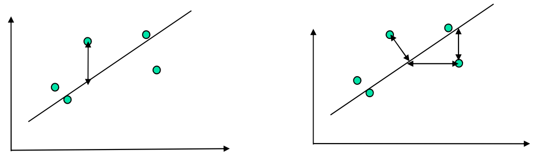
Type II models

Type I vs II

- Recall an assumption of GLM is “X” or independent variables measured exactly
- This is a Type I model
- Type II models have error/variance associated with X
  - Regression X has measurement error
  - ANOVA X is a representative example

Model II regression

- If no error in x, least squares of ($y-y_{est}$) makes sense
- If error in x should use different rule
  - Regress y on x gives different result than x on y
- Results in different slopes
- Example – allometry: metabolic rate vs. body size



Model II regression

- Lots of alternatives for Model II
  - Major axis (principal component)
    - Minimizes perpendicular distance
  - Reduced MA (version 1 RMA) (reduced major axis)
    - Minimizes geometric mean distance
    - $b_{RMA}=b_{OLS}/r=(sxy/sx2)/(sxy/(sxsy))=sy/sx$
  - If x & y in different units, then use:
    - SA or SMA - x&y are scaled (z-scored)
    - Ranged MA (version 2 RMA)
      - scale x & y to 0-1: x’=(x-xmin)/(xmax-xmin)
      - Legendre recommends

Type II ANOVA

- Have random effects
  - Everything so far has been a fixed effect
- Estimate variance between levels instead of mean of each level
- Many reasons to use random effects

Reasons to use random effects

- Traditional/philosophical
- Blocks/repeated measures
- Nested design
- Multilevel models
- Hierarchical models

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Model II ANOVA

- Often called fixed (model I) vs random (model II) effect
- Fixed is repeatable and inherently biologically interesting
  - Current and year 2100 levels of ambient CO_2
  - Male/female
  - 100, 200, 300 g N/m^2
  - $Y_{ij}=\theta+a_i+\varepsilon_{ij}$
  - Mostly interested in mean treatment effects
- Random is non-repeatable and represents a sample of large population
  - Pigs A,B,C,D fed a diet
  - Is 100, 200,300 g N random?
  - Another experimenter can't repeat
  - Want to make general statement about all pigs
  - $Y_{ij}=\theta+W_i+\varepsilon_{ij}$, $w\sim N(0,\sigma_w)$
  - Mostly interested in variance of treatment effects (is it nonzero)
  - H_o: $\sigma_w=0$

Consequences for ANOVA

- One-way
  - Interpretation only
    - Calculations tests/identical
  - EG weight~sites
  - H_0 =no difference among those sites (fixed)
  - H_0=no difference among all sites (random)
- Different sampling strategies
  - Fixed: emphasize n (replicates)
  - Random: emphasize # treatments

Two-way ANOVA w/ random

- In two-way ANOVAs it changes the calculations
  - If have a fixed and a random term it is called "mixed"
- Different sum squares tables
  - Look it up (Gotelli, Zar)
- Controversial
  - Is there an interaction between a random and a fixed factor
  - Newman paper

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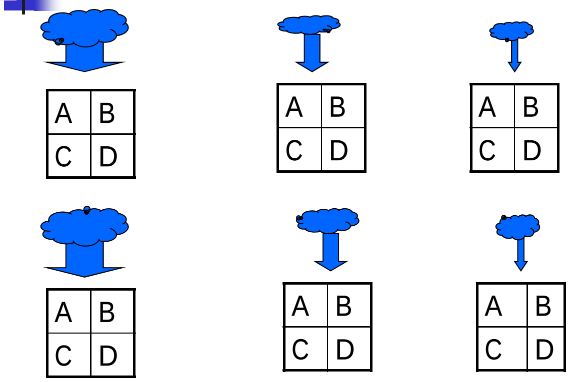
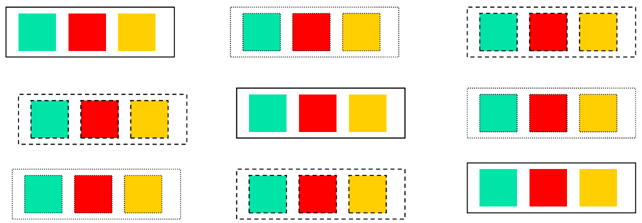
A blocking example

