

# Mixed / Multilevel Models

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## 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

## Remember our model structure

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

$$\mu_i = \alpha + \beta x_i$$

In this case:

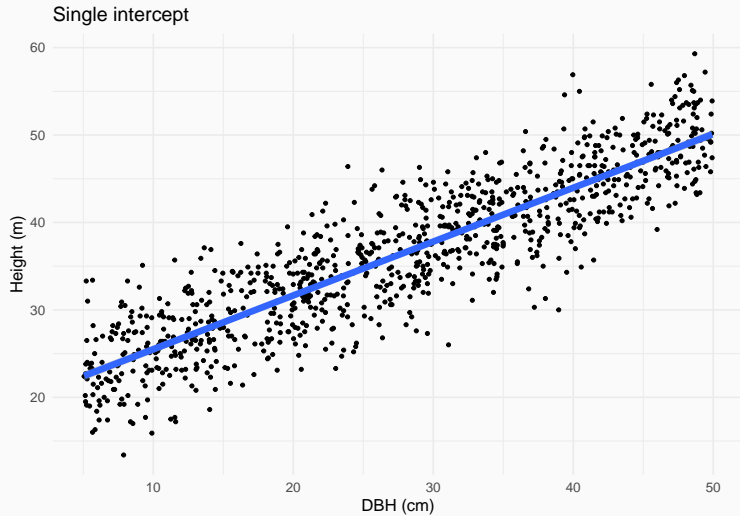
$$\text{Height}_i \sim N(\mu_i, \sigma^2)$$

$$\mu_i = \alpha + \beta \text{DBH}_i$$

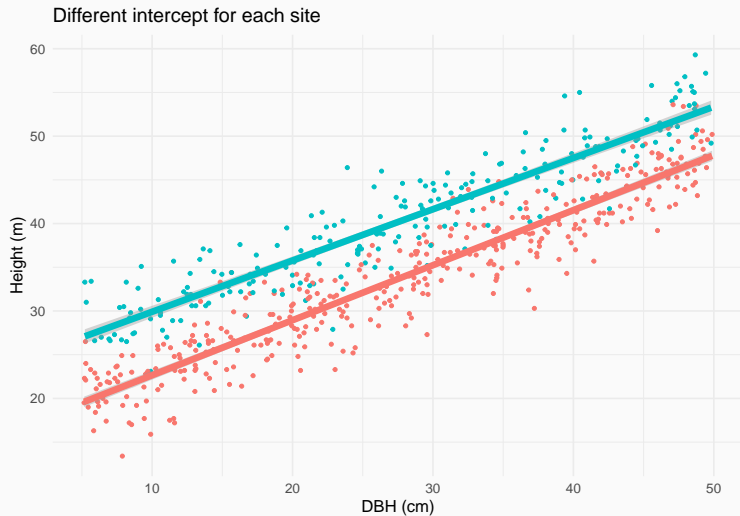
$\alpha$ : expected height when DBH = 0

$\beta$ : how much height increases with every unit increase of DBH

# There is only one intercept



## What if allometry varies among sites?





# Fitting a varying intercepts model with `lm`

Call:

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

Residuals:

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

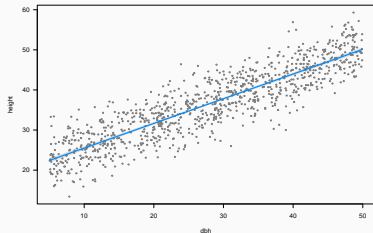
Coefficients:

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

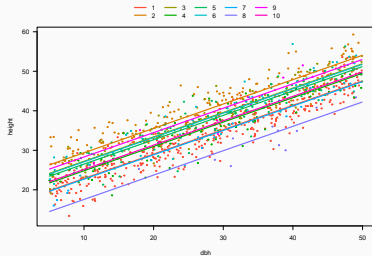
---

# Single vs varying intercept

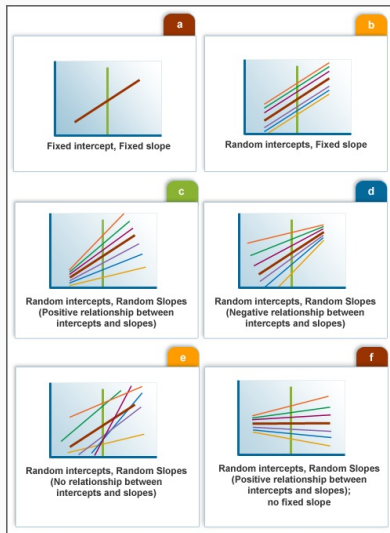
Single intercept



Different intercept for each site



# Mixed models enable us to account for variability



## Mixed model with varying intercepts

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

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

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

In our example:

$$\text{Height}_i = a + \text{site}_j + b \cdot \text{DBH}_i + \varepsilon_i$$

$$\text{site}_j \sim N(0, \tau^2)$$

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

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/](http://andrewgelman.com/2005/01/25/why_i_dont_use/)

## 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.

[http://andrewgelman.com/2005/01/25/why\\_i\\_dont\\_use/](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.
3. Fixed when sample exhausts the population; random when the sample is small part of the population.

