

Adv_Covariates_part2

Eleftherios Meletis

Sonja Hartnack

Procedure

- Data file in data_emidfin
 - Script files
 - Init files
-
- 1) Put all files in the same working directory
 - 2) Run the model in Jags with the file «tojags.R»
 - 3) Analyse the .txt files

Data file (echinococcus in fecal samples foxes)

- 300 obs
- 3 tests for echinococcus:
 - Necropsy (sp = 1)
 - PCR
 - Elisa
- Binary covariate
 - Taenia (yes/no)
- Ones

```
N<-
300

m.short <-
  structure(c(0L, 1L, 0L, 0L, 0L, 1L, 0L, 1L, 0L, 1L,
              1L, 1L, 1L, 0L, 0L, 1L, 1L, 1L, 1L, 1L,
              1L, 0L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L,
              1L, 0L, 0L, 0L, 0L, 0L, 1L, 1L, 1L, 1L,
              1L, 0L, 0L, 1L, 0L, 0L, 0L, 1L, 0L, 0L,
              1L, 1L, 1L, 1L, 1L, 1L, 0L, 1L, 0L, 0L,
              0L, 0L, 0L, 0L, 1L, 1L, 0L, 0L, 0L, 0L,
              0L, 1L, 1L, 0L,
              ...

              0L, 0L, 0L, 1L, 0L, 1L, 0L, 0L, 0L),
  .Dim = c(300L, 6L), .Dimnames = list(NULL,
  c("Necropsy", "PCR", "ELISA_olddiff",
    "Sex", "Age", "Cestodes")))
```

[illegible]

Model files: with and without a covariate

- Similar to model yesterday
- Save it as a .bug file

```
# model developed initially by Fraser Lewis
```

```
var p[N], q[N,8], pr[N], L[N], checks[N,16];
```

```
model {
```

```
  for(i in 1:N){
```

```
    q[i,1]<-pr[i]*(s1*s2*s3+covs12+covs13+covs23)  
    +(1-pr[i])*((1-c1)*(1-c2)*(1-c3)+covc12+covc13+covc23);
```

```
    q[i,2]<-pr[i]*(s1*s2*(1-s3)+covs12-covs13-covs23)  
    +(1-pr[i])*((1-c1)*(1-c2)*c3+covc12-covc13-covc23);
```

```
    q[i,3]<-pr[i]*(s1*(1-s2)*s3-covs12+covs13-covs23)  
    +(1-pr[i])*((1-c1)*c2*(1-c3)-covc12+covc13-covc23);
```

```
    q[i,4]<-pr[i]*(s1*(1-s2)*(1-s3)-covs12-covs13+covs23)  
    +(1-pr[i])*((1-c1)*c2*c3-covc12-covc13+covc23);
```

```
    q[i,5]<-pr[i]*((1-s1)*s2*s3-covs12-covs13+covs23)  
    +(1-pr[i])*(c1*(1-c2)*(1-c3)-covc12-covc13+covc23);
```

```
    q[i,6]<-pr[i]*((1-s1)*s2*(1-s3)-covs12+covs13-covs23)  
    +(1-pr[i])*(c1*(1-c2)*c3-covc12+covc13-covc23);
```

```
    q[i,7]<-pr[i]*((1-s1)*(1-s2)*s3+covs12-covs13-covs23)  
    +(1-pr[i])*(c1*c2*(1-c3)+covc12-covc13-covc23);
```

```
    q[i,8]<-pr[i]*((1-s1)*(1-s2)*(1-s3)+covs12+covs13+covs23)  
    +(1-pr[i])*(c1*c2*c3+covc12+covc13+covc23);
```

