

# Linear Mixed Effects Models

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology



# Learning objectives: Correlated Data / Mixed models

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- Understand some relatively simple ways to deal with correlated data (bootstrap, Generalized Estimating Equations [later])

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  - Understand why generalized linear mixed effects can be difficult to fit

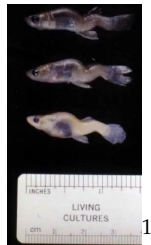
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  - Understand why generalized linear mixed effects can be difficult to fit
- Be able to describe models and their assumptions using equations and text and match parameters in these equations to estimates in computer output.



# Selenium and Fish



Selenium, Se, a bi-product of burning coal is measured in...

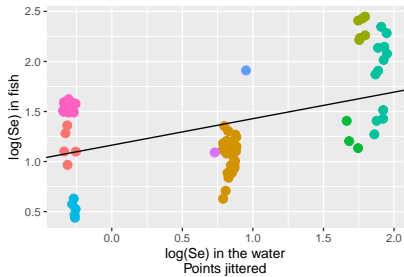
- A set of 9 lakes
- 1 to 34 fish in each lake (total of 83 observations)

Goal: determine the relationship between mean (log) Se in lake and mean (log) Se in fish.

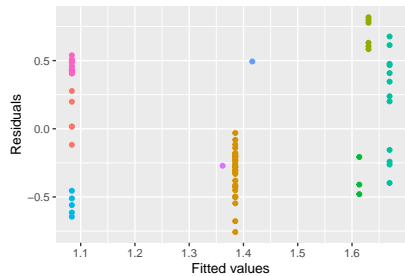
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<sup>1</sup><http://appvoices.org/tag/appalachian-voices/page/7/>

Se in Fish vs Se Water with linear regression line



Residual vs. fitted values



# Selenium Example

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*What strategies might we use to analyze these data?*

Note: our main question involves a predictor-response relationship in which the predictor is constant within each cluster or sample unit

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Lets do this!

**Mixed models**

Model Selection/Model Building Strategies

Dealing with statistical dependence

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When you want to generalize to a larger population of sample units

- **Fixed effects**: allow inference to only the sample units in the data set
- **Random effects**: allow us to generalize to a population of sample units by assuming cluster-specific regression parameters come from a common distribution

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- Provides a framework for modeling data where the independence assumption is violated

# Pines data (book example)

Study objective: investigate tradeoffs between growth rate, size, and lifespan of Mountain pines (*Pinus montana*) in Switzerland (Bigler, 2016).

Is it better to grow quick but die young? Grow more slowly and live longer?

Sample units:

- 160 dead standing trees sampled at 20 sites

Variables:

- dbh = diameter at breast height (size of tree)
- maximum age (i.e., lifespan)
- Aspect of study site

## Sampling Effort:

- 9 beaches (high, medium, low exposure)
- 5 stations at each beach.

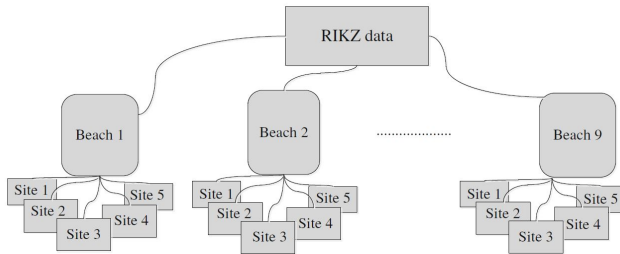
## Interest lies in modeling:

- Richness = species richness (number of species counted).

## Using macro-fauna and abiotic variables:

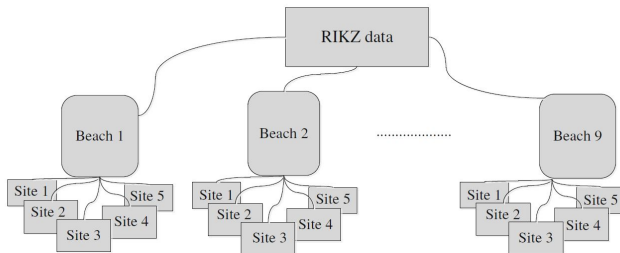
- Exposure = low or high exposure to waves, length of surf zone, slope, grain size, and depth of the anaerobic layer
- NAP = height of the sampling station compared to mean tidal level





**Fig. 5.1** Set up of the RIKZ data. Measurements were taken on 9 beaches, and on each beach 5 sites were sampled. Richness values at sites on the same beach are likely to be more similar to each other than to values from different beaches

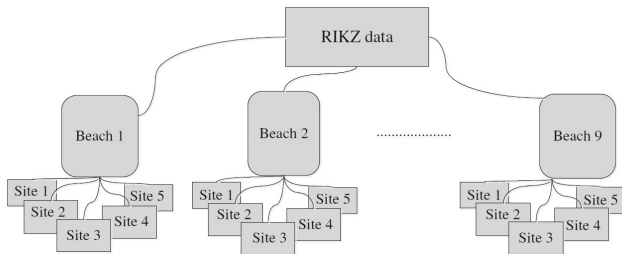
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Is that reasonable in this case?