[http://andrewgelman.com/2005/01/25/why\\_i\\_dont\\_use/](http://andrewgelman.com/2005/01/25/why_i_dont_use/)

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

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## Random vs Fixed effects?

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

[http://andrewgelman.com/2005/01/25/why\\_i\\_dont\\_use/](http://andrewgelman.com/2005/01/25/why_i_dont_use/)



## What is a random effect, really?

- Varies by group

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

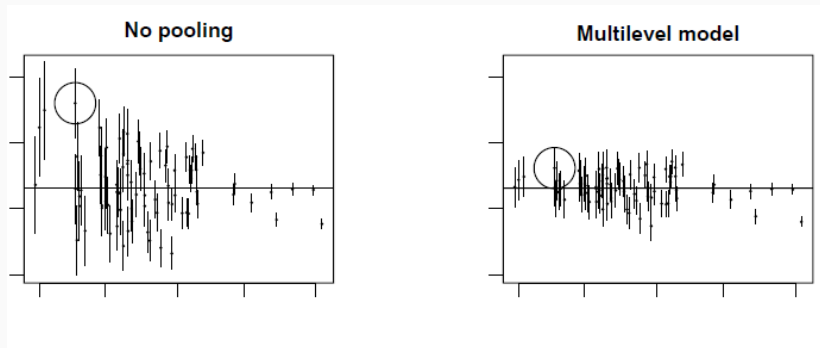
# What is a random effect, really?

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

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

# Shrinkage improves parameter estimation

Especially for groups with low sample size



*From Gelman & Hill p. 253*

# Fitting mixed/multilevel models

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

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

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

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
site	(Intercept)	10.007	3.163
Residual		9.252	3.042

Number of obs: 1000, groups: site, 10

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	19.014671	1.045018	18.20	<2e-16 ***
dbh	0.616911	0.007569	81.51	<2e-16 ***

---

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

# Fitting mixed/multilevel models

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

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

```
REML criterion at convergence: 5108.3
```

```
Scaled residuals:
```

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

```
Random effects:
```

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

```
Number of obs: 1000, groups: site, 10
```

```
Fixed effects:
```

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

```
Correlation of Fixed Effects:
```

```
(Intr)  
dbh -0.197
```

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

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

## Retrieve model coefficients

```
coef(mixed)
```

```
$site
```

```
  (Intercept)      dbh
```

1	16.70800	0.6169271
2	23.19162	0.6169271
3	21.04229	0.6169271
4	18.64086	0.6169271
5	20.32995	0.6169271
6	20.88200	0.6169271
7	16.61686	0.6169271
8	11.88302	0.6169271
9	21.84779	0.6169271
10	18.97228	0.6169271

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

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

## Compare site effects between mixed and lm

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



## Broom: model estimates in tidy form

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

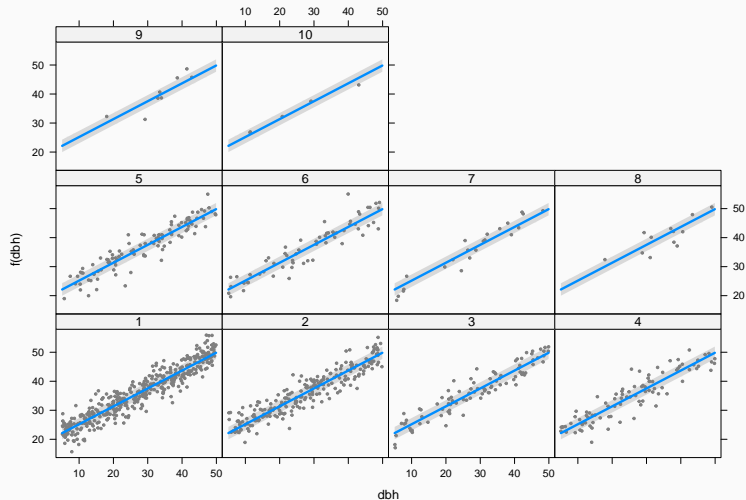
```
# A tibble: 4 x 6
```

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

See also [broom.mixed](#)

