

# 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

Residual standard error: 4.093 on 998 degrees of freedom

## Remember our model structure

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

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

In this case:

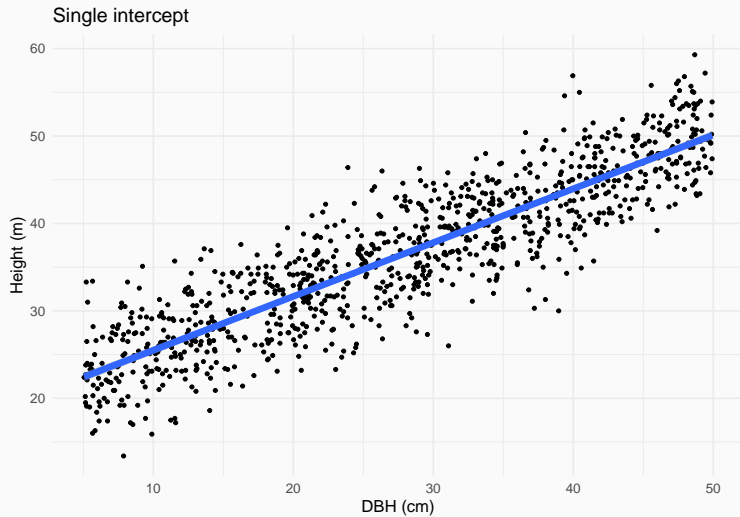
$$\text{Height}_i \sim N(\mu_i, \sigma^2)$$

