Mixed effects models
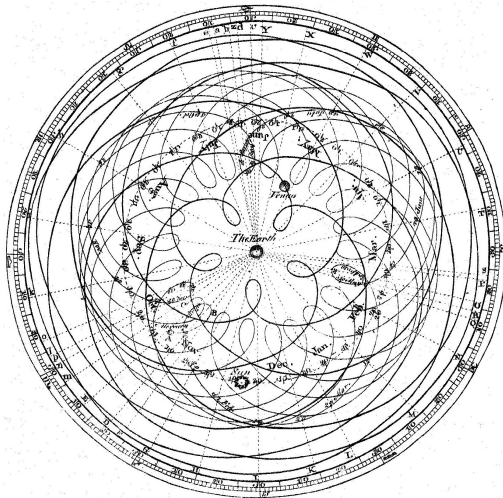## "Wheels within wheels"

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Outline

- Linear mixed effects models (LMMs)
  - A bit of math
  - Fixed vs. random effects
  - Random intercepts and slopes
- Generalized linear mixed effects models (GLMMs)
  - Residuals checks
  - Some sage advice
- Hypothesis testing and inference
  - Slopes and intercepts
  - Entire terms
  - AIC, R^2, and Star-Gazing

Part 1: Mixed effects models

Problem: group-level variation

- Sometimes we have to sample within groups: different field sites, individual organisms, etcetera
- However, often we're not really interested in each group *per se*, but in the **average group**
- e.g. "What is the effect of **x** if you remove group-to-group variation?"
- If you have a small number of groups, you can just include it in your model: `lm(y ~ x + group)`
  - If you have few samples for each group, this can create problems
- Another solution is to use **mixed effects models**

What are mixed effects models?

Many different names:

1. Mixed effects models
2. Random effects models
3. Hierarchical models
4. Empirical/Bayesian hierarchical models
5. Latent variable models
6. Split-plot models
7. Variance partitioning

I usually use the term *heirarchical models*, as this is the closest to what I will teach you

Scary math

Unfortunately, we need a review of matrix algebra in order to explain this:

- This is a matrix:

$$A = \begin{bmatrix} 1 & 4 & 7 \\ 2 & 5 & 8 \\ 3 & 6 & 9 \end{bmatrix}$$

- This is a vector:

$$b = \begin{bmatrix} 1 & 2 & 3 \end{bmatrix}$$

- Multiplying them looks like this:

$$A \times b = Ab = 1 \times \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix} + 2 \times \begin{bmatrix} 4 \\ 5 \\ 6 \end{bmatrix} + 3 \times \begin{bmatrix} 7 \\ 8 \\ 9 \end{bmatrix} = \begin{bmatrix} 30 \\ 36 \\ 42 \end{bmatrix}$$

Why do we call them "linear models"?

- *Linear* mapping of **coefficients** onto a **model matrix** (from your data)
- Coefficients:

$$\beta = \begin{bmatrix} 0.1 & 1.8 & -0.03 \end{bmatrix}$$

- Model matrix:

$$X = \begin{bmatrix} 1 & 1 & 10 \\ 1 & 1 & 12 \\ 1 & 0 & 9 \\ \vdots & \vdots & \vdots \end{bmatrix}$$

- Multiplying them looks like:

$$\hat{y} = X\beta = \begin{bmatrix} 1.60 \\ 1.54 \\ -0.17 \\ \vdots \end{bmatrix}$$

This is exactly what R does to fit models:

```r
head(dat)
```

```
##           y         x site
## 1  1.5101095 -4.248450    g
## 2  3.7190900  5.766103    j
## 3 -4.3737644 -1.820462    f
## 4 30.1459331  7.660348    n
## 5  0.2777422  8.809346    o
## 6 -3.6978175 -9.088870    p
```

```r
m1 <- lm(y~x,data=dat) #Uses x to predict y
summary(m1)
```

```
##
## Call:
## lm(formula = y ~ x, data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -18.2574  -4.1262   0.0296   3.1854  25.2780
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.7306     0.5772   4.731 4.92e-06 ***
## x             0.7213     0.1020   7.074 4.60e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.3 on 158 degrees of freedom
## Multiple R-squared:  0.2405, Adjusted R-squared:  0.2357
```

This is exactly what R does to fit models (cont.):

```
head(model.matrix(m1))
```

```
##   (Intercept)        x
## 1           1 -4.248450
## 2           1  5.766103
## 3           1 -1.820462
## 4           1  7.660348
## 5           1  8.809346
## 6           1 -9.088870
```

```
coef(m1)
```

```
## (Intercept)        x
##   2.7305689  0.7212867
```

```
pred2 <- model.matrix(m1) %*% coef(m1) #predicted = matrix * coefs
head(data.frame(pred1=predict(m1),pred2)) #same thing!
```

```
##        pred1      pred2
## 1 -0.3337812 -0.3337812
## 2  6.8895819  6.8895819
## 3  1.4174942  1.4174942
## 4  8.2558758  8.2558758
## 5  9.0846325  9.0846325
## 6 -3.8251119 -3.8251119
```

Groups are coded by "dummy variables" (0s and 1s)

```
m2 <- lm(y~site,data=dat) #Use site to predict y
head(model.matrix(m2)) #0s and 1s used to identify groups
```

```
##   (Intercept) siteb sitec sited sitee sitef siteg siteh sitei sitej sitek sitel
## 1           1     0     0     0     0     0     1     0     0     0     0     0
## 2           1     0     0     0     0     0     0     0     0     1     0     0
## 3           1     0     0     0     0     1     0     0     0     0     0     0
## 4           1     0     0     0     0     0     0     0     0     0     0     0
## 5           1     0     0     0     0     0     0     0     0     0     0     0
## 6           1     0     0     0     0     0     0     0     0     0     0     0
##   sitem siten siteo sitep
## 1     0     0     0     0
## 2     0     0     0     0
## 3     0     0     0     0
## 4     0     1     0     0
## 5     0     0     1     0
## 6     0     0     0     1
```

```
coef(m2) #This uses the 1st site as the "control" group
```

```
## (Intercept)        siteb        sitec        sited        sitee        sitef
##    7.192416   -11.998464   -14.632803     1.983649    -7.765354    -4.523079
##       siteg        siteh        sitei        sitej        sitek        sitel
##   -3.439621    -8.280601    -4.306456    -4.085855    -5.663021    -5.155112
##       sitem        siten        siteo        sitep
##   -6.226642     8.403599    -8.626661   -10.934182
```

Structure of LMs... now with matrices!

