Occupancy models

Bayesian statistics 9 – latent variable modelling

Frédéric Barraquand (CNRS, IMB)

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- Often arise in the context of modelling your observations with two submodels
- Full model = Observation submodel + Process submodel (hidden)

A Hollywood archeology example

Indy & Lara criss-cross the Amazonian jungle in search of artefacts from hidden civilizations. They have a map with 100 x 100 km quadrats. In each quadrat, there could be cultural signs but these may not be visible. Thus we consider a probability of detection p. We want to know how rich the region is, i.e., what is the probability that a quadrat is truly occupied ψ.

Figure 1: Upper Amazon - screenshot Google Earth

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- We number the site $i \in \{1, .., I\}$.
- Variable $X_{it} = 1$ if there was an artefact observed at time t in site i, 0 otherwise. They visit the sites at various times.
- Variable Z_i is the latent state, i.e., has value 1 there truly an artefact within quadrat i.

What is the model?

[Pen & paper moment]

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Solution. For all i

$$X_{it}|Z_i \sim \text{Bernoulli}(Z_i p)$$

$$Z_i \sim \text{Bernoulli}(\psi)$$

Is that OK?

One can prove this is equivalent to

$$X_{it} \sim \text{Bernoulli}(p\psi)$$

(btw: true with binomial not just Bernoulli variables)

Problem: $p\psi$ is just one parameter.

Proof: $\mathbb{P}(X_{it} = 1) = \mathbb{P}(X_{it} = 1 | Z_i = 1)\mathbb{P}(Z_i = 1) + \mathbb{P}(X_{it} = 1 | Z_i = 0)\mathbb{P}(Z_i = 0) = p \times \psi + 0 \times (1 - \psi)$

Better occupancy model

i site index in $\{1, ..., I\}$

t visit index in $\{1, ..., T\}$

$$X_{it}|Z_i \sim \text{Bernoulli}(Z_i p)$$

$$Z_i \sim \text{Bernoulli}(\psi)$$

'Robust design': T repeats within each site i. Parameters identifiable now.

(McKenzie et al. 2002)

Simulating the occupancy model

```r
#set.seed(42)
I <- 250;
T <- 10;
p <- 0.4;
psi <- 0.3;

z <- rbinom(I,1,psi); # latent occupancy state
y <- matrix(NA,I,T);  # observed state
for (i in 1:I){  y[i,] <- rbinom(T,1,z[i] * p);}
```

JAGS/BUGS modelling

```
occupancy.data <- list(y=rowSums(y), T=T,nsite=I)

cat(file="occupancy.txt","
model {

  # Priors
    p~dunif(0,1)
    psi~dunif(0,1)

  # Likelihood
    for(i in 1:nsite){
      mu[i] <- p*z[i]
      z[i] ~ dbern(psi)
      y[i] ~ dbin(mu[i],T)
      }
    n<-sum(z[])
    }
")
```

Running the model I

```
# Inits function
inits <- function(){list(p = runif(1, 0, 1),
                         psi = runif(1,0,1), z = rep(1, I))}
# we need to initialize z
# see https://bcss.org.my/tut/bayes-with-jags-a-tutorial-for-wildlife-researchers/oc

# Parameters to estimate
params <- c("p","psi")

# MCMC settings
nc <- 3  ;  ni <- 2000  ;  nb <- 1000  ;  nt <- 2

# Call JAGS, check convergence and summarize posteriors
out <- jags(occupancy.data, inits, params, "occupancy.txt", n.thin = nt,
            n.chains = nc, n.burnin = nb, n.iter = ni)
```

Running the model II

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 250
##    Unobserved stochastic nodes: 252
##    Total graph size: 758
##
## Initializing model
```