Avoid mirror and include covariate

```
L[i]<- equals(valid[i],1)*(  
  equals(m.short [i,1],1)*equals(m.short[i,2],1)*equals(m.short [i,3],1)*q[i,1]  
+ equals(m.short [i,1],1)*equals(m.short[i,2],1)*equals(m.short [i,3],0)*q[i,2]  
+ equals(m.short [i,1],1)*equals(m.short[i,2],0)*equals(m.short [i,3],1)*q[i,3]  
+ equals(m.short [i,1],1)*equals(m.short[i,2],0)*equals(m.short [i,3],0)*q[i,4]  
+ equals(m.short [i,1],0)*equals(m.short[i,2],1)*equals(m.short [i,3],1)*q[i,5]  
+ equals(m.short [i,1],0)*equals(m.short[i,2],1)*equals(m.short [i,3],0)*q[i,6]  
+ equals(m.short [i,1],0)*equals(m.short[i,2],0)*equals(m.short [i,3],1)*q[i,7]  
+ equals(m.short [i,1],0)*equals(m.short[i,2],0)*equals(m.short [i,3],0)*q[i,8]  
) +(1-equals(valid[i],1)) *(1e-14);
```

```
#logit(pr[i])<-intercept+slope*m.short[i,6];
```

```
pr[i]<-prc
```

```
## this is a trick as per winbugs manual to allow a bespoke likelihood to be used  
## - since in a bernoulli density an observation of 1 has a likelihood of p[i]  
p[i] <- L[i] / 1;## divided by a constant just to ensure all p's <1  
ones[i] ~ dbern(p[i]);
```

```
}
```

```
##### ERROR CHECKING since (0,1) bounds could be exceeded
```

```
checks[i,1]<- s1*s2*s3+covs12+covs13+covs23;  
checks[i,2]<- (1-c1)*(1-c2)*(1-c3)+covc12+covc13+covc23;  
checks[i,3]<- s1*s2*(1-s3)+covs12-covs13-covs23;  
checks[i,4]<- (1-c1)*(1-c2)*c3+covc12-covc13-covc23;  
checks[i,5]<- s1*(1-s2)*s3-covs12+covs13-covs23;  
checks[i,6]<- (1-c1)*c2*(1-c3)-covc12+covc13-covc23;  
checks[i,7]<- s1*(1-s2)*(1-s3)-covs12-covs13+covs23;  
checks[i,8]<- (1-c1)*c2*c3-covc12-covc13+covc23;  
checks[i,9]<- (1-s1)*s2*s3-covs12-covs13+covs23;  
checks[i,10]<- c1*(1-c2)*(1-c3)-covc12-covc13+covc23;  
checks[i,11]<- (1-s1)*s2*(1-s3)-covs12+covs13-covs23;  
checks[i,12]<- c1*(1-c2)*c3-covc12+covc13-covc23;  
checks[i,13]<- (1-s1)*(1-s2)*s3+covs12-covs13-covs23;  
checks[i,14]<- c1*c2*(1-c3)+covc12-covc13-covc23;  
checks[i,15]<- (1-s1)*(1-s2)*(1-s3)+covs12+covs13+covs23;  
checks[i,16]<- c1*c2*c3+covc12+covc13+covc23;
```

```
valid[i]<- step(1-q[i,1])*step(q[i,1])*  
  step(1-q[i,2])*step(q[i,2])*  
  step(1-q[i,3])*step(q[i,3])*  
  step(1-q[i,4])*step(q[i,4])*  
  step(1-q[i,5])*step(q[i,5])*  
  step(1-q[i,6])*step(q[i,6])*  
  step(1-q[i,7])*step(q[i,7])*  
  step(1-q[i,8])*step(q[i,8])*  
  step(1-checks[i,1])*step(checks[i,1])*  
  step(1-checks[i,2])*step(checks[i,2])*  
  step(1-checks[i,3])*step(checks[i,3])*  
  step(1-checks[i,4])*step(checks[i,4])*  
  step(1-checks[i,5])*step(checks[i,5])*  
  step(1-checks[i,6])*step(checks[i,6])*  
  step(1-checks[i,7])*step(checks[i,7])*
```

