

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

```
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:

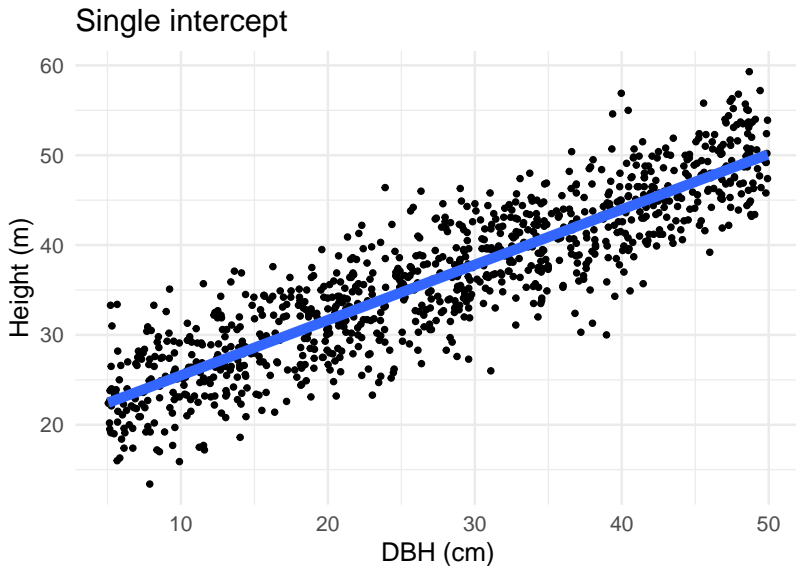
$$Height_i \sim N(\mu_i, \sigma^2)$$

$$\mu_i = \alpha + \beta DBH_i$$

α : expected height when $DBH = 0$

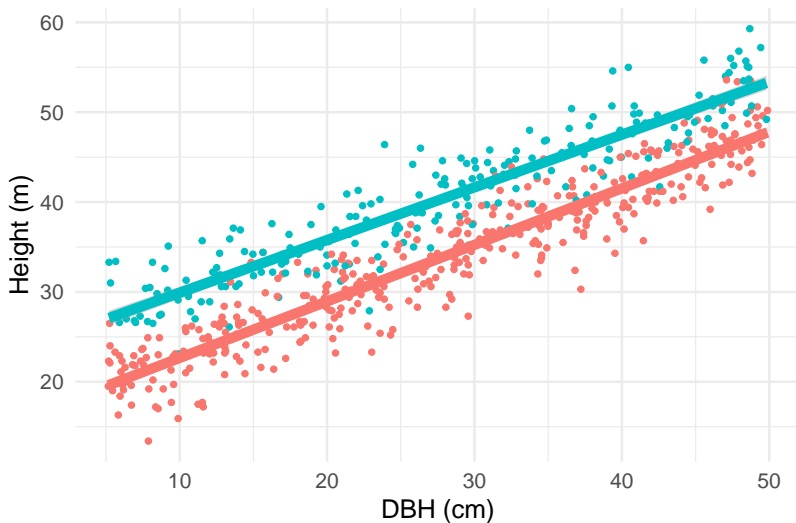
β : how much height increases with every unit increase of DBH

There is only one intercept



What if allometry varies among sites?

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 | *** |

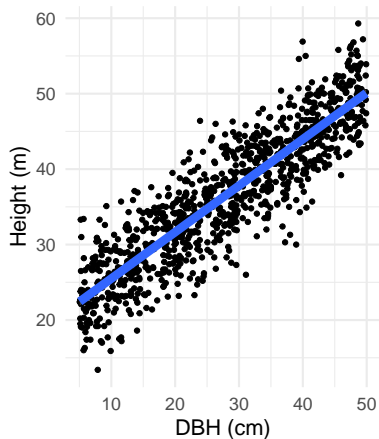
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.043 on 989 degrees of freedom

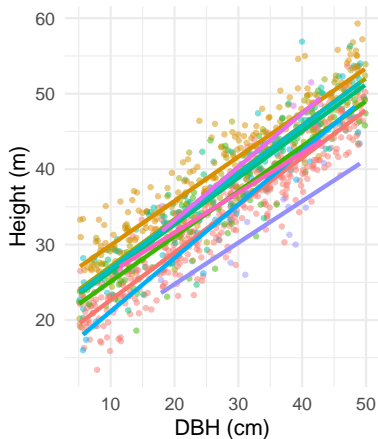
Multiple R-squared: 0.8835. Adjusted R-squared: 0.8823

Single vs varying intercept

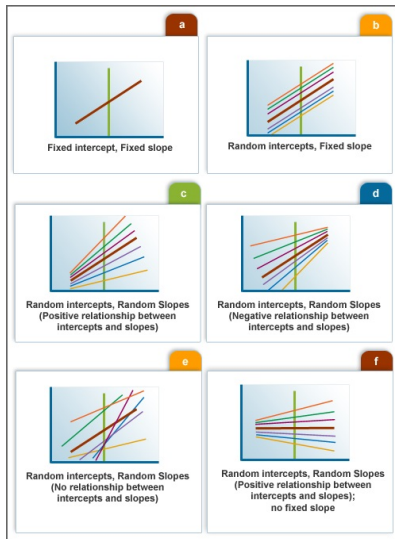
Single intercept



Different intercept for each si

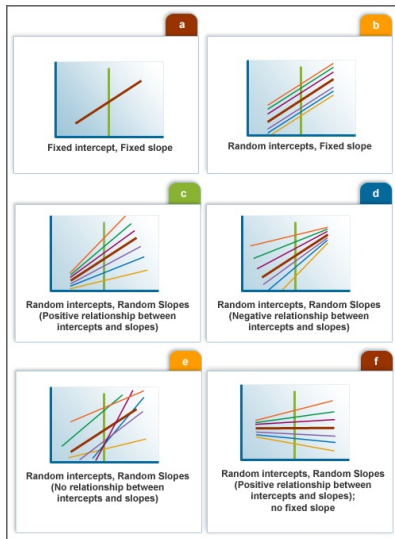


Mixed models enable us to account for variability



► Varying intercepts

Mixed models enable us to account for variability



- Varying intercepts
- Varying slopes

Mixed model with varying intercepts

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

$$\alpha_j \sim N(0, \tau^2)$$

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

En nuestro ejemplo:

$$Height_i = a + site_j + b \cdot DBH_i + \varepsilon_i$$

$$site_j \sim N(0, \tau^2)$$

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

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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Random vs Fixed effects?

