Mixed / Multilevel models

Example dataset: trees

▶ Data on 1000 trees from 10 sites.

```
head(trees)
```

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

Example dataset: trees

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

```
head(trees)
```

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

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

A simple linear model

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

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

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

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

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

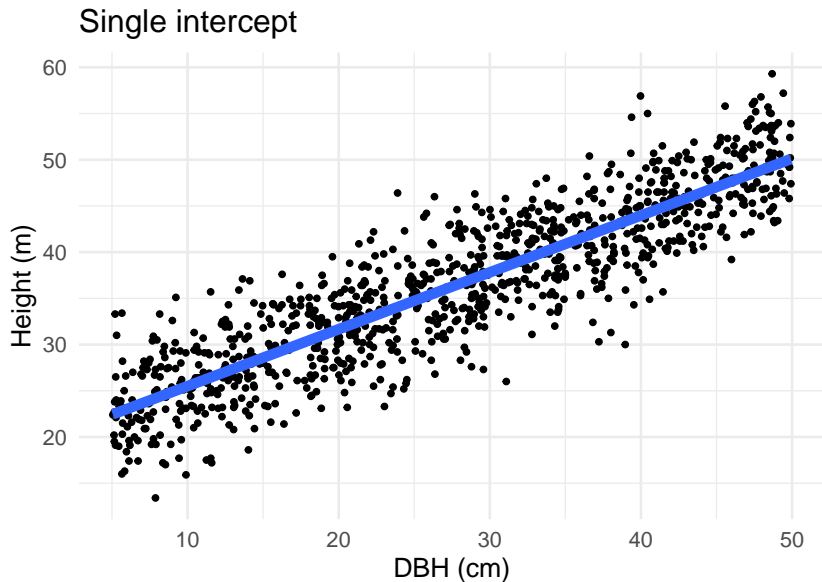$$y_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta x_i$$

In this case:

$$Height_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta DBH_i$$
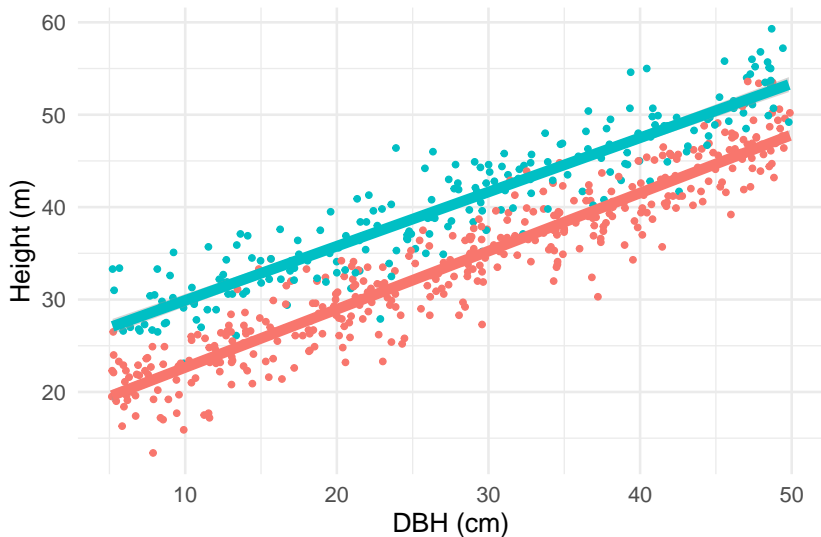
α: expected height when DBH $= 0$

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

There is only one intercept

Single intercept

What if allometry varies among sites?

