

```

anmo <- read.table("antemortem.csv",sep="," ,header=TRUE)

names(anmo)

[1] "provincie" "x.gekalfd" "kleur.ras" "totaal" "SHC" "NHC" [7] "am1SHC" "am1NHC"
"am2SHC" "am2NHC" "am3SHC" "am3NHC"

#

attach(anmo)

anmo1 <- anmo[,c(1:4,7,8)]
anmo2 <- anmo[,c(1:4,9,10)]
anmo3 <- anmo[,c(1:4,11,12)]

#

names(anmo1)[5:6] <- c("shc","nhc")
names(anmo2)[5:6] <- c("shc","nhc")
names(anmo3)[5:6] <- c("shc","nhc")

#

am <- rep(1,length(anmo1$shc))
anmo1 <- data.frame(anmo1,am)
am <- rep(2,length(anmo2$shc))
anmo2 <- data.frame(anmo2,am)
am <- rep(3,length(anmo3$shc))
anmo3 <- data.frame(anmo3,am)

#

anmo.l <- rbind(anmo1,anmo2,anmo3)
names(anmo.l)

[1] "provincie" "x.gekalfd" "kleur.ras" "totaal" "shc" "nhc"
[7] "am"

#

anmo.l <- anmo.l[!(anmo.l$nhc==0&anmo.l$shc==0),]

detach(anmo)

attach(anmo.l)

table(anmo.l$nhc,anmo.l$am)

#

```

```

xgekalfd <- cut(x.gekalfd, c(0,3,7,11),include.lowest = TRUE)

fit.0 <-
glm(cbind(nhc,shc)~factor(provincie)+factor(kleur.ras)+factor(xgekalfd)+factor(am):factor(kleur.ras)+
factor(am):factor(provincie)+factor(am):factor(xgekalfd),family=binomial,data=anmo.l)

drop1(fit.0)

summary(fit.0)

cbind(exp(confint(fit.0))[17:22,],exp(coef(fit.0)[17:22]))

tapply(nhc/(nhc+shc),list(am,provincie),mean)

tapply(fitted.values(fit.0),list(provincie,am),mean)

tapply(fitted.values(fit.0),list(kleur.ras+1,am),mean)

tapply(fitted.values(fit.0),list(x.gekalfd,am),mean)

tapply(fitted.values(fit.0),list(x.gekalfd),mean)

##

fit.0 <-
glm(cbind(nhc,shc)~factor(am)+factor(provincie)+factor(kleur.ras)+x.gekalfd+factor(am):factor(provi
ncie)+factor(am):factor(kleur.ras),family=binomial)

summary(fit.0)

drop1(fit.0,test="Chisq")

exp(confint(fit.0))

detach(anmo.l)

#####

attach(anmo)

fit.x <- glm(x.gekalfd~factor(provincie)+factor(kleur.ras),family=poisson,weight=totaal)

drop1(fit.x,test="Chisq")

summary(fit.x)

confint(fit.x)

exp(summary(fit.x)$coef[1:14])

detach(anmo)

#####

attach(anmo.l)

names(anmo.l)

[1] "provincie" "x.gekalfd" "kleur.ras" "totaal"  "shc"

```

```

[6] "nhc"    "am"

#####

am1s <- anmo[,c(1:4,7)]
names(am1s)[5] <- "amneg"
ns<-rep(0,432)
am1s <- cbind(am1s,ns)
#####

am1n <- anmo[,c(1:4,8)]
names(am1n)[5]<-"amneg"
ns<-rep(1,432)
am1n <- cbind(am1n,ns)
#####

am2s <- cbind(anmo[,1:4],anmo[,9]+anmo[,11])
names(am2s)[5]<-"ampos"
ns<-rep(0,432)
am2s <- cbind(am2s,ns)
#####

am2n <- cbind(anmo[,1:4],anmo[,10]+anmo[,12])
names(am2n)[5]<-"ampos"
ns<-rep(1,432)
am2n <- cbind(am2n,ns)

```