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

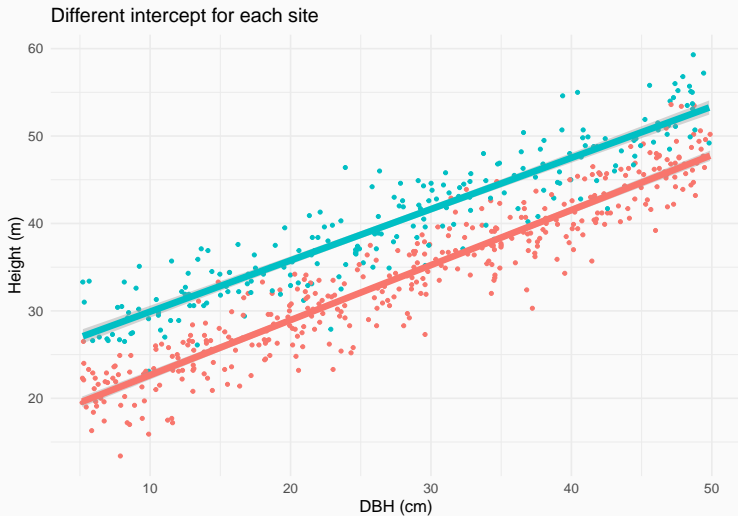
$\alpha$ : expected height when DBH = 0

$\beta$ : 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 ~ factor(site) + dbh, data = trees)
```

Residuals:

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

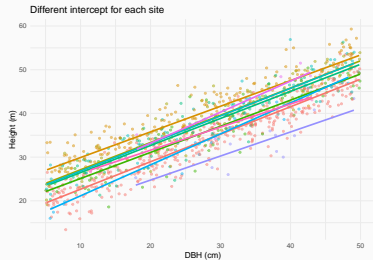
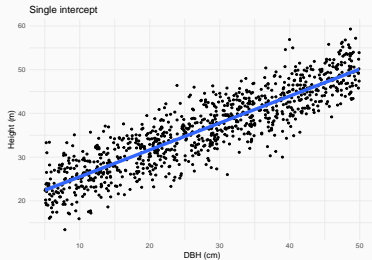
Coefficients:

	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 ***

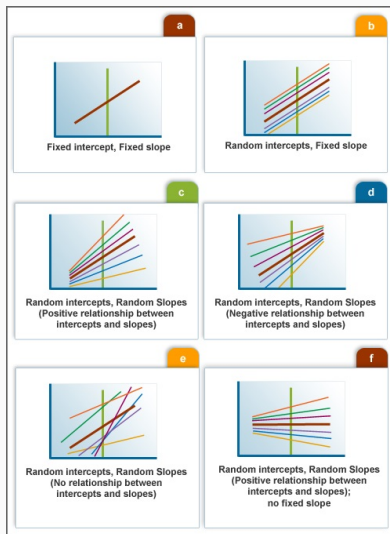
---

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

# 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.

## 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.



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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/](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.

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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*, while fixed effects are not (infinite variance).

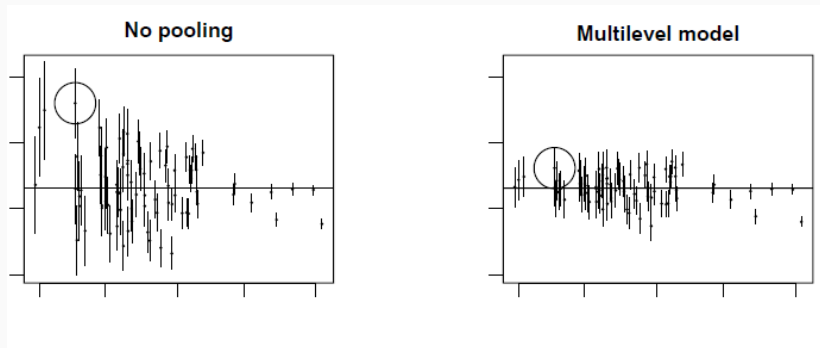
## What is a random effect, really?

- 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

## 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](#)

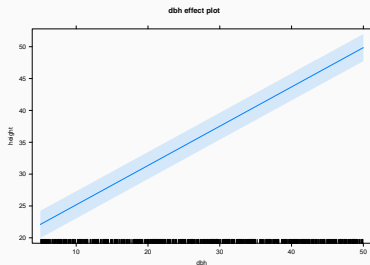
# Visualising model: allEffects