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- 2 observations from the same beach may be more alike than 2 observations taken from 2 different beaches.



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- 2 observations from the same beach may be more alike than 2 observations taken from 2 different beaches.
- $\Rightarrow$  observations from the same beach are likely correlated

# Multi-level model

Think of models at 2 levels:

- Level 1: model the how individual observations vary within a cluster

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- Level 1: model the how individual observations vary within a cluster
- Level 2: model how (cluster-specific) parameters, in the level-1 model, vary (across clusters)

## 2-stage multi-level modeling approach

Stage 1 (level 1 model):

- Build a separate model for each cluster (beach)
- Only consider variables that are NOT constant within a cluster

## 2-stage multi-level modeling approach

Stage 1 (level 1 model):

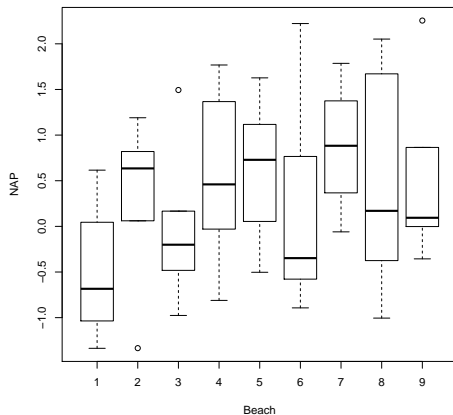
- Build a separate model for each cluster (beach)
- Only consider variables that are NOT constant within a cluster

Stage 2 (level 2 model):

- Treat the coefficients from stage 1 as 'data'
- Model the coefficients as a function of variables that are constant within a cluster

Can be useful exploratory approach when you have lots of data for each cluster, but few clusters

NAP is a “level-1” covariate (it varies within each cluster)





# RIKZdat

exposure is a “level-2” covariate (it is constant within a cluster)

```
xtabs(~ exposure + Beach, data=RIKZdat)
```

	Beach								
exposure	1	2	3	4	5	6	7	8	9
8	0	5	0	0	0	0	0	0	0
10	5	0	0	0	5	0	0	5	5
11	0	0	5	5	0	5	5	0	0

```
# Only 1 beach with lowest exposure level: modify to have 2 categories  
RIKZdat$exposure.c<-"High"  
RIKZdat$exposure.c[RIKZdat$exposure%in%c(8,10)]<-"Low"
```

## 2-Stage approach

Let  $R_{ij}$  = the species richness for the  $j^{th}$  sample on the  $i^{th}$  beach  
(note: we now need two subscripts!)

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Level 1 model: model for observations within each cluster (i.e.,  
for each beach)

$$R_{ij} = \beta_{0i} + \beta_{1i}NAP_{ij} + \epsilon_{ij}; (j = 1, 2, \dots, 5 \text{ observations for each Beach})$$

Each beach has its own intercept  $\beta_{0i}$  and slope  $\beta_{1i}$

# Modified R code

```
RIKZdat$NAPc = RIKZdat$NAP - mean(RIKZdat$NAP) #center NAP variable
Beta<-matrix(NA, 9,2) # to hold slope and intercepts
Exposure<-matrix(NA,9,1) # to hold exposure level for each beach
for(i in 1:9){
  Mi<-lm(Richness~NAPc, data=subset(RIKZdat, Beach==i))
  Beta[i,]<-coef(Mi)
  Exposure[i]<-subset(RIKZdat, Beach==i)$exposure.c[1]
}
betadat <- data.frame(Beach = 1:9, intercept = Beta[,1],
                      slope = Beta[,2], exposure.c = Exposure)
```

Note: I have centered the NAP variable

- Makes intercept more meaningful =  $R_{ij}$  at the mean value of NAP
- Helps avoid numerical problems and identifiability problems due to correlation of  $\hat{\beta}_{0i}$  and  $\hat{\beta}_{1i}$

