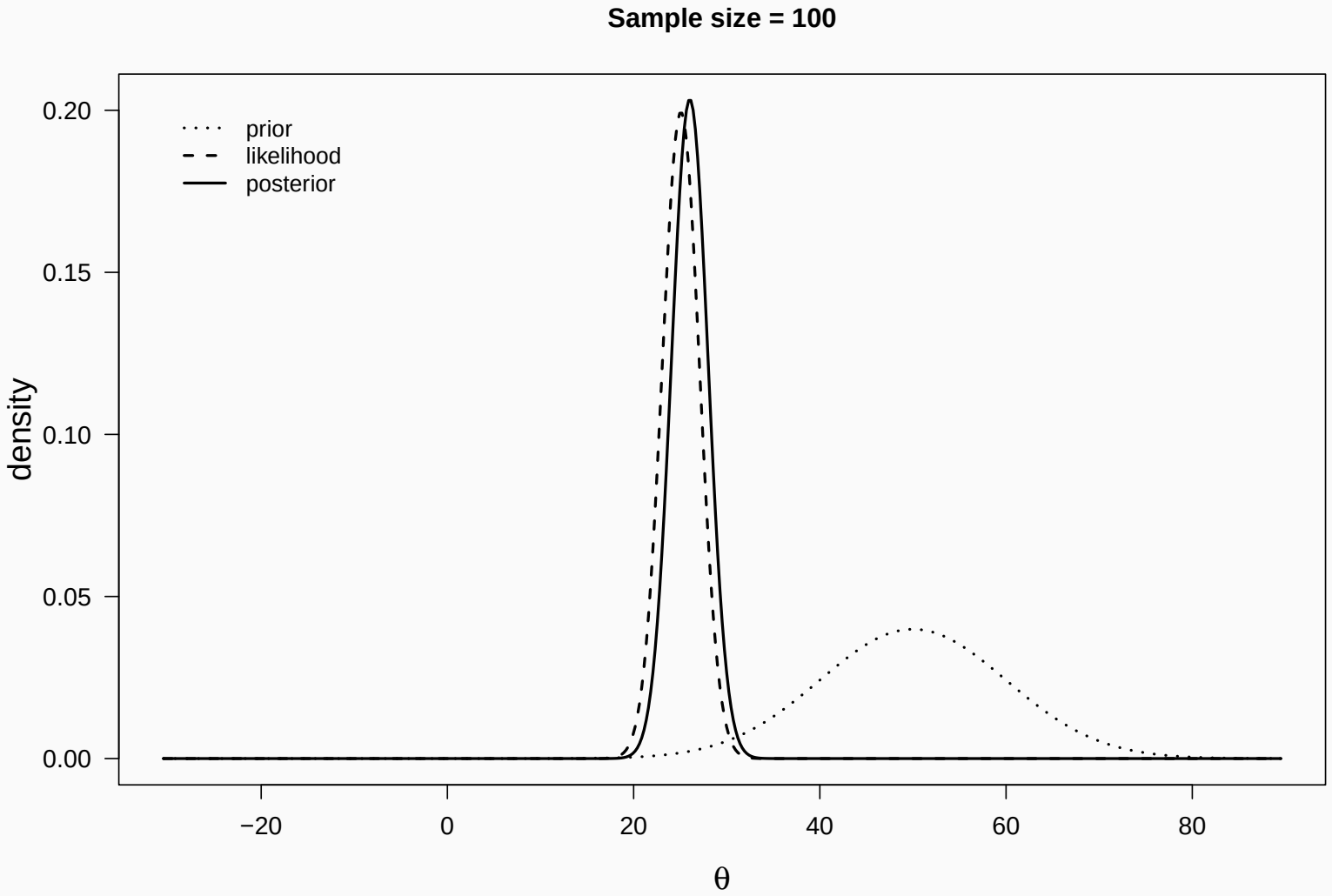


https://seeing-theory.brown.edu/bayesian-inference/index.html

Bayesian inference: prior and likelihood produce posterior



With increasing sample size, likelihood dominates prior



Bayesian statistics in practice

- Integrate information (prior)

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- Prior regularises unlikely estimates from data

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- Particularly important with limited sample sizes
- Large dataset -> prior effect diminishes
- Uncertainty / Propagate errors

Remember our model structure

$$y_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta x_i$$

In this case:

$$Height_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta DBH_i$$

α: expected height when DBH = 25 cm

β: how much height increases with every unit increase of DBH

Defining model formula

```
library('brms')

height.formu <- brmsformula(height ~ dbh.c)
```

We must define **prior distributions** for every parameter

brms default priors

```
get_prior(height.formu, data = trees)
```

```
                  prior     class  coef group resp dpar nlpar lb ub
                 (flat)         b                                  
                 (flat)         b dbh.c                            
 student_t(3, 36.5, 10.2) Intercept                                
    student_t(3, 0, 10.2)     sigma                             0  
       source
      default
 (vectorized)
      default
      default
```

Choosing priors

Avoid 'non-informative' priors

Use *weakly informative* (e.g. relatively wide Normal or t-student distributions)

or *strongly informative* priors based on previous knowledge and common sense.

