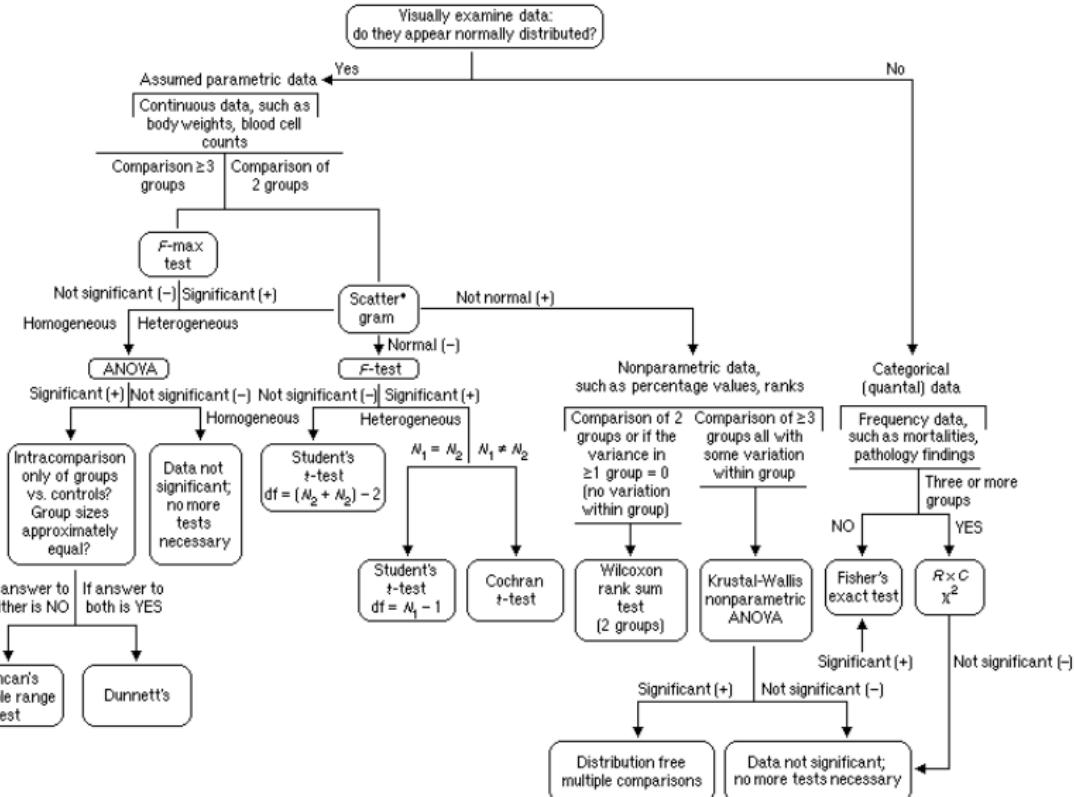


GLM as a unified framework for data analysis

Francisco Rodríguez-Sánchez

<https://frodriguezsanchez.net>

How I was taught statistics



So many questions

- Why should we really use analysis Y over Z?

So many questions

- Why should we really use analysis Y over Z?
- What if my data are **not Normal**?

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- What if they are **not independent**?

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- Why am I getting **different p-values** with different tests?

So many questions

- Why should we really use analysis Y over Z?
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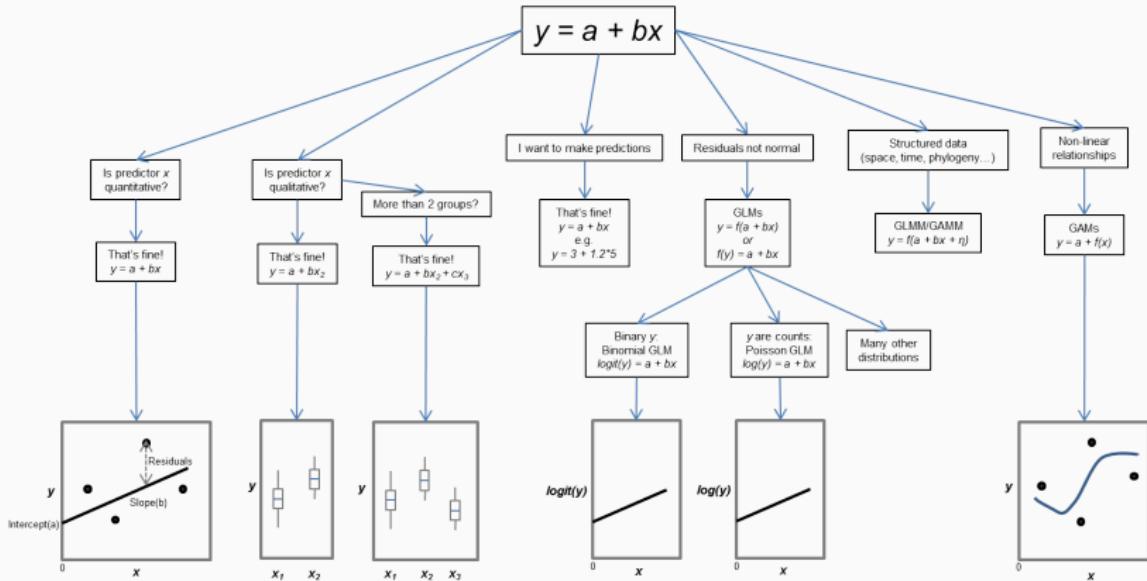
So many questions

- 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?

So many questions

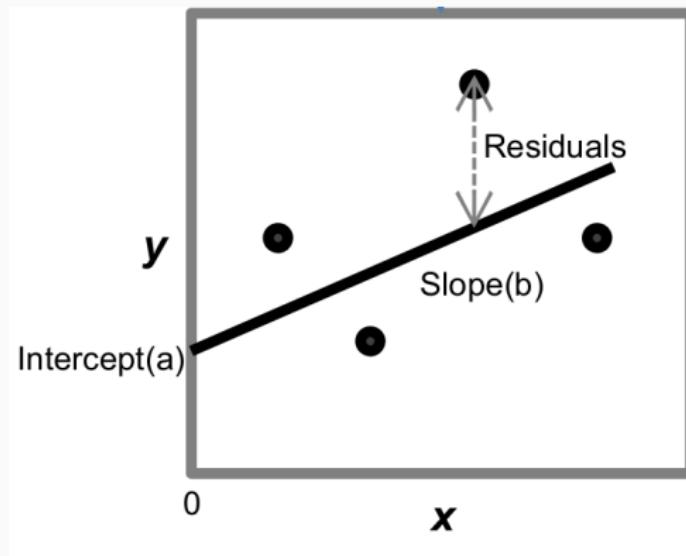
- Why should we really use analysis Y over Z?
- What if my data are **not Normal**?
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- Why am I getting **different p-values** with different tests?
- What even is a **p-value**?
- How can I take **different factors** into account?
- Can I make **predictions**?

A unified framework



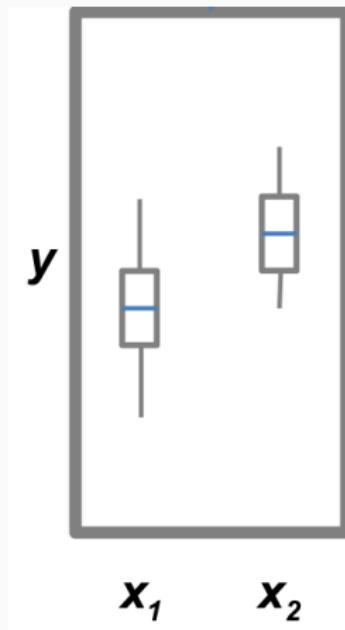
Linear regression

$$y = a + bx$$



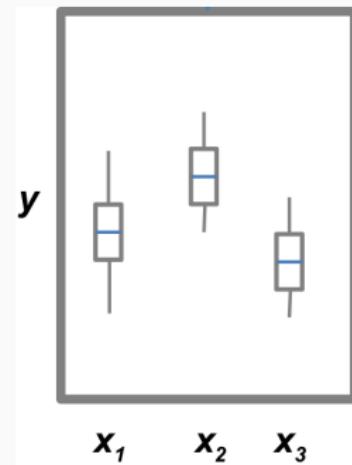
Is predictor X qualitative?

$$y = a + bx_2$$



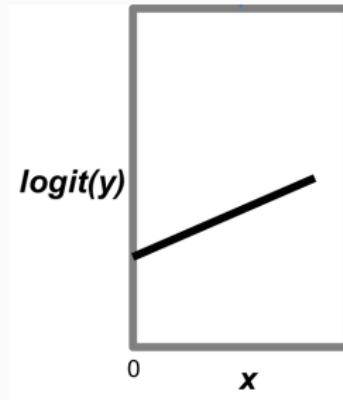
More than 2 groups?

$$y = a + bx_2 + cx_3$$



My data (residuals) are not Normal

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

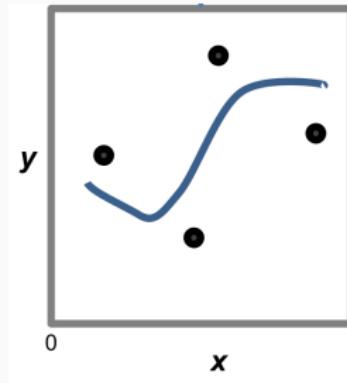


My data are structured (space, time, phylogeny)

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

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:

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

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

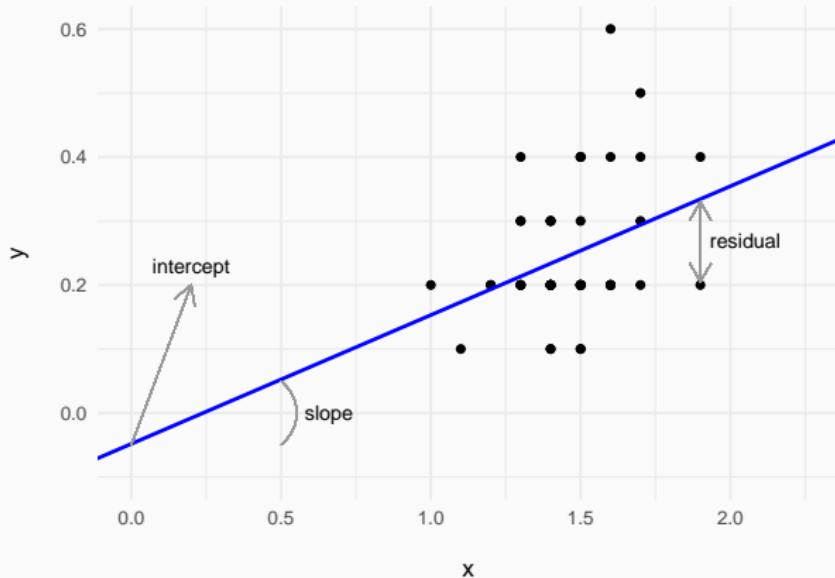
Francisco Rodríguez-Sánchez

<https://frodriguezsanchez.net>

Our unified regression framework (GLM)

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

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



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 $x = 0$:

- $y = a + b \cdot 0$

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 $x = 10 \rightarrow y = 0.5 + 2 * 10 = 20.5$

If x increases 1 unit, y increases 2 units

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 $x = 10 \rightarrow y = 0.5 + 2 * 10 = 20.5$
- If $x = 11 \rightarrow y = 0.5 + 2 * 11 = 22.5$

If x increases 1 unit, y increases 2 units

Slopes can be negative

If we have model

$$y = 0.5 - 2 * x$$

- If $x = 10 \rightarrow y = 0.5 - 2 * 10 = -19.5$

If x increases 1 unit, y decreases 2 units

Slopes can be negative

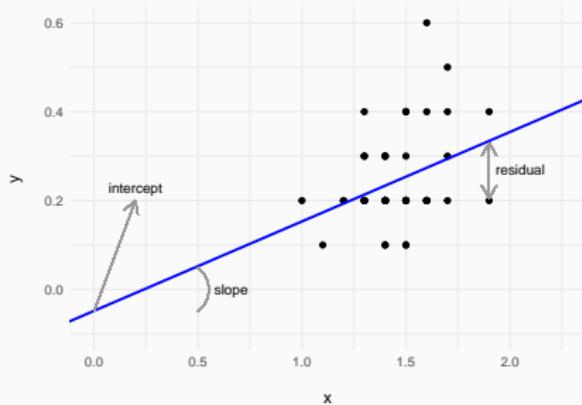
If we have model

$$y = 0.5 - 2 * x$$

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

If x increases 1 unit, y decreases 2 units

What are residuals?



How far points fall from the regression line

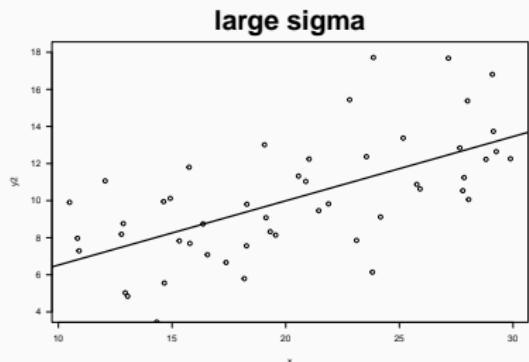
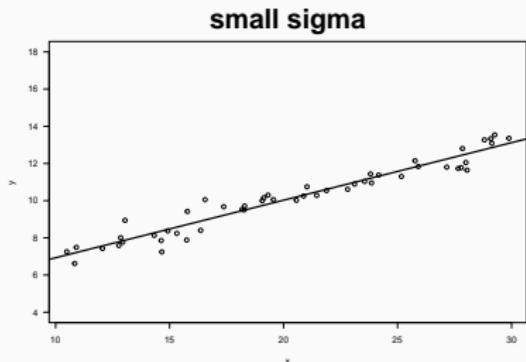
Difference between observed values and values predicted by model
(regression line)

If sigma is large, residuals are larger

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

If sigma is larger:

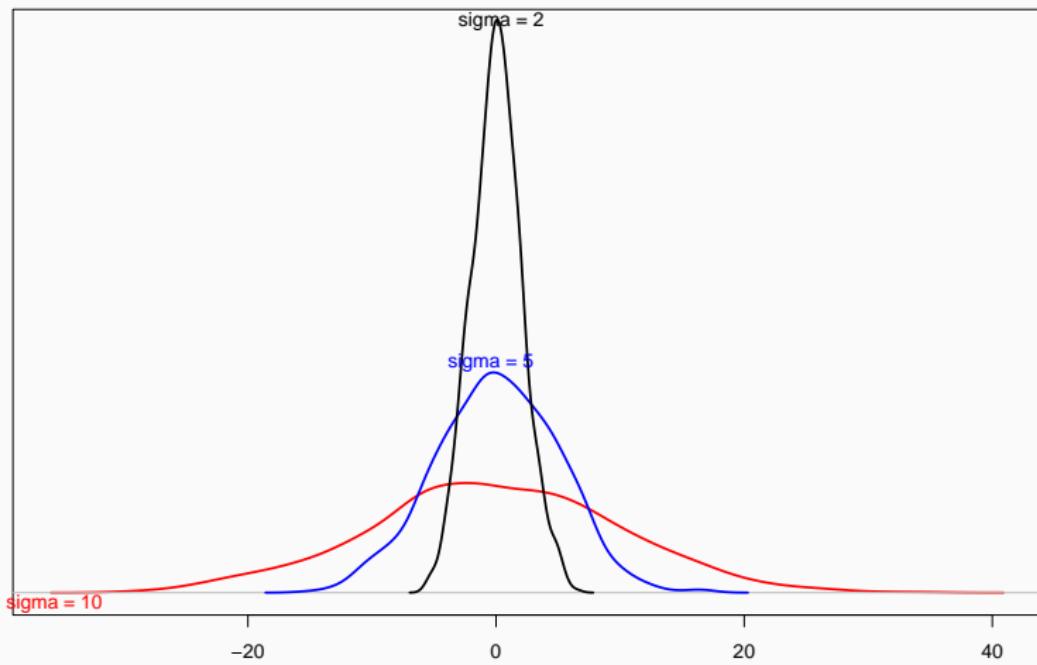
- points farther from regression line
- larger difference of observed - predicted values



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

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

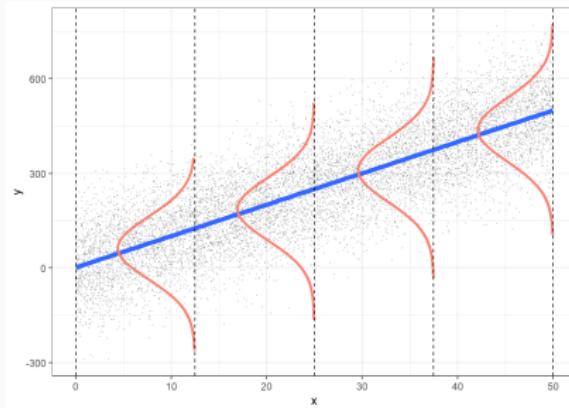
Distribution of residuals



In a general linear model we assume residuals are

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

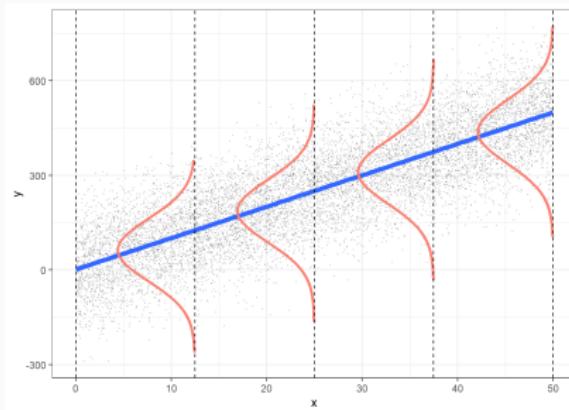
- Normal



In a general linear model we assume residuals are

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

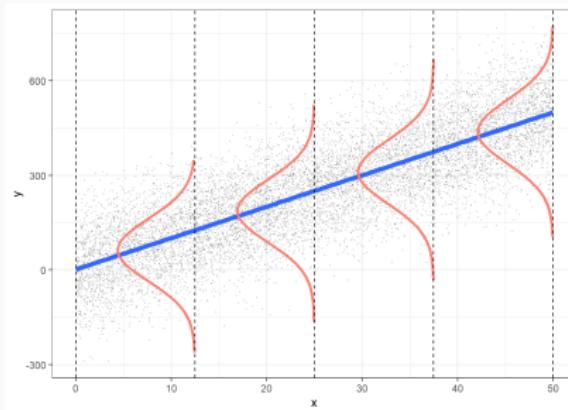
- Normal
- Centred on 0 (no bias)



In a general linear model we assume residuals are

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

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



Different ways to write same model

$$y_i = a + b x_i + \varepsilon_i$$

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

$$y_i \sim N(\mu_i, \sigma^2)$$

$$\mu_i = a + b x_i$$

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

Quiz

<https://pollev.com/franciscorod726>

Linear models

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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:

```
trees <- read.csv("data/trees.csv")  
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```

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6	1	10.82	26.2	male	0

Questions

- What is the relationship between DBH and height?

Questions

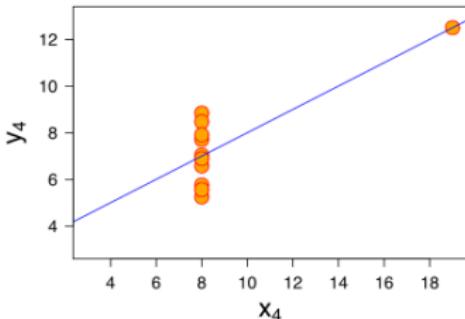
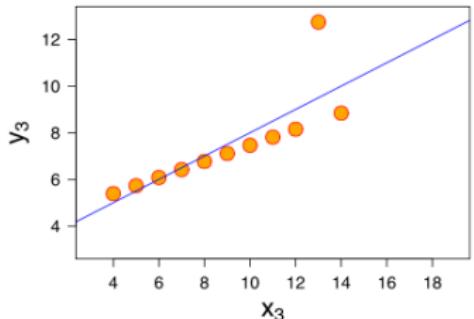
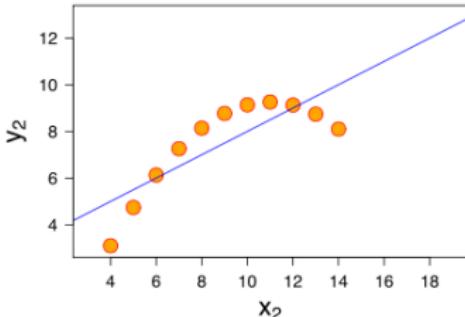
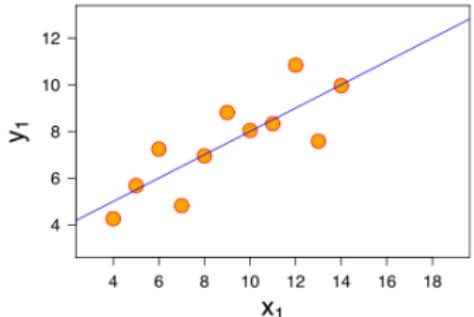
- What is the relationship between DBH and height?
- Do taller trees have bigger trunks?

Questions

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

Always plot your data first!

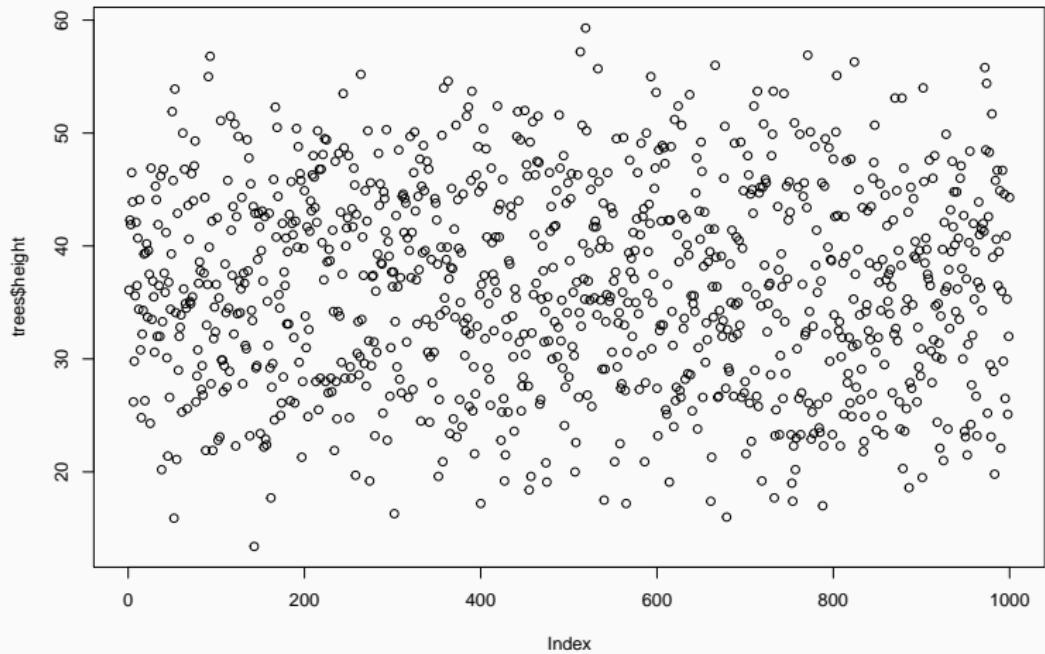
Always plot your data first!



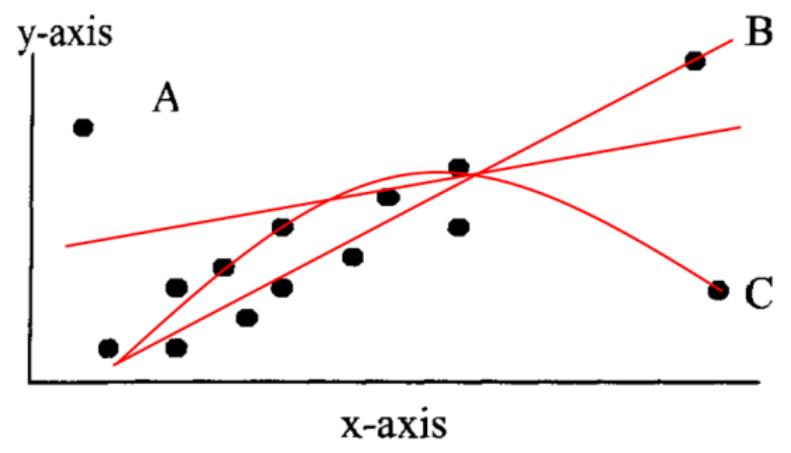
Exploratory Data Analysis (EDA)

Outliers

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



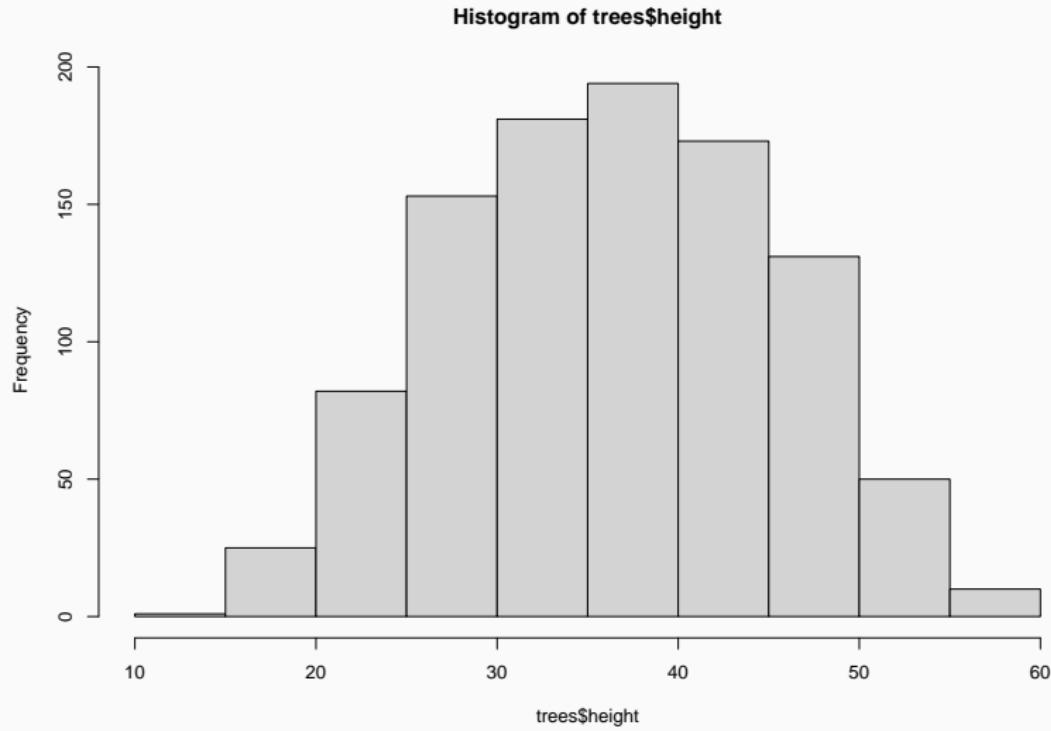
Outliers impact on regression



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

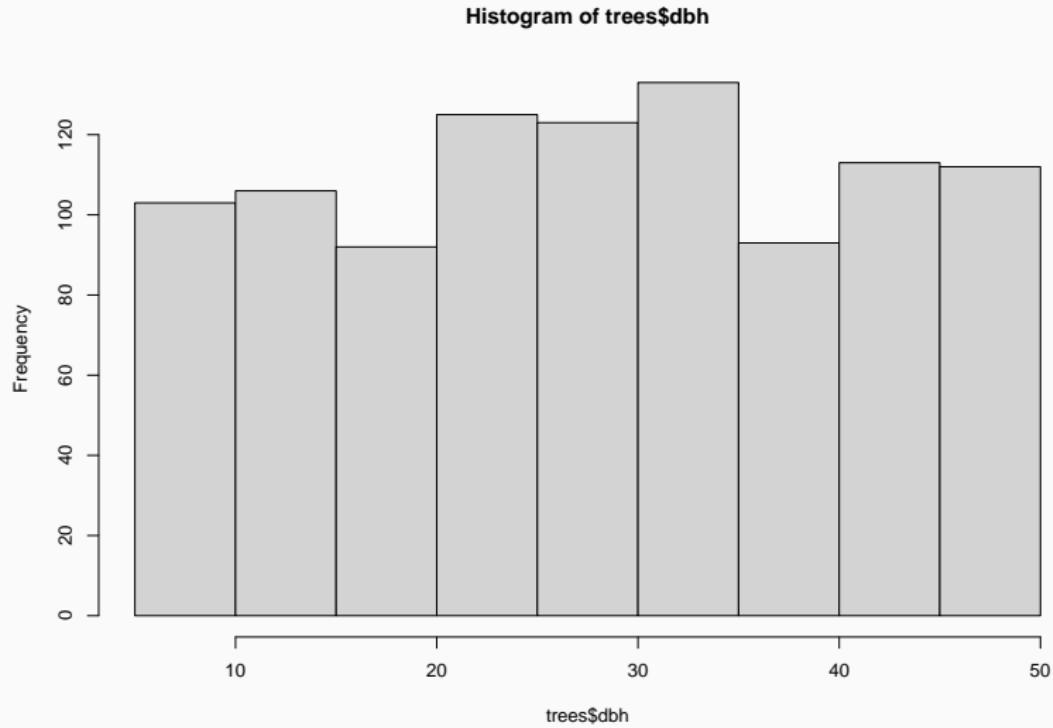
Histogram of response variable

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



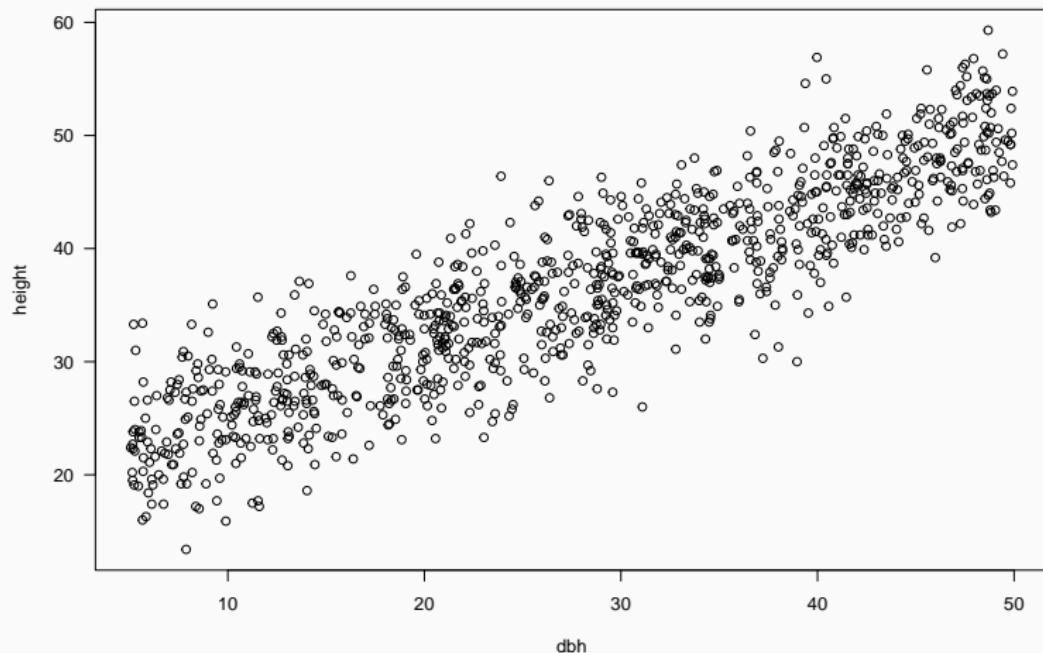
Histogram of predictor variable

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



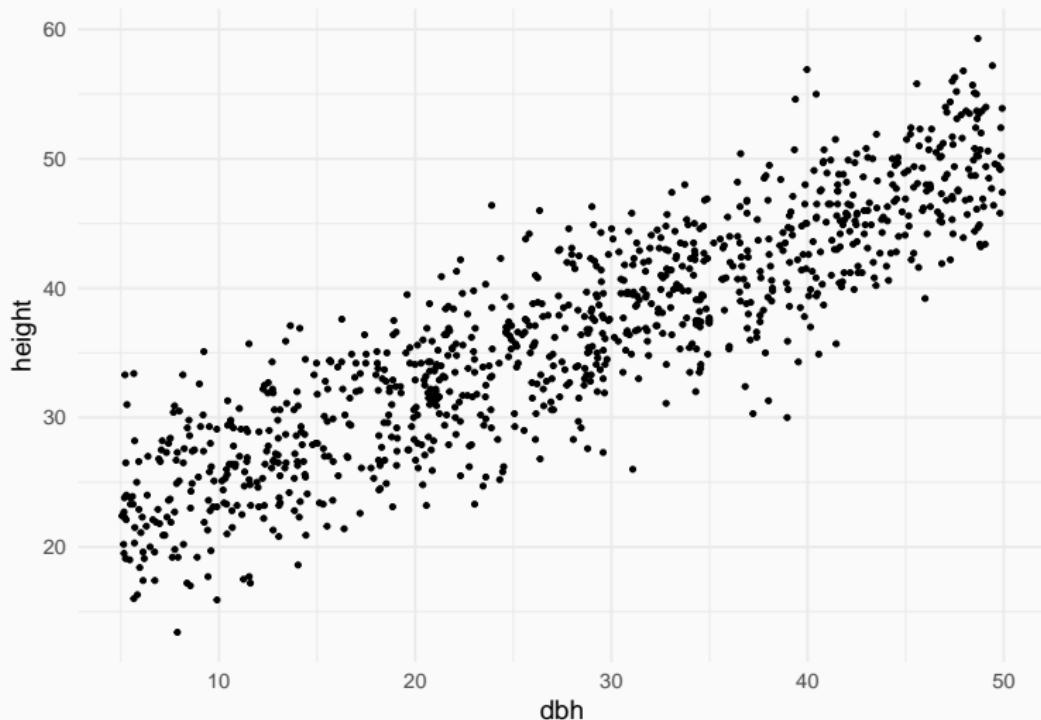
Scatterplot

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



Scatterplot

