Linear, Generalized, and Mixed/Multilevel models - an introduction with R

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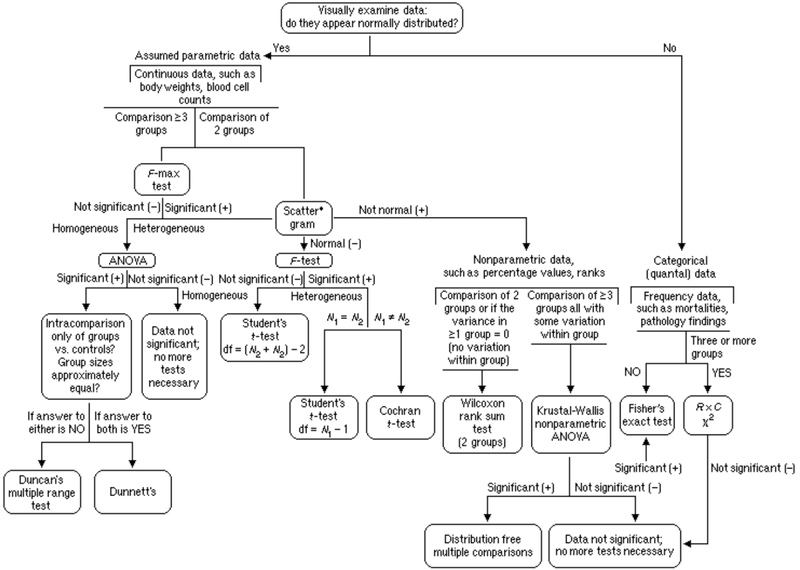
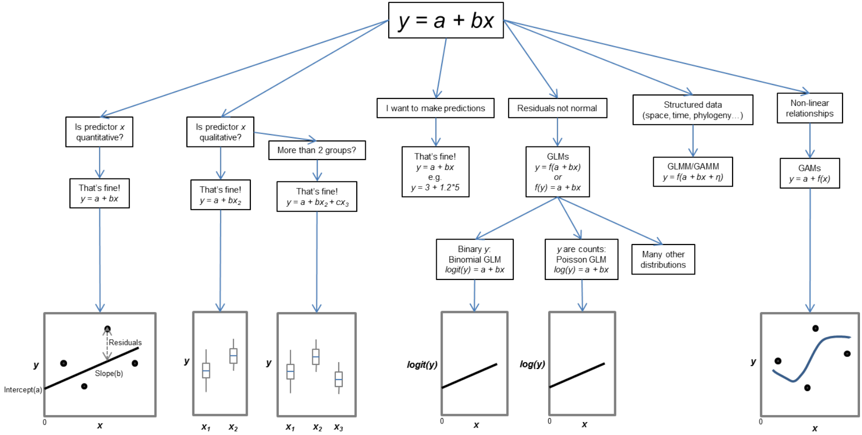
https://frodriguezsanchez.net

Introduction to linear models

Modern statistics are easier than this

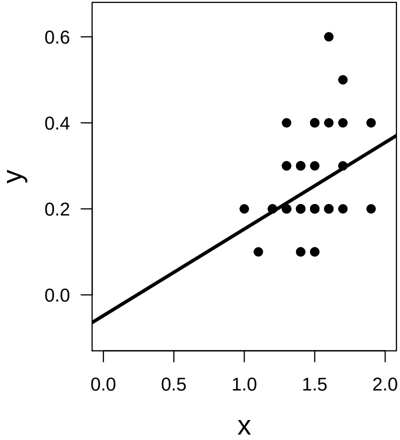


A unified framework



Our unified regression framework

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

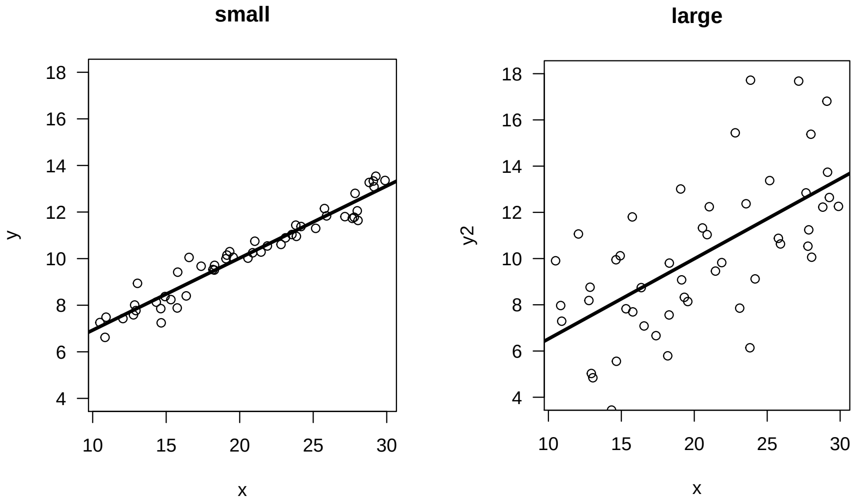


Data
y = response variable
x = predictor

Parameters
a = intercept
b = slope
σ = residual variation

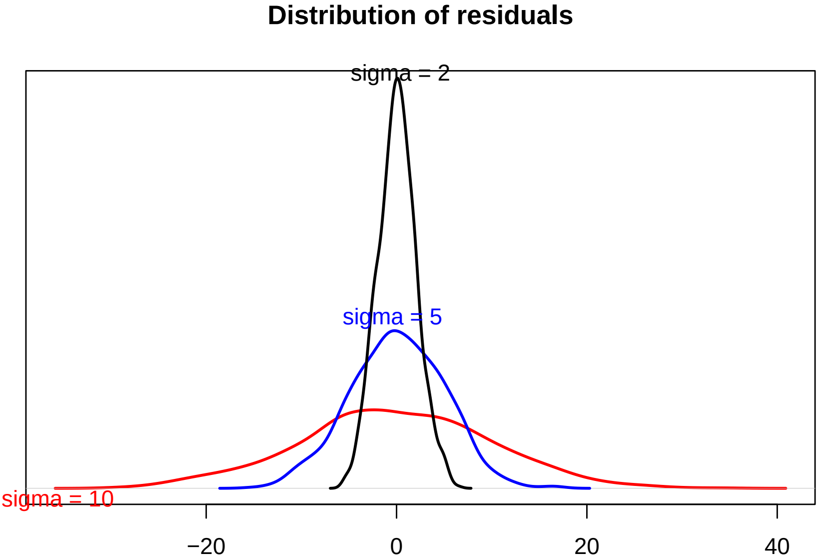
ε = residuals

Residual variation (error)

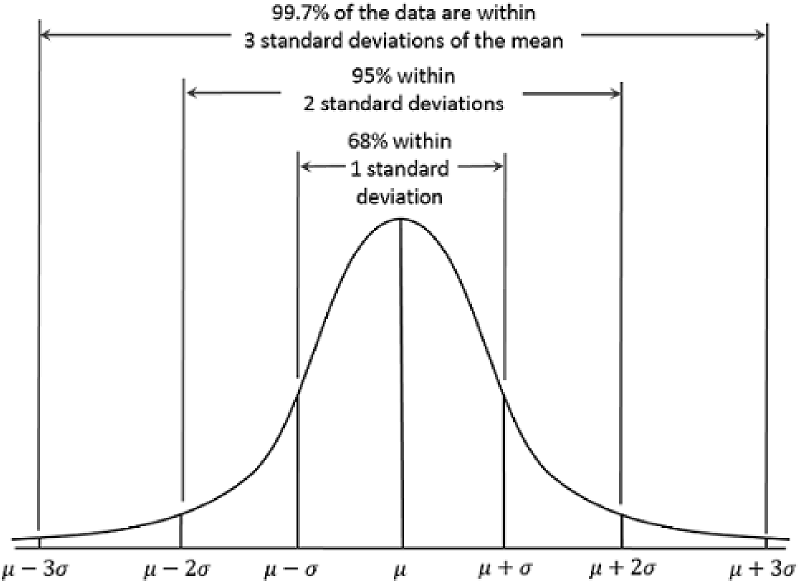


Residual variation

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



In a Normal distribution



Different ways to write same model

$$
\begin{aligned}
y_i &= a + bx_i + \varepsilon_i \\
\varepsilon_i &\sim N\left(0, \sigma^2\right)
\end{aligned}
$$

.

$$
\begin{aligned}
y_i &\sim N\left(\mu_i, \sigma^2\right) \\
\mu_i &= a + bx_i \\
\varepsilon_i &\sim N\left(0, \sigma^2\right)
\end{aligned}
$$

Quiz

https://pollev.com/franciscorod726

Linear models

Example dataset: forest trees

- Download this dataset (or the entire zip file)

```r
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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5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Questions

- What is the relationship between DBH and height?

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- Do taller trees have bigger trunks?

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

Always plot your data first!

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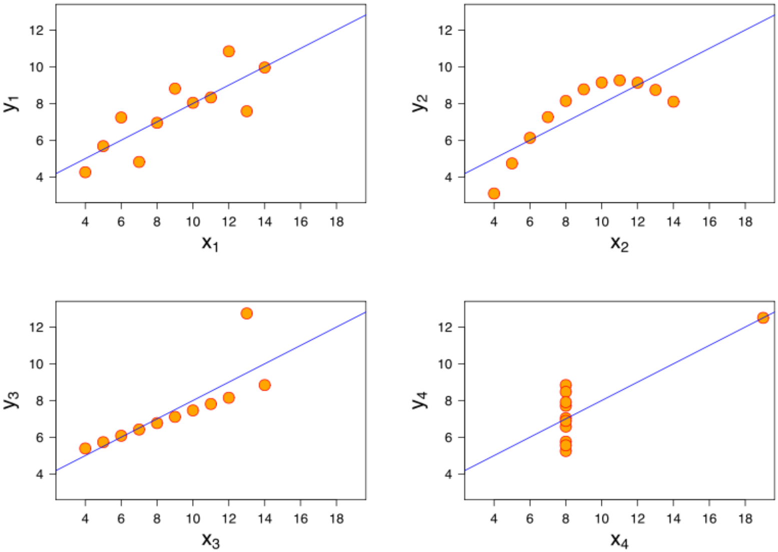
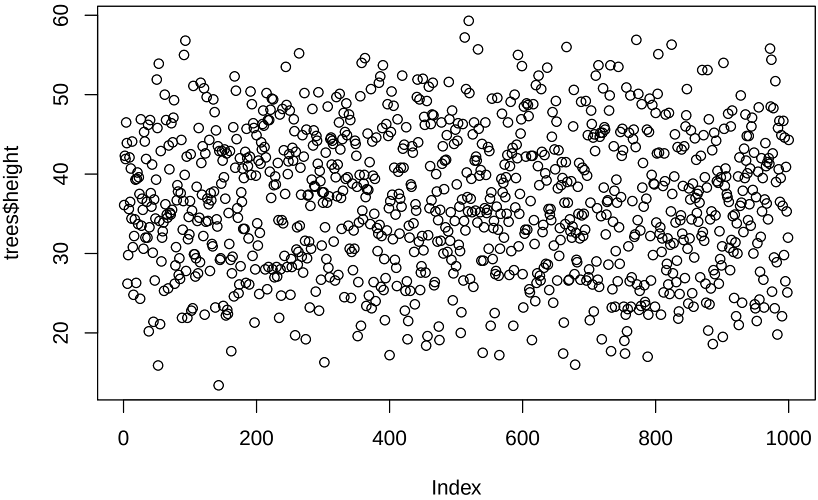


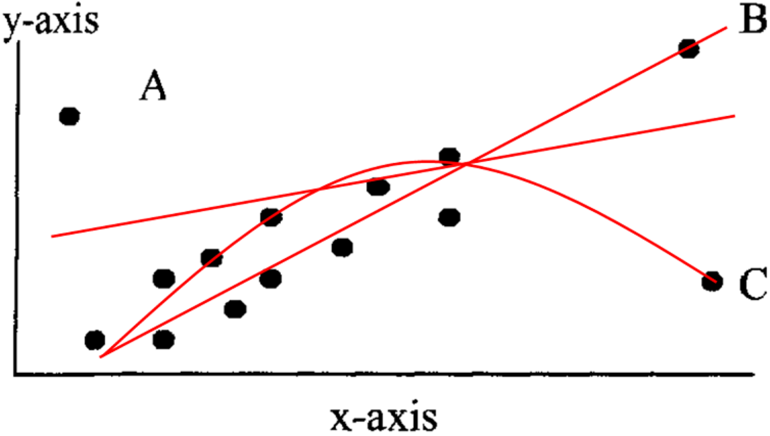
Exploratory Data Analysis (EDA)

Outliers

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



Outliers impact on regression



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

Histogram of response variable

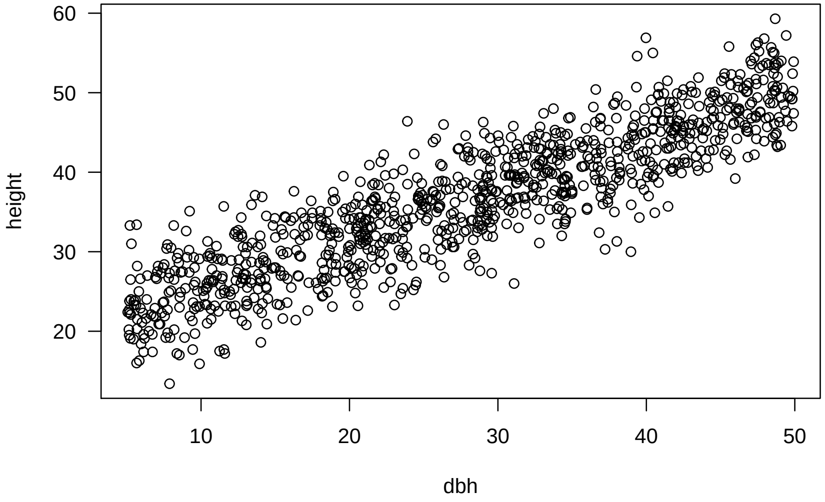
```r
hist(trees$height)
```

Histogram of predictor variable

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

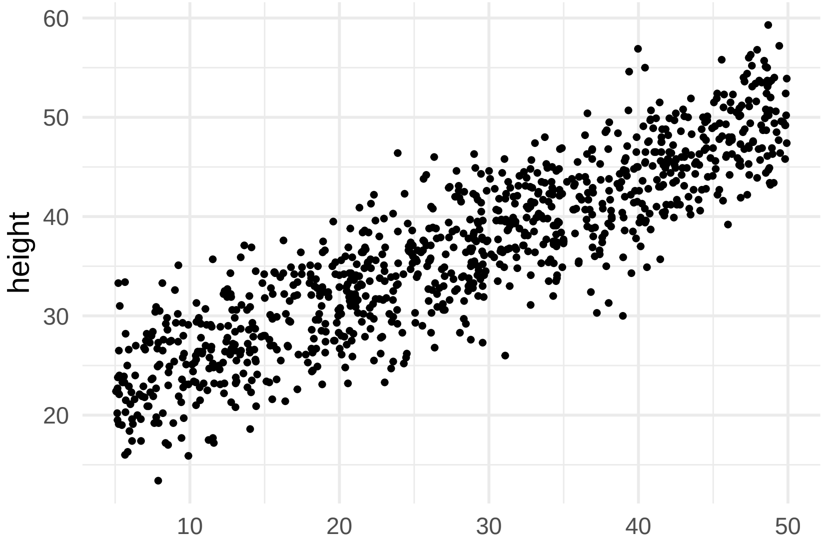
Scatterplot

```
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

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

Model interpretation

What does this mean?

```
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
```

Quiz

https://pollev.com/franciscorod726

Communicating results

Avoid dichotomania of statistical significance

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EDITORIAL · 20 MARCH 2019

It's time to talk about ditching statistical significance

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

Avoid dichotomania of statistical significance

MENU nature Subs

EDITORIAL · 20 MARCH 2019

It's time to talk about ditching statistical significance

- 'Never conclude there is 'no difference' or 'no association' just because $p > 0.05$ or CI includes zero'
- Estimate and communicate effect sizes and their uncertainty

Avoid dichotomania of statistical significance

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EDITORIAL · 20 MARCH 2019

It's time to talk about ditching statistical significance

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

Communicating results

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

Presenting model results

```r
kable(xtable::xtable(m1), digits = 2)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	19.34	0.31	62.26	0
dbh	0.62	0.01	60.79	0

Presenting model results

```r
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 2: Statistical models

Retrieving model coefficients

```r
coef(m1)
```

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

Tidy up model coefficients with broom

```r
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
```

```r
glance(m1)
```

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

Confidence intervals

```
confint(m1)
```

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

Using effects package

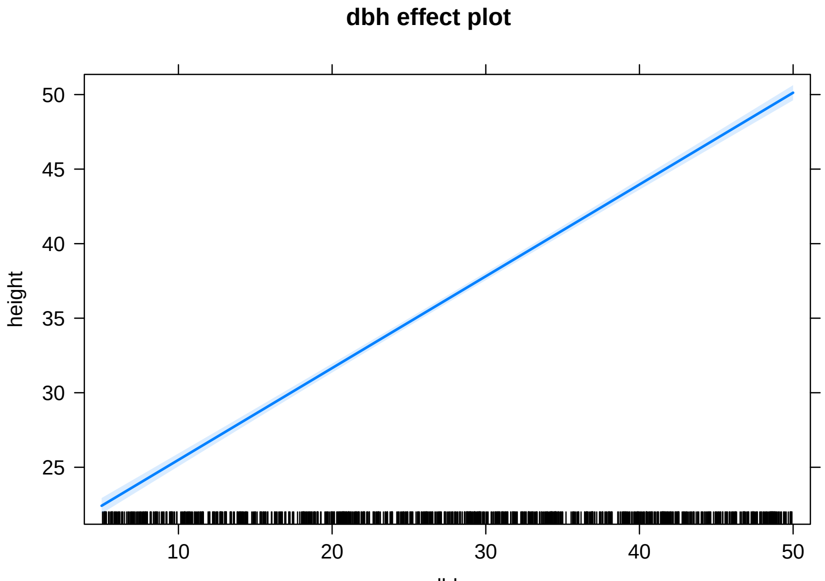
```r
library(effects)
summary(allEffects(m1))
```

```
 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 
```

Visualising fitted model

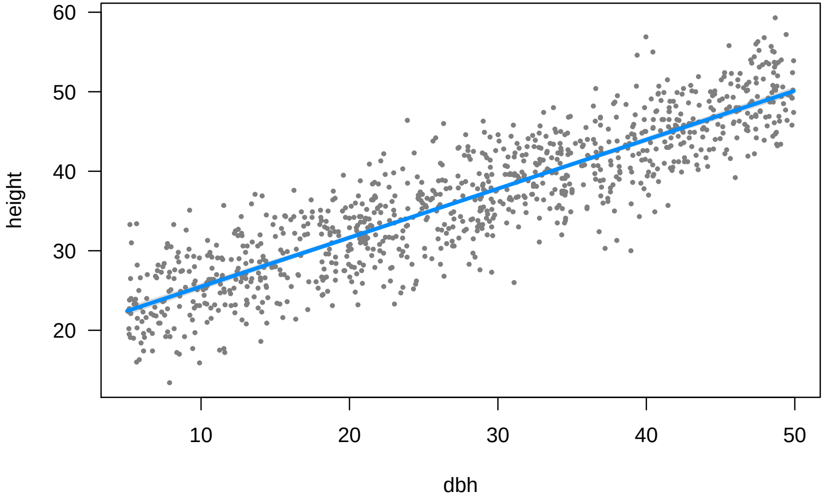
Plot effects

```
plot(allEffects(m1))
```



Plot model (visreg)

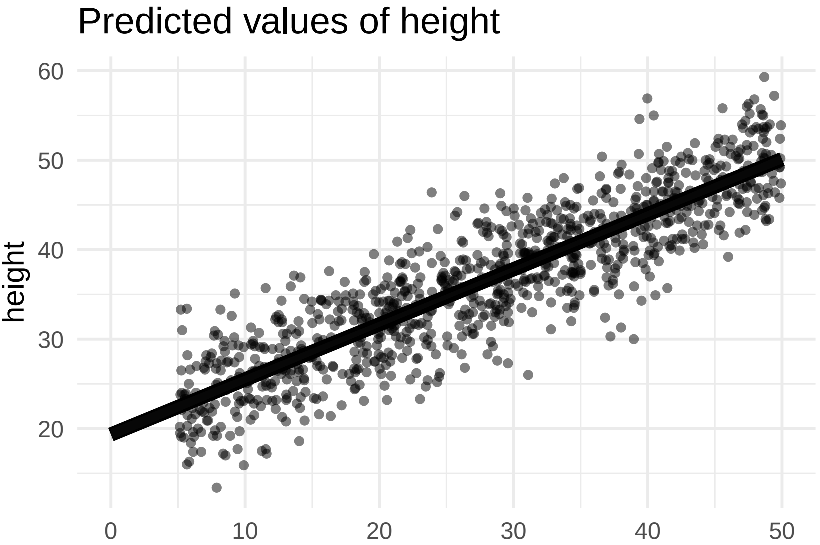
```r
library(visreg)
visreg(m1)
```



Plot model (sjPlot - ggplot2)

```
sjPlot::plot_model(m1, type = "eff", show.data = TRUE, line.size
```

```
$dbh
```



Model checking

Linear model assumptions

- Linearity (transformations, GAM...)

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- Residuals:

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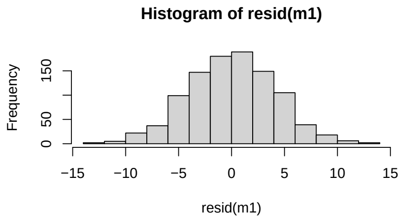
Linear model assumptions

- Linearity (transformations, GAM...)
- Residuals:
  - Independent
  - Equal variance
  - Normal
- No measurement error in predictors

Are residuals normal?