- Imagine 9 sites, each site 3 fields, each field 1 nitrogen treatment (randomly assigned L/M/H N) for a balanced complete block design
- To block you need
  - B fixed: Y~N+B   2+8 parameters (+1 mean, 1 variance)
  - B random: Y~N+B 2+1 parameter
    - Estimate σ instead of $\beta_1,\beta_2,\beta_3,\ldots$
- Now imagine in regression (N continuous)
  - B fixed, varying slope: y~N*b $y_i=b_i+(\beta+b_{is})Ni+\varepsilon i$
    - 16 parameters!
  - B random, varying slope:
    - 3 β σ_s σ_i

Split-plot block design



Marine larval settlement



Repeated measures (ANOVAR)

- Also known as longitudinal studies
- Following course over time:
  - Growth rates
  - Before/after treatment
  - Controlling of variation (e.g. photosynthesis at high/low CO_2)
- Blocking but on individual
  - Multiple measures are not subplots within block but repeated measures on individual
  - Like paired-t-test
- Statistically the same as blocking
  - Add as a factor, probably random, interaction??

Reasons to use random effects

- Traditional/philosophical
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- Nested design
- Multilevel models
- Hierarchical models

Nested models

- A factor that clearly is contained within another:
  - Batches/brands of pesticide within pesticide type
  - Genus within family
  - Subplots within plots
- Variances clearly vary with level
  - Species/Genus/Family
    - s_s, s_g, s_f
- Have a variance for each level
  - Think about this two ways
    - Nesting of errors
    - Nested factors are naturally random not fixed

Variance components

- We are now estimating variances
- Can be meaningful to compare relative amount of variances (instead of effect sizes of factors)
- Called variance components
- Normally rescale so add to 1
  - $\tau_1/(\tau_1+\tau_2+\ldots)$

Reasons to use random effects

- Traditional/philosophical
- Blocks/repeated measures
- Nested design
- Multilevel models
- Hierarchical models

Useful in mutilevel (aka hierarchical)

- Imagine:
  - Lifespan as a function of body size
  - Multiple measurements per species
  - May have species level predictor of life span (e.g. altricial/precocial)

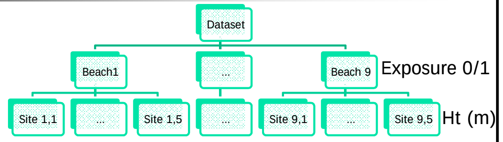
T	M	Care
42	32	A
39	30	A
50	40	P
55	42	P
48	39	P

	T	M	Care
Sp1	42	32	A
	39	30	
Sp2	50	40	P
	55	42	
	48	39	

Other multilevel

- Site/Blocking factor with measurement at multiple locations within
  - Location & Site level factors
  - IE nested spatial design
- Species/Family
  - Species & family level traits

Spatial nesting example



- Sites within beach
  - Exposure per beach
  - Height above mean tide per site
  - Richness at each site (R_{ij})
- Issues
  - Pseudoreplication: errors at site 1,1 and site 1,5 not independent
  - Some variables (exposure) not at base

Two step approach

- $R_{ij}=\alpha+\beta_1*NAP_{ij}+\beta_2*exposure_i+\varepsilon_{ij}$
  - Oops – pseudoreplicated
    - ε_{ij} and $\varepsilon_{ij'}$ certainly not independent
    - Literally copied exposure$_i$ 5 times each
- $R_{ij}=\alpha+\beta_i*NAP_{ij}+\varepsilon_{ij}$ for j=1..5
  - 9 times (i=1..9)
  - →9 β_i
- Second level
  - $\beta_i=\eta+\gamma*Exposure_i+b_i$ with 9 data points
- Now
  - Given NAP_{ij} and exposure$_i$ can predict R_{ij}
  - No pseudoreplication
  - But, 12 parameters (α, η, γ, 9xβ_i)+2 variances (ε_{ij},β_i)
- Alternative – mean approach
  - Take average richness per beach (across 5 sites)
  - Regress average richness vs. exposure
  - But can't include NAP, throwing away data, possible biasing if set of NAPs differ across beaches