```
ggplot(trees) +  
  geom_point(aes(dbh, height))
```



Model fitting

Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

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

which corresponds to

$$\begin{aligned} \text{Height}_i &= a + b \cdot DBH_i + \varepsilon_i \\ \varepsilon_i &\sim N(0, \sigma^2) \end{aligned}$$

Package equatiomatic returns model structure

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

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

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

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

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 ***							

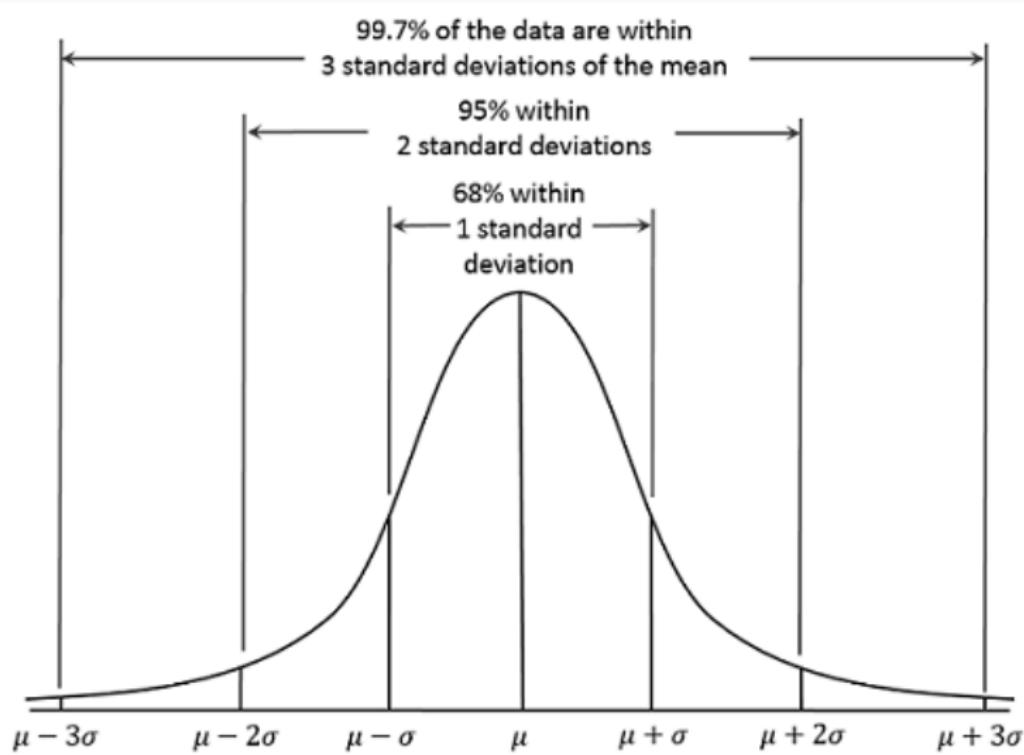
Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

Residual standard error: 4.093 on 998 degrees of freedom

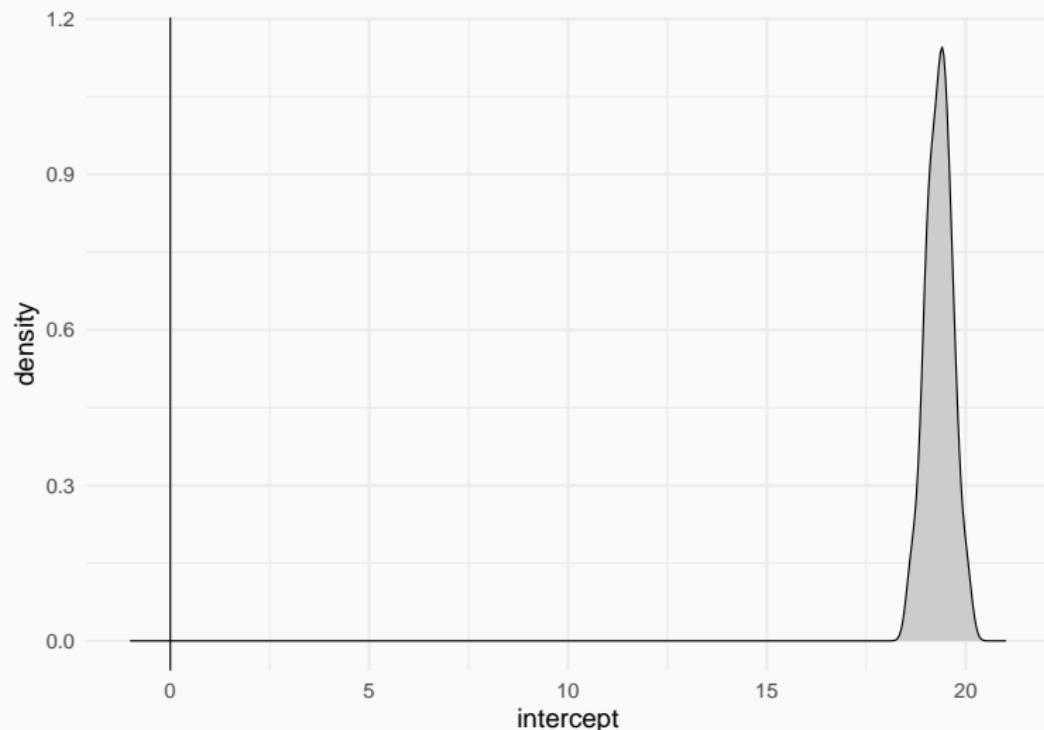
Multiple R-squared: 0.7874, Adjusted R-squared: 0.7871

F-statistic: 3695 on 1 and 998 DF, p-value: < 2.2e-16

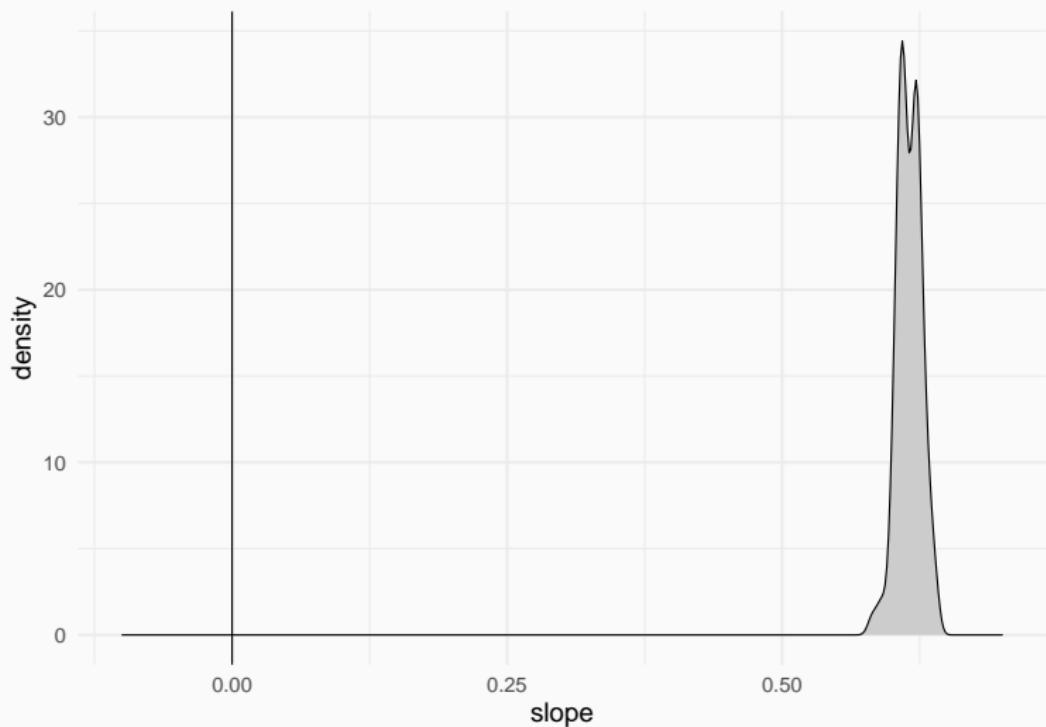
Remember that in a Normal distribution



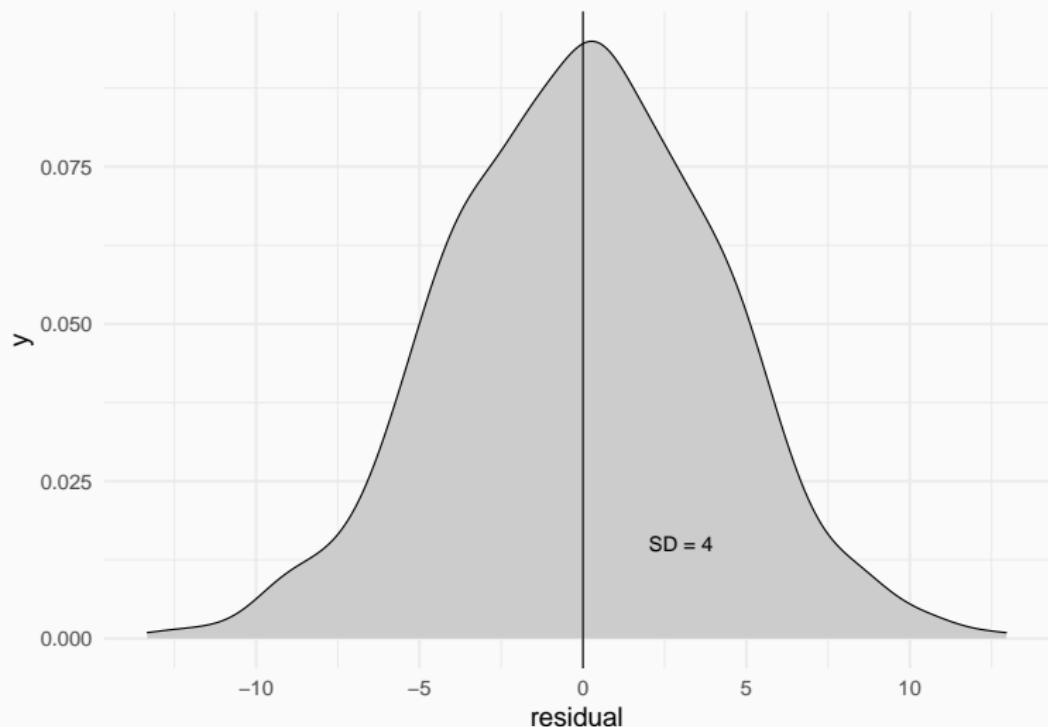
Estimated distribution of the intercept parameter



Estimated distribution of the slope parameter



Distribution of residuals



Degrees of freedom

$$DF = n - p$$

n = sample size

p = number of estimated parameters

R-squared

Proportion of ‘explained’ variance

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

Adjusted R-squared

Accounts for model complexity (number of parameters)

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

Quiz

<https://pollev.com/franciscorod726>

Retrieving model coefficients

```
coef(m1)
```

	dbh
(Intercept)	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.sq~1 adj.r~2 sigma stati~3 p.value     df logLik     AIC     BIC devia~4 df.re~5
  <dbl>   <dbl> <dbl>   <dbl>   <dbl> <dbl> <dbl> <dbl>   <dbl>   <dbl>   <int>
1 0.787   0.787  4.09   3695.     0     1 -2827. 5660. 5675. 16716.    998
# ... with 1 more variable: nobs <int>, and abbreviated variable names
#   1: r.squared, 2: adj.r.squared, 3: statistic, 4: deviance, 5: df.residual
```

<https://broom.tidymodels.org/>

Retrieving model parameters with `parameters` package

```
library("parameters")
parameters(m1)
```

Parameter	Coefficient	SE	95% CI	t(998)	p
<hr/>					
(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/>

Understanding the fitted effects with `effects` package

```
library("effects")
summary(allEffects(m1))
```

model: height ~ dbh

dbh effect

dbh

5 20 30 40 50

22.41771 31.65327 37.81030 43.96734 50.12438

Lower 95 Percent Confidence Limits

dbh

5 20 30 40 50

21.89682 31.35487 37.55287 43.61733 49.61669

Upper 95 Percent Confidence Limits

dbh

5 20 30 40 50

22.93861 31.95167 38.06774 44.31735 50.63207

Communicating results

Avoid dichotomania of statistical significance

The screenshot shows a web page from the journal 'nature'. At the top, there is a red header bar with a 'MENU ▾' button, the 'nature' logo, and a 'Subs' button. Below the header, the word 'EDITORIAL' is followed by a small dot and the date '20 MARCH 2019'. The main title of the article is 'It's time to talk about ditching statistical significance', displayed in a large, bold, serif font.

- “Never conclude there is ‘no difference’ or ‘no association’ just because $p > 0.05$ or CI includes zero”

Avoid dichotomania of statistical significance

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- “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

Avoid dichotomania of statistical significance

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- “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 ($p < 0.05$).

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

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 ($R^2 = 0.79$, $F(1, 998) = 3695.40$, $p < .001$, adj. $R^2 = 0.79$). 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: `xtable`

```
library("xtable")
xtable(m1, digits = 2)
```

% latex table generated in R 4.2.1 by xtable 1.8-4 package % Sat Sep 17 21:12:52 2022

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	19.34	0.31	62.26	0.00
dbh	0.62	0.01	60.79	0.00

Generating table with model results: `texreg`

```
library("texreg")
texreg(m1, single.row = TRUE)
```

Model 1	
(Intercept)	19.34 (0.31)***
dbh	0.62 (0.01)***
R ²	0.79
Adj. R ²	0.79
Num. obs.	1000

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$

Table 1: Statistical models

Generating table with model results: `modelsummary`

```
library("modelsummary")
modelsummary(m1, output = "markdown")
```

Model 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

Generating table with model results: `gtsummary`

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

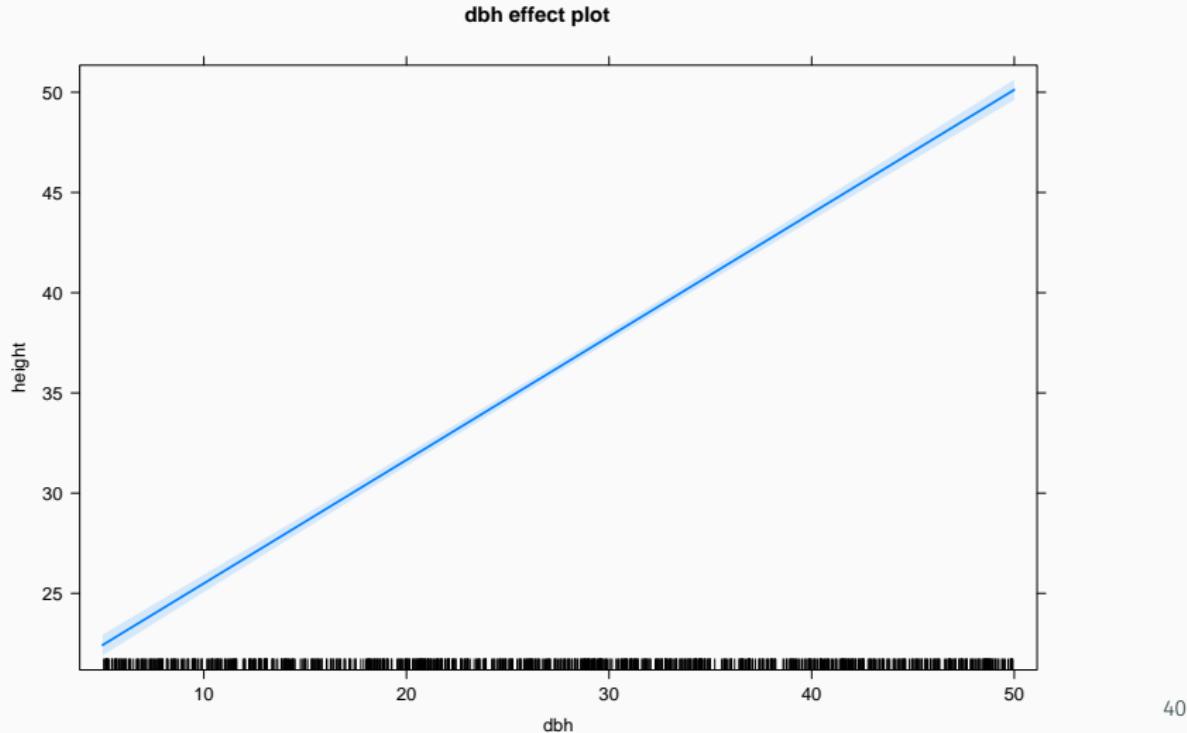
Characteristic	**Beta**	**95% CI**	**p-value**
(Intercept)	19	19, 20	<0.001
dbh	0.62	0.60, 0.64	<0.001

<https://www.danieldsjoberg.com/gtsummary>

Visualising fitted model

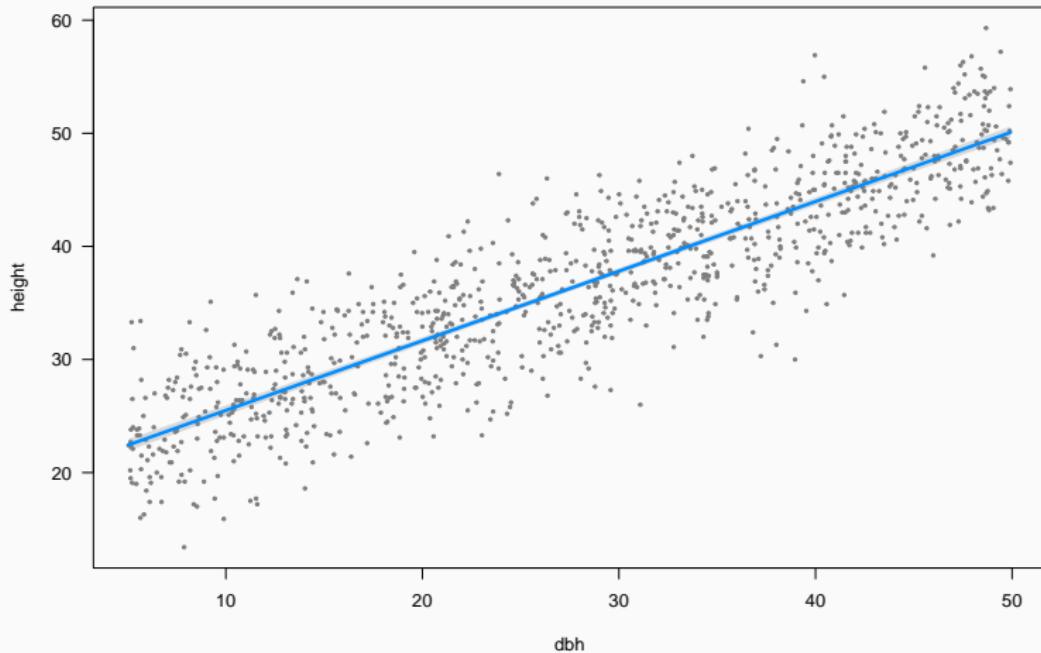
Plot model: effects package

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



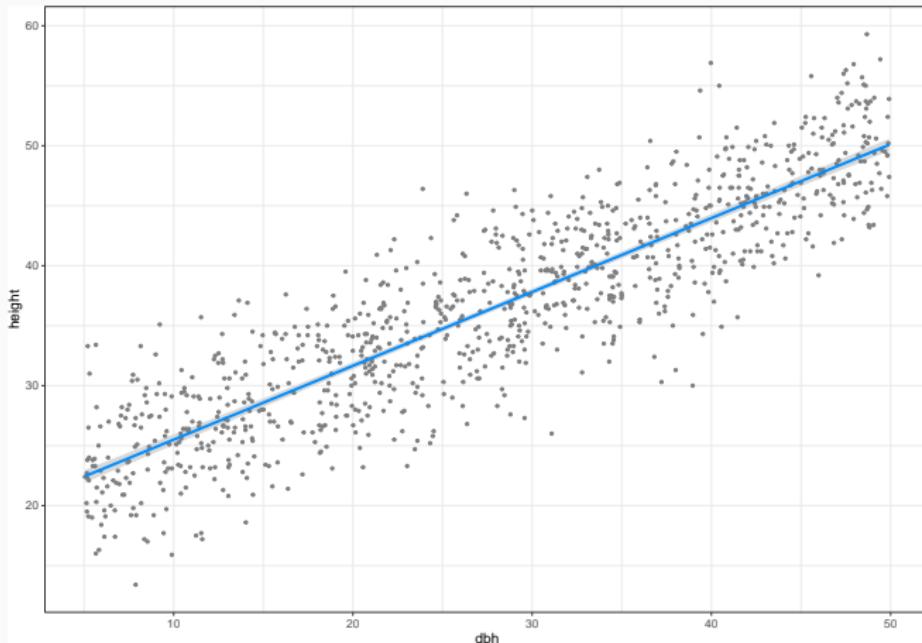
Plot model: visreg

```
library("visreg")
visreg(m1)
```



visreg can use ggplot2 too

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

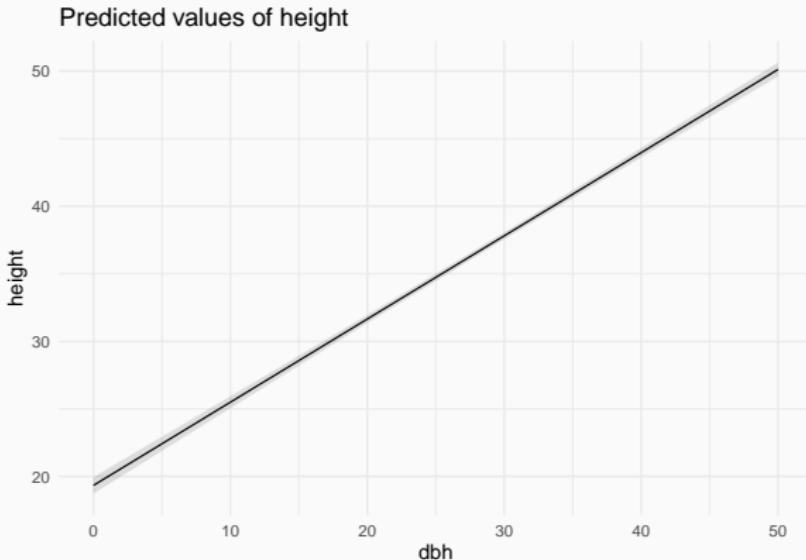


<https://pbreheny.github.io/visreg>

Plot model: sjPlot

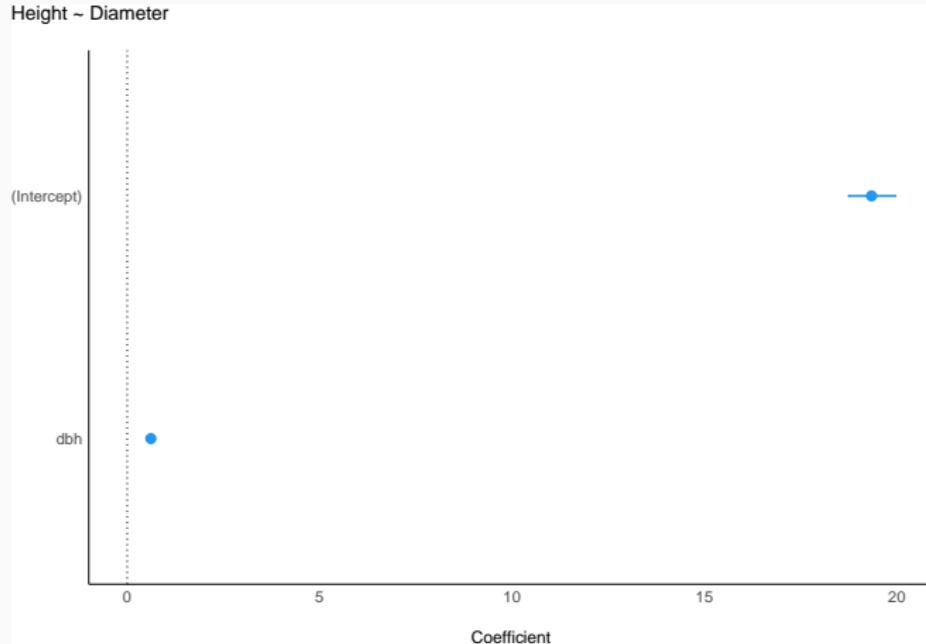
```
library("sjPlot")
plot_model(m1, type = "eff")
```

\$dbh



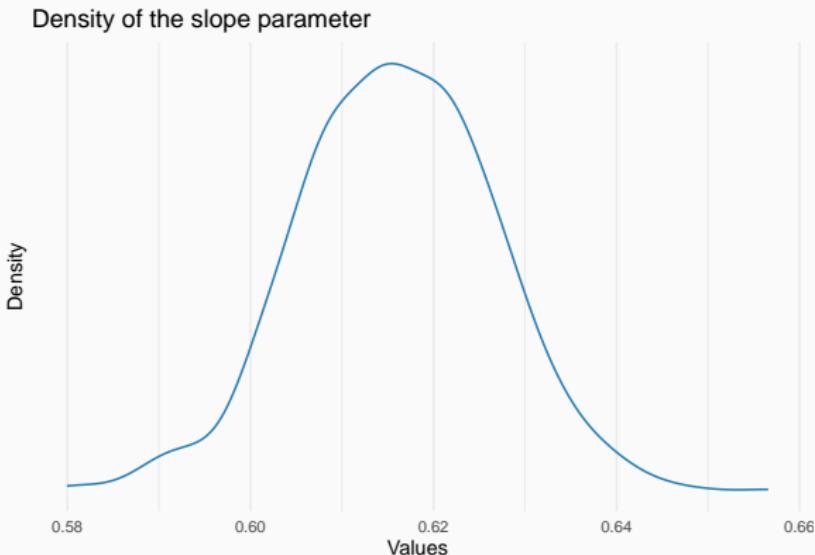
Plot model: see

```
library("see")
plot(parameters(m1), show_intercept = TRUE) +
  labs(title = "Height ~ Diameter") # ggplot2
```



Plot parameters' estimated distribution: see

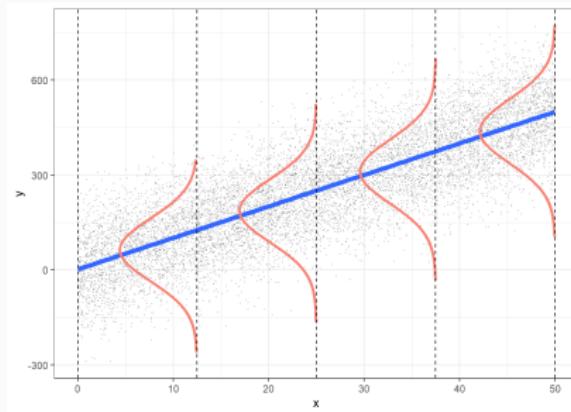
```
plot(simulate_parameters(m1)) +  
  labs(title = "Density of the slope parameter")
```



Model checking

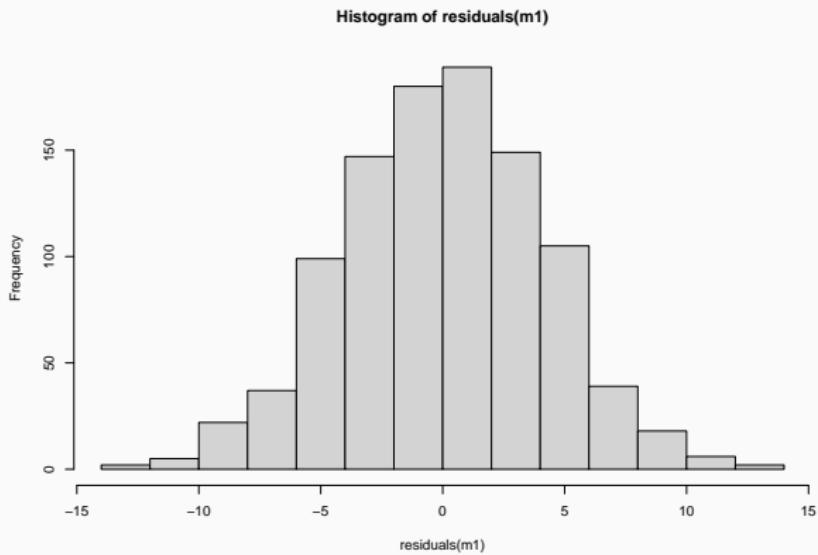
Linear model assumptions

- Linearity (transformations, GAM...)
- Residuals:
 - Independent
 - Equal variance
 - Normal
- Negligible measurement error in predictors



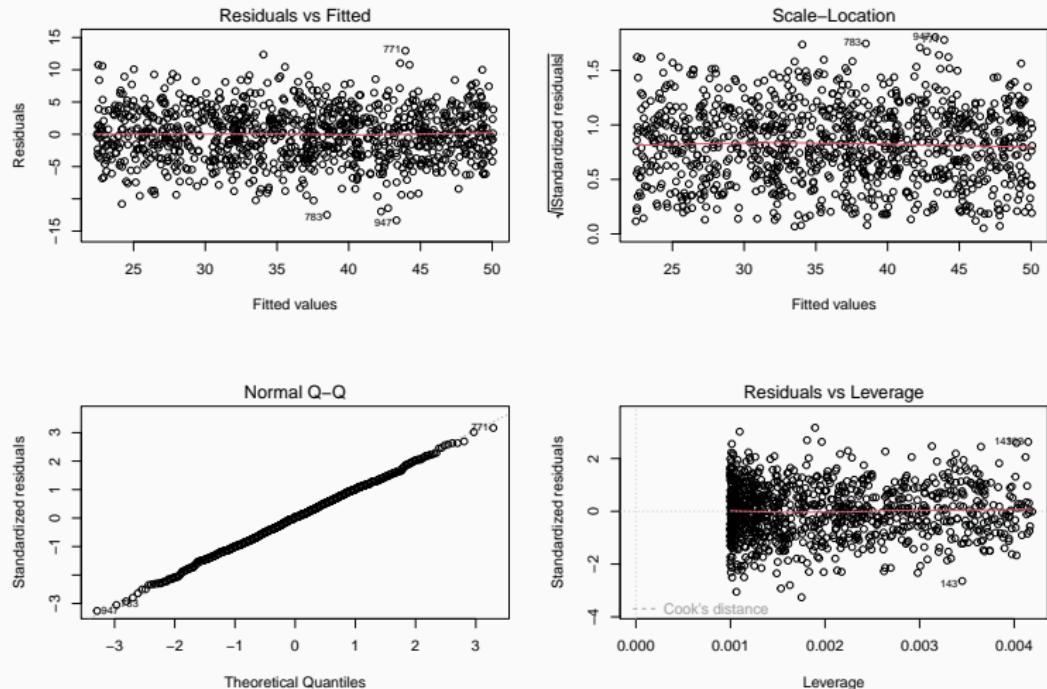
Are residuals normal?

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



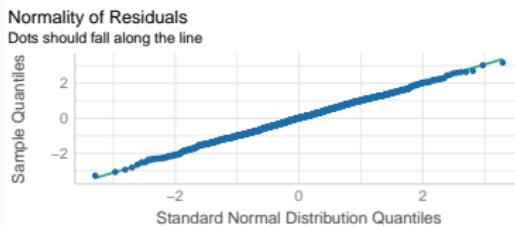
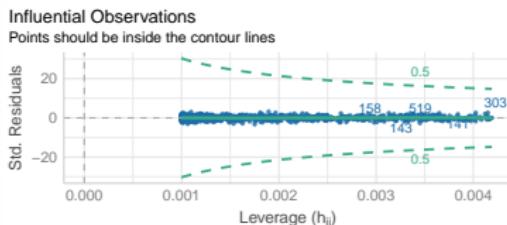
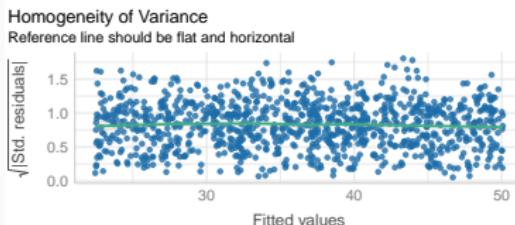
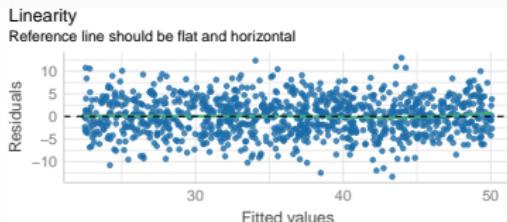
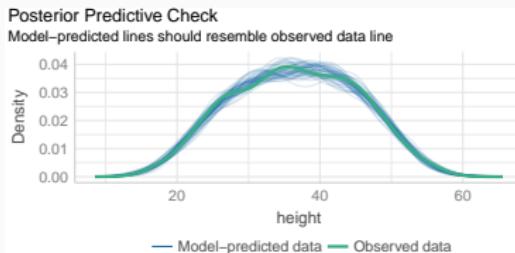
SD = 4.09

Model checking: `plot(model)`



Model checking with performance package

```
library("performance")
check_model(m1)
```



A dashboard to explore the full model

```
library("easystats")
model_dashboard(m1)
```

Using model for prediction

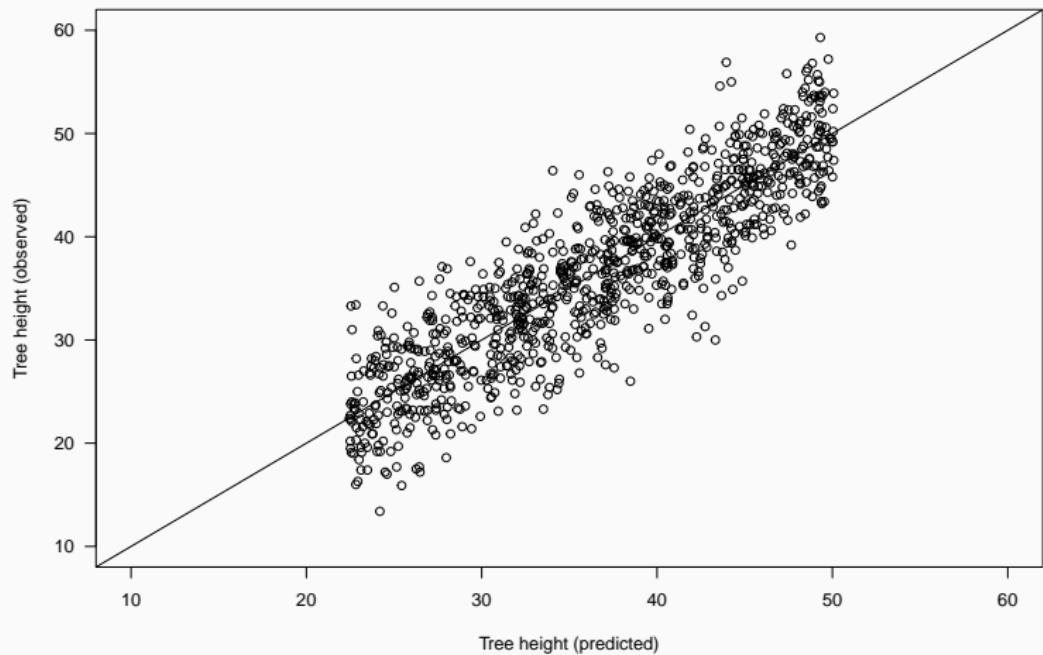
How good is the model in predicting tree height?