- All linear models take the form:

$$\hat{y} = X\beta = b_0 1 + b_1 x_1 ... + b_i x_i$$
$$y \sim Normal(\hat{y}, \sigma)$$

- y is a vector of data you want to predict
- $\hat{y}$ is a vector of *predicted values* for y
- $X = \{1, x_1 ...\}$ is a matrix of *predictors* for y
- $\beta = \{b_0, b_1, ...\}$ is a vector of *coefficients*
- $y \sim Normal(\hat{y}, \sigma)$ means:
  - "y follows a Normal distribution with mean $\hat{y}$ and SD σ"

Fixed effects vs. Random effects

Say that X is a model matrix coding for 10 sites[1], and y is something we're interested in predicting

$$\hat{y} = b_0 + X\beta$$
$$y \sim Normal(\hat{y}, \sigma)$$

$$\hat{y} = b_0 + X\zeta$$
$$y \sim Normal(\hat{y}, \sigma)$$
$$\zeta \sim Normal(0, \sigma_{site})$$

- Site coefficients (β) are unrelated to each other
- σ is the SD of *residuals*
- Site is a **fixed effect**

- Site coefficients (ζ) are related to each other via a *Normal* distribution
- σ is the SD of *residuals*, σ_{site} is the SD of *sites*
- Site is a **random effect**

---

[1]Intercept is a separate variable

Mixed effects = fixed + random effects

A mixed effects model has both **fixed** and **random** effects

$$\hat{y} = X\beta + U\zeta$$
$$y \sim Normal(\hat{y}, \sigma)$$
$$\zeta \sim Normal(0, \sigma_{site})$$

- X = fixed effects matrix (e.g. intercept, temperature)
- β = fixed effects coefficients
- U = random effects matrix (e.g. sites)
- ζ = random effects coefficients
- σ, σ_{site} = variance terms

Mixed effect model example

Let's go back to our earlier example:

- We're interested in predicting *y* using *x* (fixed effects)
- Data was collected at a number of *sites*, which may affect *y* "somehow"
- Effect of each site is normally distributed

```
head(dat)
```

```
##            y          x site
## 1  1.5101095 -4.248450    g
## 2  3.7190900  5.766103    j
## 3 -4.3737644 -1.820462    f
## 4 30.1459331  7.660348    n
## 5  0.2777422  8.809346    o
## 6 -3.6978175 -9.088870    p
```

```
library(lme4) #Mixed effects library
mm1 <- lmer(y ~ x + (1|site),data=dat) #site is fit as "random intercepts"
```

Mixed effect model example

```
summary(mm1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ x + (1 | site)
##    Data: dat
##
## REML criterion at convergence: 1040.4
##
## Scaled residuals:
##     Min      1Q   Median      3Q      Max
## -2.50816 -0.71380 -0.02682  0.69401  3.01951
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 26.78    5.175
##  Residual             31.68    5.628
## Number of obs: 160, groups: site, 16
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  2.00331    1.38297   1.449
## x            0.76192    0.08083   9.426
##
## Correlation of Fixed Effects:
##   (Intr)
## x -0.002
```

Results from `lmer` model:

- Random effects:
  - *residual* and *site* variance (σ, σ_{site})
- Fixed effects:
  - Intercept and slope estimates (β)
  - No d.f. and p-value [2]
  - If you need p-values for parameters, you can use the *lmerTest* package (or just calculate them yourself using means/SEs)

[2]'lme4' author doesn't think they can be calculated. I somewhat agree

Mixed effect model results

- In a *random intercepts* model, the regression line of x on y is allowed to move up or down around the main regression line for each site
- These changes in intercepts are *normally distributed*
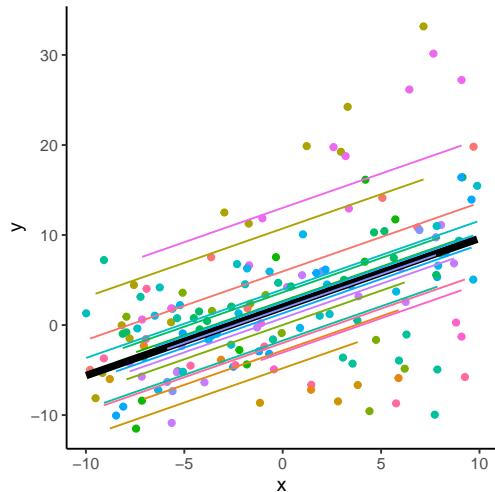
Mixed effect model results (cont.)

- For plotting, we want a partial effects plot that marginalizes across sites (i.e. "What does the trend look like at the average site?")
- `ggpredict` works well for this. If you want partial residuals, you'll have to add them in yourself using `predict` and `residual`
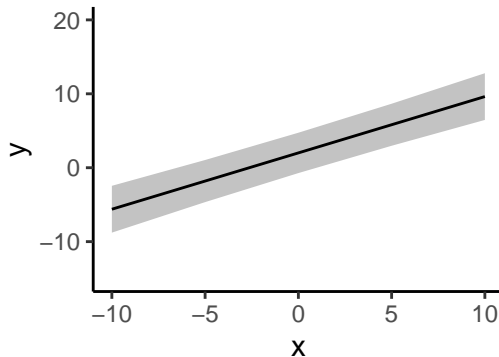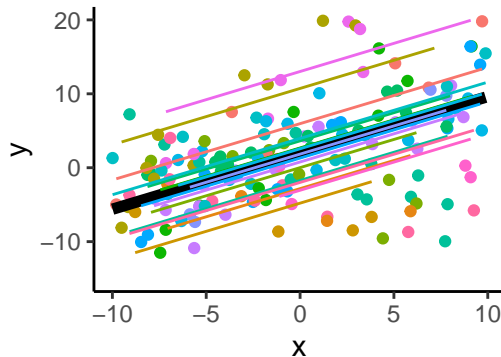
First challenge

How does forest cover influence fish size? Maybe some of the species do better in forested streams?