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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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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.

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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?

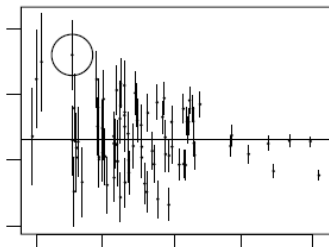
- ▶ Varies by group
- ▶ Variation estimated with **probability model**

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

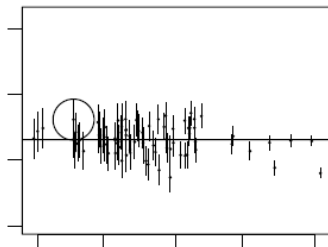
Shrinkage improves parameter estimation

Especially for groups with low sample size

No pooling



Multilevel model



From Gelman & Hill p. 253

Fitting mixed/multilevel models

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

Linear mixed model fit by REML ['lmerMod']

Formula: height ~ dbh + (1 | site)

Data: trees

REML criterion at convergence: 5108.3

Scaled residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|--------|--------|--------|
| -3.3199 | -0.6607 | 0.0227 | 0.6716 | 3.7328 |

Random effects:

| Groups | Name | Variance | Std.Dev. |
|----------|-------------|----------|----------|
| site | (Intercept) | 11.195 | 3.346 |
| Residual | | 9.261 | 3.043 |

Number of obs: 1000, groups: site, 10

Fixed effects:

| | Estimate | Std. Error | t value |
|-------------|-----------|------------|---------|
| (Intercept) | 19.011468 | 1.100444 | 17.28 |
| dbh | 0.616927 | 0.007572 | 81.47 |

Correlation of Fixed Effects:

(Intr)

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

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