Some tips for setting priors:

- https://github.com/stan-dev/stan/wiki/Prior-Choice-Recommendations

Run **prior predictive checks** (just priors, no data)

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- Priors chapter in The BUGS book
- https://doi.org/10.1111/oik.05985

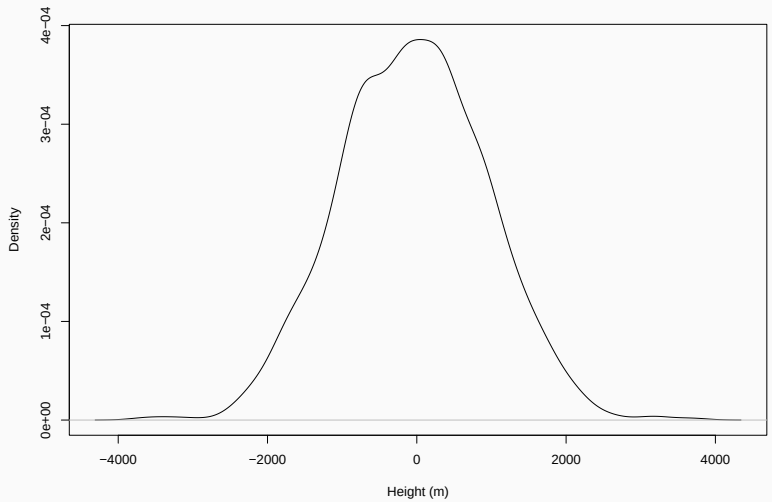
Run **prior predictive checks** (just priors, no data)

Probability distribution explorer

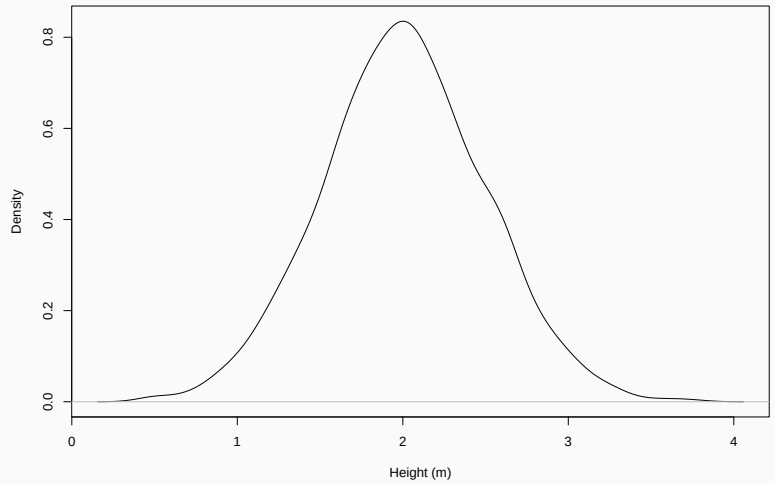
https://distribution-explorer.github.io/