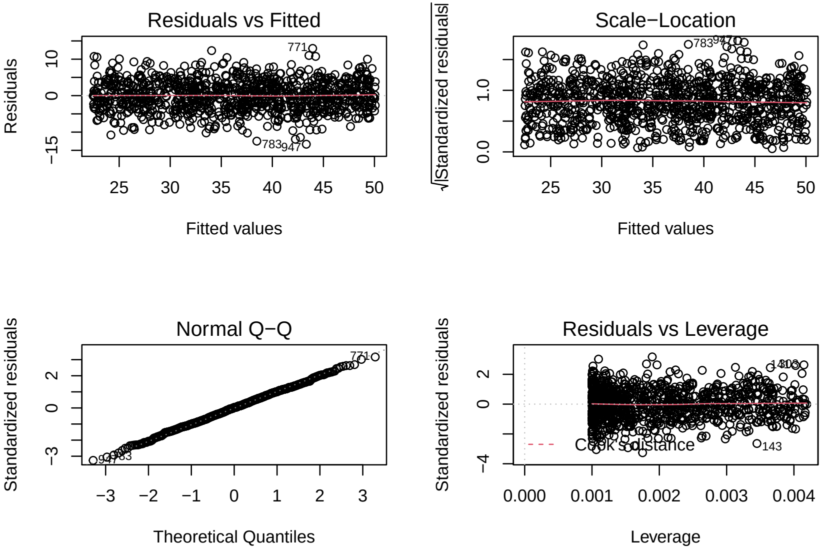
```r
hist(resid(m1))
```




```
lm(formula = height ~ dbh, data = trees)
            coef.est coef.se
(Intercept) 19.34    0.31
dbh          0.62    0.01
---
n = 1000, k = 2
residual sd = 4.09, R-Squared = 0.79
```

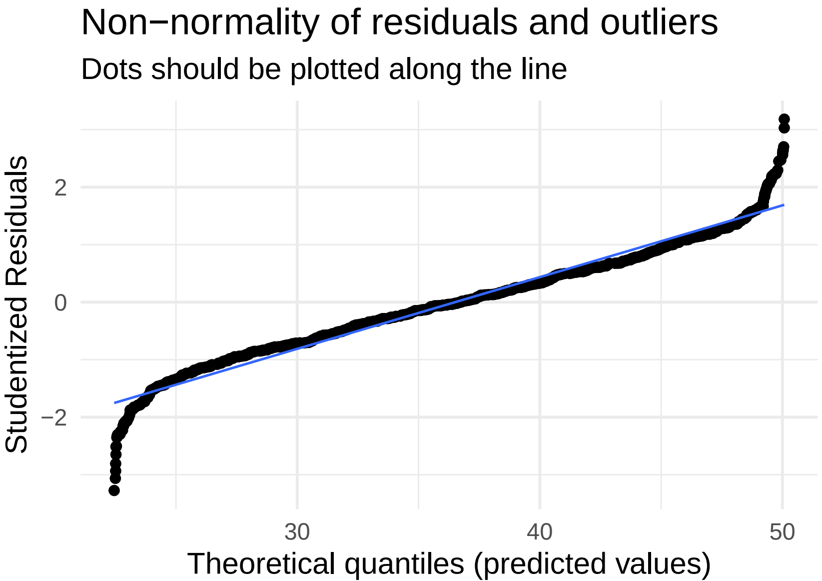
SD of residuals = 4.09 coincides with estimate of `sigma`.

Model checking: residuals



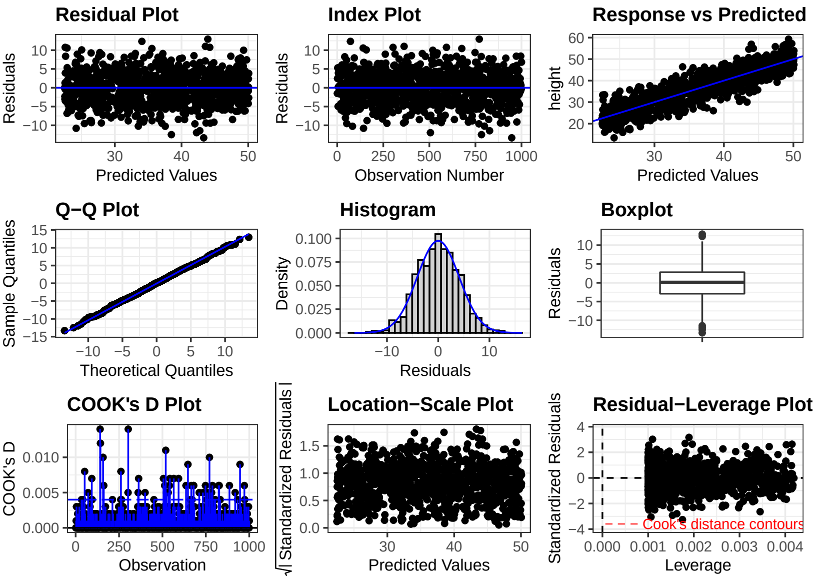
Model checking (sjPlot)

```
plot_model(m1, type = "diag")[[1]]
```



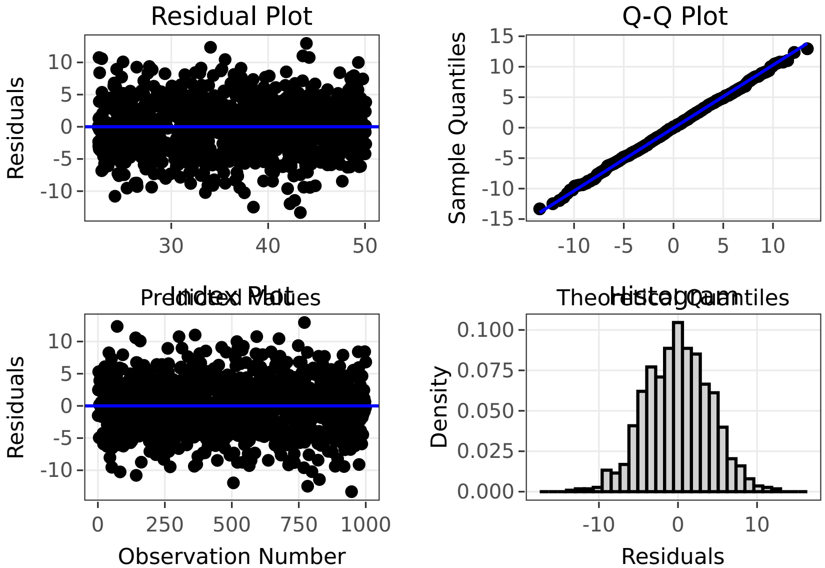
Model checking (ggResidpanel)

```
ggResidpanel::resid_panel(m1, plots = "all")
```



Interactive model checking (ggResidpanel)

```
ggResidpanel::resid_interact(m1)
```



Using model for prediction

How good is the model in predicting tree height?

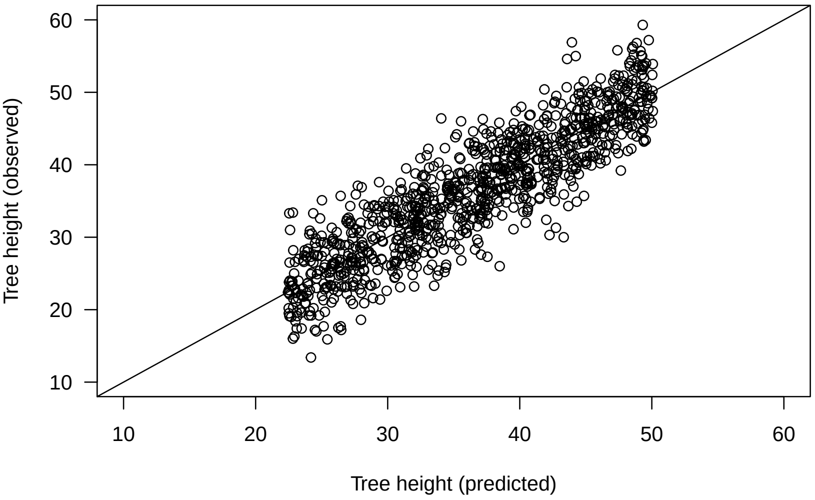
`fitted` gives predictions for each observation

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

```
  site   dbh height    sex dead height.pred
1    4 29.68   36.1   male    0    37.61328
2    5 33.29   42.3   male    0    39.83597
3    2 28.03   41.9 female    0    36.59737
4    5 39.86   46.5 female    0    43.88114
5    1 47.94   43.9 female    0    48.85603
6    1 10.82   26.2   male    0    26.00111
```

Calibration plot: Observed vs Predicted values

```r
plot(trees$height.pred, trees$height,
     xlab = "Tree height (predicted)", ylab = "Tree height (obse
```



Using fitted model for prediction

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
```

Using fitted model for prediction

Q: Expected tree height if DBH = 39 cm?

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

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

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

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

Workflow

- **Visualise data**

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- **Understand fitted model** (`summary`, `allEffects`…)

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Workflow

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- **Check model** (`plot`, `resid_panel`, calibration plot...)

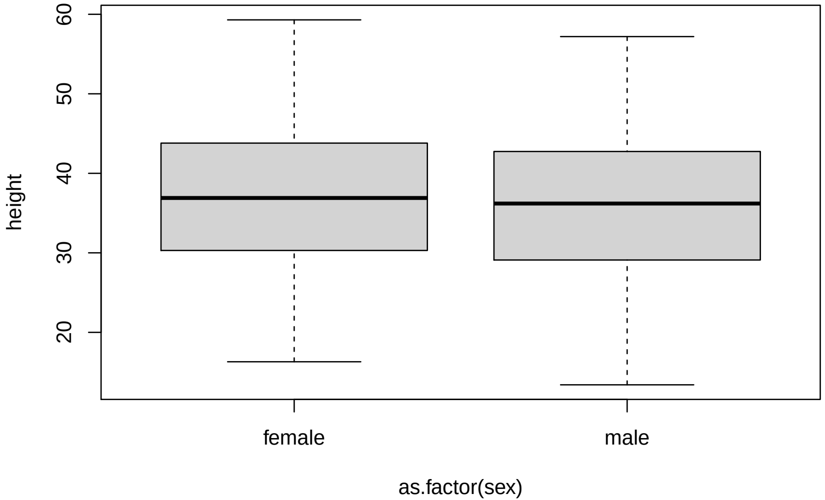
Workflow

- **Visualise data**
- **Understand fitted model** (`summary`, `allEffects`…)
- **Visualise model** (`plot(allEffects)`, `visreg`, `plot_model`…)
- **Check model** (`plot`, `resid_panel`, 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

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

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

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

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

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

Linear model with categorical predictors

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

corresponds to

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

Model height ~ sex

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

```

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

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```

Quiz

https://pollev.com/franciscorod726

Presenting model results

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	36.93	0.40	92.78	0.00
sexmale	-0.84	0.56	-1.50	0.13

Effects: Height ~ sex

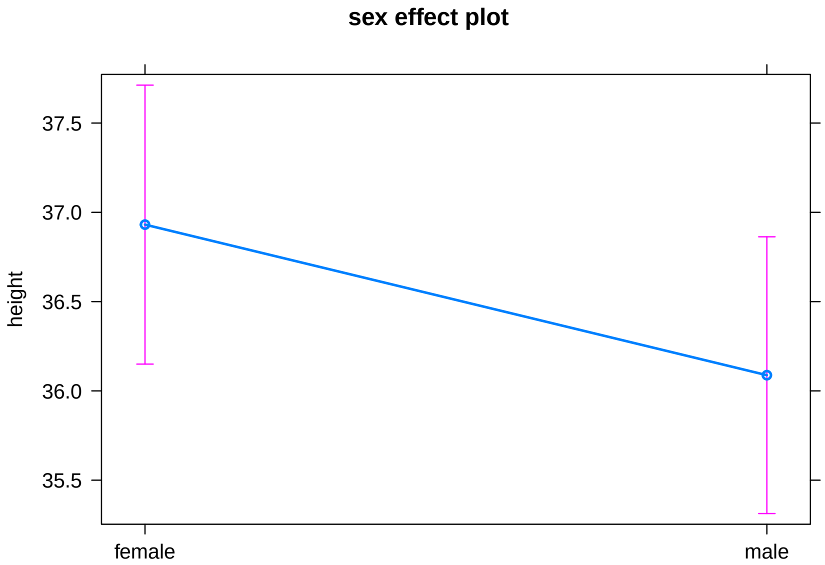
Compare CIs

```r
summary(allEffects(m2))
```

```
 model: height ~ sex

 sex effect
sex
  female     male
36.93125 36.08810

 Lower 95 Percent Confidence Limits
sex
  female     male
36.15012 35.31319

 Upper 95 Percent Confidence Limits
sex
  female     male
37.71238 36.86300
```

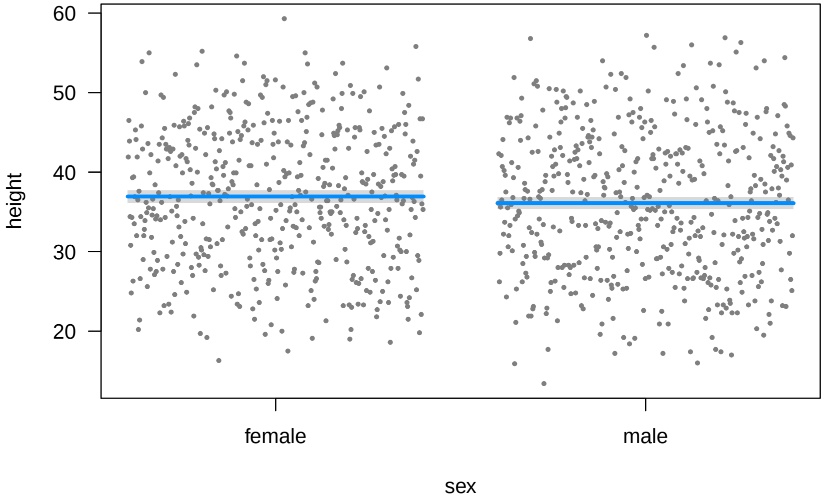
Plot

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



Plot (visreg)

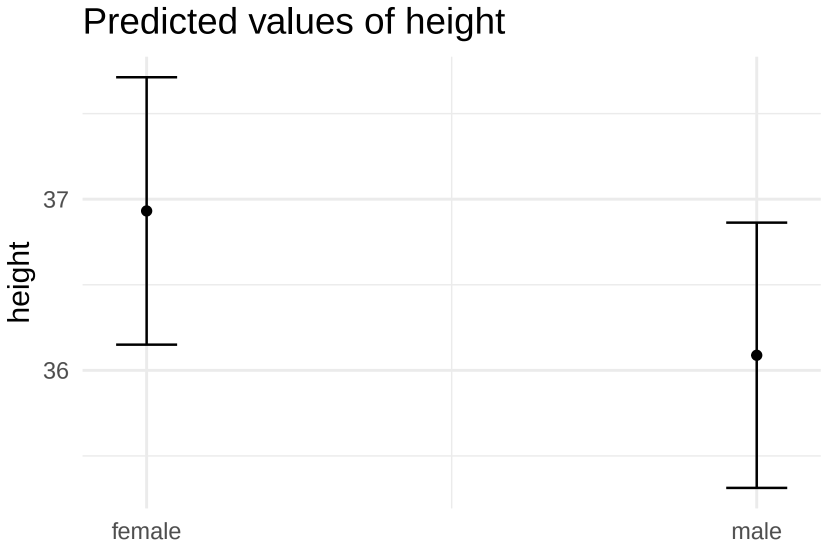
```
visreg(m2)
```



Plot model (sjPlot)

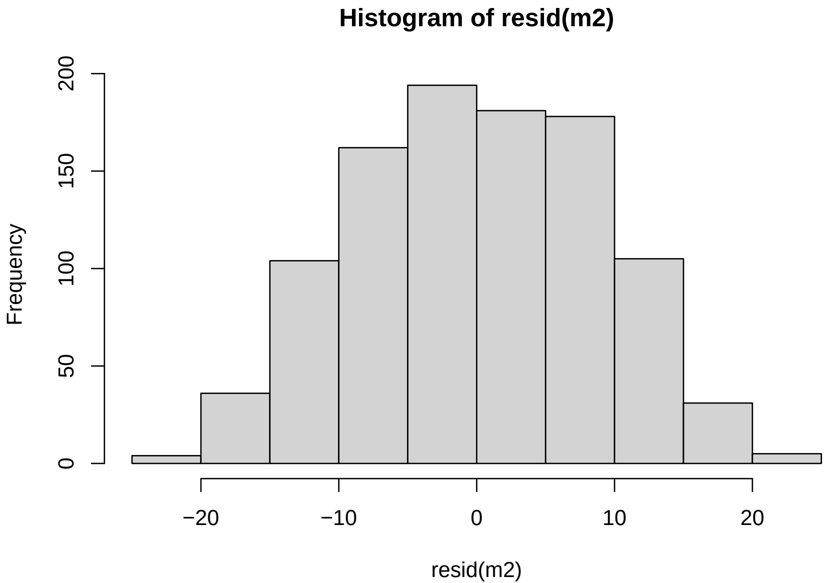
```
plot_model(m2, type = "eff")
```

```
$sex
```

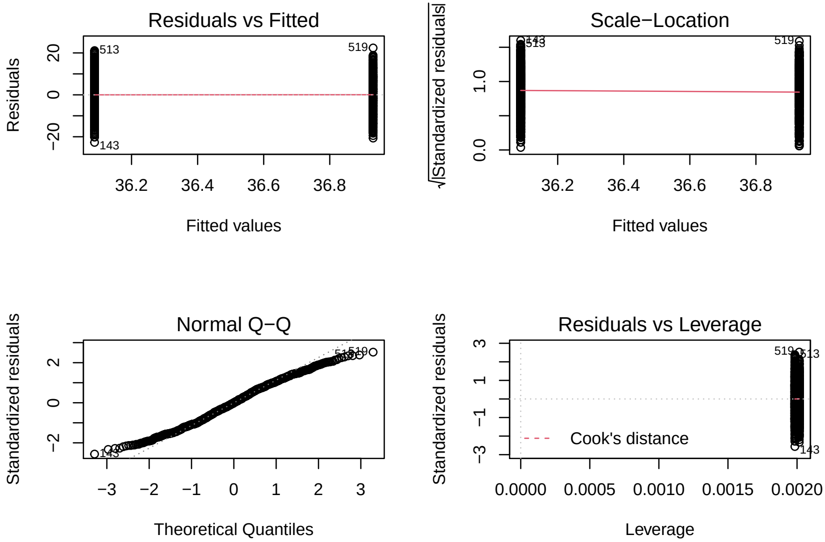


Model checking: residuals

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

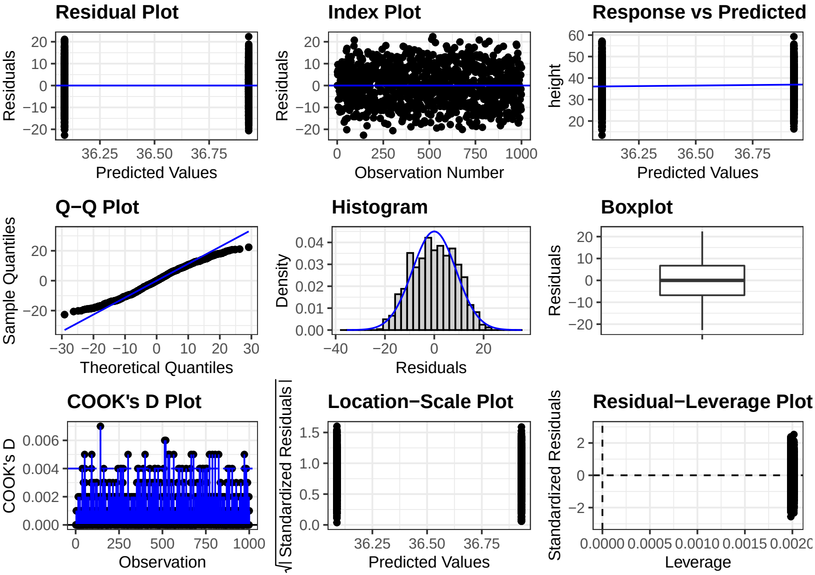


Model checking: residuals



Model checking (ggResidpanel)

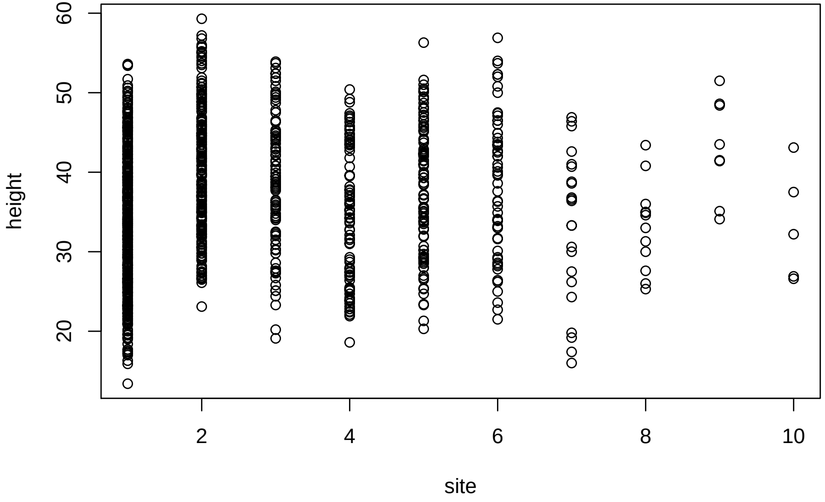
```
ggResidpanel::resid_panel(m2, plots = "all")
```



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)
```

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

Model Height ~ site

All right here?

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

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

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

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

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

site is a factor!

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

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
```

Presenting model results

```r
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

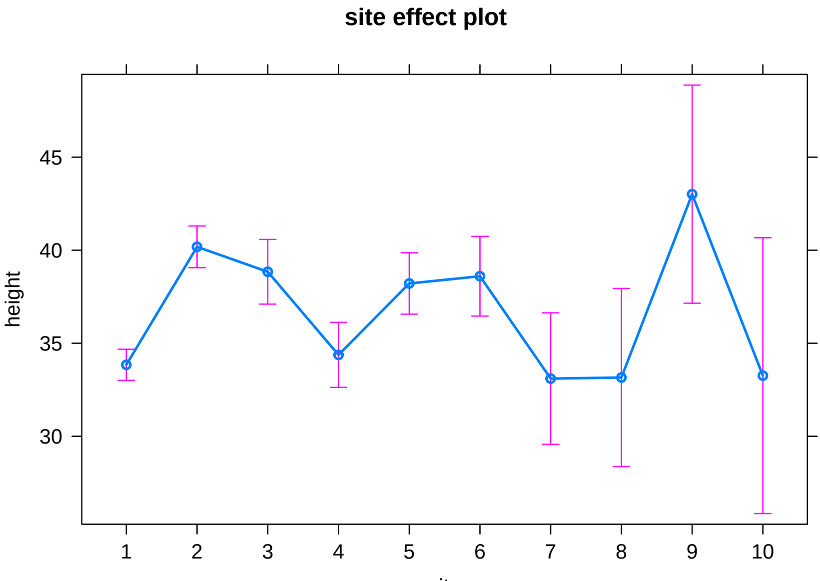
Estimated tree heights for each site