```
# A tibble: 4 x 5
```

| | term <chr> | estimate <dbl> | std.error <dbl> | statistic <dbl> | group <chr> |
|---|-------------------------|-------------------|--------------------|--------------------|----------------|
| 1 | (Intercept) | 19.0 | 1.10 | 17.3 | fixed |
| 2 | dbh | 0.617 | 0.00757 | 81.5 | fixed |
| 3 | sd_(Intercept).site | 3.35 | NA | NA | site |
| 4 | sd_Observation.Residual | 3.04 | NA | NA | Residual |

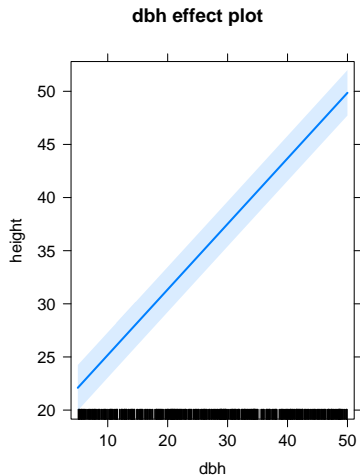
See also broom.mixed

Visualising model: allEffects

```
model: height ~ dbh
```

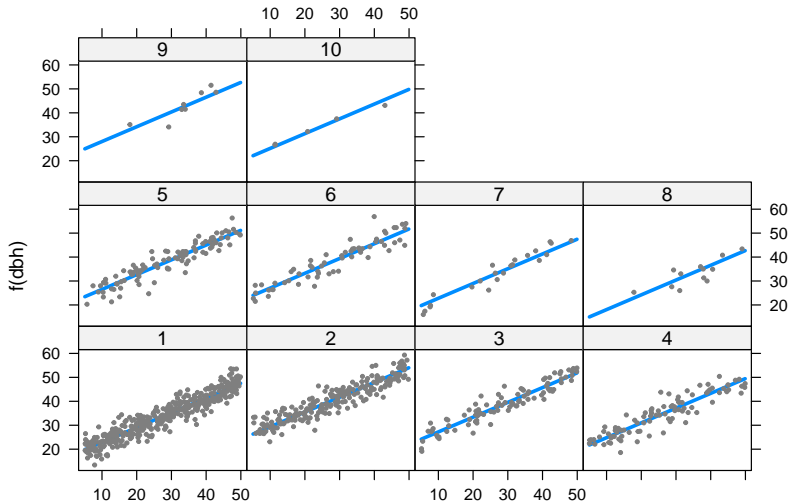
```
dbh effect
```

| dbh | 5 | 20 | 30 | 40 | 50 |
|-----|----------|----------|----------|----------|----------|
