

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
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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:

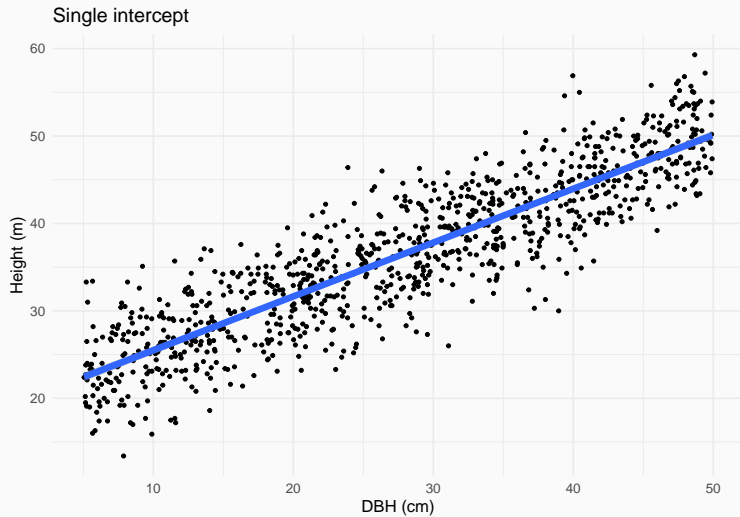
$$\text{Height}_i \sim N(\mu_i, \sigma^2)$$

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

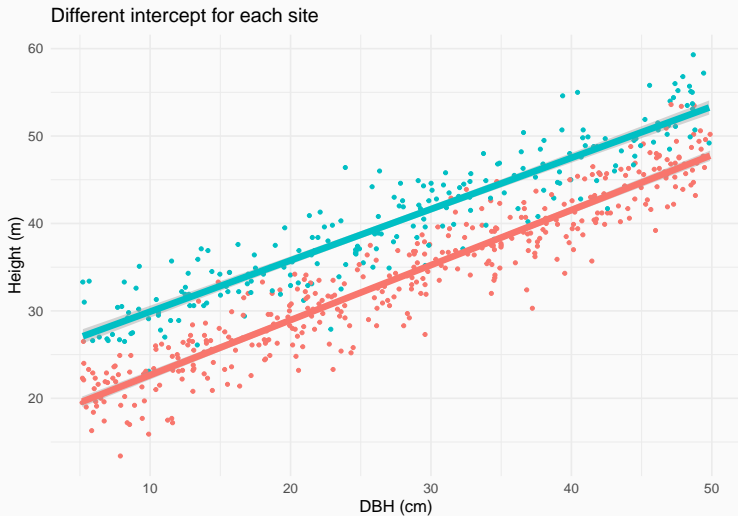
α : expected height when DBH = 0

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)
```

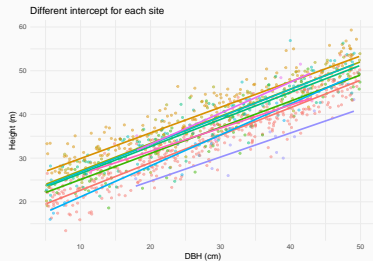
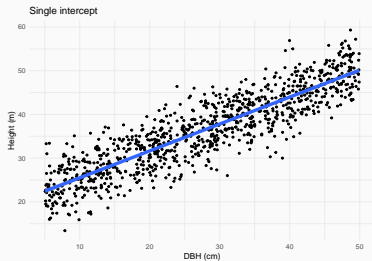
Residuals:

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

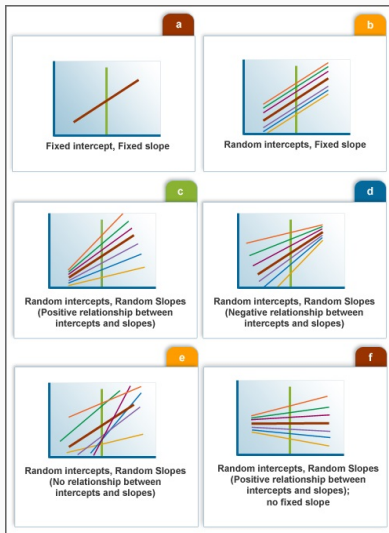
Coefficients:

	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 ***

Single vs varying intercept



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.

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- 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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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).

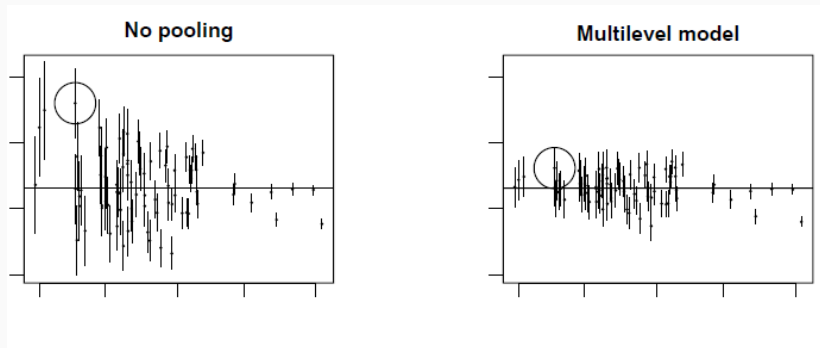
What is a random effect, really?

- 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