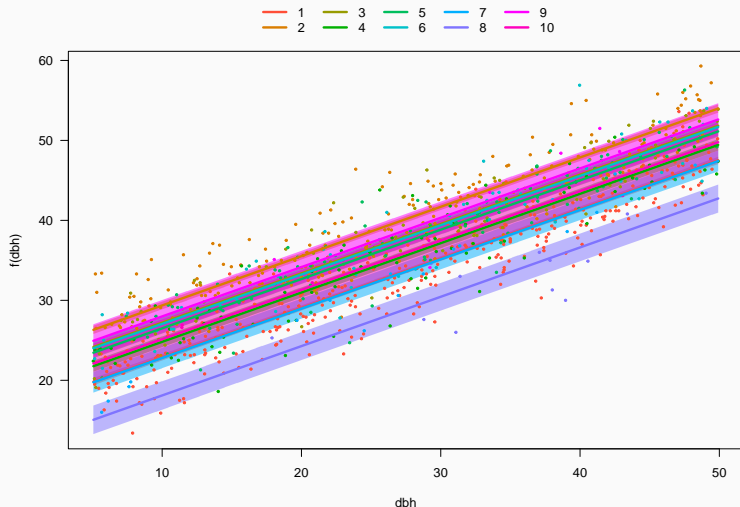
# Visualising model: visreg

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



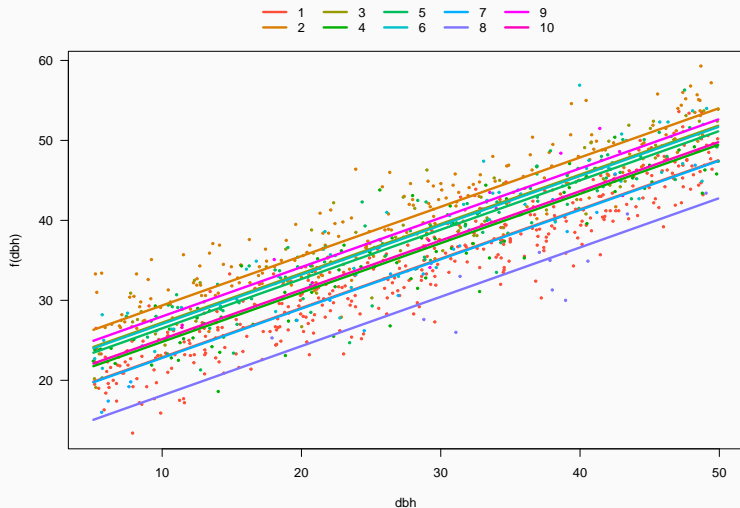
# Visualising model

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



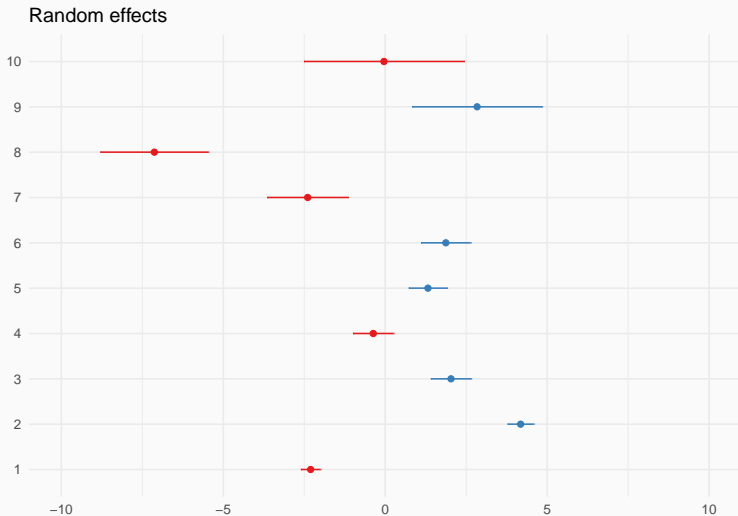
# Visualising model

```
visreg(mixed, xvar = "dbh", by = "site", overlay = TRUE, band = FALSE)
```



