

Appendix B

R_code - GLM Randomization

```
#Set up data frame
data.name<-read.delim("filename.txt")
names(data.name)
library(car)
pairs(with(data.name,cbind(var.1,var.2,var.3,var.4,...)))
#Run Generalized Linear Model
model.name<-with(data.name,glm(response.variable~var.1+var.2+var.3+var.4+...,family=family))
plot(fitted(model.name),resid(model.name))
#Evaluate assumptions - independence, homogeneity, straight line, and normal error
lag.plot(resid(model.name),diag=FALSE,do.lines=FALSE)
qqnorm(resid(model.name))
qqline(resid(model.name))
#Check link function for over/under fitting
plot(fitted(model.name),with(data.name,response.variable))
abline(lm(with(data.name,response.variable)~fitted(model.name)))
coef(lm(with(data.name,response.variable)~fitted(model.name)))
#Check dispersion. deviance/df < 4 ?
deviance(model.name)
df.residual(model.name)
deviance(model.name)/df.residual(model.name)
#Obtain adjusted delta deviance and capture chi statistic for each term in model
Anova(model.name,type="III")
exp.chi<-data.frame(data.frame(Anova(model.name,type="III"))[,1])
#Capture randomized statistic for each term in model
rand.chi<-
data.frame(rbind(replicate(####,c(data.frame(with(data.name,Anova(glm(sample(response.variable,##,FALSE)~va
r.1+var.2+var.3+var.4+...,family=family),type="III"))[,1])))
#Calculate right tail p-value for each term in model
summary(c(rand.chi[1,])>exp.chi[1,])
summary(c(rand.chi[2,])>exp.chi[2,])
summary(c(rand.chi[...])>exp.chi[...])

# NEGATIVE BINOMIAL VARIANT
library(MASS)
model.name<-with(data.name,glm.nb(response.variable~var.1+var.2+var.3+var.4+...,link=link))
rand.chi<-
data.frame(rbind(replicate(####,c(data.frame(with(data.name,Anova(glm.nb(sample(response.variable,##,FALSE)
~var.1+var.2+var.3+var.4+..., link=link),type="III"))[,1])))

# RANDOMIZED SELECTION OF AUTHORSHIP
sample(c(1:6),6,FALSE)
```