####Relative Risk and Odds Ratio Disease Model

#Where “experimental” refers to corals exposed to disease homogenate

#Where “control” refers to corals exposed to healthy homogenate

#RRISK refers to relative risk

#OR refers to odds ratio

# Where “a” is the proportion of experimental corals with disease

# Where “b” is the proportion of experimental corals with no disease

# Where “c” is the proportion of control corals with disease

# Where “d” is the proportion of control corals without disease

# Where “h” is the total number of experimental corals with disease

# Where “r” is the total number of experimental corals

# Where “l” is the total number of control corals with disease

# Where “m” is the total number of control corals

model

{

for (i in 1:k) {

#Prior

a[i] ~dbeta(1,1)

c[i] ~dbeta(1,1)

# Likelihood

h[i] ~ dbin(a[i],r[i])

l[i] ~ dbin(c[i],m[i])

RRISK[i] <- a[i]/c[i]

OR[i]<- (a[i]/(1-a[i]))/(c[i]/(1-c[i]))

lnOR[i]<-log(OR[i])

ppos[i]<-step(OR[i]-1)

}

}

##Ofav by genotype

Data list(k=10,

h = c(3,5,4,2,3,1,3,3,3,4),

r=c(12,12,12,12,12,12,12,12,12,12),

l = c(0,0,0,0,0,0,0,0,0,0),

m=c(12,12,12,12,12,12,12,12,12,12))

##Pcli by genotype

Data list(k=3,

h = c(7,3,3),

r=c(12,12,12),

l = c(0,0,0),

m=c(12,12,12))

##Ofav by treatment: control, oa, ow, oaow

Data list(k=4,

h = c(14,3,2,12),

r=c(30,30,30,30),

l = c(0,0,0,0),

m=c(30,30,30,30))

##Pcli by treatment: control, oa, ow, oaow

Data list(k=4,

h = c(4,1,5,3),

r=c(9,9,9,9),

l = c(0,0,0,0),

m=c(9,9,9,9))

##Ofav by genotype by treatment: control

Data list(k=10,

h = c(3,2,2,1,0,0,2,1,2,2),

r=c(3,3,3,3,3,3,3,3,3,3),

l = c(0,0,0,0,0,0,0,0,0,0),

m=c(3,3,3,3,3,3,3,3,3,3))

##Ofav by genotype by treatment: OA

Data list(k=10,

h = c(0,1,0,0,1,0,1,0,0,0),

r=c(3,3,3,3,3,3,3,3,3,3),

l = c(0,0,0,0,0,0,0,0,0,0),

m=c(3,3,3,3,3,3,3,3,3,3))

##Ofav by genotype by treatment: OW

Data list(k=10,

h = c(0,0,0,0,1,0,0,1,0,0),

r=c(3,3,3,3,3,3,3,3,3,3),

l = c(0,0,0,0,0,0,0,0,0,0),

m=c(3,3,3,3,3,3,3,3,3,3))

##Ofav by genotype by treatment: OAOW

Data list(k=10,

h = c(1,2,3,1,0,0,0,0,3,2),

r=c(3,3,3,3,3,3,3,3,3,3),

l = c(0,0,0,0,0,0,0,0,0,0),

m=c(3,3,3,3,3,3,3,3,3,3))

model

{

for (i in 1:k) {

#Prior

a[i] ~dbeta(1,1)

c[i] ~dbeta(1,1)

# Likelihood

h[i] ~ dbin(a[i],r[i])

l[i] ~ dbin(c[i],m[i])

RRISK[i] <- a[i]/c[i]

OR[i]<- (a[i]/(1-a[i]))/(c[i]/(1-c[i]))

lnOR[i]<-log(OR[i])

ppos[i]<-step(OR[i]-1)

}

}

##Pcli by genotype by treatment: Control

Data list(k=3,

h = c(2,1,1),

r=c(3,3,3),

l = c(0,0,0),

m=c(3,3,3))

##Pcli by genotype by treatment: OA

Data list(k=3,

h = c(1,0,0),

r=c(3,3,3),

l = c(0,0,0),

m=c(3,3,3))

##Pcli by genotype by treatment: OW

Data list(k=3,

h = c(3,1,1),

r=c(3,3,3),

l = c(0,0,0),

m=c(3,3,3))

##Pcli by genotype by treatment: OAOW

Data list(k=3,

h = c(1,1,1),

r=c(3,3,3),

l = c(0,0,0),

m=c(3,3,3))