`fitted` gives expected value for each observation

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

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

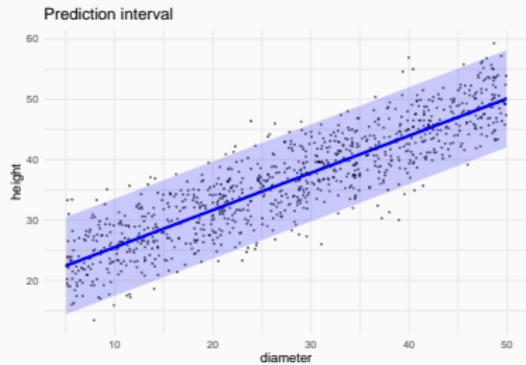
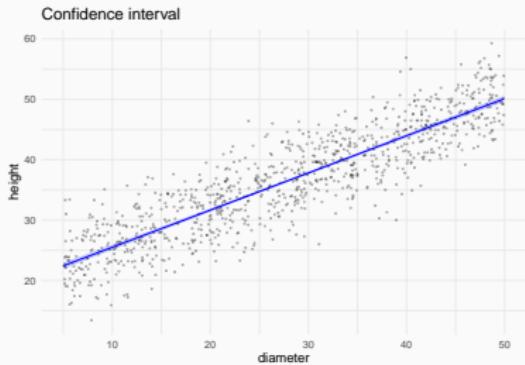
```
predict(m1, new.dbh, interval = "confidence")
```

	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



Workflow

- Visualise data

Workflow

- Visualise data
- Understand fitted model (`summary`, `allEffects`...)

Workflow

- Visualise data
- Understand fitted model (`summary`, `allEffects`...)
- Visualise model (`plot(allEffects)`, `visreg`, `see`, `plot_model`...)

Workflow

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

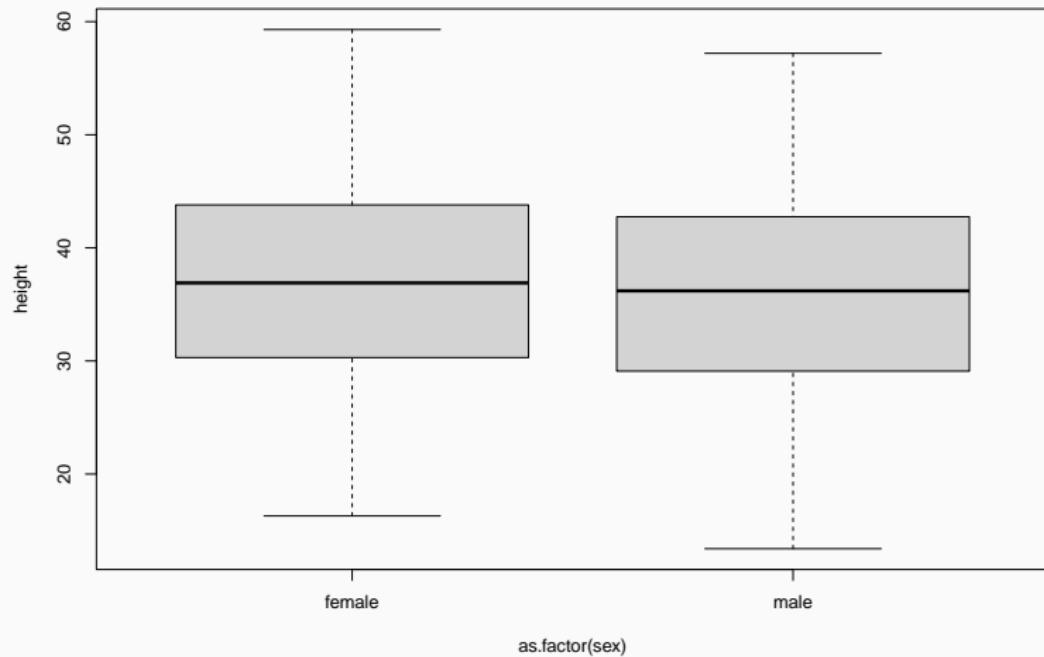
Workflow

- Visualise data
- Understand fitted model (`summary`, `allEffects`...)
- Visualise model (`plot(allEffects)`, `visreg`, `see`, `plot_model`...)
- Check model (`plot`, `check_model`, calibration plot...)
- Predict (`fitted`, `predict`)

Categorical predictors (factors)

Q: Does tree height vary with sex?

```
plot(height ~ as.factor(sex), data = trees)
```



Model height ~ sex

```
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

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

corresponds to

$$Height_i = a + b_{male} + \varepsilon_i$$

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

Model height ~ sex

```
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

Quiz

<https://pollev.com/franciscorod726>

Let's read the model report...

```
report(m2)
```

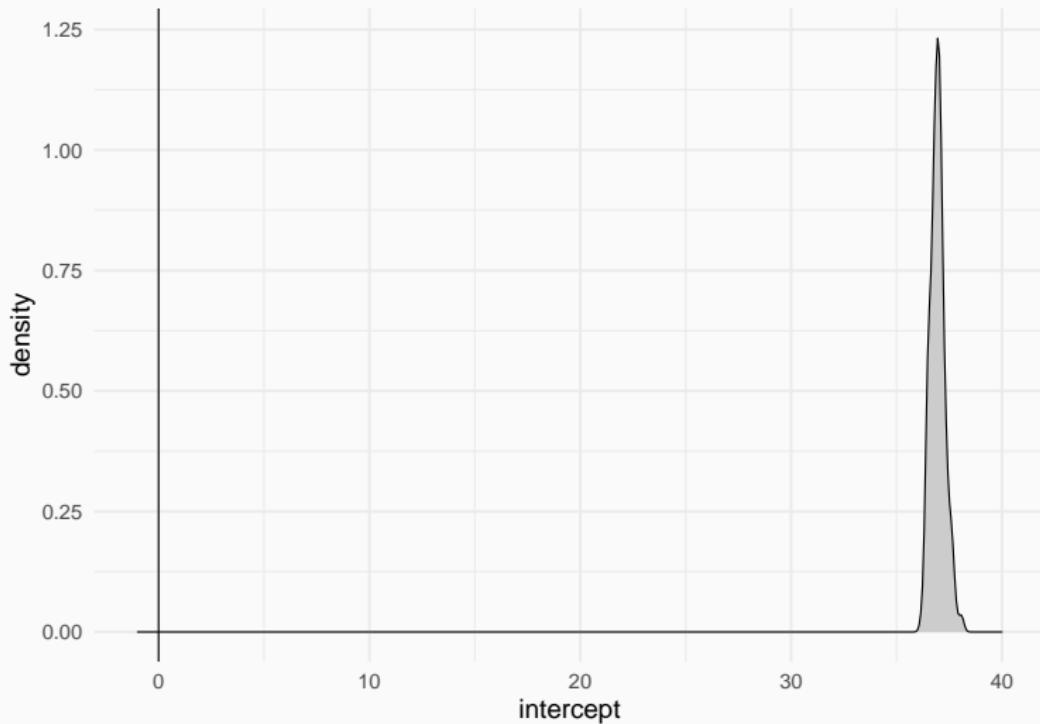
We fitted a linear model (estimated using OLS) to predict height with sex (formula: height ~ sex). The model explains a statistically not significant and very weak proportion of variance ($R^2 = 2.26e-03$, $F(1, 998) = 2.26$, $p = 0.133$, adj. $R^2 = 1.26e-03$). The model's intercept, corresponding to 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.

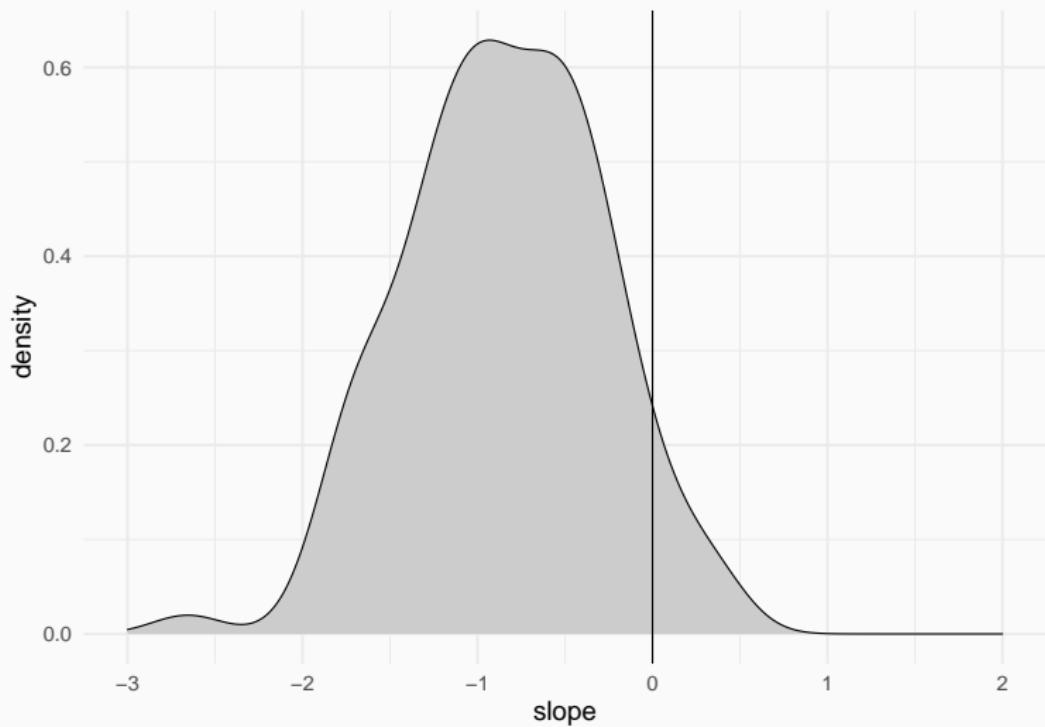
Estimated distribution of the intercept parameter

Intercept = Height of females



Estimated distribution of the *beta* parameter

beta = height difference of males vs females



Analysing differences among factor levels

```
library("modelbased")
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

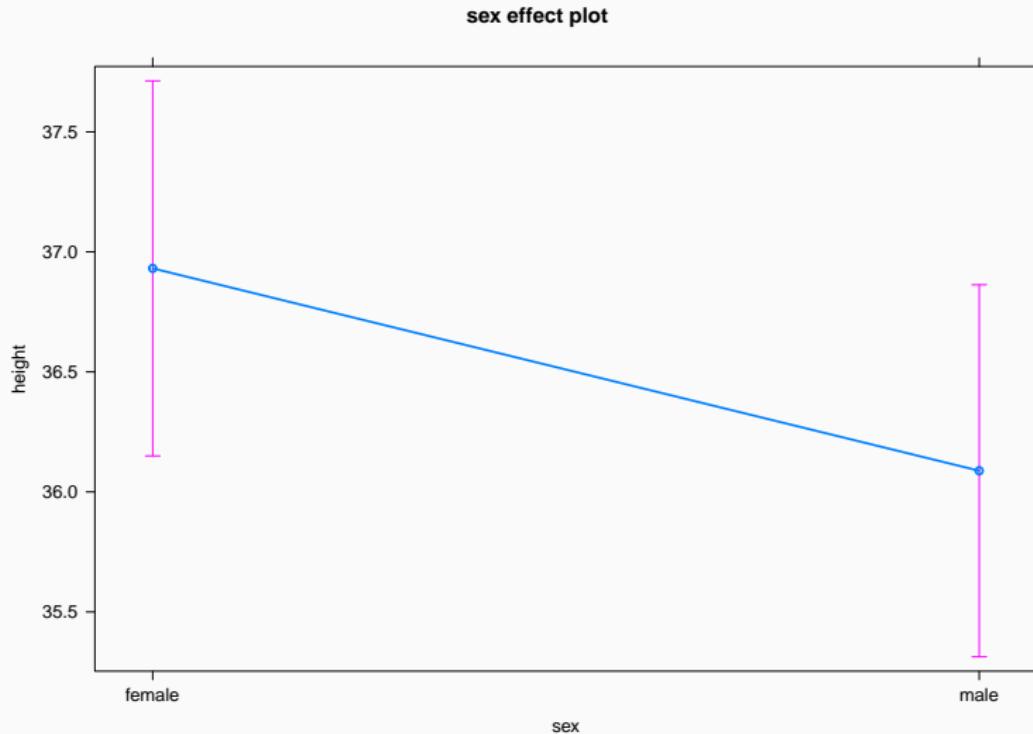
male		female		-0.84		[-1.94, 0.26]		0.56		-1.50		0.133

Marginal contrasts estimated at sex

p-value adjustment method: Holm (1979)

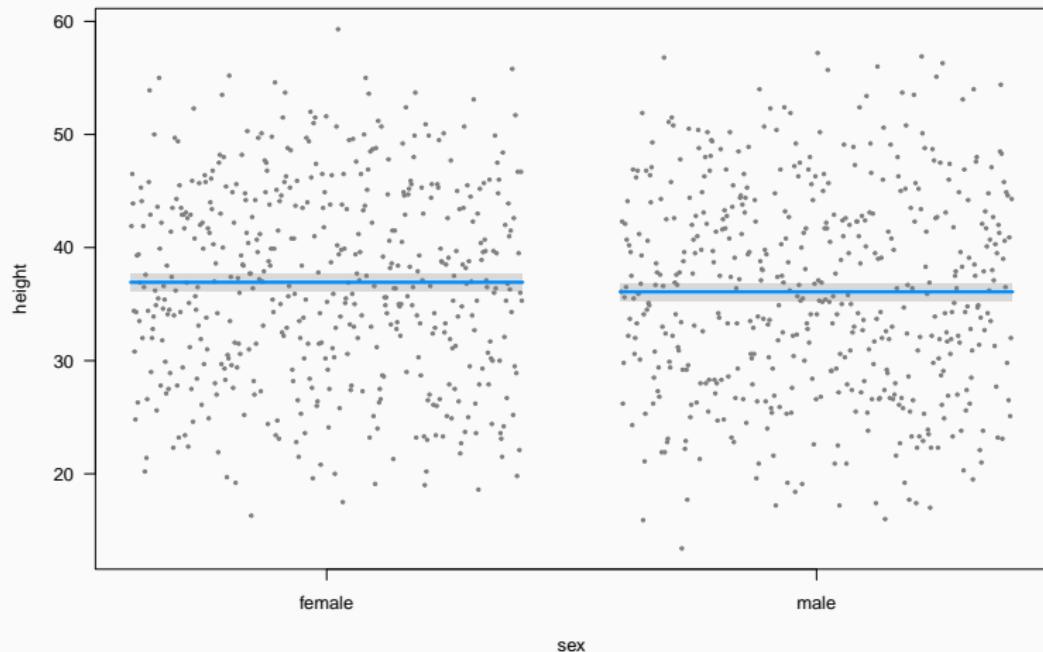
Plot

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



Plot (visreg)

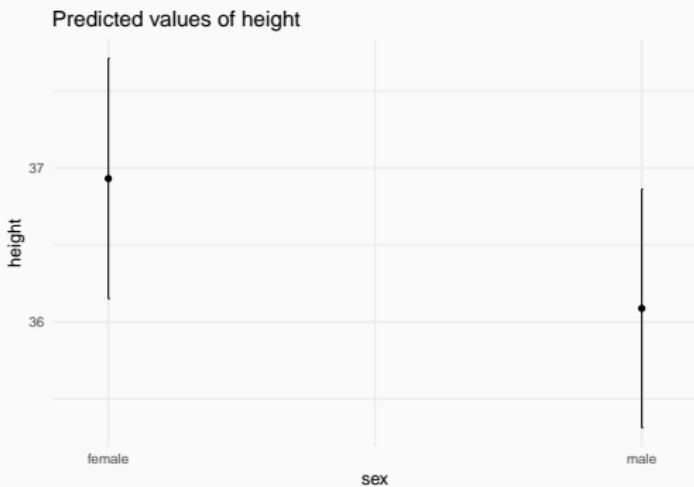
```
visreg(m2)
```



Plot model (sjPlot)

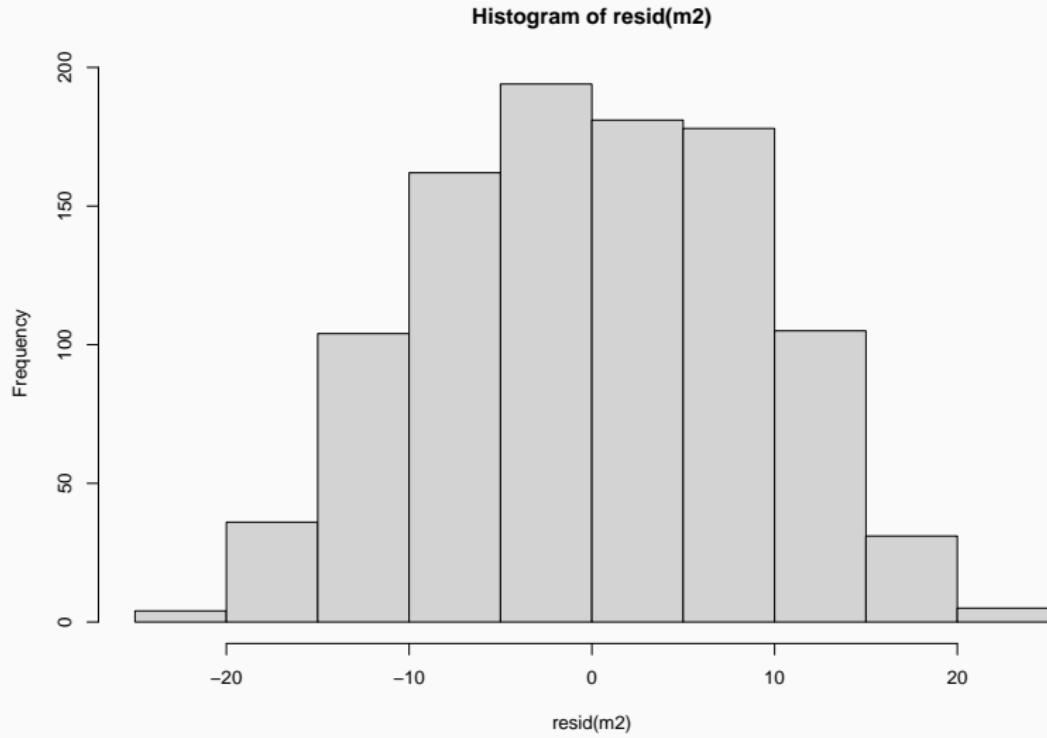
```
plot_model(m2, type = "eff")
```

\$sex

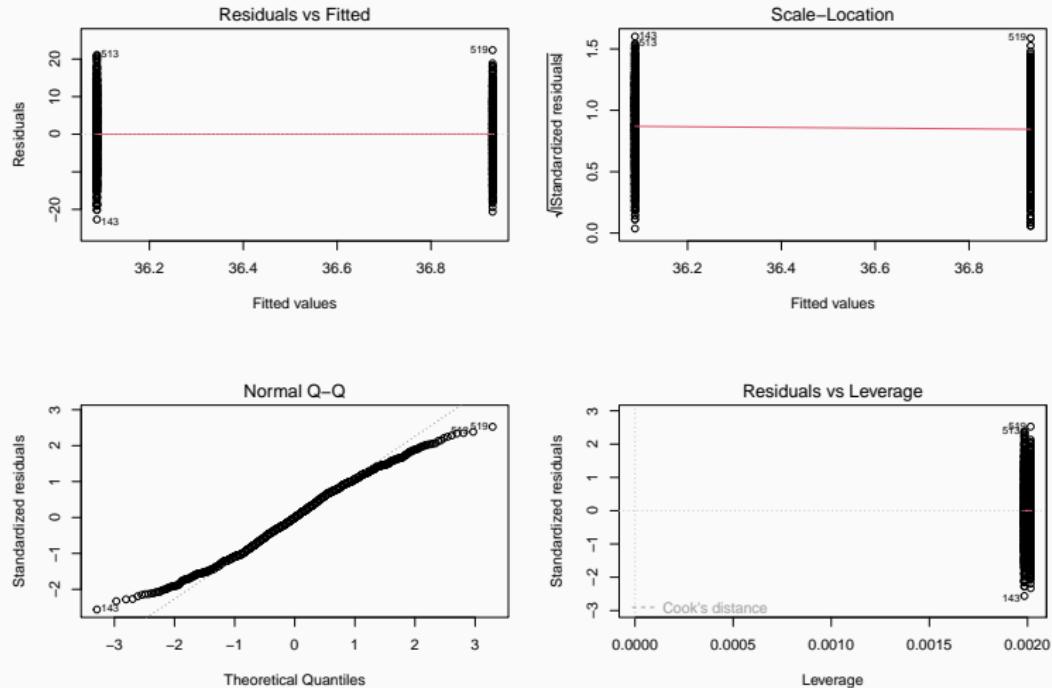


Model checking: residuals

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

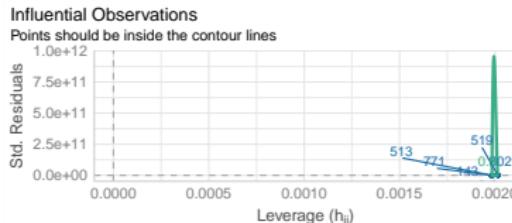
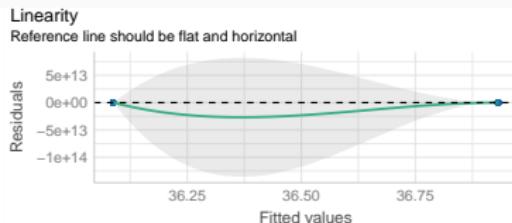
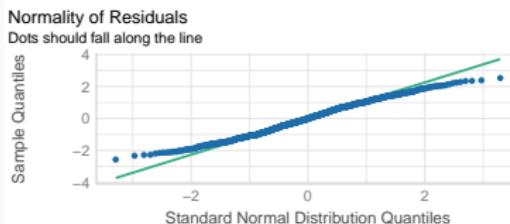
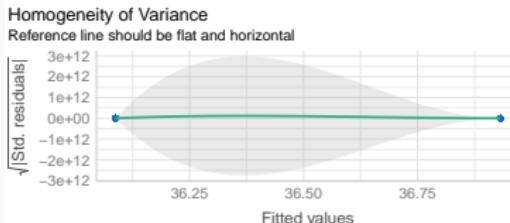
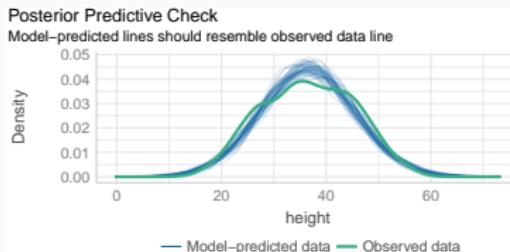


Model checking: residuals



Model checking

```
library("performance")
check_model(m2)
```



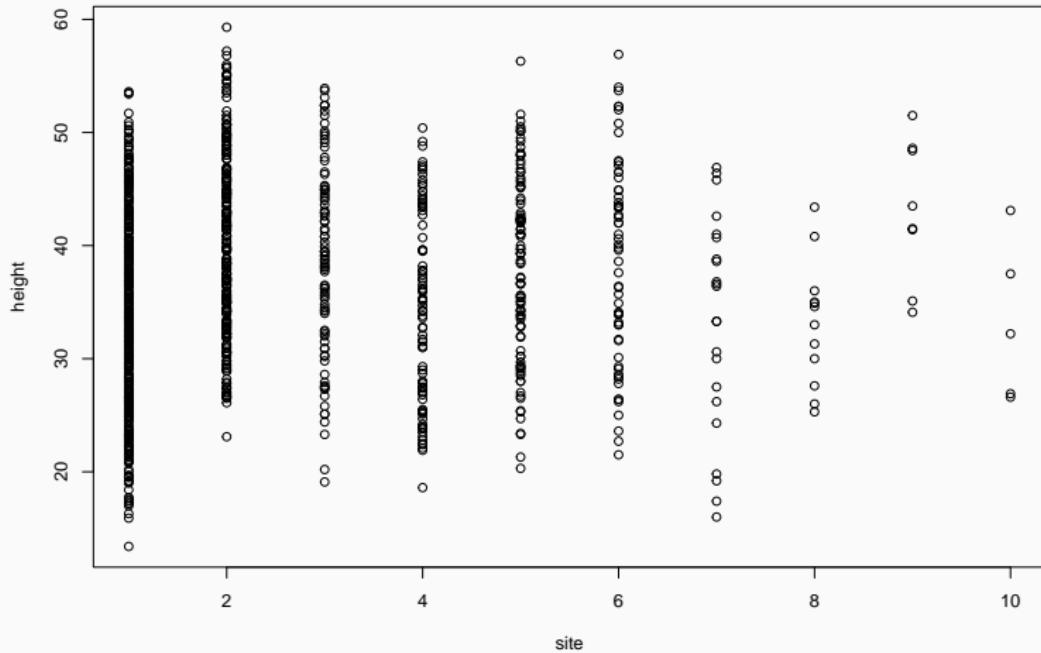
Model dashboard

```
model_dashboard(m2)
```

Q: Does height differ among field sites?

Plot data first

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



Linear model with categorical predictors

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

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + \dots + \varepsilon_i$$
$$\varepsilon_i \sim N(0, \sigma^2)$$

Model Height ~ site

All right here?

```
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)
```

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

site is a factor!

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

Let's check model structure with `equatiomatic`

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

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

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

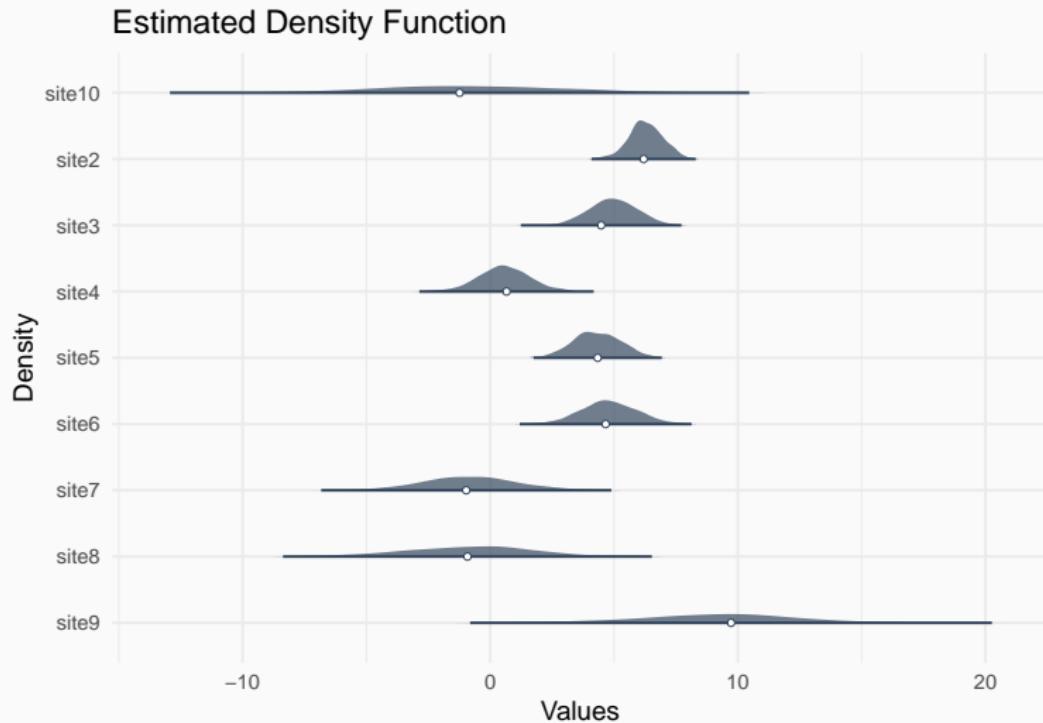
Residual standard error: 8.446 on 990 degrees of freedom

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)
```



Analysing differences among factor levels

```
library("modelbased")
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]

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	0.073
site2	site10	6.92	[-5.57, 19.42]	3.82	1.81	0.728
site2	site3	1.34	[-2.10, 4.79]	1.05	1.27	0.959
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	0.643
site2	site6	1.58	[-2.44, 5.61]	1.23	1.28	0.957
site2	site7	7.08	[0.90, 13.26]	1.89	3.75	0.007
site2	site8	7.02	[-1.17, 15.21]	2.50	2.81	0.136
site2	site9	-2.83	[-12.77, 7.11]	3.04	-0.93	0.995
site3	site10	5.58	[-7.11, 18.27]	3.88	1.44	0.915
site3	site4	4.47	[0.36, 8.57]	1.26	3.56	0.014
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	0.118
site3	site8	5.68	[-2.80, 14.17]	2.59	2.19	0.464
site3	site9	-4.17	[-14.36, 6.01]	3.11	-1.34	0.944
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	0.055
site4	site6	-4.23	[-8.83, 0.38]	1.41	-3.00	0.081

Presenting model results

```
kable(xtable::xtable(m3), digits = 2)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	33.84	0.43	79.33	0.00
site2	6.34	0.71	8.90	0.00
site3	5.00	0.98	5.09	0.00
site4	0.53	0.99	0.54	0.59
site5	4.37	0.94	4.64	0.00
site6	4.76	1.17	4.07	0.00
site7	-0.74	1.85	-0.40	0.69
site8	-0.68	2.48	-0.28	0.78
site9	9.17	3.02	3.04	0.00
site10	-0.58	3.80	-0.15	0.88

Estimated tree heights for each site

```
summary(allEffects(m3))
```

model: height ~ site

site effect

site

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

Lower 95 Percent Confidence Limits

site

	1	2	3	4	5	6	7	8
33.00444	39.06264	37.10317	32.62733	36.56463	36.46190	29.56629	28.37367	
9	10							
37.15251	25.84764							

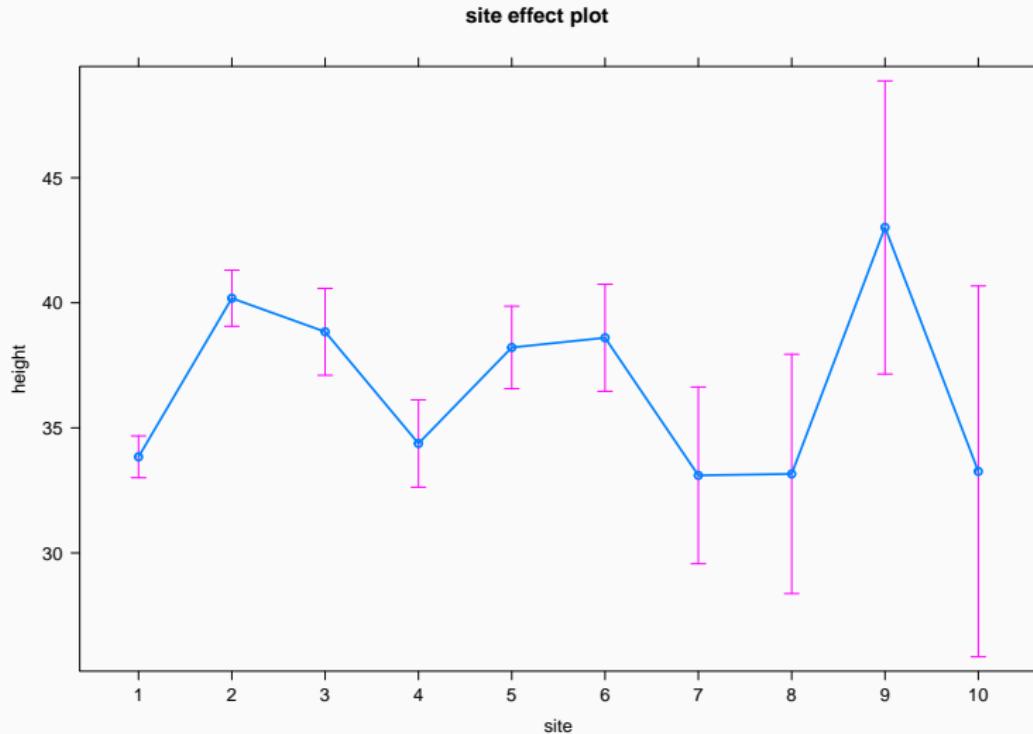
Upper 95 Percent Confidence Limits

site

	1	2	3	4	5	6	7	8
34.67872	41.30265	40.57814	36.12156	39.86309	40.74143	36.63371	37.94299	
9	10							
48.87249	40.67236							

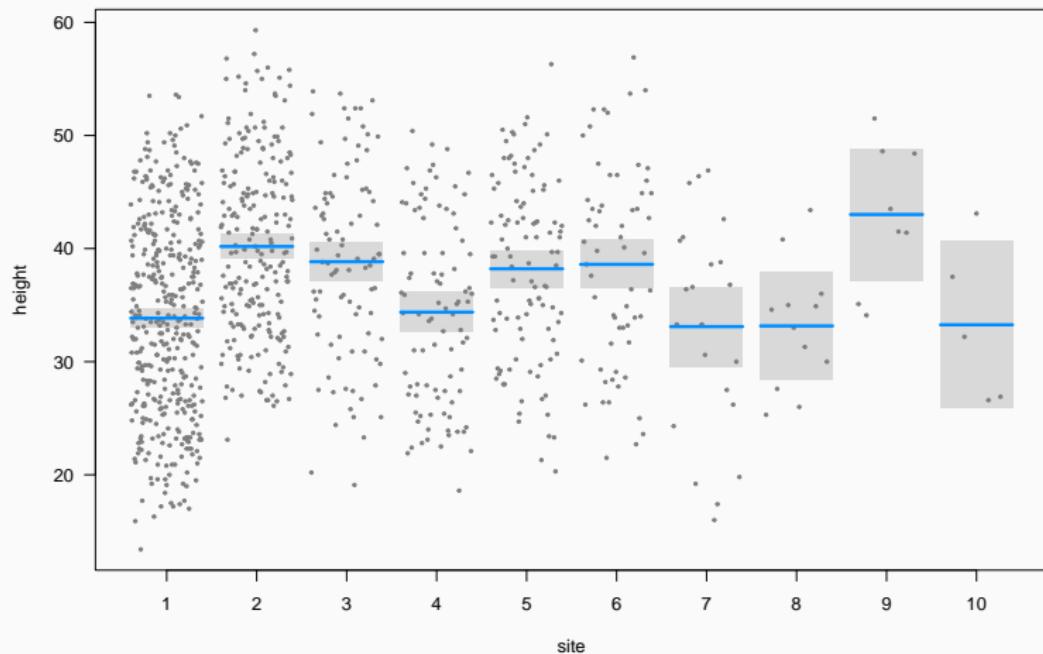
Plot

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



Plot (visreg)