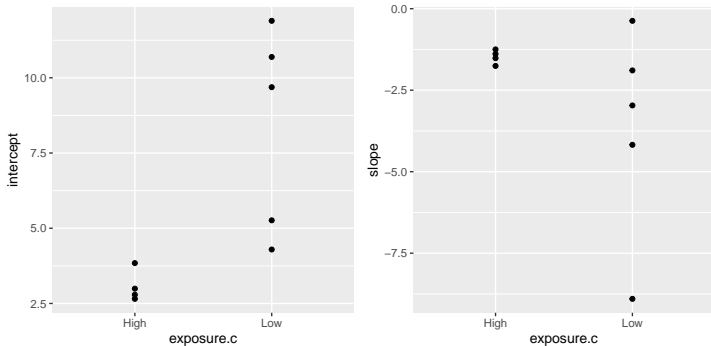
This gives us a data frame of coefficients and level-2 predictors for a level-2 model:

```
betadat
```

	Beach	intercept	slope	exposure.c
1	1	10.692614	-0.3718279	Low
2	2	11.893999	-4.1752712	Low
3	3	2.790385	-1.7553529	High
4	4	2.653600	-1.2485766	High
5	5	9.688335	-8.9001779	Low
6	6	3.841864	-1.3885120	High
7	7	2.992969	-1.5176126	High
8	8	4.293257	-1.8930665	Low
9	9	5.263276	-2.9675304	Low

For a tidyverse solution - see book/R code.

```
library(ggplot2); library(patchwork)
g1 <-ggplot(betadat, aes(exposure.c, intercept)) + geom_point()
g2 <-ggplot(betadat, aes(exposure.c, slope)) + geom_point()
g1+g2
```



## Level-2 model

Model for the slope and intercept parameters (analyze the summary statistics,  $\hat{\beta}_{0i}, \hat{\beta}_{1i}$ ) using level-2 predictors (ones that are constant within a cluster)

- $\hat{\beta}_{0i} = \beta_0 + \gamma_0 Exposure_i + b_{0i}$
- $\hat{\beta}_{1i} = \beta_1 + \gamma_1 Exposure_i + b_{1i}$

For now, ignore the fact that the variability of  $b_{0i}, b_{1i}$  seems to depend on exposure level (“low”, “high”).

# Level-2 Model: Intercepts

```
summary(lm(intercept ~ exposure.c, data = betadat))
```

Call:

```
lm(formula = intercept ~ exposure.c, data = betadat)
```

Residuals:

Min	1Q	Median	3Q	Max
-4.0730	-0.4161	-0.0767	1.3220	3.5277

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.070	1.291	2.378	0.0491 *
exposure.cLow	5.297	1.732	3.058	0.0184 *