- You've weighed fish in streams with different forest covers (`fishMass.csv`). However, perhaps some of the variation is caused by "other things" about the site?
- Fit a mixed effects model with the fixed effects you're interested in (**forest cover**, **species**), and include **site** as a random *intercept*
- How does this compare to a simple linear model where you *ignore* site?
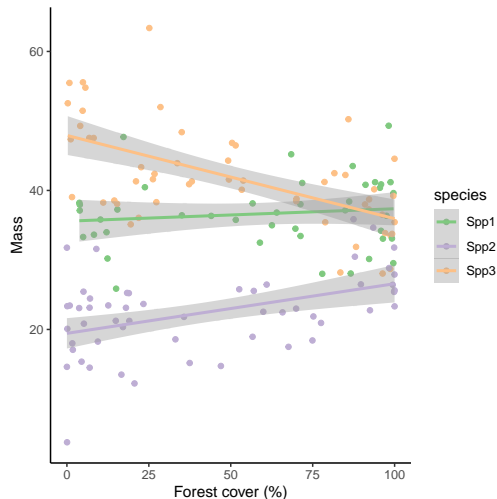
First challenge results

```
##
## Call:
## lm(formula = mass ~ species * forest, data = fishDat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.6767 -3.1422  0.0415  3.3364 18.4631
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       35.57610    1.68256  21.144  < 2e-16 ***
## speciesSpp2      -16.13571    2.02625  -7.963 4.60e-13 ***
## speciesSpp3       12.34080    2.11876   5.825 3.59e-08 ***
## forest            0.01792    0.02413   0.743   0.4590
## speciesSpp2:forest 0.05348    0.03152   1.697   0.0919 .
## speciesSpp3:forest -0.13769   0.03187  -4.321 2.88e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.468 on 144 degrees of freedom
## Multiple R-squared:  0.7391, Adjusted R-squared:  0.73
## F-statistic: 81.57 on 5 and 144 DF,  p-value: < 2.2e-16
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mass ~ species * forest + (1 | sites)
##    Data: fishDat
##
## REML criterion at convergence: 807.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.3538 -0.5868  0.0548  0.6296  2.1122
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  sites    (Intercept) 25.931   5.092
##  Residual              8.381   2.895
## Number of obs: 150, groups:  sites, 15
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)       33.78928    1.63228  20.701
## speciesSpp2      -14.65711    1.13614 -12.901
## speciesSpp3       15.68085    1.19467  13.126
## forest            0.02365    0.01353   1.747
## speciesSpp2:forest 0.05650    0.01720   3.285
## speciesSpp3:forest -0.17411   0.01785  -9.754
##
## Correlation of Fixed Effects:
##            (Intr) spcsS2 spcsS3 forest spcS2:
## speciesSpp2 -0.501
## speciesSpp3 -0.480  0.681
## forest      -0.513  0.734  0.702
## spcsSpp2:fr  0.390 -0.815 -0.532 -0.771
```
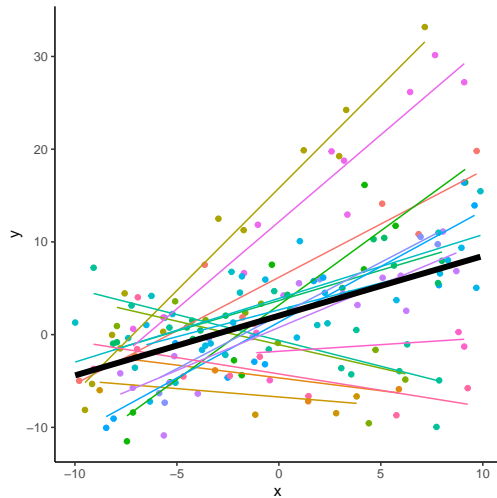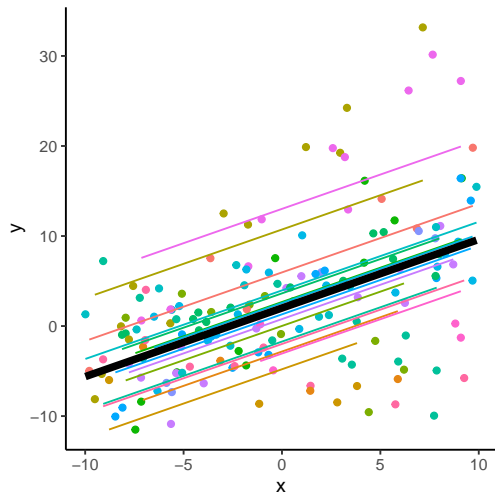
First challenge results (cont.)
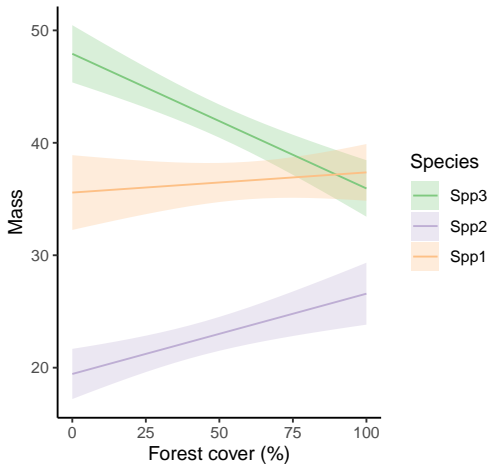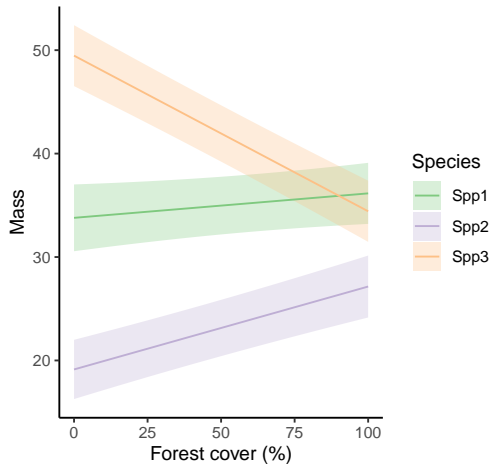
More random effects: slopes!

Random slopes + intercepts

Suppose that y wasn't just higher or lower at each site, but that the effect of x on y was higher or lower at each site

$$\hat{y} = X\beta + U\zeta_{int} + U_x\zeta_{slope}$$
$$y \sim Normal(\hat{y}, \sigma)$$
$$\zeta_{int} \sim Normal(0, \sigma_{int})$$
$$\zeta_{slope} \sim Normal(0, \sigma_{slope})$$

- X = fixed effects matrix (e.g. intercept, temperature)
- β = fixed effects coefficients
- U = random intercept matrix (e.g. sites)
- U_x = random slopes matrix (e.g. temperature)
- $\zeta_{int}, \zeta_{slope}$ = random intercept and slope coefficients
- $\sigma, \sigma_{int}, \sigma_{slope}$ = variance terms