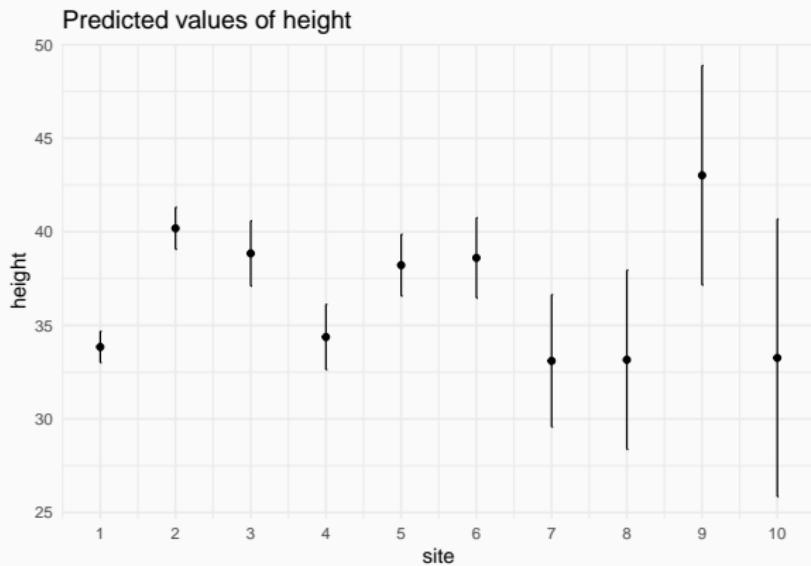
```
visreg(m3)
```



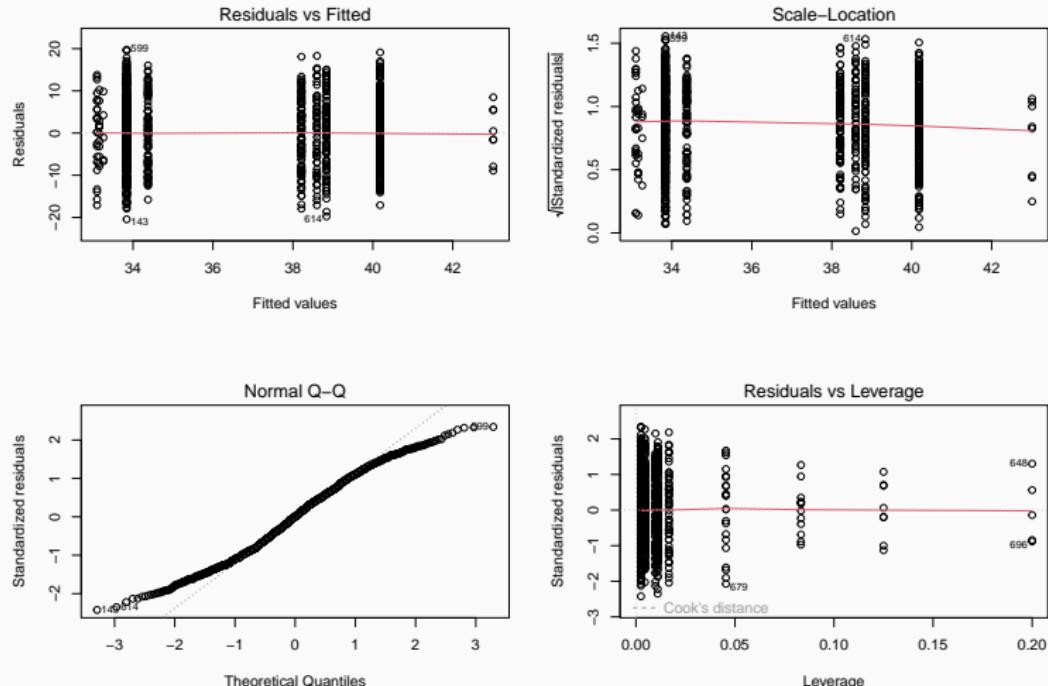
Plot model (sjPlot)

```
plot_model(m3, type = "eff")
```

\$site

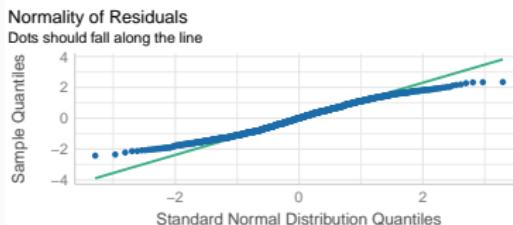
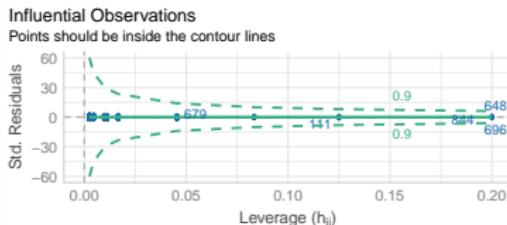
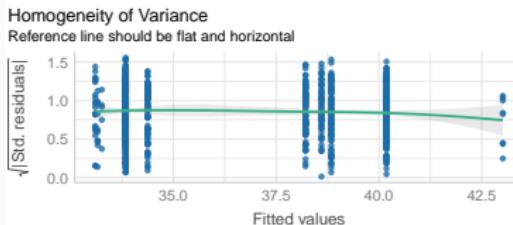
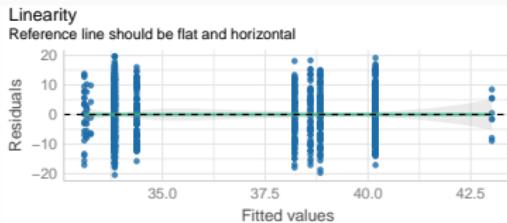
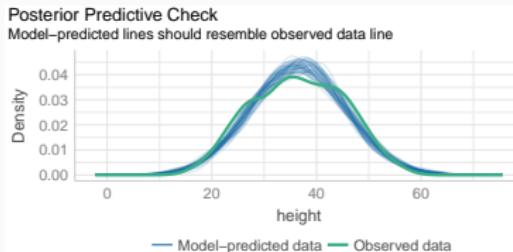


Model checking: residuals



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

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + \dots + k \cdot DBH_i + \varepsilon_i$$
$$\varepsilon_i \sim N(0, \sigma^2)$$

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 .
	'	'	'	'

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
<hr/>					
(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

```
summary(allEffects(m4))
```

model: height ~ site + dbh

site effect

site

	1	2	3	4	5	6	7	8
33.90437	40.40868	38.26183	35.83902	37.54181	38.10889	33.72818	28.59173	
9	10							
39.34142	36.16771							

Lower 95 Percent Confidence Limits

site

	1	2	3	4	5	6	7	8
33.60276	40.00512	37.63569	35.20858	36.94739	37.33787	32.45495	26.86438	
9	10							
37.22831	33.49623							

Upper 95 Percent Confidence Limits

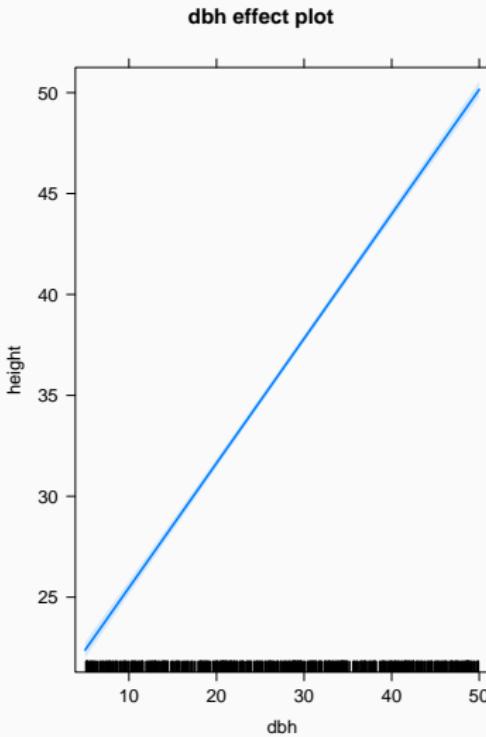
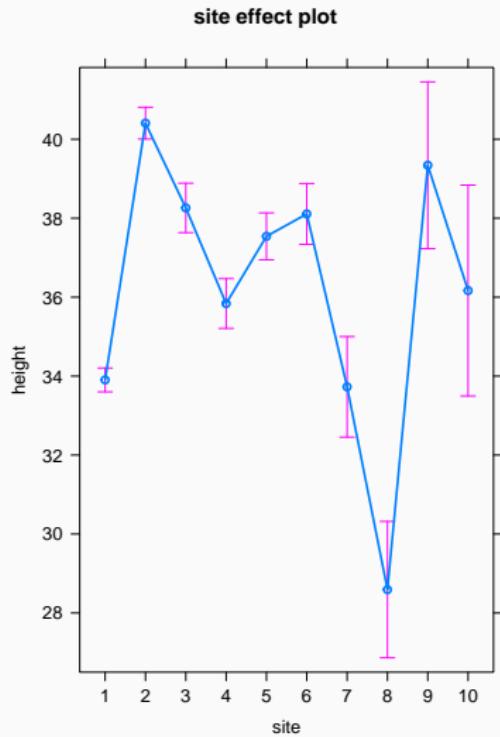
site

	1	2	3	4	5	6	7	8
34.20599	40.81223	38.88798	36.46947	38.13622	38.87990	35.00141	30.31907	
9	10							
41.45454	38.83919							

dbh effect

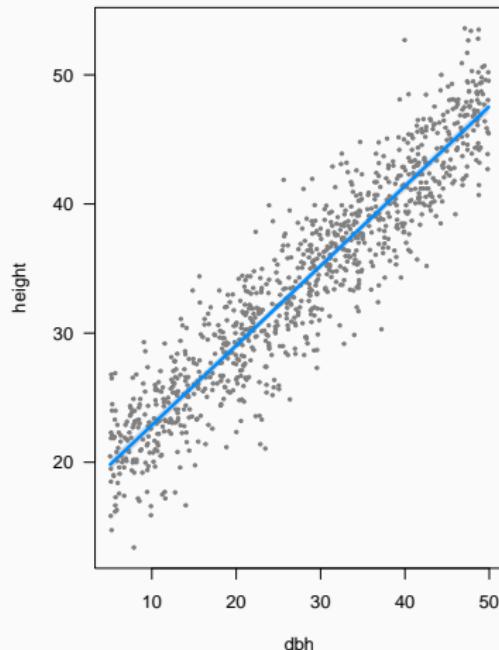
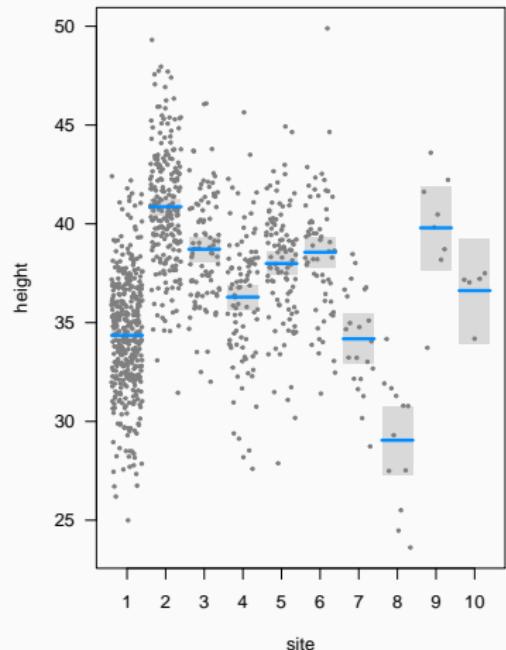
Plot

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



Plot (visreg)

```
visreg(m4)
```

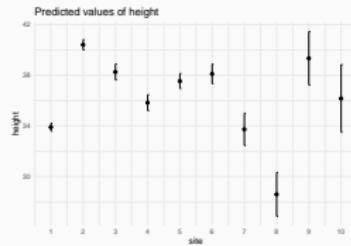


null device

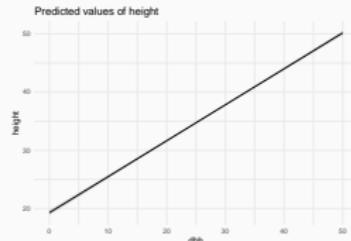
Plot model (sjPlot)

```
plot_model(m4, type = "eff")
```

\$site

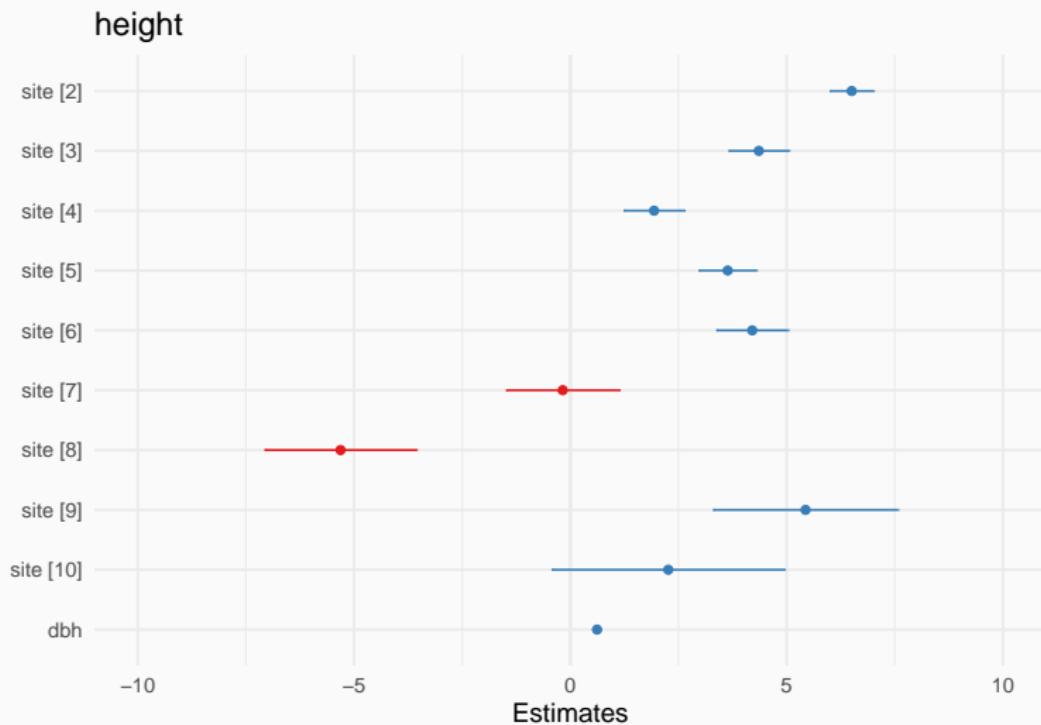


\$dbh



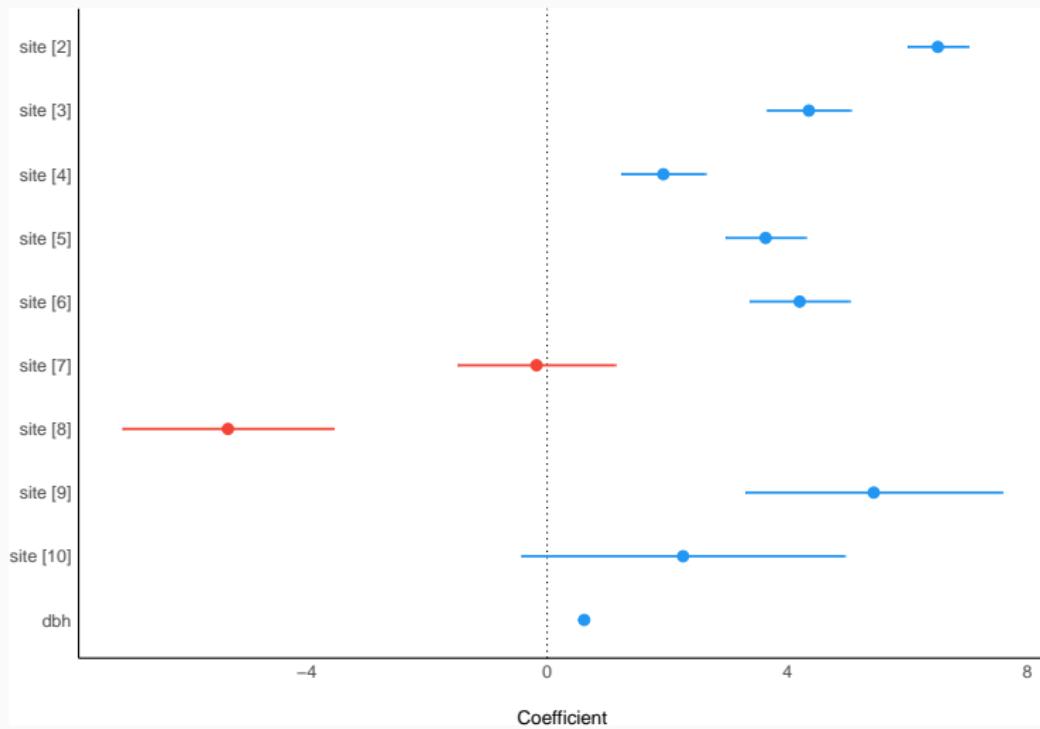
Plot model (sjPlot)

```
plot_model(m4, type = "est")
```

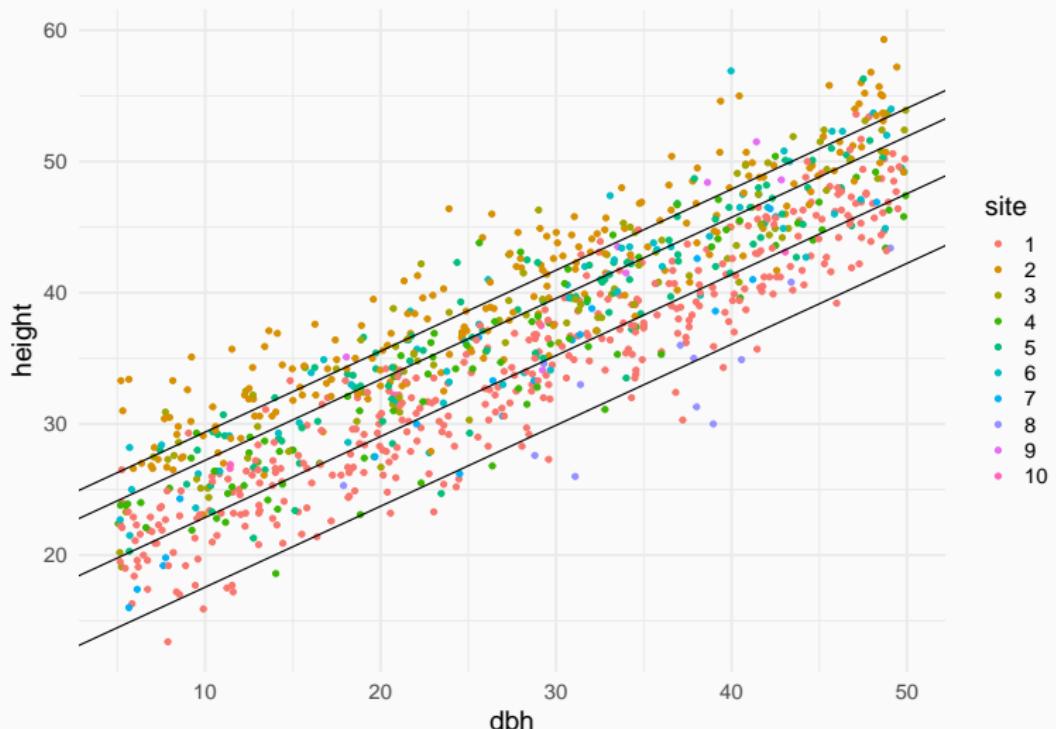


Plot model (see)

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



We have fitted model w/ many intercepts and single slope



Slope is the same for all sites

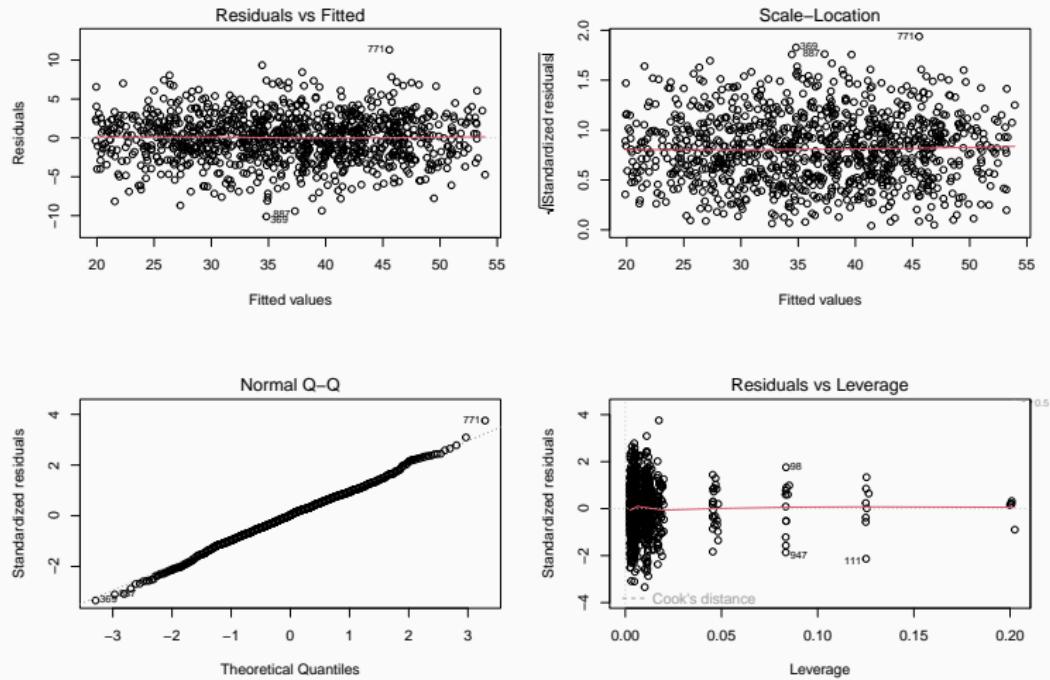
```
estimate_slopes(m4)
```

Estimated Marginal Effects

Coefficient	SE	95% CI	t(989)	p
<hr/>				
0.62	7.57e-03	[0.60, 0.63]	81.47	< .001

Marginal effects estimated for dbh

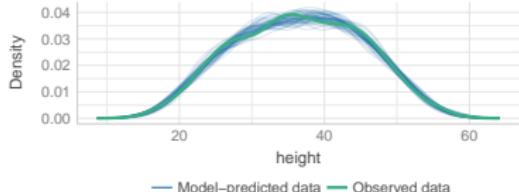
Model checking: residuals



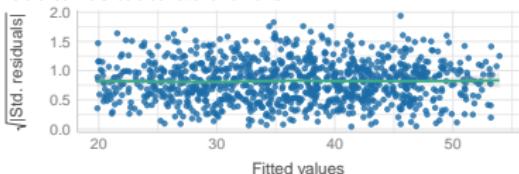
Model checking: residuals

```
check_model(m4)
```

Posterior Predictive Check
Model-predicted lines should resemble observed data line



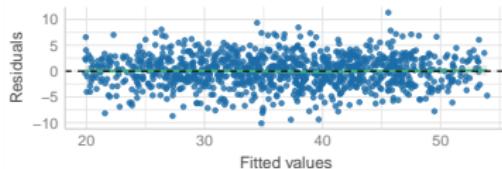
Homogeneity of Variance
Reference line should be flat and horizontal



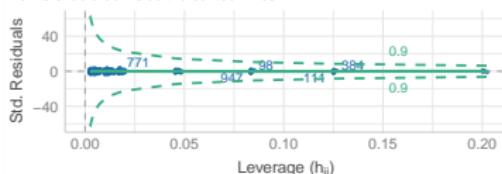
Collinearity
High collinearity (VIF) may inflate parameter uncertainty



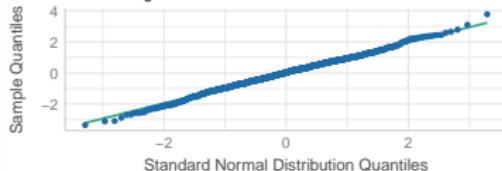
Linearity
Reference line should be flat and horizontal



Influential Observations
Points should be inside the contour lines

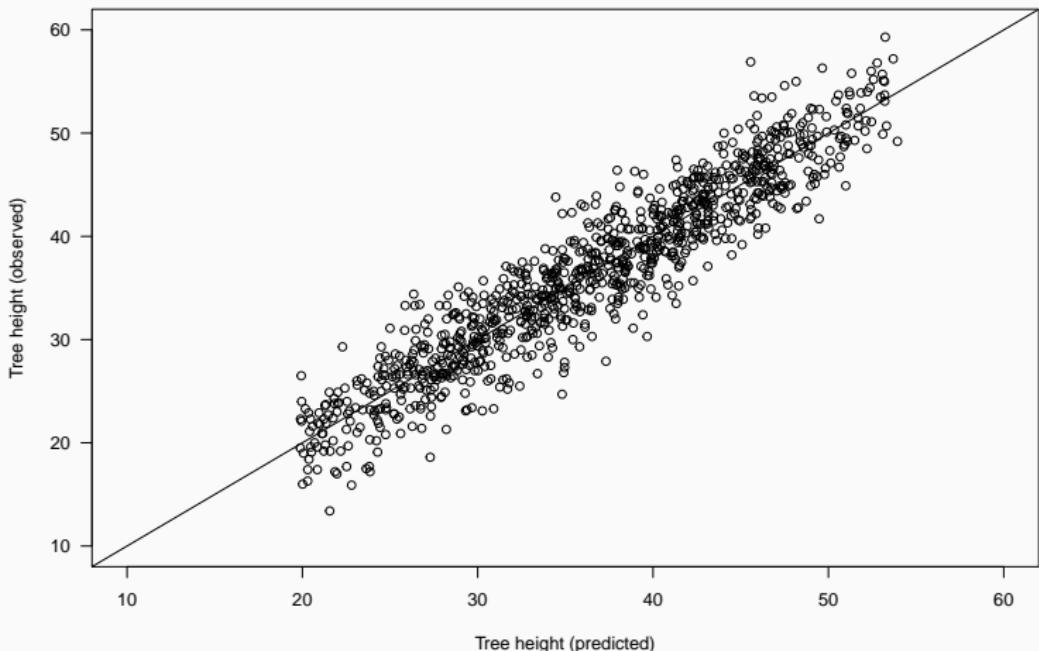


Normality of Residuals
Dots should fall along the line



How good is this model? Calibration plot

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



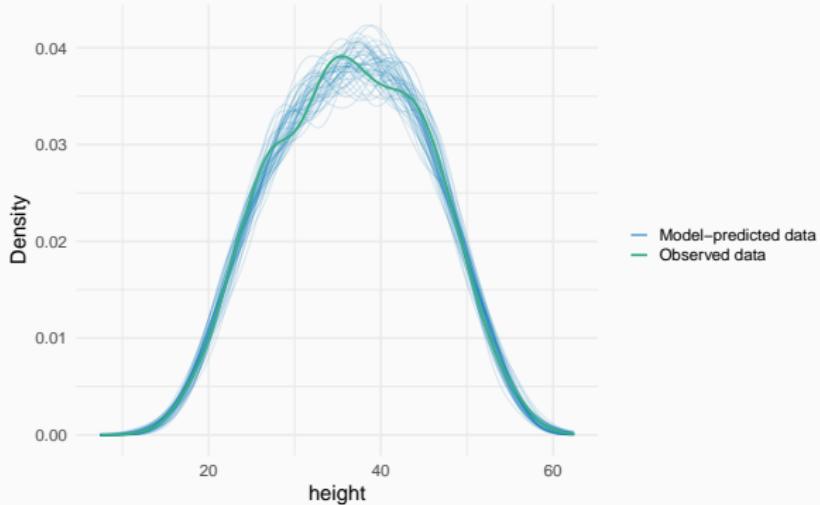
Posterior predictive checking

Simulating response data from fitted model (y_{rep})

and comparing with observed response (y)

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

Posterior Predictive Check
Model-predicted lines should resemble observed data line



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[,10], 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[,10], 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

Q: 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							

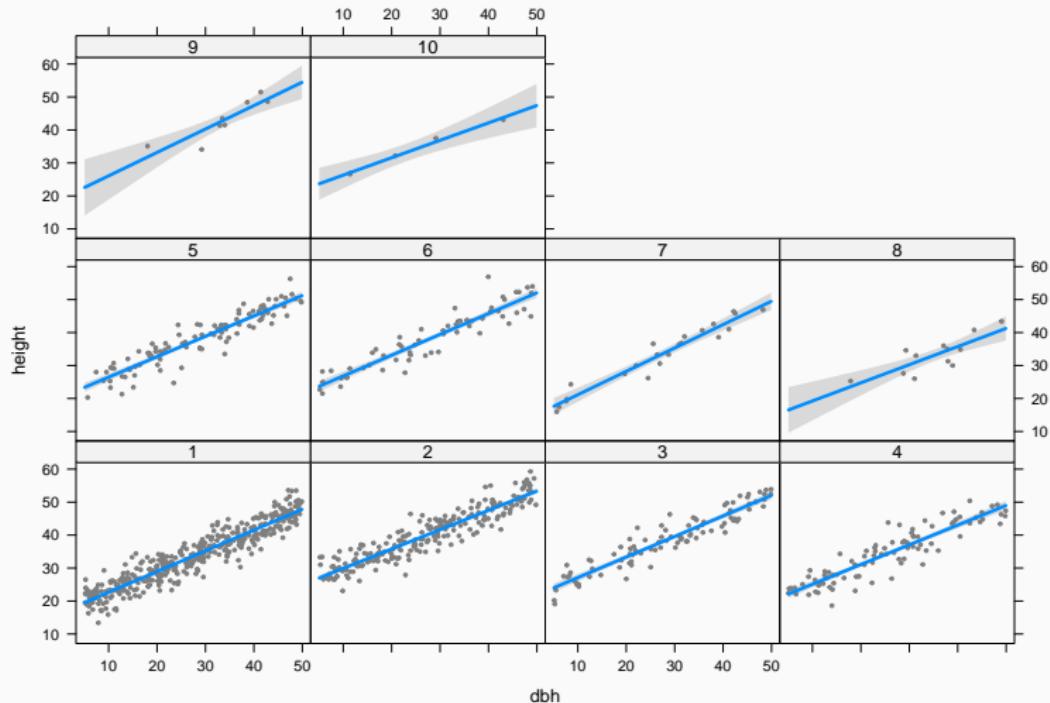
Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