Example: estimating people height across countries

Unreasonable prior



Reasonable prior

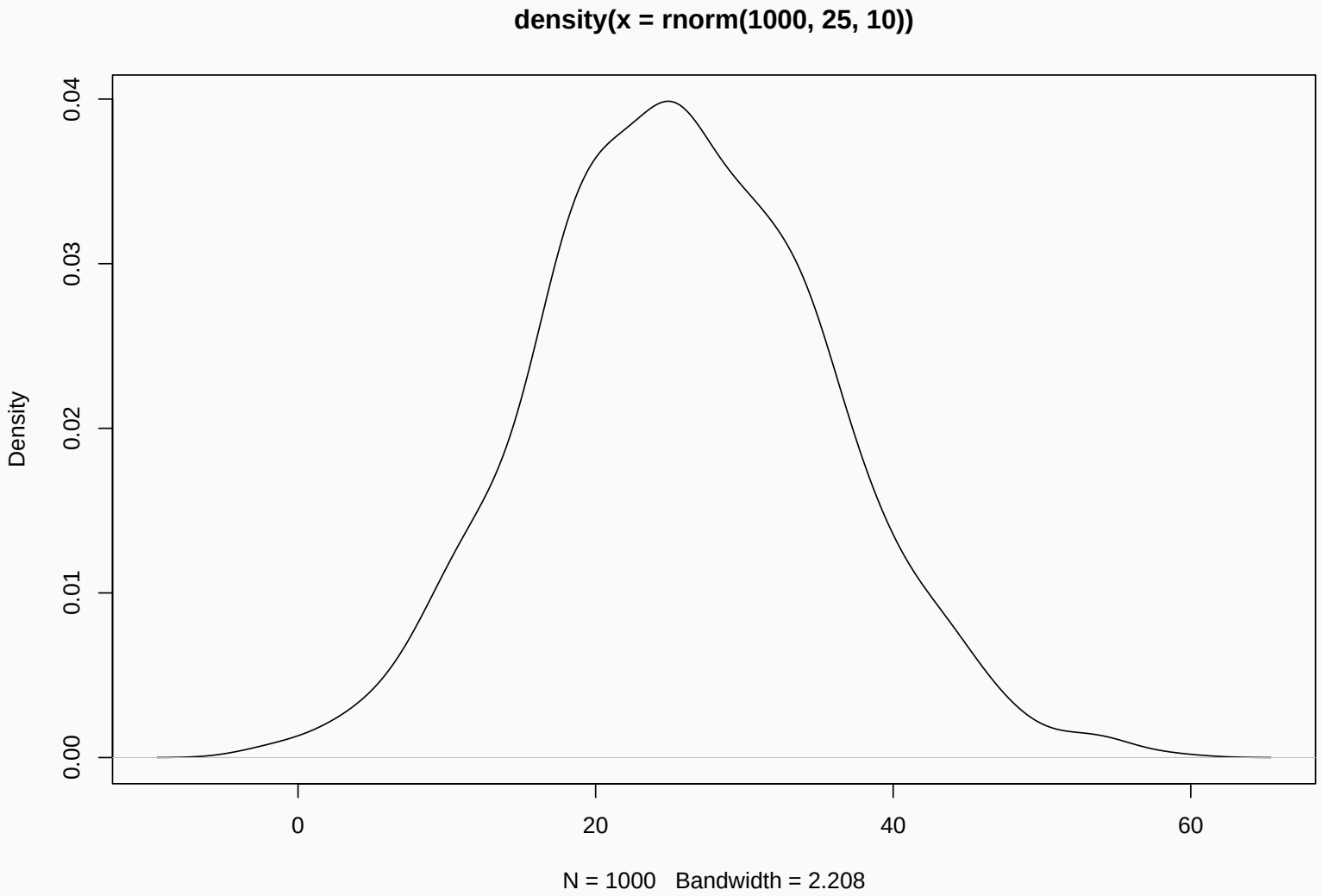


Defining priors for our trees example

```
priors <- c(
  set_prior('normal(30, 10)', class = 'Intercept'),
  set_prior('normal(0.5, 0.4)', class = 'b'),
  set_prior('normal(0, 5)', class = 'sigma')
)
```

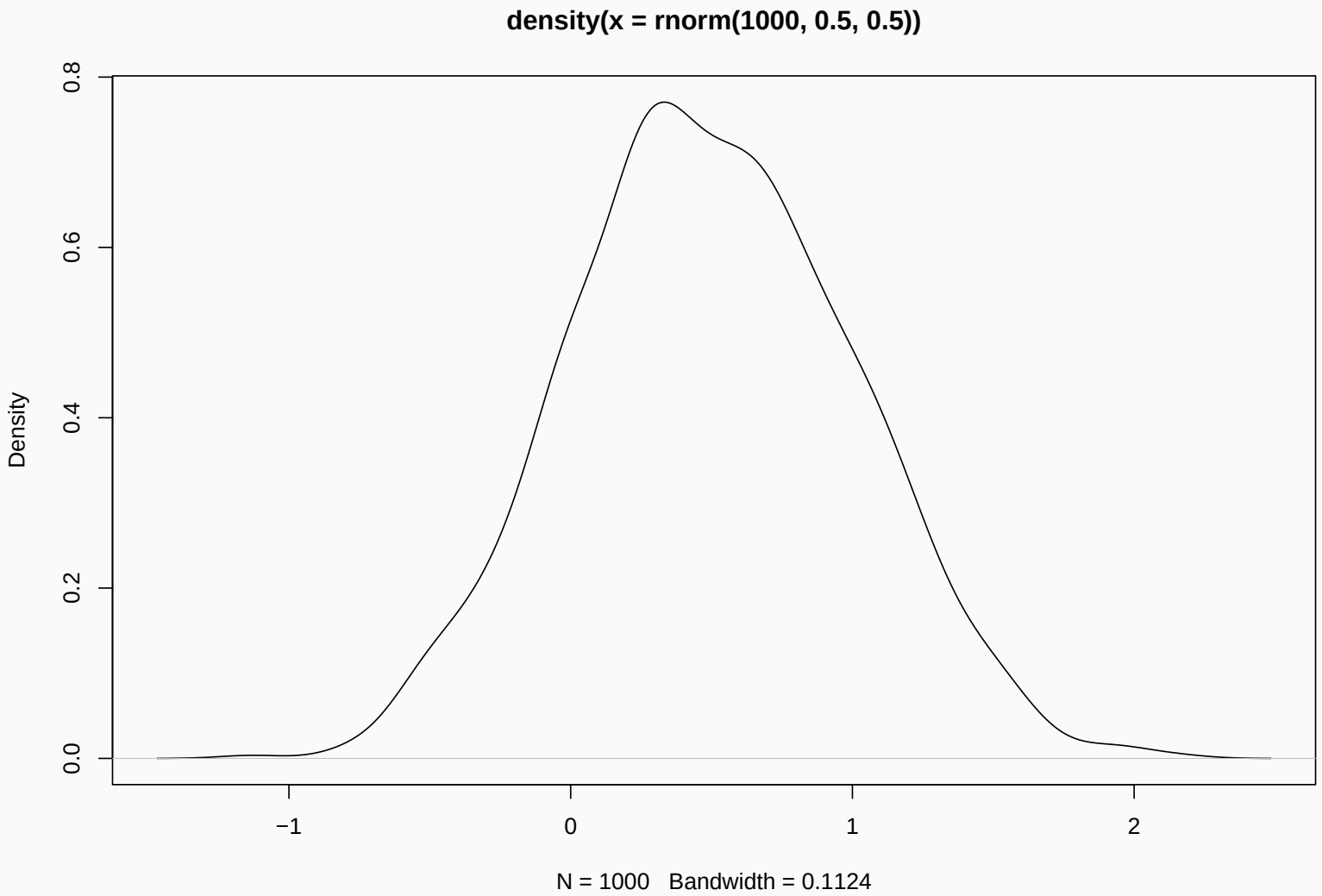
Prior for intercept (average height of 25-cm diameter tree)

```
plot(density(rnorm(1000, 25, 10)))
```