Random slope and intercept example:

```
#Intercept varies with site, and slope of x can
#   also vary with site (both hierarchical)
mm2 <- lmer(y ~ x + (x|site),data=dat)
summary(mm2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ x + (x | site)
##    Data: dat
##
## REML criterion at convergence: 900.6
##
## Scaled residuals:
##     Min      1Q   Median      3Q     Max
## -2.10500 -0.64857  0.02414  0.61137  2.22996
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 35.2210  5.9347
##           x            0.7889  0.8882   0.82
##  Residual              9.3162  3.0522
## Number of obs: 160, groups:  site, 16
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   2.0383     1.5091   1.351
## x             0.6438     0.2275   2.830
##
## Correlation of Fixed Effects:
##    (Intr)
```

Results from `lmer` model:

- Random effects:
  - *residual*, *slope*, and *site* variance (σ, σ_{int}, σ_{slope})
  - Correlation b/w intercept and slope $= 0.82$
    - Sites with higher intercept *also* have a higher slope
- Fixed effects:
  - Intercept and slope estimates

Model matrices

X: Fixed effects model matrix

```
##   (Intercept)         x
## 1           1 -4.248450
## 2           1  5.766103
## 3           1 -1.820462
## 4           1  7.660348
## 5           1  8.809346
## 6           1 -9.088870
```

U: Random intercept model matrix

```
##   sitea siteb sitec sited sitee sitef siteg siteh sitei
## 1     0     0     0     0     0     0     1     0     0
## 2     0     0     0     0     0     0     0     0     0
## 3     0     0     0     0     0     1     0     0     0
## 4     0     0     0     0     0     0     0     0     0
## 5     0     0     0     0     0     0     0     0     0
## 6     0     0     0     0     0     0     0     0     0
##   sitej sitek sitel sitem siten siteo sitep
## 1     0     0     0     0     0     0     0
## 2     1     0     0     0     0     0     0
## 3     0     0     0     0     0     0     0
## 4     0     0     0     0     1     0     0
## 5     0     0     0     0     0     1     0
## 6     0     0     0     0     0     0     1
```

U_x: Random slope model matrix

```
##   sitea siteb sitec sited sitee sitef siteg siteh sitei
## 1     0     0     0     0     0  0.00 -4.25     0     0
## 2     0     0     0     0     0  0.00  0.00     0     0
## 3     0     0     0     0     0 -1.82  0.00     0     0
## 4     0     0     0     0     0  0.00  0.00     0     0
## 5     0     0     0     0     0  0.00  0.00     0     0
## 6     0     0     0     0     0  0.00  0.00     0     0
##   sitej sitek sitel sitem siten siteo sitep
## 1  0.00     0     0     0  0.00  0.00  0.00
## 2  5.77     0     0     0  0.00  0.00  0.00
## 3  0.00     0     0     0  0.00  0.00  0.00
## 4  0.00     0     0     0  7.66  0.00  0.00
## 5  0.00     0     0     0  0.00  8.81  0.00
## 6  0.00     0     0     0  0.00  0.00 -9.09
```

Mixed effect model results

- Regression line of x on y is allowed to move up or down for each site (random intercepts)
- Slope of regression line can be more or less steep for each site (random slopes)
- Changes in intercepts and slopes are *normally distributed*, and in this example are *correlated* with each other
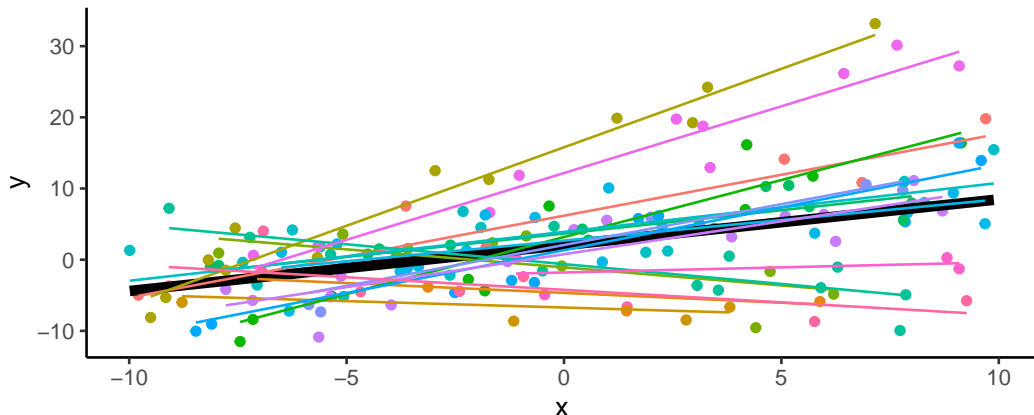
Why do we need to do any of this?

"My supervisor told me to just use site as a fixed effect. Why can't I do that?"

- You can do it this way, but you may encounter the following problems:
  - You lose the *partial pooling* that occurs in mixed effects models = Worse estimates of site effects!
  - You lose 1 d.f. for each site = Type II error $\uparrow$ = You may not find the fixed effect of interest, even if it's there!
  - Sites with low sample sizes may cause your models to break
  - People[3] who have read statistics books published after 1980 may ask questions
- However, if you have a low number of sites (1-10), fixed effects may work better
  - Hard to estimate σ_{site} if number of sites is low
  - If stakes are high, it may be better to be more conservative about site intercepts
 - Easier to interpret (p-values, ANOVA, etc.)

---

[3]e.g. me

Second challenge

- Let's go back to the fish weight model...
- Fit a mixed effects model with the fixed effects you're interested in (**forest cover**, **species**), and include **site** as a random effect (*intercept* **or** *slope*)
- Your supervisor doesn't like hierarchical models, and tells you to just use site as another fixed term in an `lm` model. Do you get different results if you use their approach?