---

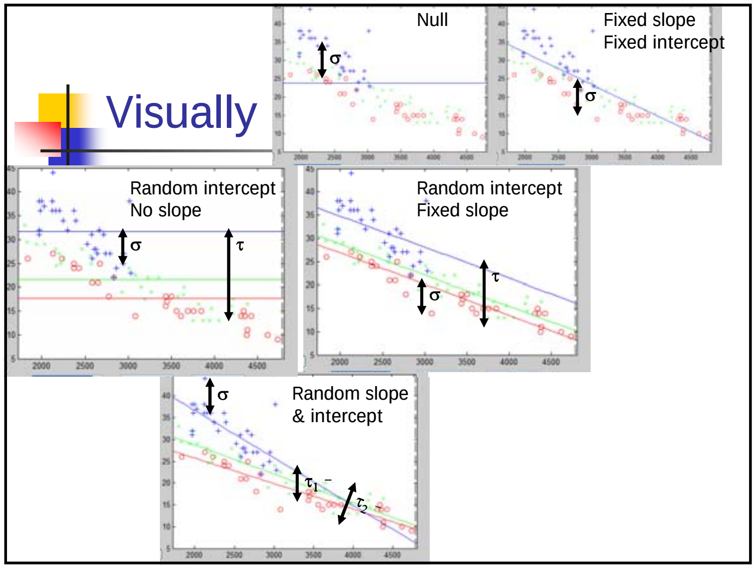
Pulling together – a better way

- Matrix notation to get rid of j
- Lower level (0): $R_i=Z_i x\beta_i+\varepsilon_i$
- Higher level (1): $\beta_i=K_i x\gamma+b_i$
- Combine: $R_i=Z_i x(K_i x\gamma+b_i)+\varepsilon_i$
  - $=Z_iK_i\gamma+Z_ib_i+\varepsilon_i=X_i\gamma+Z_ib_i+\varepsilon_i$
- Mixed model w: fixed, random, error

Nested special cases: ANCOVA w/ discrete (blocking) variable random

- 1 Level
  - ANOVA random factor (1-way)
    - $y_{ij} \sim \mu+\alpha_j+\varepsilon_{ij} \rightarrow \alpha_j \sim N(0,\tau_a)$
  - Simple regression (no random)
    - $y_i \sim \mu+\beta N+\varepsilon_i \rightarrow$ N/A (only for discrete)
- 2-level
  - Varying intercepts (ANCOVA) (1 random)
    - $y_{ij} \sim \mu+\alpha_j+\beta N+\varepsilon_{ij} \rightarrow \alpha_j \sim N(0,\tau_a)$
  - Varying slope & intercepts (ANCOVA) (2 random)
    - $y_{ij} \sim \mu+\alpha_j+\beta_j N+\varepsilon_{ij} \rightarrow \alpha_j \sim N(0,\tau_a)$, $\beta_j \sim N(0,\tau_b)$

Visually



Reasons to use random effects

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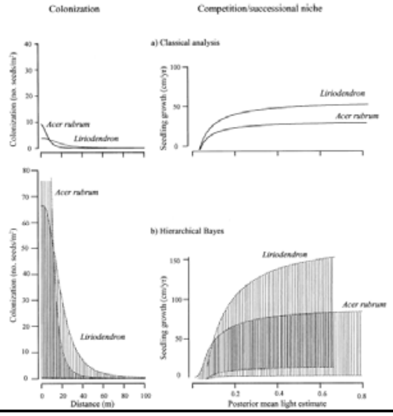
Hierarchical normal model

- 10 individuals within S species, measure mass
  - m_{ij} where i=1..S, j=1..10
  - Species is essentially a block
- Traditional:
  - $m_{ij} \sim N(\mu,\sigma)$
- Hierarchical
  - $\mu_i \sim N(\mu,\sigma)$
  - $m_{ij} \sim N(\mu_i,\tau)$