```r
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 
```

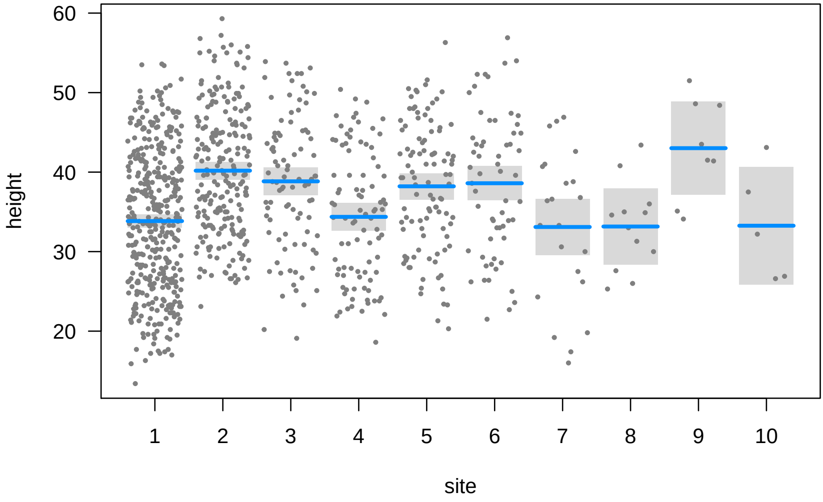
Plot

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



Plot (visreg)

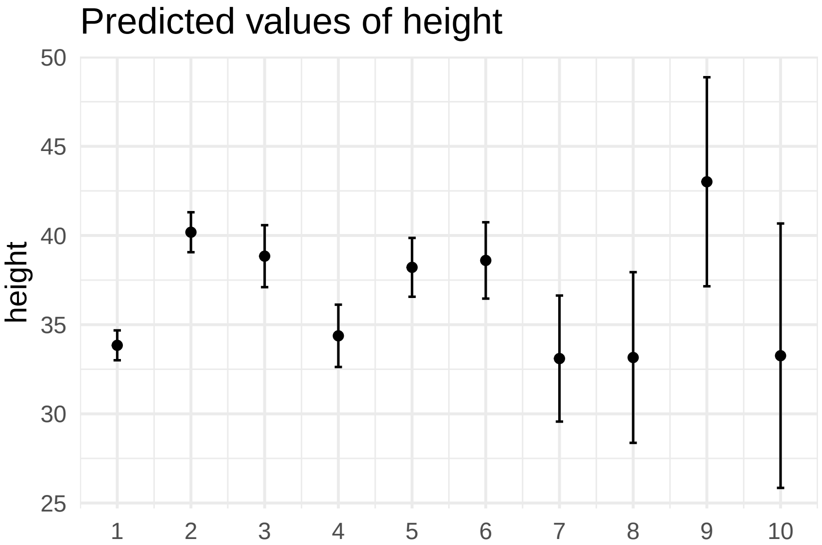
```
visreg(m3)
```



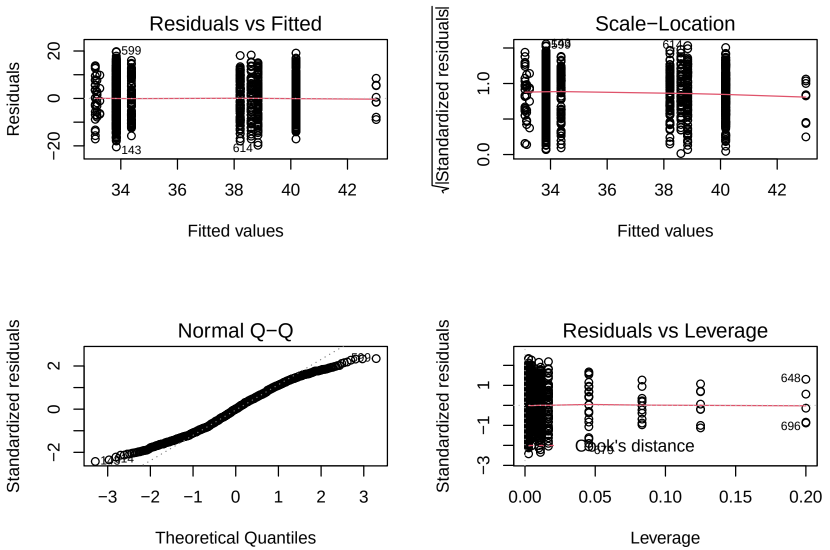
Plot model (sjPlot)

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

```
$site
```



Model checking: residuals



Combining continuous and categorical predictors

Predicting tree height based on dbh and site

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

corresponds to

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

Predicting tree height based on dbh and site

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

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

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

Residual standard error: 3.043 on 989 degrees of freedom
Multiple R-squared:  0.8835,    Adjusted R-squared:  0.8823
F-statistic:   750 on 10 and 989 DF,  p-value: < 2.2e-16
```

Presenting model results

```
kable(xtable::xtable(m4), digits = 2)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	16.70	0.26	64.09	0.00
site2	6.50	0.26	25.34	0.00
site3	4.36	0.35	12.30	0.00
site4	1.93	0.36	5.43	0.00
site5	3.64	0.34	10.71	0.00
site6	4.20	0.42	9.97	0.00
site7	-0.18	0.67	-0.26	0.79
site8	-5.31	0.89	-5.95	0.00
site9	5.44	1.09	5.00	0.00
site10	2.26	1.37	1.65	0.10
dbh	0.62	0.01	81.47	0.00

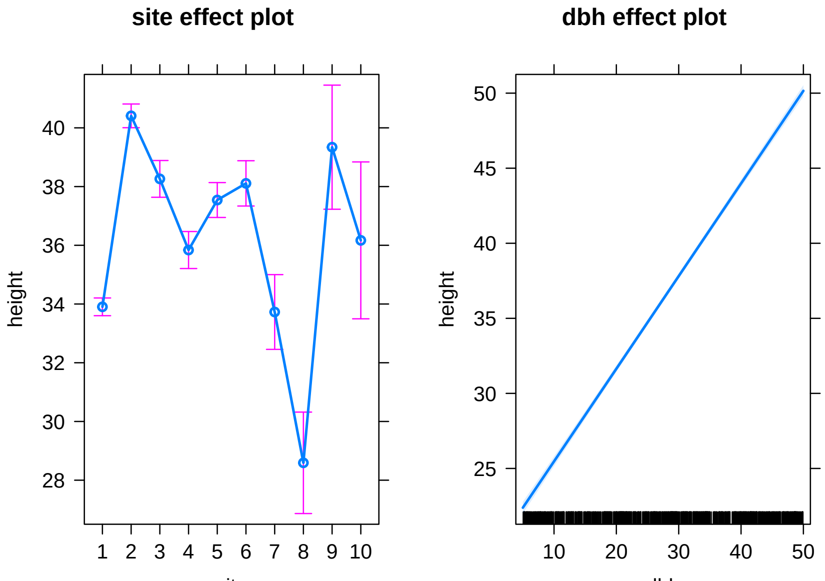
Estimated tree heights for each site

```r
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
dbh
       5       20       30       40       50 
22.38634 31.64246 37.81321 43.98396 50.15471 

 Lower 95 Percent Confidence Limits
```

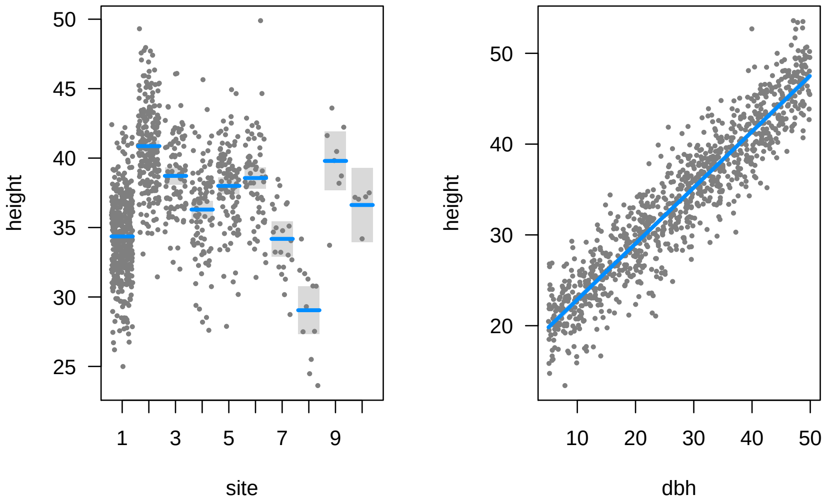
Plot

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



Plot (visreg)

```
visreg(m4)
```

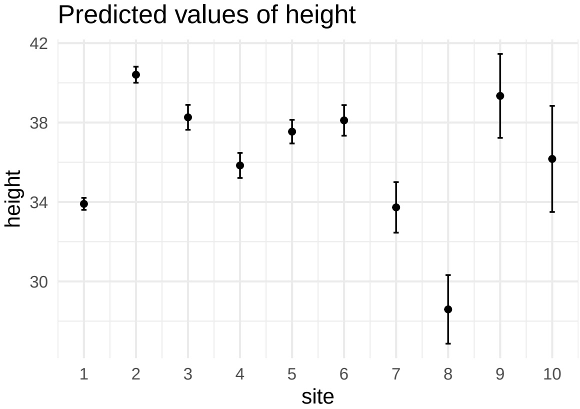



```
null device
          1
```

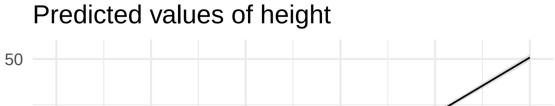
Plot model (sjPlot)

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

```
$site
```

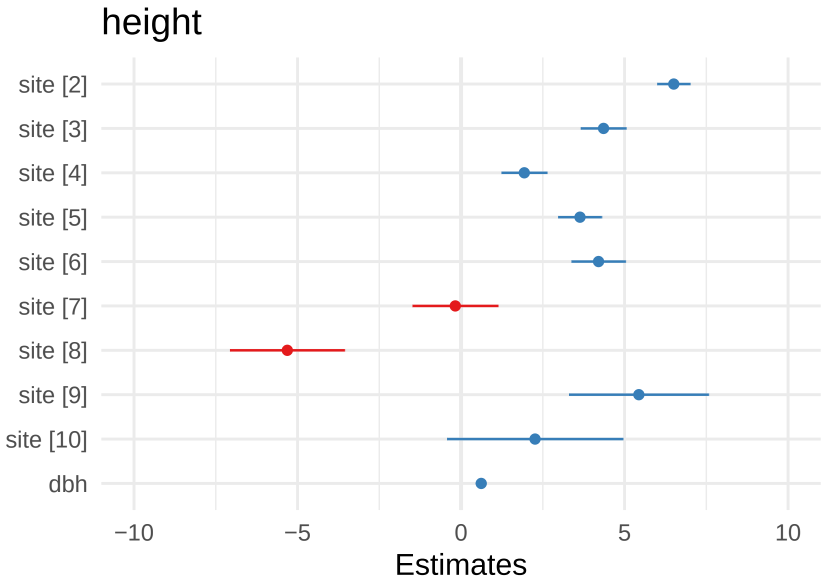



```
$dbh
```

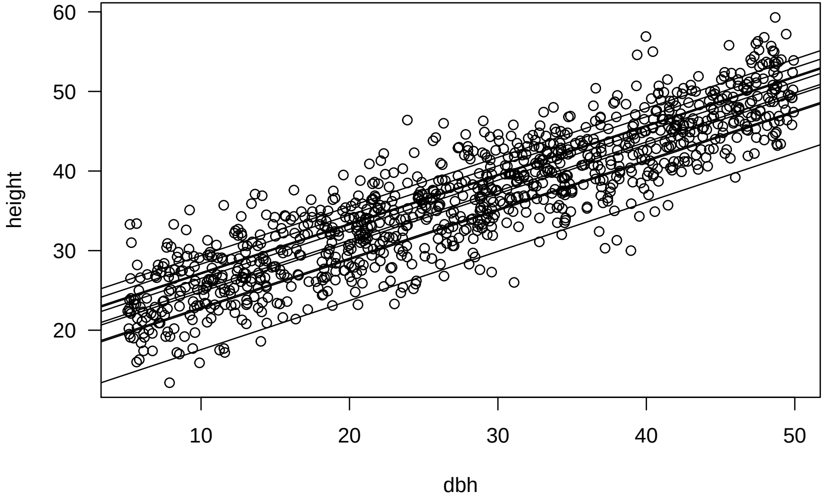


Plot model (sjPlot)

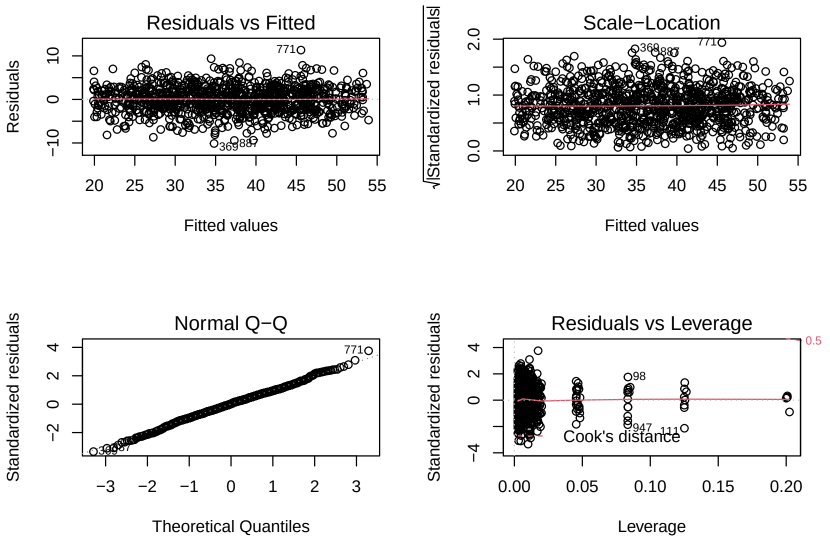
```
plot_model(m4, type = "est")
```



We have fitted model w/ many intercepts and single slope

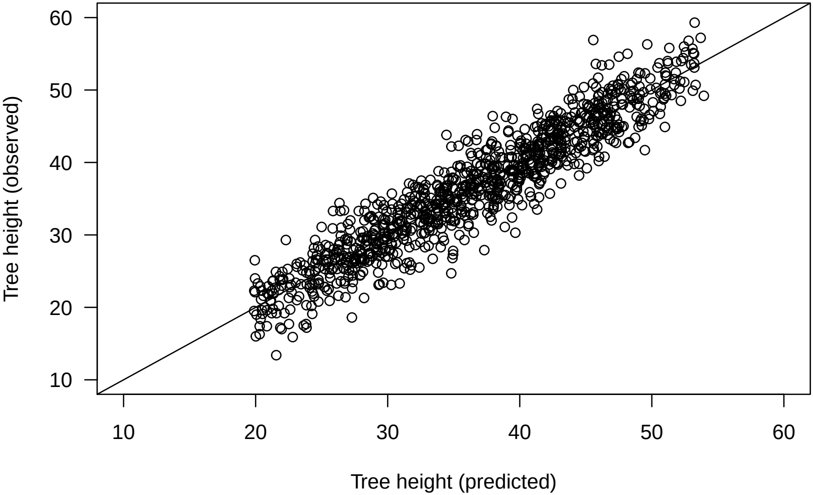


Model checking: residuals



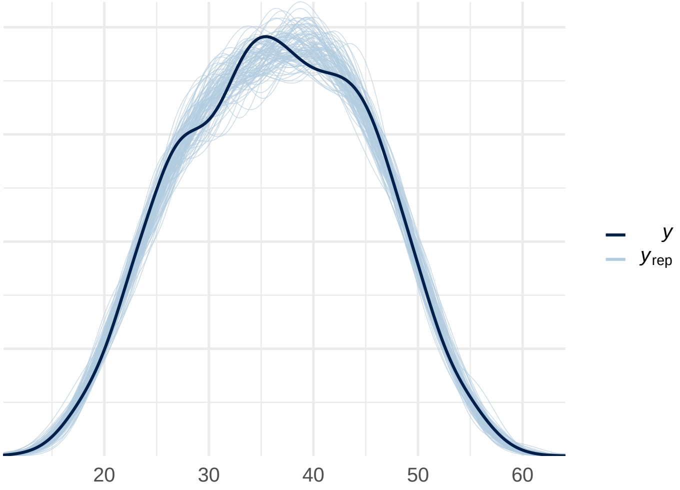
How good is this model? Calibration plot

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



Model checking with simulated data

```
library(bayesplot)
sims <- simulate(m4, nsim = 100)
ppc_dens_overlay(trees$height, yrep = t(as.matrix(sims)))
```



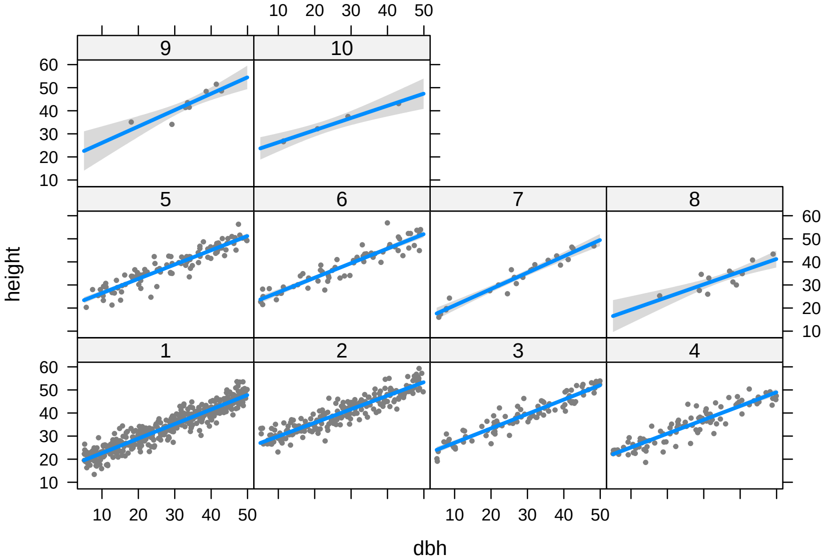
Q: Does allometric relationship between DBH and Height vary among sites?

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
F-statistic: 395.7 on 19 and 980 DF,  p-value: < 2.2e-16
```

Does slope vary among forests?

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



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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- mammal sleep: Are sleep patterns related to diet?
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- Penguins data: Body mass $\sim$ Flipper length, Bill length $\sim$ Bill depth, differences across sites...

Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?
- mammal sleep: Are sleep patterns related to diet?
- iris: Predict petal length $\sim$ petal width and species
- Penguins data: Body mass $\sim$ Flipper length, Bill length $\sim$ Bill depth, differences across sites...
- racing pigeons: is speed related to sex?

Generalised Linear Models: Logistic regression

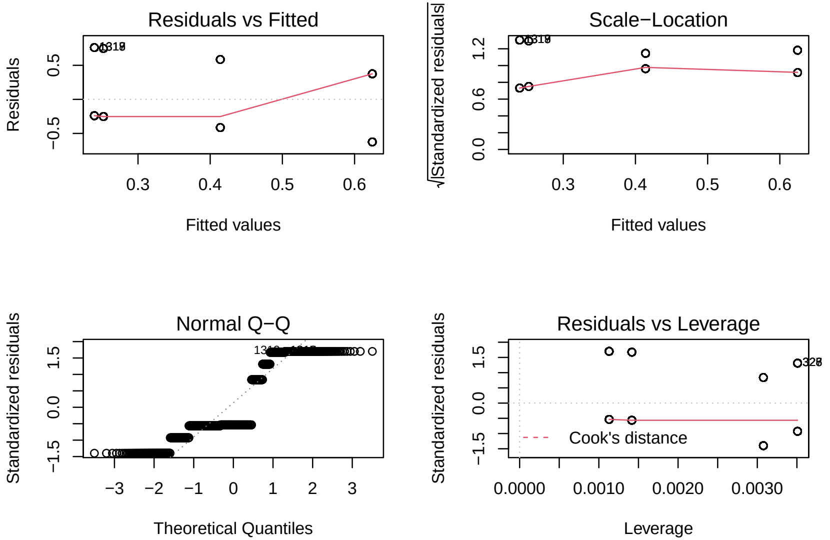
Q: Survival of passengers on the Titanic ∼ Class

Read `titanic_long.csv` dataset.

```
  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
```

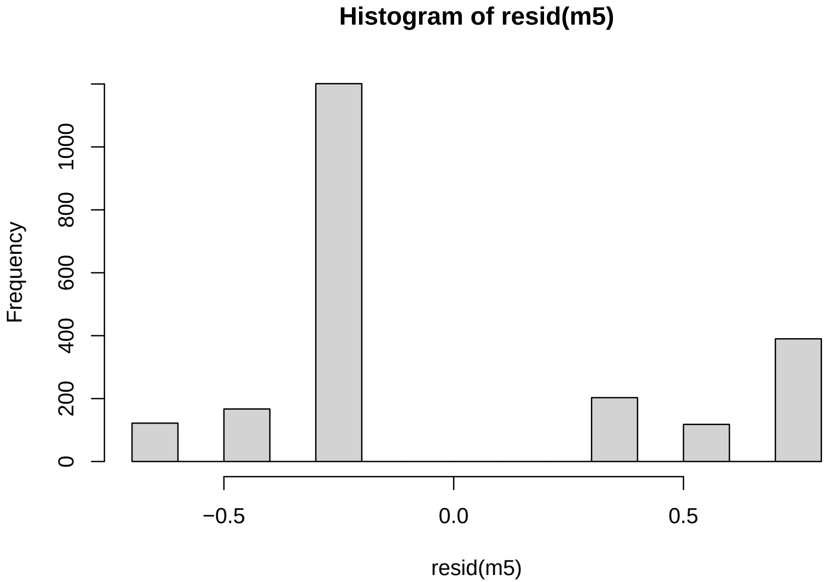
Let's fit linear model:

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




```
null device
          1
```

Weird residuals!