```
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.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](#)

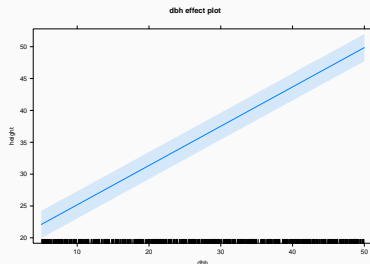
Visualising model: allEffects

```
allEffects(mixed)
```

```
model: height ~ dbh
```

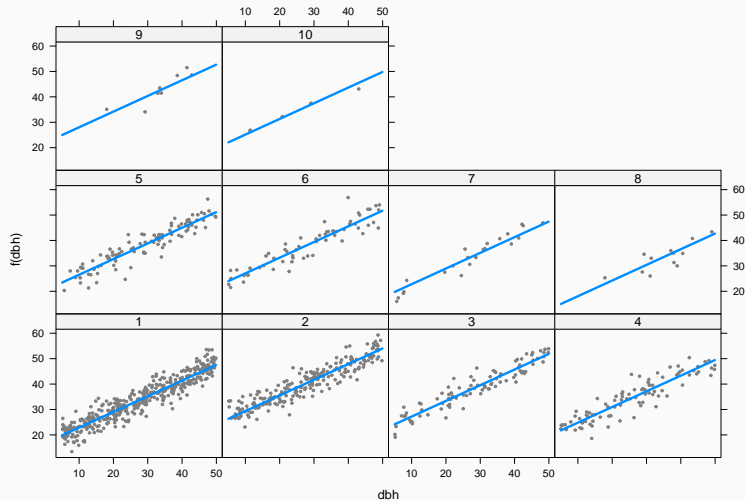
```
dbh effect
```

dbh	5	20	30	40	50
	22.09610	31.35001	37.51928	43.68855	49.85782



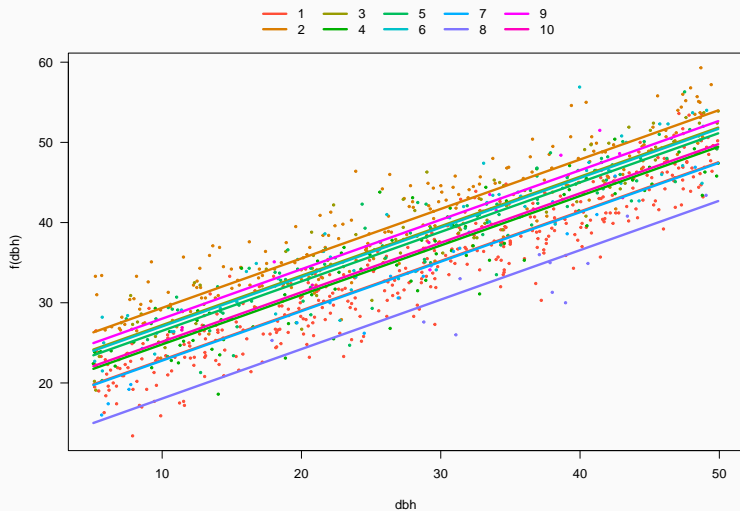
Visualising model: visreg

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



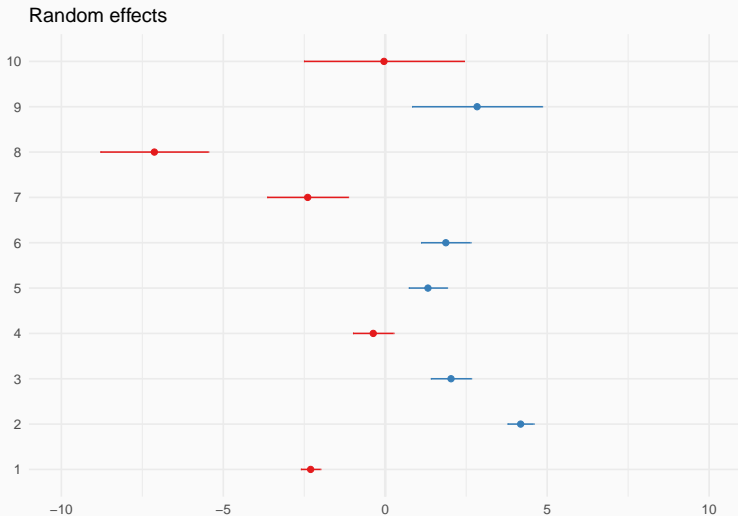
Visualising model

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



Visualising model: sjPlot

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

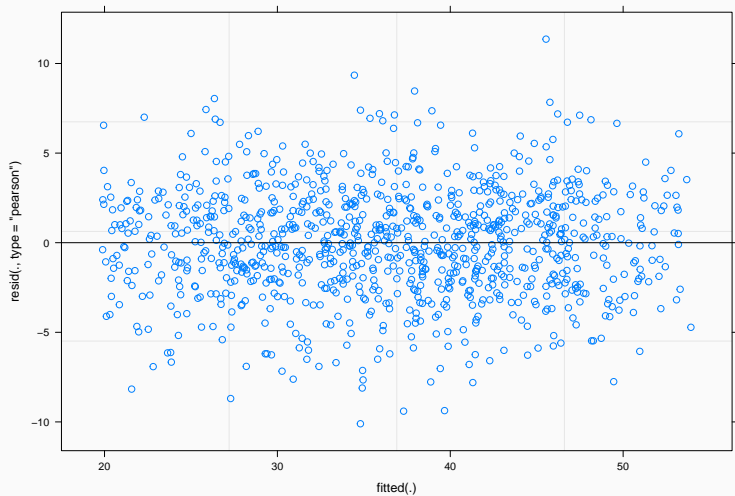


Using merTools to understand fitted model