# Visualising model: sjPlot

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

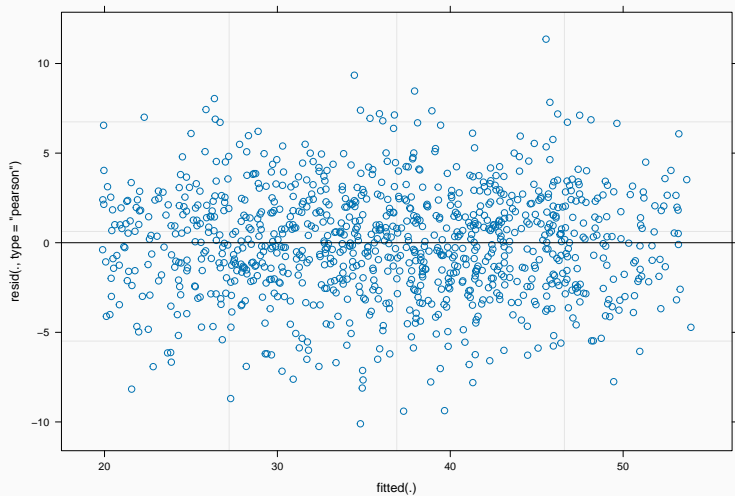


## Using merTools to understand fitted model

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

# Checking residuals

```
plot(mixed)
```

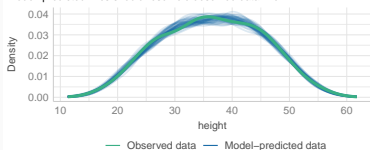


# Checking residuals

```
library("performance")  
check_model(mixed)
```

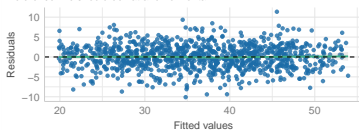
## Posterior Predictive Check

Model-predicted lines should resemble observed data line



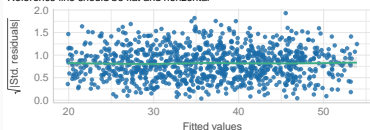
## Linearity

Reference line should be flat and horizontal



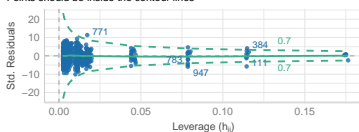
## Homogeneity of Variance

Reference line should be flat and horizontal



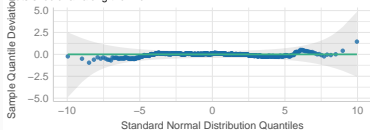
## Influential Observations

Points should be inside the contour lines



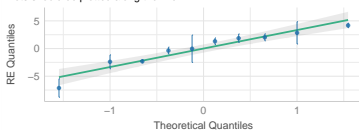
## Normality of Residuals

Dots should fall along the line



## Normality of Random Effects (site)

Dots should be plotted along the line

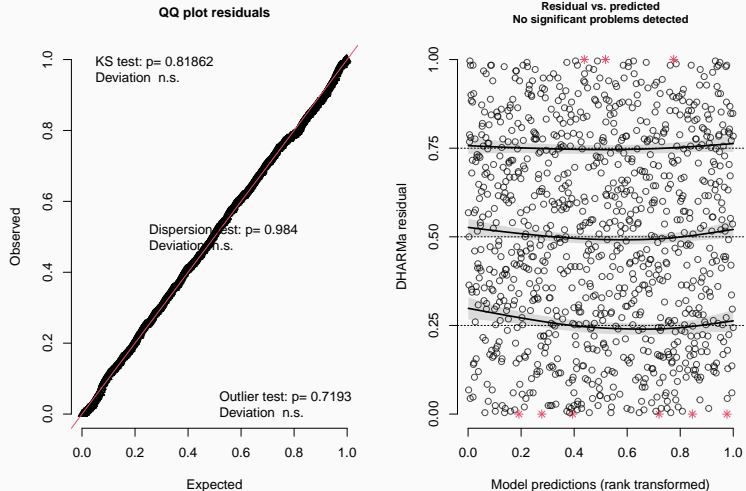




# Checking residuals (DHARMA)

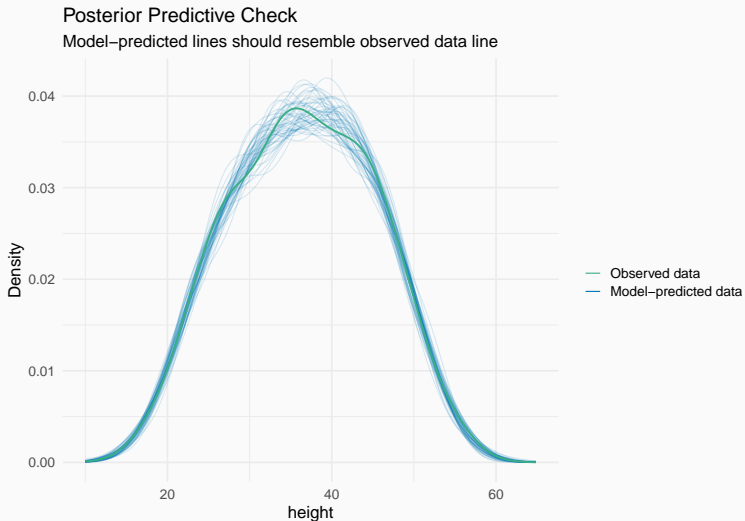
```
DHARMA::simulateResiduals(mixed, plot = TRUE, re.form = NULL)
```

DHARMA residual



# Model checking with simulated data

```
check_predictions(mixed)
```



# R-squared for GLMMs

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

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

```
r2(mixed)
```

```
# R2 for Mixed Models
```

```
Conditional R2: 0.888
```

```
  Marginal R2: 0.753
```