```
model: height ~ dbh
```

```
dbh effect
```

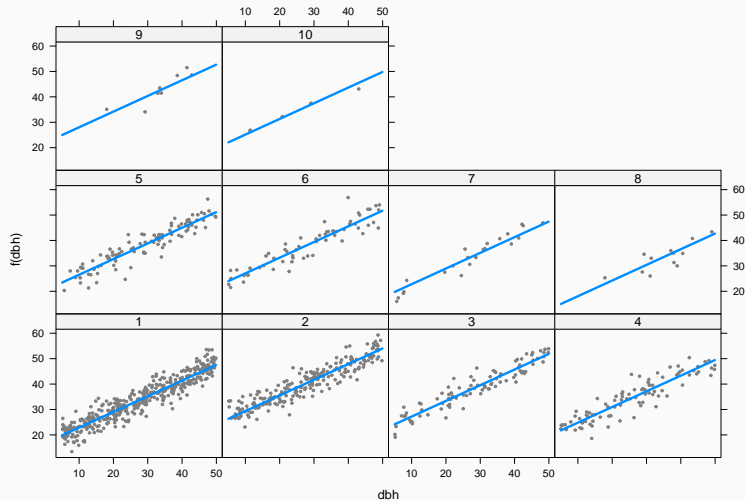
```
dbh
```

	5	20	30	40	50
	22.09610	31.35001	37.51928	43.68855	49.85782



# Visualising model: visreg

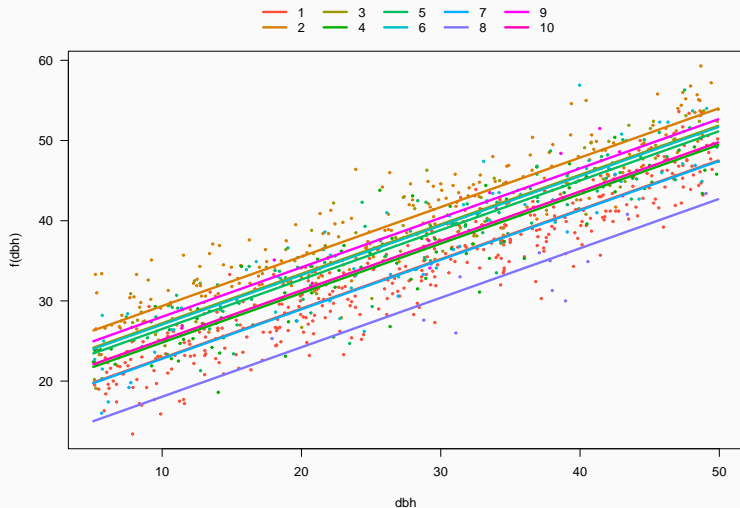
```
visreg(mixed, xvar = "dbh", by = "site", re.form = NULL)
```





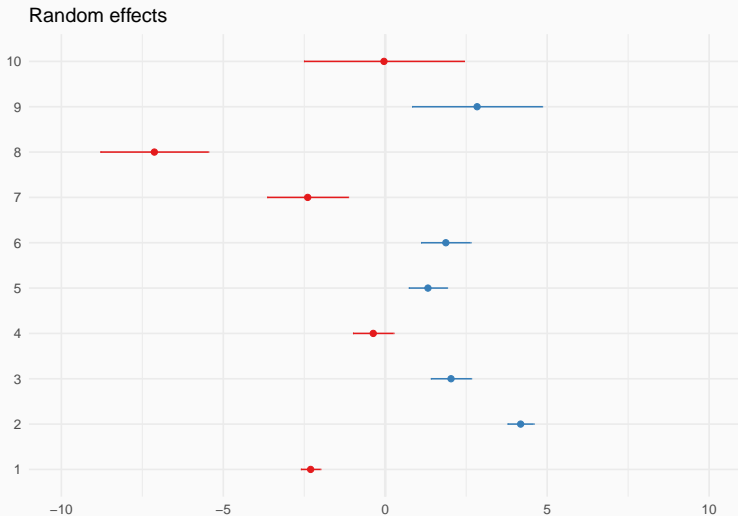
# Visualising model

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



# Visualising model: sjPlot

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

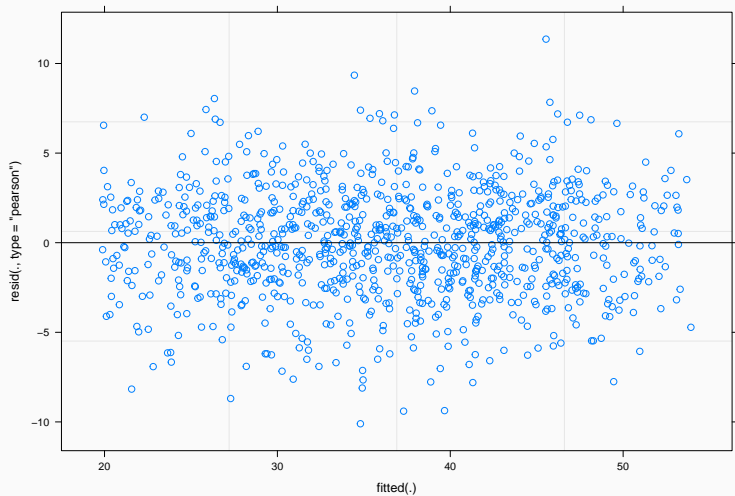


## Using merTools to understand fitted model

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

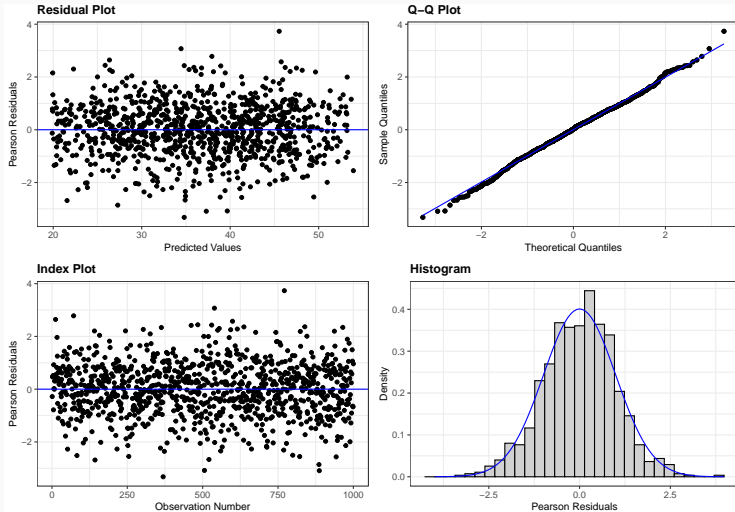
# Checking residuals