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

Checking residuals

```
plot(mixed)
```

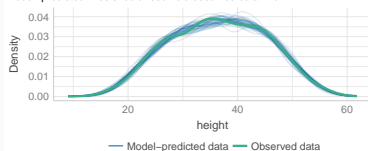


Checking residuals

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

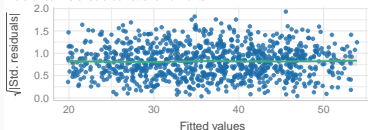
Posterior Predictive Check

Model-predicted lines should resemble observed data line



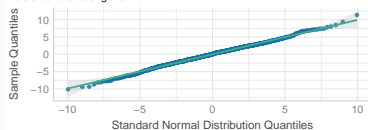
Homogeneity of Variance

Reference line should be flat and horizontal



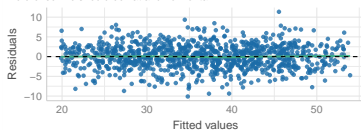
Normality of Residuals

Dots should fall along the line



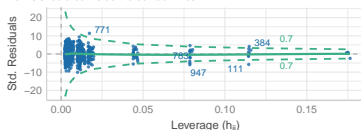
Linearity

Reference line should be flat and horizontal



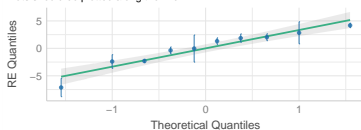
Influential Observations

Points should be inside the contour lines



Normality of Random Effects (site)