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

- Binary variables (0/1)

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

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

Generalised Linear Models

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

Generalised Linear Models

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

Generalised Linear Models

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

Generalised Linear Models

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

Generalised Linear Models

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

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit, probit

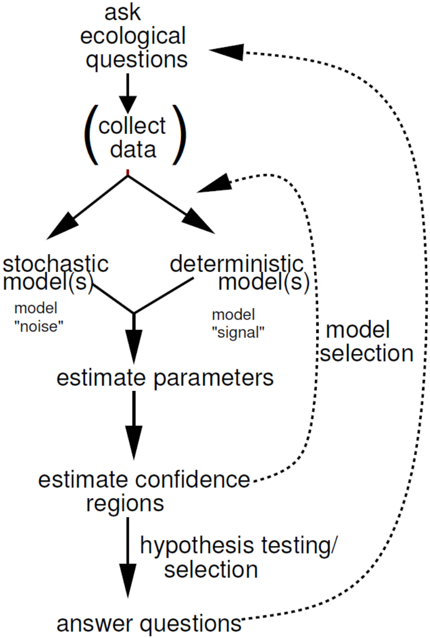
Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
    - Gaussian: identity
    - Binomial: logit, probit
    - Poisson: log...

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit, probit
   - Poisson: log...
   - See `family`.

The modelling process



Bernouilli - Binomial distribution (Logistic regression)

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

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

Then

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

Bernouilli - Binomial distribution (Logistic regression)

- Response variable: **Yes/No** (e.g. survival, sex, presence/absence)
- Link function: `logit` (others possible, see `family`).

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

Then

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

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
```

Back to survival of Titanic passengers (dplyr)

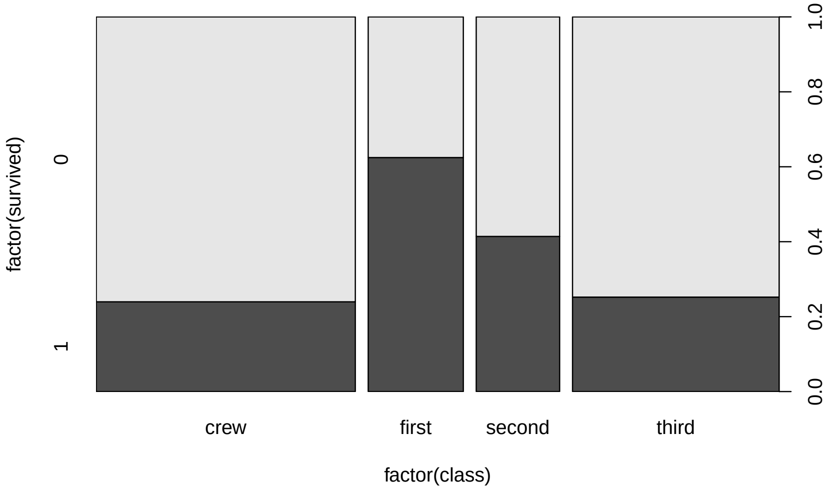
Passenger survival according to class

```
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
```

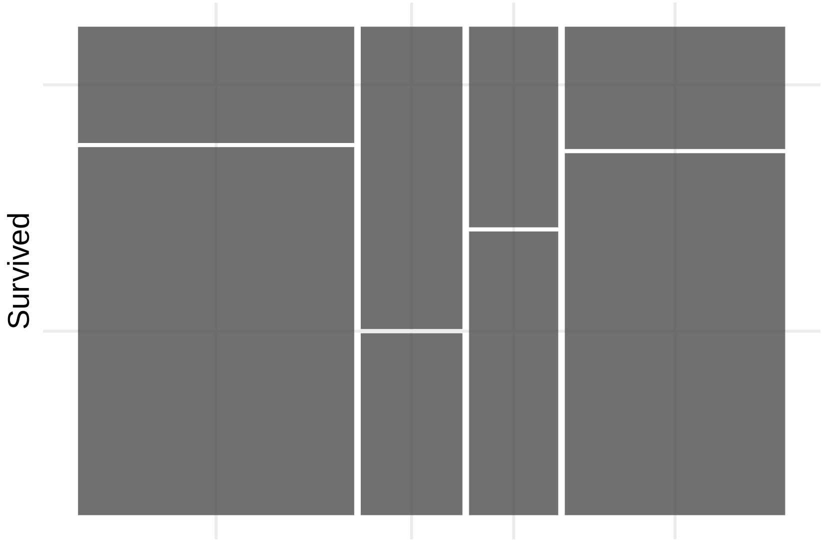
Or graphically...

```r
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

$$logit(Pr(survival)_i) = a + b \cdot class_i$$
$$logit(Pr(survival)_i) = a + b_{first} + c_{second} + d_{third}$$

Fitting GLMs in R: glm

```r
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 ***
classsecond  0.80785    0.14375   5.620 1.91e-08 ***
classthird   0.06785    0.11711   0.579    0.562
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

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

Number of Fisher Scoring iterations: 4
```

These estimates are in logit scale!

Interpreting logistic regression output

Parameter estimates (logit-scale)

```
(Intercept)  classfirst classsecond  classthird
-1.15515905  1.66434399  0.80784987  0.06784632
```

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

Crew probability of survival:

```r
plogis(coef(tit.glm)[1])
```

```
(Intercept)
   0.239548
```

Looking at the data, the proportion of crew who survived is

```
[1] 0.239548
```

Q: Probability of survival for 1st class passengers?

```
plogis(coef(tit.glm)[1] + coef(tit.glm)[2])
```

```
(Intercept)
  0.6246154
```

Must add intercept (baseline) to the parameter estimate. Again this value matches the data:

```
sum(titanic$survived[titanic$class == "first"]) /
  nrow(titanic[titanic$class == "first", ])
```

```
[1] 0.6246154
```

Model interpretation using `effects` package

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

```
 model: survived ~ class

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

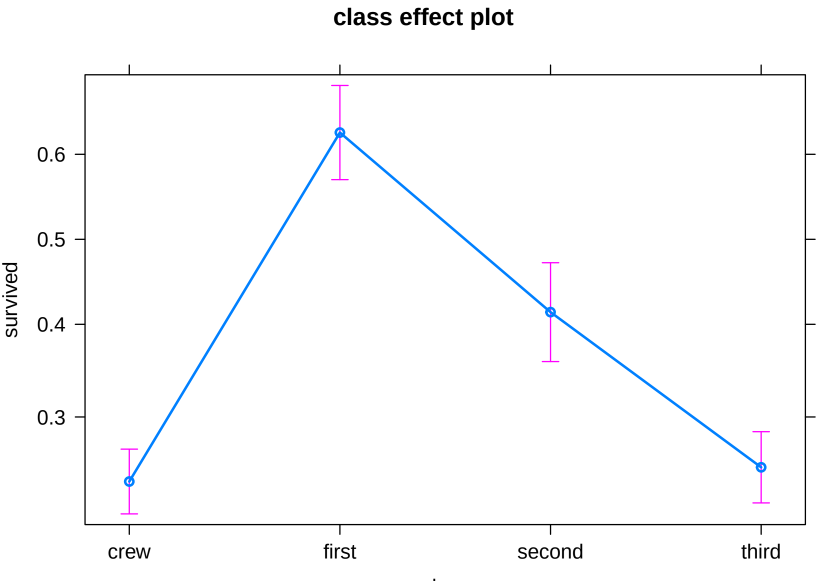
Presenting model results

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

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

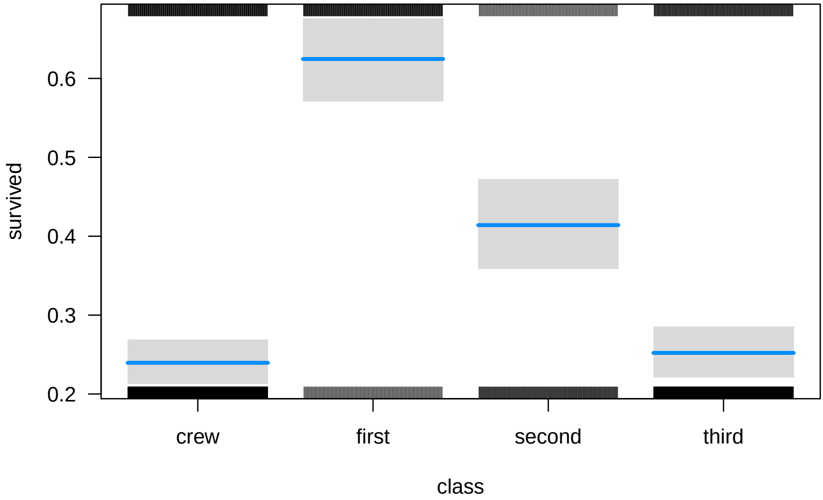
Visualising model: `effects` package

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



Visualising model: `visreg` package

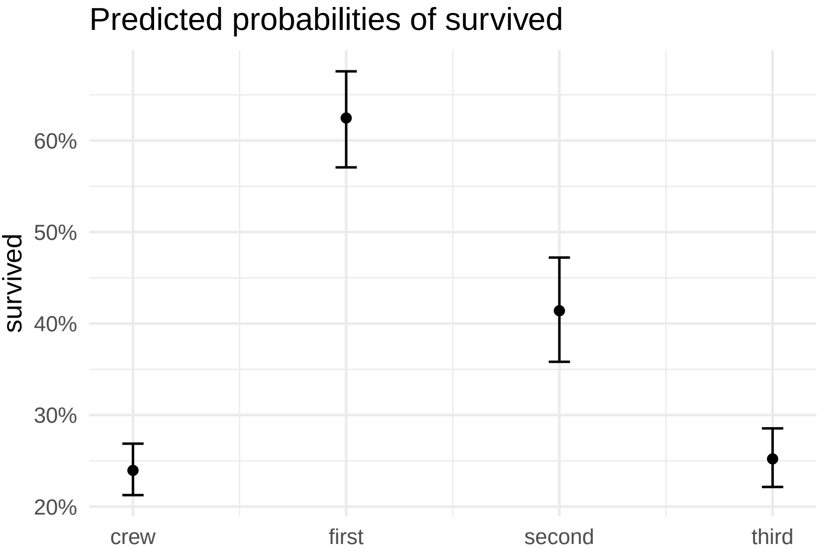
```
visreg(tit.glm, scale = "response")
```



Visualising model: `sjPlot` package

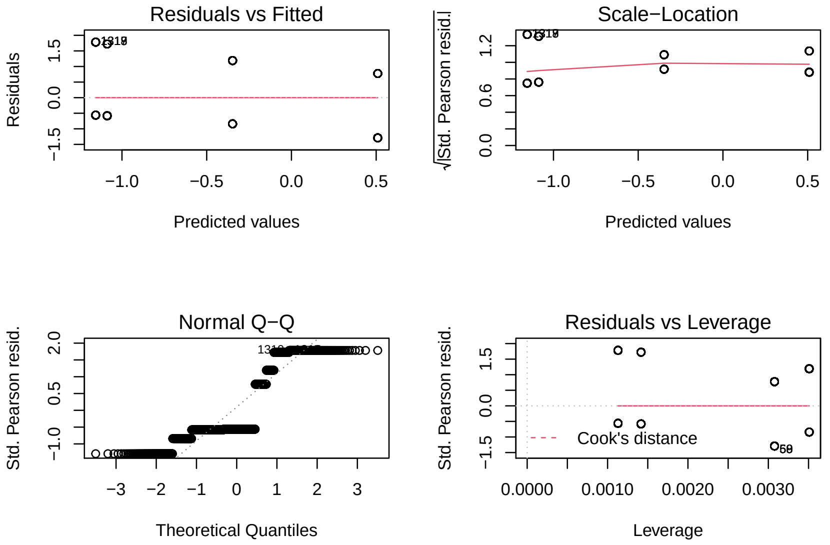
```
sjPlot::plot_model(tit.glm, type = "eff")
```

```
$class
```



Logistic regression: model checking

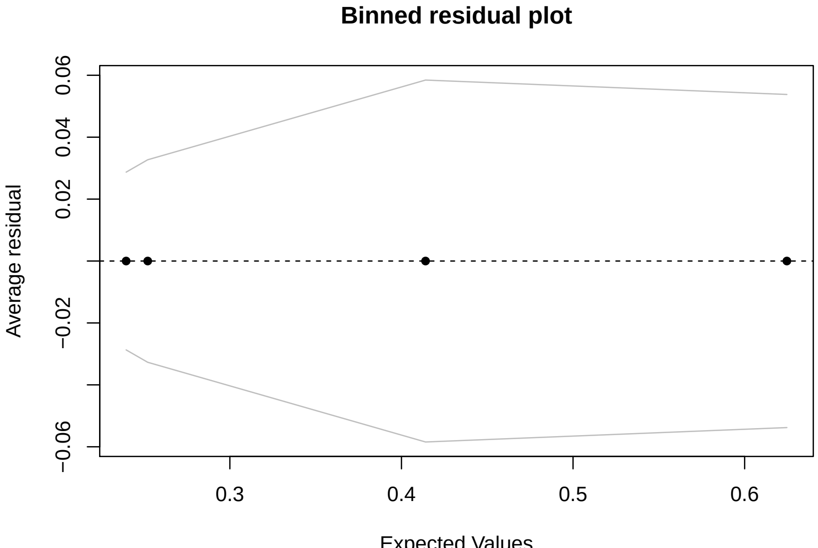
Not very useful




```
null device
```

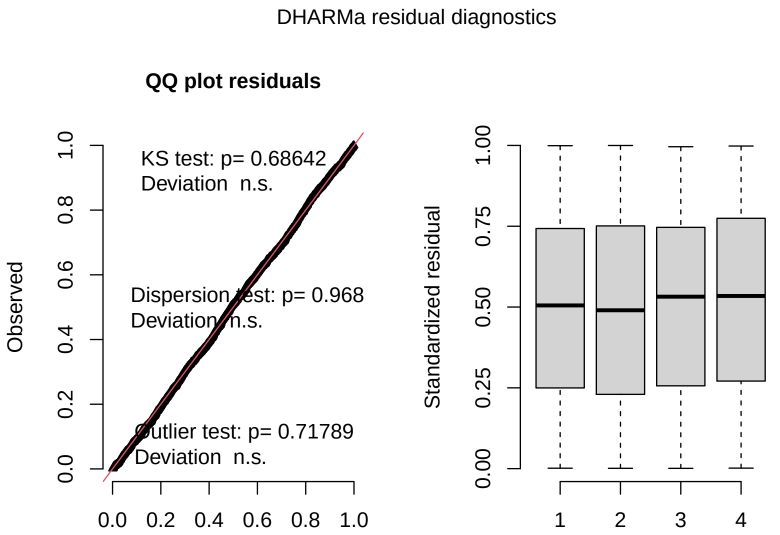
Binned residual plots for logistic regression

```r
predvals <- predict(tit.glm, type="response")
arm::binnedplot(predvals, titanic$survived - predvals)
```



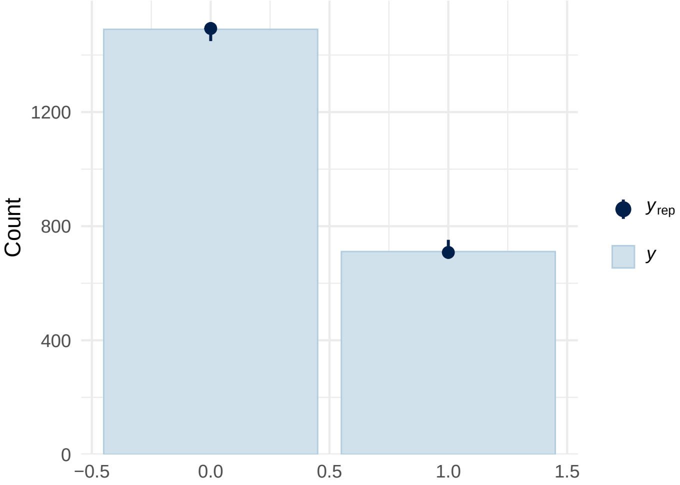
Residual diagnostics with DHARMa

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



Model checking with simulated data

```
library(bayesplot)
sims <- simulate(tit.glm, nsim = 100)
ppc_bars(titanic$survived, yrep = t(as.matrix(sims)))
```



Pseudo R-squared for GLMs

```r
library(performance)
r2(tit.glm)
```

```
$R2_Tjur
 Tjur's R2
0.08650663
```

But many caveats apply! (e.g. see here and here)

Recapitulating

1. **Visualise data**

Recapitulating

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

Recapitulating

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

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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`)
5. **Plot model**: `plot(allEffects(model))`, `visreg`, `plot_model`...

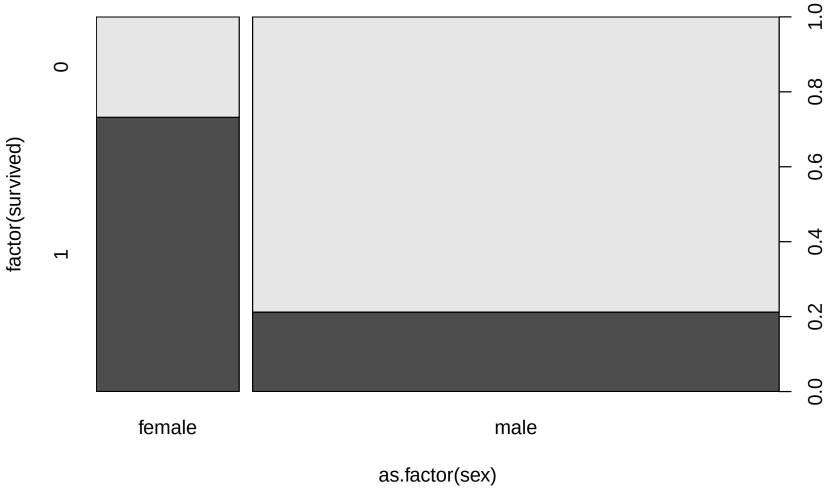
Recapitulating

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`)
5. **Plot model**: `plot(allEffects(model))`, `visreg`, `plot_model`...
6. **Examine residuals**: `DHARMa::simulateResiduals`.

Q: Did men have higher survival than women?

Plot first

```
plot(factor(survived) ~ as.factor(sex), data = titanic)
```

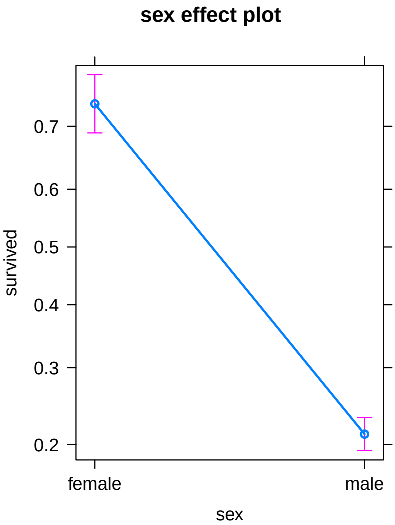


Fit model

```
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
```

Effects

```
 model: survived ~ sex

 sex effect
sex
   female      male
0.7319149 0.2120162
```



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

Let's look at the data

```r
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
```

Mmmm...

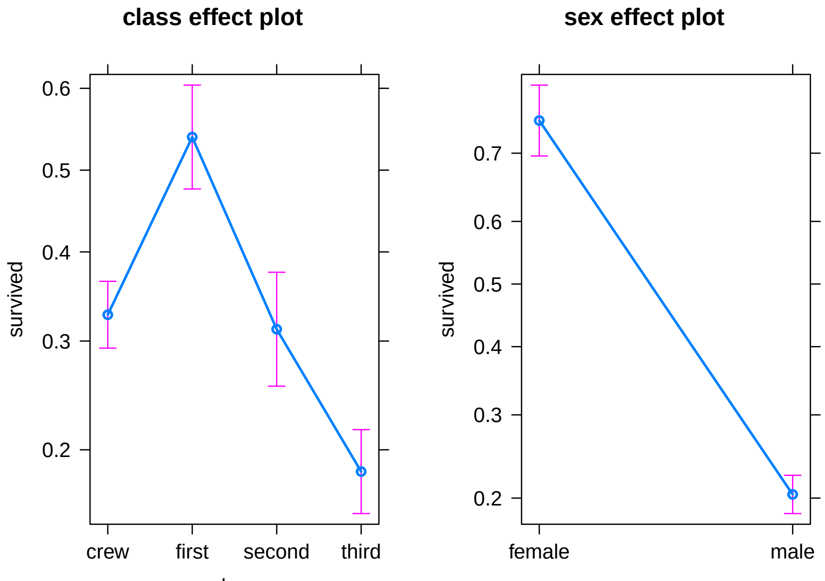
Fit additive model with both factors

```
tit.sex.class <- glm(survived ~ class + sex, family = binomial,
```

```
glm(formula = survived ~ class + sex, family = binomial, data =
            coef.est coef.se
(Intercept)  1.19     0.16
classfirst   0.88     0.16
classsecond -0.07     0.17
classthird  -0.78     0.14
sexmale     -2.42     0.14
---
  n = 2201, k = 5
  residual deviance = 2228.9, null deviance = 2769.5 (difference
```

Plot additive model

```
plot(allEffects(tit.sex.class))
```



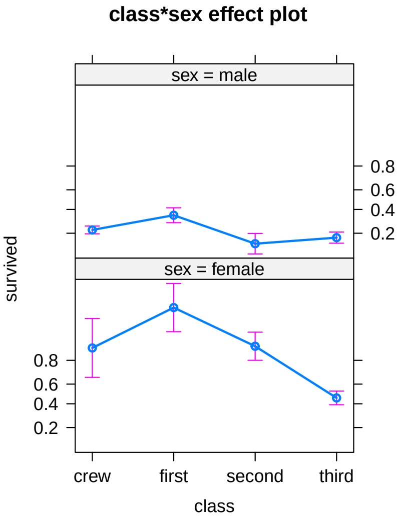
Fit model with both factors (interactions)

