#LOAD MGCV AND MASS

require(mgcv)

require(MASS)

#LOAD MONTHLY DATA FOR ONE SEROTYPE

TEMP0<-read.csv("TEMP0.csv", header = TRUE)

# COUNT = REPORTED CASES

#FYR = FISCAL YEAR

#FMO = FISCAL MONTH

#LN\_POP = NATURAL LOGARITHM(POPULATION OF ORIGINAL FOODNET SITES)

# GENERALIZED POISSON MONTHLY DATA

#ORIGINAL SITES: COUNT ~ FYR FMO

M0<-gam(COUNT~s(FYR, k = 6, fx =FALSE, bs ="ps", m = c(2,2))+

s(FMO, k = 6, fx =FALSE, bs ="ps", m = c(2,2)),

family = poisson(link = log), data = TEMP0, method="GCV.Cp",

offset = LN\_POP, scale = -1)

summary(M0)

p0<-predict(M0, type = "link", se.fit = TRUE)

lpfit0<-p0$fit

write(lpfit0,file="lpfit0.csv",ncolumns=1, sep = ",")

lpsefit0<-p0$se.fit

write(lpsefit0,file="lpsefit0.csv",ncolumns=1, sep = ",")

#LOAD ANNUAL DATA FOR ONE SEROTYPE

TEMP1<-read.csv("TEMP1.csv", header = TRUE)

# COUNT = REPORTED CASES

#YEAR = CALENDAR YEAR

#LN\_POP = NATURAL LOGARITHM(POPULATION OF ORIGINAL FOODNET SITES)

#GENERALIZED POISSON ANNUAL DATA

#ORIGINAL SITES: COUNT ~ YEAR

M1<-gam(COUNT~s(YEAR, k = 6, fx =FALSE, bs ="ps", m = c(2,2)),

family = poisson(link = log), data = TEMP1, method="GCV.Cp",

offset = LN\_POP, scale = -1)

summary(M1)

p1<-predict(M1, type = "link", se.fit = TRUE)

lpfit1<-p1$fit

write(lpfit1,file="lpfit1.csv",ncolumns=1, sep = ",")

lpsefit1<-p1$se.fit

write(lpsefit1,file="lpsefit1.csv",ncolumns=1, sep = ",")