---

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

Residual standard error: 2.582 on 7 degrees of freedom

Multiple R-squared: 0.5719, Adjusted R-squared: 0.5107

F-statistic: 9.349 on 1 and 7 DF, p-value: 0.01838



# Level-2 Model: Slopes

```
summary(lm(slope ~ exposure.c, data = betadat))
```

Call:

```
lm(formula = slope ~ exposure.c, data = betadat)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-5.2386	-0.2778	0.0890	0.6940	3.2897

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-1.478	1.229	-1.202	0.268
exposure.cLow	-2.184	1.649	-1.325	0.227

Residual standard error: 2.458 on 7 degrees of freedom

Multiple R-squared: 0.2005, Adjusted R-squared: 0.08625

F-statistic: 1.755 on 1 and 7 DF, p-value: 0.2268

# Putting things together: Composite Equation

Level-1 Model:

- $R_{ij} = \beta_{0i} + \beta_{1i}NAP_{ij} + \epsilon_{ij}$

Level-2 Model:

- $\beta_{0i} = \beta_0 + \gamma_0 Exposure_i + b_{0i}$

- $\beta_{1i} = \beta_1 + b_{1i}$

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Substitute into level-1 equation to get the *composite equation*

$$R_{ij} = (\beta_0 + \gamma_0 Exposure_i + b_{0i}) + (\beta_1 + b_{1i})NAP_{ij} + \epsilon_{ij}$$

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$$R_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})NAP_{ij} + \gamma_0 Exposure_i + \epsilon_{ij}$$

$\Rightarrow$  *random intercepts and slopes model (or random coefficients model)*

# Mixed Models

Rather than use a 2-stage approach, we could just posit a model for the data using random and fixed effects.

**Random Intercepts Model:**

$$R_{ij} = \beta_0 + b_{0i} + \beta_1 NAP_{ij} + \beta_2 Exposure_i + \epsilon_{ij}$$
$$b_{0i} \sim N(0, \tau^2) \quad \epsilon_{ij} \sim N(0, \sigma^2)$$

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Can think of  $b_{0i}$  and  $b_{1i}$  as deviations from the average intercept ( $\beta_0$ ) and slope ( $\beta_1$ ), respectively.

Or, think in terms of beach-level intercepts and slopes:  $\beta_{0i} = \beta_0 + b_{0i}$  and  $\beta_{1i} = \beta_1 + b_{1i}$ , with  $(\beta_{0i}, \beta_{1i}) \sim MVN(\beta, D)$



# Fitting Mixed Effects Models in R

Two popular packages: `nlme` and `lme4`:

`nlme` (older)

- More flexibility for modeling within-cluster correlation and heterogeneity (e.g., time series data, spatial data), but slowly being replaced by other options (e.g., `glmmTMB`, `INLA`);
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`lme4` (newer)

- Better options for fitting non-normal data: generalized linear mixed effects models [GLMMS] for count or binary data
- Easier to fit non-nested or 'crossed' random effects (e.g., `year` and `Beach` if we had many years of data).
- Cannot handle within-cluster correlation or heterogeneity

## Other Packages

Many others too... see:

<http://glmm.wikidot.com/pkg-comparison>

Two others that we will consider:

- glmmTMB
- GLMMadaptive

For now, let's fit the random intercept and random intercept and slope models using the `lmer` function in the `lme4` package!

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$$b_{0i} \sim N(0, \tau^2) \quad \epsilon_{ij} \sim N(0, \sigma^2)$$

Fit this model in R using `lmer` and identify  $\hat{\beta}_0, \hat{\beta}_1, \hat{\sigma}, \hat{\tau}$ !

## Random Intercepts and Slopes Model:

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$$(b_{0i}, b_{1i}) \sim N(0, D)$$

$$D = \begin{bmatrix} var(b_{0i}) & cov(b_{0i}, b_{1i}) \\ cov(b_{0i}, b_{1i}) & var(b_{1,i}) \end{bmatrix}$$

Fit this model in R and identify the different parameters:

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Fit this model in R and identify the different parameters:

- $var(\epsilon_{ij}) = \sigma^2 = 6.50$  (variance within a Beach)
- $var(b_{0i}) = 4.750$  (variance among beach intercepts)
- $var(b_{1i}) = 3.567$  (variance among beach slopes)
- $Cor(b_{0i}, b_{1i}) = \frac{Cov(b_{0i}, b_{1i})}{\sqrt{var(b_{0i})var(b_{1i})}} = -0.557$

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If you are a Bayesian, you can ignore the distinction between “prediction” and “estimation”... ALL parameters are random variables!

## Fixed versus Random Comparison

Each beach also has its own intercept. What if we modeled Beach using fixed effects?

# Fixed versus Random Comparison

Each beach also has its own intercept. What if we modeled Beach using fixed effects?

```
lm.fe <- lm(Richness~factor(Beach)-1+NAPc, data=RIKZdat)
summary(lm.fe)
```

Call:

```
lm(formula = Richness ~ factor(Beach) - 1 + NAPc, data = RIKZdat)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-4.8518	-1.5188	-0.1376	0.7905	11.8384

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
factor(Beach)1	8.9392	1.4301	6.251	3.61e-07	***
factor(Beach)2	12.0173	1.3690	8.778	2.29e-10	***
factor(Beach)3	2.5343	1.3796	1.837	0.074716	.
factor(Beach)4	2.9063	1.3723	2.118	0.041364	*
factor(Beach)5	8.0409	1.3746	5.850	1.22e-06	***
factor(Beach)6	3.7161	1.3697	2.713	0.010271	*
factor(Beach)7	3.5025	1.3934	2.514	0.016705	*
factor(Beach)8	4.3862	1.3707	3.200	0.002920	**
factor(Beach)9	5.1572	1.3731	3.756	0.000629	***
NAPc	-2.4928	0.5023	-4.963	1.79e-05	***

---

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

Residual standard error: 3.06 on 35 degrees of freedom

Multiple R-squared: 0.8719, Adjusted R-squared: 0.8353

F-statistic: 23.82 on 10 and 35 DF, p-value: 9.56e-13

# Fixed versus random

Fixed effects:

- `lm.fe <- lm(Richness~factor(Beach)-1+NAPc, data=RIKZdat)`
- each beach has its own intercept which we estimate

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Random effects:

- `lme.fit<-lme(Richness~NAPc+exposure.c + (1 | Beach), data=RIKZdat)`
- each beach has its own intercept
- we further assume  $\beta_i \sim N(\beta, \sigma_{b_{oi}}^2)$  or equivalently  $b_{oi} \sim N(0, \sigma_{b_{oi}}^2)$
- we estimate the variance of the intercepts and “predict” the beach-level intercepts

## Downsides to fixed effects model

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```
lm.fe2 <- lm(Richness~factor(Beach)-1+NAPc+exposure.c, data=RIKZdat)
coef(lm.fe2)
```

```
factor(Beach)1 factor(Beach)2 factor(Beach)3 factor(Beach)4 factor(Beach)5
      8.939200      12.017303      2.534266      2.906323      8.040936
factor(Beach)6 factor(Beach)7 factor(Beach)8 factor(Beach)9      NAPc
      3.716094      3.502535      4.386168      5.157177      -2.492836
exposure.cLow
      NA
```

# Downsides to fixed effects model

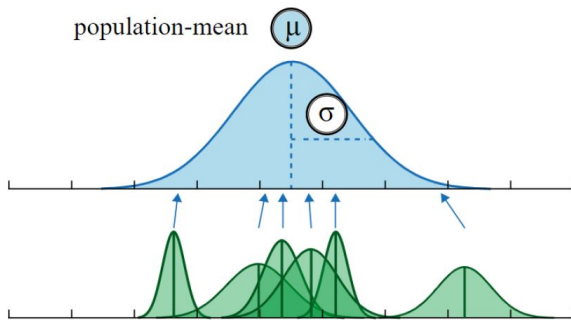
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exposure.cLow
           NA
```

- Random coefficients would require interactions between Beach and NAP (another 8 parameters)

# Shrinkage (demonstration in R!)



[https://benediktehinger.de/glm2018/mm\\_slides.html](https://benediktehinger.de/glm2018/mm_slides.html)

Shrinkage depends on:

- how variable the coefficients are across clusters
- the degree of uncertainty associated with individual estimates

## Predicted values

$$R_{ij}|b_i \sim N(\mu_i, \sigma^2)$$

$$\mu_i = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})NAP_{ij} + \beta_2 Exposure_i$$

$$b_i = (b_{0i}, b_{1i}) \sim N(0, D) \text{ with } D = \begin{bmatrix} var(b_{0i}) & cov(b_{0i}, b_{1i}) \\ cov(b_{0i}, b_{1i}) & var(b_{1,i}) \end{bmatrix}$$

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**Subject-Specific** (lines for a particular beach):

- $E[R_{ij}|X_{ij}, b_i] = \mu_i = \beta_0 + b_{0i} + (\beta_1 + b_{1i})NAP + \beta_2(\text{exposure}=\text{"LOW"})$

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**Population Average** (averages over beaches):

- $E[R_{ij}|X_{ij}] = E(E[R_{ij}|X_{ij}, b_i]) = \beta_0 + \beta_1 NAP + \beta_2(\text{exposure} = \text{"low"})$

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R for a demonstration!



# Diagnostics

## Random Intercepts and Slopes Model:

$$R_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})NAP_{ij} + \beta_2 Exposure_i + \epsilon_{ij}$$
$$(b_{0i}, b_{1i}) \sim N(0, D)$$

What are our assumptions?

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$$(b_{0i}, b_{1i}) \sim N(0, D)$$

What are our assumptions?

1. Linearity:

$$E[Richness|NAP, Exposure] = \beta_0 + \beta_1 NAP + \beta_p Exposure$$

2. Residuals are Normally distributed with constant variance:

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2. Residuals are Normally distributed with constant variance:

$$\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$$

3. Beaches are independent

4.  $(b_{0i}, b_{1i}) \sim MVN(0, D)$ , independent of  $\epsilon_{ij}$

# Diagnostic plots

- Default plot method: plot of within beach residuals,  $\hat{\epsilon}_{ij}$  versus beach-level predictions

$$\hat{R}_{ij} = \hat{\beta}_0 + \hat{b}_{0i} + (\hat{\beta}_1 + \hat{b}_{1i})NAP + \hat{\beta}_2(exposure = "low")$$

# Diagnostic plots

- Default plot method: plot of within beach residuals,  $\hat{\epsilon}_{ij}$  versus beach-level predictions
$$\hat{R}_{ij} = \hat{\beta}_0 + \hat{b}_{0i} + (\hat{\beta}_1 + \hat{b}_{1i})NAP + \hat{\beta}_2(exposure = "low")$$
- `check_model` function offers many more checks
  - QQplots to evaluate Normality of residuals
  - QQplots to evaluate Normality of the random effects
  - Residual versus fitted values and scale-location plot for constant variance
  - Posterior predictive checks
  - Collinearity, influential observation

See R for a demonstration!