Second challenge results
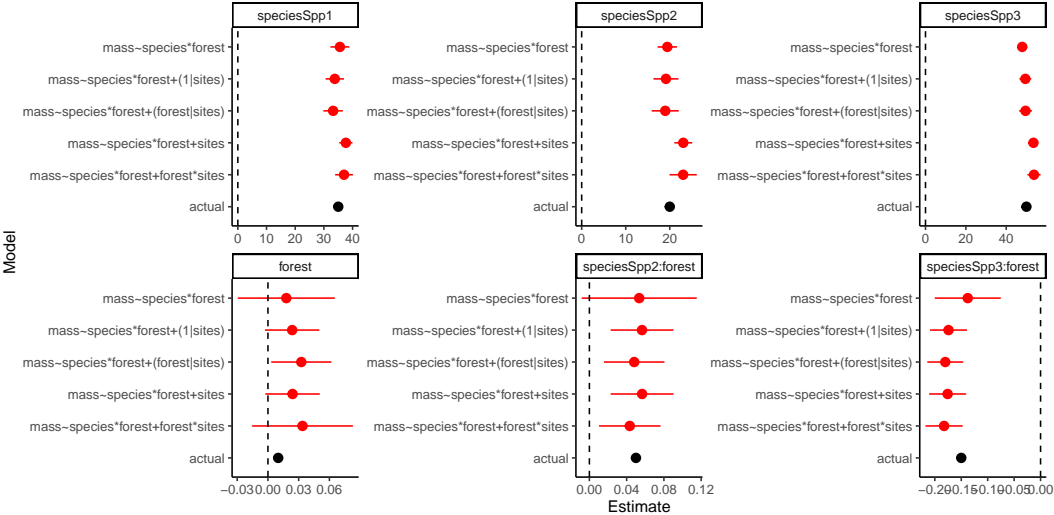
Second challenge results (cont.):
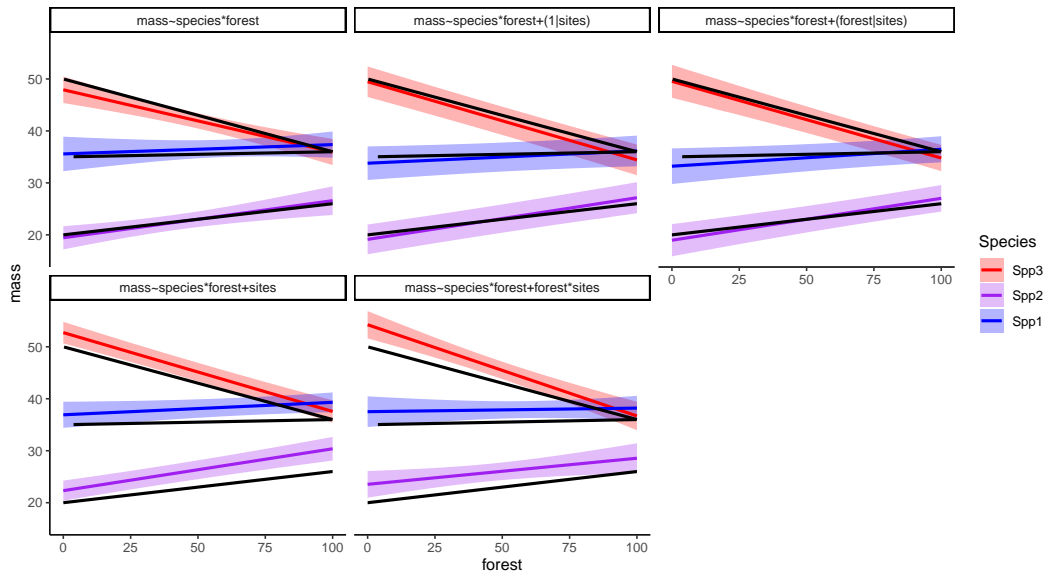
Part 2: GLMMs

What if my response variable is non-normal?

- Linear model (LM)

$$\hat{y} = X\beta$$
$$y \sim Normal(\hat{y}, \sigma)$$

- Linear mixed effects model (LMM)

$$\hat{y} = X\beta + U\zeta$$
$$y \sim Normal(\hat{y}, \sigma)$$
$$\zeta \sim Normal(0, \sigma_{site})$$

- Generalized linear model (GLM)

$$logit(\hat{\phi}) = X\beta$$
$$y \sim Binomial(\hat{\phi})$$

- Generalized linear mixed effects model (GLMM)

$$logit(\hat{\phi}) = X\beta + U\zeta$$
$$y \sim Binomial(\hat{\phi})$$
$$\zeta \sim Normal(0, \sigma_{site})$$

How do I fit GLMMs?

- `glmer()` and `glmer.nb()` from `lme4` work for Binomial, Poisson, and Negative Binomial data

```
library(lme4)
glmm1 <- glmer.nb(y~x+(x|site),data=dat2) #Negative binomial GLMM
summary(glmm1) #glmer.nb takes a long time to run
```

- `glmmTMB()` from `glmmTMB` works for those above, *plus* a bunch of others (Zero-inflation, Beta-binomial), and it's generally faster

```
library(glmmTMB)
glmm2 <- glmmTMB(y~x+(x|site),data=dat2,family=nbinom2())
summary(glmm2) #Similar results, but quicker
```

Fitting GLMMs

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: Negative Binomial(5.1294) ( log )
## Formula: y ~ x + (x | site)
##    Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
##    627.8    646.3   -307.9    615.8      154
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.3745 -0.7098 -0.3946  0.5108  2.5367
##
## Random effects:
##  Groups Name        Variance Std.Dev. Corr
##  site   (Intercept) 1.43500  1.1979
##         x           0.02878  0.1697   0.92
## Number of obs: 160, groups: site, 16
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.32746    0.32166   1.018   0.3087
## x            0.10830    0.04681   2.314   0.0207 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##   (Intr)
## x 0.799
```

```
## Family: nbinom2  ( log )
## Formula:          y ~ x + (x | site)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
##    627.8    646.2   -307.9    615.8      154
##
## Random effects:
##
## Conditional model:
##  Groups Name        Variance Std.Dev. Corr
##  site   (Intercept) 1.43543  1.1981
##         x           0.02892  0.1701   0.92
## Number of obs: 160, groups: site, 16
##
## Dispersion parameter for nbinom2 family (): 5.12
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.34132    0.32172   1.061   0.2887
## x            0.11026    0.04697   2.348   0.0189 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual checks for LMMs/GLMMs

- Unfortunately, residual plotting functions aren't set up for mixed effects models. However, you can extract deviance residuals from `lmer`, `glmer`, or `glmmTMB` models and make your own plots:

- Added complication: **we also need to check whether the random effects are normally distributed**

```
#Example with LMMs (fish model from before)
devRes <- residuals(m2,type='deviance') #Get deviance residuals
m2RE <- ranef(m2)$sites #Get random effects (intercept + slope)
par(mfrow=c(2,2))
plot(fitted(m2),devRes,xlab='Fitted',ylab='Deviance residual',main='Residuals'); abline(h=0,lty=2)
qqnorm(devRes,main='Residual Q-Q'); qqline(devRes) #Deviance residual Q-Q
qqnorm(m2RE[,1],main='Intercepts Q-Q'); qqline(m2RE[,1]) #Intercepts
qqnorm(m2RE[,2],main='Slopes Q-Q'); qqline(m2RE[,2]) #Slopes Q-Q
par(mfrow=c(1,1))
```