| | 22.09610 | 31.35001 | 37.51928 | 43.68855 | 49.85782 |



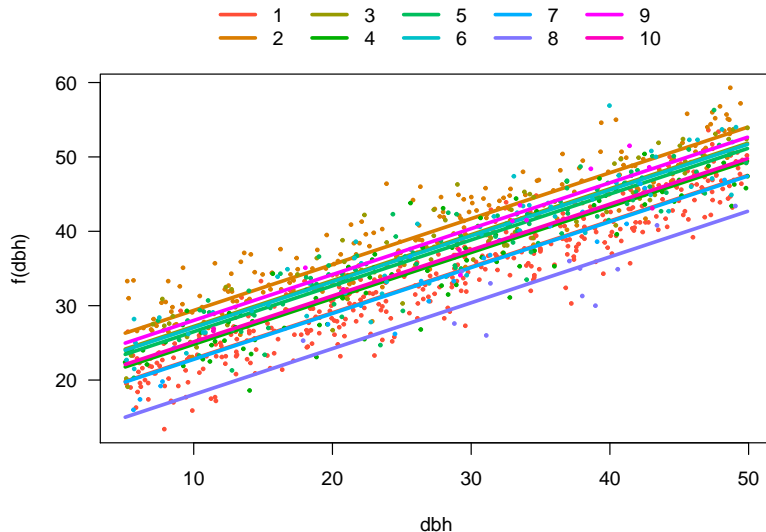
Visualising model: visreg

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



Visualising model

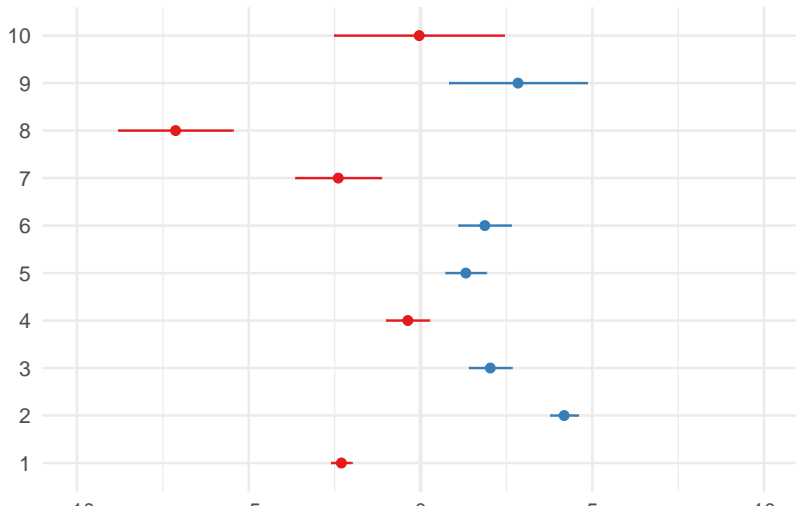
```
visreg(mixed, xvar = "dbh", by = "site", re.form = NULL, overlay
```



Visualising model: sjPlot

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

Random effects

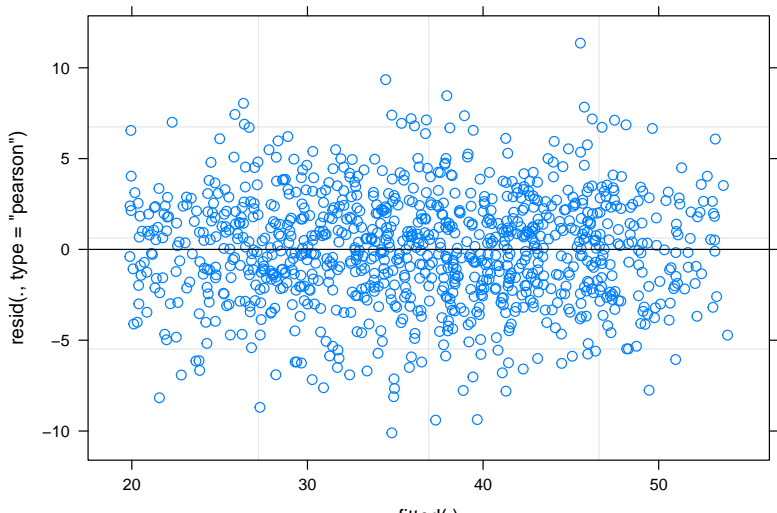


Using merTools to understand fitted model

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

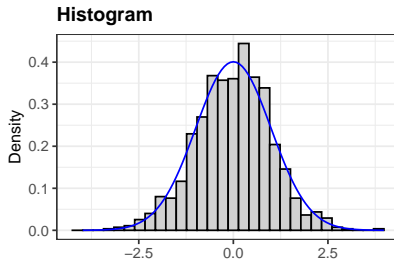
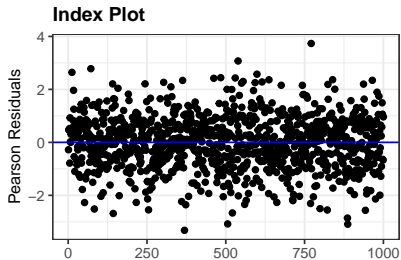
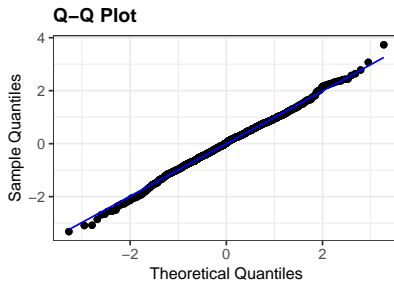
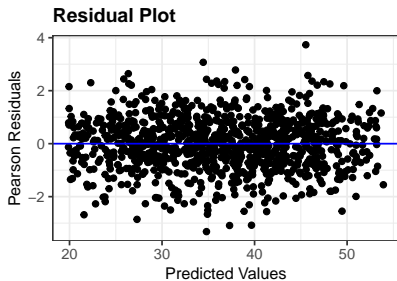
Checking residuals