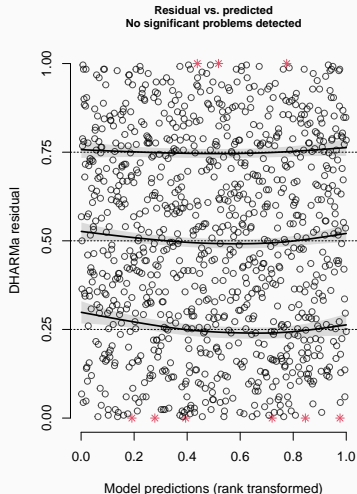
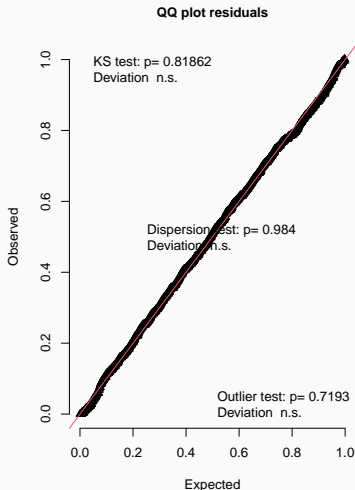
Dots should be plotted along the line



Checking residuals (DHARMA)

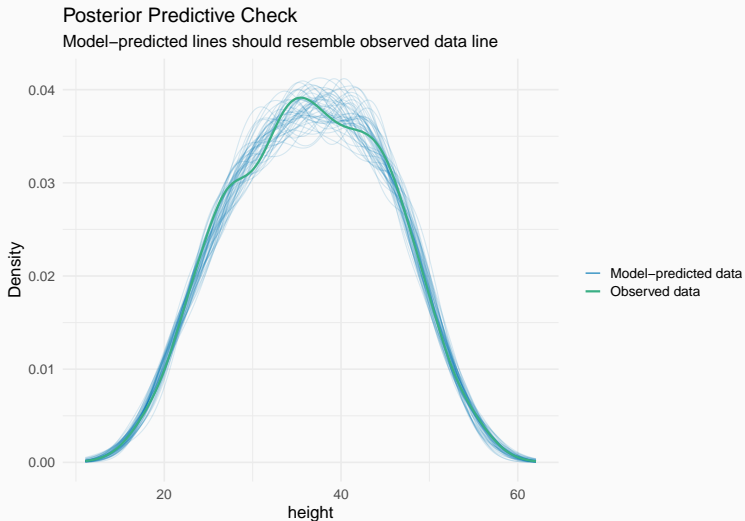
```
DHARMA::simulateResiduals(mixed, plot = TRUE, re.form = NULL)
```

DHARMA residual



Model checking with simulated data

```
check_predictions(mixed)
```



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

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:

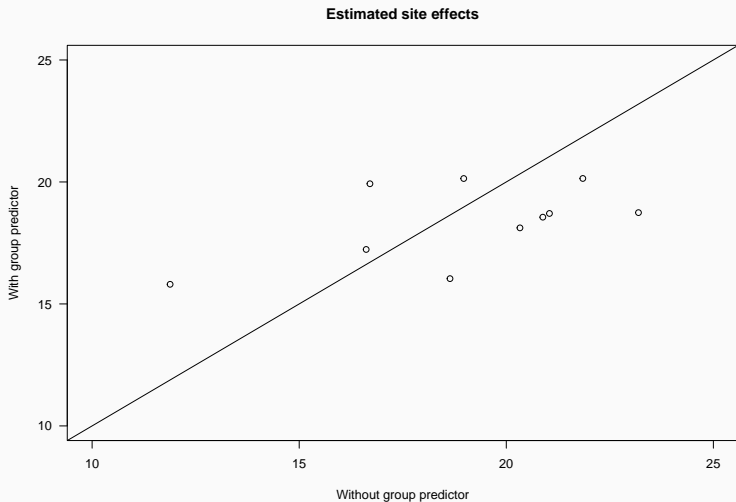
	Estimate	Std. Error	t value
(Intercept)	18.340954	0.655054	27.999
dbh	0.616894	0.007571	81.484
temp.c	1.115104	0.248000	4.496