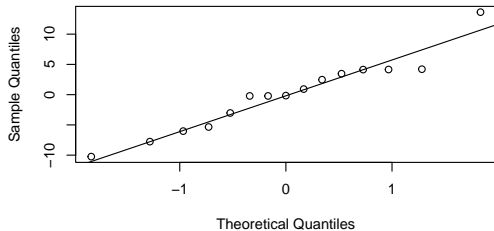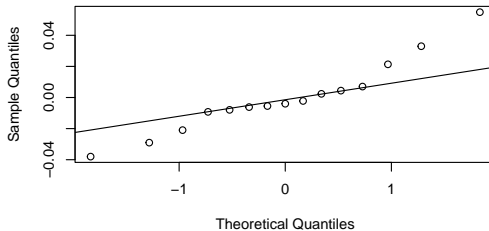# Residual checks for LMMs/GLMMs (cont.)
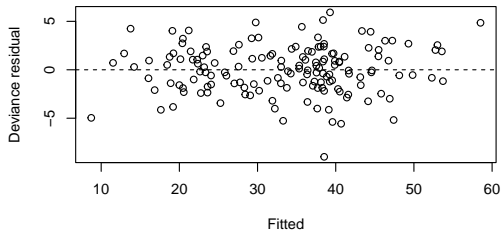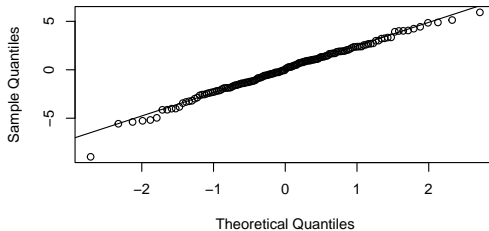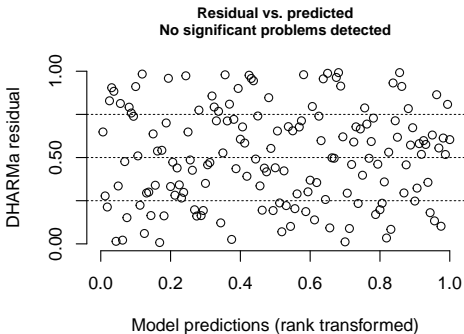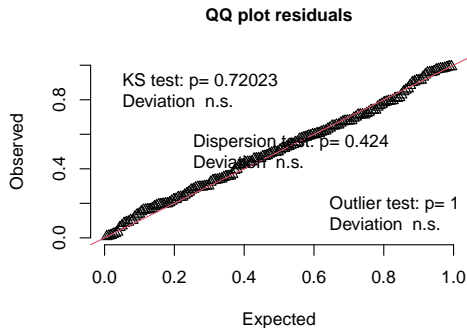
Alternative approach: simulation

- Residual plots can be misleading, and can hide information from you. A better way is to compare a set of *simulated data* from your model to the *actual data*
- The `simulateResiduals` from DHARMa (see here) works well for `glmmTMB` models, as well as LMs, GLMs, and more, so it's worth learning
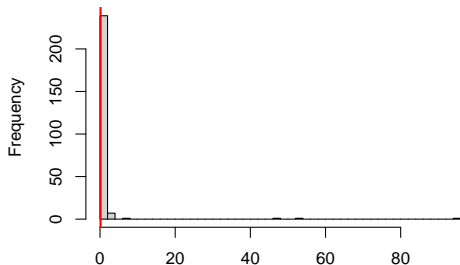

DHARMa residual

Simulation (cont.)

- `DHARMa` also has useful functions for checking overdispersion and zero-inflation. Both of these tests indicate that a) this model is not overdispersed, and b) there seems to be no zero-inflation (see here for more examples)
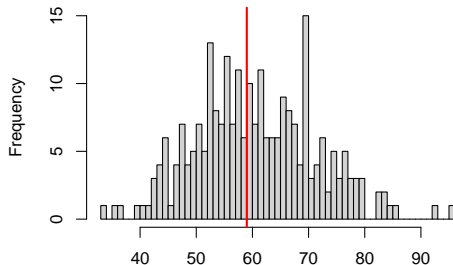

DHARMa nonparametric dispersion test via sd of residuals fitted vs. simulated

Simulated values, red line = fitted model. p−value (two.sided) = 0.4

DHARMa zero−inflation test via comparison to expected zeros with simulation under H0 = fitted model

Simulated values, red line = fitted model. p−value (two.sided) = 0.9

```
##
## DHARMa nonparametric dispersion test via sd of
## residuals fitted vs. simulated
```

```
##
## DHARMa zero-inflation test via comparison to expected
## zeros with simulation under H0 = fitted model
```
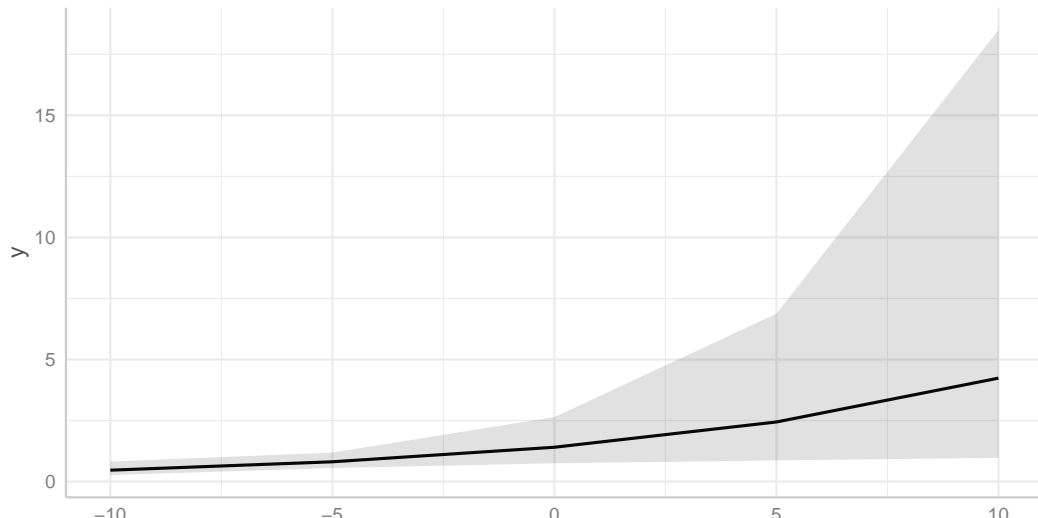
Partial residual plots for glmmTMB models

- ggpredict() from library(ggeffects) works with glmmTMB models

Predicted counts of y

Third challenge

- Remember that `canolaPlants.csv` data I gave you last week, which you all dutifully fit GLMs of? (See here)
- That `Field` column indicates which farmer's field the plants came from. You'll also notice that there are groupings at each `Distance`, indicating distinct `Plots` that each plant came from.
- Fit a GLMM of pod success with distance, using Field and Plot as random effects.
- Check the assumptions of your model with `DHARMa`.

