MIxed Effect ANOVAs

Here we revisit an ANOVA you have already conducted as a a factorial, randomized block experiment. This experiment used whole wetlands as units in a 3-way factorial design, where treatments were:
- either intensive land use or seminatural lands,
- cattle were exclosed with fence or not), and
- prescribed fire applied or not (Boughton et al. 2015).

The goal is to evaluate the interactive effects of these common ranch practices on plant diversity (here $D = e^{H'}$ - see Jost (2006) for more details on how D is calculated). The plantdata06-15.csv data set lists species codes for each wetland (called ponds in the data), from 2006 (when only pasture treatments had been applied) through 2015. We want to calculate diversity (D). We can do that using the vegan package:

First import and attach the plantdata06-15.csv file. Below I assume you called it "data."

Now let's get D calculated. If not already installed, install and then load the vegan package. We will use the diversity command – if you read that in the Help or Package tab, you will see that it expects a simple data matrix, where unlabelled rows are matched with columns containing species' counts. If we are clever we can get R to get us just the diversity per row (i.e., a pond in each year).

```
ncol(data) # calculate the number of columns in data = 203
# we know from looking at data that non-species info is in columns 1-6. So we
calculate diversity on the other columns.
div <- diversity(data[7:203, index="shannon"]

# this calculates Shannon diversity. We want that as e raised to that power.
D <- exp(div)

# And because we want to re-connect the info in columns 1-6 with D, we can
bind D to the info (leaving all the species aside):

info <- data[1:6]
Ddata <- cbind(info, D) # to get our info columns and just D (leaving all the
species aside).
Ddata$fyear <- factor(year) # to make year a factor in Ddata
Ddata$fblock <- factor(block) # to make fence a factor in Ddata
Ddata$ffence <- factor(fence) # to make fence a factor in Ddata
Ddata$fburn <- factor(burn) # to make burn a factor in Ddata
```

Below we use dplyr, glmmADMB, and bbmle - so load those packages. Simple analyses in glmmADMB match simple lm but more advanced models are also possible.

```
library(dplyr) # to make selecting subsets easy
library(glmmADMB) # to run glm and glmm
library(bbmle) # for AICs
```

This command sets up ADMB to run plenty of iterations, if needed, plus some other controls

```
admbControl(impSamp=0,maxfn=10000,imaxfn=10000,maxph=5,noinit=FALSE,shess=FALS
E, run=TRUE, ZI_kluge=FALSE, poiss_prob_bound=FALSE)
```

Let's re-run a former ANOVA, where blocks were handled as fixed effects. We will be a wee bit advanced by using glm to adjust/test distribution assumptions, and focus on just 2009 (two years after all treatments had been applied).

```
yr2009 <- filter(Ddata, year == 2009)

fmodelgau <- glmmadmb(D ~ pasture*ffence*fburn + fblock, data=yr2009,
family="gaussian")
fmodelgam <- glmmadmb(D ~ pasture*ffence*fburn + fblock, data=yr2009,
family="gamma")
fmodelp <- glmmadmb(D ~ pasture*ffence*fburn + fblock, data=yr2009,
family="poisson")
fmodeln <- glmmadmb(D ~ pasture*ffence*fburn + fblock, data=yr2009,
family="nbinom")

AICctab(fmodelgau,fmodelgam,fmodelp,fmodeln, base=T,delta=T,weights=T)
```

Which distribution assumption works "best"?

summary(YOU FILL IN THE MODEL)

What pops out as a result?

Now we handle blocks as a random effect, rather than a fixed effect. We use glmmadmb again, and assume the gaussian model was most plausible above – if not, change it:

```
rmodelgau <- glmmadmb(D ~ pasture*ffence*fburn, random= ~1|fblock,
data=yr2009, family="gaussian")
```

Did treating blocks as random effects improve the "story"?

summary(YOU FILL IN THE MODEL)

So now let's include years as a second random factor. 2006 was a pasture-only year. Fences were installed in winter 2006-2007, and then fire was applied in winter 2007-2008. Fire has been applied periodically since, too. So we expect changes through time. Again, make the family match your choice.

```
tempmodel <- glmmadmb(D ~ pasture*ffence*fburn, random= ~ (1|fblock) + (1|
fyear), data=Ddata, family="gaussian")
```

Note that >1 random effect must be in ()

```
summary(tempmodel)
```

Near the bottom are estimates of random effect variance. Random effects contributed about 8% of the story in D, and blocks ~ 4%, using the StdDev column as a guide.

Finally, let's consider what would have happened if we mistakenly considered each year as an independent replicate, used a plain ol' lm (family="gaussian"), and didn't think of blocks.

```
wrongmodel <- glmmadmb(D ~ pasture*ffence*fburn, data=Ddata,
family="gaussian")
summary(wrongmodel)
```

Compare coefficients (effect sizes) and their std. errors among models. Are they different?
What about residual variance (leftover, unexplained variation)?
Also compare models for AICcs – which most parsimoniously explains the data, even if it was a bit more complicated to construct?

```
AICctab(wrongmodel,tempmodel, base=T,delta=T,weights=T)
```

Or compare models with analysis of deviance:

```
anova(tempmodel,wrongmodel)
```

Bottom Lines = The model that best captures variance best represents effects. Mixed effect models can represent a lot of variation that fixed effect models cannot. Expect to use mixed effect models!

References
- Boughton EH, et al. 2015. Interactive effects of pasture management intensity, release from grazing, and prescribed fire on forty subtropical wetland plant assemblages. J. Applied Ecology 53:159-170.
- Jost, L. 2006. Entropy and diversity. Oikos 113:363-375.