Correlation of Fixed Effects:

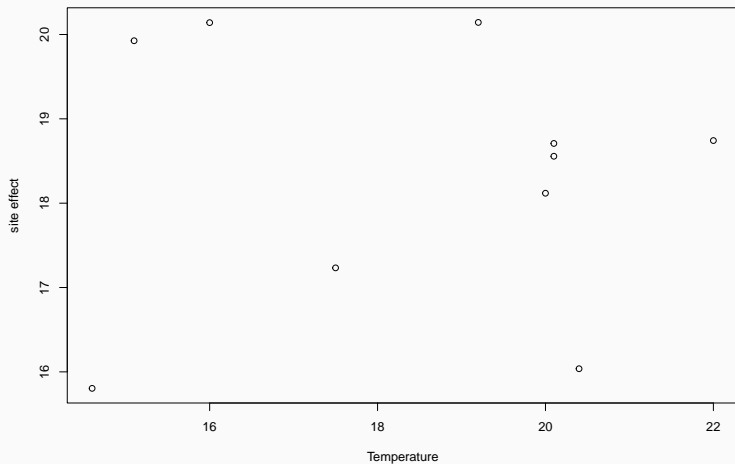
(Intr) dbh


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

Comparing site effects with and without group predictor



Are site effects related to temperature?



Varying intercepts and slopes

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

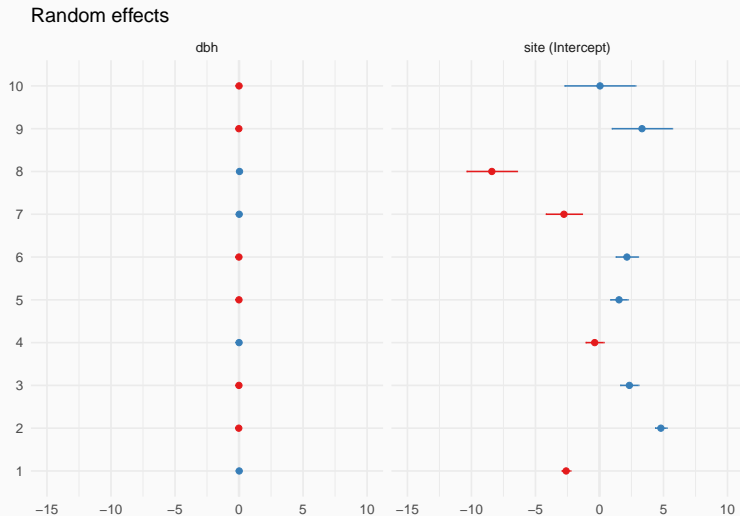
Varying intercepts and slopes

```
$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"
```