```r
tit.sex.class <- glm(survived ~ class * sex, family = binomial,
```

```
glm(formula = survived ~ class * sex, family = binomial, data =
                      coef.est coef.se
(Intercept)            1.90     0.62
classfirst             1.67     0.80
classsecond            0.07     0.69
classthird            -2.06     0.64
sexmale               -3.15     0.62
classfirst:sexmale    -1.06     0.82
classsecond:sexmale   -0.64     0.72
classthird:sexmale     1.74     0.65
---
  n = 2201, k = 8
  residual deviance = 2163.7, null deviance = 2769.5 (difference
```

Effects

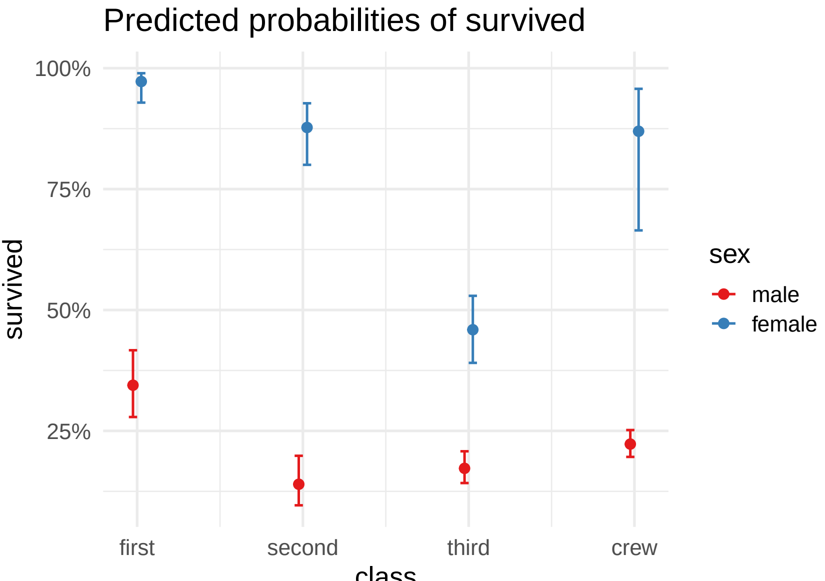
```
model: survived ~ class * sex

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
```



So, women had higher probability of survival than men, even within the same class.

Effects (sjPlot)

```
plot_model(tit.sex.class, type = "int")
```



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

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

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

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)
```

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 raw data:

```
 model: survived ~ class

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

Same results!

Logistic regression with continuous predictors

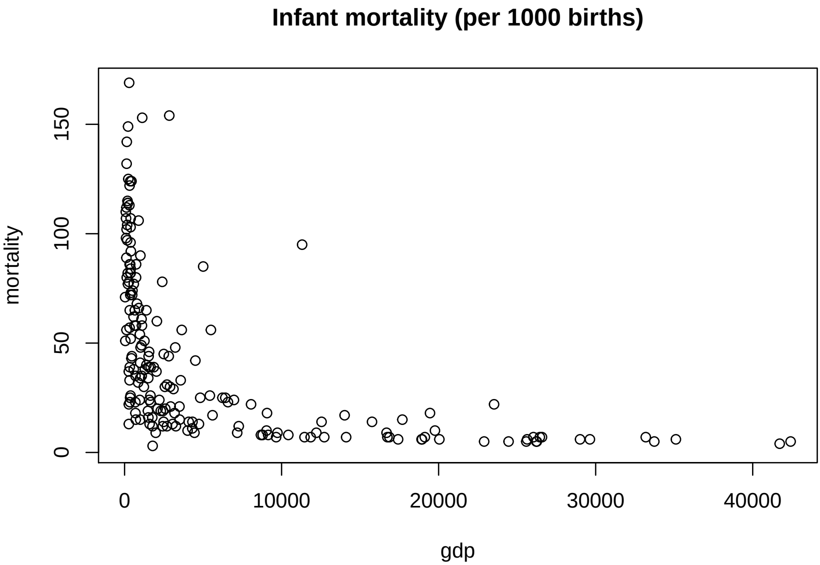
Example dataset: GDP and infant mortality

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
```

EDA

```
plot(mortality ~ gdp, data = gdp, main = "Infant mortality (per
```



Fit model

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

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

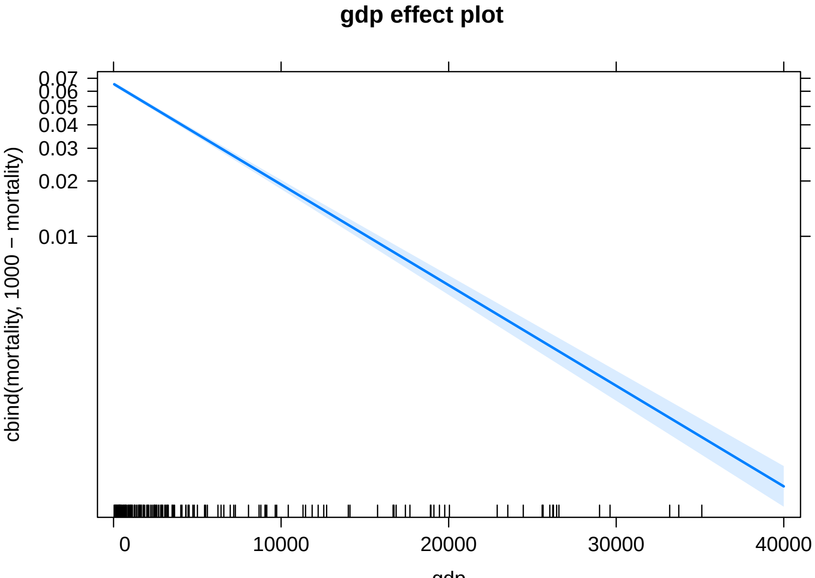
Effects

```r
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
```

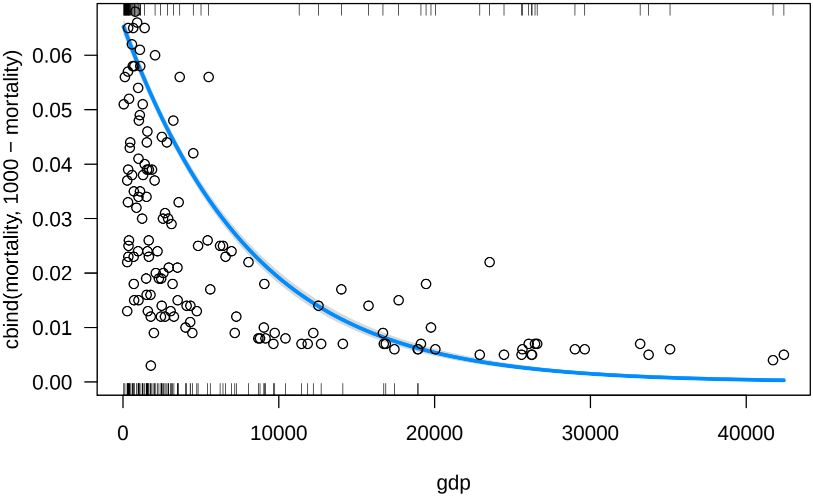
Effects plot

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



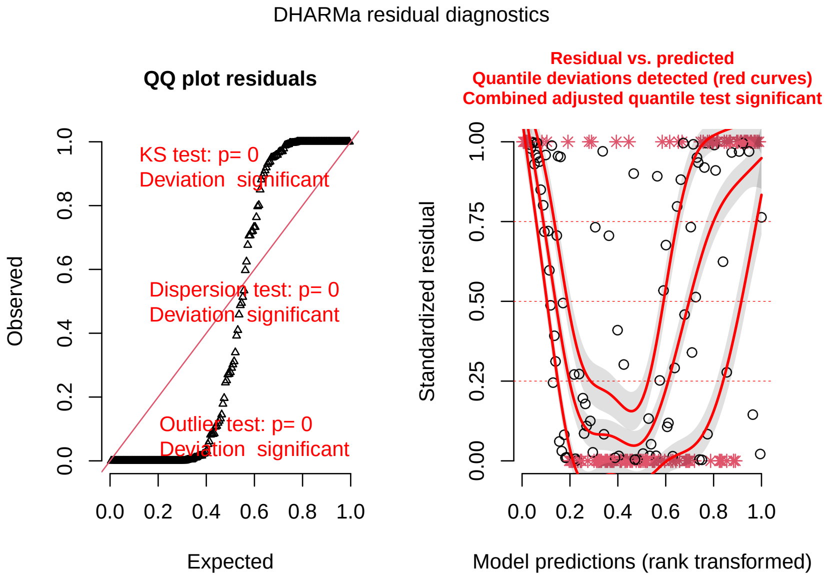
Plot model using visreg:

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



Residuals diagnostics with DHARMa

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



Overdispersion

Testing for overdispersion (DHARMa)

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

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

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

Overdispersion in logistic regression with proportion data

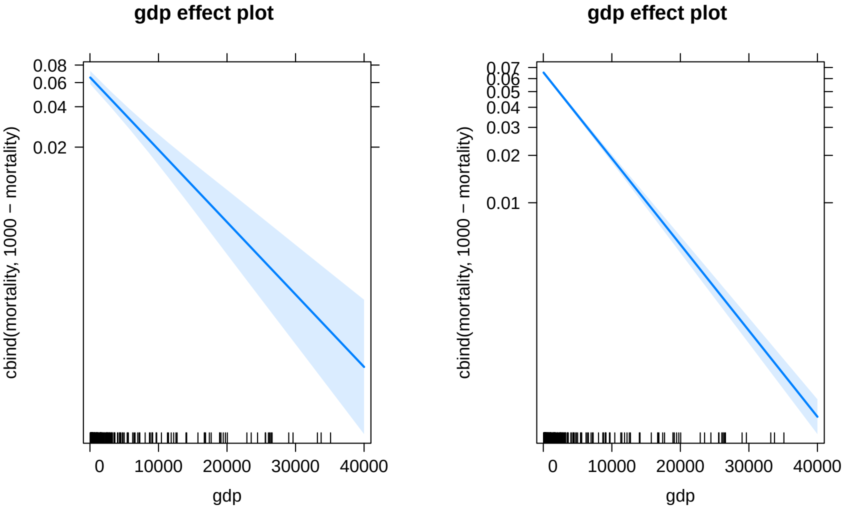
```r
gdp.overdisp <- glm(cbind(mortality, 1000 - mortality) ~ gdp,
                    data = gdp, family = quasibinomial)
```

```
Call:
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family =
    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 20.79
```

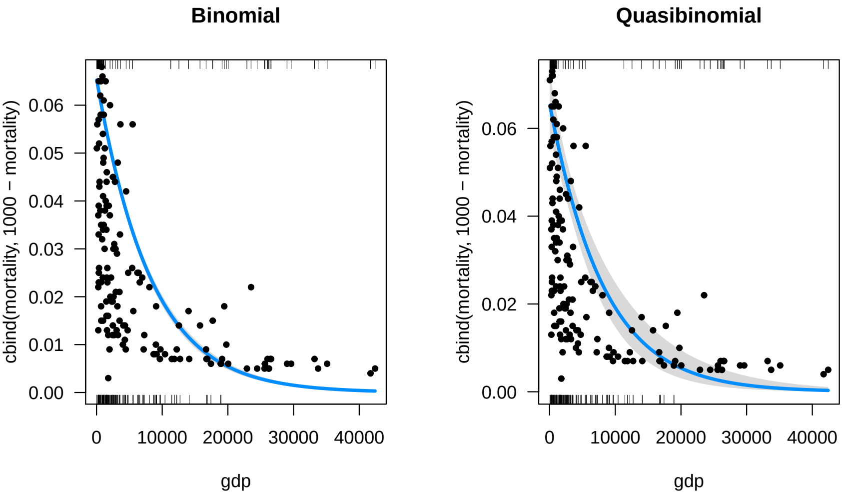
Mean estimates do not change after accounting for overdispersion

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

 gdp effect
gdp
         40        10000        20000        30000        40000
0.0652177296 0.0191438829 0.0054028095 0.0015096074 0.0004206154
 model: cbind(mortality, 1000 - mortality) ~ gdp

 gdp effect
gdp
         40        10000        20000        30000        40000
0.0652177296 0.0191438829 0.0054028095 0.0015096074 0.0004206154
```

But standard errors (uncertainty) do!



Plot model and data

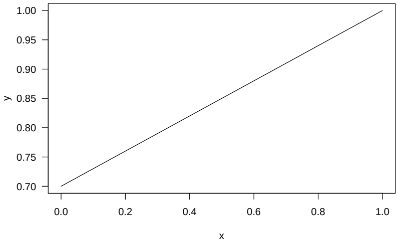


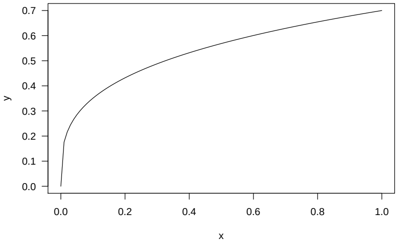
Overdispersion

Whenever you fit logistic regression to **proportion** data, check family `quasibinomial`.

Think about the shape of relationships

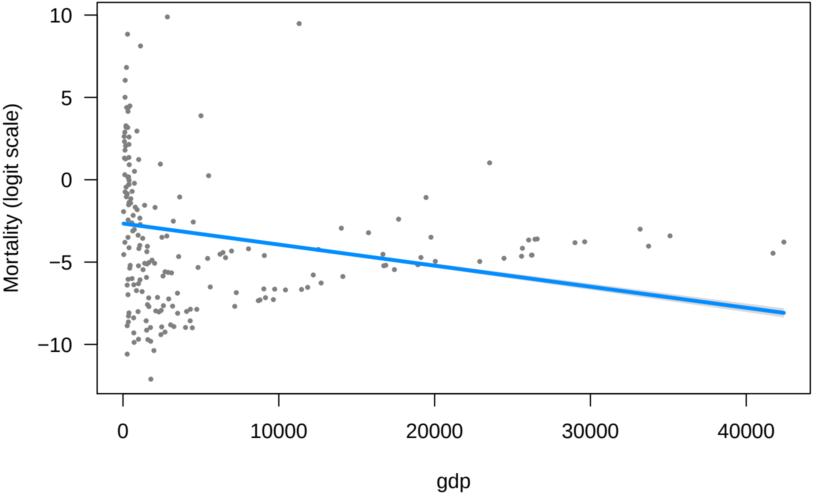
$y \sim x + z$
Really? Not everything has to be linear! Actually, it often is not.
Think about shape of relationship. See chapter 3 in Bolker's book.



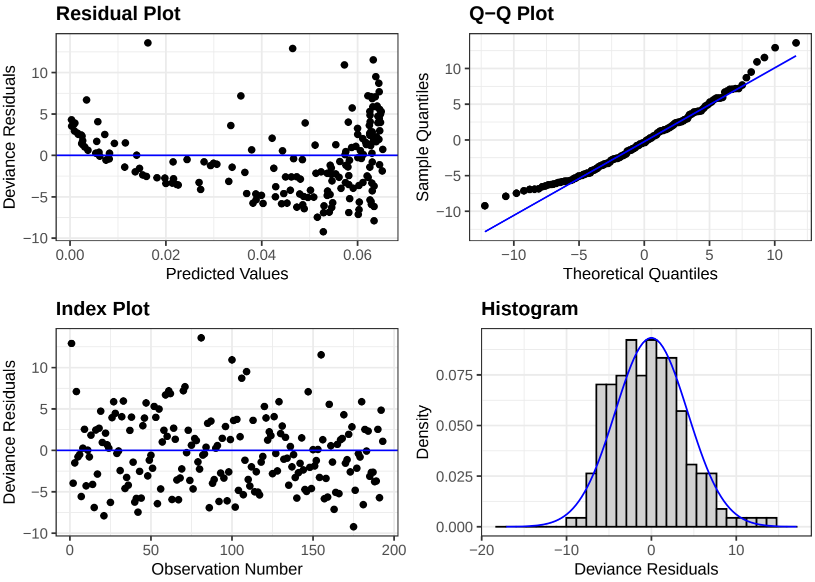


Think about the shape of relationships

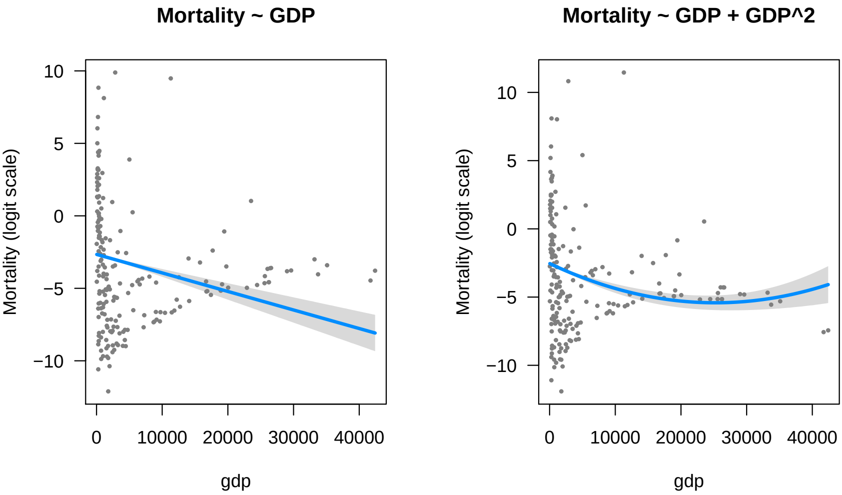
```
visreg(gdp.glm, ylab = "Mortality (logit scale)")
```



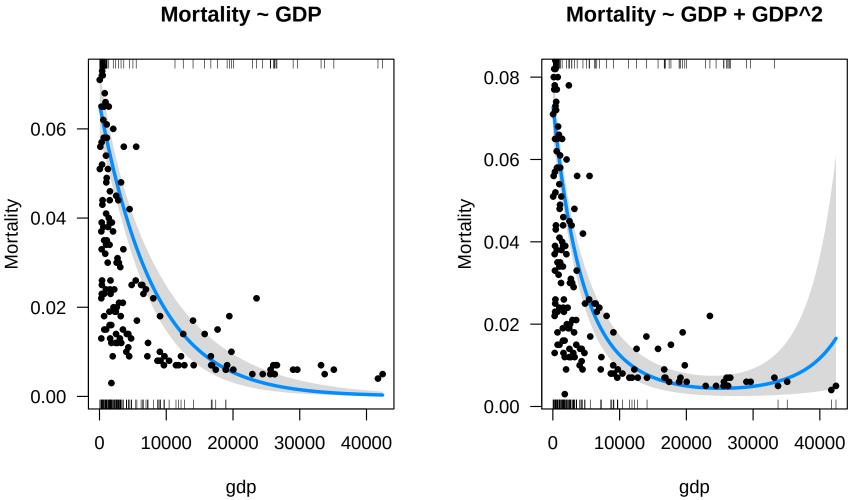
Think about the shape of relationships



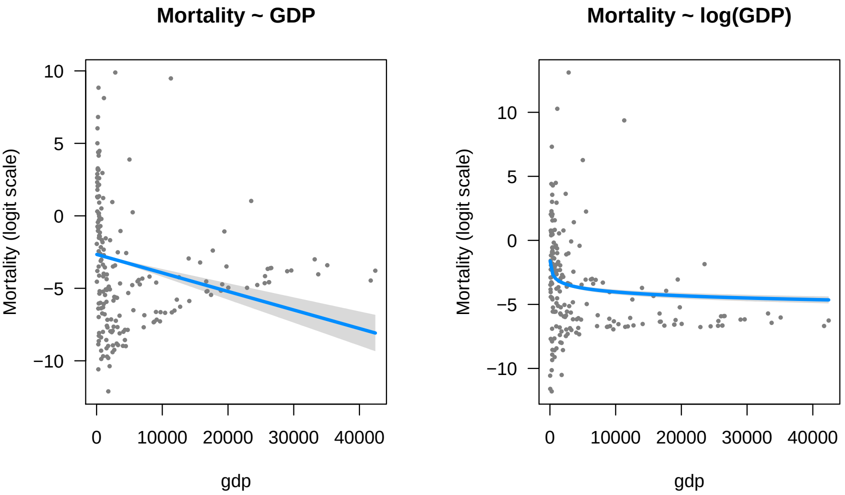
Think about the shape of relationships



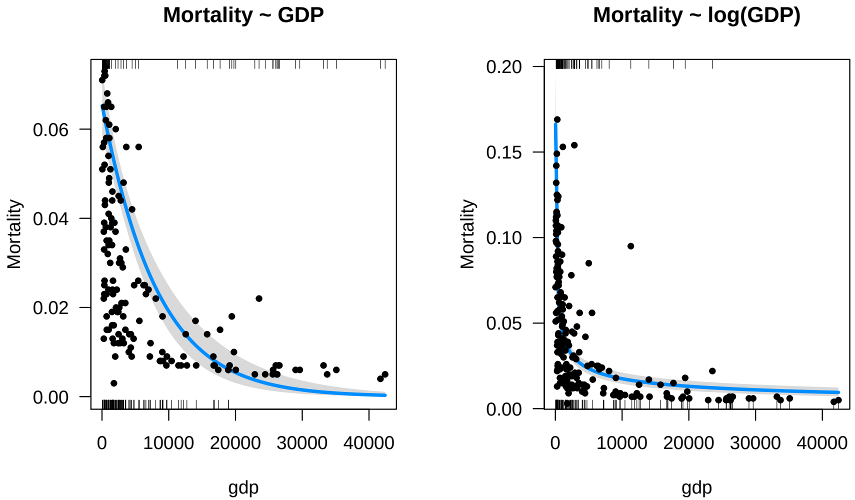
Think about the shape of relationships



Think about the shape of relationships



Think about the shape of relationships




```
gdp.log <- glm(cbind(mortality, 1000 - mortality) ~ log(gdp),
```

More examples

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

Seed set among plants

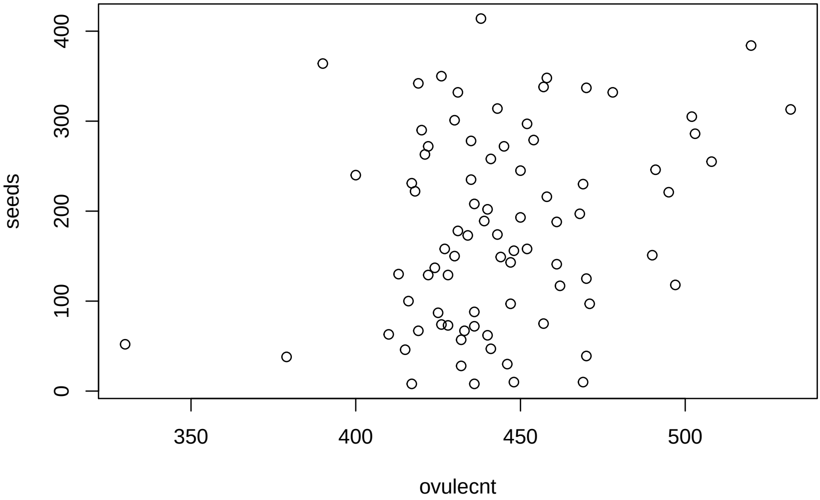
```
seed <- readr::read_csv("data/seedset.csv")
head(seed)
```