Different intercept for each site

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
```
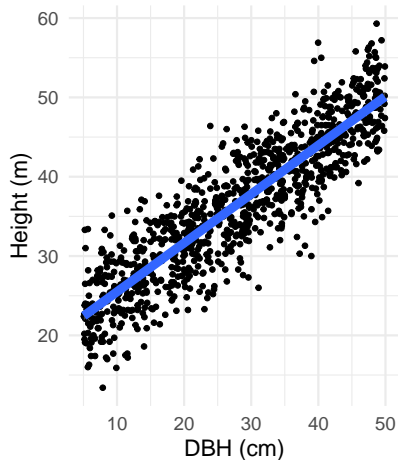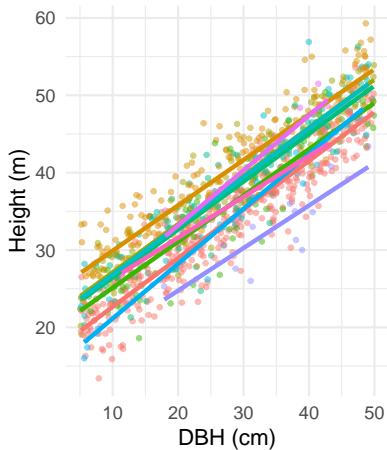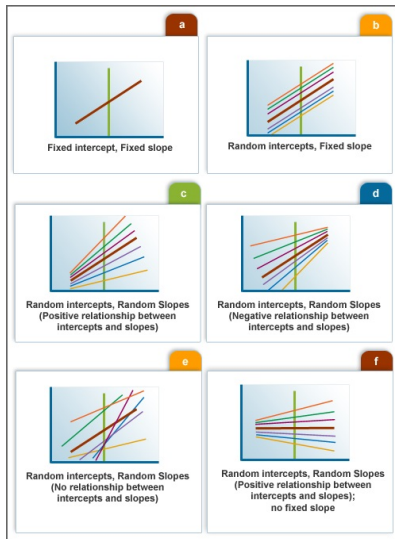
Single vs varying intercept

Mixed models enable us to account for variability

www.esourceresearch.org/

▶ Varying intercepts

Mixed models enable us to account for variability

www.esourceresearch.org/
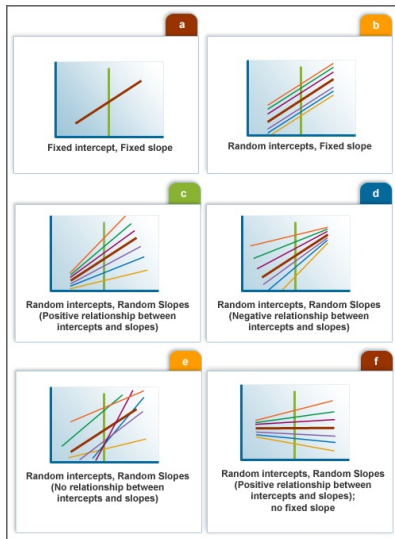
▶ Varying intercepts
▶ Varying slopes

Mixed model with varying intercepts

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

En nuestro ejemplo:

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

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

Hence there's gradient between

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

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  ▶ `lm (height ~ dbh)`

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

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► **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/

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

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Random vs Fixed effects?

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

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

What is a random effect, really?

▶ Varies by group

Random effects are estimated with *partial pooling*, while fixed effects are not (infinite variance).
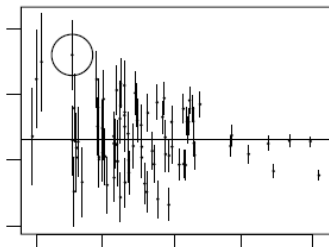
What is a random effect, really?

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

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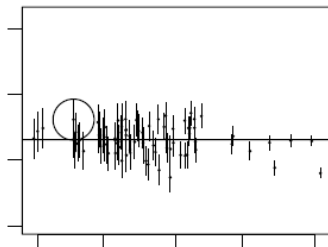
Shrinkage improves parameter estimation

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)
dbh
```

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
```
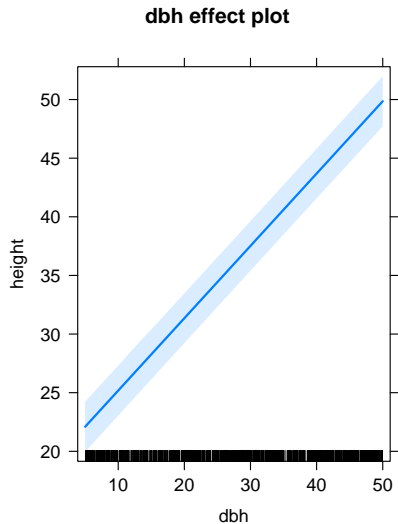
See also broom.mixed

Visualising model: `allEffects`

dbh effect plot