## Growing the hierarchy: adding site-level predictors

---

## Model with group-level predictors

We had:

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

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

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

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?

$$\text{Height}_i = \text{site}_j + b \cdot \text{DBH}_i + \varepsilon_i$$

$$\text{site}_j \sim N(\mu_j, \tau^2)$$

$$\mu_j = a + \delta \cdot \text{Temperature}_j$$

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

## 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

```
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 °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:

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site	(Intercept)	3.158	1.777
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Number of obs: 1000, groups: site, 10

Fixed effects:

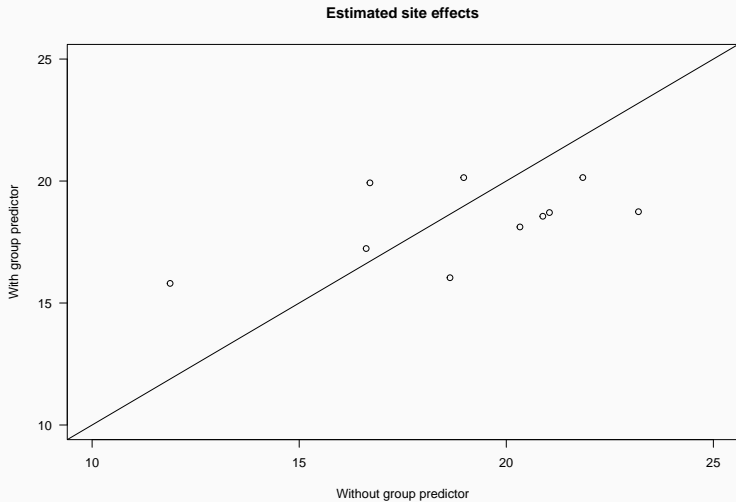
	Estimate	Std. Error	t value
(Intercept)	18.340954	0.655054	27.999
dbh	0.616894	0.007571	81.484
temp.c	1.115104	0.248000	4.496

Correlation of Fixed Effects:

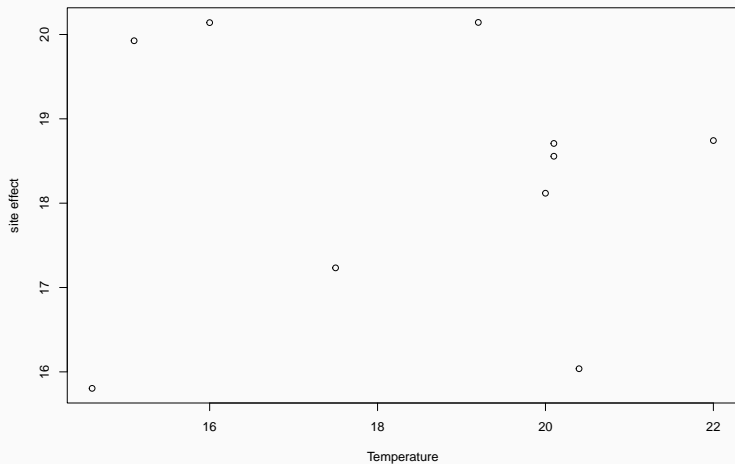
(Intr) dbh

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

## Comparing site effects with and without group predictor



## Are site effects related to temperature?

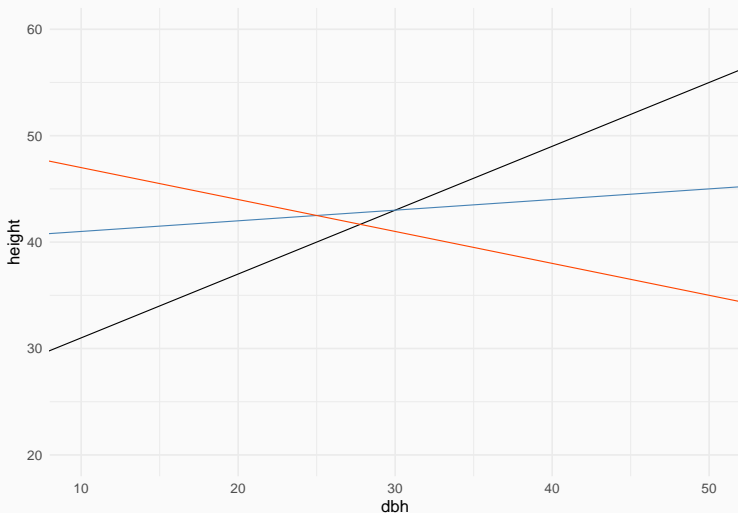


## Varying intercepts and slopes

---

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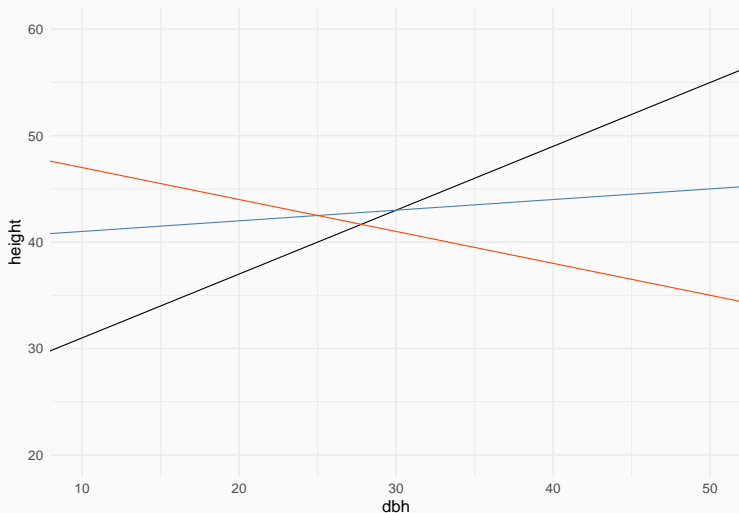
- There is overall difference in height among sites (different intercepts)





## Varying intercepts and slopes

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



## Varying intercepts and slopes

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

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

# Varying intercepts and slopes

Linear mixed model fit by REML ['lmerMod']

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

Data: trees

REML criterion at convergence: 5105.1

Scaled residuals:

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

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
site	(Intercept)	1.566e+01	3.95671	
	dbh	3.087e-04	0.01757	-1.00