Modify priors

```
covs12 ~ dunif(-1,1);
covs13 <- 0;
covs23 <- 0;
covc12 <- 0;
covc13 <- 0;
covc23 <- 0;
prc ~ dbeta(37.9836,31.2593);      # Prev 95%; >0.45, m 0.55
c1 <- 1;                          # SP necropsy
c2 ~ dbeta(1,1);                  # SP PCR
c3 ~ dbeta(1,1);                  # SP ELISA
s1 ~ dbeta(99.6983,6.1946);        # SE necropsy 95%, >0.9, m 0.95
s2 ~ dbeta(37.9836,31.2593);      # SE PCR 95%, >0.5, m 0.55
s3 ~ dbeta(1,1);                  # SE ELISA
#intercept~dnorm(0,0.001);
#slope~dnorm(0,0.001);

logL<-sum(log(p[1:N]));

}
```

Script files and init files

- Script file
 - thinning
 - monitor
 - Output txt files

- Init file

```
model in model1.bug
data in data_emidfin.R
load dic
compile, nchains(1)
parameters in inits1.R, chain(1)
initialize
update 5000, by(1000)
monitor prc, thin(10)
monitor c1, thin(10)
monitor c2, thin(10)
monitor c3, thin(10)
monitor s1, thin(10)
monitor s2, thin(10)
monitor s3, thin(10)
monitor deviance, thin(10)
monitor covs12, thin(10)
monitor covs13, thin(10)
monitor covs23, thin(10)
monitor covc12, thin(10)
monitor covc13, thin(10)
monitor covc23, thin(10)
#monitor slope, thin(10)
#monitor intercept, thin(10)
update 20000, by(1000)
coda *, stem("model1.without")
```

```
".RNG.name" <- "base::Mersenne-Twister"
".RNG.seed" <- 100022
```

Run model in jags

- tojags

```
setwd("C:\\Users\\admin\\Documents\\COST\\cestode")

library(rjags)

# first run models without a covariate

system("jags script1.without.R");
system("jags script2.without.R");
system("jags script3.without.R")
```


Analyse

- Summarise posteriors
- Trace plots
- Obtain OR and prevalences in Taenia pos and Taenia neg

Analyse

- Read posterior values in

```
library(coda);  
  
# analysis for model without covariates  
res1 <- read.coda("model1.withoutchain1.txt",  
                  "model1.withoutindex.txt");  
res2 <- read.coda("model2.withoutchain1.txt",  
                  "model2.withoutindex.txt");  
res3 <- read.coda("model3.withoutchain1.txt",  
                  "model3.withoutindex.txt");
```

Analyse posteriors

```
all<-mcmc.list(res1,res2,res3);  
plot(all)
```

```
par(mfrow=c(1,1))  
plot(density(c(res1[, "s1"])),col="red");  
lines(density(c(res2[, "s1"])),col="darkgreen");  
lines(density(c(res3[, "s1"])),col="blue");
```