```
model: height ~ dbh

 dbh effect
dbh
       5        20        30        40        50
22.09610 31.35001 37.51928 43.68855 49.85782
```
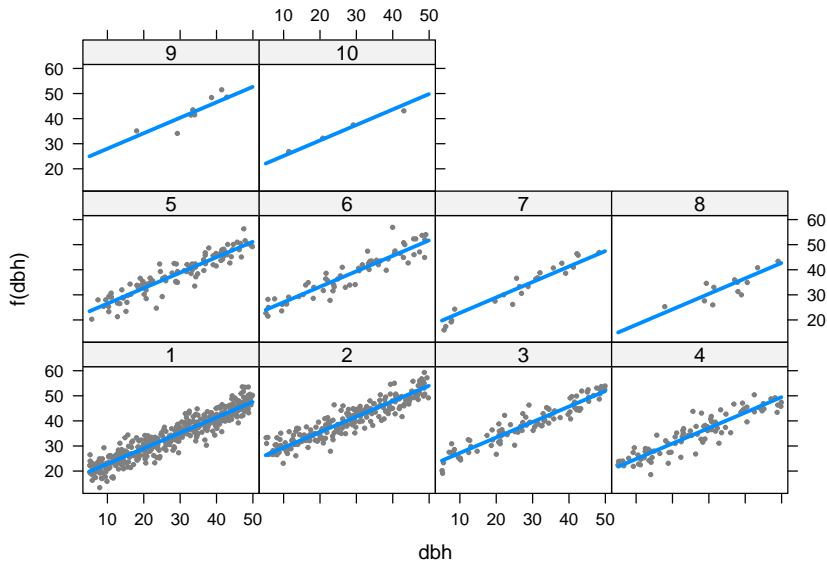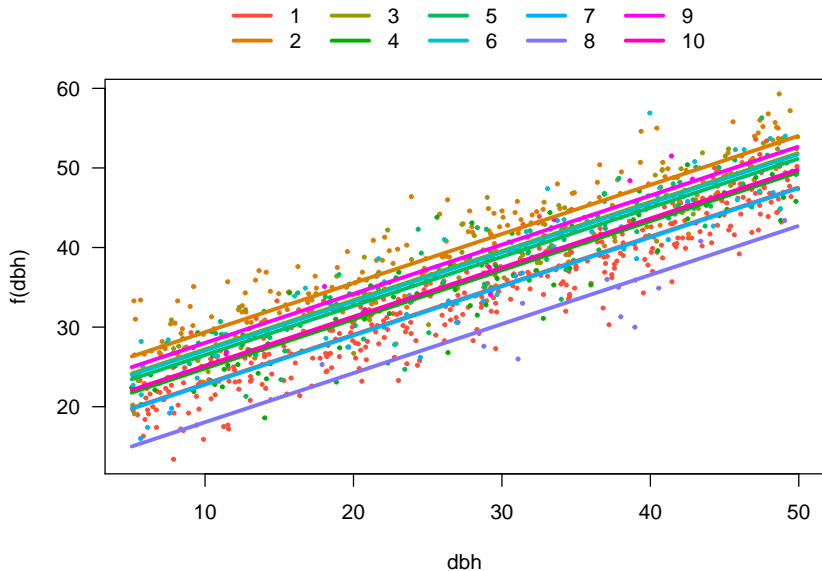
Visualising model: visreg

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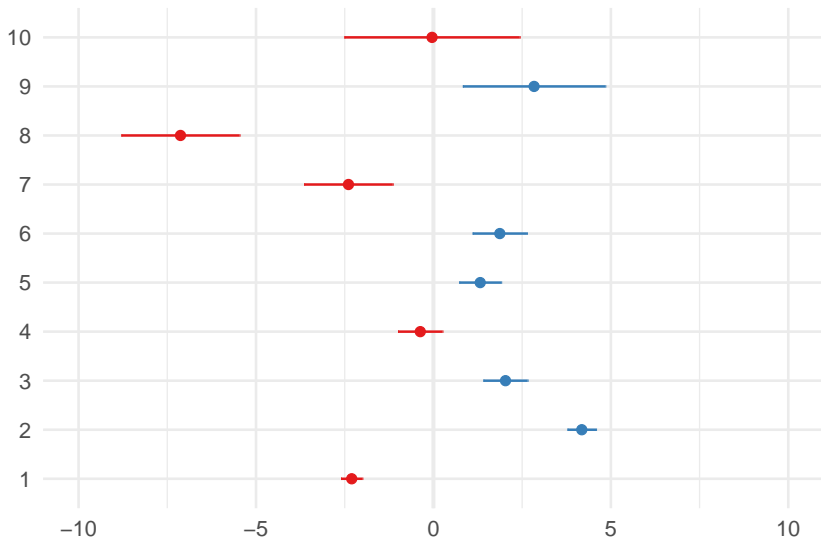
Visualising model

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