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")
```



Examining fitted model with {modelStudio}

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

Extra exercises

- [paperplanes](#): How does flight distance differ with age, gender or paper type?

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- [mammal sleep](#): Are sleep patterns related to diet?

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Extra exercises

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- [racing pigeons](#): is speed related to sex?

Variable and model selection

Francisco Rodríguez-Sánchez

<https://frodriguezsanchez.net>

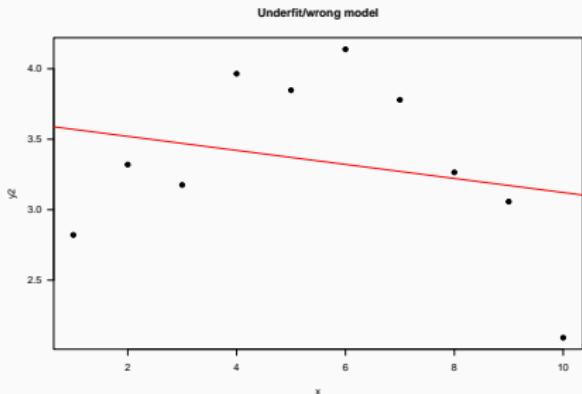
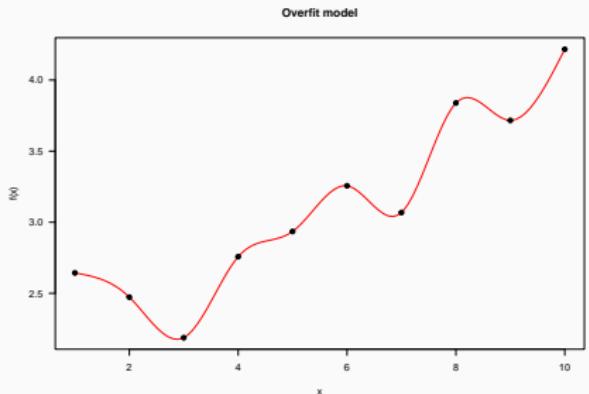
Overfitting and balanced model complexity

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

Overfitting and balanced model complexity

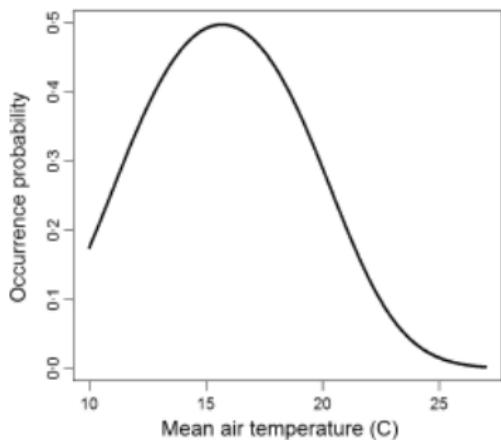
- On one hand, we want to **maximise fit**.
- On the other hand, we want to **avoid overfitting** and overly complex models.

Overfitting and balanced model complexity

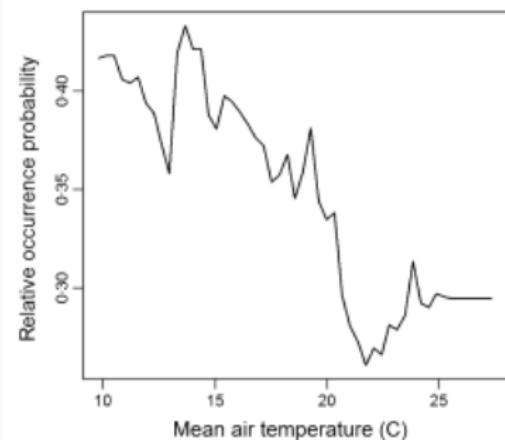


Overfitting and balanced model complexity

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:

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Evaluating models' predictive accuracy

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- All these methods have flaws!

AIC (Akaike Information Criteria)

$$AIC = -2 * \text{LogLikelihood} + 2K$$

- First term: model fit

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- 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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- 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

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 - Or combine 2 or more in a synthetic variable (e.g. water deficit ~ Temp + Precip).
 - Many methods available, e.g. sequential, ridge regression...
 - Measurement error can seriously complicate things (Biggs et al 2009; Freckleton 2011)

Choosing predictors

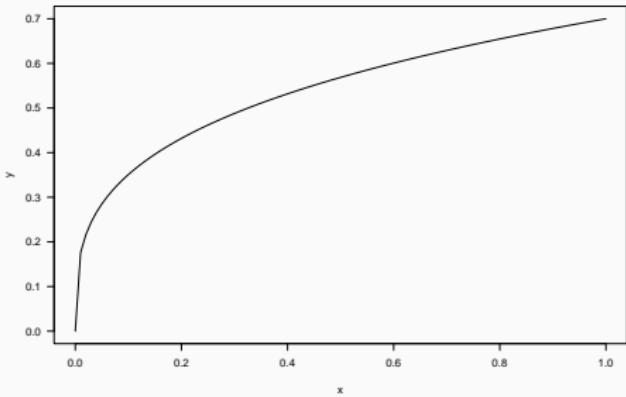
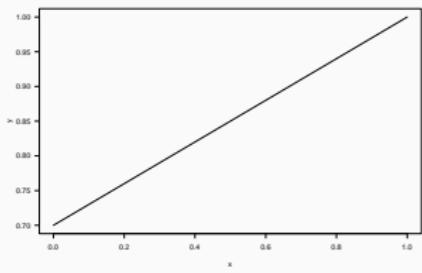
- Choose variables based on **background knowledge**, rather than throwing plenty of them in a fishing expedition.
- Propose single global model or small set (< 10 - 20) of **reasonable** candidate models.
- Number of variables **balanced with sample size** (e.g. at least 10 - 30 obs per param)
- Assess collinearity between predictors ([Dormann et al 2013](#))
 - If $|r| > 0.5 - 0.7$, consider leaving one variable out, but keep it in mind when interpreting model results.
 - Or combine 2 or more in a synthetic variable (e.g. water deficit ~ Temp + Precip).
 - Many methods available, e.g. sequential, ridge regression...
 - Measurement error can seriously complicate things (Biggs et al 2009; Freckleton 2011)
- For predictors with large effects, **consider interactions**.

Think about the shape of relationships

$$y \sim x + z$$

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

Think about shape of relationship.



Removing predictors

Stepwise regression has many problems

- Whittingham et al. (2006) Why do we still use stepwise modelling in ecology and behaviour? *J. Animal Ecology*.

Stepwise regression has many problems

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- Mundry & Nunn (2009) Stepwise Model Fitting and Statistical Inference: Turning Noise into Signal Pollution. *Am Nat.*

Stepwise regression has many problems

- Whittingham et al. (2006) Why do we still use stepwise modelling in ecology and behaviour? *J. Animal Ecology*.
- Mundry & Nunn (2009) Stepwise Model Fitting and Statistical Inference: Turning Noise into Signal Pollution. *Am Nat.*
- 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

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)

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

Summary

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 - Beware collinearity

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 - Keep good n/p ratio

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 - Consider interactions for strong main effects
3. If > 1 model have similar support, consider model averaging (or blending).
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

```
library("performance")
compare_performance(m1, m2, m3, m4)
```

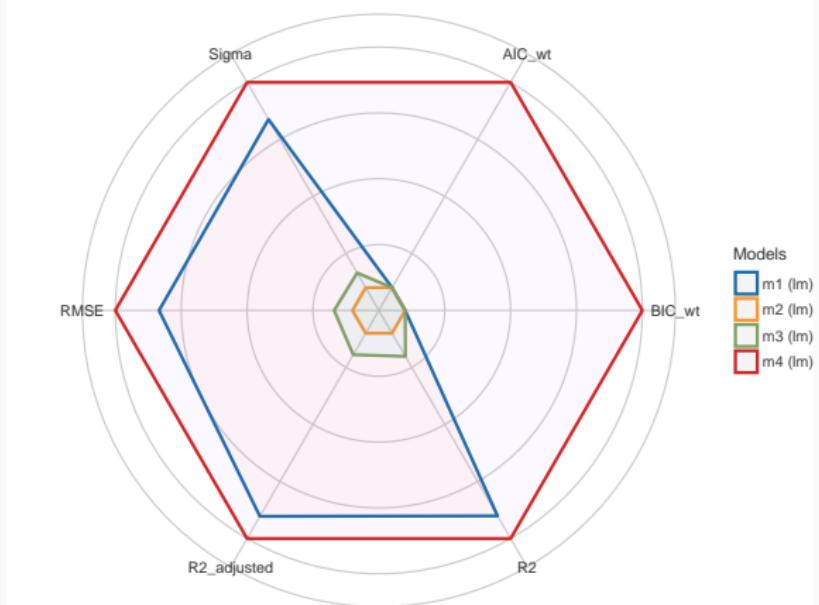
```
# Comparison of Model Performance Indices
```

Name	Model	AIC	AIC weights	BIC	BIC weights	R2	R2 (adj.)
<hr/>							
m1	lm	5660.250	8.39e-126	5674.973	1.28e-106	0.787	0.787
m2	lm	7206.145	0.00e+00	7220.868	0.00e+00	0.002	0.001
m3	lm	7117.264	0.00e+00	7171.250	0.00e+00	0.102	0.093
m4	lm	5084.253	1.00	5187.316	1.00	0.885	0.882

Compare model performance

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

Comparison of Model Indices



Compare parameters

```
library("parameters")
compare_parameters(m1, m2, m3, m4)
```

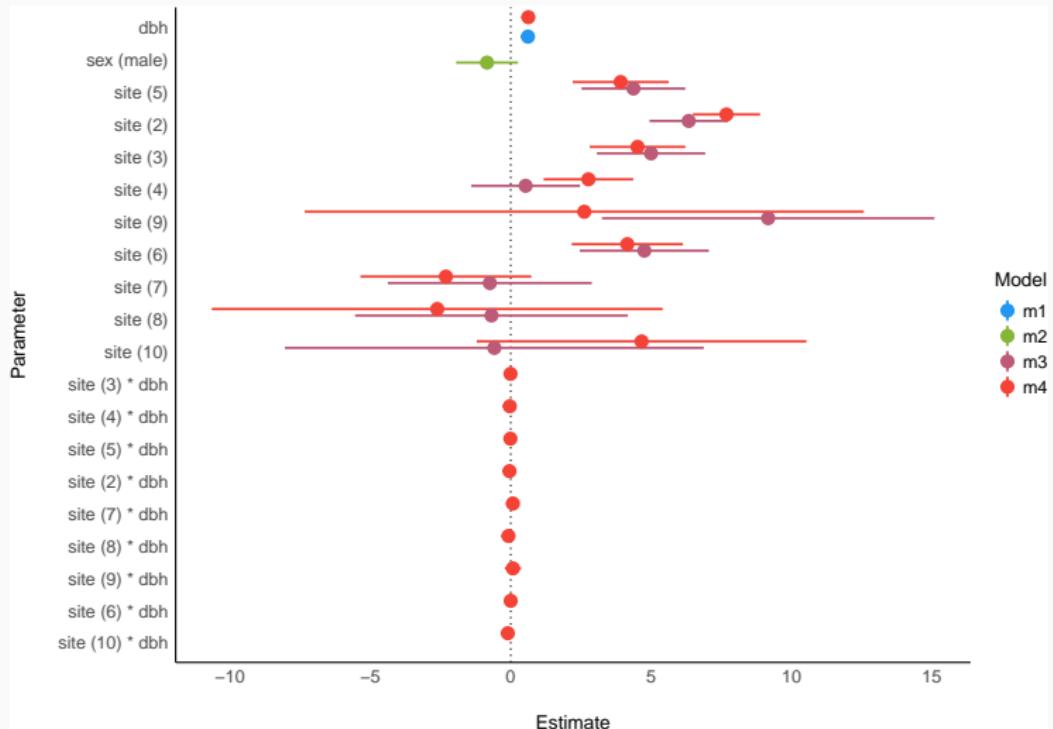
Parameter	m1	m2	m3	m4

(Intercept)	19.34 (18.73, 19.95)	36.93 (36.15, 37.71)	33.84 (33.00, 34.68)	16.36 (15.65, 17.07)
dbh	0.62 (0.60, 0.64)			0.63 (0.61, 0.65)
sex (male)		-0.84 (-1.94, 0.26)		
site (5)			4.37 (2.52, 6.22)	3.92 (2.21, 5.63)
site (2)			6.34 (4.94, 7.74)	7.68 (6.49, 8.88)
site (3)			5.00 (3.87, 6.93)	4.52 (2.82, 6.22)
site (4)			0.53 (-1.40, 2.47)	2.77 (1.17, 4.37)
site (9)			9.17 (3.25, 15.09)	2.62 (-7.34, 12.58)
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 (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)
site (5) * dbh				-0.01 (-0.06, 0.04)
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 (9) * dbh				0.08 (-0.21, 0.37)
site (6) * dbh				1.34e-03 (-0.06, 0.06)
site (10) * dbh				-0.10 (-0.33, 0.12)

Observations	1000	1000	1000	1000

Compare parameters

```
library("parameters")
plot(compare_parameters(m1, m2, m3, m4))
```



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).

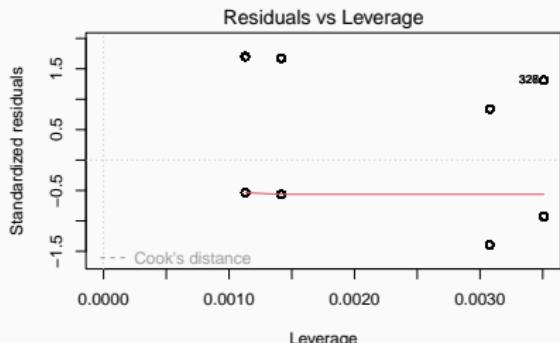
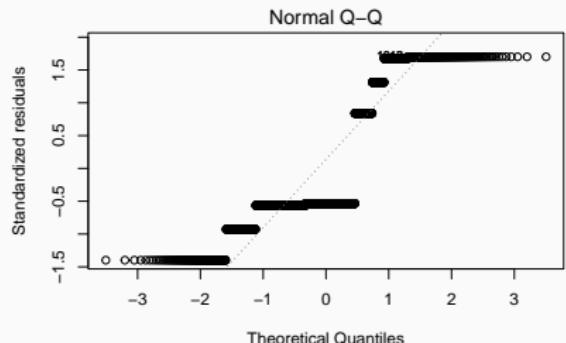
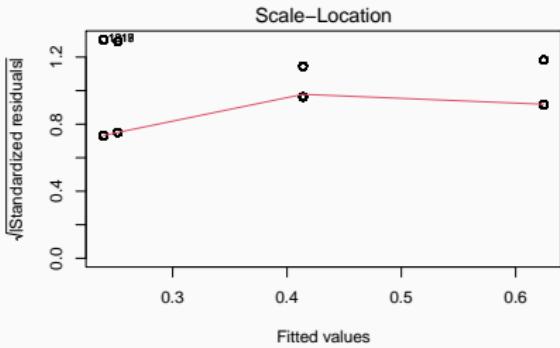
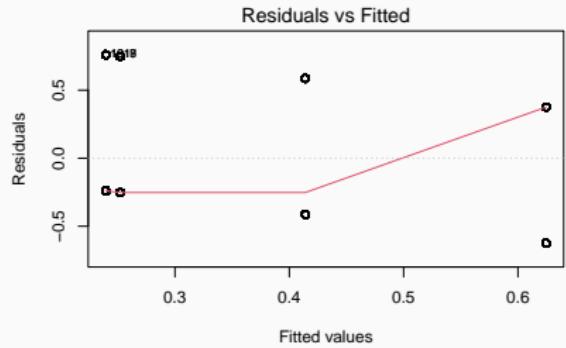
```
class    age   sex survived
1 first  adult male      1
2 first  adult male      1
3 first  adult male      1
4 first  adult male      1
5 first  adult male      1
6 first  adult male      1
```

Quiz: Did passenger class influence survival?

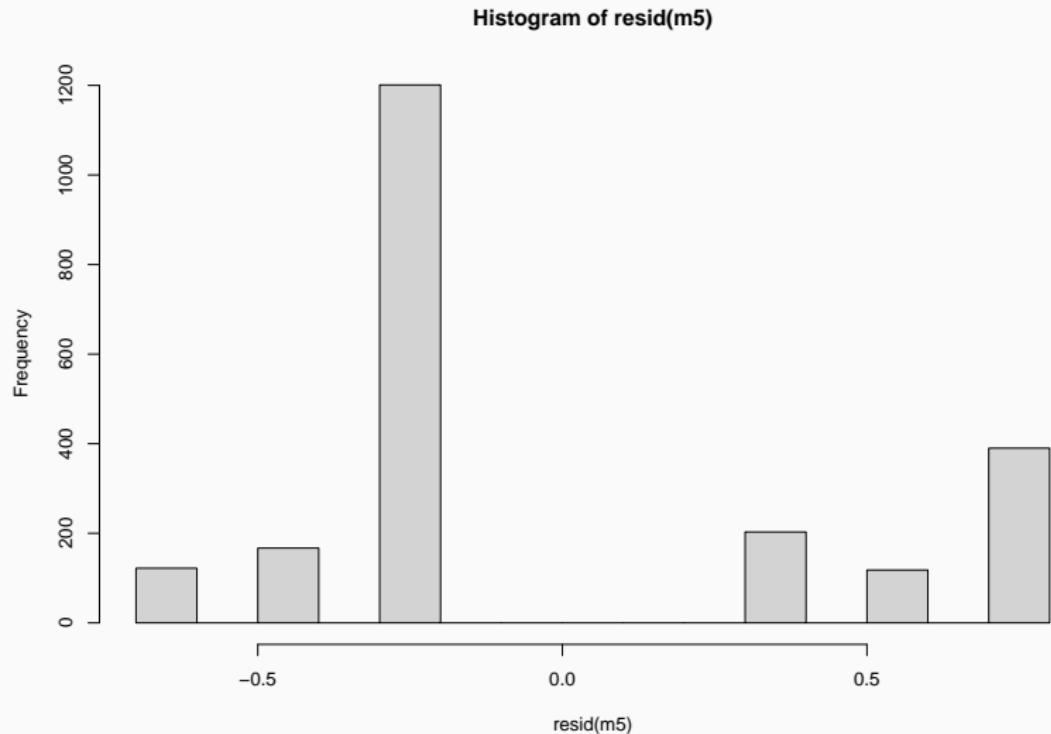
<https://pollev.com/franciscorod726>

Let's check linear model:

```
m5 <- lm(survived ~ class, data = titanic)
```



Weird residuals!



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
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Generalised Linear Models

1. Response variable - distribution family

- Bernouilli - Binomial
- Poisson
- Gamma
- etc

Generalised Linear Models

1. Response variable - distribution family

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- etc

2. Predictors (continuous or categorical)

Generalised Linear Models

1. Response variable - distribution family

- Bernouilli - Binomial
- Poisson
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- etc

2. Predictors (continuous or categorical)

3. Link function

Generalised Linear Models

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- Gaussian: identity

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Generalised Linear Models

1. Response variable - distribution family

- Bernouilli - Binomial
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- etc

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- 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

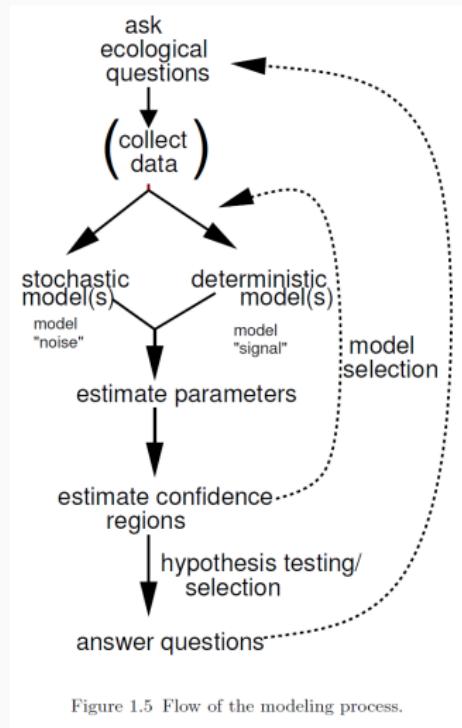


Figure 1.5 Flow of the modeling process.

Bernoulli - 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**)

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

Then

$$\begin{aligned}\text{logit}(P(\text{alive})) &= a + bx \\ P(\text{alive}) &= \text{invlogit}(a + bx) = \frac{e^{a+bx}}{1 + e^{a+bx}}\end{aligned}$$

Where is the variance?

In a Gaussian GLM

$$y \sim \text{Normal}(\mu, \sigma)$$

In a Binomial GLM

$$y \sim \text{Binomial}(n, p)$$

n = number of trials

p = probability of success

$$\text{Var}(y) = np(1 - p)$$

(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

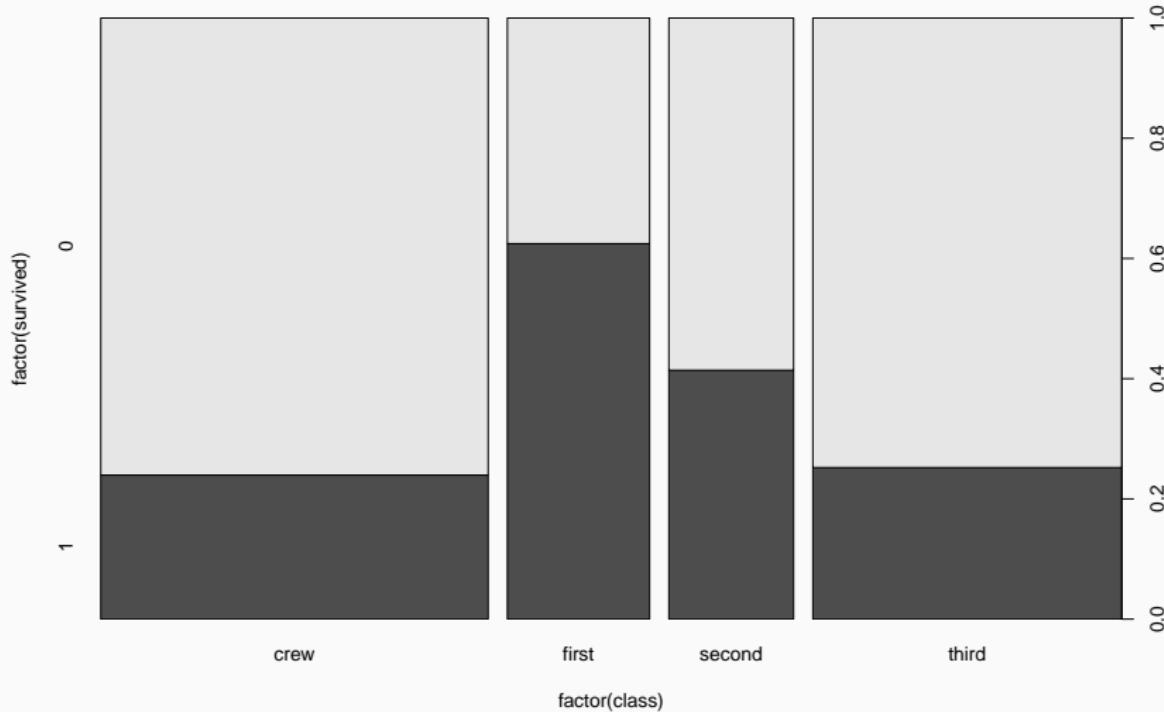
How many survived in each class? (*dplyr*)

```
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
```

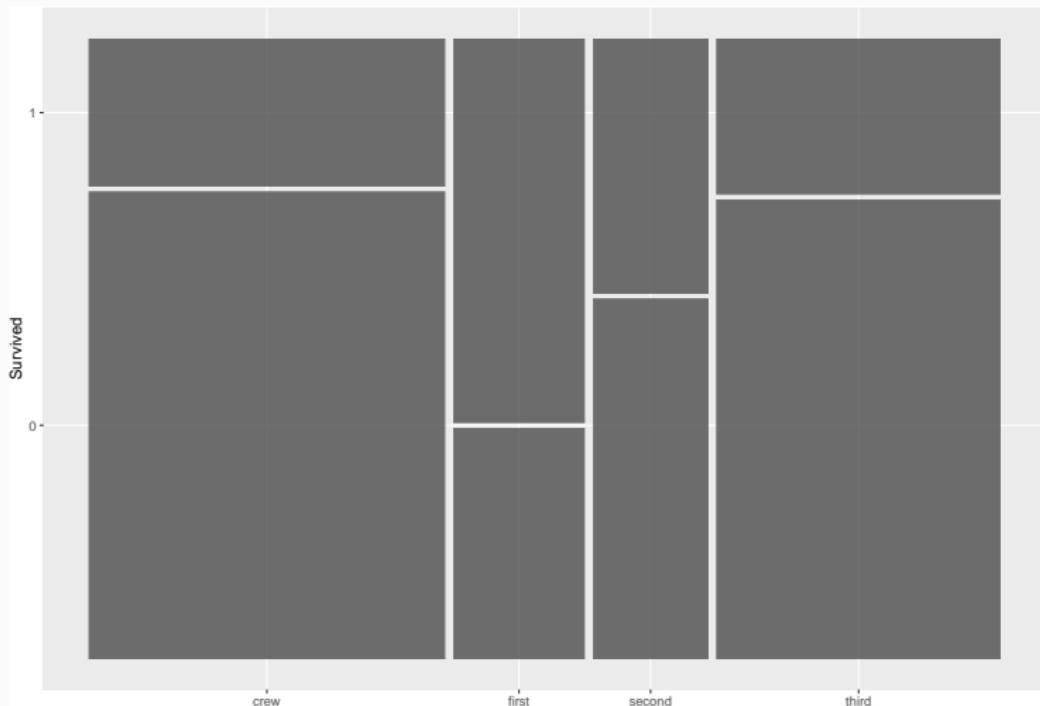
Data visualisation (mosaic plot)

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



Mosaic plots (ggplot2)

```
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

$$\text{logit}(P(\text{survival})_i) = a + b \cdot \text{class}_i$$

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

Interpreting binomial GLM

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

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.3999	-0.7623	-0.7401	0.9702	1.6906

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 ***
classesecond	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: `effects`, `modelbased`, etc.

Interpreting logistic regression output (effects pkg)

```
library("effects")
allEffects(tit.glm)
```

model: survived ~ class

```
class effect
class
    crew      first     second     third
0.2395480 0.6246154 0.4140351 0.2521246
```

Interpreting logistic regression output (effects pkg)

Including confidence intervals:

```
summary(allEffects(tit.glm))
```

```
model: survived ~ class

class effect
class
  crew      first     second     third
0.2395480 0.6246154 0.4140351 0.2521246

Lower 95 Percent Confidence Limits
class
  crew      first     second     third
0.2125668 0.5706887 0.3582390 0.2214588

Upper 95 Percent Confidence Limits
class
  crew      first     second     third
0.2687850 0.6756185 0.4721282 0.2854798
```

Interpreting logistic regression output (easystats)

```
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)

```
library("easystats")    # 'modelbased' pkg  
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		0.938

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)
```

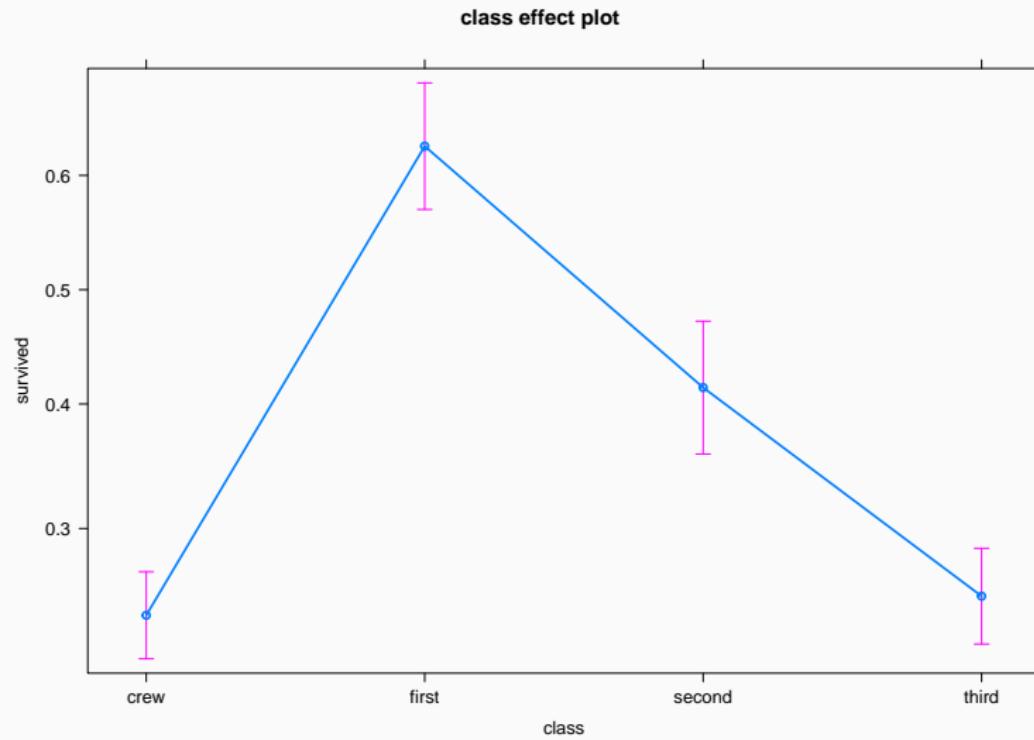
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.16	0.08	-14.67	0.00
classfirst	1.66	0.14	11.97	0.00
classesecond	0.81	0.14	5.62	0.00
classthird	0.07	0.12	0.58	0.56

Presenting model results

```
library("modelsummary")
modelsummary(tit.glm)
```

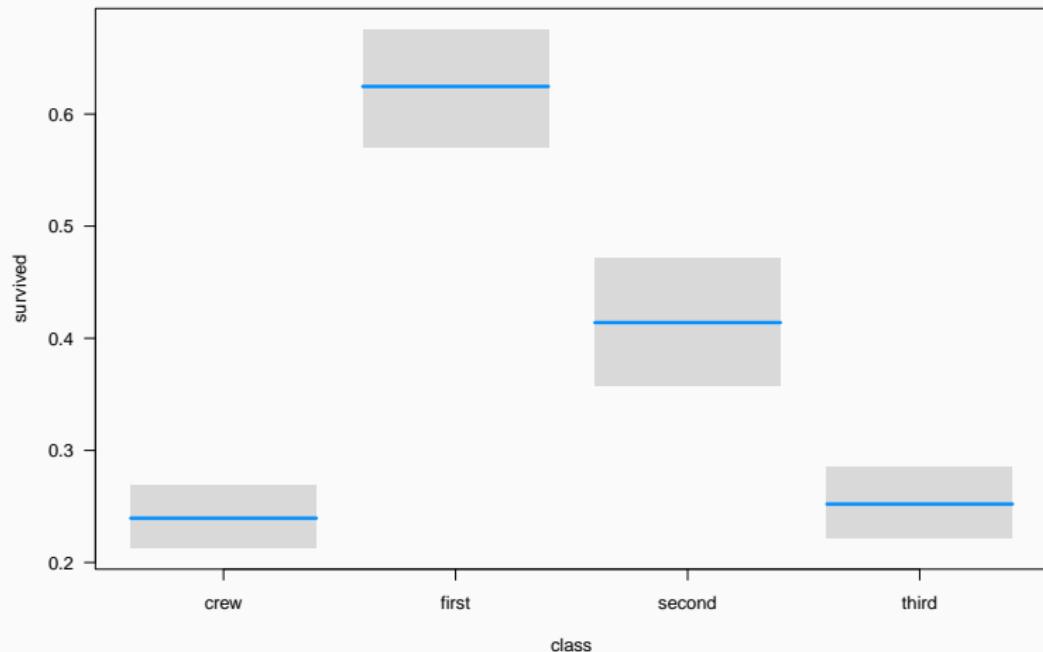
Visualising model: effects package

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



Visualising model: visreg package

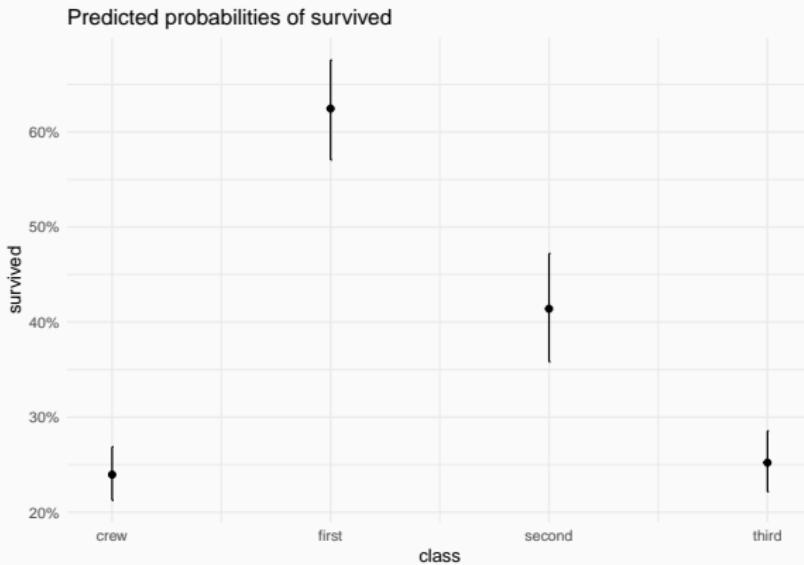
```
visreg(tit.glm, scale = "response", rug = FALSE)
```



Visualising model: sjPlot package

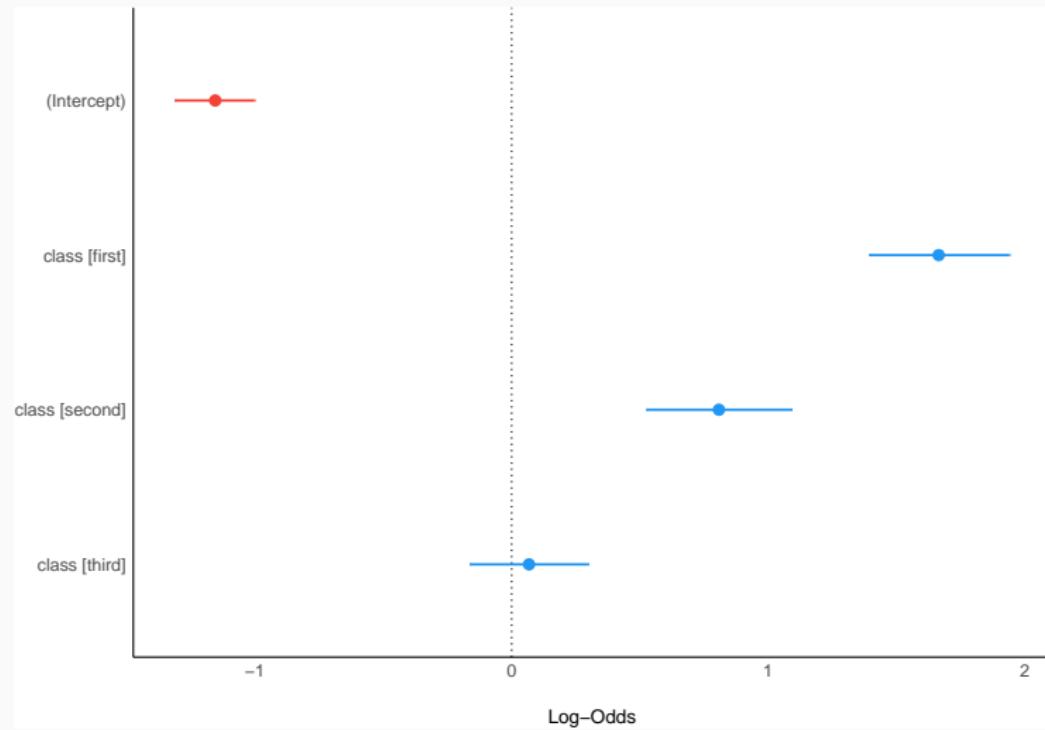
```
sjPlot::plot_model(tit.glm, type = "eff")
```

\$class



Visualising model: easystats (see package)

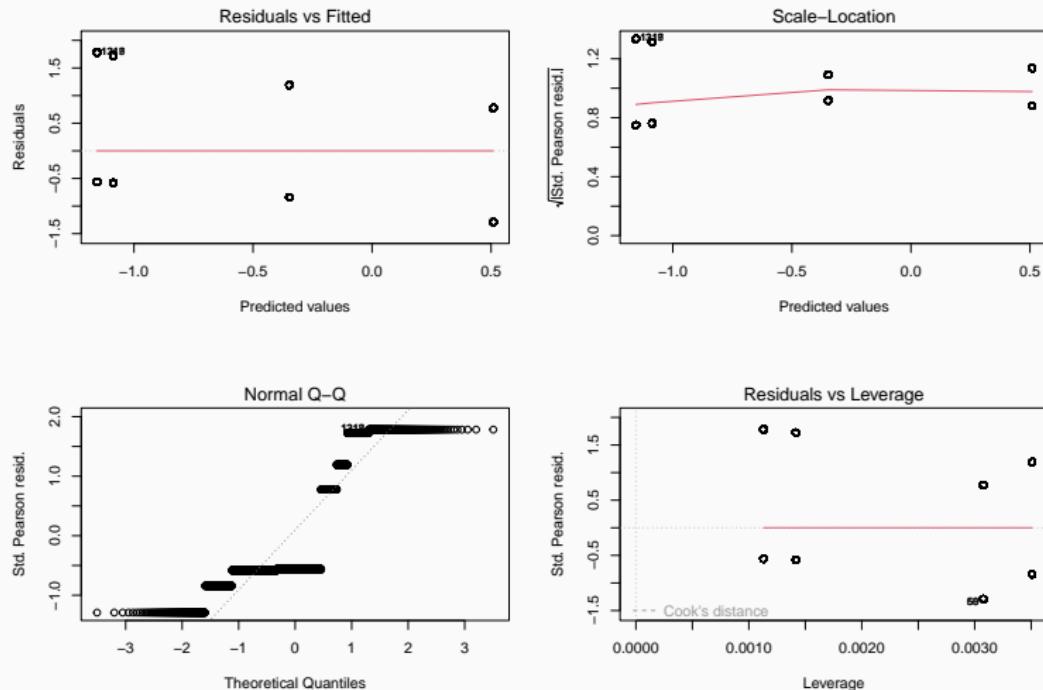
```
plot(parameters(tit.glm), show_intercept = TRUE)
```



Model checking

plot(model) not very useful with binomial GLM

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