```
plot(mixed)
```



Checking residuals

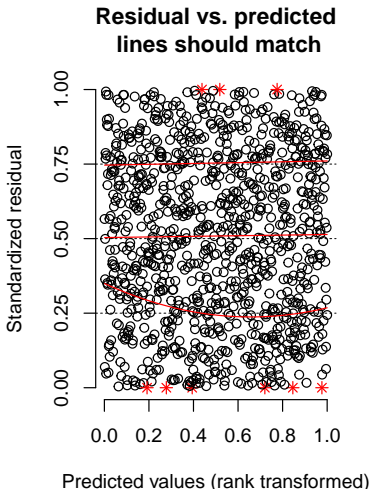
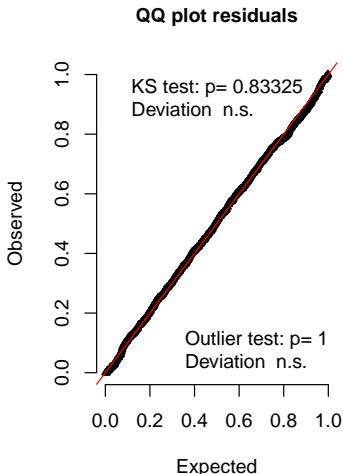
```
ggResidpanel::resid_panel(mixed)
```



Checking residuals (DHARMA)

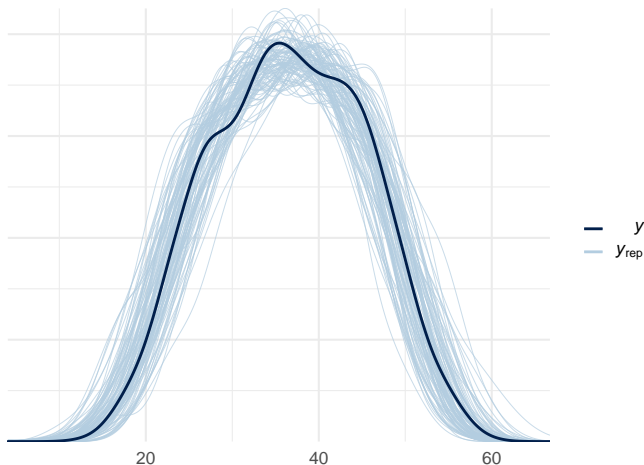
```
DHARMA::simulateResiduals(mixed, plot = TRUE, use.u = TRUE)
```

DHARMA scaled residual plots



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

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

$$\alpha_j \sim N(\mu_j, \tau^2)$$

$$\mu_j = \delta \cdot \text{Predictor}_j$$

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

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-raw/sitedata.csv")  
sitedata
```