Visualising model: `sjPlot`

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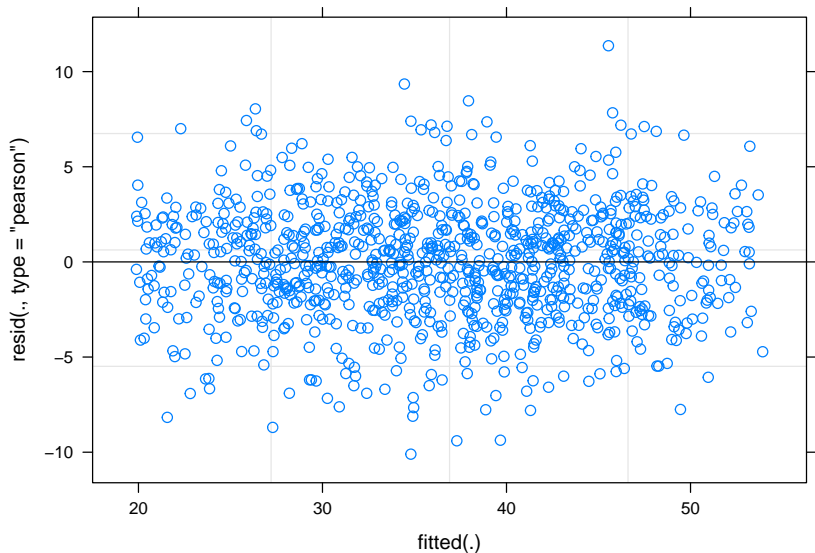

Random effects

Using merTools to understand fitted model
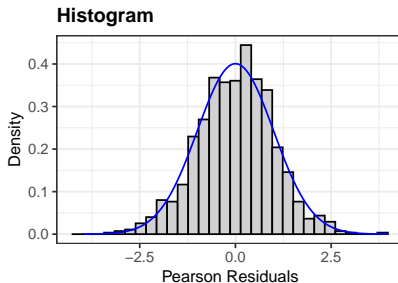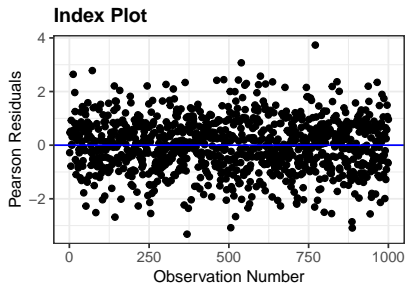
```
library(merTools)
shinyMer(mixed)
```
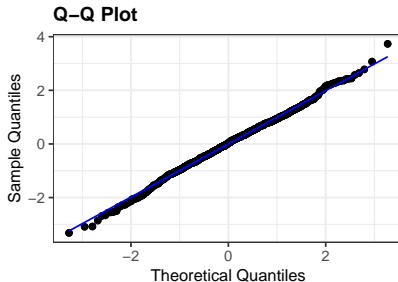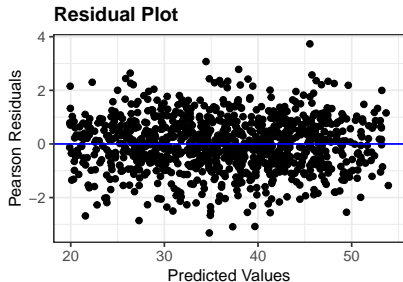
Checking residuals