The importance of individual variation

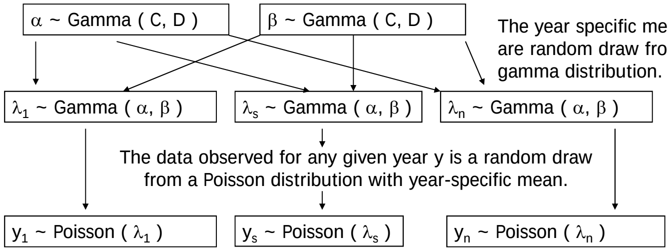


Clark et al 2004

Hierarchical non-normal model

- Imagine measure population size at several plots
  - Traditional N~Pois(λ)
  - Error is picked up by Poisson
- Alternative
  - λ really does vary from site to site
  - N~Pois(λ_i)
  - λ~Gamma(a,b)
  - [Bayesian: a~Gamma(A,B), b~Gamma(C,D)]

Graphical Representation of the Hierarchical Gamma-Poisson Model



The prior parameters α and β are unknown. Both α and β are assumed to be drawn from Gamma distributions

$\alpha \sim$ Gamma (C, D)

$\beta \sim$ Gamma (C, D)

The year specific means λ_t are random draw from a gamma distribution.

$\lambda_1 \sim$ Gamma (α, β)

$\lambda_s \sim$ Gamma (α, β)

$\lambda_n \sim$ Gamma (α, β)

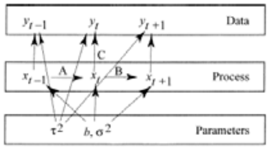
The data observed for any given year y is a random draw from a Poisson distribution with year-specific mean.

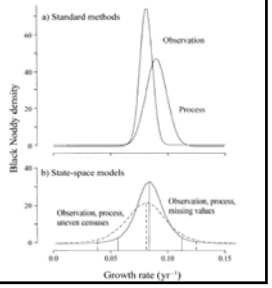
$y_1 \sim$ Poisson (λ_1)

$y_s \sim$ Poisson (λ_s)

$y_n \sim$ Poisson (λ_n)

Process models & latent variables





- Exponential growth
  - Random variation in growth rate b
  - Random measurement error
  - Typically merge into one error
    - Process error: $n_t=n_{t-1}e^{b+\varepsilon t}$
    - Observation error: $n_t=n_{t-1}e^{b}+w_t$
  - But exponential growth compounds growth rate variability but NOT observation error
- $n_t=n_{t-1}e^{b+\varepsilon t}$
  - ε~N(0,σ^2)
- o_t=g(N_t)+w_t
  - w~N(0, τ^2)

Clark & Bjornstad 2004

What we’ve seen

- Some factors/treatments are random
- Grouping structures
  - Simple block or repeated measure (2 levels – block/measurement)
  - Nested (several levels) – only intercept (site/plot/subplot)
  - Multilevel (HLM) – 2+ levels w/ treatments
  - Hierarchical – nested structure with different parameters/distributions at each level
- Common theme: nesting/grouping
  - Must treat or pseudoreplication
  - |level/level/level

When randomness multiplies!

- Random factors and nestedness and hierarchy lead to estimating variances for not just ε but for factors
- $Y=X\beta+Zb+\varepsilon \quad b\sim N(0,\tau^2) \quad \varepsilon\sim N(0,\sigma^2)$
- Note GLS ($\varepsilon\sim N(0,\Sigma)$) is a trivial extension once solving LMM
  - Blocking can be in Σ or in Zb (GLS or LMM)
- A discrete variable is always involved (possibly nested)
  - Called a group and denoted by “|” (and “/”) in formulas

Solving LMM/GLMM

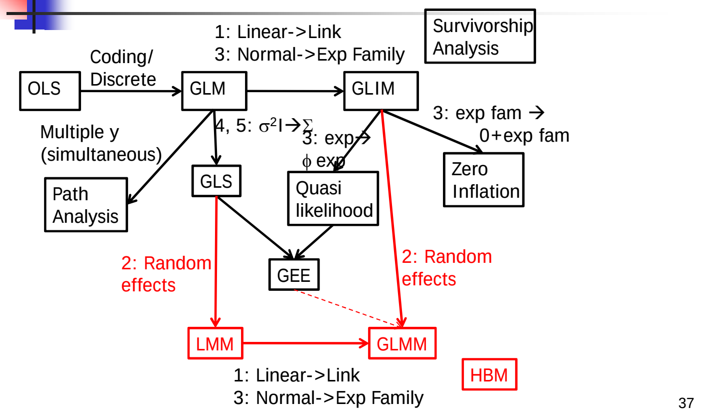
- Changes calculation methods
  - SS doesn’t work use ML, REML
    - ML for comparison of models (likelihood ratios)
    - REML for variance comparisons
  - Need new command
    - lme in package nlme
    - lmer in lme4