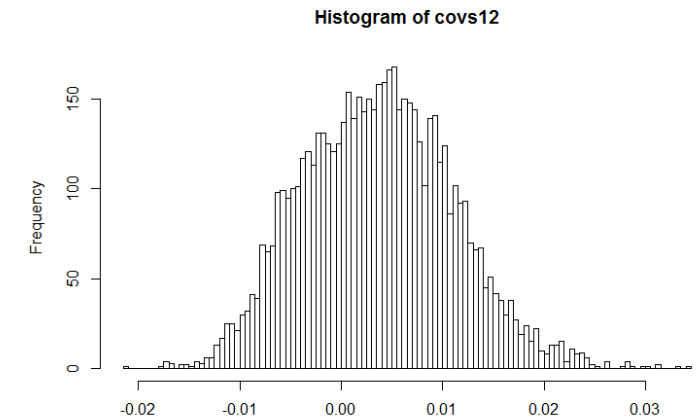
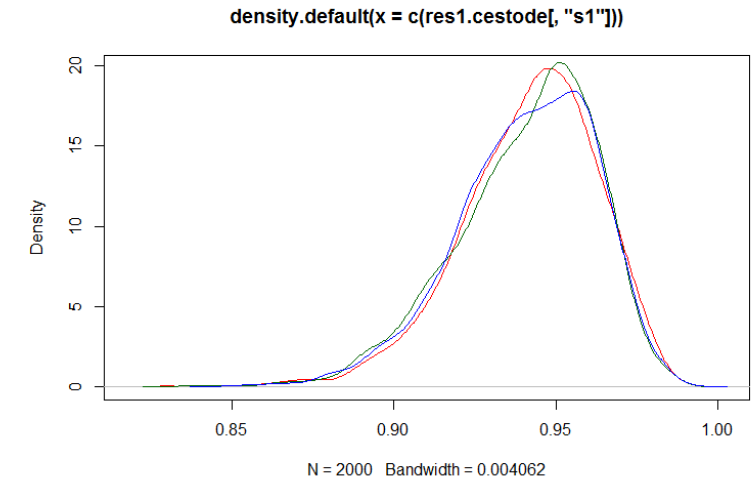
```
cbind(prettyNum(apply(rbind(res1),2,mean)))  
cbind(prettyNum(apply(rbind(res2),2,mean)))  
cbind(prettyNum(apply(rbind(res3),2,mean)))
```

```
cbind(prettyNum(apply(rbind(res1,res2,res3),2,mean)))
```

```
t(apply(rbind(res1),2,quantile,probs=c(0.025,0.975)))  
t(apply(rbind(res2),2,quantile,probs=c(0.025,0.975)))  
t(apply(rbind(res3),2,quantile,probs=c(0.025,0.975)))
```

```
t(apply(rbind(res1,res2,res3),2,quantile,probs=c(0.025,0.975)))
```

```
hist(c(res1[, "covs12"],  
      res2[, "covs12"],  
      res3[, "covs12"]),100,  
      main="Histogram of covs12",xlab="")
```



Analyse covariate effect

```
# for OR
comb[15] # slope
exp(as.numeric(comb[15])) # OR

# prevalence in Taenia neg. population
comb[16] # intercept
exp(as.numeric(comb[16]))

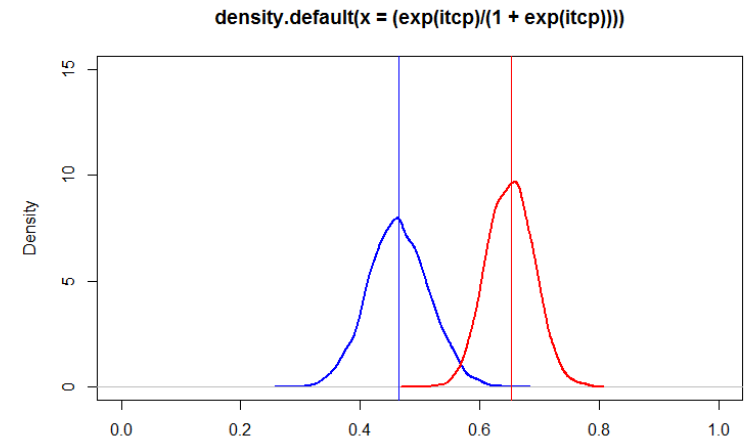
PrTneg <- exp(as.numeric(comb[16]))/(1+exp(as.numeric(comb[16])))

# prevalence in Taenia pos. population
exp(as.numeric(comb[15])+as.numeric(comb[16]))

PrTpos <- exp(as.numeric(comb[15])
             +as.numeric(comb[16]))/(1+exp(as.numeric(comb[15])+as.numeric(comb[16])))
```

```
#Plot for effect of taenia on prevalence
slopd<-cbind(res1.cestode[, "slope"],
             res2.cestode[, "slope"],
             res3.cestode[, "slope"]);
itcp<-cbind(res1.cestode[, "intercept"],
            res2.cestode[, "intercept"],
            res3.cestode[, "intercept"]);

plot(density((exp(itcp)/(1+exp(itcp)))),
     col="blue",ylim=c(0,15),xlim=c(0,1),xlab="",lwd=2);
lines(density((exp(itcp+slopd)/(1+exp(itcp+slopd)))),
     col="red",lwd=2)
abline(v = PrTneg, col = "blue")
abline(v = PrTpos, col = "red")
```



Open questions

- Now, just the prevalence varies with the covariate
 - Need to let simultaneously vary se and sp ?