```r
plot(mixed)
```

Checking residuals

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

Checking residuals (DHARMa)

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

DHARMa residual diagnostics
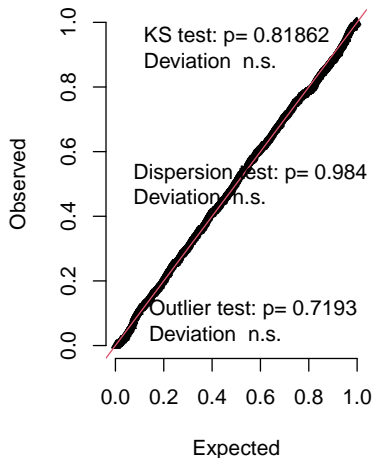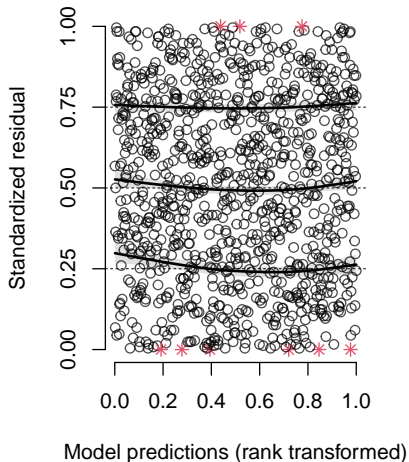
Model checking with simulated data

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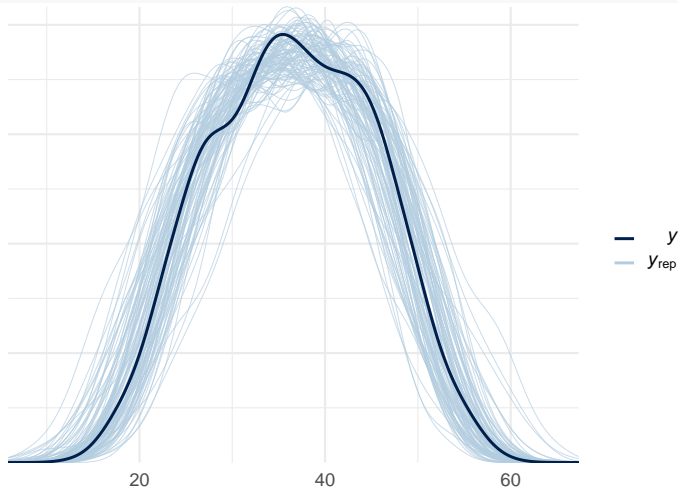
R-squared for GLMMs

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:

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

Now

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

Are height differences among sites related to temperature?

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

Are height differences among sites related to temperature?

```
sitedata <- read.csv("data/sitedata.csv")
sitedata
   site temp
1     1 15.1
2     2 22.0
3     3 20.1
4     4 20.4
5     5 20.0
6     6 20.1
7     7 17.5
8     8 14.6
9     9 19.2
10   10 16.0
```

Merging trees and site data

```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

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

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

REML criterion at convergence: 5098.2

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

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

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

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

Too strong correlation of parameters!