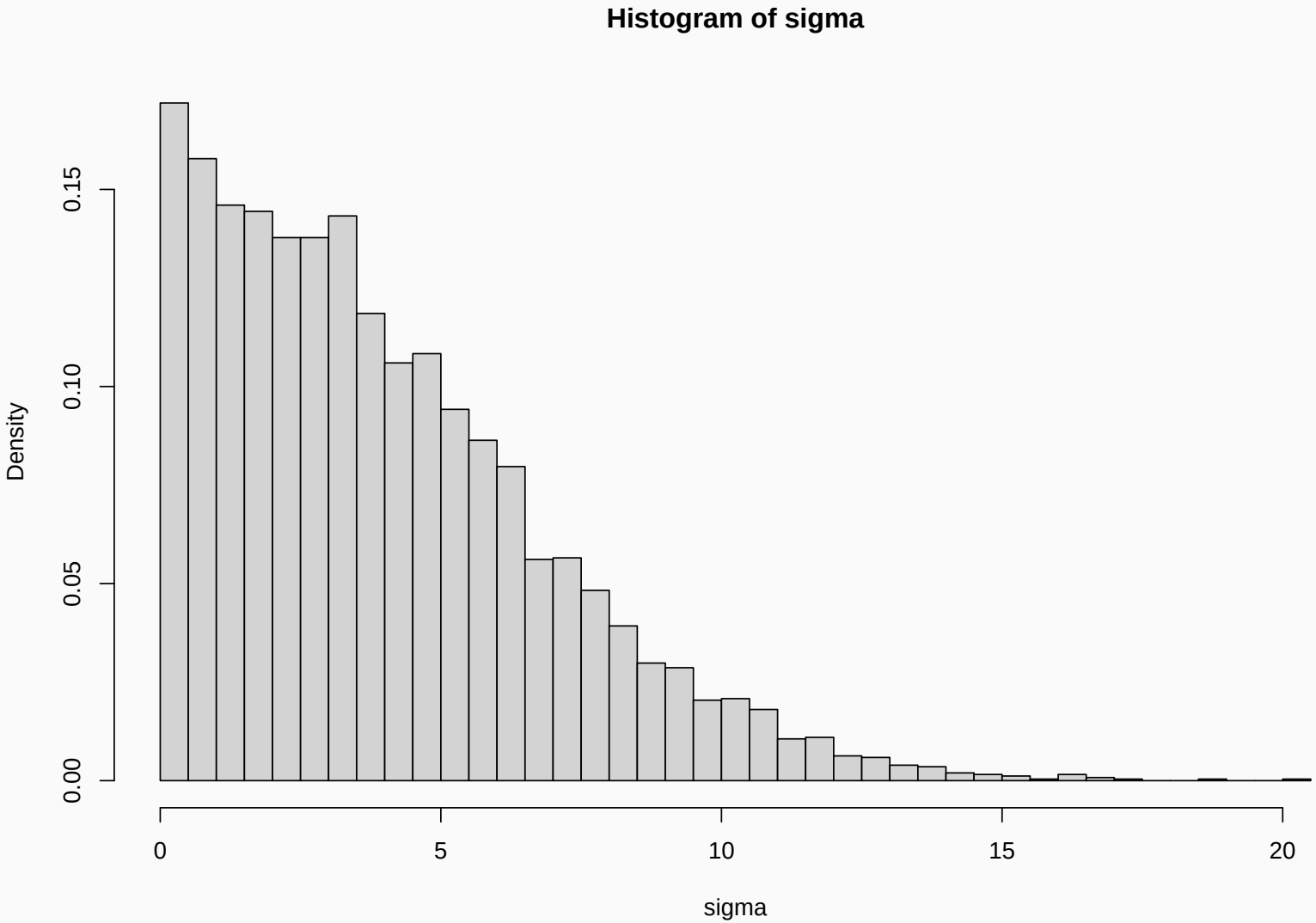


Prior for slope

```
plot(density(rnorm(1000, 0.5, 0.5)))
```



Prior for sigma (residual sd)

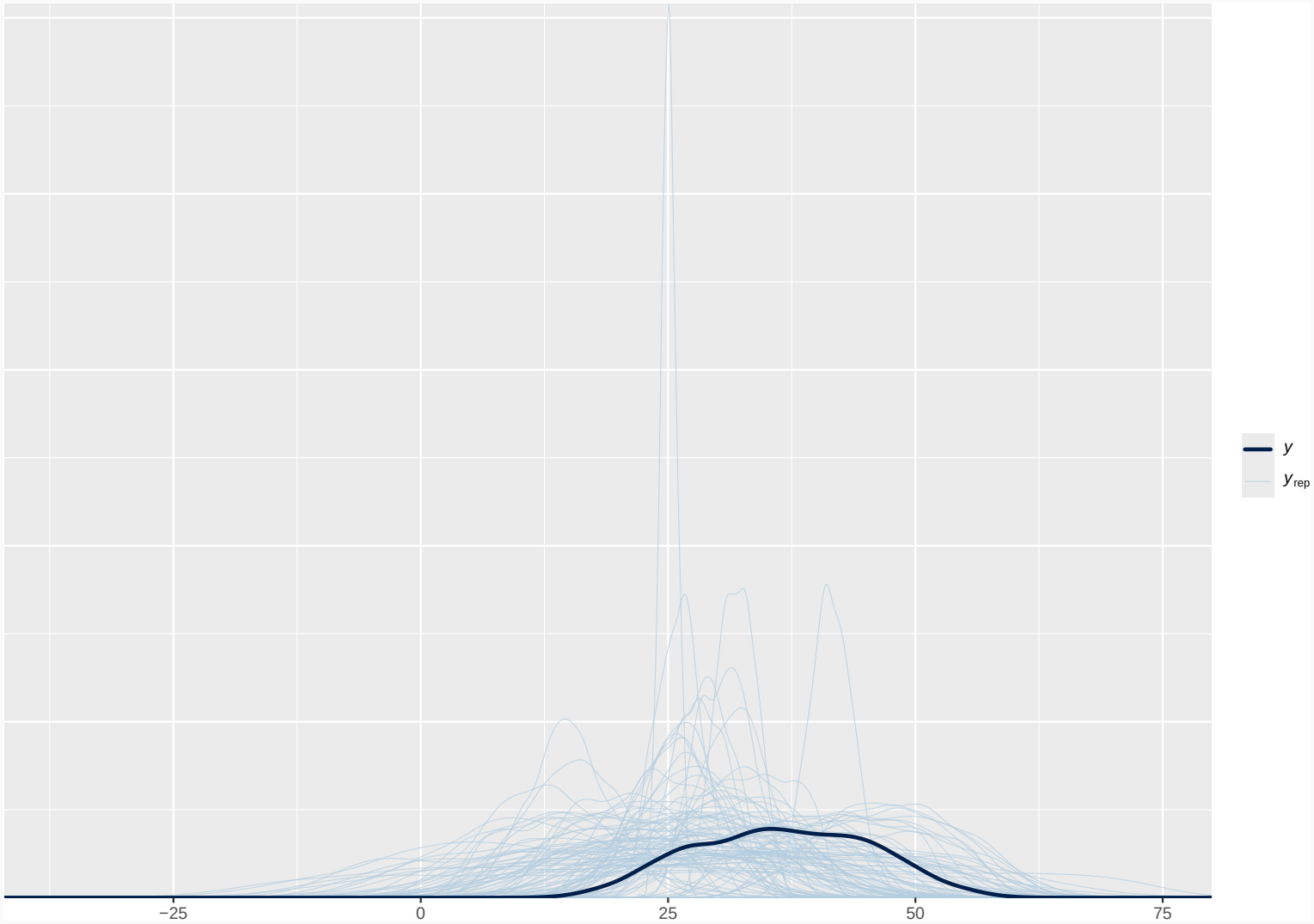


Prior predictive check

```
height.mod <- brm(height.formu,
          data = trees,
          prior = priors,
          sample_prior = 'only')
```