Model selection by Zuur et al

1. Use an overinclusive fixed effect model
2. Vary random effects to pick best (using REML)
3. Now hold random effects constant & vary fixed effects to pick best (using MLE)
4. Estimate parameters using (REML)

Road map

1. Linear
2. Error in Y only
3. Errors normal
4. Errors independent
5. Errors homoscedasti



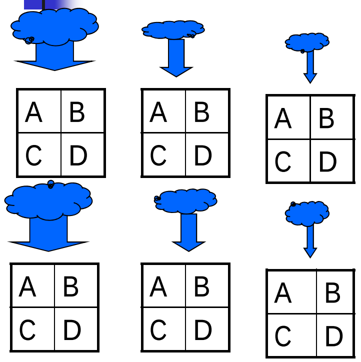
Summary

- If you have:
  - Random factors
  - Nesting
  - Blocking/ANOVAR/longitudinal
  - Predictors at multiple levels
- Then you
  - Are doing mixed models
  - Need to use lme (nlme) or lmer (lme4)
  - Specify the fixed and random components
- Because
  - Avoid pseudoreplication (non-independence)
  - Estimate variance more interesting

General notation

- Use formulas with 3 extensions
  - | means group by – implies acknowledgement of pseudoreplication
  - / means in – implies nested acknowledgement of pseudoreplication
  - 2 formulas
    - fixed (same as before) – everything of ecological interest
    - random – everything of pseudoreplication potential

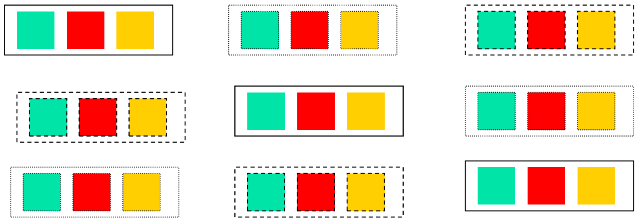
Split-plot block design



Level	Treatment	N	Fixed	Random
Experiment	N/A	1	N	N (top, N=1)
Treatment	Moisture*	3	Y	N (no grouping creating pseudoreplication)
Tray*	N/A	2	N	Y (grouping creating pseudo replication)
Well	Fertilizer*	4	Y	N (bottom)

Yield~Fertilizer*Moisture,random=~1|Tray

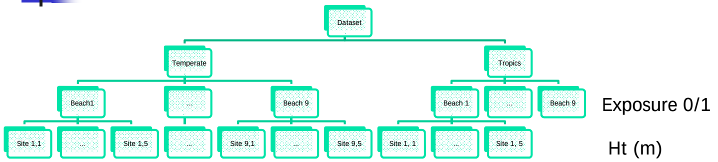
Marine larval settlement – split-plot



Level	Treatment / Interest	N	Fixed	Random
Experiment	N/A	1	N	N (top, N=1)
Treatment	Predation type	3	Y	N (no grouping creating pseudoreplication)
Cage	N/A	3	N	Y (grouping creating pseudo replication)
Brick	Substrate	3	Y	N (bottom)

Abund~predation*substrate,random=~1|cage

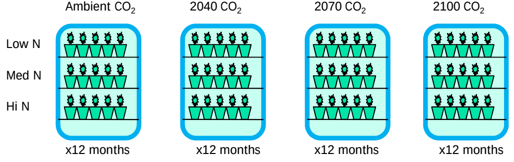
Observational example



Level	Treatment	Interest Var	N	Fixed	Random
Experiment	N/A	N/A	1	N	N (top, N=1)
biogeog	N/A	Biogeog	2	Y	Y (grouping could create pseudo replication)
beach	N/A	Exposure	9	Y	Y (grouping creating pseudo replication)
site	Substrate	Ht	5	Y	N (bottom)

