

```
setwd("~/Documents/Working Directory/PNAS")
rm(list=ls())
```

```
#####
```

```
# Libraries #
```

```
#####
```

```
library("tidyverse")
```

```
library("rjags")
```

```
library("coda")
```

```
library("matrixStats")
```

```
library("ggplot2")
```

```
#####
```

```
# #
```

```
# 1. PREPARE CR REARING DATA #
```

```
# #
```

```
#####
```

```
#####
```

```
# Read in Data #
```

```
#####
```

```
file<-read.csv( "CostRica.csv", header=TRUE)
```

```
file<-subset(file, lepgen!="Eois" & lepgen!= "Quadrus")
```

```
#####
```

```
# Plot ("plot" or "gencol") ####
```

```
#####
```

```

#Designate factor called "collect_method" which has two levels "plot" or "gencol"
#Plot means data was collected from standardized plot
#gencol means data was collected via haphazard collection
file$collect_method<- ifelse(grepl("plot", file$loc, ignore.case = F), "plot", "gencol")
file$collect_method[grepl("succ plot",file$loc, ignore.case = F)]<-"gencol"
file$collect_method[grepl("trial plot",file$loc, ignore.case = F)]<-"gencol"

#subset and read out df
file<- file[,c("ID", "loc", "date", "day", "month", "year", "lepsz", "lepfam", "collect_method", "lepgen")]

#####
# file: Add super family column
#####
file$superfam[file$lepfam=="Bombycidae"]<-"Bombycoidea"
file$superfam[file$lepfam=="Depressariidae"]<-"Gelechioidea"
file$superfam[file$lepfam=="Gracillariidae"]<-"Gracillarioidea"
file$superfam[file$lepfam=="Limacodidae"]<-"Zygaenoidea"
file$superfam[file$lepfam=="Notodontidae"]<-"Noctuoidea"
file$superfam[file$lepfam=="Pieridae" ]<-"Papilionoidea"
file$superfam[file$lepfam=="Thyrididae"]<-"Thyridoidea"
file$superfam[file$lepfam=="Apatelodidae"]<-"Bombycoidea"
file$superfam[file$lepfam=="Choreutidae"]<-"Choreutoidea"
file$superfam[file$lepfam=="Erebidae" ]<-"Noctuoidea"
file$superfam[file$lepfam=="Hedylidae" ]<-"Hedyloidea"
file$superfam[file$lepfam=="Lycaenidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="Nymphalidae" ]<-"Papilionoidea"
file$superfam[file$lepfam=="Pyralidae"]<-"Pyraloidea"
file$superfam[file$lepfam=="Tortricidae"]<-"Tortricoidea"
file$superfam[file$lepfam=="Arctiidae"]<-"Noctuoidea"

```

```

file$superfam[file$lepfam=="Choruetidae"]<-"Choreutoidea"
file$superfam[file$lepfam=="Gelechiidae"]<-"Gelechioidea"
file$superfam[file$lepfam=="Hesperidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="megalopygidae"]<-"Zygaenoidea"
file$superfam[file$lepfam=="Ocophoridae"]<-"Gelechioidea"
file$superfam[file$lepfam=="Riodinidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="Uraniidae"]<-"Geometroidea"
file$superfam[file$lepfam=="Arctiinae"]<-"Noctuoidea"
file$superfam[file$lepfam=="Cossidae"]<-"Cossoidea"
file$superfam[file$lepfam=="Geometridae"]<-"Geometroidea"
file$superfam[file$lepfam=="Hesperiidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="Noctuidae"]<-"Noctuoidea"
file$superfam[file$lepfam=="Oecophoridae"]<-"Gelechioidea"
file$superfam[file$lepfam=="Saturniidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="Yponomeutidae"]<-"Yponomeutoidea"
file$superfam[file$lepfam=="Artiidae"]<-"Noctuoidea"
file$superfam[file$lepfam=="Crambidae"]<-"Pyraloidea"
file$superfam[file$lepfam=="Glyphipterigidae"]<-"Yponomeutoidea"
file$superfam[file$lepfam=="Lasiocampidae"]<-"Lasiocampoidea"
file$superfam[file$lepfam=="Nolidae"]<-"Noctuoidea"
file$superfam[file$lepfam=="Papilionidae"]<-"Papilionoidea"
file$superfam[file$lepfam=="sphingidae"]<-"Bombycoidea"
file<-droplevels(file)
file$superfam<-as.factor(file$superfam)