```
null device
```

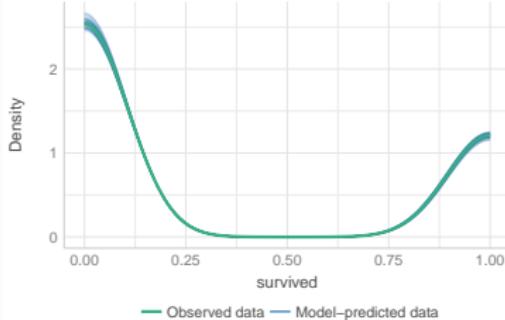
```
1
```

easystats::check_model

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

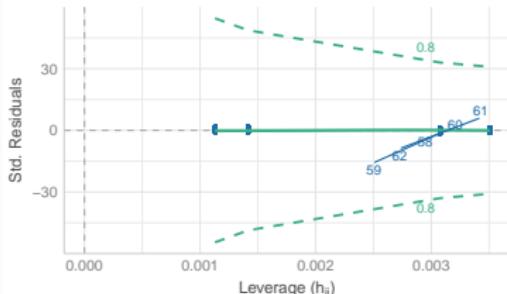
Posterior Predictive Check

Model-predicted lines should resemble observed data line



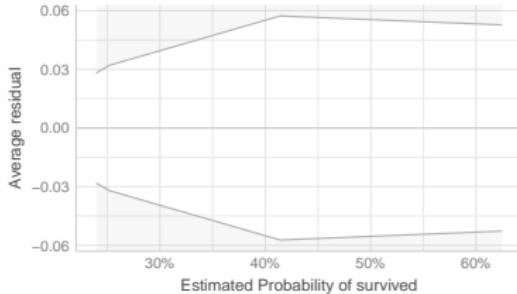
Influential Observations

Points should be inside the contour lines



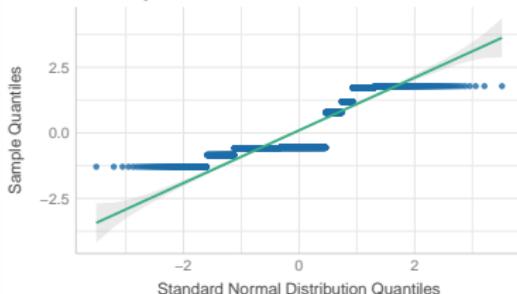
Binned Residuals

Points should be within error bounds



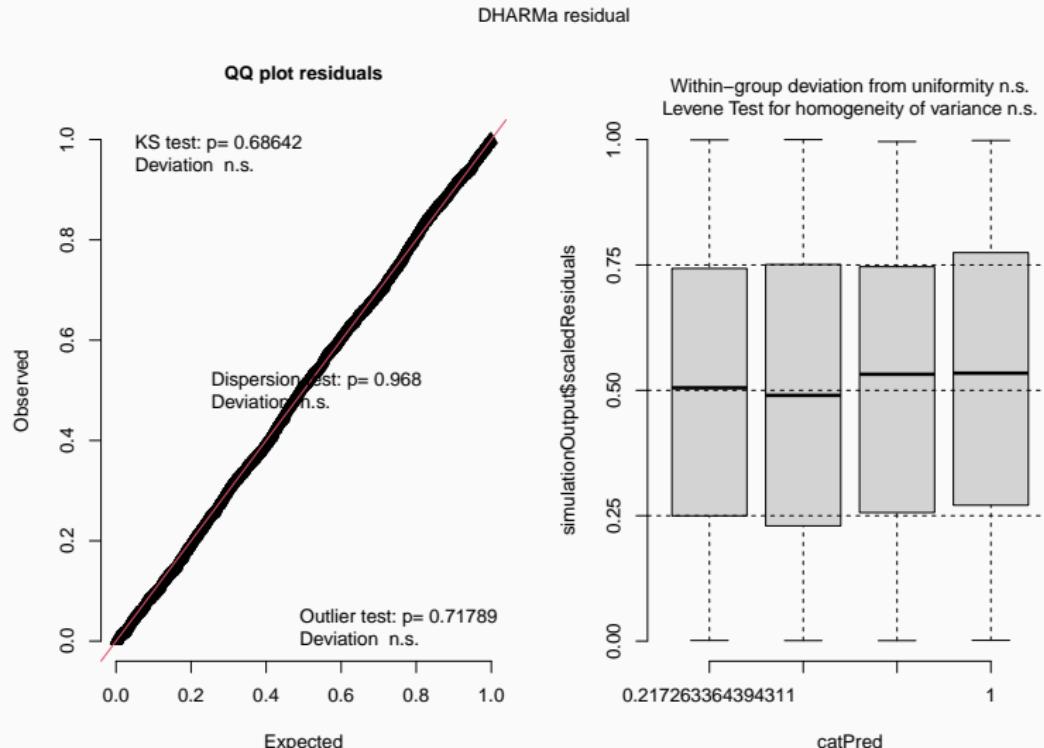
Normality of Residuals

Dots should fall along the line



Residual diagnostics with DHARMA

```
library("DHARMA")
simulateResiduals(tit.glm, plot = TRUE)
```

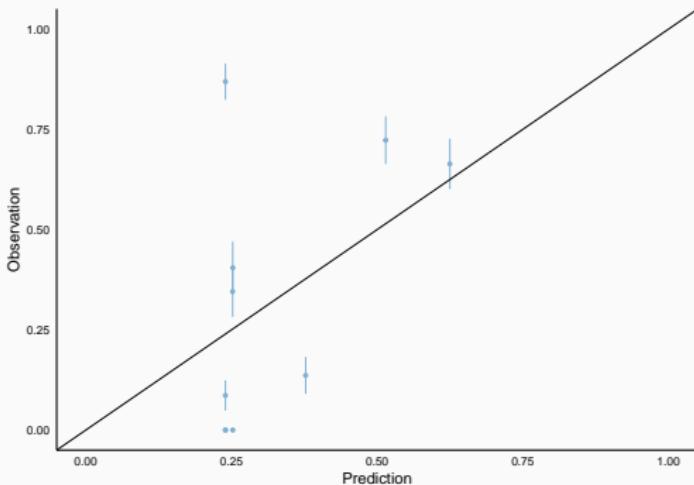


Calibration plot

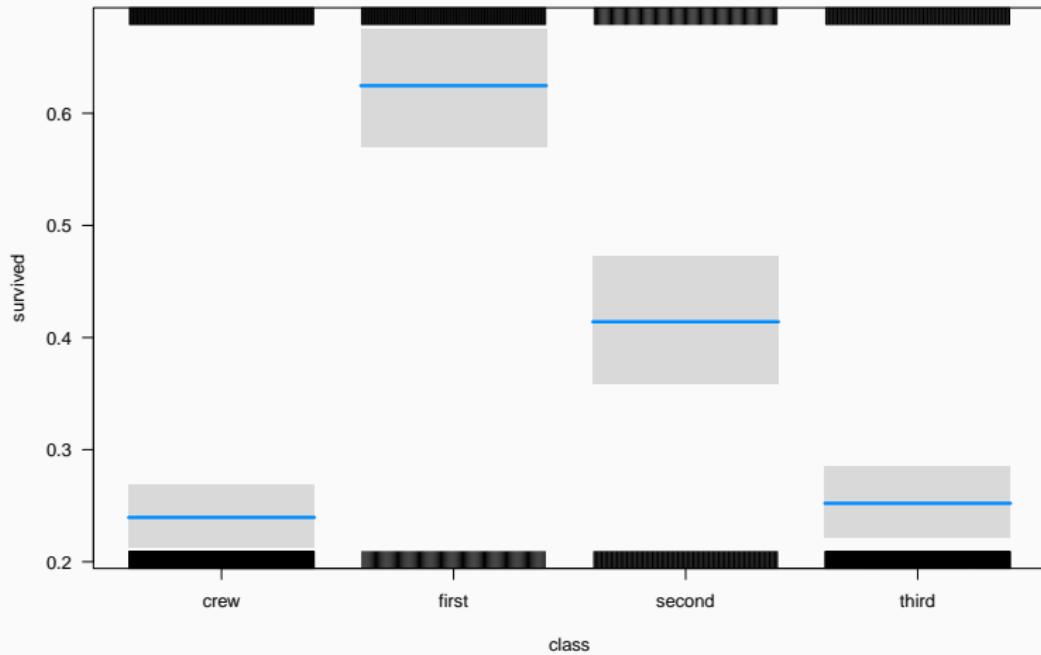
Compares predicted vs observed probabilities (grouped by quantiles)

```
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

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

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(e.g. `allEffects`, `estimate_means`)

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(e.g. `allEffects`, `estimate_means`)
5. Plot model: `plot(allEffects(model))`, `visreg`, `plot_model...`

Recapitulating

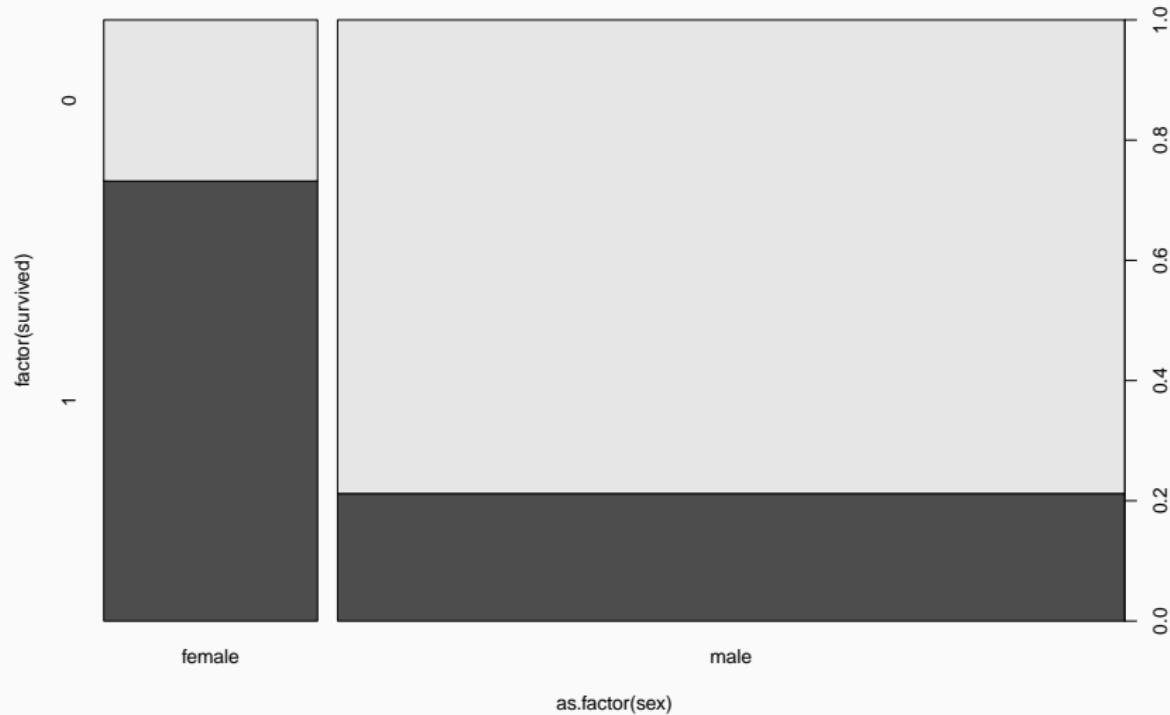
1. Visualise data
2. Fit model: `glm`. Don't forget to specify `family`!
3. Examine model: `summary`
4. Back-transform parameters from `logit` into probability scale
(e.g. `allEffects`, `estimate_means`)
5. Plot model: `plot(allEffects(model))`, `visreg`, `plot_model...`
6. Check model: `check_model`, `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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.6226	-0.6903	-0.6903	0.7901	1.7613

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

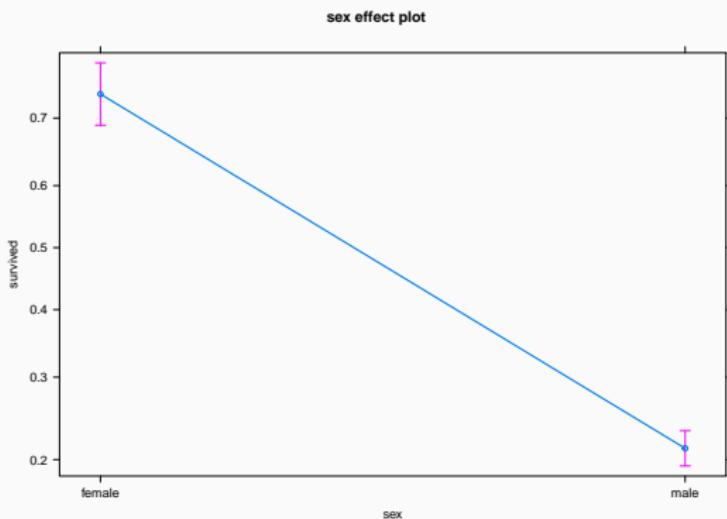
Model interpretation

```
model: survived ~ sex
```

```
sex effect
```

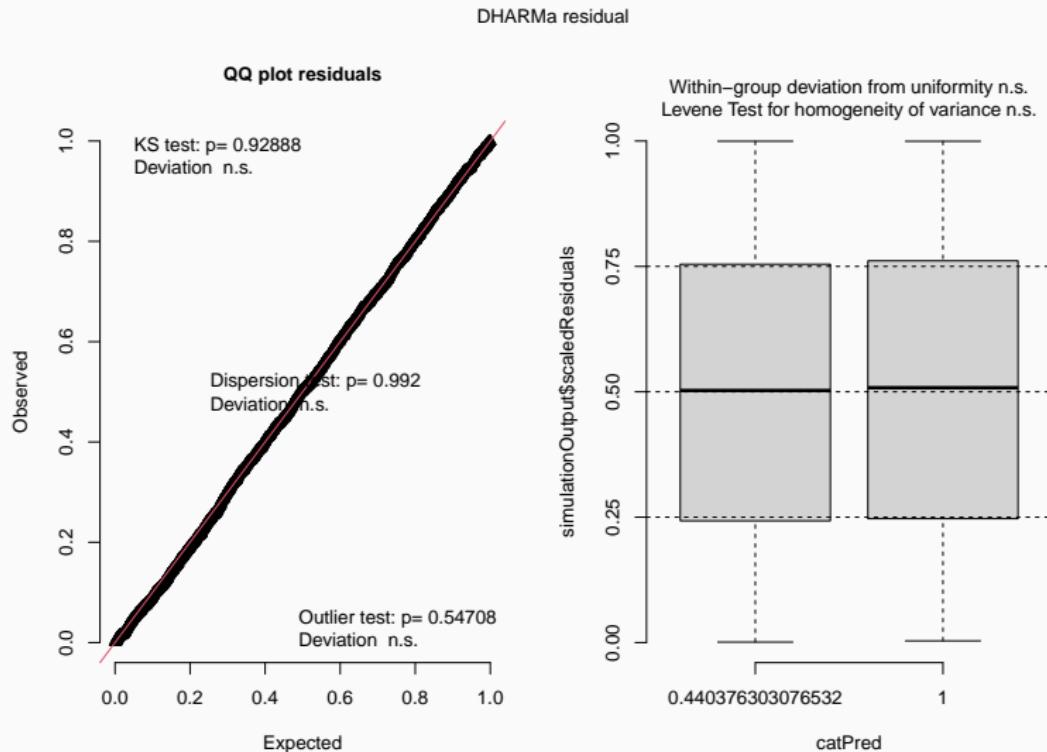
```
sex
```

female	male
0.7319149	0.2120162



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?



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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.0915	-0.7149	-0.5012	0.7297	2.0673

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 ***

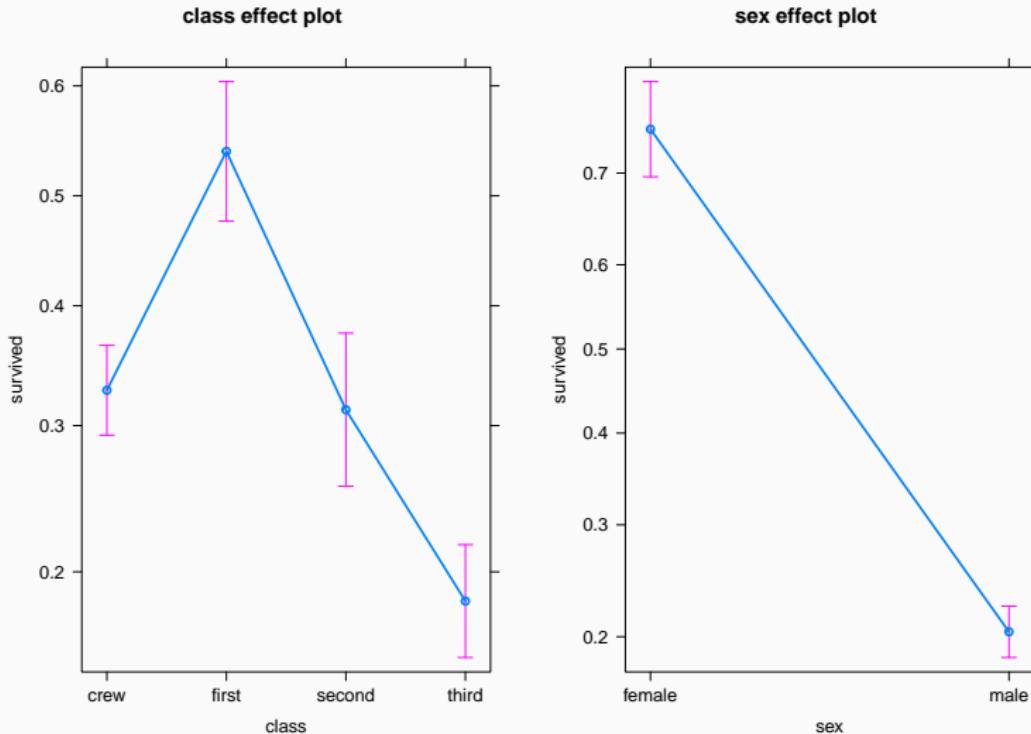
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(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

Plot additive model



Fit model with the interaction of both factors

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.6797	-0.7099	-0.6155	0.5115	1.9842

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)

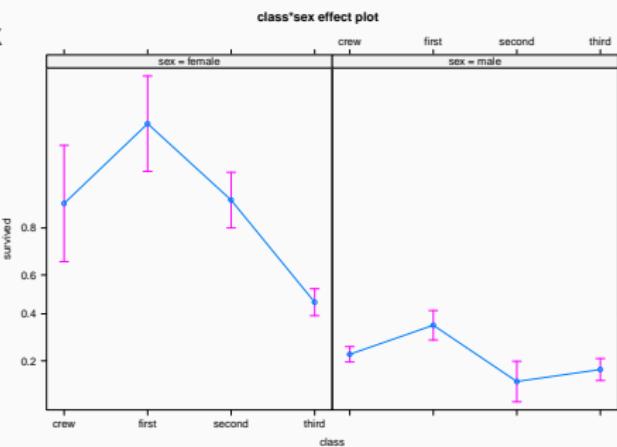
Women had higher survival than men, even within the same class

model: survived ~ class * sex

class*sex effect

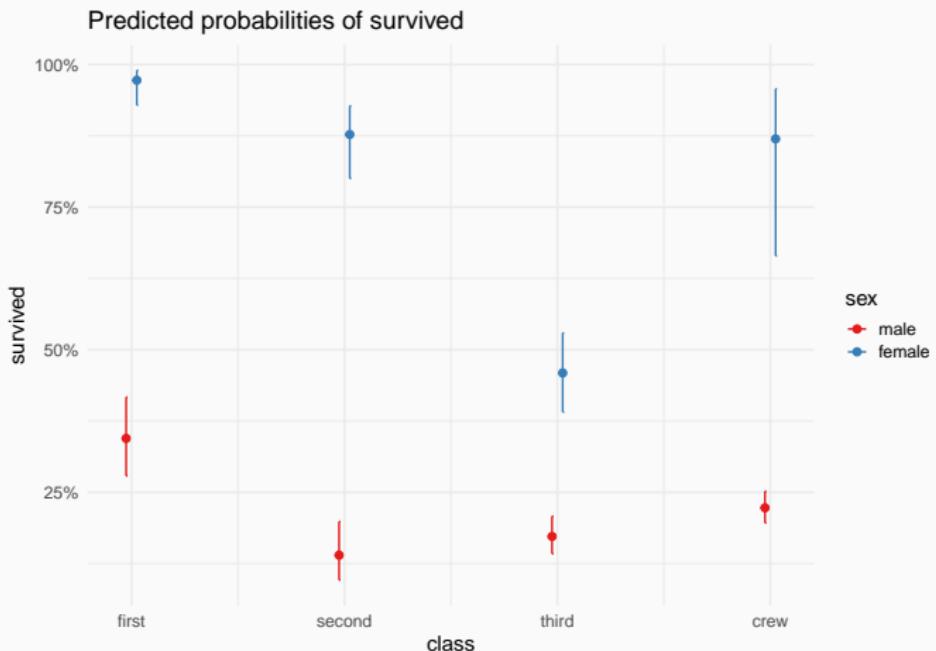
sex

class	female	male
crew	0.8695652	0.2227378
first	0.9724138	0.3444444
second	0.8773585	0.1396648
third	0.4591837	0.1725490



Visualising model (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)	Tjur's R2	RMS
<hr/>						
tit.sex.class.add	glm	2238.9 (<.001)	2238.9 (<.001)	2267.4 (<.001)	0.248	0.40
tit.sex.class.int	glm	2179.7 (>.999)	2179.8 (>.999)	2225.3 (>.999)	0.271	0.39

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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.6404	-0.2915	1.5698	5.0366	10.1516

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

Effects

```
model: cbind(Yes, No) ~ Class
```

Class effect

Class

1st	2nd	3rd	Crew
-----	-----	-----	------

0.6246154	0.4140351	0.2521246	0.2395480
-----------	-----------	-----------	-----------

Compare with former model based on binary data:

```
model: survived ~ class
```

class effect

class

crew	first	second	third
------	-------	--------	-------

0.2395480	0.6246154	0.4140351	0.2521246
-----------	-----------	-----------	-----------

Logistic regression with continuous predictors

Example dataset: [GDP and infant mortality](#)

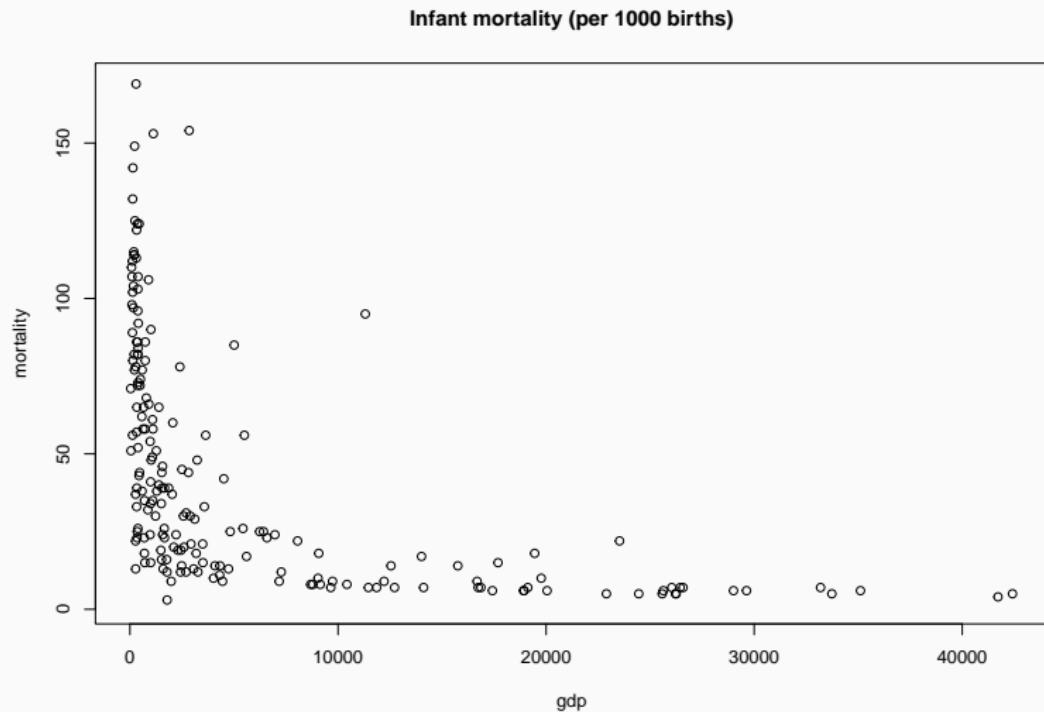
Read `UN_GDP_infantmortality.csv`.

```
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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.2230	-3.5163	-0.5697	2.4284	13.5849

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

Effects

```
allEffects(gdp.glm)
```

```
model: cbind(mortality, 1000 - mortality) ~ gdp
```

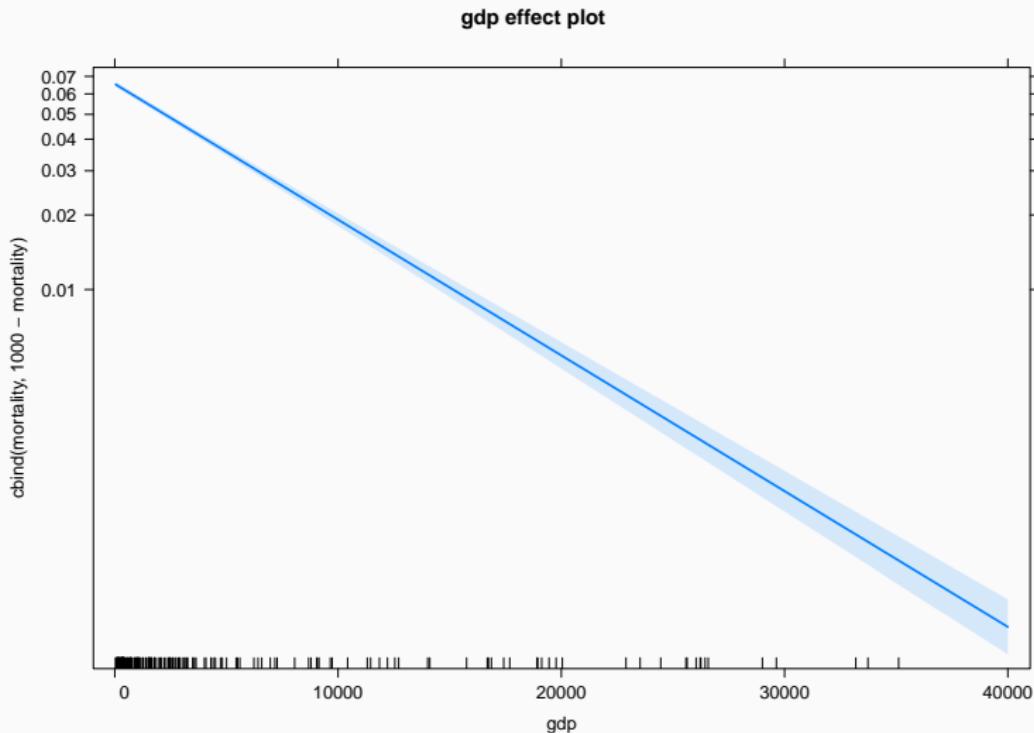
```
gdp effect
```

```
gdp
```

40	10000	20000	30000	40000
----	-------	-------	-------	-------

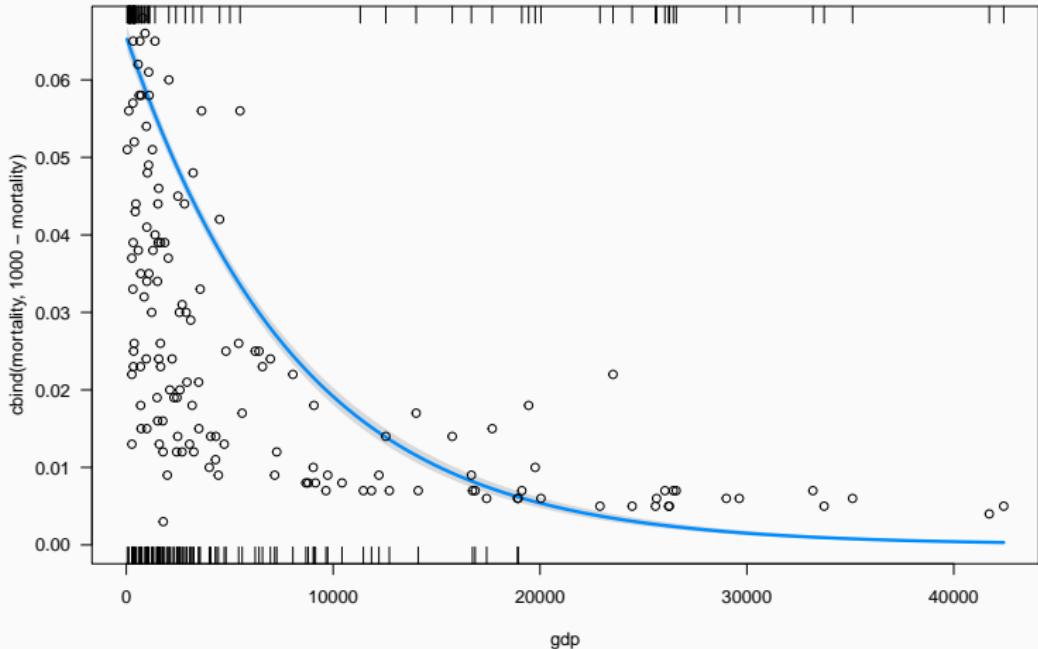
0.0652177296	0.0191438829	0.0054028095	0.0015096074	0.0004206154
--------------	--------------	--------------	--------------	--------------

Effects plot



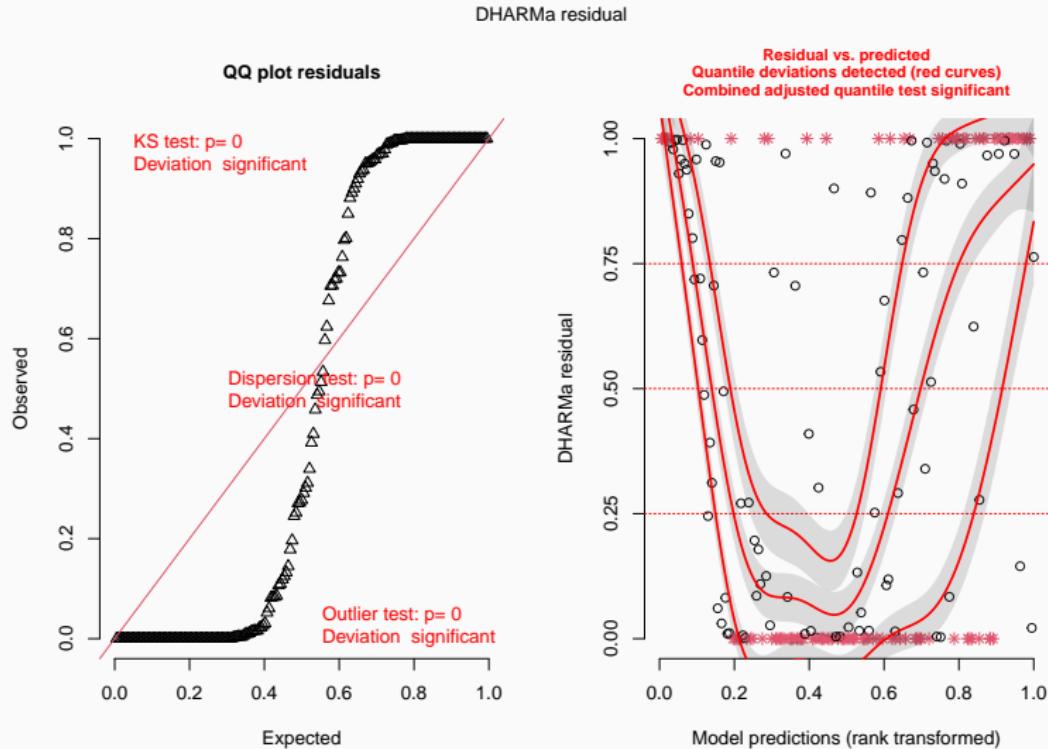
Plot model using visreg:

```
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

$$\text{Var}(y) = np(1 - p)$$

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
```

`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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.2230	-3.5163	-0.5697	2.4284	13.5849

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

Mean estimates do not change after accounting for overdispersion

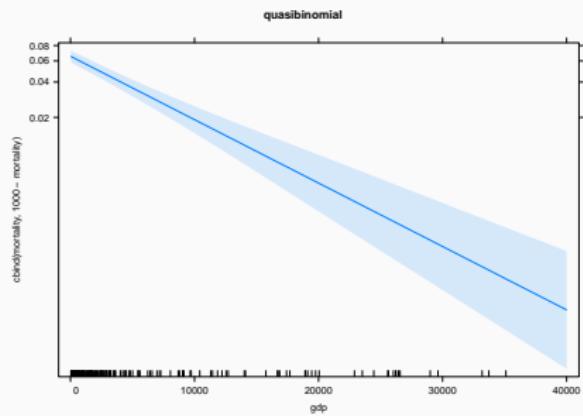
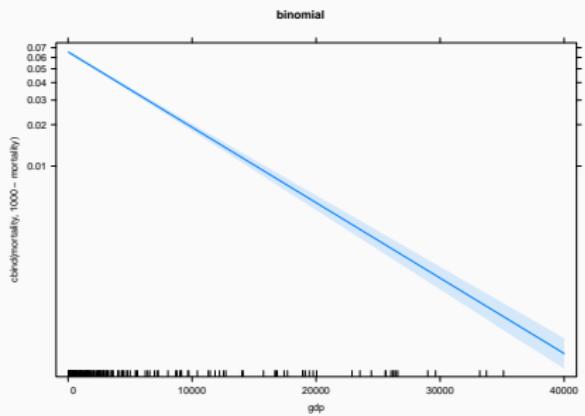
```
coef(gdp.overdisp)
```