```
# 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
```

```
seed$plant <- as.factor(seed$plant)
```

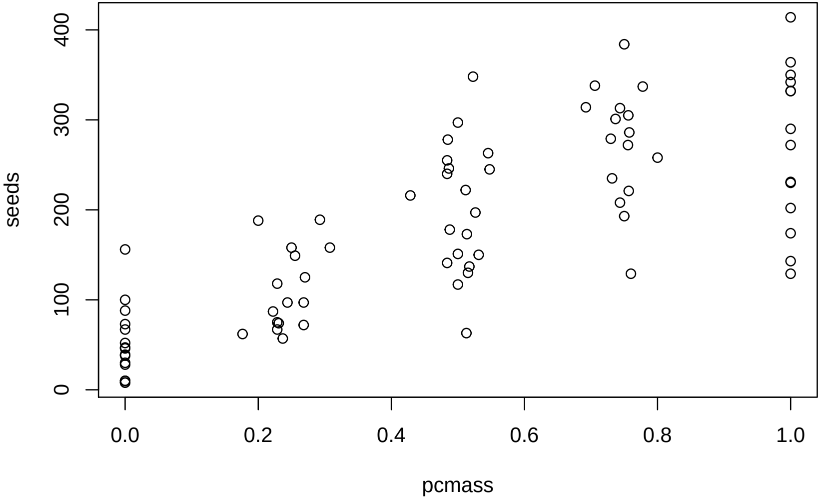
Number of seeds vs Number of ovules

```
plot(seeds ~ ovulecnt, data = seed)
```

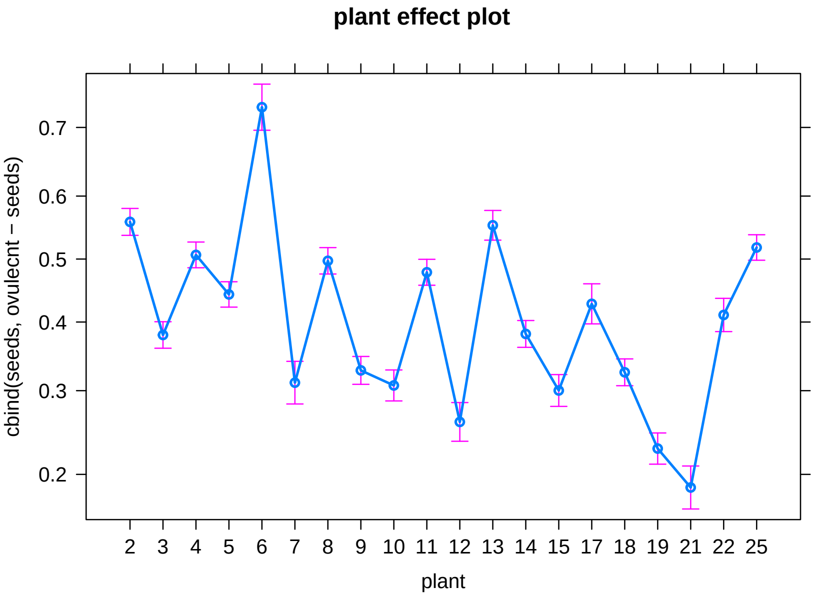


Number of seeds vs Proportion outcross pollen

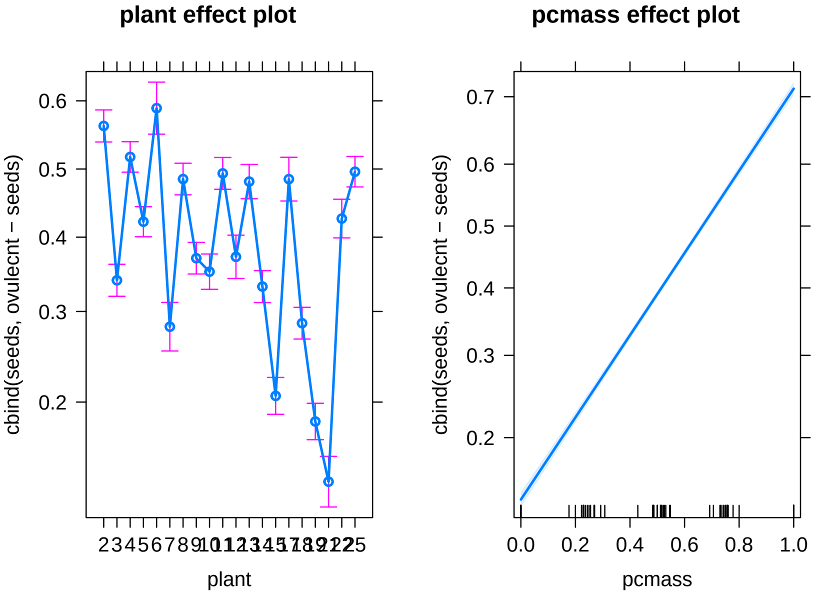
```r
plot(seeds ~ pcmass, data = seed)
```



Seed set across plants



Seed set $\sim$ outcross pollen



GLM for count data: Poisson regression

Types of response variable

- Gaussian: `lm`

Types of response variable

- Gaussian: `lm`
- Bernouilli / Binomial: `glm` (family `binomial` / `quasibinomial`)

Types of response variable

- Gaussian: `lm`
- Bernouilli / Binomial: `glm` (family `binomial / quasibinomial`)
- Counts: `glm` (family `poisson / quasipoisson`)

Poisson regression

- Response variable: Counts (0, 1, 2, 3...) - discrete

Then

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

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

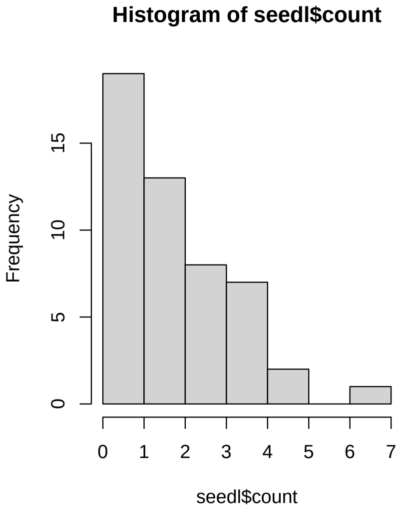
```r
seedl <- read.csv("data/seedlings.csv")
```

```
       X             count            row          col             l
 Min.   : 1.00   Min.   :0.00   Min.   :1   Min.   : 1.0   Min.
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:2   1st Qu.: 3.0   1st Q
 Median :25.50   Median :2.00   Median :3   Median : 5.5   Media
 Mean   :25.50   Mean   :2.14   Mean   :3   Mean   : 5.5   Mean
 3rd Qu.:37.75   3rd Qu.:3.00   3rd Qu.:4   3rd Qu.: 8.0   3rd Q
 Max.   :50.00   Max.   :7.00   Max.   :5   Max.   :10.0   Max.
      area
 Min.   :0.25
 1st Qu.:0.25
 Median :0.50
 Mean   :0.62
 3rd Qu.:1.00
 Max.   :1.00
```

EDA

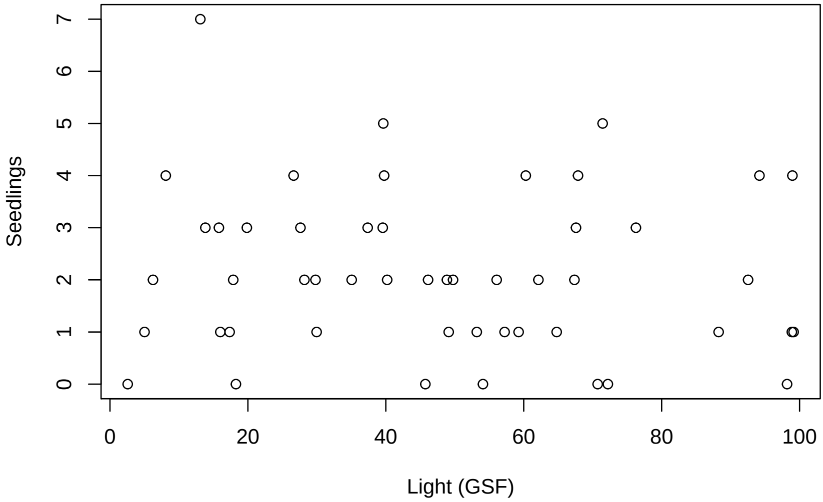
```
table(seedl$count)
```

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



Q: Relationship between Nseedlings and light?

```
plot(seedl$light, seedl$count, xlab = "Light (GSF)", ylab = "See
```



Let's fit model (Poisson regression)

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

Interpreting Poisson regression output

Parameter estimates (log scale):

```
coef(seedl.glm)
```

```
 (Intercept)        light
 0.881805022 -0.002575656
```

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

```
exp(coef(seedl.glm))
```

```
(Intercept)       light
  2.4152554   0.9974277
```

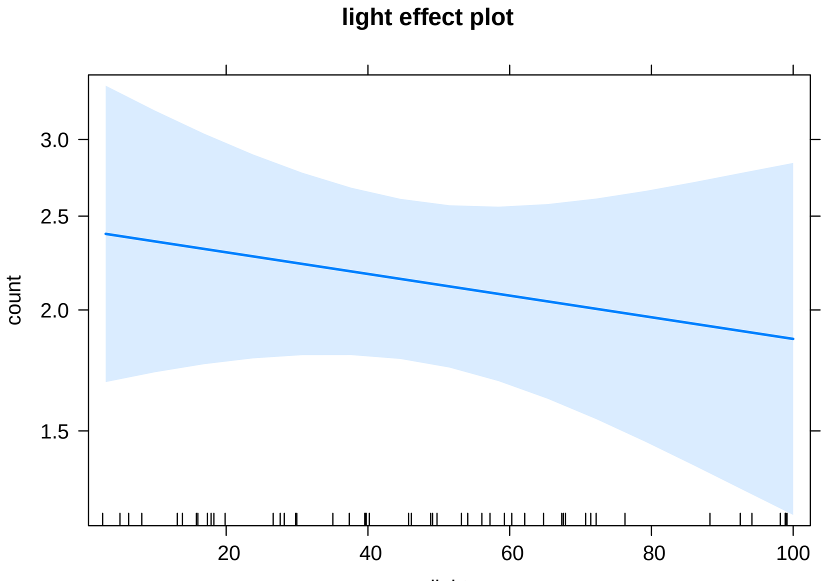
Using effects package

```r
summary(allEffects(seedl.glm))
```

```
 model: count ~ light

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

 Lower 95 Percent Confidence Limits
light
       3       30       50       70      100
1.684579 1.795202 1.753373 1.567785 1.228247

 Upper 95 Percent Confidence Limits
light
       3       30       50       70      100
3.409754 2.784179 2.571535 2.594398 2.837408
```

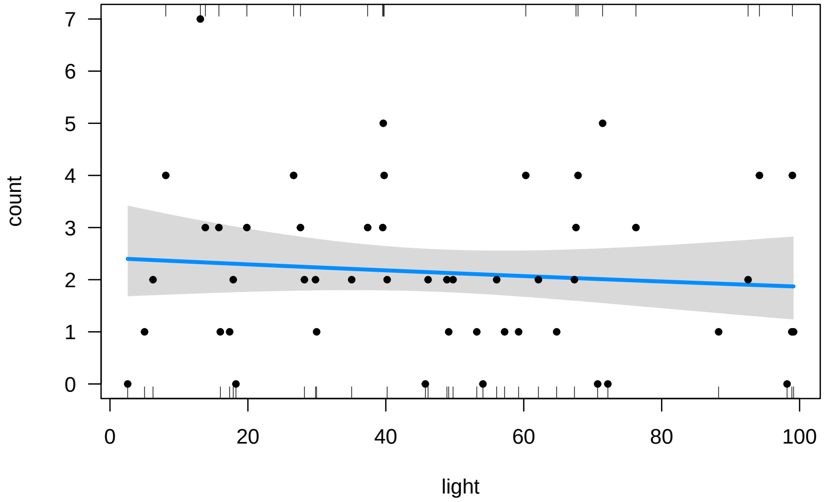
So what's the relationship between Nseedlings and light?

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



Using visreg

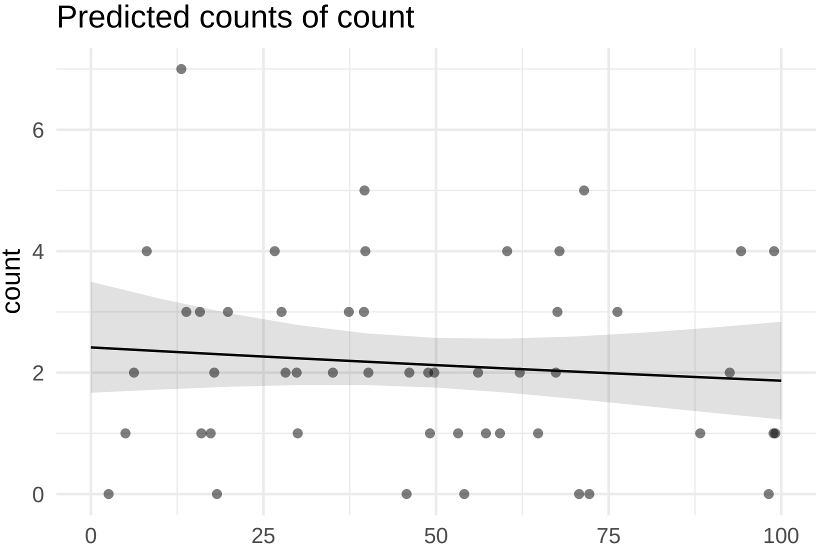
```
visreg(seedl.glm, scale = "response", ylim = c(0, 7))
points(count ~ light, data = seedl, pch = 20)
```



Using sjPlot

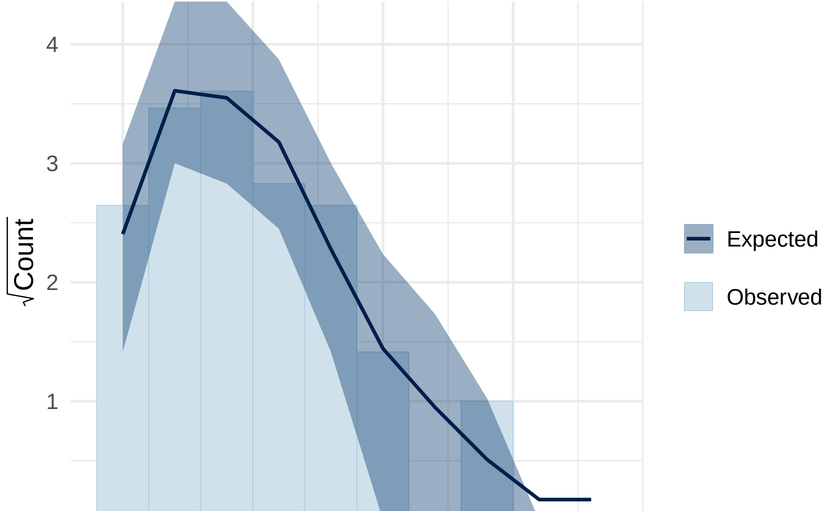
```
sjPlot::plot_model(seedl.glm, type = "eff", show.data = TRUE)
```

```
$light
```

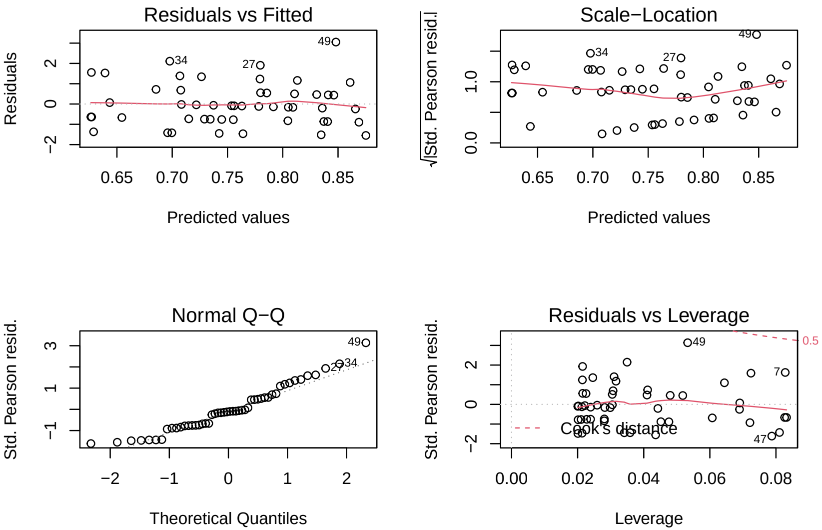


Calibration plot with count data: rootograms

```r
sims <- simulate(seedl.glm, nsim = 100)
yrep <- t(as.matrix(sims))
bayesplot::ppc_rootogram(seedl$count, yrep)
```



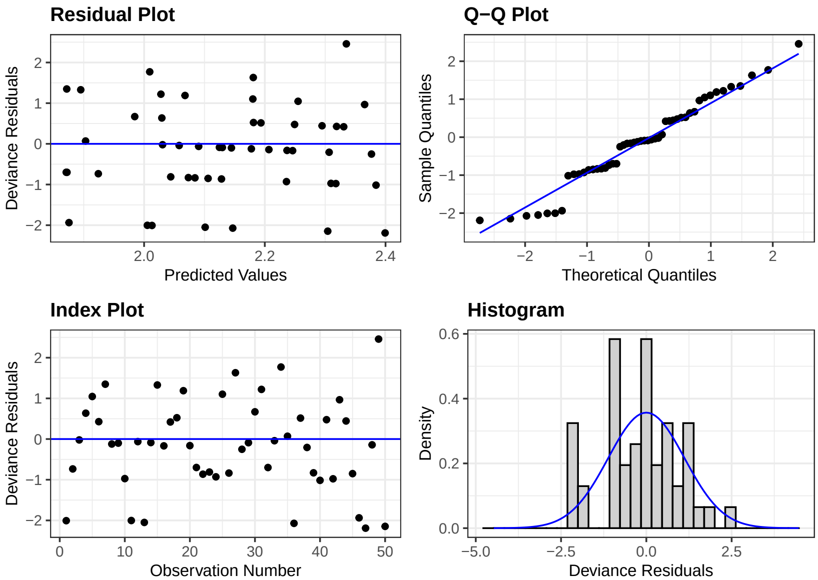
Poisson regression: model checking




```
null device
          1
```

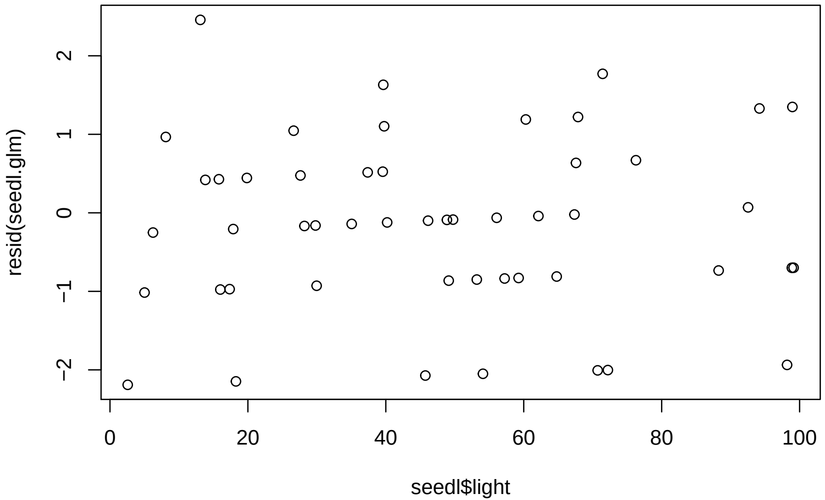
Poisson regression: model checking

```
ggResidpanel::resid_panel(seedl.glm)
```



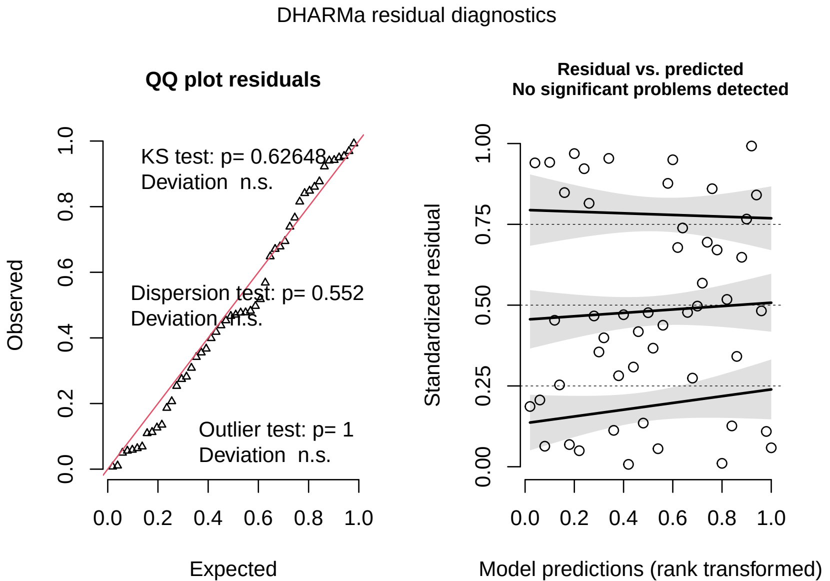
Is there pattern of residuals along predictor?

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



Residuals diagnostics with DHARMa

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



Poisson regression: Overdispersion

Always check overdispersion with count data

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

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

data:  simres
dispersion = 1.1655, p-value = 0.432
alternative hypothesis: two.sided
```

Accounting for overdispersion in count data

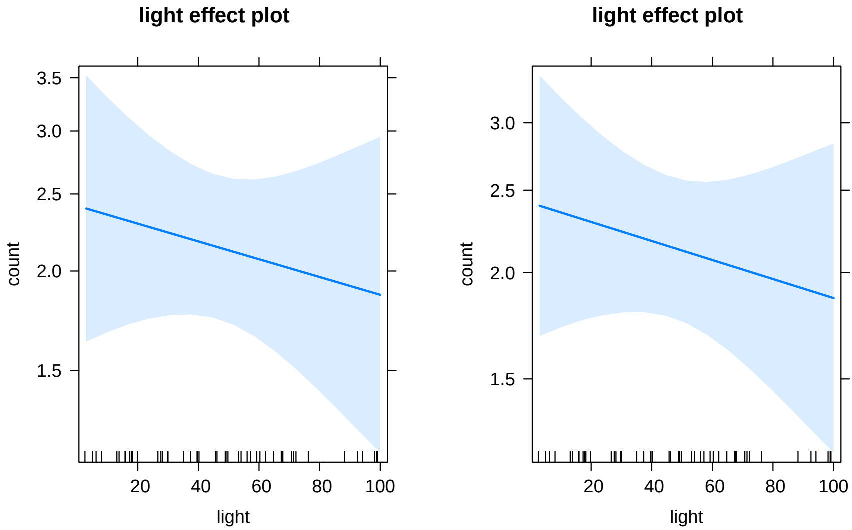
Use family quasipoisson

```
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 1.1349

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

Mean estimates do not change after accounting for overdispersion

```
 model: count ~ light

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



What if survey plots have different area?