```
plot(mixed)
```



# Checking residuals

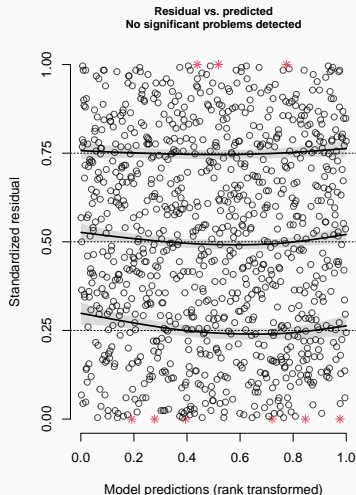
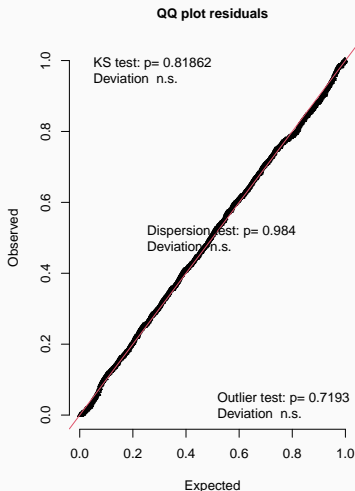
```
ggResidpanel::resid_panel(mixed)
```



# Checking residuals (DHARMA)

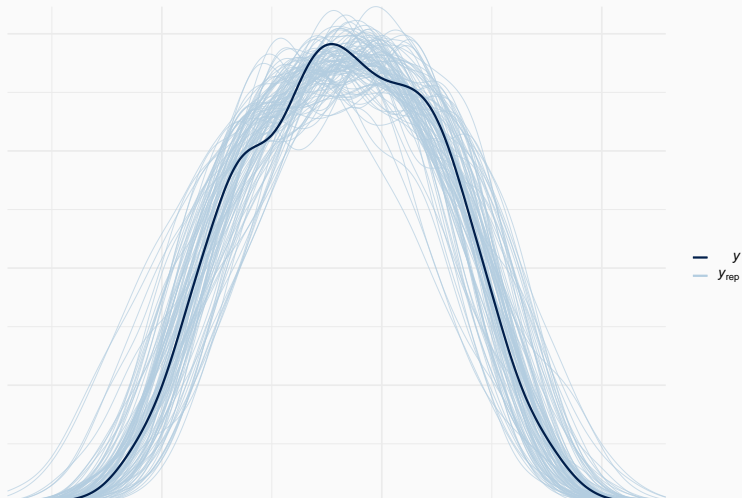
```
DHARMA::simulateResiduals(mixed, plot = TRUE, use.u = TRUE)
```

DHARMA 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

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

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

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

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

## 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

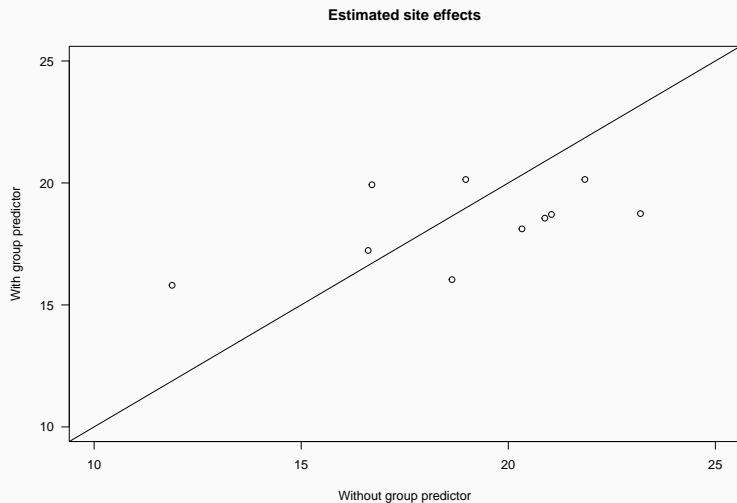
Correlation of Fixed Effects:

(Intr) dbh

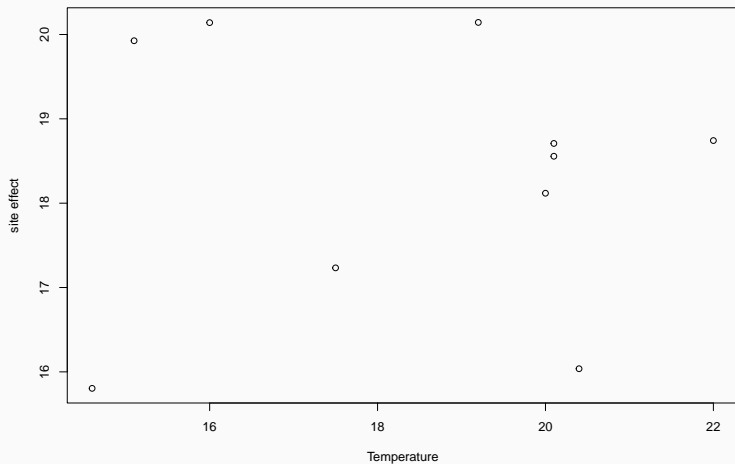