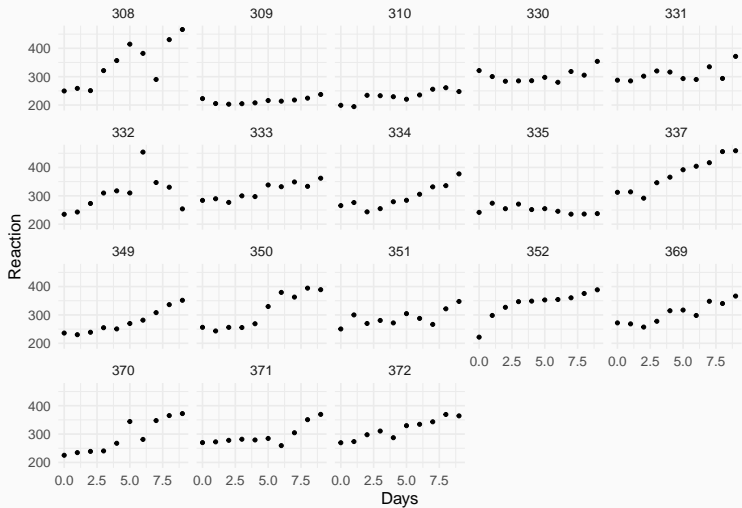
Visualising model: sjPlot

```
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:

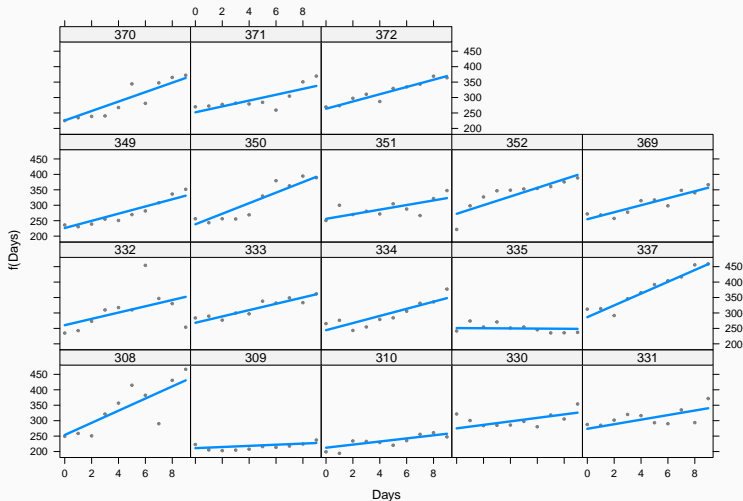
	Estimate	Std. Error	t value
(Intercept)	251.405	6.825	36.838
Days	10.467	1.546	6.771

Correlation of Fixed Effects:

(Intr)

Varying intercepts and slopes (lme4)

```
visreg(sleep, xvar = "Days", by = "Subject", 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)	298.51	9.05	32.98	<2e-16 ***

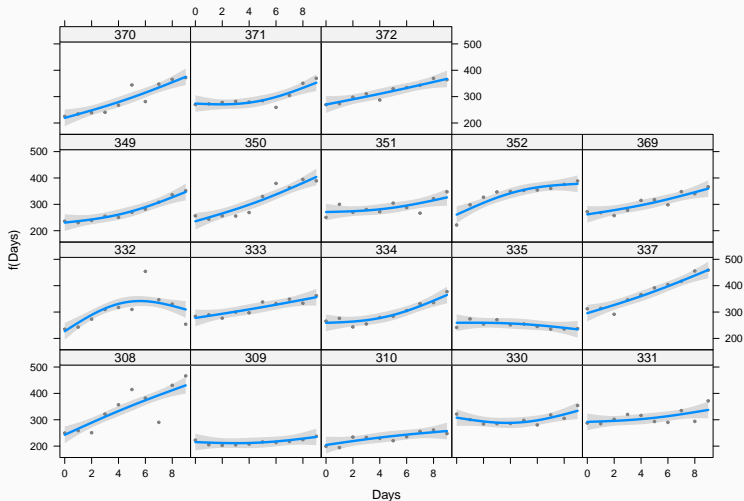
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

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

Fitting multilevel models (GAMM) with mgcv

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



Hierarchical generalized additive models: an introduction with mgcv

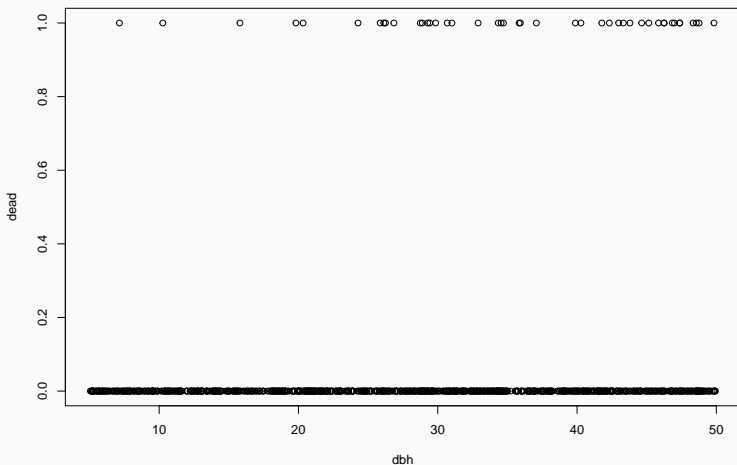
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<https://doi.org/10.7287/peerj.preprints.27320v1>