	Residual	9.226e+00	3.03744	

Number of obs: 1000, groups: site, 10

Fixed effects:

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

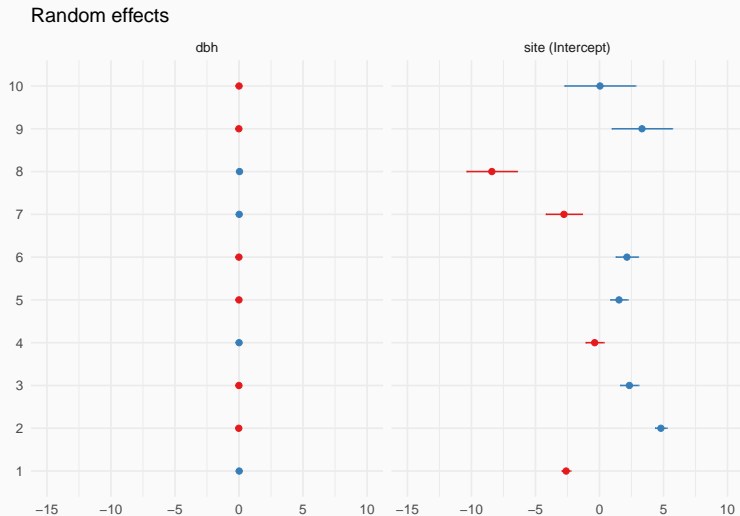
## Varying intercepts and slopes

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

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

# Visualising model: sjPlot

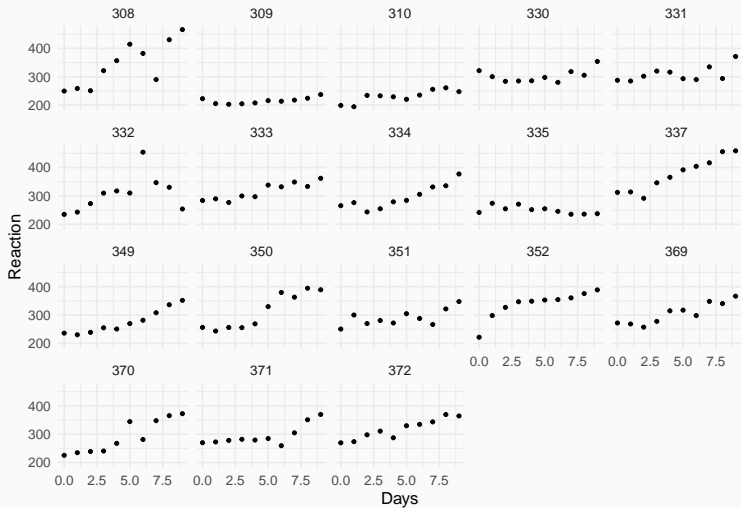
```
plot_model(mixed.slopes, type = "re")
```



## More examples

---

# sleepstudy (repeated measures)



# Varying intercepts and slopes (lme4)

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

Linear mixed model fit by REML ['lmerMod']

Formula: Reaction ~ Days + (1 + Days | Subject)

Data: sleepstudy

REML criterion at convergence: 1743.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9536	-0.4634	0.0231	0.4634	5.1793

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Subject	(Intercept)	612.10	24.741	
	Days	35.07	5.922	0.07
Residual		654.94	25.592	

Number of obs: 180, groups: Subject, 18

Fixed effects:

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

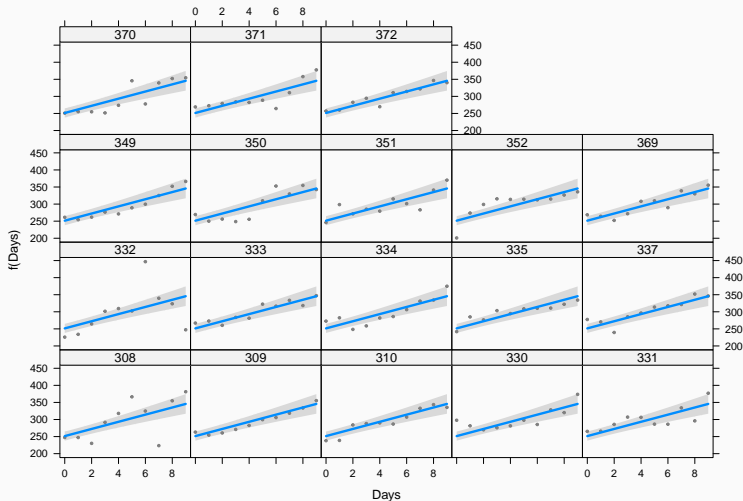
Correlation of Fixed Effects:

(Intr)



# Varying intercepts and slopes (lme4)

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



# Fitting multilevel models (GAMM) with mgcv

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

Family: gaussian

Link function: identity

Formula:

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

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	298.51	9.05	32.98	<2e-16 ***

---

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

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(Days,Subject)	45.67	53	17.11	<2e-16 ***

---

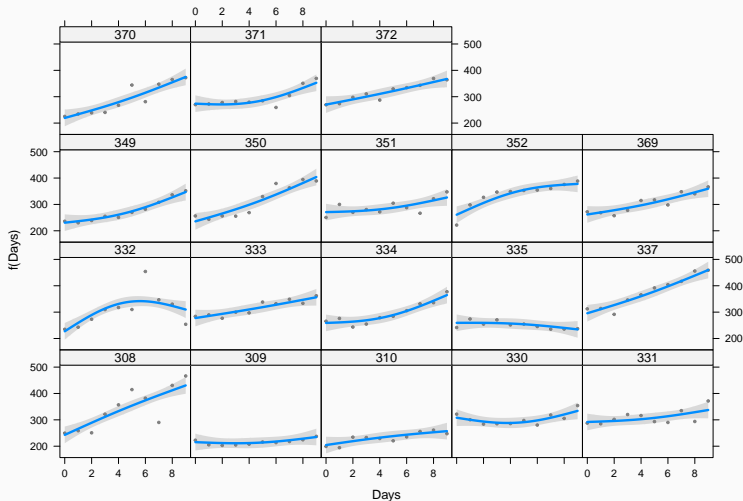
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.835 Deviance explained = 87.7%

-REML = 883.64 Scale est. = 523.2 n = 180

## Fitting multilevel models (GAMM) with mgcv

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



## **Hierarchical generalized additive models: an introduction with mgcv**

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

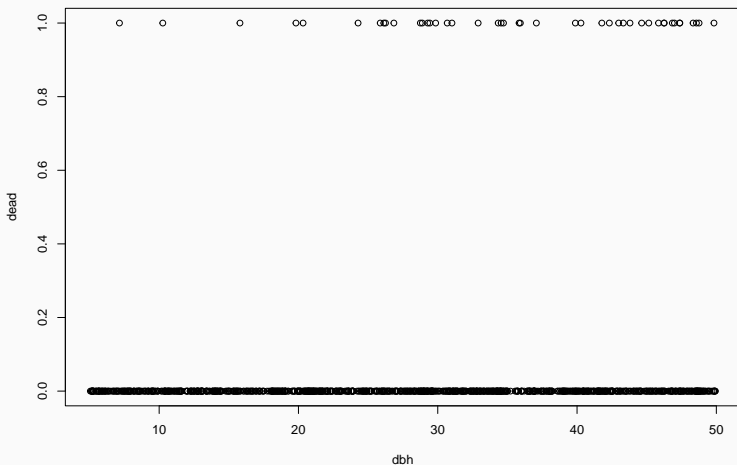
<https://doi.org/10.7287/peerj.preprints.27320v1>

