Mixed effects models 2
Even more bells and whistles

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Motivation

- How do I check if model results are valid?
  - Residual checks
  - Hypothesis testing
- What if my response variable is non-normal?
  - Generalized linear mixed models (GLMMs)
- Sampling over time or space
  - "Continuous" random effects
- Christmas-themed exercise!

# Mixed effect model example

Let's go back to our earlier example:

```
lmer(y ~ x + (x|site), data = dat)
```
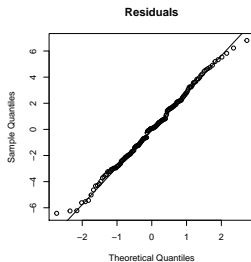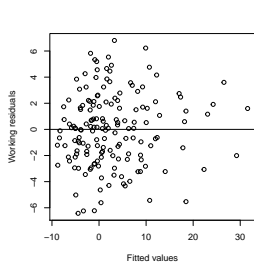
- We're interested in predicting y using x (fixed effects)
- Data was collected at a number of *sites*, which may affect y
- Effect of each site is normally distributed (random intercept)
- Effect of site on slope of x is normally distributed (random slope)
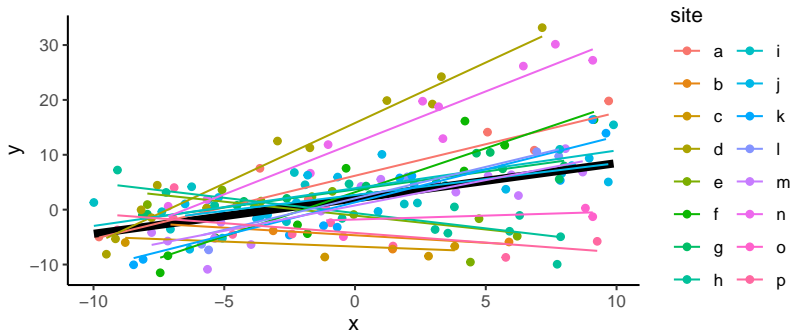
Validation

- Similar to linear models, but we *also* check whether the random intercepts are normally distributed
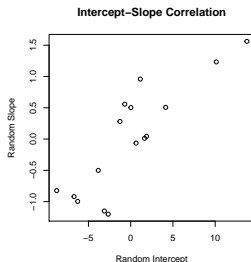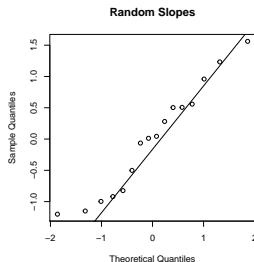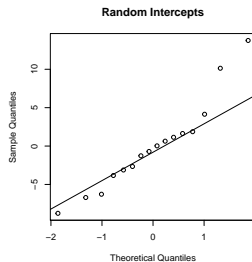
Hypothesis testing

Is this fixed effect important? (e.g. ANOVA)

- Use likelihood-based test via drop1 (likelihood ratio test, AIC)
- Be careful to fit model with REML = FALSE!

```
lmm1 <- update(lmm1,REML=FALSE) #Refit model using ML rather than REML
drop1(lmm1,test='Chisq') #x has a strong effect
```

```
## Single term deletions
##
## Model:
## y ~ x + (x | site)
##          npar    AIC     LRT   Pr(Chi)
## <none>          913.08
## x           1  917.85  6.7697  0.009272 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hypothesis testing (cont.)

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

```
##              x
## 0.004659069
```

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

What if my response variable is non-normal?

- Linear model (LM)

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

- Generalized linear model (GLM)

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

- 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 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 `library(lme4)` work for Binomial, Poisson, and Negative Binomial data

```
library(lme4)
glmm1 <- glmer.nb(y2~x+(x|site),data=dat) #Negative binomial GLMM
summary(glmm1) #glmer.nb takes a LONG time to run
```

- glmmTMB from `library(glmmTMB)` works for those above, *plus* a bunch of others
  - e.g. Zero-inflation, Beta-binomial, Spatial Models

```
library(glmmTMB)
glmm2 <- glmmTMB(y2~x+(x|site),data=dat,family=nbinom2())
summary(glmm2) #Similar results, but quicker
```

Fitting GLMMs - `glmer.nb`

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: Negative Binomial(5.1295)  ( log )
## Formula: y2 ~ x + (x | site)
##    Data: dat
##
##      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) 1.43502  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)  0.32745    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
```

Fitting GLMMs - `glmmTMB`

```
##  Family: nbinom2  ( log )
## Formula:          y2 ~ x + (x | site)
## Data: dat
##
##      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
##
## Overdispersion 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 on `glmmTMB` objects

- Extract residuals and make your own plots, or use `simulateResiduals` from `library(DHARMa)` (see here)
- DHARMa also has useful functions for checking overdispersion and zero-inflation (found here)

```
## This is DHARMa 0.3.3.0. For overview type '?DHARMa'. For recent changes, type news(package = 'DHARMa')
```

DHARMa residual diagnostics