Prior predictive check

```
pp_check(height.mod, ndraws = 100)
```



Fit model (now with data)

```
height.mod <- brm(height.formu,
          data = trees,
          prior = priors)
```

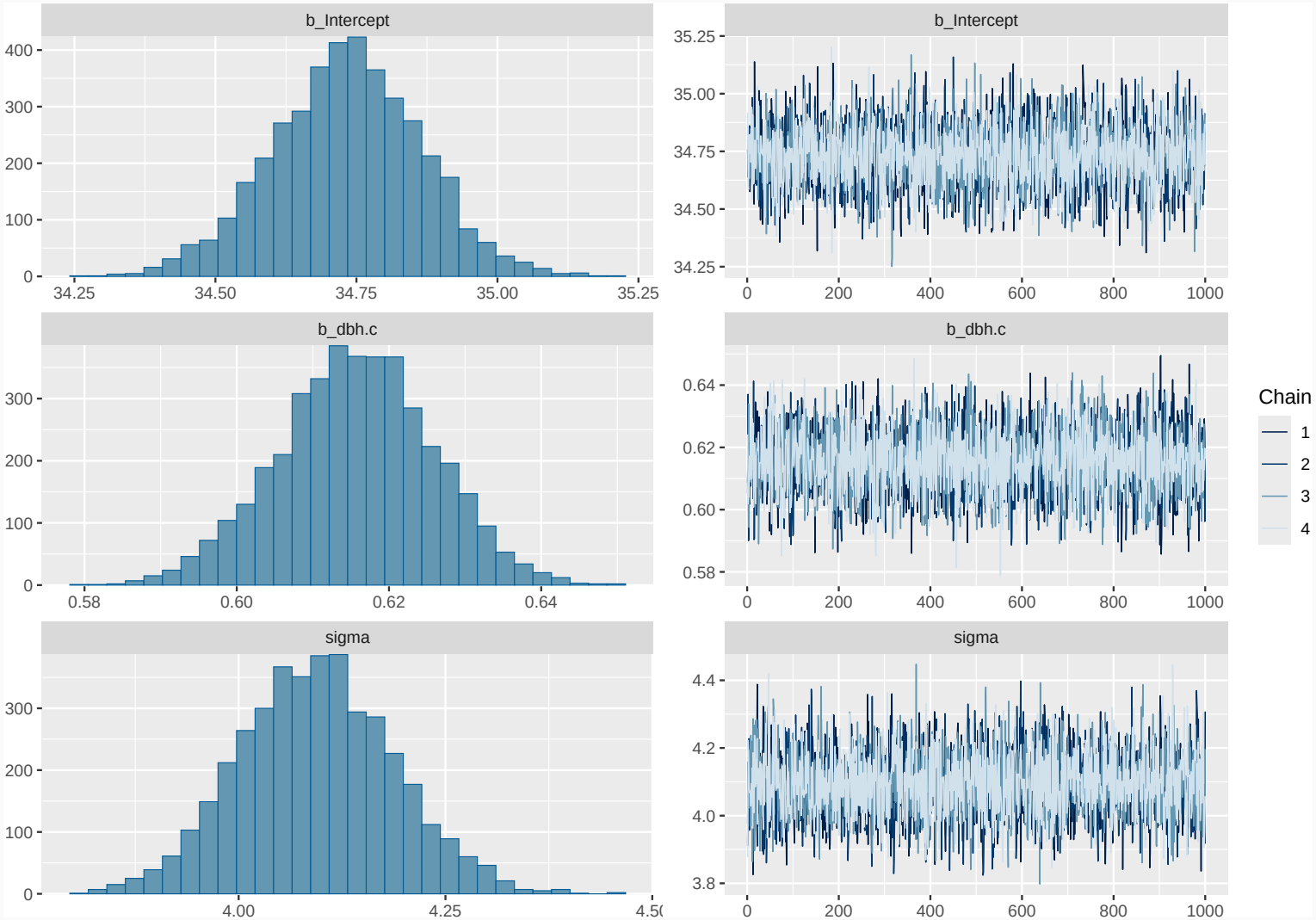
Model summary

```
summary(height.mod)
```

```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: height ~ dbh.c
   Data: trees (Number of observations: 1000)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Regression