```
(Intercept)          gdp  
-2.6574663734 -0.0001278976
```

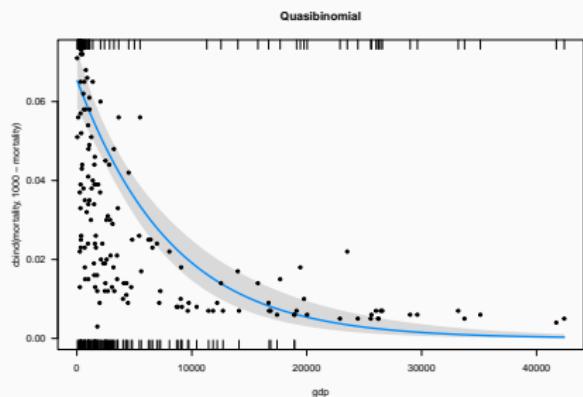
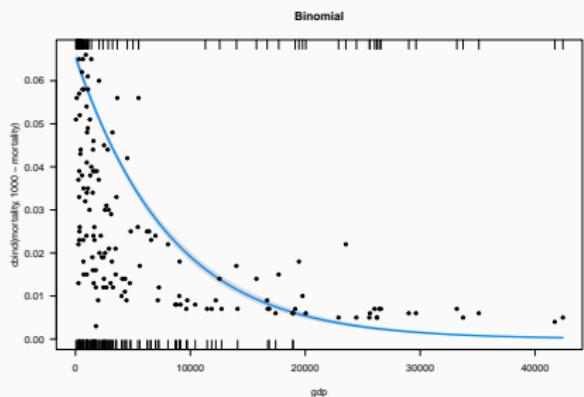
```
coef(gdp.glm)
```

```
(Intercept)          gdp  
-2.6574663734 -0.0001278976
```

But standard errors (uncertainty) do!



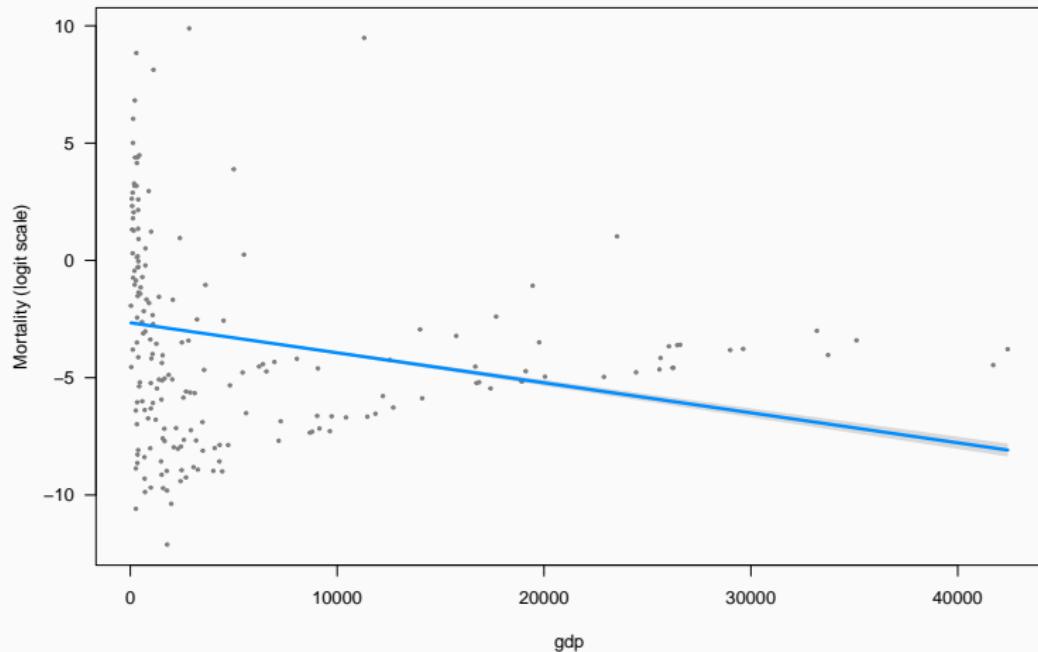
Plot model and data



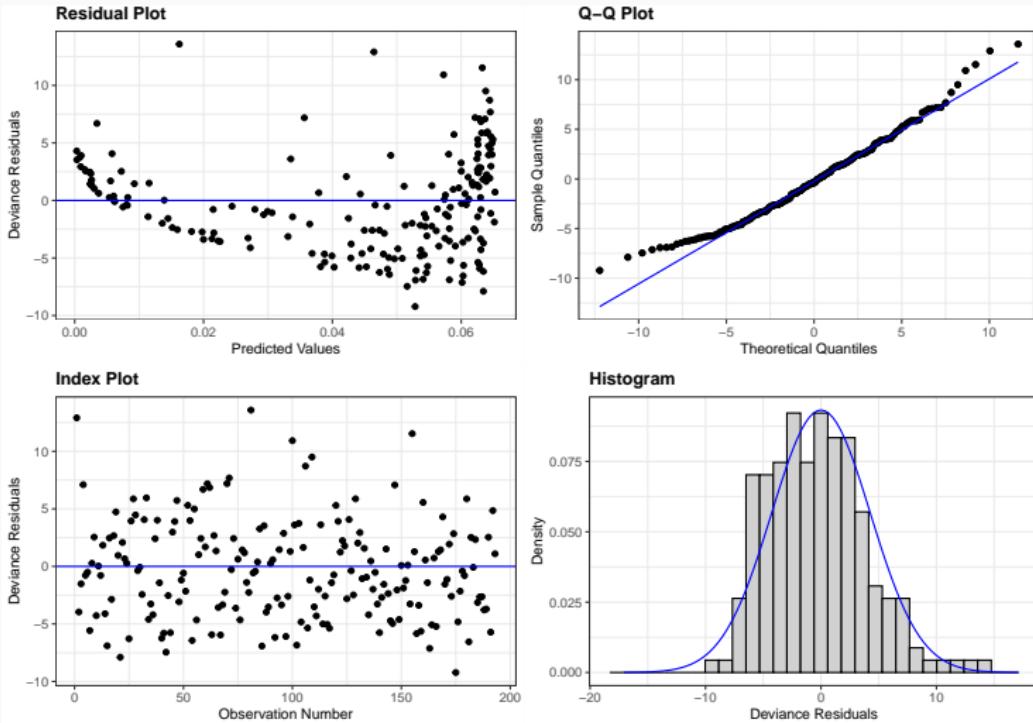
Think about the shape of
relationships

Think about the shape of relationships

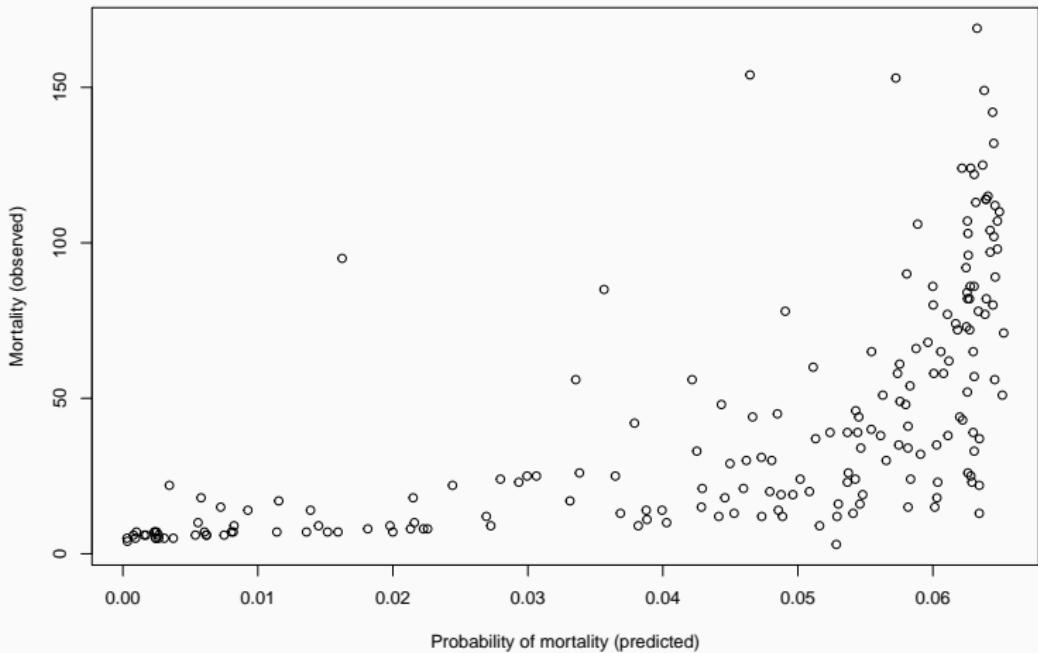
Not everything has to be linear...



Residuals show non-linear pattern

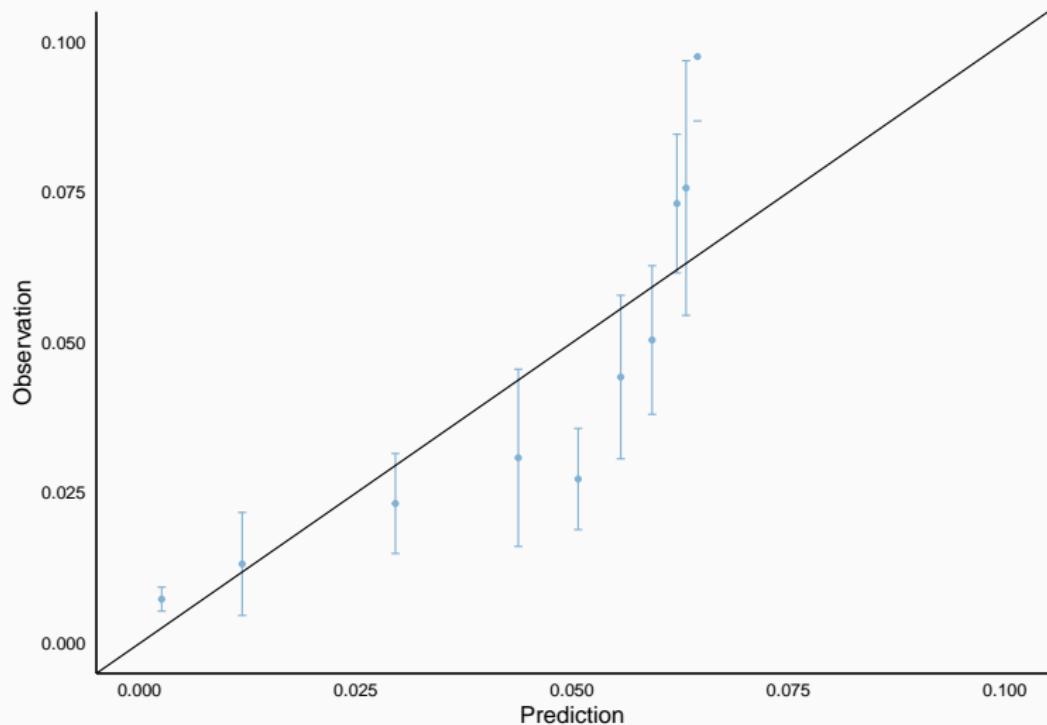


Calibration plot shows non-linear pattern

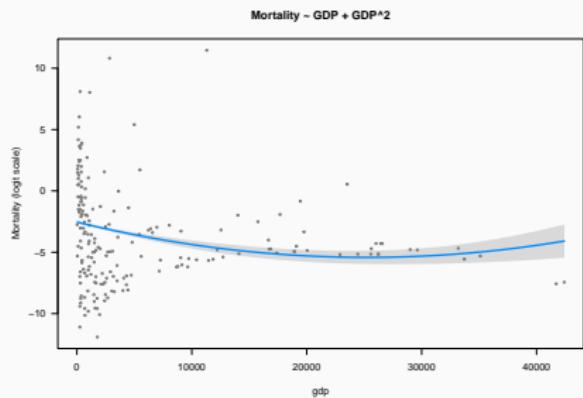
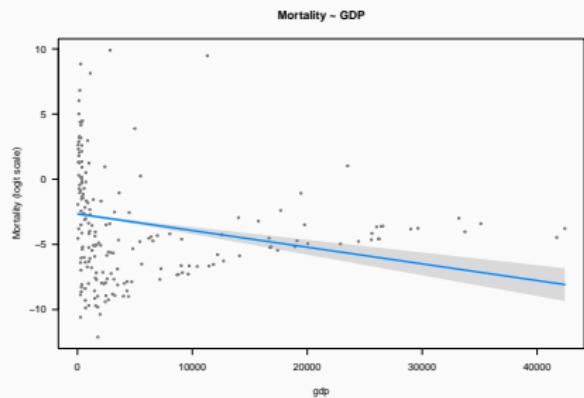


Calibration plot shows non-linear pattern

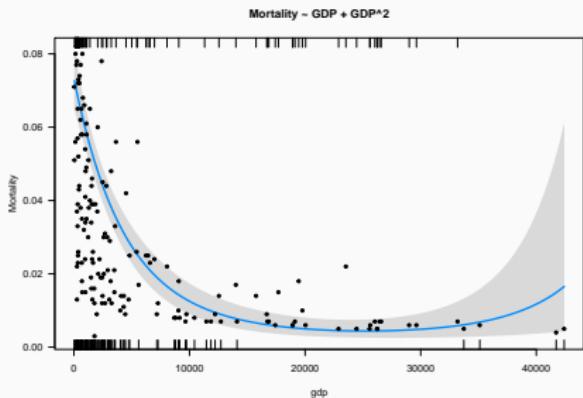
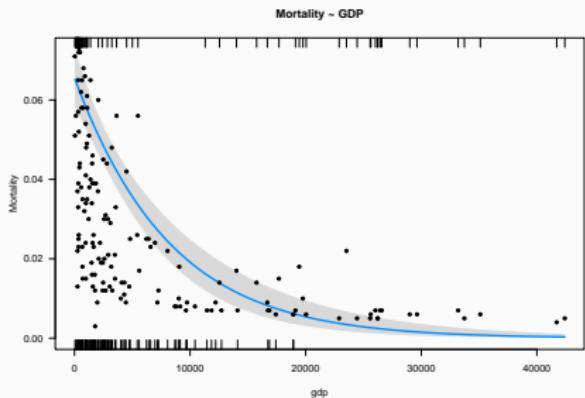
\$calibration_plot



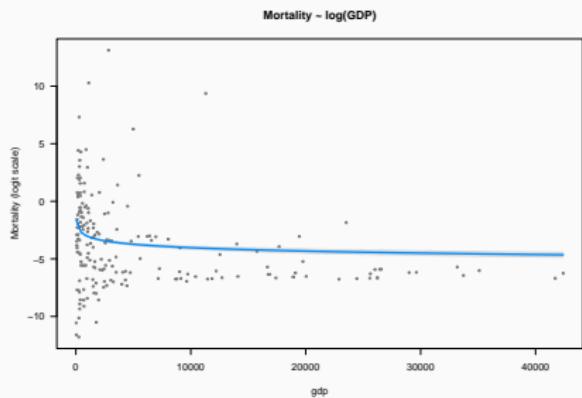
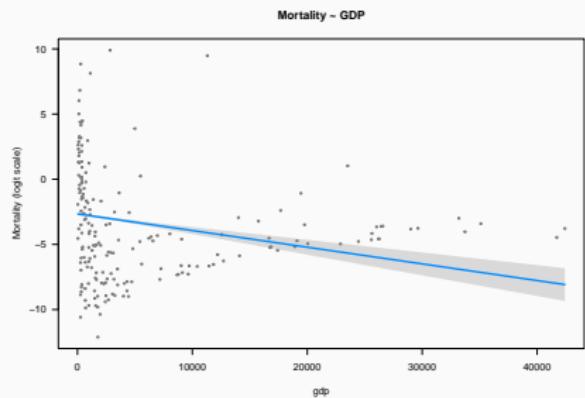
Trying polynomial predictor ($\text{GDP} + \text{GDP}^2$)



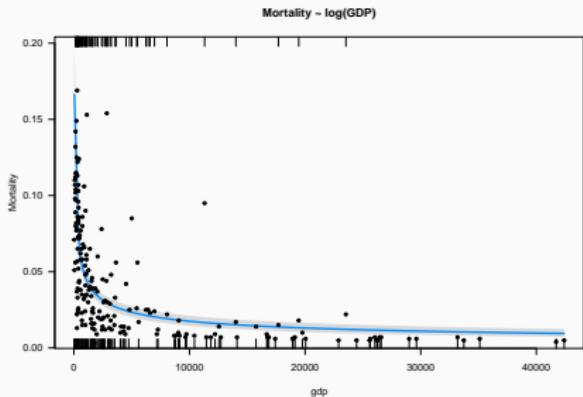
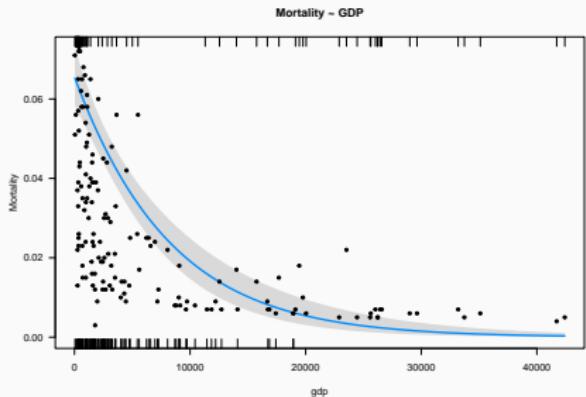
Think about the shape of relationships



Trying $\log(\text{GDP})$



Trying $\log(\text{GDP})$



More examples

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

More examples

- `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](#))

More examples

- **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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2681	-1.3310	0.1386	1.1062	2.1885

Coefficients:

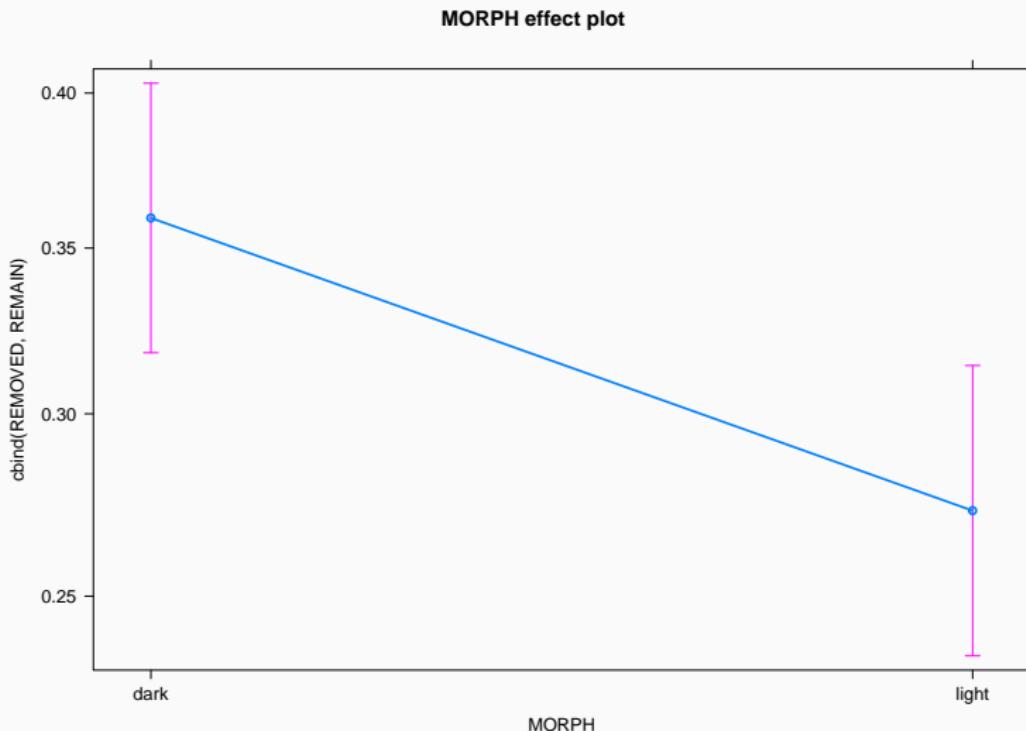
	Estimate	Std. Error	z value	Pr(> z)		
(Intercept)	-0.57752	0.09473	-6.097	1.08e-09 ***		
MORPHlight	-0.40331	0.13925	-2.896	0.00377 **		

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

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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.9764	-0.9411	-0.1206	1.0887	2.7666

Coefficients:

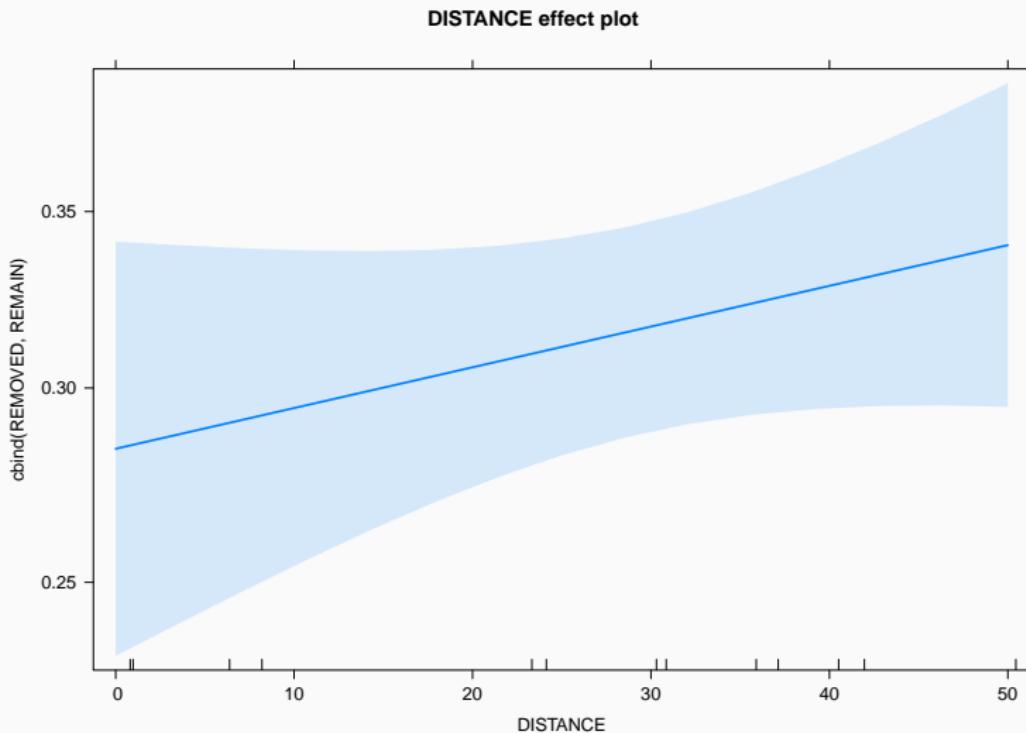
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.925861	0.136634	-6.776	1.23e-11 ***
DISTANCE	0.005268	0.003984	1.322	0.186

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

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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.21183	-0.39883	0.01155	0.68292	1.31242

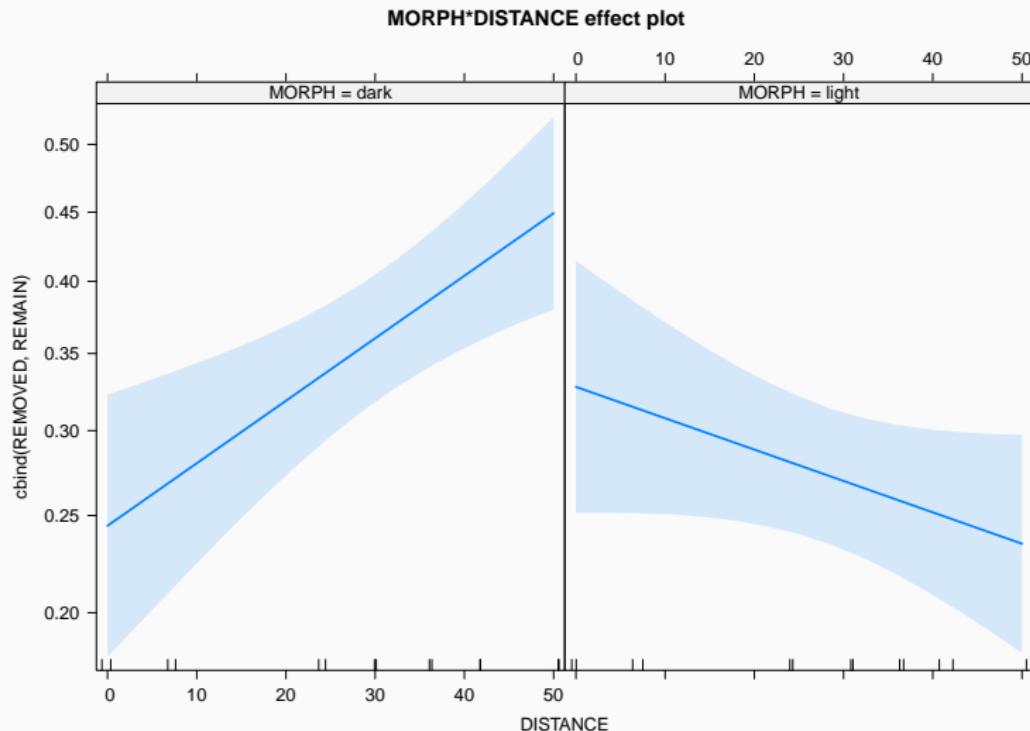
Coefficients:

	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

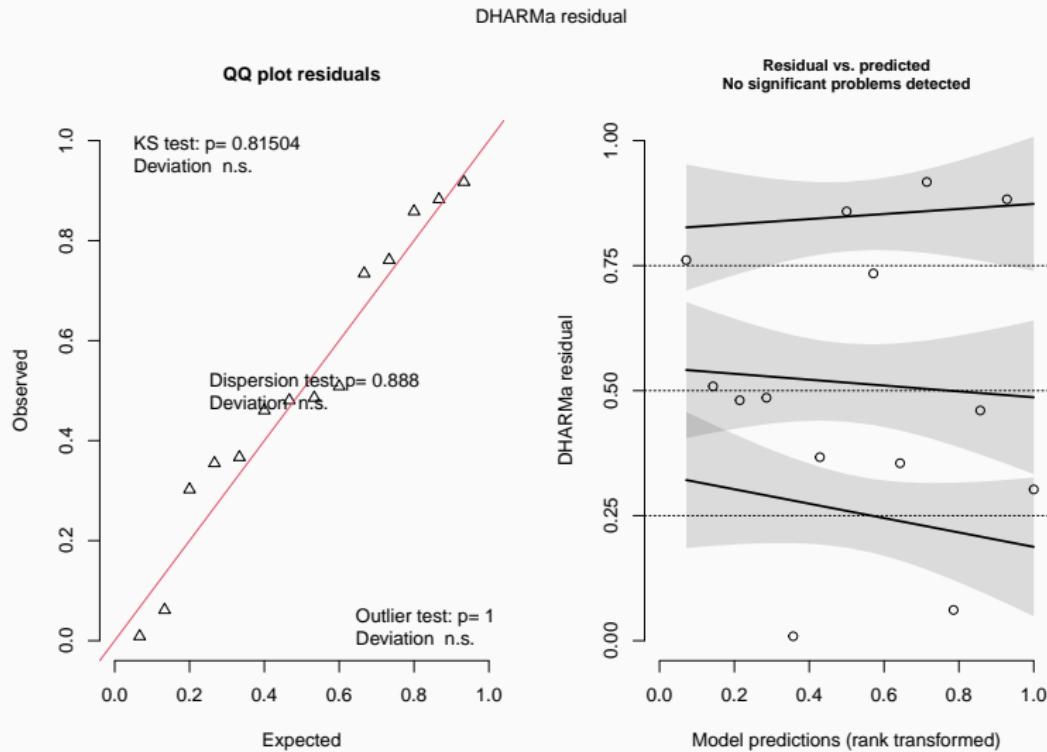
(Dispersion parameter for binomial family taken to be 1)

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>

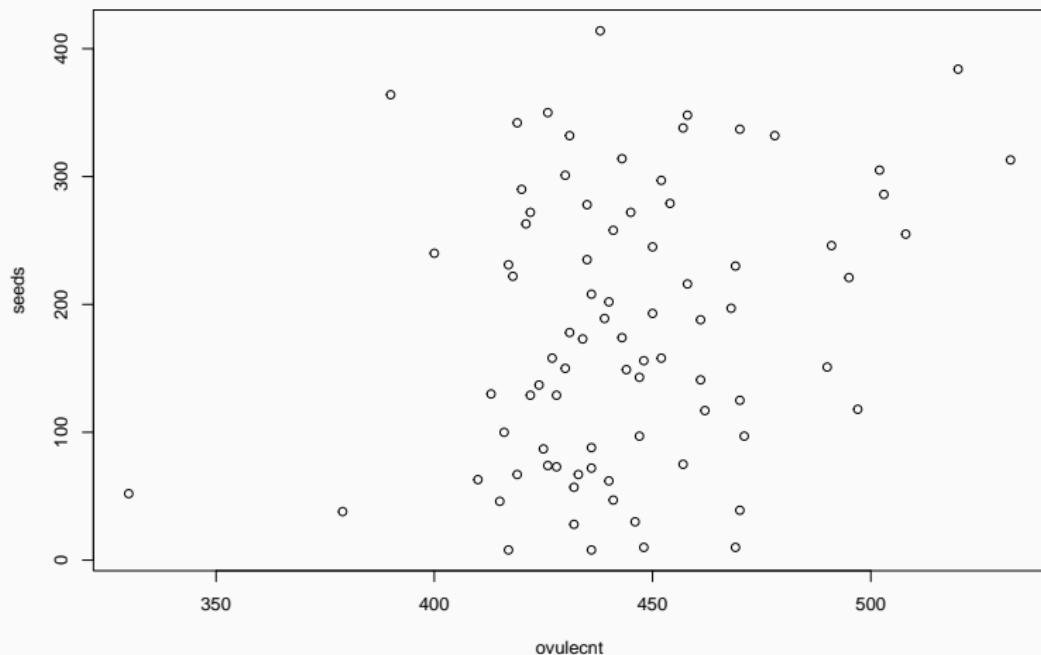
- Is seed set related to proportion of outcross pollen (pcmass)?

Questions:

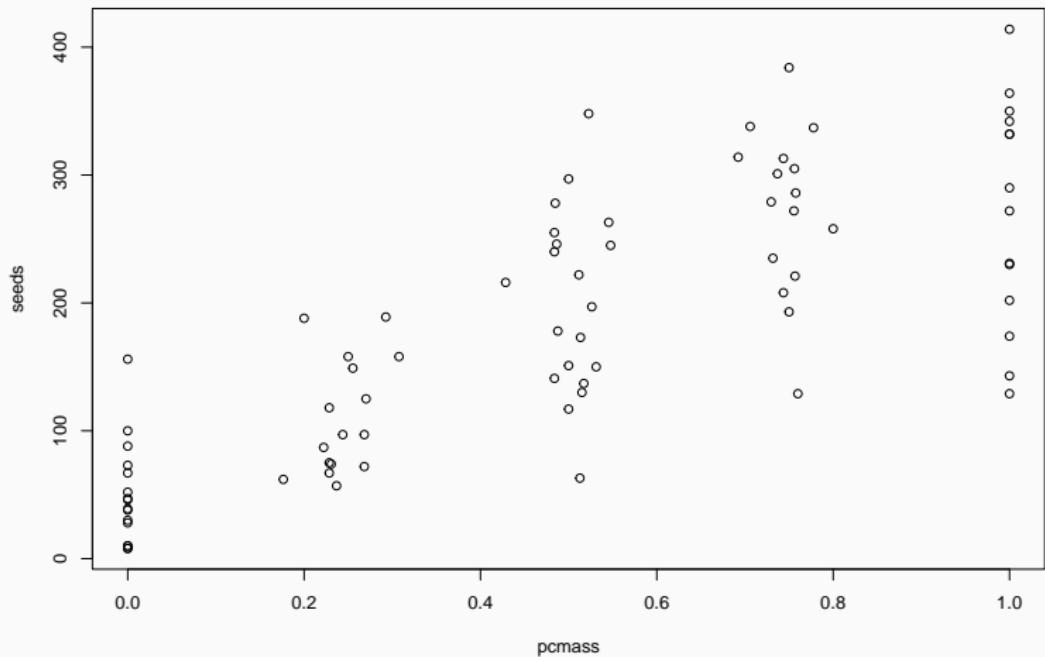
<https://pollev.com/franciscorod726>

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

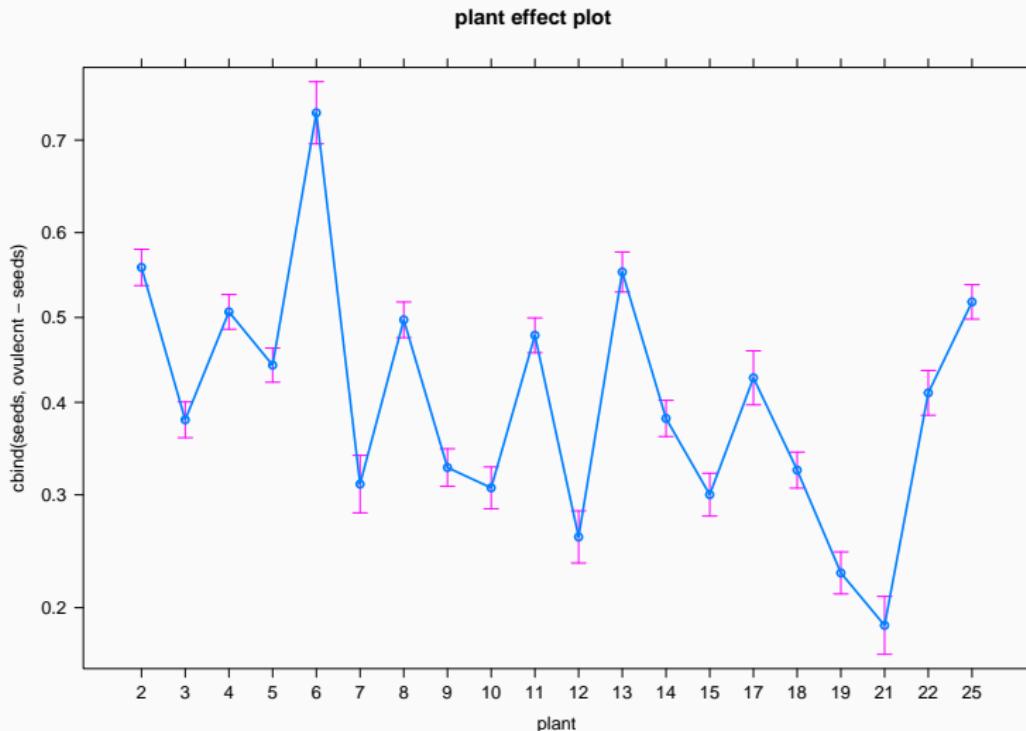
Number of seeds vs Number of ovules



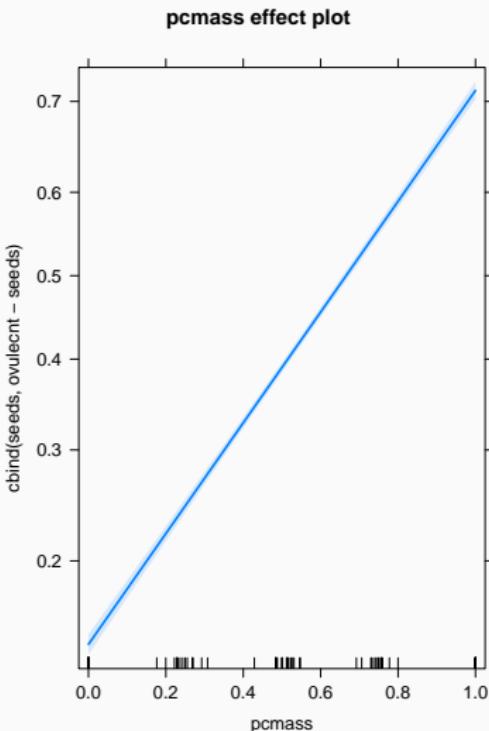
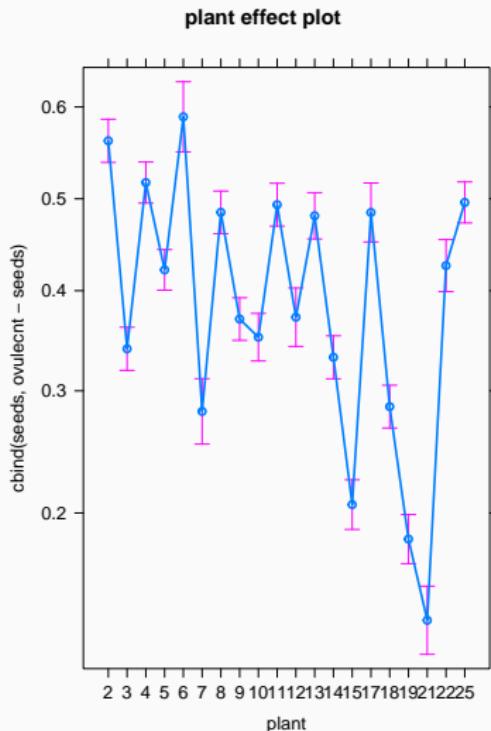
Number of seeds vs Proportion outcross pollen



Seed set across plants



Seed set ~ outcross pollen



Probability of scoring penalty

Data on penalty shots

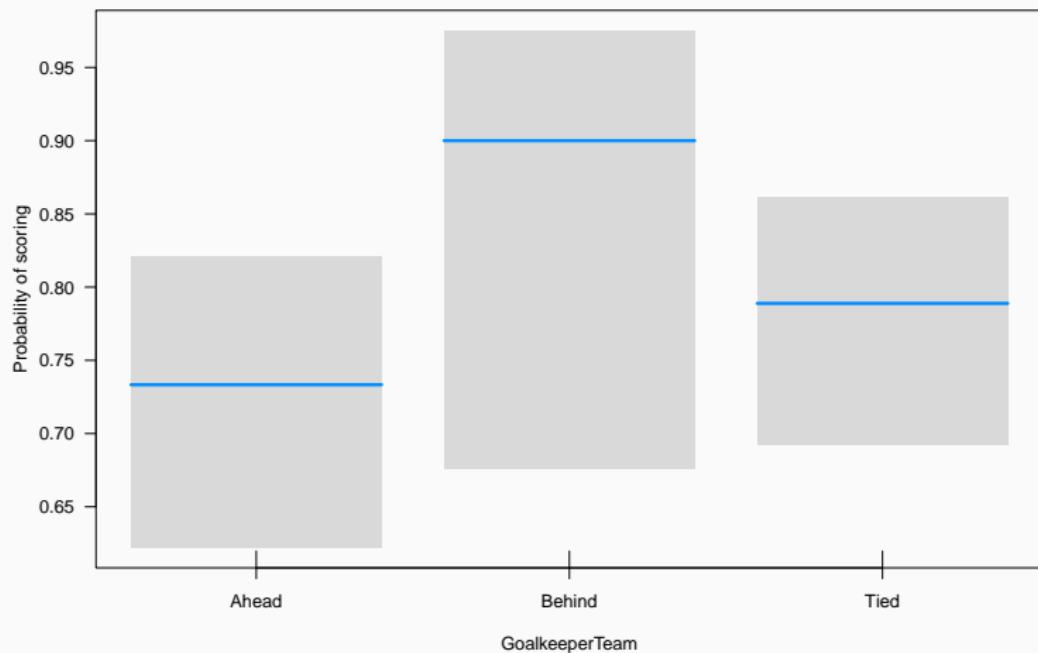
```
soccer <- read.csv("data/soccer.csv")  
soccer
```

	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: Poisson regression

Francisco Rodríguez-Sánchez

<https://frodriguezsanchez.net>

Types of response variable

- Gaussian: lm

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- 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

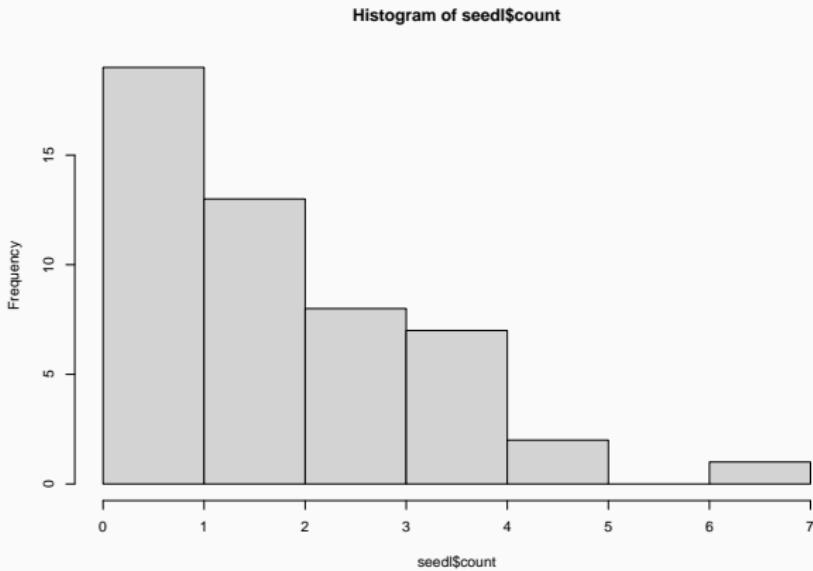
```
seedl <- read.csv("data/seedlings.csv")
```

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

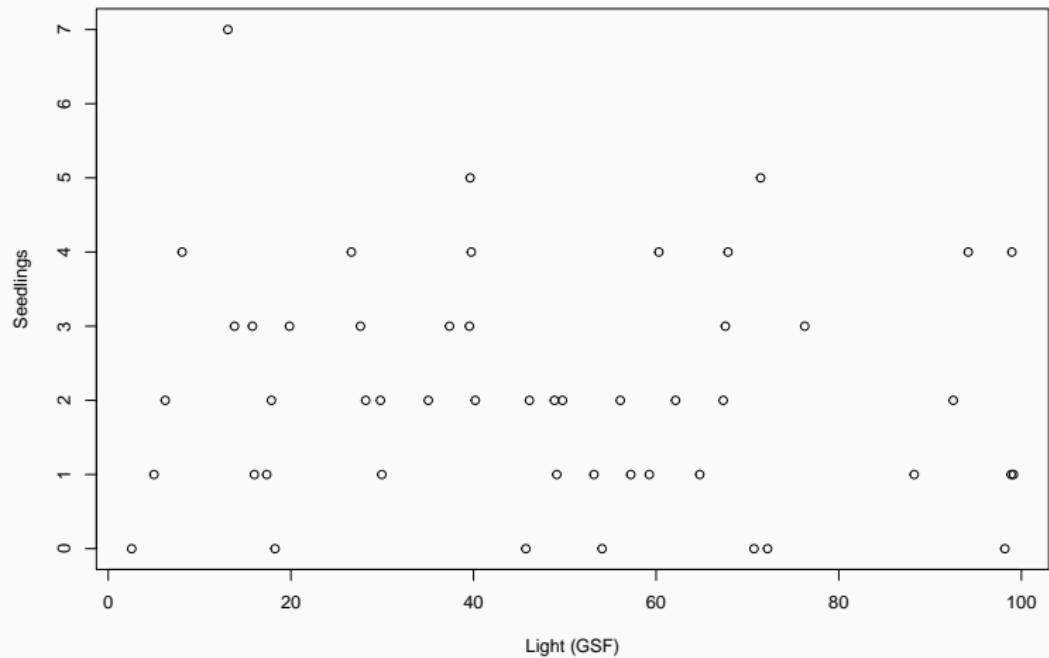
Exploring the data