```
shinyMer(group.pred)
```

# 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

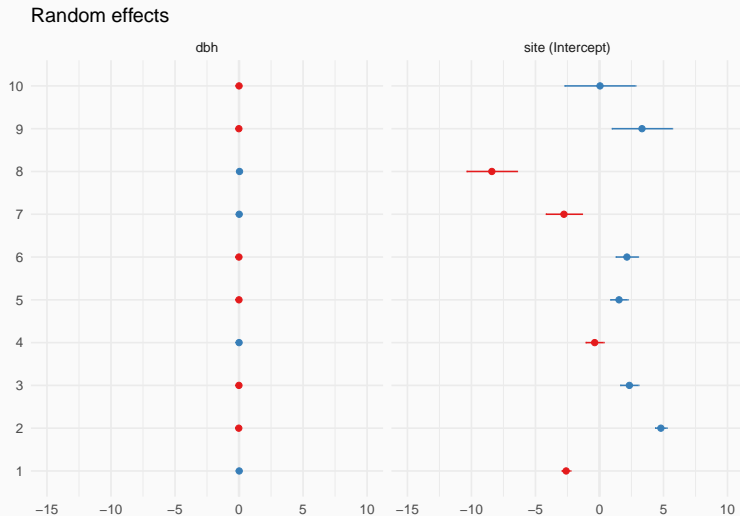
## Varying intercepts and slopes

```
$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")
```

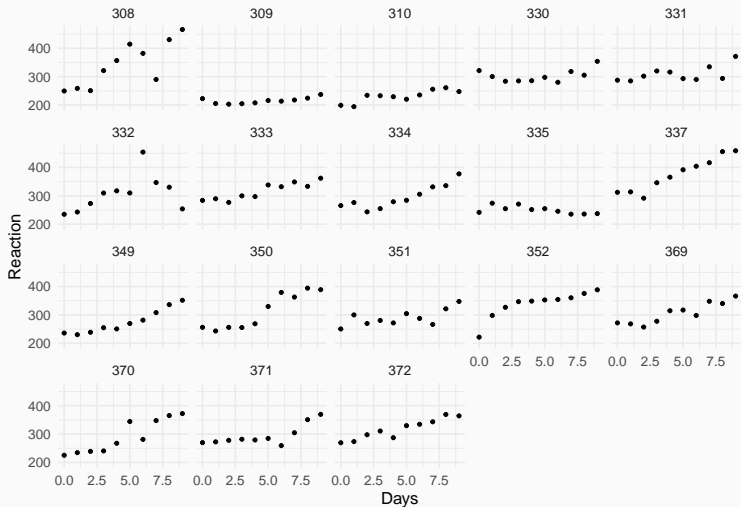




## More examples

---

# 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)	295.22	10.49	28.15	<2e-16 ***

---

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

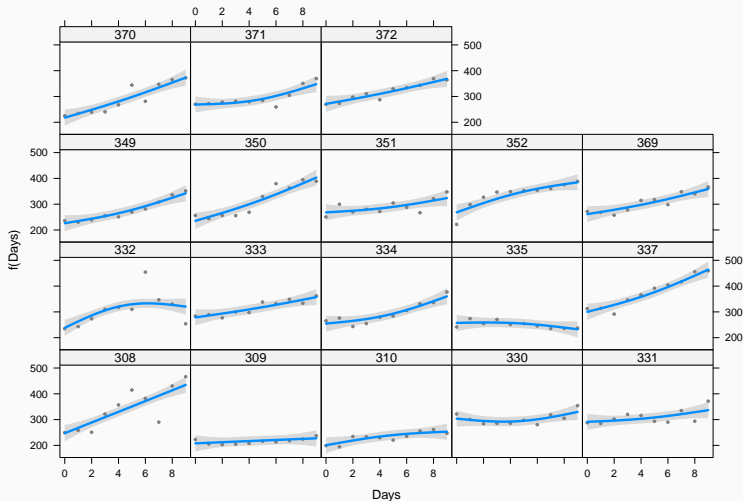
Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(Days,Subject)	42.2	53	16.05	<2e-16 ***

---

## Fitting multilevel models (GAMM) with mgcv