Third challenge results

Big plants have proportionally more pods
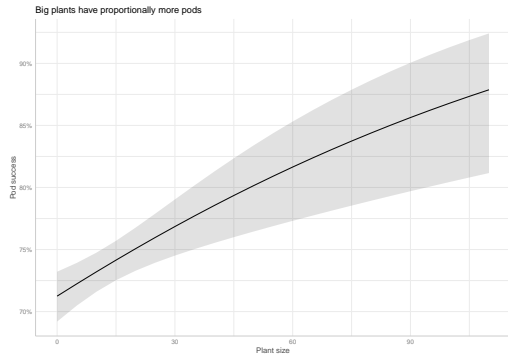
Third challenge results (cont.)

DHARMa residual
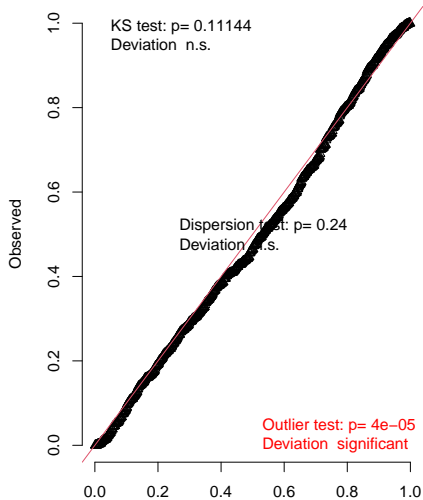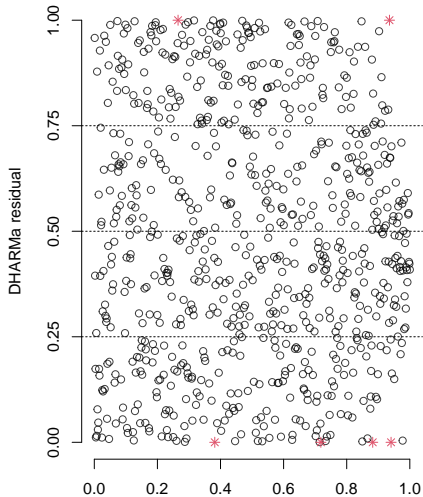
Third challenge results (cont.)

Outlier test significant
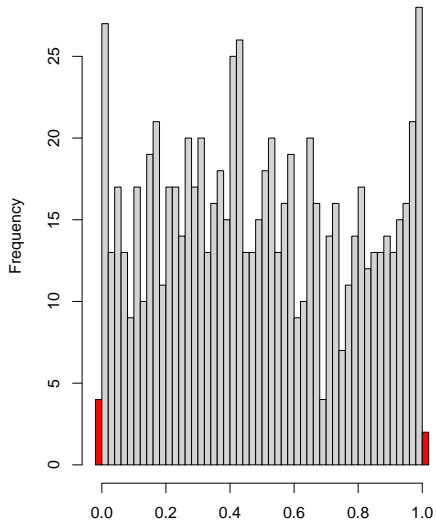
Histogram of frequBoot
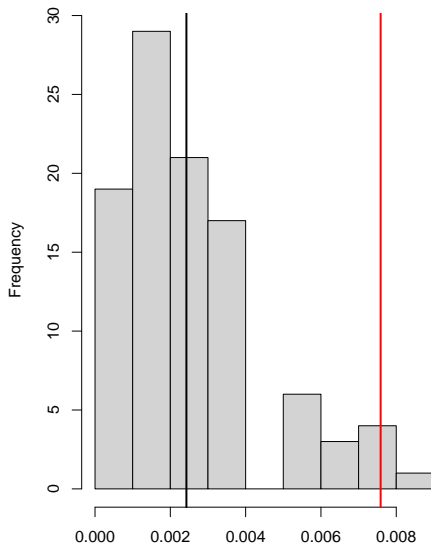
Third challenge results (cont.)

DHARMa nonparametric dispersion test via sd of residuals fitted vs. simulated
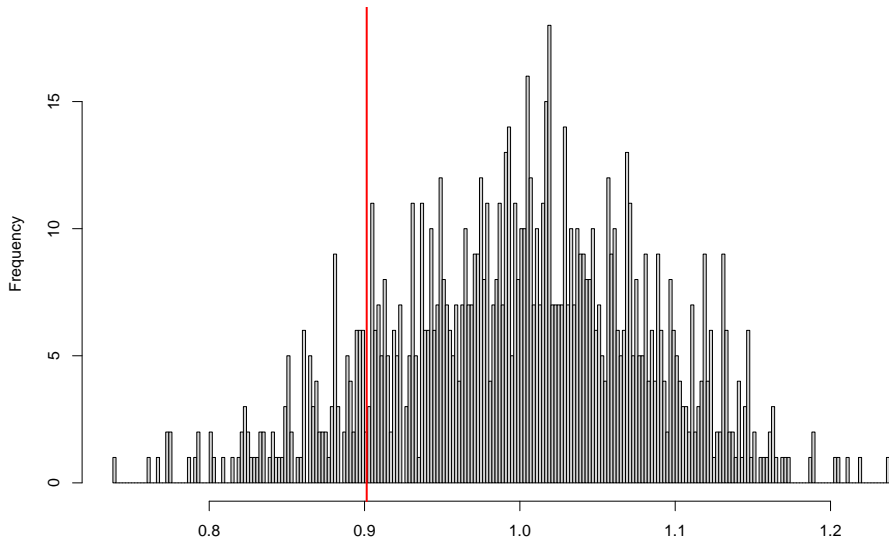
Part 3: Hypothesis testing and inference

I fit a model... now what?

- Congratulations, your model ran and it met the assumptions of regression...
- Time to see if your predictions are supported by your data!
- For each of the terms in your model:
  - Was the term "important" for your model?
  - If so, what direction was the effect in?
- How well did your model fit your data (overall)?
- Some other sage advice

Step 1: was the term "important"?