Centre (and scale) continuous variables

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

```
[1] 18.5
```

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

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

Fit multilevel model

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

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

REML criterion at convergence: 5098.2

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

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

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

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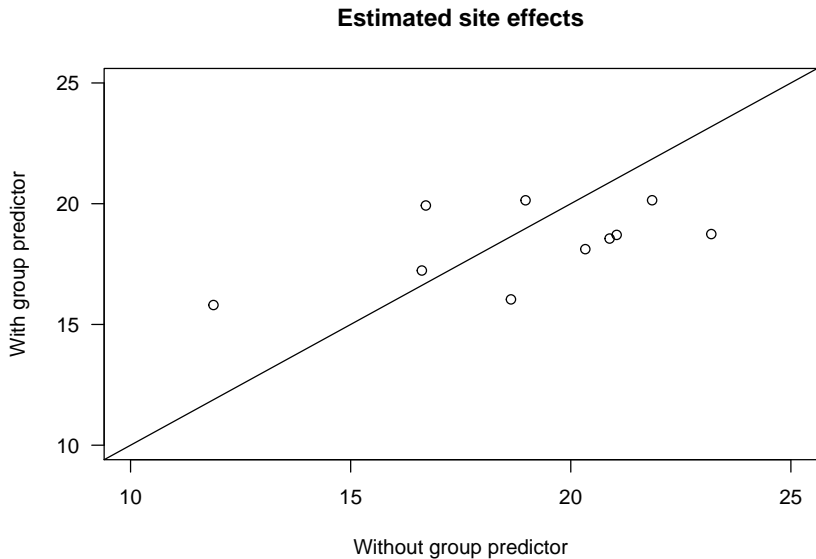
Examine model with merTools

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

Comparing site effects with and without group predictor

Estimated site effects

Are site effects related to temperature?
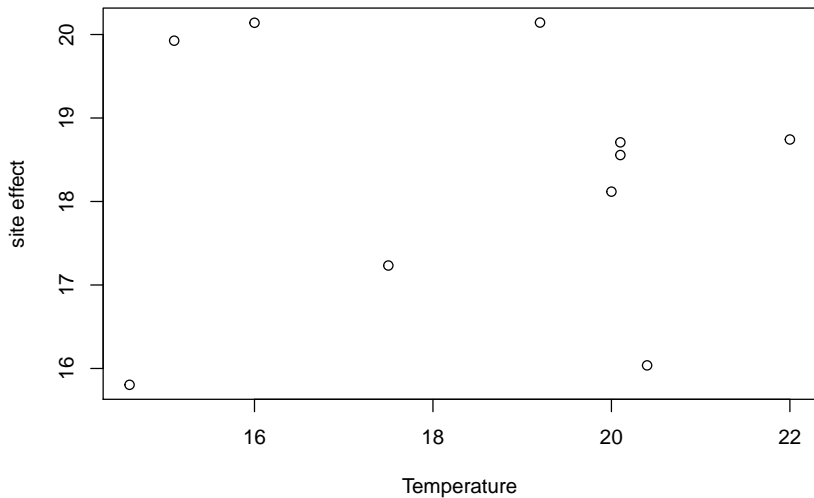
Varying intercepts and slopes

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)
```

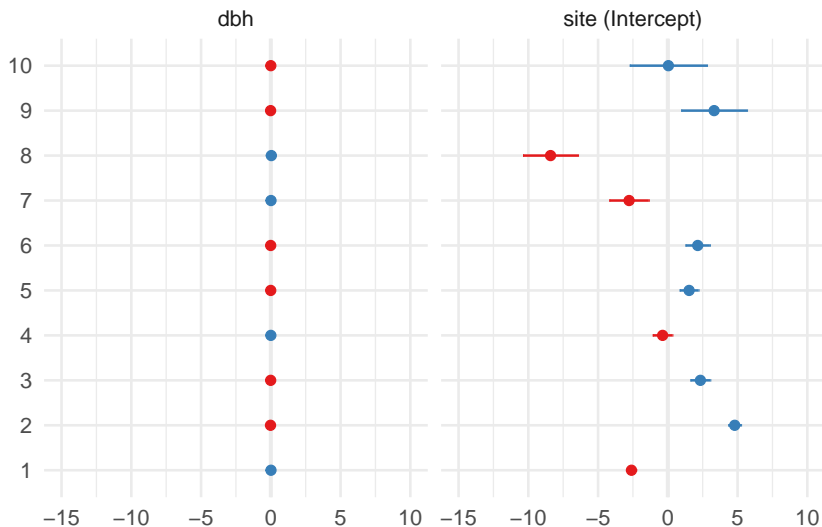# Varying intercepts and slopes

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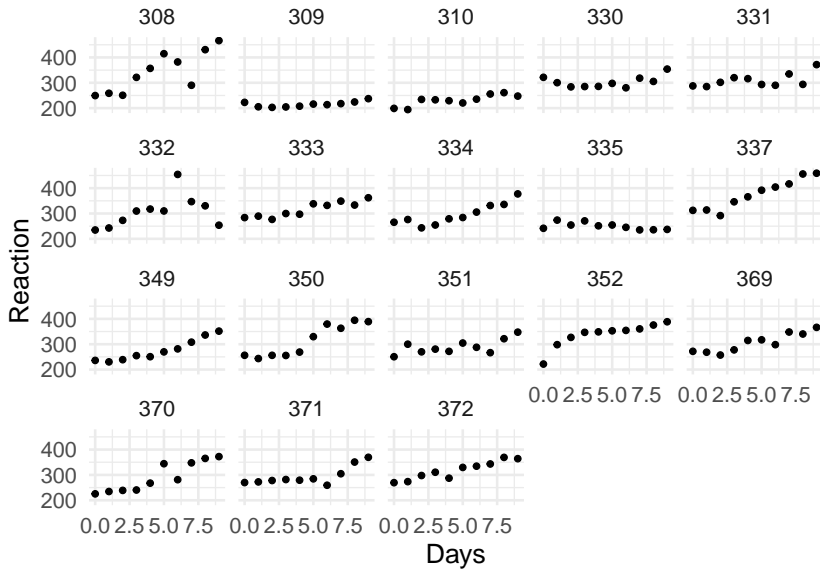
```
plot_model(mixed.slopes, type = "re")
```

Random effects

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)

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

Fitting multilevel models (GAMM) with `mgcv`

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