Avoid regression of ratios

seedlings/area $\sim$ light

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†

Use offset to standardise response variables in GLMs

```r
seedl.offset <- glm(count ~ light, offset = seedl$area, data = s
summary(seedl.offset)
```

```

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

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.6926  -0.8532   0.1491   0.5211   3.1051

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.299469   0.185468   1.615    0.106
light       -0.004498   0.003441  -1.307    0.191

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 70.263  on 49  degrees of freedom
Residual deviance: 68.535  on 48  degrees of freedom
```

Note estimates now referred to area units

```r
exp(coef(seedl.offset))
```

```
(Intercept)       light
  1.3491422   0.9955123
```

Other examples

- Infant mortality $\sim$ GDP

Other examples

- Infant mortality $\sim$ GDP
- Number of cones consumed by squirrels (data)

Mixed / Multilevel models

Example dataset: trees

- Data on 1000 trees from 10 sites.

```r
head(trees)
```

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

Example dataset: trees

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

```
head(trees)
```

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

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

A simple linear model

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

```

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

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

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

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 our model structure

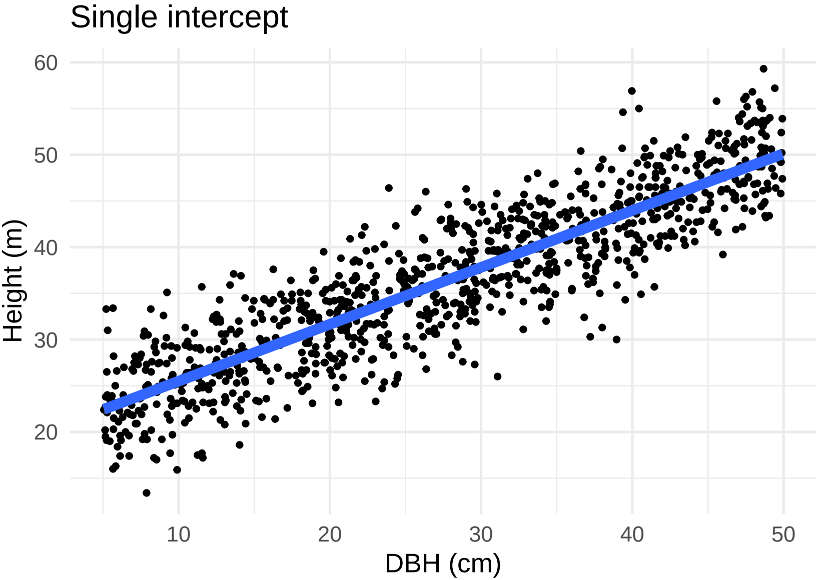
$$y_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta x_i$$

In this case:

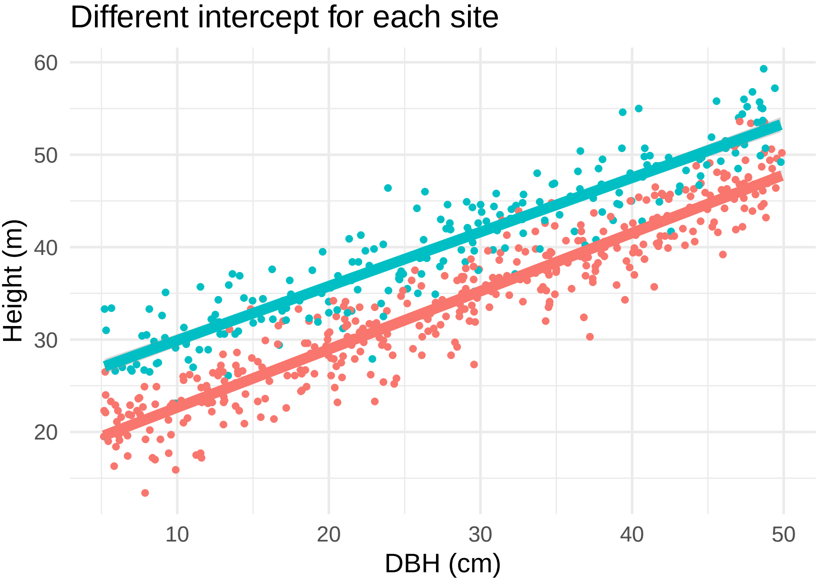
$$Height_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta DBH_i$$

α: expected height when DBH $= 0$
β: how much height increases with every unit increase of DBH

There is only one intercept



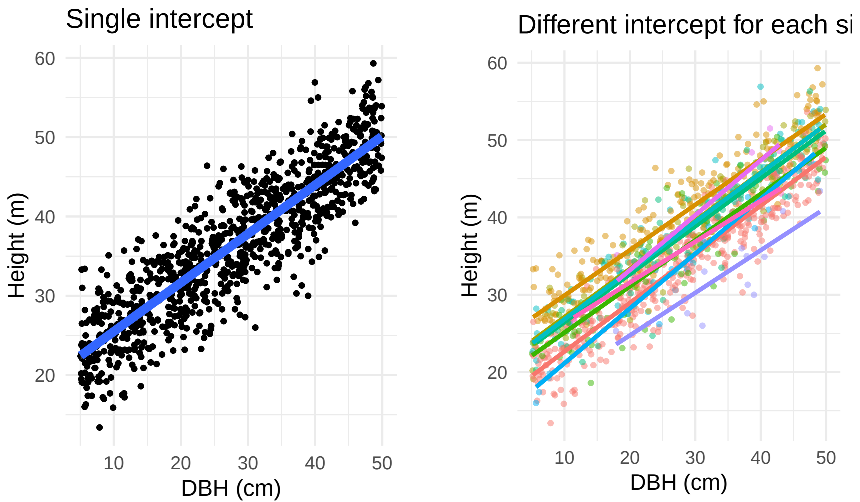
What if allometry varies among sites?



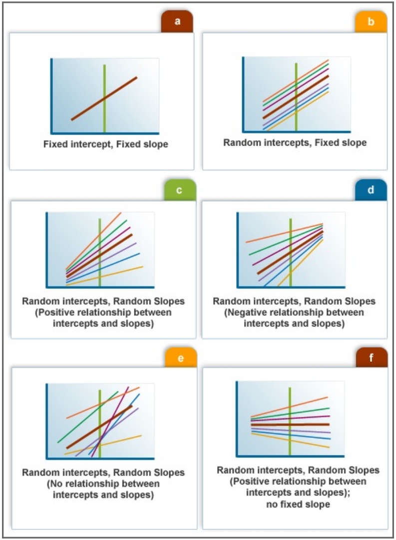
Fitting a varying intercepts model with `lm`

```
Call:
lm(formula = height ~ factor(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 ***
factor(site)2   6.504303   0.256730  25.335  < 2e-16 ***
factor(site)3   4.357457   0.354181  12.303  < 2e-16 ***
factor(site)4   1.934650   0.356102   5.433 6.98e-08 ***
factor(site)5   3.637432   0.339688  10.708  < 2e-16 ***
factor(site)6   4.204511   0.421906   9.966  < 2e-16 ***
factor(site)7  -0.176193   0.666772  -0.264   0.7916    
factor(site)8  -5.312648   0.893603  -5.945 3.82e-09 ***
factor(site)9   5.437049   1.087766   4.998 6.84e-07 ***
factor(site)10  2.263338   1.369986   1.652   0.0988 .  
dbh             0.617075   0.007574  81.473  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

Single vs varying intercept



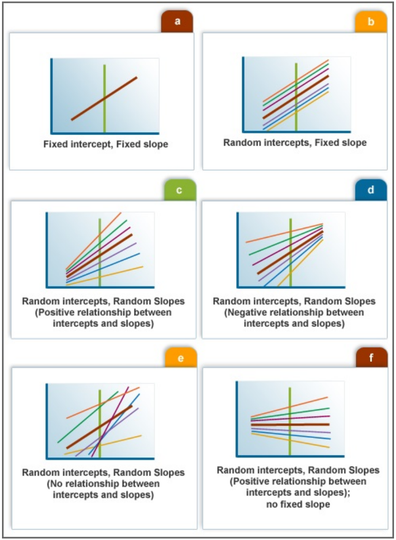
Mixed models enable us to account for variability



www.esourceresearch.org/

- Varying intercepts

Mixed models enable us to account for variability



www.esourceresearch.org/

- Varying intercepts
- Varying slopes

Mixed model with varying intercepts

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

En nuestro ejemplo:

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

Mixed models estimate varying parameters (intercepts and/or slopes) with pooling among levels (rather than considering them fully independent)

Hence there's gradient between

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

Hence there's gradient between

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

Hence there's gradient between

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

Hence there's gradient between

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

Hence there's gradient between

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

Hence there's gradient between

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

Random vs Fixed effects?

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

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

Random vs Fixed effects?

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

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

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Random vs Fixed effects?

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

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

What is a random effect, really?

- Varies by group

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

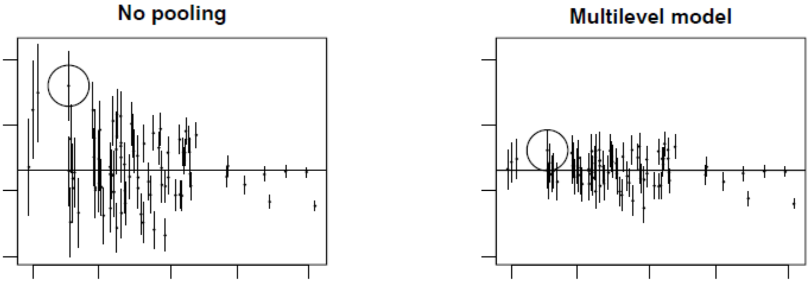
What is a random effect, really?

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

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

Shrinkage improves parameter estimation

Especially for groups with low sample size



From Gelman & Hill p. 253

Fitting mixed/multilevel models

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

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

REML criterion at convergence: 5108.3

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

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

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

Correlation of Fixed Effects:
    (Intr)
```

Retrieve model coefficients

```
coef(mixed)
```

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

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

Broom: model estimates in tidy form

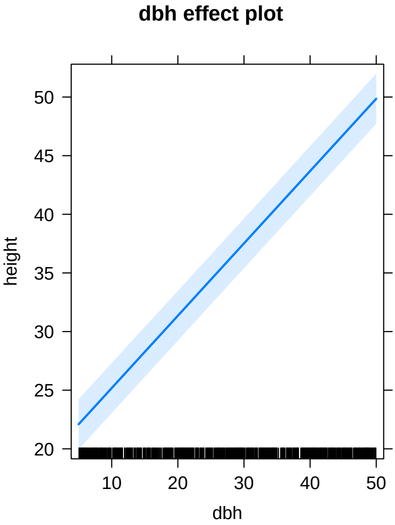
```r
library(broom.mixed)
tidy(mixed)
```

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

See also broom.mixed

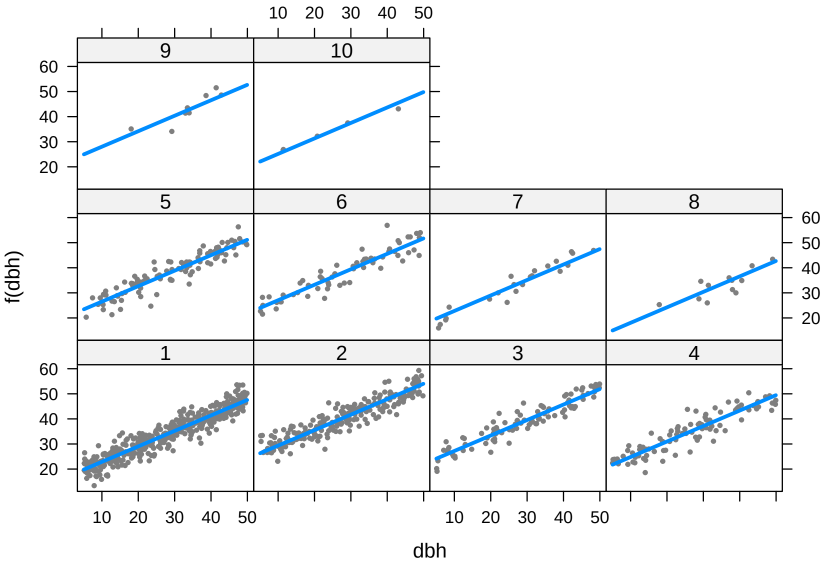
Visualising model: `allEffects`

```
 model: height ~ dbh

 dbh effect
dbh
       5       20       30       40       50
22.09610 31.35001 37.51928 43.68855 49.85782
```



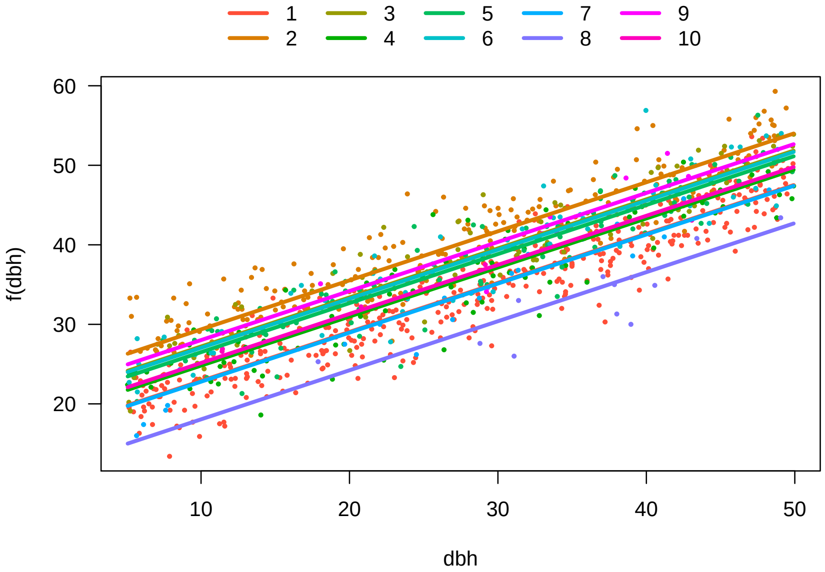
Visualising model: visreg

```
visreg(mixed, xvar = "dbh", by = "site", re.form = NULL)
```



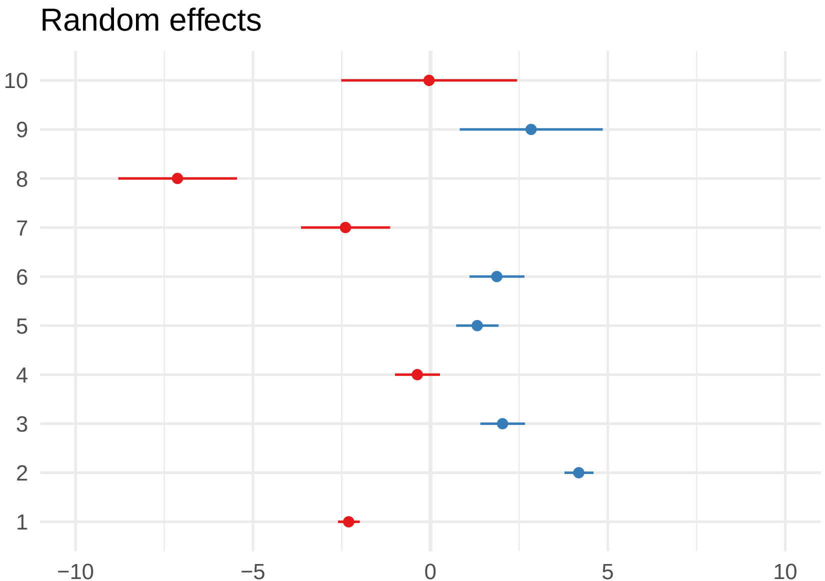
Visualising model

```r
visreg(mixed, xvar = "dbh", by = "site", re.form = NULL, overlay
```



Visualising model: `sjPlot`

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

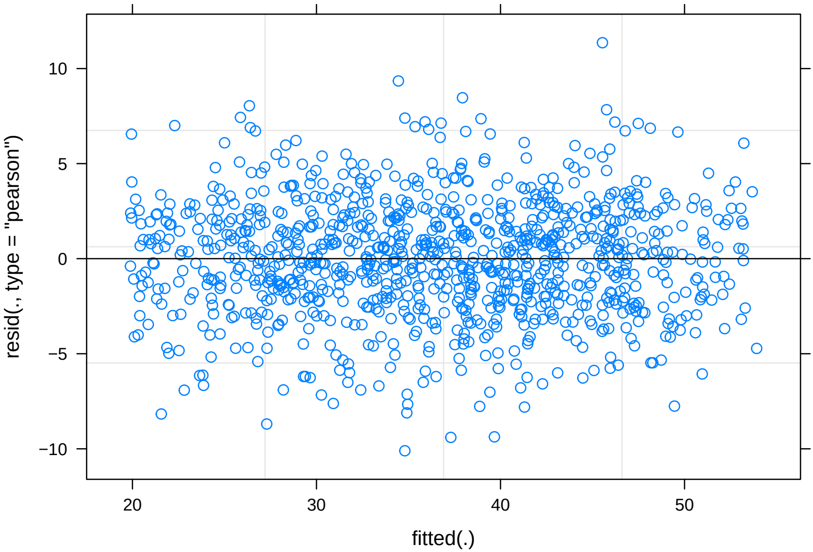


Using merTools to understand fitted model

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

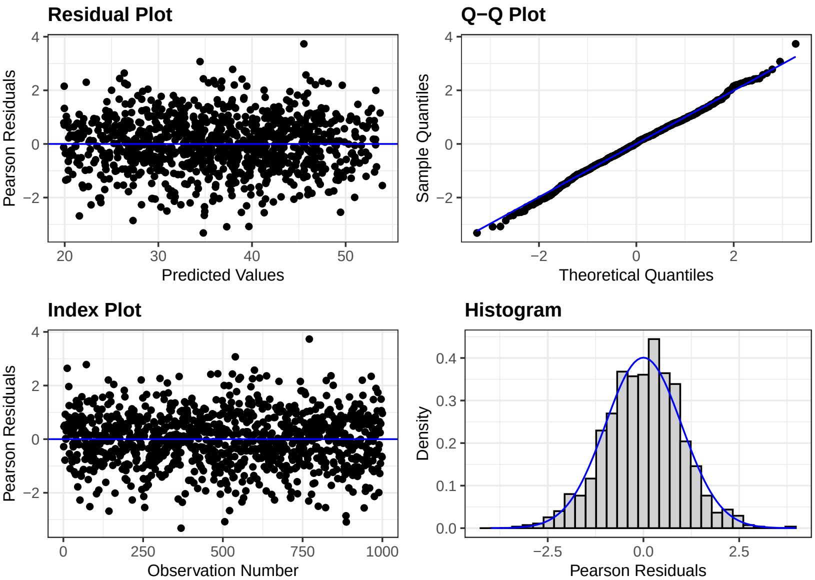
Checking residuals

```
plot(mixed)
```



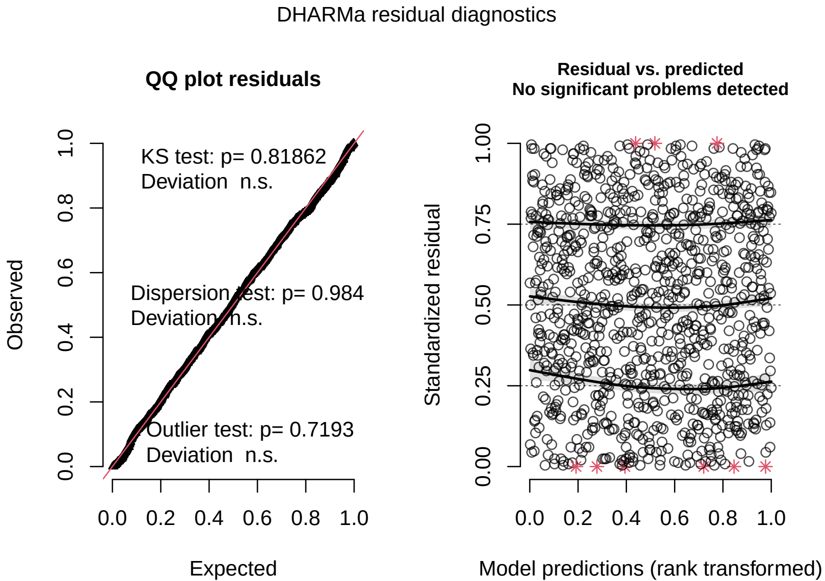
Checking residuals

```r
ggResidpanel::resid_panel(mixed)
```



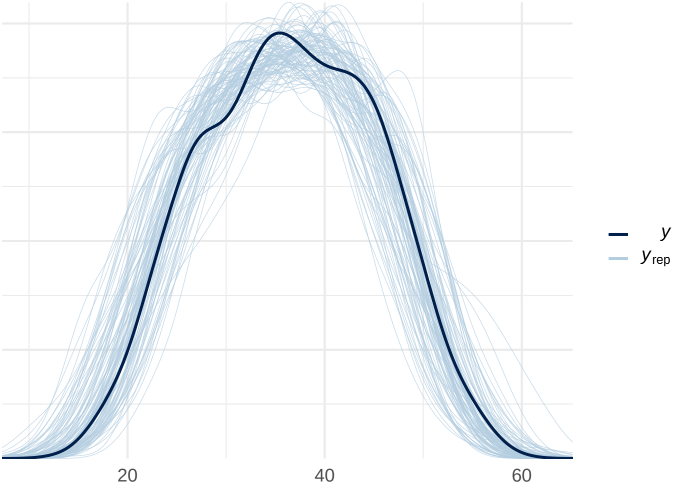
Checking residuals (DHARMa)

```
DHARMa::simulateResiduals(mixed, plot = TRUE, use.u = TRUE)
```



Model checking with simulated data

```
library(bayesplot)
sims <- simulate(mixed, nsim = 100)
ppc_dens_overlay(trees$height, yrep = t(as.matrix(sims)))
```



R-squared for GLMMs

Many approaches! Somewhat polemic (e.g. see this).
Nakagawa & Schielzeth propose **marginal** (considering fixed effects only) and **conditional** R^2 (including random effects too):

```
library(MuMIn)
r.squaredGLMM(mixed)
```

```
          R2m       R2c
[1,] 0.752535 0.8879656
```

Growing the hierarchy: adding site-level predictors

Model with group-level predictors

We had:

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

Now

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

Are height differences among sites related to temperature?

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

Are height differences among sites related to temperature?