```
table(seed1$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)
```

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

Interpreting Poisson GLM

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1906	-0.8466	-0.1110	0.5220	2.4577

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

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 effects package

```
allEffects(seed1.glm)
```

```
model: count ~ light
```

```
light effect
```

```
light
```

```
3
```

```
30
```

```
50
```

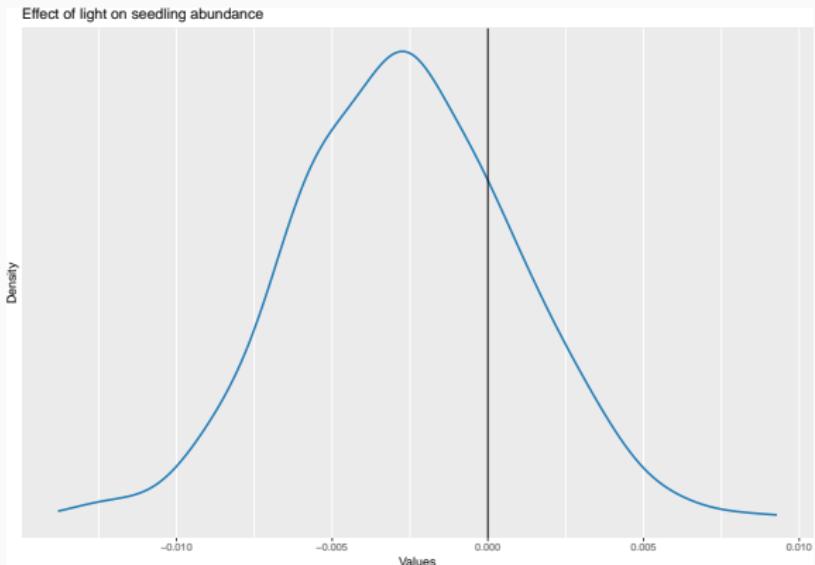
```
70
```

```
100
```

```
2.396665 2.235657 2.123408 2.016794 1.866826
```

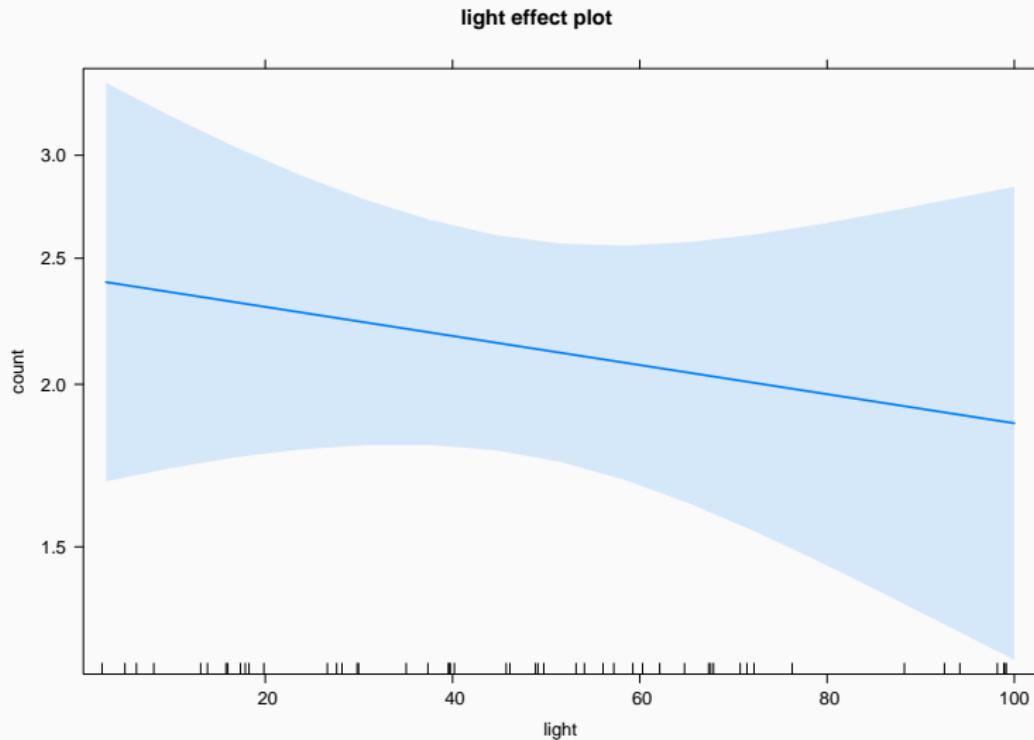
Estimated distribution of the slope parameter

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



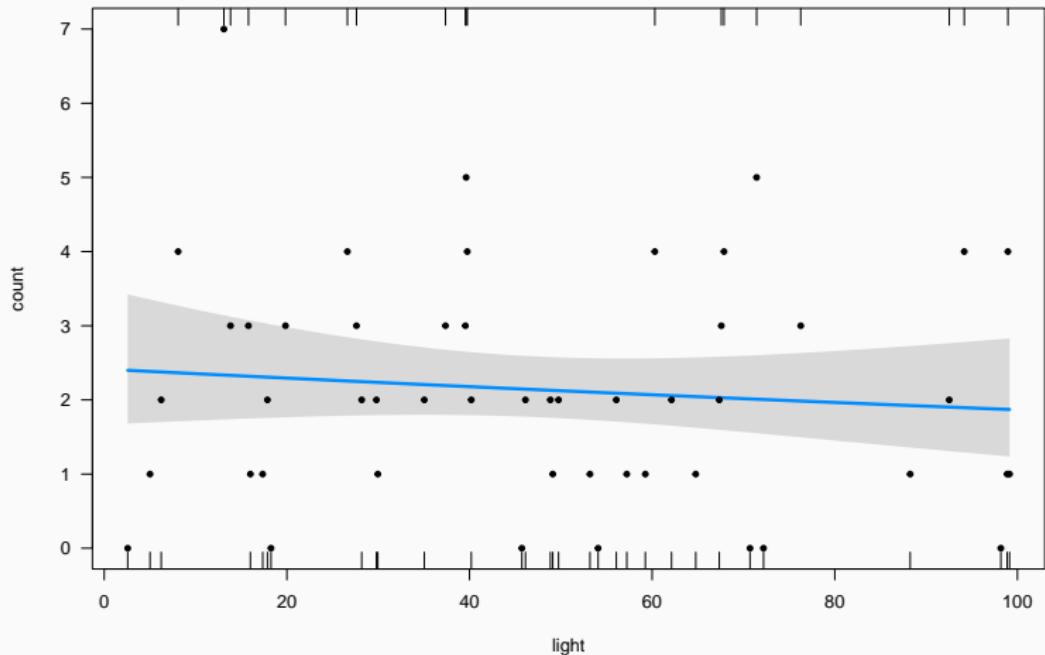
So what's the relationship between Nseedlings and light?

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



Using visreg

```
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 ($\log \text{response} \sim \text{predictors}$)

Assumptions of Poisson regression

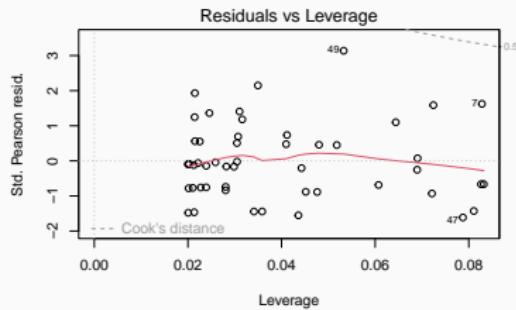
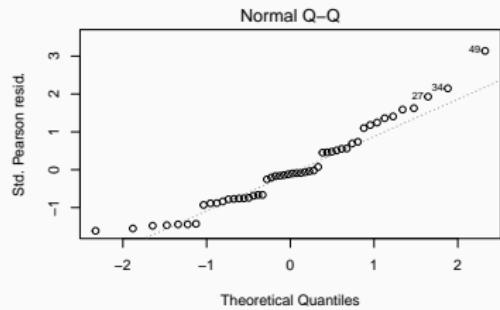
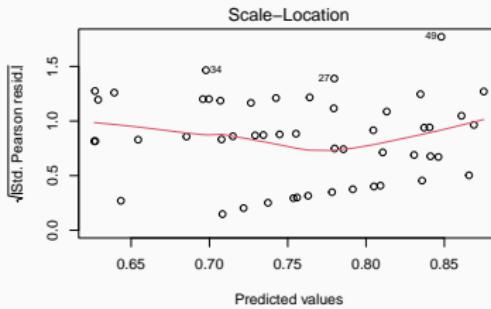
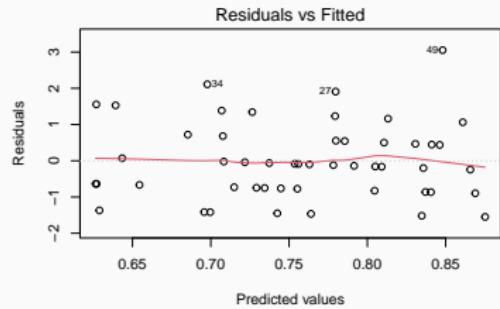
- Linearity (\log response ~ predictors)
- Observations are independent

Assumptions of Poisson regression

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

Checking Poisson GLM

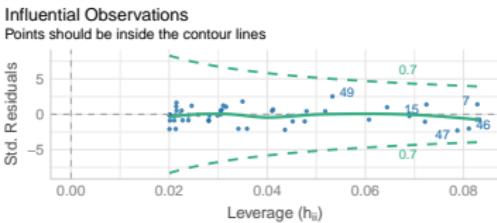
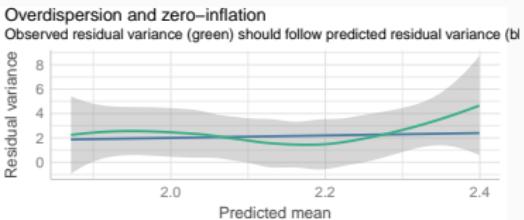
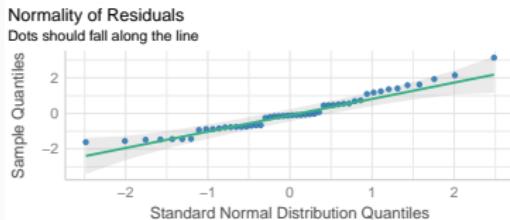
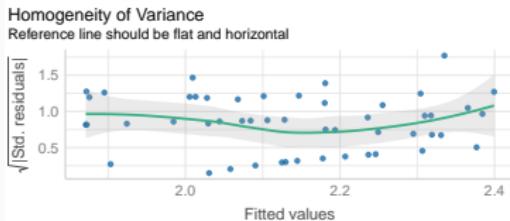
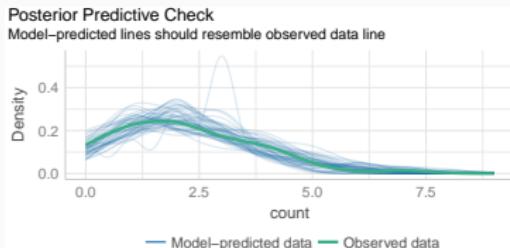
```
plot(seedl.glm)
```



```
null device
```

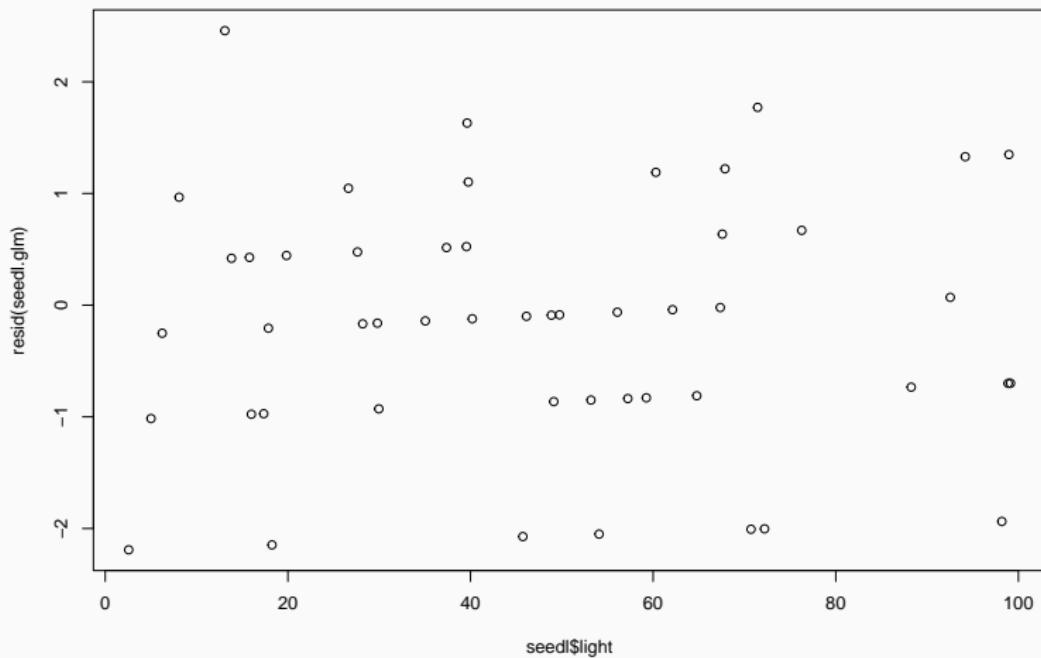
Checking Poisson GLM

```
check_model(seed1.glm)
```



Is there pattern of residuals along predictor?

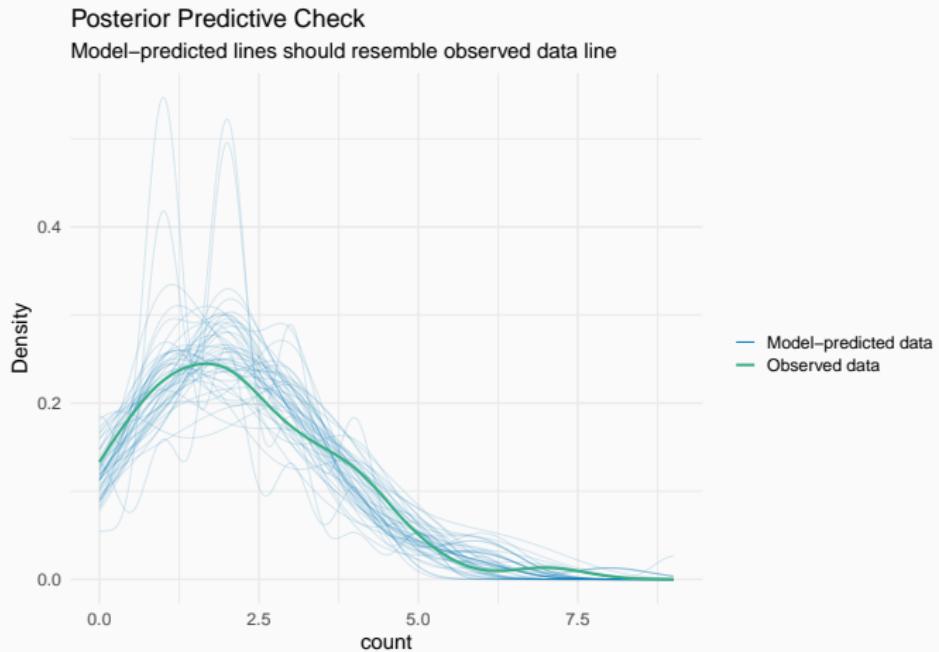
```
plot(seedl$light, resid(seedl.glm))
```



Posterior predictive checking

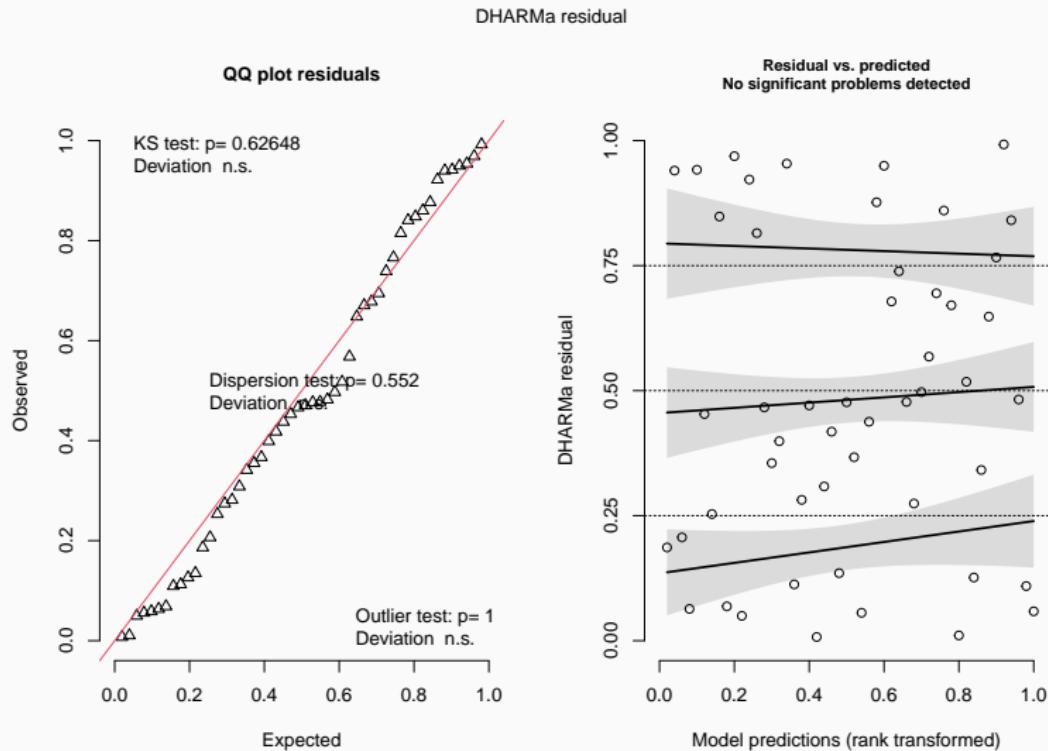
Simulate data from fitted model (y_{rep}) and compare with observed data (y)

```
check_predictions(seed1.glm)
```



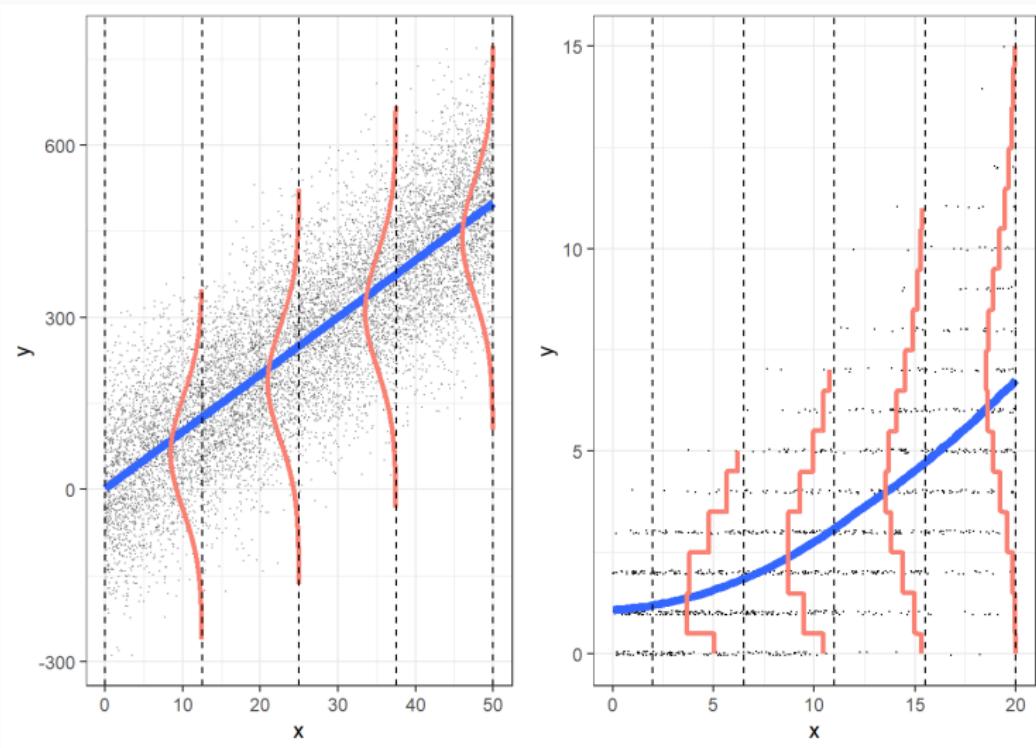
Residuals diagnostics with DHARMA

```
simulateResiduals(seed1.glm, plot = TRUE)
```



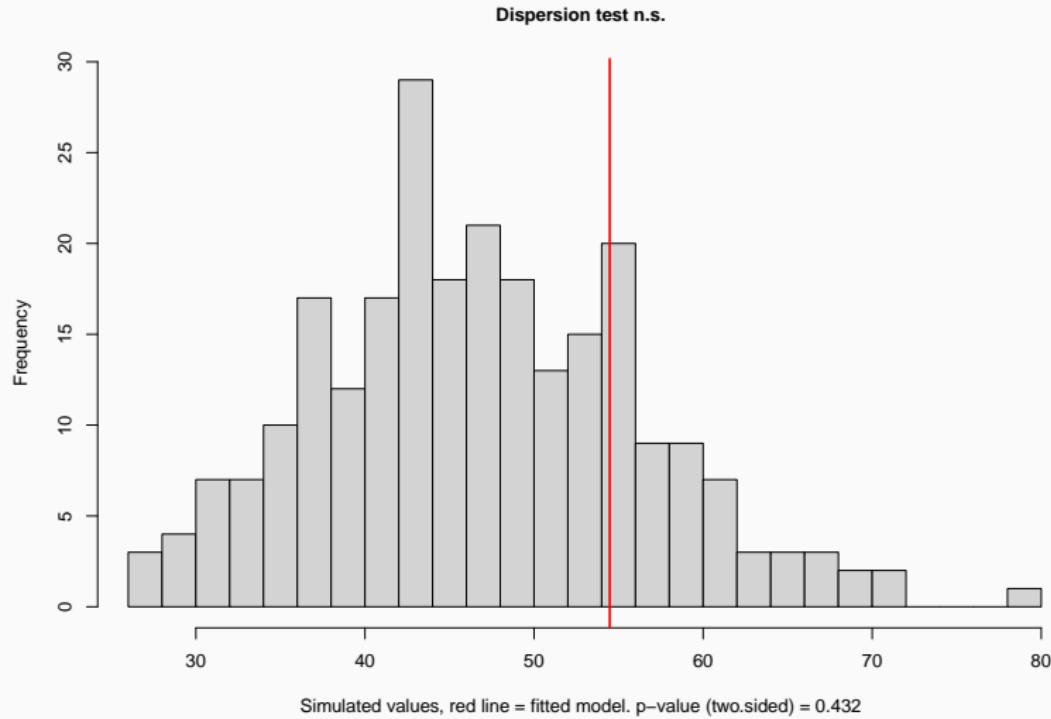
Overdispersion

Poisson GLM assumes mean = variance



Always check overdispersion with count data

```
simres <- simulateResiduals(seed.l.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)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1906	-0.8466	-0.1110	0.5220	2.4577

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

```
allEffects(seedl.overdisp)
```

```
model: count ~ light

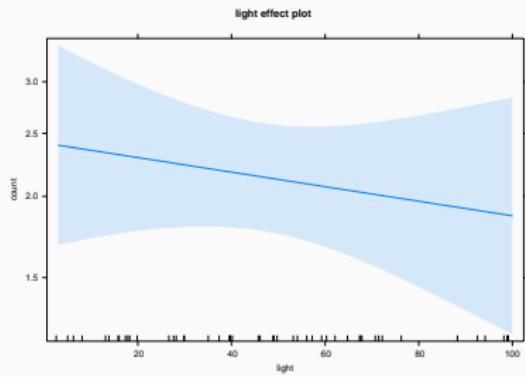
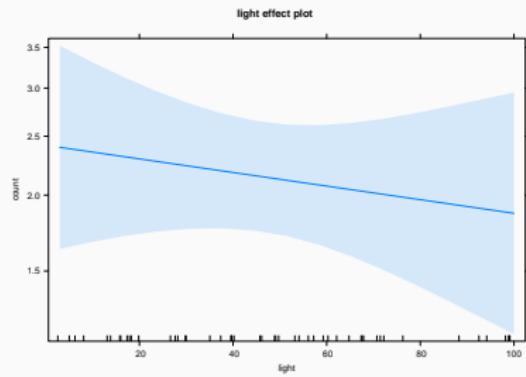
light effect
light
      3       30       50       70       100
2.396665 2.235657 2.123408 2.016794 1.866826
```

```
allEffects(seedl.glm)
```

```
model: count ~ light

light effect
light
      3       30       50       70       100
2.396665 2.235657 2.123408 2.016794 1.866826
```

But standard errors may change



Accounting for overdispersion using negative binomial

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

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1349	-0.8162	-0.1061	0.4954	2.2814

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

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		AIC weights		BIC		BIC weights		Nagelkerke's R2		RMSE	
seedl.glm		glm		182.034		0.710		185.858		0.864		0.015		1.529	
seedl.nb		negbin		183.827		0.290		189.563		0.136		0.014		1.529	

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))
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.9918	-1.0142	0.1673	0.8401	3.8230

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)

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
```

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](#))