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

Merging trees and site data

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

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

Fit multilevel model

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

Linear mixed model fit by REML ['lmerMod']

Formula: height ~ dbh + (1 | site) + temp

Data: trees.full

REML criterion at convergence: 5098.2

Scaled residuals:

| | Min | 1Q | Median | 3Q | Max |
|--|---------|---------|--------|--------|--------|
| | -3.3247 | -0.6517 | 0.0192 | 0.6663 | 3.7268 |

Random effects:

| Groups | Name | Variance | Std.Dev. |
|----------|-------------|----------|----------|
| site | (Intercept) | 3.158 | 1.777 |
| Residual | | 9.266 | 3.044 |

Number of obs: 1000, groups: site, 10

Fixed effects:

| | Estimate | Std. Error | t value |
|-------------|-----------|------------|---------|
| (Intercept) | -1.730911 | 4.671336 | -0.371 |
| dbh | 0.616894 | 0.007571 | 81.484 |
| temp | 1.115104 | 0.248001 | 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 °C (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 | 0.655055 | 27.999 |
| dbh | 0.616894 | 0.007571 | 81.484 |
| temp.c | 1.115104 | 0.248001 | 4.496 |

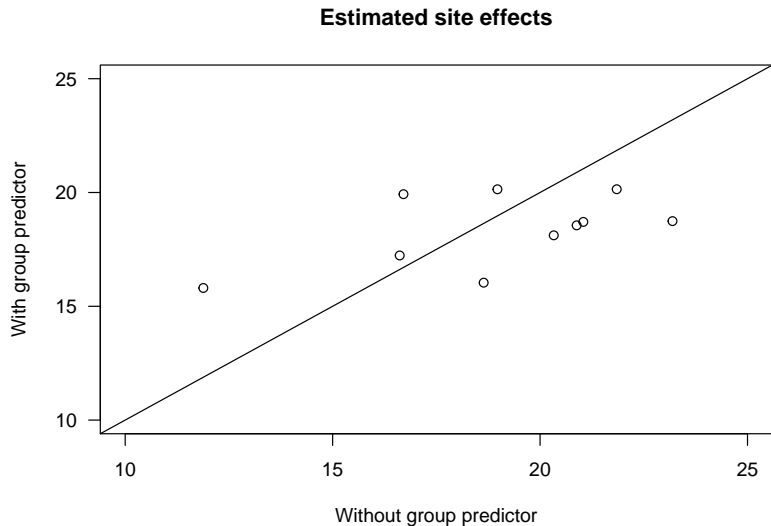
Correlation of Fixed Effects:

| | (Intr) dbh |
|--------|--------------|
| dbh | -0.333 |
| temp.c | -0.250 0.008 |

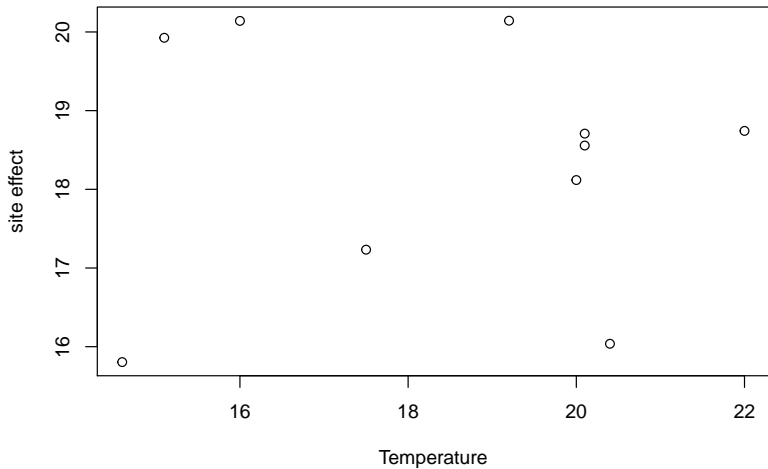
Examine model with merTools

```
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

convergence code: 0

Varying intercepts and slopes

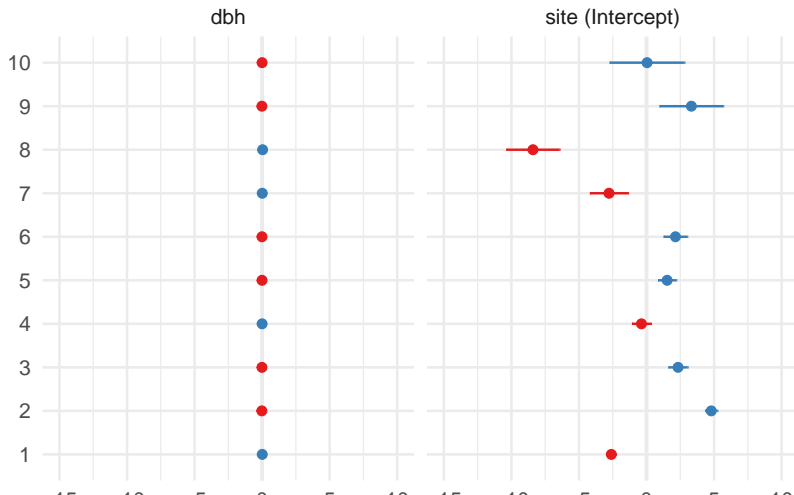
```
$site
  (Intercept)      dbh
1    16.34655 0.6299443
2    23.74733 0.5970814
3    21.28802 0.6080019
4    18.57844 0.6200337
5    20.47961 0.6115916
6    21.09608 0.6088542
7    16.17675 0.6306983
8    10.54681 0.6556978
9    22.27301 0.6036281
10   18.99463 0.6181856
```

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


Visualising model: sjPlot

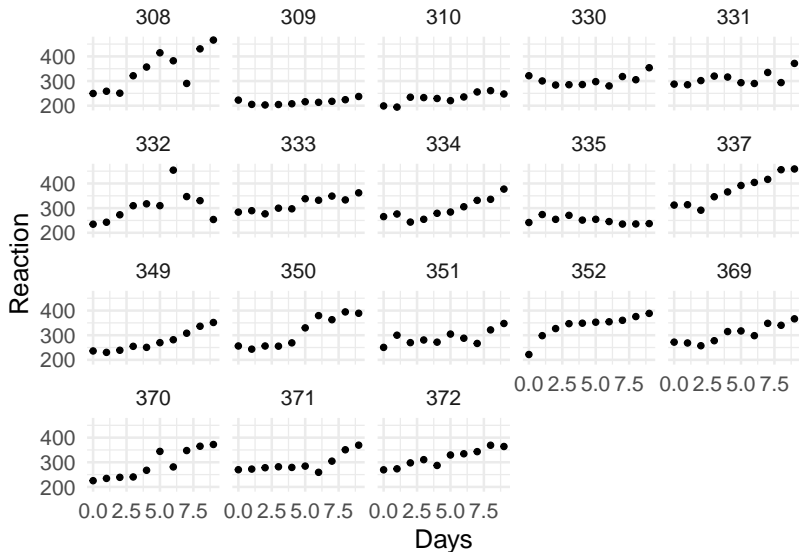
```
plot_model(mixed.slopes, type = "re")
```

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 | 0.4633 | 5.1793 |

Random effects:

| Groups | Name | Variance | Std.Dev. | Corr |
|----------|-------------|----------|----------|------|
| Subject | (Intercept) | 611.90 | 24.737 | |
| | Days | 35.08 | 5.923 | 0.07 |
| Residual | | 654.94 | 25.592 | |

Number of obs: 180, groups: Subject, 18

Fixed effects:

| | Estimate | Std. Error | t value |
|-------------|----------|------------|---------|
| (Intercept) | 251.405 | 6.824 | 36.843 |
| 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