Multilevel logistic regression

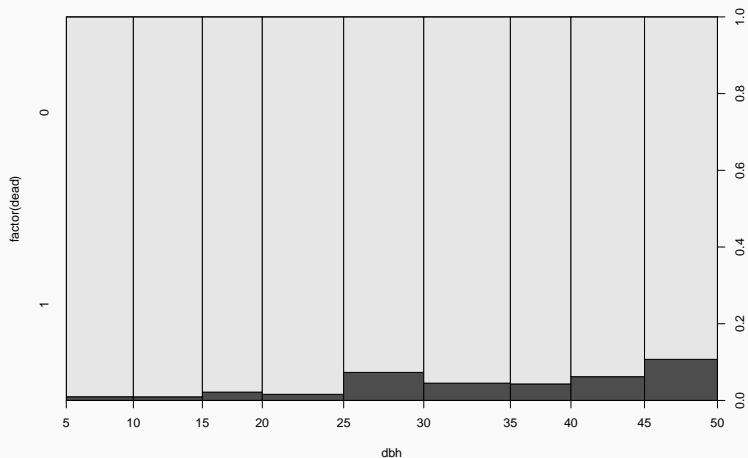
Q: Relationship between tree size and mortality

```
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
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 + 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
```

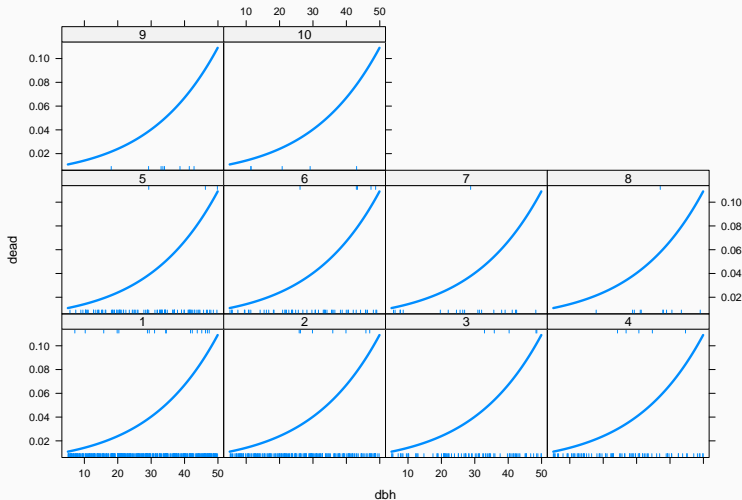
1	-4.778744	0.05364989
2	-4.778744	0.05364989
3	-4.778744	0.05364989
4	-4.778744	0.05364989
5	-4.778744	0.05364989
6	-4.778744	0.05364989
7	-4.778744	0.05364989
8	-4.778744	0.05364989
9	-4.778744	0.05364989
10	-4.778744	0.05364989

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

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

Visualising model: visreg

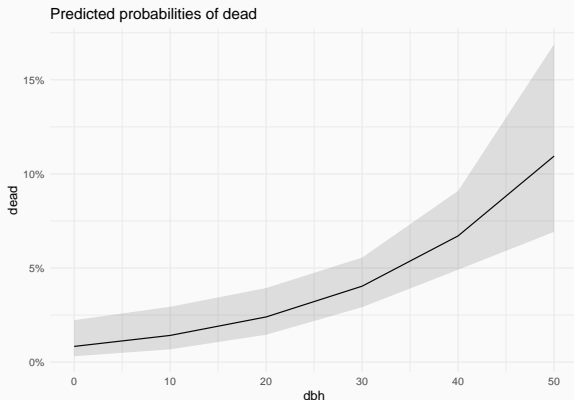
```
visreg(mixed.logis, xvar = "dbh", by = "site", scale = "response")
```



Visualising model: sjPlot

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

\$dbh



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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**

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

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