- Rich~biogeog+Exposure+Ht, random=~1|biogeog/beach

ANOVAR



Level	Treatment	N	Fixed	Random
Experiment	N/A	1	N	N (top, N=1)
Chamber	CO2	4	Y	Y (grouping could create pseudoreplication)
Shelf	N	3	Y	Y??? (grouping creating pseudoreplication)
Pot/plant	N/A	5	Y	Y (repeated measures on individual→pseudorep)
Month	Growth	12	Y (interaction)	N (bottom)

y~(CO2+N)*ordered(Month),random=~1|CO2/N/PlantID #errors/intercept grouped
y~(CO2+N)*ordered(Month),random=~Month|CO2/N/PlantID #also slope wrt month aka variable slope

lme

- library(nlme) #download package
- Blocking
  - m=lme(y~N,random=~1|block,...)
    - #random intercept $y=(\alpha+a_i)+\beta N+\varepsilon$
  - m=lme(y~N,random=~N|block,...)
    - #random intercept & slope $y=(\alpha+a_i)+(\beta+b_\iota)N+\varepsilon$
  - m=lme(y~N,random=~(N-1)|block,...) ????
    - #random slope ONLY $y=\alpha+(\beta+b_\iota)N+\varepsilon$
  - m=lme(y~I(N-mean(N)), random=~I(N-mean(N))|block, ..)
    - Centering is often a good idea
      - Intercepts have more meaning/easier to interpret
      - Eliminates correlation between parameters (more independent, better estimated
- ANOVAR
  - m=lme(ht~t,random=~1|individual,...)
  - m=lme(ht~t,random=~t|individual,...)

lme II

- Nested
    - m=lme(log10(ab)~1,random=~1|Order/Family/Genus/Species,...)
    - varcomp(m,1) #varcomp is in library ape
- Hierarchical
    - m=lme(T~M+care,random=~M|species,...)
- For lme: method="REML" (variance components) vs method="ML" (model comparison)
- Plotting:
    - plot(groupedData(ht~t|individual,data=..))
    - xyplot(Rich~Time|Field,data=d,type=c("p","smooth","grid"))
    - coplot

lme4

- Newer package
    - Command lmer
    - Key differences
        - Don't specify nesting (figures it out automatically) so no /
        - No random, just put +(1|block) in formula
    - E.g.
        - `m<-lmer(abund~mass+(1|species)+(1|genus),…)`
    - Supports glmer for GLIM type analyses
    - Does NOT give p-values (df not clear)

In R – simple block (or ANOVAR)

```
library(AED)
data(RIKZ)
str(RIKZ)
summary(m.lm<-
  lm(Richness~Exposure+Beach,data=RIKZ))
library(nlme)
summary(m.mm<-
  lme(Richness~Exposure,random=~1|Beach,data=
  RIKZ))
```

In R II – exploring the data

```
library(lattice)
RIKZ$Beach=factor(RIKZ$Beach)
RIKZ[RIKZ$Exposure==8,"Exposure"]=10 #only one 8 – merge to 10
RIKZ$Exposure=factor(RIKZ$Exposure)
xyplot(Richness~NAP|Beach,data=RIKZ,type=c("p","smooth","grid"))
xyplot(Richness~NAP|Beach,data=RIKZ,type=c("p","l","grid"))
   #in general in the type, p=points, l=timeseries line,
   r=regression line, smooth=loess
bwplot(Richness~Exposure|Beach,data=RIKZ) #oops
```

In R - III

```
#two step
beta<-vector(length=9)
for (i in 1:9) {
   mi<-
   summary(lm(Richness~NAP,subset=(Beach==i),data=RIKZ))
   beta[i]<-mi$coefficients[2,1]
}
beta
bchExp<-RIKZ[seq(1,45,by=5),"Exposure"]
bchExp
summary(lm(beta~bchExp,data=RIKZ))
#average
bchRich<-tapply(RIKZ$Richness,RIKZ$Beach,mean)
bchRich
summary(lm(bchRich~bchExp))
```