```

#----Get an idea of how many samples per super family so that we can create minimum threshold to be included in study

```
temp <-
```

```
file%>%
```

```
filter(!is.na(superfam))%>%
group_by(year, superfam) %>%
dplyr::summarize(freq = n())
```

```
ggplot(temp, aes(x=year, y=freq, colour=superfam)) +
  geom_point() +
  geom_smooth(method=lm, se=FALSE)+
  facet_wrap(~superfam)
```

```
#Remove (removed below) the following family bc these superfamilies were samped only 1-3 years:
#Yponomeutoidea, Hedyloidea, Gracillarioidea, Cossoidea
```

```
#Remove the following family bc these superfamilies were samped only 1-3 years:
#Yponomeutoidea, Hedyloidea, Gracillarioidea, Cossoidea
```

```
file<- file[!(file$superfam %in% c("Yponomeutoidea", "Hedyloidea", "Gracillarioidea", "Cossoidea")),]
file<-droplevels(file)
```

```
year<-file
month_df<-file
```

```
#####
# Summarise frequency table
#####
```

```
#----ANNUAL SUMMARY
a_year <-
year%>%
filter(!is.na(superfam))%>%
group_by(year, superfam) %>%
dplyr::summarize(freq = n())
```

```
p_year <-  
  year%>%  
  filter(collect_method=="plot", !is.na(superfam))%>%  
  group_by(year, superfam) %>%  
  dplyr::summarize(freq = n())
```

```
g_year <-  
  year%>%  
  filter(collect_method=="gencol", !is.na(superfam))%>%  
  group_by(year, superfam) %>%  
  dplyr::summarize(freq = n())
```

#-----MONTHLY SUMMARY

#-----Count of super fam freq per month and collection method

```
month_df <-  
  month_df%>%  
  filter(!is.na(superfam))%>%  
  group_by(year, month, collect_method) %>%  
  dplyr::summarize(freq = n())
```

```
all_methods <-  
  month_df%>%  
  group_by(year, month) %>%  
  dplyr::summarize(freq = sum(freq))  
all_methods$collect_method<- "all"  
month<-rbind(as.data.frame(month_df), as.data.frame(all_methods))
```

```
#####  
# #  
# 4. BAYESIAN ANALYSES #  
# #  
#####
```

```
dat<-a_year  
temp<-dat  
dat$freq <- as.numeric(scale(log(dat$freq)))  
dat$year <- as.numeric(scale(dat$year))  
dat<-dat[ which( ! dat$year %in% NA ) , ]  
  
library("rjags")  
library("coda")  
library("matrixStats")  
## put into list format jags wants  
dataForJags <- list(freq=dat$freq, year=dat$year, superfam=dat$superfam,  
Ncol=length(levels(dat$superfam)), N=length(dat$freq))  
  
## specify model, priors etc.  
model <- "model{  
for(i in 1:N){  
freq[i] ~ dnorm(alpha[i], tau)  
alpha[i] <- mu[superfam[i]] + beta1[superfam[i]]*year[i]  
}  
# coefficients for individual collection_method (conditional priors)
```

```

for(j in 1:Ncol){
beta1[j] ~ dnorm(beta1mu, beta1tau)
mu[j] ~ dnorm(mumu, mutau)
}
tau ~ dgamma(0.1,0.1)

# hyperpriors for coefficients
beta1mu ~ dnorm(0,0.001)
mumu ~ dnorm(0,0.001)

# hyperpriors for precisions
beta1tau ~ dgamma(0.1,0.1)
mutau ~ dgamma(0.1,0.1)
}"

## compile
mod1 <- jags.model(textConnection(model),data= dataForJags,n.chains=2)

## run it
samples<-jags.samples(model= mod1,variable.names=c("beta1","mu","beta1mu","mumu",
"beta1tau","mutau","tau"),n.iter=1000000)

#take beta1mu (coefficient and 95%CI for highest level of heirarchy) to later ass to caterpillar plot
keyBits <-round(quantile(samples$beta1mu[,,],probs=c(0.5,0.1,0.9)),3)

#Calculate probability of Negative slope
probNeg<-as.vector(samples$beta1mu[,,1])
probNeg <- length(probNeg[probNeg<0]) / length(as.vector(samples$beta1mu[,,1]))

vec <- data.frame(site= "CR", superfam= "Overall Beta Coefficient", mid=keyBits[1], lower=keyBits[2],
upper=keyBits[3], probNeg=probNeg)