```
print(out, dig = 3)     # Bayesian analysis
```

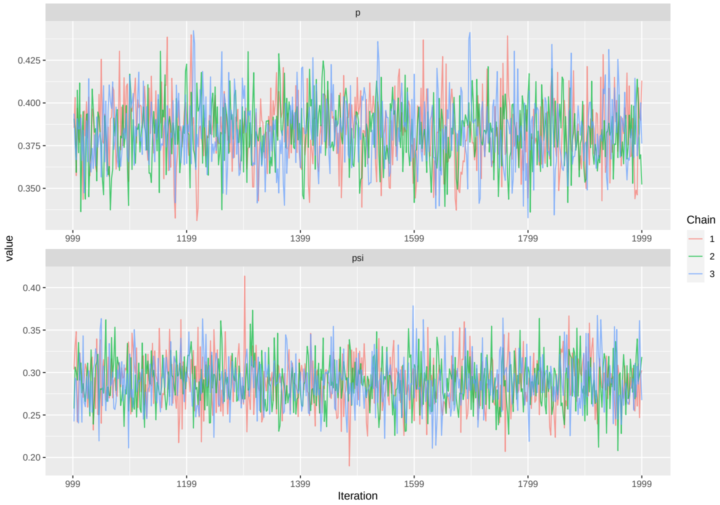
```
## Inference for Bugs model at "occupancy.txt", fit using jags,
##  3 chains, each with 2000 iterations (first 1000 discarded), n.thin = 2
##  n.sims = 1500 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%   97.5% Rhat n.eff
## p          0.383   0.019   0.345   0.370   0.382   0.395   0.420    1  1500
## psi        0.288   0.028   0.235   0.269   0.288   0.306   0.348    1  1500
## deviance 253.374   7.743 246.516 246.887 249.236 257.038 273.418    1  1500
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
```

Running the model III

```
## pD = 30.0 and DIC = 283.4
## DIC is an estimate of expected predictive error (lower deviance is better).
```

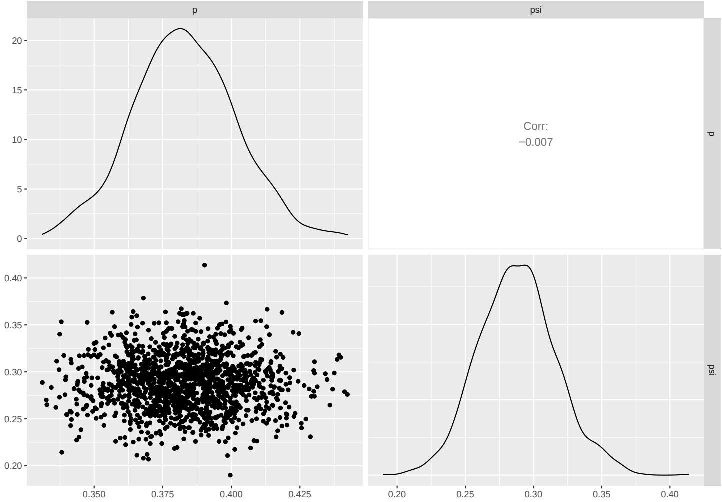
Showing traceplots

```
S<-ggs(as.mcmc(out)) #R2jags
S<-filter(S,Parameter != "deviance")
ggs_traceplot(S)
```



Showing correlations (p,ψ)

```
ggs_pairs(S)
```



Adding covariates

Possible to add covariates on detection probability

$p_{it} = \text{logistic}(\alpha_{k[i]} + \beta \times \text{survey duration}_{it})$

or

$\text{logit}(p_{it}) = \ln(\frac{p_{it}}{1-p_{it}}) = \alpha_{k[i]} + \beta \times \text{survey duration}_{it}$

Covariates on occupancy probability, e.g.

$\psi_i = \text{logistic}(\alpha_\psi + \beta_\psi \times \text{population density}_i)$

Real-life example

FIGURE 13.4 The remarkable "blue bug", the cerambycid beetle *Rosalia alpina*, Switzerland, 2009 (Photograph by T. Marent).

Figure 2: Bluebug *Rosalia alpina* from Kéry (2010)

The dataset

- 27 sites (woodpiles), 6 replicated counts for each.
- Covariates: `forest_edge` (edge or more interior), `date`, `hour` (date and hour of day, both of these are control variables)
- Detection at 10 of 27 woodpiles and from 1 to 5 times
- Questions:
  - Have some bluebugs been likely missed in some sites?
  - How many times should one visit a woodpile?
  - Effect of forest edge? (bluebugs are a typical forest species)