```
visreg(sgam, 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>

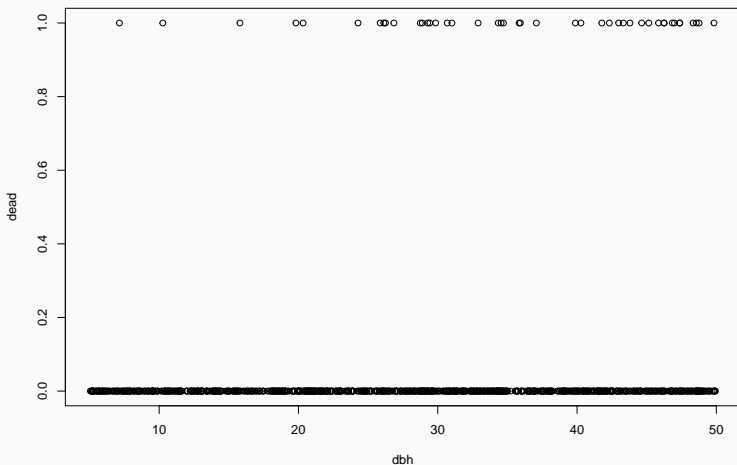
## Multilevel logistic regression

---



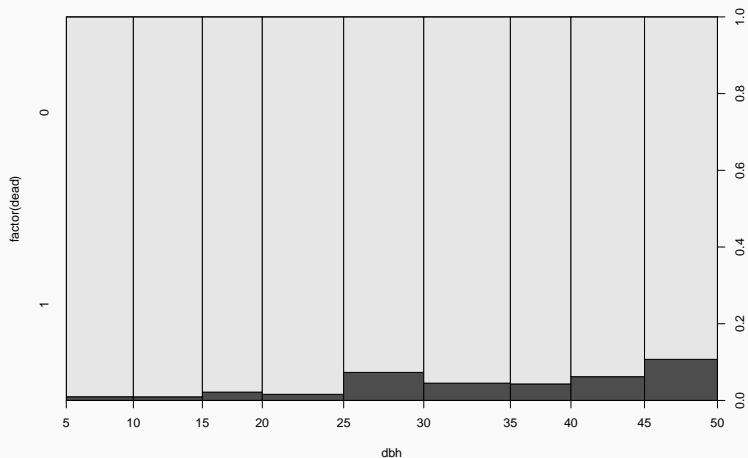
## Q: Relationship between tree size and mortality

```
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)
```

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)

## 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

# 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 )
----------	------------	---------	----------

## 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

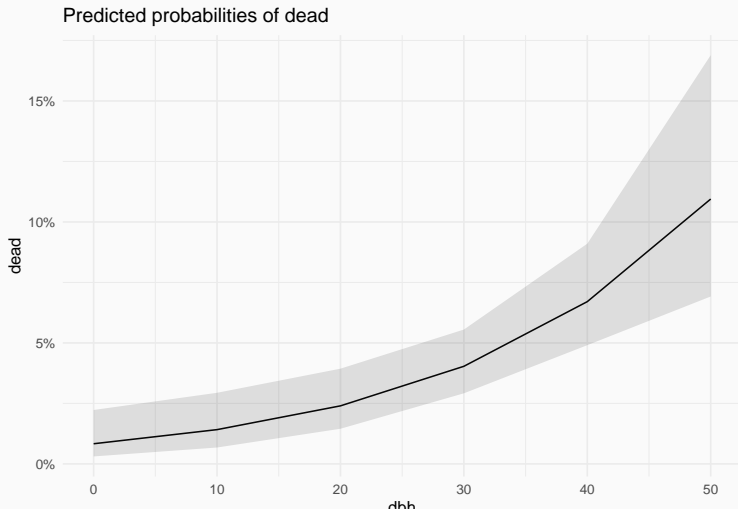
```
attr(,"class")
```

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

# Visualising model: sjPlot

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

\$dbh



## Poisson multilevel regression

---



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- Using all the data to perform inferences for groups with small sample size

- Varying intercepts

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

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