Linear Mixed Effects Regression

<2014.2.10>

AC's attempts at learning to do this in R.

Added package **lme4** to R. http://cran.r-project.org/web/packages/lme4/lme4.pdf

Also added **plyr** package, because it has a rename() function for renaming columns in a data frame: (http://www.cookbook-r.com/Manipulating_data/Renaming_columns_in_a_data_frame/)

However, I found it easier to do this:

```
colnames(x) <- c("name1","name2"...)
```

based on guidance from:

https://stat.ethz.ch/R-manual/R-devel/library/base/html/colnames.html

and from

http://cran.r-project.org/doc/manuals/r-devel/R-data.html

```
Column names can be given explicitly via the col.names; explicit names override
the header line (if present).
```

Added **arm** package: http://cran.r-project.org/web/packages/arm/index.html

```
arm: Data Analysis Using Regression and Multilevel/Hierarchical Models R
functions for processing lm, glm, svy.glm, merMod and polr outputs.
```

arm package provides the coefplot() function for plotting the regression coefficient values and std. errors.

Need to specify that subjects is a nominal variable, using the *factor* command:

http://www.statmethods.net/input/datatypes.html

```
Tell R that a variable is nominal by making it a factor. The factor stores the
nominal values as a vector of integers in the range [ 1… k ] (where k is the
number of unique values in the nominal variable), and an internal vector of
character strings (the original values) mapped to these integers.
```

Interpretation of glmer output

A nice description from:

https://stat.ethz.ch/pipermail/r-sig-mixed-models/2011q1/015590.html

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In this case the coefficient corresponds to one of the terms in the model and I would advocate performing a likelihood ratio test comparing the two models

```
fm <- glmer(SameSite~BreedSuc1+Sex+(1|Bird), family="binomial")
fm0 <- glmer(SameSite~Sex+(1|Bird), family="binomial")  # the null
hypothesis model
anova(fm0, fm)
```

Even though the function is called anova it will, in this case, perform a likelihood ratio test (LRT). It also prints the values of AIC and BIC if you prefer to compare models according to one of those criteria but I prefer using the likelihood ratio for nested models.

However, before doing that comparison you should ask yourself whether you want to compare models that have the, apparently unnecessary term for Sex in them. The way I would approach the model building is first to reduce the model to

```
fm1 <- lmer(SameSite~BreedSuc1+(1|Bird), family="binomial")
```

You could then compare

```
anova(fm1, fm)
```

which I presume will give a large p-value for the LRT, so we prefer the simpler model, fm1. After that, I would compare

```
fm2 <- lmer(SameSite ~ 1 + (1|Bird), family="binomial")
```

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