In R – IV – ignore exposure

```
# random effects – calculate means across groupings
summary(m.re<-lme(Richness~1,random=~1|Beach,data=RIKZ))
#compare with lm (random factor in error)
summary(lm(Richness~1,data=RIKZ))
#random intercept – regress vs NAP, let b0 (intercept) vary
summary(m.ri<-lme(Richness~NAP,random=~1|Beach,data=RIKZ))
#random slope & intercept
summary(m.ris<-lme(Richness~NAP,random=~NAP|Beach,data=RIKZ))
#random slope only
summary(m.rs<-lme(Richness~NAP,random=~(NAP-1)|Beach,data=RIKZ))
```

```
> # random effects – calculate means across groupings
> summary(m.re<-lme(Richness~1,random=~1|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  267.1142 272.4668 -130.5571

Random effects:
 Formula: ~1 | Beach
        (Intercept) Residual
StdDev:    3.237112 3.938415

Fixed effects: Richness ~ 1
               Value Std.Error DF  t-value p-value
(Intercept) 5.688889  1.228419 36 4.631066       0

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-1.77968689 -0.50704111 -0.09795286  0.25468670  3.80631705

Number of Observations: 45
Number of Groups: 9
#compare with lm (random factor in error)
summary(lm(Richness~1,data=RIKZ))
Call:
lm(formula = Richness ~ 1, data = RIKZ)

Residuals:
   Min     1Q Median     3Q    Max
-5.689 -2.689 -1.689  2.311 16.311

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.6889     0.7459   7.627 1.39e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5.004 on 44 degrees of freedom

> #random intercept – regress vs NAP, let b0 (intercept) vary
> summary(m.ri<-lme(Richness~NAP,random=~1|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  247.4802 254.5250 -119.7401

Random effects:
 Formula: ~1 | Beach
        (Intercept) Residual
StdDev:    2.944065  3.05977

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.581893 1.0957618 35  6.006682       0
NAP         -2.568400 0.4947246 35 -5.191574       0
 Correlation:
    (Intr)
NAP -0.157

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.4227495 -0.4848006 -0.1576462  0.2518966  3.9793918

Number of Observations: 45
Number of Groups: 9
Number of Groups: 9
```

```
> #random slope & intercept
> summary(m.ris<-lme(Richness~NAP,random=~NAP|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  244.3839 254.9511 -116.1919

Random effects:
 Formula: ~NAP | Beach
 Structure: General positive-definite, Log-Cholesky parametrization
            StdDev   Corr
(Intercept) 3.549068 (Intr)
NAP         1.714957 -0.99
Residual    2.702824

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.588703 1.2647622 35  5.209441   0e+00
NAP         -2.830027 0.7229385 35 -3.914616   4e-04
 Correlation:
    (Intr)
NAP -0.819

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.8213275 -0.3411044 -0.1674619  0.1921281  3.0397126

Number of Observations: 45
Number of Groups: 9
> #random slope only
> summary(m.rs<-lme(Richness~NAP,random=~(NAP-1)|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
      AIC      BIC    logLik
  260.201 267.2458 -126.1005

Random effects:
 Formula: ~(NAP - 1) | Beach
                 NAP Residual
StdDev: 0.0001123315 4.159929

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.685662 0.6577579 35 10.164320   0e+00
NAP         -2.866853 0.6307186 35 -4.545376   1e-04
 Correlation:
    (Intr)
NAP -0.333

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.2181663 -0.6636488 -0.1930031  0.3253447  3.3347473

Number of Observations: 45
```