```
Family: gaussian
Link function: identity

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

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   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%
```
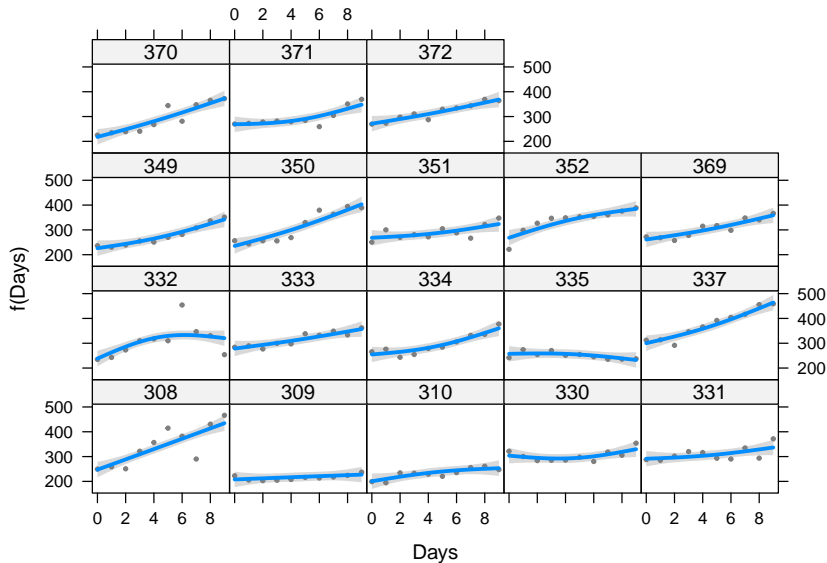
Fitting multilevel models (GAMM) with `mgcv`

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

Fitting multilevel models (GAMM) with `mgcv`

Hierarchical generalized additive models: an introduction with mgcv
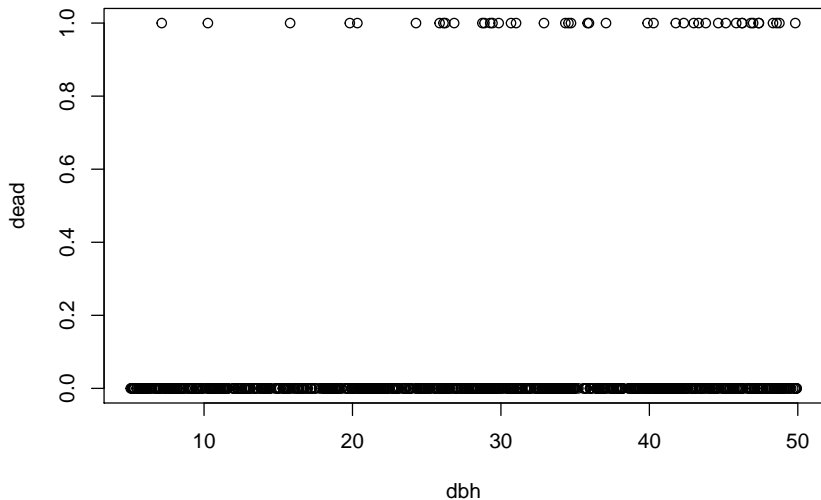
Eric J Pedersen [Corresp.,] [1, 2] , David L. Miller [3, 4] , Gavin L. Simpson [5] , Noam Ross [6]

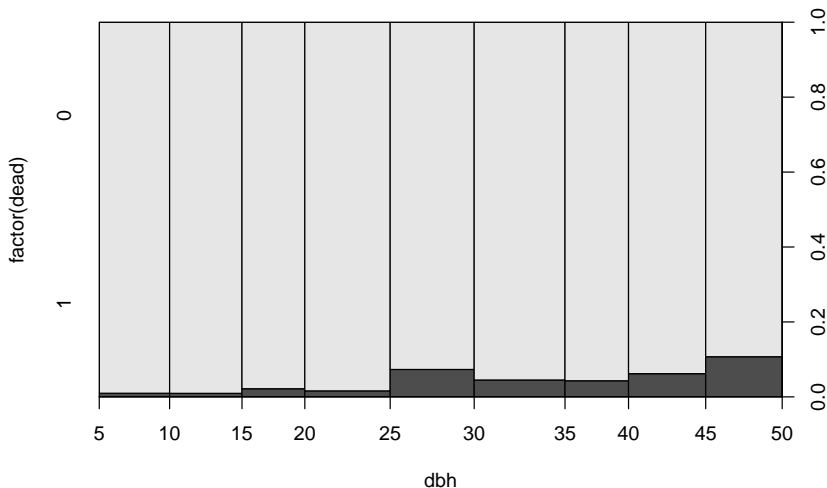# Multilevel logistic regression

Q: Relationship between tree size and mortality

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

Q: Relationship between tree size and mortality

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

Fit simple logistic regression

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

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

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