## Multilevel logistic regression

---

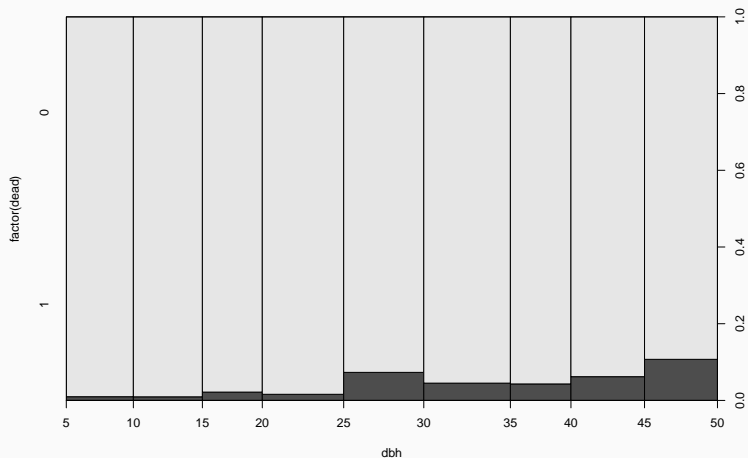
## Q: Relationship between tree size and mortality

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



## Q: Relationship between tree size and mortality

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



# Fit simple logistic regression

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

Call:

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

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.77874	0.50902	-9.388	< 2e-16 ***
dbh	0.05365	0.01377	3.895	9.82e-05 ***

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 360.91 on 999 degrees of freedom  
Residual deviance: 343.69 on 998 degrees of freedom  
AIC: 347.69

Number of Fisher Scoring iterations: 6



# Logistic regression with *independent* site effects

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

Call:

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

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.80123	0.54985	-8.732	<2e-16 ***
dbh	0.05371	0.01381	3.889	0.0001 ***
site2	-0.29692	0.46073	-0.644	0.5193
site3	0.21275	0.52799	0.403	0.6870
site4	0.39841	0.53025	0.751	0.4524
site5	-0.42557	0.64018	-0.665	0.5062
site6	0.66861	0.53656	1.246	0.2127
site7	0.11862	1.06211	0.112	0.9111
site8	0.43899	1.08058	0.406	0.6846
site9	-13.63389	840.90382	-0.016	0.9871
site10	-13.17148	1042.21823	-0.013	0.9899

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 360.91 on 999 degrees of freedom  
Residual deviance: 338.58 on 989 degrees of freedom

# Fit multilevel logistic regression

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

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

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

Scaled residuals:

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

Random effects:

Groups	Name	Variance	Std.Dev.
site	(Intercept)	0	0

Number of obs: 1000, groups: site, 10

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.77874	0.50904	-9.388	< 2e-16 ***
dbh	0.05365	0.01377	3.895	9.83e-05 ***

---

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

## Retrieve model coefficients

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