In linear models, this is done using an ANOVA F-test (also shown at the bottom of a `summary()` statement):

```
## Analysis of Variance Table
##
## Response: mpg
##            Df Sum Sq Mean Sq F value    Pr(>F)
## disp        1 808.89  808.89 73.9959 1.788e-09 ***
## gear        1   0.14    0.14  0.0132    0.9093
## Residuals  29 317.01   10.93
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

But wait, there's more!

Unfortunately, if we have more than 1 term in the model, the order of terms can change your answer:

- ```
  ## Analysis of Variance Table
  ##
  ## Response: mpg
  ##           Df Sum Sq Mean Sq F value    Pr(>F)
  ## disp       1 808.89  808.89 73.9959 1.788e-09 ***
  ## gear       1   0.14    0.14  0.0132    0.9093
  ## Residuals 29 317.01   10.93
  ## ---
  ## Signif. codes:
  ## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
  ```

- ```
  ## Analysis of Variance Table
  ##
  ## Response: mpg
  ##           Df Sum Sq Mean Sq F value    Pr(>F)
  ## gear       1 259.75  259.75 23.762 3.595e-05 ***
  ## disp       1 549.28  549.28 50.248 8.465e-08 ***
  ## Residuals 29 317.01   10.93
  ## ---
  ## Signif. codes:
  ## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
  ```

Solution: use a Type II ANOVA

- We're usually interested in the importance of a term on its own, *not just after other terms are accounted for* (Type I ANOVA).

- For this, we use a Type II ANOVA. This can be done using drop1() (or Anova() in the car package)

-
```
## Single term deletions
##
## Model:
## mpg ~ disp + gear
##       Df Sum of Sq    RSS    AIC F value    Pr(>F)
## <none>              317.01  79.383
## disp   1    549.28 866.30 109.552 50.2476 8.465e-08 ***
## gear   1      0.14 317.16  77.397  0.0132    0.9093
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

-
```
## Single term deletions
##
## Model:
## mpg ~ gear + disp
##       Df Sum of Sq    RSS    AIC F value    Pr(>F)
## <none>              317.01  79.383
## gear   1      0.14 317.16  77.397  0.0132    0.9093
## disp   1    549.28 866.30 109.552 50.2476 8.465e-08 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interactions make ANOVA testing a bit strange

- If interactions are present, it doesn't really make sense to test the main terms **because they depend on the interactions**

- For example:

```
## Single term deletions
##
## Model:
## mpg ~ gear * disp
##           Df Sum of Sq    RSS    AIC F value  Pr(>F)
## <none>                 278.60 77.250
## gear:disp  1   38.412 317.01 79.383 3.8604 0.05943 .
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Anova from the car package tests other terms *after* interactions, but the meaning isn't the same. I prefer to keep things simple and just use drop1()

```
## Anova Table (Type II tests)
##
## Response: mpg
##           Sum Sq Df F value    Pr(>F)
## gear        0.14  1  0.0145   0.90502
## disp      549.28  1 55.2038 4.312e-08 ***
## gear:disp  38.41  1  3.8604   0.05943 .
## Residuals 278.60 28
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

GLMs, LMMs, and GLMMs

- drop1 also works with GLMs, LMMs, and GLMMs, but we use a χ^2 *likelihood ratio test* rather than an F-test

- Unfortunately, different numbers of data points change your likelihood, so this can wreck LRTs. This happens a lot if you have NAs in your predictor columns, so *clean up your data before using it in models*.

```
drop1(m1,test='Chisq')
```

```
## Single term deletions
##
## Model:
## mass ~ species * forest - 1 + (1 | sites)
##                npar    AIC    LRT   Pr(Chi)
## <none>                806.04
## species:forest    2 932.51 130.47 < 2.2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ML vs REML - a mathematical aside

- Maximum likelihood (ML) estimates of variance (e.g. SD) are always smaller than the actual variance (biased)
- Restricted maximum likelihood (REML) uses a mathematical trick to get around this, but. . .
- This means that models with *different numbers of fixed effects* don't have the same REML estimates
- Likelihood between these models technically can't be compared!

Solution:

1. Use ML if comparing between models with different fixed effects, then. . .
2. Re-fit with REML once you've decided on a model

Step 2: what was the direction of the effect?

How do I know this effect is different from x? (Usually zero) - Use Wald Z-test (2-sided p-value from Z-test)

```
## x
## 0
```

- glht from library(multcomp) works with lmer models if you are comparing between coefficients (e.g. "Is treatment A different from B and C?")

Step 3: How well did your model fit your data?

In a simple linear model, a common measure of model fit is *adjusted R^2*, which can be found in the summary() statement

```
##
## Call:
## lm(formula = mass ~ species * forest - 1, data = fishDat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.6767 -3.1422  0.0415  3.3364 18.4631
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## speciesSpp1        35.57610    1.68256  21.144  < 2e-16 ***
## speciesSpp2        19.44039    1.12903  17.219  < 2e-16 ***
## speciesSpp3        47.91690    1.28769  37.212  < 2e-16 ***
## forest              0.01792    0.02413   0.743   0.4590
## speciesSpp2:forest  0.05348    0.03152   1.697   0.0919 .
## speciesSpp3:forest -0.13769    0.03187  -4.321 2.88e-05 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.468 on 144 degrees of freedom
## Multiple R-squared:  0.9766, Adjusted R-squared:  0.9756
## F-statistic:  1002 on 6 and 144 DF,  p-value: < 2.2e-16
```

How well did your model fit your data? (cont.)

- For GLMs, LMMs, and GLMMs, there isn't really one standard way to get "R^2". See here for a widely-read paper on the topic
- Likelihood Ratio Tests or AIC (*Akaike's Information Criterion*) can be used to compare between different models *of the same dataset*, but likelihood and AIC don't mean anything on their own
- Both `MuMIn` and `r2glmm` implement versions of the Nakagawa R^2 for mixed effects models. *Caveat emptor*:

```
## Warning: 'r.squaredGLMM' now calculates a revised statistic.       ##   Effect Rsq upper.CL lower.CL
## See the help page.                                                 ## 1  Model 0.96    0.969    0.951
```

```
##            R2m       R2c
## [1,] 0.7094007 0.9290197
```

Above all: avoid selecting models based on R^2 or AIC alone

Some final advice

- LMMs and GLMMs are *hard* to both understand and fit. They are not as forgiving as LMs and GLMs, and will often fail to fit, take a very long time, or give you very strange answers without any explanation.
  - Check the model output and make sure the coefficients and SEs aren't weirdly large or small
  - Andrew Gelman's Modeling Rule-of-Thumb: "It's not me, it's you!"
- My advice: Once you have a model you'd like to fit, start off with simpler "incorrect" version of it, and add terms until you have the final "correct" model
- In the canola model, I started off with a Field-level intercept, then added a Plot-level intercept, and finally a random slope term
- One of my interim models had a random `Distance` slope term, which caused the model to fail (reason: only 1 distance per plot!)