Coefficients:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept    34.73      0.13    34.47    34.99 1.00     4222     3247
dbh.c         0.62      0.01     0.60     0.64 1.00     4499     2673

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     4.09      0.09     3.92     4.28 1.00     4430     3153

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

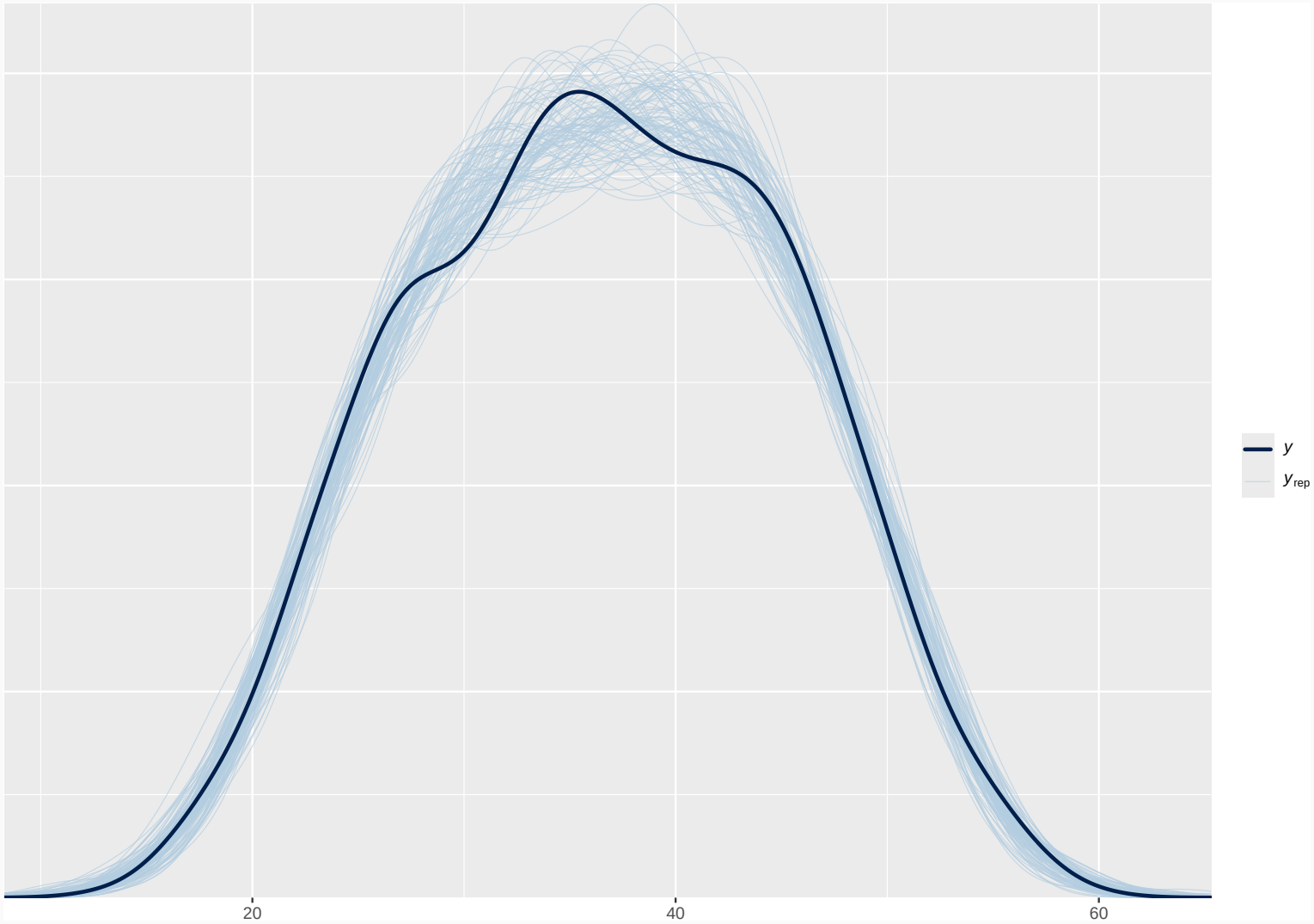
Model visualisation