```
$site
```

```
  (Intercept)      dbh
```

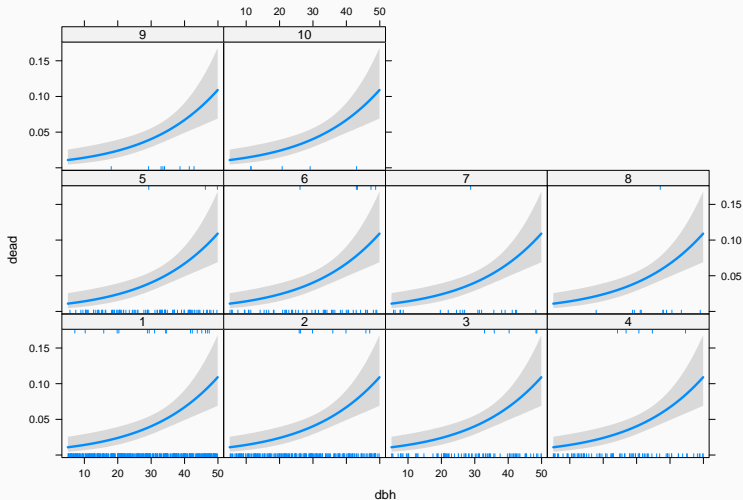
1	-4.778744	0.05364989
2	-4.778744	0.05364989
3	-4.778744	0.05364989
4	-4.778744	0.05364989
5	-4.778744	0.05364989
6	-4.778744	0.05364989
7	-4.778744	0.05364989
8	-4.778744	0.05364989
9	-4.778744	0.05364989
10	-4.778744	0.05364989

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

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

## Visualising model: visreg

```
visreg(mixed.logis, xvar = "dbh", by = "site", scale = "response")
```



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

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- Allow predictions for **unobserved groups**

- Varying intercepts

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## Formula syntax for different models

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

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

<http://mfviz.com/hierarchical-models/>

- Starlings: body mass growth depending on nest type



- Starlings: body mass growth depending on nest type
- Mixed\_binom: Species presence/absence ~ environment

- Starlings: body mass growth depending on nest type
- Mixed\_binom: Species presence/absence ~ environment
- Mixed\_count: Species counts ~ environment