# Degrees of Freedom (lme)

```
library(nlme)
lme.fit<-lme(Richness~NAPc+exposure.c, random=~1|Beach, data=RIKZdat)
summary(lme.fit)
```

Linear mixed-effects model fit by REML

Data: RIKZdat

	AIC	BIC	logLik
	240.5538	249.2422	-115.2769

Random effects:

Formula: ~1 | Beach

(Intercept) Residual

StdDev: 1.907175 3.059089

Fixed effects: Richness ~ NAPc + exposure.c

	Value	Std.Error	DF	t-value	p-value
(Intercept)	3.170680	1.1739987	35	2.700752	0.0106
NAPc	-2.581708	0.4883901	35	-5.286160	0.0000
exposure.cLow	4.532777	1.5755610	7	2.876929	0.0238

Correlation:

(Intr) NAPc

NAPc -0.028

exposure.cLow -0.746 0.037

Standardized Within-Group Residuals:

Degrees of Freedom (differ for level-1 and level-2 predictors):

- $NAP_c = 35$
- `exposure.cLow = 7`

Level-1: within-subjects degrees of freedom calculated as the number of observations minus the number of groups minus the number of level-1 regressors in the model.

```
nrow(RIKZdat) - length(unique(RIKZdat$Beach)) - 1
```

```
[1] 35
```



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```

```
[1] 35
```

Level-2: among-subjects degrees of freedom calculated as the number of groups minus the number of level-2 regressors in the model - 1 for the intercept.

```
length(unique(RIKZdat$Beach)) - 1 - 1
```

```
[1] 7
```

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The formula are not important. . . . what is:

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- we have more information about the effect of NAP on species richness than exposure since NAP varies between and within beaches.

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The formula are not important. . . . what is:

- we have more information about the effect of NAP on species richness than `exposure` since NAP varies between and within beaches.
- `lme` accounts for the data structure when carrying out statistical tests.

## Degrees of Freedom: More accurately

Note: lme's df are essentially correct for **balanced data** (all clusters have an equal number of observations). For unbalanced data, the tests (and df) are only approximate.

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- thus, a decision was made to NOT report p-values for models fit with `lmer` in `lme4`
- there are “better” degrees of freedom approximations for unbalanced data (see, e.g., *lmerTest* package and Section 18.12.3 of the book and R code).

Mixed models

**Model Selection/Model Building Strategies**

Dealing with statistical dependence



# Comparing the 2 Models

AIC comparisons and likelihood ratio tests are complicated by the fact that the variance parameter is “on the boundary”

See: <https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#testing-significance-of-random-effects>

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See: <https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#testing-significance-of-random-effects>

Number of parameters for calculating AIC also depends on focus (on individual subjects or population)

- See:  
<http://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#can-i-use-aic-for-mixed-models-how-do-i-count-the-number-of-degrees-of-freedom-for-a-random-effect>

# Simulation-based testing

See `LectureMixedMods.Rmd` for an option, or have a look at the `RLRsim` or `pbkrtest` packages for simulation-based alternatives.

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- Simulate data from the simpler model
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p-value = proportion of simulated observations that are as extreme, or more extreme than the likelihood ratio statistic calculated using the observed data.

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- Determine random effects structure by comparing models fit using REML (all w/ the same fixed effects)
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For more, see:

- Zuur et al. 5.6

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2. Compare models with different random effects structures (via AIC, LR tests). Use method = “REML” and keep fixed component constant.
3. Compare fixed effects models (using AIC, LR tests) using the random structure from step [2]. Use method = “ML” and keep random component constant.
4. Refit the ‘best’ model from step [4] using method = “REML”.
5. Look at diagnostic plots, and modify model as needed

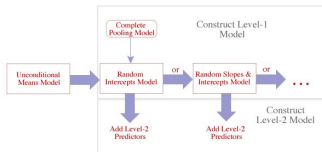


Fig. 1 A general flowchart for fitting multilevel models

Jack Weiss suggests fitting a series of models:

- Pooled model (assuming independence), include level-1 predictors [predictors that vary within clusters]  $\text{lm}(y \sim x1)$
- Unconditional means model or variance components model (no predictors, just random intercepts)  $\text{lmer}(y \sim 1 + (1|\text{site}))$
- Random intercepts (with level 1 predictors)  $\text{lmer}(y \sim x1 + (1|\text{site}))$
- Random intercepts and slopes (with level 1 predictors)  $\text{lmer}(y \sim x1 + (1 + x1|\text{site}))$

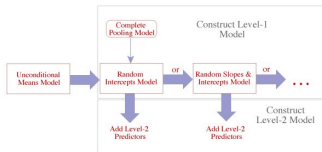


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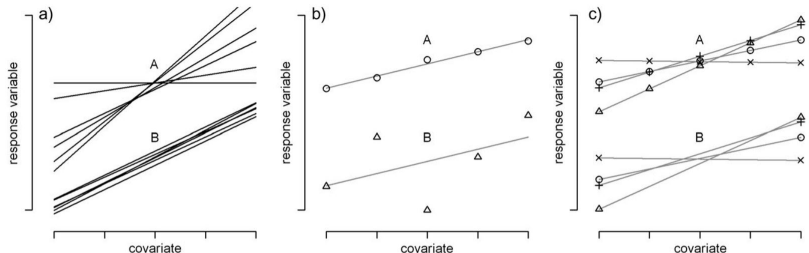
Pick the best of these, then add level-2 predictors (predictors that are constant within clusters).

Strategy outlined by: Singer, J. D. and Willett, J. B. (2003) *Applied Longitudinal Data Analysis: Modeling Change and Event Occurrence*. (Oxford University Press, Oxford, UK).

# Random intercepts versus random coefficient models

Although random intercepts models are common. . .

Schielzeth and Forstmeier (2009) suggest random slopes are usually appropriate for level-1 predictors (i.e., when  $x$  varies within a subject).



**Figure 1**

Schematic illustrations of more (A) and less (B) problematic cases for the estimation of fixed-effect covariates in random-intercept models. (a) Regression lines for several individuals with high (A) and low (B) between-individual variation in slopes ( $\sigma_\beta$ ). (b) Two individual regression slopes with low (A) and high (B) scatter around the regression line ( $\sigma_\epsilon$ ). (c) Regression lines with (A) many and (B) few measurements per individual (independent of the number of levels of the covariate).

See *Readings, Linear Mixed Effects Page* for a copy of Schielzeth and Forstmeier (2009)

# Maximal model

Attempt to make inference from a maximal model:

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Lots of debate on how best to approach model building/selection.

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## Induced correlation: random intercepts model

$$R_{ij} = \beta_0 + b_{0i} + \beta_1 NAP_{ij} + \beta_2 Exposure_i + \epsilon_{ij}$$

$$\text{Variance of } R_{ij} = \text{var}(b_{0i} + \epsilon_{ij}) = \text{var}(b_{0i}) + \text{var}(\epsilon_{ij}) = \tau^2 + \sigma^2$$



## Induced correlation: random intercepts model

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Variance of  $R_{ij} = var(b_{0i} + \epsilon_{ij}) = var(b_{0i}) + var(\epsilon_{ij}) = \tau^2 + \sigma^2$

Covariance  $(Y_{ij}, Y_{ij'}) = \tau^2$  (2 observations, same cluster [beach] since they share  $b_{0i}$ )

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Covariance ( $Y_{ij}, Y_{ij'}$ ) =  $\tau^2$  (2 observations, same cluster [beach] since they share  $b_{0i}$ )

Covariance ( $Y_{ij}, Y_{i'j}$ ) = 0 (2 observations taken from 2 different clusters [beaches])

## Induced correlation: random intercepts model

$$R_{ij} = \beta_0 + b_{0i} + \beta_1 NAP_{ij} + \beta_2 Exposure_i + \epsilon_{ij}$$

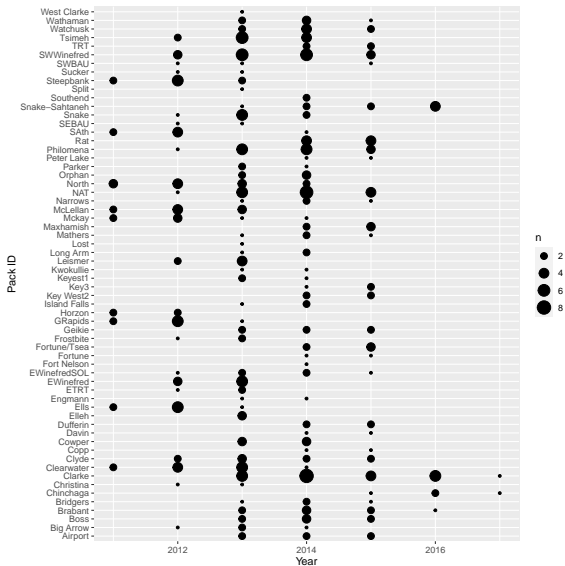
Variance of  $R_{ij} = var(b_{0i} + \epsilon_{ij}) = var(b_{0i}) + var(\epsilon_{ij}) = \tau^2 + \sigma^2$