```
plot(height.mod)
```



Posterior predictive checking

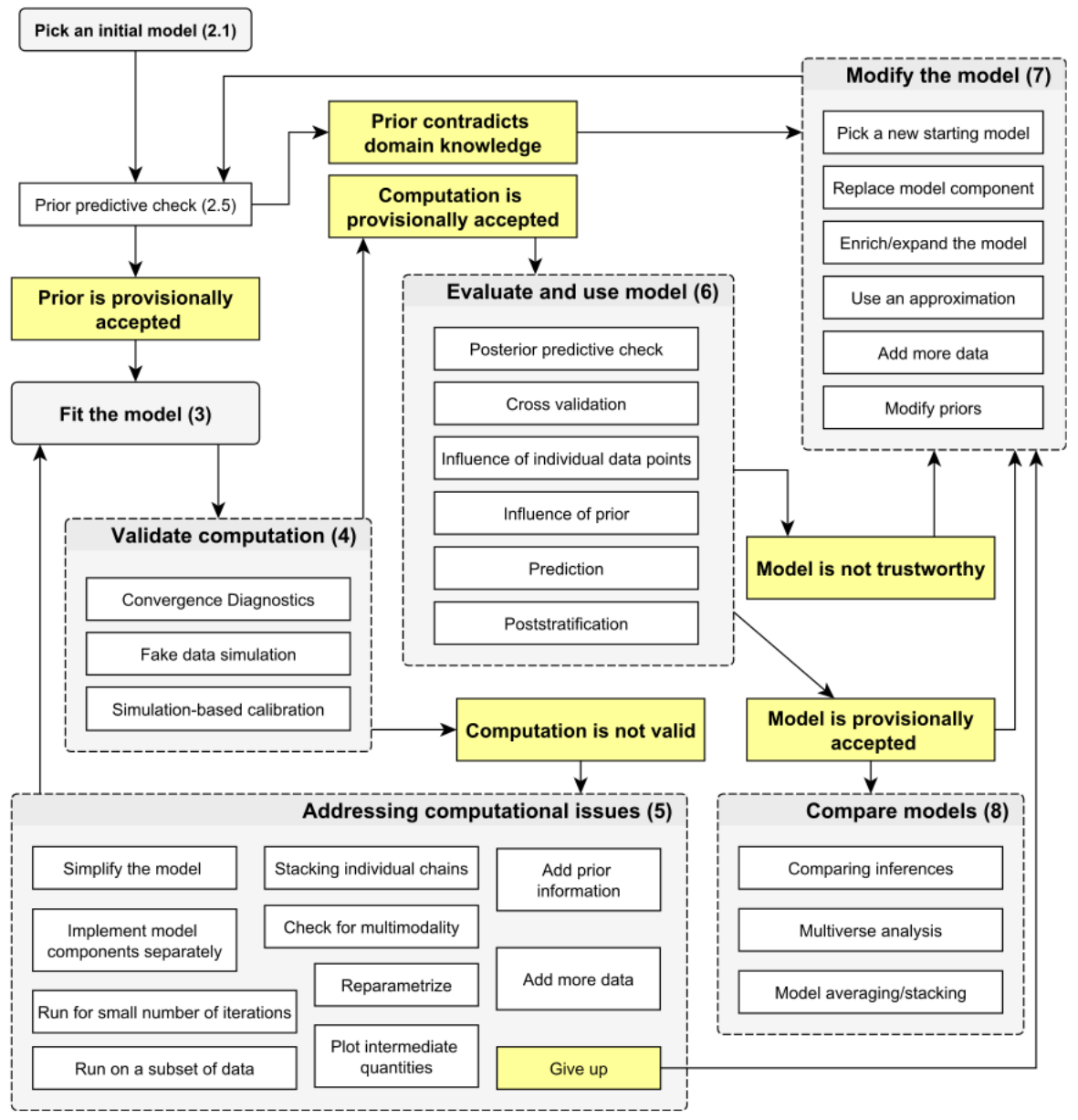
```
pp_check(height.mod, ndraws = 100)
```



Interactive model exploration