```

vec

```
#### generate a table of genus-specific slopes and intervals
```

```
mid <- NA
```

```
lower <- NA
```

```
upper <- NA
```

```
probNeg <- NA
```

```
res <- samples$beta1
```

```
for(i in 1:length(levels(dat$superfam))){
```

```
  sub <- res[i,,]
```

```
  mid[i] <- quantile(sub,0.5)
```

```
  upper[i] <- quantile(sub,0.9)
```

```
  lower[i] <- quantile(sub,0.1)
```

```
  probNeg[i] <- length(sub[sub<0]) / length(sub)
```

```
  print(i)
```

```
}
```

```
new <- data.frame(levels(dat$superfam),mid,lower,upper, probNeg)
```

```
new <- new[order(new$mid,decreasing=T),]
```

```
colnames(new)[1] <- "superfam"
```

```
new$site<- "CR"
```

```
new<-rbind(new, vec)
```

```
#hist(new$mid, col="green",xlim=c(-0.2, 0.0001))
```

```
head(new)
```

```
write.csv(new, "new.csv")
```

```
#####
```

```
#
```

```
#
```

```
#
```

```
4. GRAPHS
```

```
#
```

```
#
```

```
#
```



```
#####
```

```
#####
```

```
# Caterpillar Plot
```

```
#
```

```
#####
```

```
#Use for a_year
```

```
new$border_color <- c(rep("#3B94ED", 1), rep("#00008B", 10), "#1B1E23")
```

```
new$fill_color <- c(rep("#3B94ED", 1), rep("#00008B", 10), "#1B1E23")
```

```
#Use for p_year
```

```
new$border_color <- c(rep("#51B700", 9), rep("#3B94ED", 3), "#1B1E23")
```

```
new$fill_color <- c(rep("#51B700", 9), rep("#3B94ED", 3), "#1B1E23")
```

```
#Use for g_year
```

```
new$border_color <- c(rep("#3B94ED", 2), rep("#00008B", 10), "#1B1E23")
```

```
new$fill_color <- c(rep("#3B94ED", 2), rep("#00008B", 10), "#1B1E23")
```

```
quartz(width=7,height=9)
```

```
## plot those point estimates and credible intervals in caterpillar plot
```

```
layout(matrix(c(1,1,1,2,1,1,1,3,1,1,1,4,1,1,1,5,1,1,1,6),5,4,byrow=T))
```

```
par(mar=c(5,1,0,5))
```

```
par(oma=c(12,0,1,4))
```

```
plot(new$mid,12:1,yaxt="n",ylab="",xlab="",xlim=c(-1,0.5),ylim=c(1,12),cex.axis=2, cex=3, font=2,  
cex.lab=5, pch=21,col=new$border_color, bg= alpha(new$fill_color, 0.7), lwd=2)
```

```
mtext("Change in Annual Frequency",1,line=2.5,cex=1.5, font= 2)
```

```
arrows(new$lower, 12:1, new$upper, 12:1,length=0,lwd=2, col=new$border_color)
```

```
abline(v=0,lty=2)
```

```
axis(4,labels= new$superfam,at=12:1,las=2,cex.axis=2,font=2,tck=-0.02)
grid(nx=10,ny=20)
```

```
#####
```

```
# Box Plot: Monthly Freq Across Years
```

```
#
```

```
#####
```

```
# Box Plot: Monthly Freq Across Years
```

```
# purple: plot
```

```
# blue: gencol
```

```
# forest green= all
```

```
cr <-
```

```
  month%>%
```

```
  group_by(year, collect_method) %>%
```

```
  dplyr::summarize(mean=mean(freq), sd=sd(freq), n=n_distinct(month))
```

```
cr <-
```

```
  cr%>%
```

```
  group_by(year, collect_method ) %>%
```

```
  dplyr::mutate( se=(sd/sqrt(n)))
```

```
cr$mean<-scale(cr$mean)
```

```
cr$se<-scale(cr$se)
```

```
cr$sd[is.na(cr$sd)] <- 0
```

```
cr$year<-as.factor(cr$year)
```

```
lvls<-levels(cr$year)
```

```
ggplot(cr, aes(x=as.factor(year), y=mean, color= collect_method))+  
  geom_pointrange(aes(ymin = mean-se, ymax = mean+se, color=  
collect_method),position=position_jitterdodge(-2),alpha=0.8, size=0.75)+  
  scale_x_discrete(limits=lvls,breaks=lvls[seq(1,length(lvls),by=2)])+  
  scale_color_manual(values = c( "#000000", "#CDCDCD", "#878787"))+  
  labs( x="", y=expression(paste("Frequency of Encounter")))+  
  theme_classic()+  
  theme(axis.text.x = element_text(face= "bold", size= 20, angle=18, hjust = 1),  
        axis.text.y =element_text(face= "bold", size=20),  
        axis.title.x= element_text( size = rel(2.5)),  
        axis.title.y= element_text( size = rel(2.5)))
```