Covariance  $(Y_{ij}, Y_{ij'}) = \tau^2$  (2 observations, same cluster [beach] since they share  $b_{0i}$ )

Covariance  $(Y_{ij}, Y_{i'j'}) = 0$  (2 observations taken from 2 different clusters [beaches])

Intraclass correlation =  $Cor(Y_{ij}, Y_{ij'}) = \frac{\tau^2}{\tau^2 + \sigma^2} = 0.28$ , correlation among observations taken from the same cluster.

# Multiple random effects



# Crossed random effects Year and PackID

```
modell <- lmer(log(HRsize) ~ Season + StudyArea + DiffDTScaled + LFD★E
```

Different levels of correlation induced by  $(1 \mid \text{PACKID}) + (1 \mid \text{Year})$

- two observations from same pack will be correlated due to sharing a “PackID” random effect
- two observations from same year will be correlated due to sharing a random a Year random effect.

R for demonstration!

# Marginal Distribution

$$Y_i = X_i\beta + z_ib + \epsilon_i$$

$$\epsilon_i \sim N(0, \Sigma_i)$$

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If we average over (or integrate out) the random effects, we get the **marginal Distribution of  $Y$** .

$$Y_i \sim N(X_i\beta, V_i), V_i = Z_i D Z_i' + \Sigma_i$$

This is actually what R uses to fit the data.



# Marginal model is what R is fitting

For random intercepts model:

$$Y_i \sim N(X_i\beta, V_i)$$
$$V_i = \begin{bmatrix} \sigma^2 & \rho & \cdots & \rho \\ \rho & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \rho \\ \rho & \cdots & \rho & \sigma^2 \end{bmatrix} \quad \rho = \frac{\tau^2}{\tau^2 + \sigma^2}$$

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$$\text{Var/Cov matrix for } Y \text{ (all data)} = \begin{bmatrix} V_i & 0 & \cdots & 0 \\ 0 & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & V_i \end{bmatrix}$$

## Fitting the marginal model using `gls`

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See Ch 4 Zuur et al. and the section of the course on `gls` models.

# Marginal Model fit using gls

```
gls.fit<-gls(Richness~NAPc+exposure.c, method="REML",  
             correlation=corCompSymm(form=~1|Beach),  
             data=RIKZdat)  
summary(gls.fit)
```

Generalized least squares fit by REML

Model: Richness ~ NAPc + exposure.c

Data: RIKZdat

	AIC	BIC	logLik
	240.5538	249.2422	-115.2769

Correlation Structure: Compound symmetry

Formula: ~1 | Beach

Parameter estimate(s):

	Rho
	0.2798938

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	3.170680	1.1739987	2.700752	0.0099
NAPc	-2.581708	0.4883901	-5.286160	0.0000
exposure.cLow	4.532777	1.5755610	2.876929	0.0063

Correlation:

	(Intr)	NAPc
NAPc	-0.028	
exposure.cLow	-0.746	0.037

Standardized residuals:

	Min	Q1	Med	Q3	Max
	-1.5551728	-0.6415409	-0.1554932	0.4150315	3.3566242

Residual standard error: 3.604905

Degrees of freedom: 45 total; 42 residual

```
tab_model(gls.fit, lme.fit, show.r2 = FALSE)
```

<i>Predictors</i>	<b>Richness</b>			<b>Richness</b>		
	<i>Estimates</i>	<i>CI</i>	<i>p</i>	<i>Estimates</i>	<i>CI</i>	<i>p</i>
(Intercept)	3.17	0.87 – 5.47	<b>0.010</b>	3.17	0.79 – 5.55	<b>0.011</b>
NAPc	-2.58	-3.54 – -1.62	<b>&lt;0.001</b>	-2.58	-3.57 – -1.59	<b>&lt;0.001</b>
exposure.c [Low]	4.53	1.44 – 7.62	<b>0.006</b>	4.53	0.81 – 8.26	<b>0.024</b>
N	<sup>9</sup> Beach					
Observations	45					
		45				