```r
sitedata <- read.csv("data/sitedata.csv")
sitedata
```

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

Merging trees and site data

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

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

Fit multilevel model

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

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

REML criterion at convergence: 5098.2

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

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

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

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

Too strong correlation of parameters!

Centre (and scale) continuous variables

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

```
[1] 18.5
```

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

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

Fit multilevel model

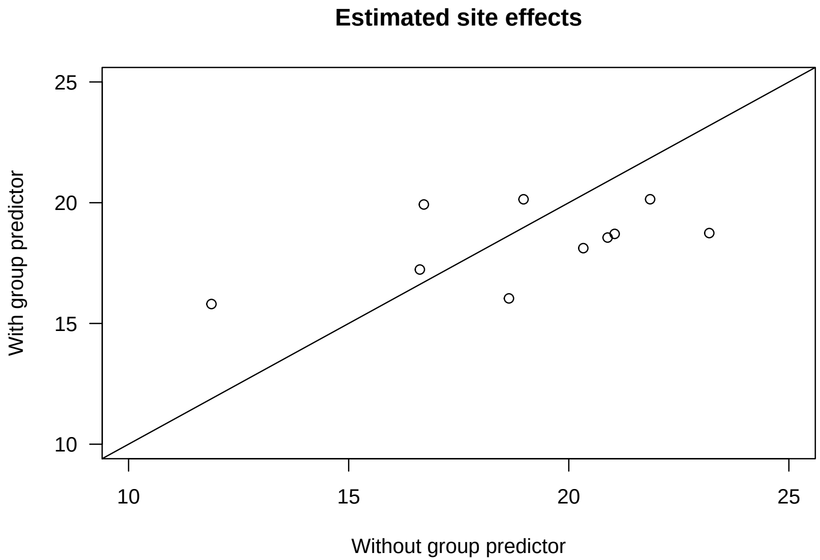
```
group.pred <- lmer(height ~ dbh + (1 | site) + temp.c, data = trees.full)
```

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

REML criterion at convergence: 5098.2

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

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

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

Correlation of Fixed Effects:
       (Intr) dbh
dbh    -0.333
temp.c -0.250  0.008
```

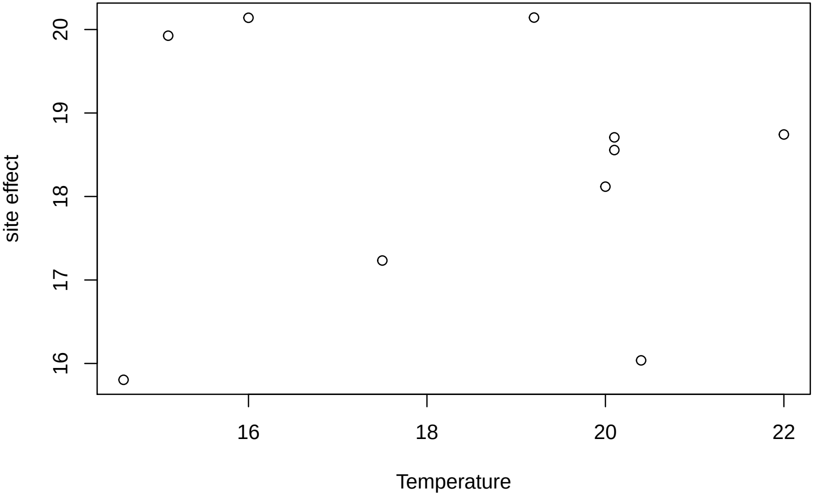
Examine model with merTools

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

Comparing site effects with and without group predictor



Are site effects related to temperature?



Varying intercepts and slopes

Varying intercepts and slopes

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

AND

Relationship between DBH and Height varies among sites (different slopes)

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

Varying intercepts and slopes

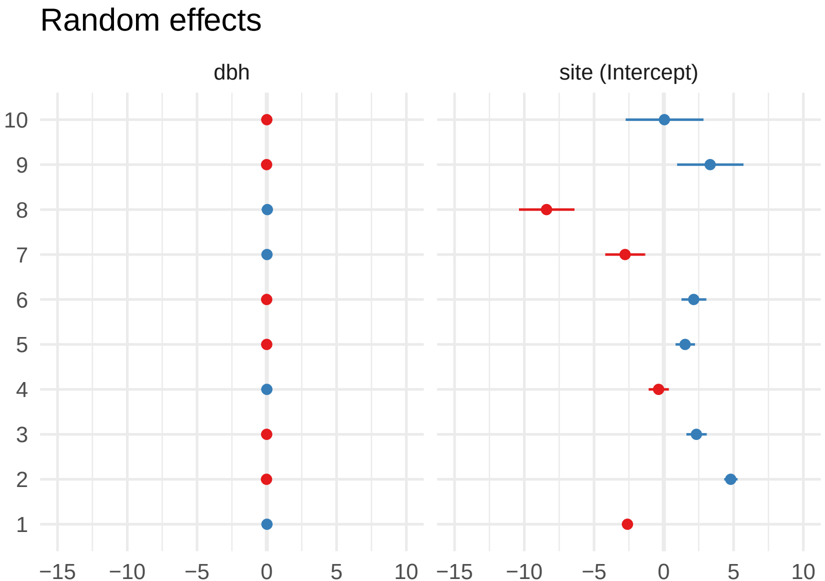
```
Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 + dbh | site)
   Data: trees

REML criterion at convergence: 5105.1

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

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

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

Correlation of Fixed Effects:
    (Intr)
dbh -0.722
optimizer (nloptwrap) convergence code: 0 (OK)
```

Varying intercepts and slopes

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

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

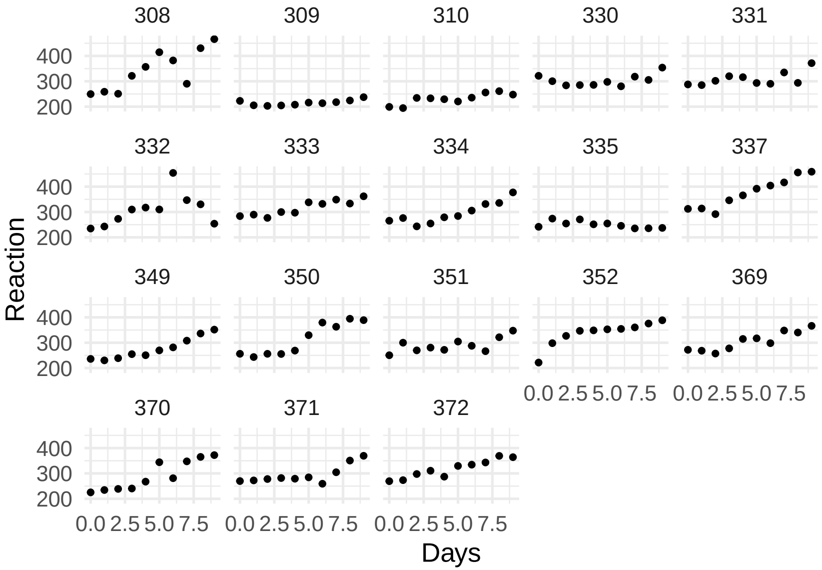
Visualising model: sjPlot

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



More examples

sleepstudy (repeated measures)



Varying intercepts and slopes (lme4)

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

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

REML criterion at convergence: 1743.6

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

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

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

Correlation of Fixed Effects:
     (Intr)
Days -0.138
```

Varying intercepts and slopes (lme4)

```
visreg(sleep, xvar = "Days", by = "Subject", re.form = NULL)
```

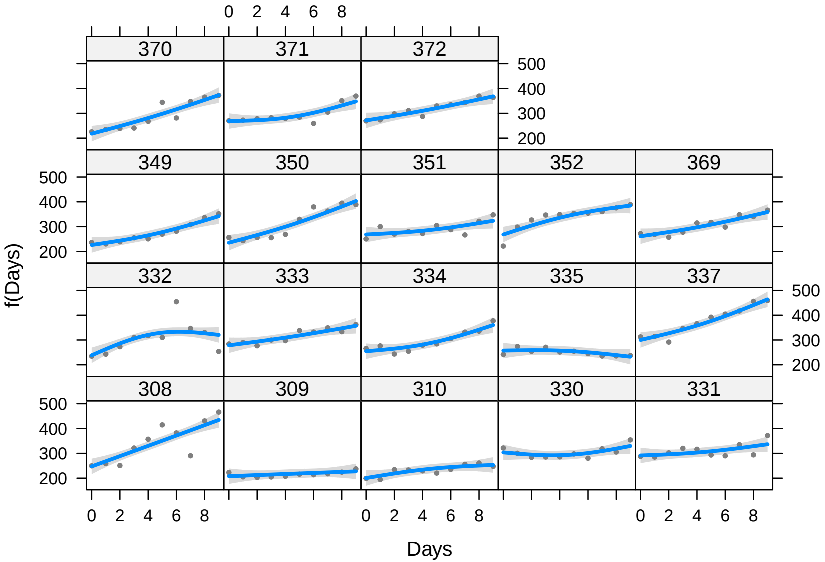
Fitting multilevel models (GAMM) with mgcv

```r
sgamm <- mgcv::gam(Reaction ~ s(Days, Subject, k = 3, bs = "fs"),
                   data = sleepstudy, method = "REML")
```

```

Family: gaussian
Link function: identity

Formula:
Reaction ~ s(Days, Subject, k = 3, bs = "fs")

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   295.22      10.49   28.15   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
                  edf Ref.df     F p-value
s(Days,Subject) 42.2     53 16.05  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.826   Deviance explained = 86.7%
```

Fitting multilevel models (GAMM) with mgcv

```r
visreg(sgamm, xvar = "Days", by = "Subject")
```



Fitting multilevel models (GAMM) with `mgcv`

Hierarchical generalized additive models: an introduction with mgcv

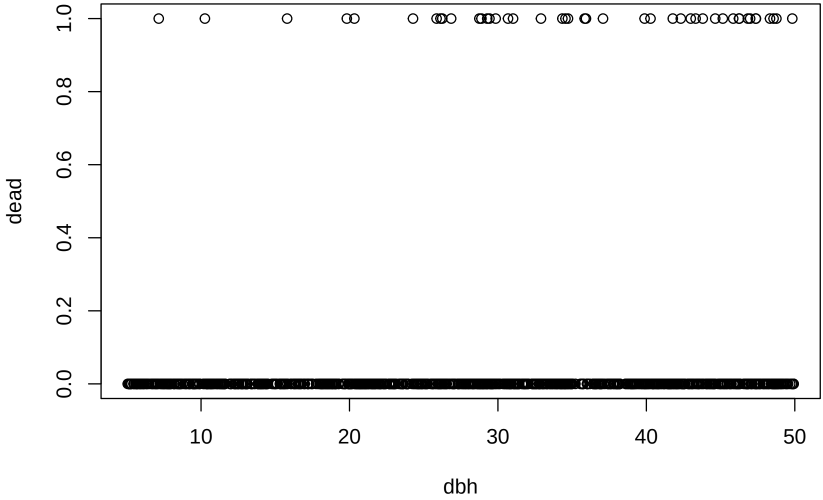
Eric J Pedersen [Corresp., 1, 2], **David L. Miller** [3, 4], **Gavin L. Simpson** [5], **Noam Ross** [6]

https://doi.org/10.7287/peerj.preprints.27320v1

Multilevel logistic regression

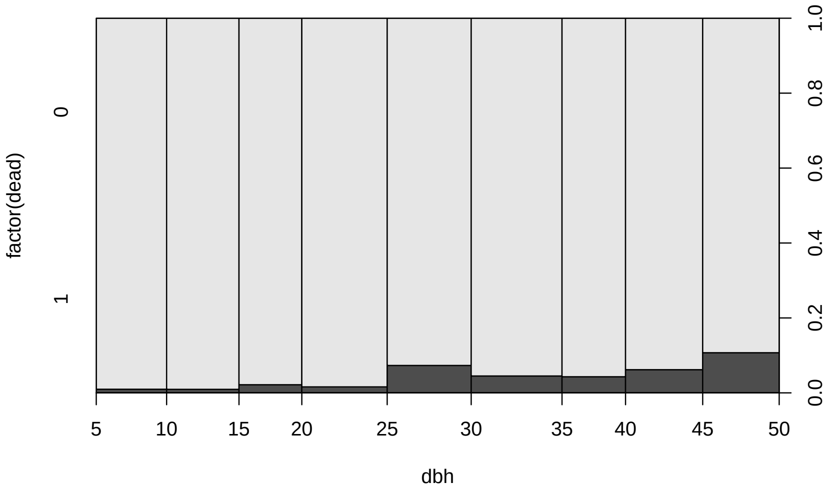
Q: Relationship between tree size and mortality

```r
plot(dead ~ dbh, data = trees)
```



Q: Relationship between tree size and mortality

```
plot(factor(dead) ~ dbh, data = trees)
```



Fit simple logistic regression

```
simple.logis <- glm(dead ~ dbh, data = trees, family=binomial)
```

```
Call:
glm(formula = dead ~ dbh, family = binomial, data = trees)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.4805  -0.3520  -0.2647  -0.1928   2.9690

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.77874    0.50902  -9.388  < 2e-16 ***
dbh          0.05365    0.01377   3.895 9.82e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 360.91  on 999  degrees of freedom
Residual deviance: 343.69  on 998  degrees of freedom
```

Logistic regression with *independent* site effects

```r
logis2 <- glm(dead ~ dbh + factor(site), data = trees, family=binomial)
```

```
Call:
glm(formula = dead ~ dbh + factor(site), family = binomial, data = trees)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.6359  -0.3449  -0.2561  -0.1852   2.9763

Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)      -4.80123    0.54985  -8.732   <2e-16 ***
dbh               0.05371    0.01381   3.889   0.0001 ***
factor(site)2    -0.29692    0.46073  -0.644   0.5193
factor(site)3     0.21275    0.52799   0.403   0.6870
factor(site)4     0.39841    0.53025   0.751   0.4524
factor(site)5    -0.42557    0.64018  -0.665   0.5062
factor(site)6     0.66861    0.53656   1.246   0.2127
factor(site)7     0.11862    1.06211   0.112   0.9111
factor(site)8     0.43899    1.08058   0.406   0.6846
factor(site)9   -13.63389  840.90382  -0.016   0.9871
factor(site)10  -13.17148 1042.21823  -0.013   0.9899
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

Fit multilevel logistic regression

```r
mixed.logis <- glmer(dead ~ dbh + (1|site), data=trees, family = binomial)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: dead ~ dbh + (1 | site)
   Data: trees

     AIC      BIC   logLik deviance df.resid
   349.7    364.4   -171.8    343.7      997

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.3498 -0.2528 -0.1888 -0.1370  9.0031

Random effects:
 Groups Name        Variance Std.Dev.
 site   (Intercept) 0        0
Number of obs: 1000, groups:  site, 10

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.77874    0.50904  -9.388  < 2e-16 ***
dbh          0.05365    0.01377   3.895 9.83e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Retrieve model coefficients

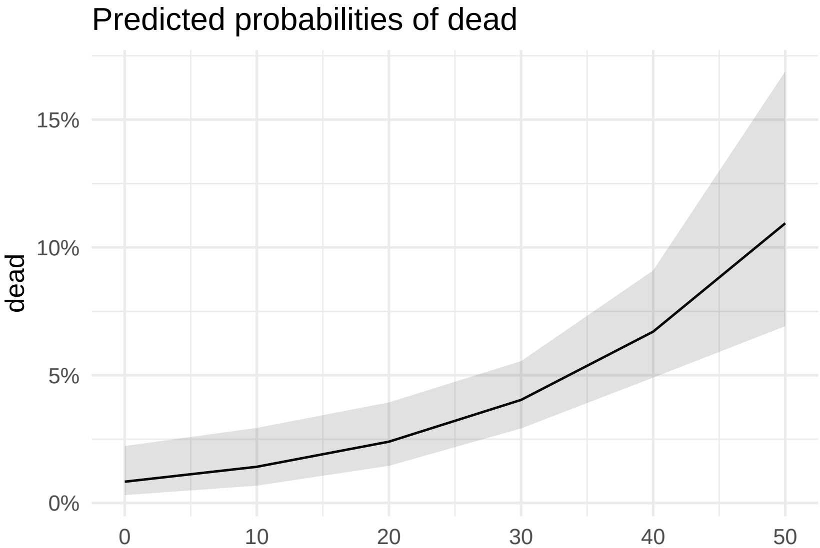
```r
coef(mixed.logis)
```

```
$site
   (Intercept)        dbh
1    -4.778744 0.05364989
2    -4.778744 0.05364989
3    -4.778744 0.05364989
4    -4.778744 0.05364989
5    -4.778744 0.05364989
6    -4.778744 0.05364989
7    -4.778744 0.05364989
8    -4.778744 0.05364989
9    -4.778744 0.05364989
10   -4.778744 0.05364989

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

Visualising model: sjPlot

```
plot_model(mixed.logis, type = "eff", show.ci = TRUE)
```

```
$dbh
```



Poisson multilevel regression

Advantages of multilevel models

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Advantages of multilevel models

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- Accommodate **variation** in treatment effects
- More **efficient inference** of regression parameters
- Using all the data to perform inferences for groups with small sample size

Formula syntax for different models

- Varying intercepts

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- Varying intercepts
  - `y ~ x + (1 | group)`

Formula syntax for different models

- Varying intercepts
  - `y ~ x + (1 | group)`
- Varying intercepts and slopes

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Formula syntax for different models

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  - `y ~ x + (1 | group1) + (1 | group2)`

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  - `y ~ x + (1 + x | group)`
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  - `y ~ x + (1 | group1) + (1 | group2)`
- Varying intercepts, 2 groups (nested)
  - `y ~ x + (1 | group/subgroup)`

Formula syntax for different models

- Varying intercepts
  - `y ~ x + (1 | group)`
- Varying intercepts and slopes
  - `y ~ x + (1 + x | group)`
- Varying intercepts, 2 groups (crossed)
  - `y ~ x + (1 | group1) + (1 | group2)`
- Varying intercepts, 2 groups (nested)
  - `y ~ x + (1 | group/subgroup)`
  - This is equivalent to `y ~ x + (1 | group1) + (1 | group2)` with distinct labelling of group levels.

Formula syntax for different models

- Varying intercepts
  - `y ~ x + (1 | group)`
- Varying intercepts and slopes
  - `y ~ x + (1 + x | group)`
- Varying intercepts, 2 groups (crossed)
  - `y ~ x + (1 | group1) + (1 | group2)`
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Formula syntax for different models

- Varying intercepts
  - `y ~ x + (1 | group)`
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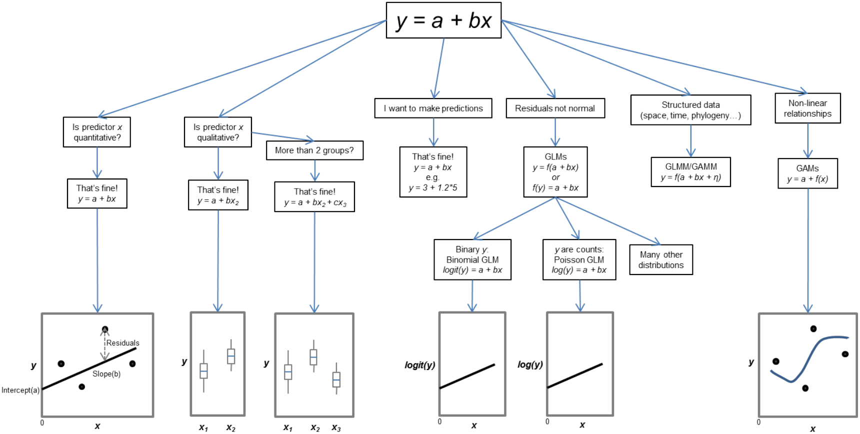
  - `y ~ x + (1 | group1) + (1 | group2)`
- Varying intercepts, 2 groups (nested)
  - `y ~ x + (1 | group/subgroup)`
  - This is equivalent to `y ~ x + (1 | group1) + (1 | group2)` with distinct labelling of group levels.
- Varying intercepts and slopes, 2 groups (crossed)
  - `y ~ x + (1 + x | group1) + (1 + x | group2)`

GLMM FAQ

https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html



y = a + bx
Is predictor x quantitative?
That's fine! y = a + bx
Is predictor x qualitative?
That's fine! y = a + bx2
More than 2 groups?
That's fine! y = a + bx2 + cx3
I want to make predictions
That's fine! y = a + bx e.g. y = 3 + 1.2*5
Residuals not normal
GLMs y = f(a + bx) or f(y) = a + bx
Binary y: Binomial GLM logit(y) = a + bx
y are counts: Poisson GLM log(y) = a + bx
Many other distributions
Structured data (space, time, phylogeny…)
GLMM/GAMM y = f(a + bx + η)
Non-linear relationships
GAMs y = a + f(x)
Residuals
Slope(b)
Intercept(a)
y
x
0
x1
x2
x3
logit(y)
log(y)

END

Source code and materials:
https://github.com/Pakillo/LM-GLM-GLMM-intro