```
library('shinystan')
launch_shinystan(height.mod)
```

The Bayesian workflow



https://arxiv.org/abs/2011.01808

Exercise

height ~ sex

To read more

Regression and other stories

Statistical Rethinking

Statistical rethinking with brms, ggplot2, and the tidyverse

Bayesian Population Analysis using WinBugs

Applied Hierarchical Modeling in Ecology

Stan user guide

Exercises

Data coming from `rstanarm` package:

- Prob. switching well ~ arsenic level + distance to safe well using wells dataset

Exercises

Data coming from `rstanarm` package:

- Prob. switching well ~ arsenic level + distance to safe well using wells dataset
- Children IQ score ~ mother characteristics data

Exercises

Data coming from `rstanarm` package:

- Prob. switching well ~ arsenic level + distance to safe well using wells dataset
- Children IQ score ~ mother characteristics data
- Number of roaches in apartments data

Exercises

Data from Zuur book:

https://highstat.com/Books/Book2/ZuurDataMixedModelling.zip

Some in `AED` package: `remotes::install_github("romunov/AED")`

- Analysing species richness (RIKZ dataset)

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- Presence absence of flatfish Solea dataset

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- Presence/absence of koalas (koalas dataset)
- Presence absence of flatfish Solea dataset
- Presence of tuberculosis in wild boar (WildBoarTb dataset)
- Bird densities (Loyn dataset)

Exercises

- Foraging ecology of bald eagles

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- Days absent from school

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- Do bigger birds lay more eggs?

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- Foraging ecology of bald eagles
- Days absent from school
- Do bigger birds lay more eggs?
- Does bird egg colour relate to closed/open nest?
- Are woody plants taller? Do they have larger seeds too?