```
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

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

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

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

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

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

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

Retrieve model coefficients

```
coef(mixed.logis)

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

attr(,"class")
[1] "coef.mer"
```
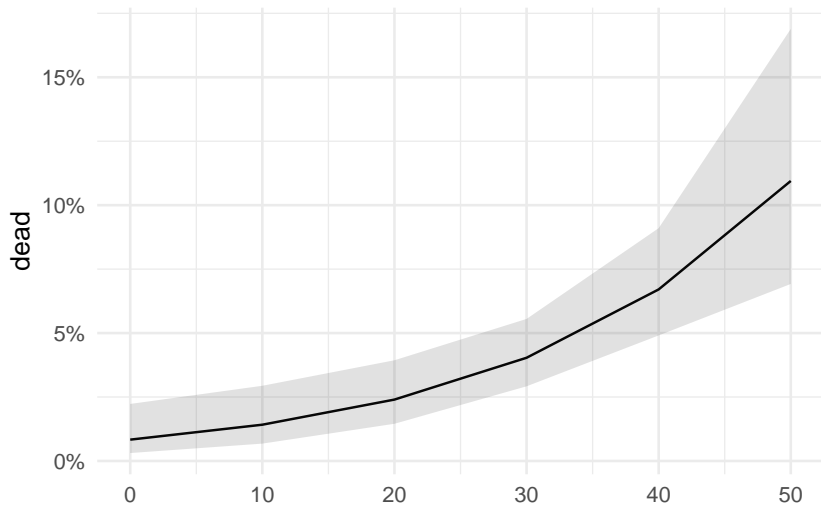
Visualising model: `sjPlot`

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

```
$dbh
```

Predicted probabilities of dead

Poisson multilevel regression

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▶ 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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  - ▶ `y ~ x + (1 | group)`

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

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GLMM FAQ

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