Proportion of Buttercups vs Different Treatments

2023-05-10

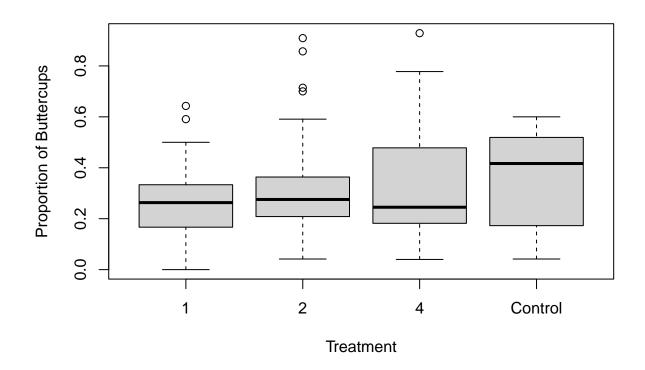
The following is an analysis on how different treatments impact the proportion of buttercups present in a paddock. Buttercups are recorded present if one or more buttercups are viable on the tip of the observers shoe after each step.

The Observer should be included as a random effect because different observers may introduce variance into the data due to factors such as the step size of the observer or their interpretation of what is meant by a weed being "exactly" at the tip of their shoe.

A binomial distribution is appropriate as it allows us to model the proportion of successes (steps with butter cup present) out of the total number of steps. This allows us to find the probability of finding a buttercup after each step.

library(lme4)

Loading required package: Matrix



```
mod1 <- glmer(y ~ Trt + Farm + (1|Observer), data = data, family = binomial)</pre>
mod2 <- glmer(y ~ Trt + (1|Observer) + (1|Farm), data = data, family = binomial)</pre>
mod3 <- glmer(y ~ Trt + (1|Observer) + (1|Farm:Plot),data = data, family = binomial)</pre>
anova(mod1, mod2, mod3)
## Data: data
## Models:
## mod2: y ~ Trt + (1 | Observer) + (1 | Farm)
## mod3: y ~ Trt + (1 | Observer) + (1 | Farm:Plot)
## mod1: y ~ Trt + Farm + (1 | Observer)
                       BIC logLik deviance Chisq Df Pr(>Chisq)
##
        npar
                AIC
## mod2
           6 482.23 498.16 -235.12
                                      470.23
## mod3
           6 478.51 494.44 -233.26
                                      466.51 3.7174 0
           9 477.48 501.36 -229.74
                                      459.48 7.0362 3
## mod1
                                                          0.07075 .
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
summary(mod1) #Best model
```

Generalized linear mixed model fit by maximum likelihood (Laplace

Approximation) [glmerMod]
Family: binomial (logit)

Data: data

##

Formula: y ~ Trt + Farm + (1 | Observer)

```
##
        AIC
##
                 BIC
                        logLik deviance df.resid
                        -229.7
                                  459.5
##
      477.5
               501.4
##
##
   Scaled residuals:
##
                                      3Q
        Min
                   10
                        Median
                                              Max
                       0.02078
##
   -2.37497 -0.88004
                                0.67377
                                          3.02819
##
##
  Random effects:
##
    Groups
             Name
                          Variance Std.Dev.
    Observer (Intercept) 0.04433 0.2105
   Number of obs: 105, groups: Observer, 5
##
##
## Fixed effects:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.30669
                            0.18257
                                      -7.157 8.24e-13 ***
## Trt2
                0.15889
                            0.12930
                                       1.229
                                               0.2191
## Trt4
                0.21855
                            0.12847
                                       1.701
                                               0.0889
## TrtControl
                                       1.433
                0.22587
                            0.15760
                                               0.1518
## FarmB
                0.19313
                            0.19957
                                       0.968
                                               0.3332
## FarmF
               -0.31136
                            0.20704
                                      -1.504
                                               0.1326
## FarmR
                -0.39467
                            0.21223
                                      -1.860
                                               0.0629 .
                0.05252
                                       0.270
## FarmS
                            0.19425
                                               0.7869
                   0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## Signif. codes:
##
## Correlation of Fixed Effects:
##
              (Intr) Trt2
                             Trt4
                                    TrtCnt FarmB
                                                   FarmF
                                                          FarmR
              -0.356
## Trt2
## Trt4
              -0.355
                       0.525
## TrtControl -0.300
                       0.427
                              0.430
## FarmB
              -0.598 -0.004 -0.009
                                     0.006
## FarmF
              -0.567 -0.021 -0.022 -0.002
                                             0.723
              -0.555 -0.015 -0.020 -0.011
                                             0.707
## FarmR
                                                    0.679
## FarmS
              -0.605 -0.012 -0.016 -0.006
                                             0.767
                                                    0.736
```

Model1 which includes observer as a random effect and treatment and farm as fixed effects is the best model. This is because it has the lowest AIC meaning it has the best tradeoff between goodness of fit and model complexity.

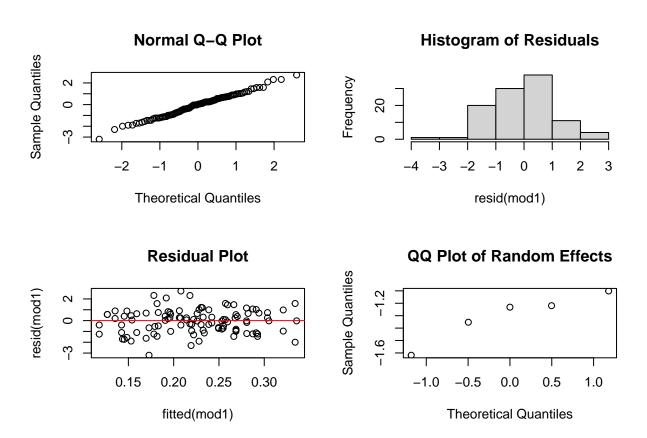
The scaled residuals look good because the median is close to 0 (0.0208) and the 1st and 3rd quartile are reasonably symetric.

The random effect coefficient of 0.044 suggests there are differences between observers when determining if a buttercup is found at the end of a step. This introduces variance into our data which we need to account for.

The fixed effects all have insignificant p-values. This means there is no significant difference between treatments in each farm. The regression equation is log odds of finding buttercup = -1.307 + (0.159 x trt2) + (0.219 x trt4) + (0.226 x control) + (0.193 x farmB) + (-0.311 x farmF) + (-0.395 x farmR) + (0.053 x farmS).

my overall conclusion is that there is no significant difference between treatments in the farms. Our original plot did not show a clear difference between the groups. This observation was backed up by generalised linear mixed effects models coefficients.

```
par(mfrow=c(2,2))
qqnorm(resid(mod1), main="Normal Q-Q Plot")
hist(resid(mod1), main="Histogram of Residuals")
plot(fitted(mod1), resid(mod1), main = "Residual Plot")
abline(0,0, col='red')
qqnorm(coef(mod1)$Observer[,1], main="QQ Plot of Random Effects")
```



The residuals appear to be normally distributed as the residuals can be fit to a straight line in our Normal Q-Q plot and create a bell curve shape in our Histogram of Residuals. The residuals are scattered above and bellow 0 in the Residual plot so we can assume there is constant variance between the residuals.

The points in the QQ Plot of Random Effects can be fit to a striaght line. This menas we can assume our random effects are normally distributed.