```
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

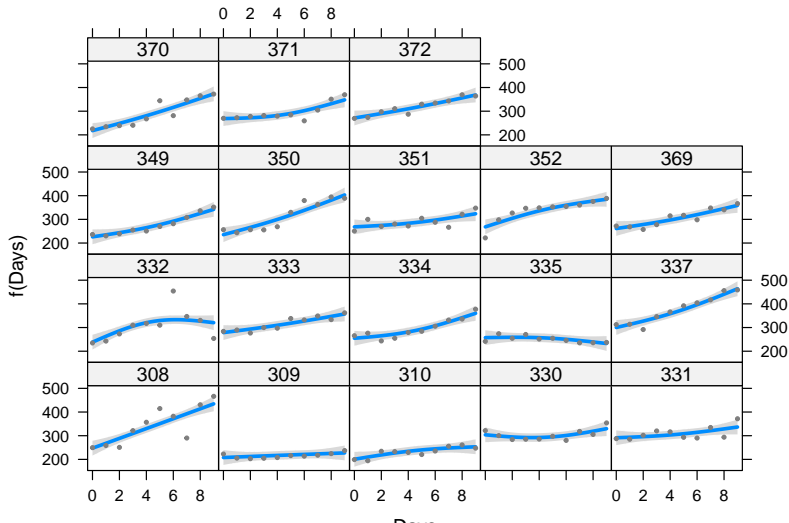
Approximate significance of smooth terms:

| | 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

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`

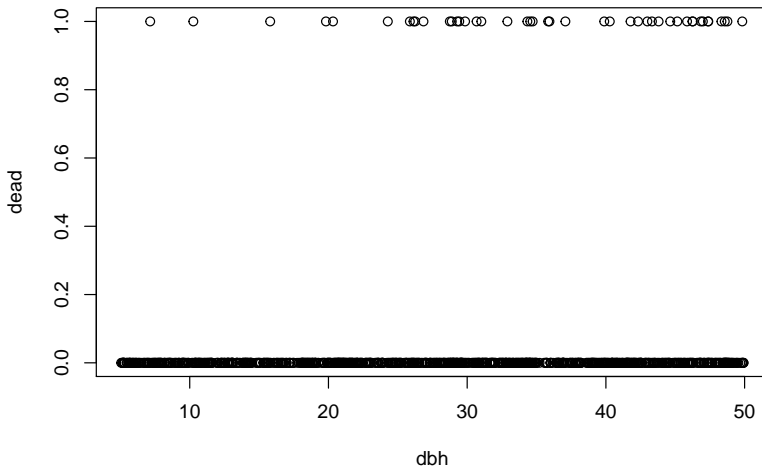
Eric J Pedersen ^{Corresp., 1,2}, David L. Miller ^{3,4}, Gavin L. Simpson ⁵, Noam Ross ⁶

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

Multilevel logistic regression

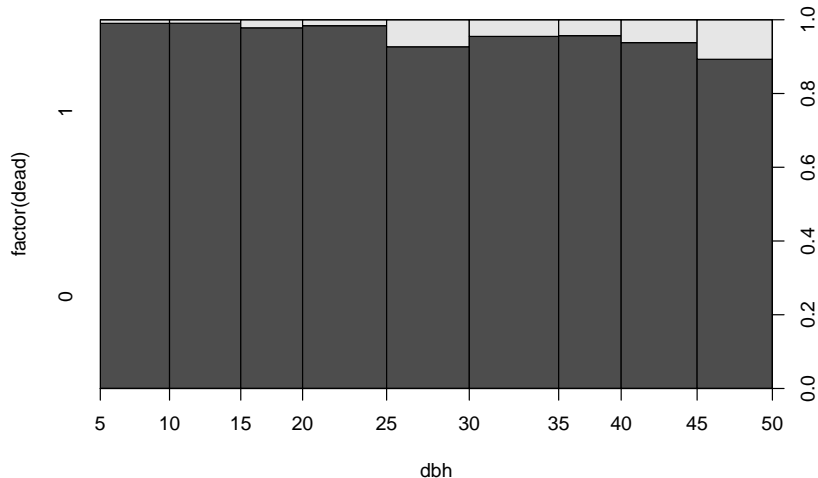
Q: Relationship between tree size and mortality

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



Q: Relationship between tree size and mortality

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



Fit simple logistic regression

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

Call:

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

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

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

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 |

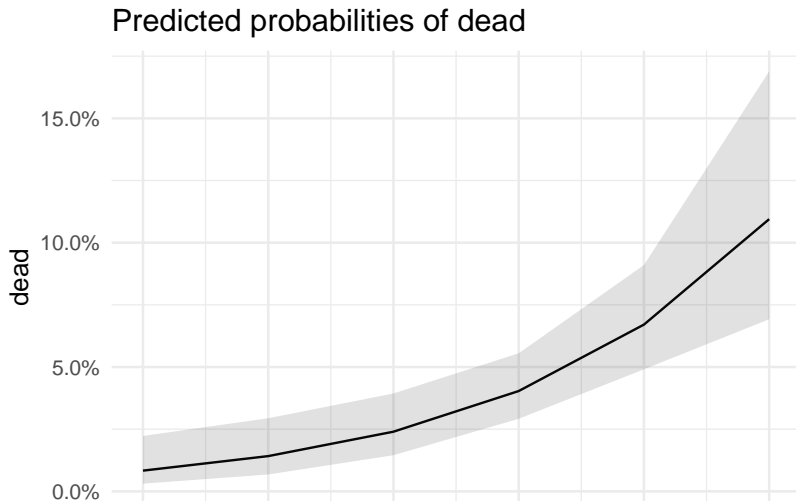
```
attr(,"class")
```

```
[1] "coef.mer"
```

Visualising model: sjPlot

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

\$dbh



Poisson multilevel regression

Advantages of multilevel models

- ▶ Perfect for **structured data** (space-time)

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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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- ▶ $y \sim x + (1 \mid \text{group})$

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- ▶ Varying intercepts and slopes, 2 groups (crossed)
 - ▶ $y \sim x + (1 + x \mid \text{group1}) + (1 + x \mid \text{group2})$

GLMM FAQ

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