In R

```
#compare GLS & LMM
summary(m.mixed<-
  lme(Richness~NAP,random=~1|Beach,method="REML",data=R
  IKZ))
summary(m.gls<-
  gls(Richness~NAP,cor=corCompSymm(form=~1|Beach),metho
  d="REML",data=RIKZ))
#no difference!

#compare REML vs. MLE
summary(m.reml<-m.mixed)
summary(m.mle<-
  lme(Richness~NAP,random=~1|Beach,method="ML",data=RIK
  Z))
#slightly different
```

```
> # random effects – calculate means across groupings
> summary(m.re<-lme(Richness~1,random=~1|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  267.1142 272.4668 -130.5571

Random effects:
 Formula: ~1 | Beach
        (Intercept) Residual
StdDev:    3.237112 3.938415

Fixed effects: Richness ~ 1
               Value Std.Error DF  t-value p-value
(Intercept) 5.688889  1.228419 36 4.631066       0

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-1.77968689 -0.50704111 -0.09795286  0.25468670  3.80631705

Number of Observations: 45
Number of Groups: 9
#compare with lm (random factor in error)
summary(lm(Richness~1,data=RIKZ))
Call:
lm(formula = Richness ~ 1, data = RIKZ)

Residuals:
   Min     1Q Median     3Q    Max
-5.689 -2.689 -1.689  2.311 16.311

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.6889     0.7459   7.627 1.39e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5.004 on 44 degrees of freedom

> #random intercept – regress vs NAP, let b0 (intercept) vary
> summary(m.ri<-lme(Richness~NAP,random=~1|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  247.4802 254.5250 -119.7401

Random effects:
 Formula: ~1 | Beach
        (Intercept) Residual
StdDev:    2.944065  3.05977

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.581893 1.0957618 35  6.006682       0
NAP         -2.568400 0.4947246 35 -5.191574       0
 Correlation:
    (Intr)
NAP -0.157

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.4227495 -0.4848006 -0.1576462  0.2518966  3.9793918

Number of Observations: 45
Number of Groups: 9
Number of Groups: 9
```

```
> #random slope & intercept
> summary(m.ris<-lme(Richness~NAP,random=~NAP|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
       AIC      BIC    logLik
  244.3839 254.9511 -116.1919

Random effects:
 Formula: ~NAP | Beach
 Structure: General positive-definite, Log-Cholesky parametrization
            StdDev   Corr
(Intercept) 3.549068 (Intr)
NAP         1.714957 -0.99
Residual    2.702824

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.588703 1.2647622 35  5.209441   0e+00
NAP         -2.830027 0.7229385 35 -3.914616   4e-04
 Correlation:
    (Intr)
NAP -0.819

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.8213275 -0.3411044 -0.1674619  0.1921281  3.0397126

Number of Observations: 45
Number of Groups: 9
> #random slope only
> summary(m.rs<-lme(Richness~NAP,random=~(NAP-1)|Beach,data=RIKZ))
Linear mixed-effects model fit by REML
 Data: RIKZ
      AIC      BIC    logLik
  260.201 267.2458 -126.1005

Random effects:
 Formula: ~(NAP - 1) | Beach
                 NAP Residual
StdDev: 0.0001123315 4.159929

Fixed effects: Richness ~ NAP
                Value Std.Error DF   t-value p-value
(Intercept)  6.685662 0.6577579 35 10.164320   0e+00
NAP         -2.866853 0.6307186 35 -4.545376   1e-04
 Correlation:
    (Intr)
NAP -0.333

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.2181663 -0.6636488 -0.1930031  0.3253447  3.3347473

Number of Observations: 45
```

Ignore – this just don't want to delete a slide with so many equations! Multilevel fits paradigm

- Multiple equations:
  - $Y_{ij}=\beta_{0j}+\beta_{1j}X_{ij}+\varepsilon_{ij}$ Level 1 (lowest – e.g. individual)
  - $\beta_{0j}=\gamma_{00}+\gamma_{01}W_j+u_{0j}$ Level 2a (highest – e.g. site)
  - $\beta_{1j}=\gamma_{10}+\gamma_{11}W_j+u_{0j}$ Level 2b (highest)
  - $\rightarrow Y_{ij}=\gamma_{00}+\gamma_{01}W_j+u_{0j}+(\gamma_{10}+\gamma_{11}W_j+u_{0j})X_{ij}+\varepsilon_{ij}$
    - $= Y_{ij}=\gamma_{00}+\gamma_{01}W_j+\gamma_{10}X_{ij}+\gamma_{11}W_jX_{ij}+[u_{0j}+u_{0j}X_{ij}+\varepsilon_{ij}]$
  - i=replicate w/in patch, j=patch, $u_{0j}\sim N(0,\tau_0)$, $u_{1j}\sim N(0,\tau_1)$, $\varepsilon_{ij}\sim N(0,\sigma)$