Models with false positive detections

OUTLINE

- Basic concepts and motivation
- Extending the basic occupancy model: a building block for false positives (Royle and Link 2006)
- The integrated model of Miller et al. (2011)

  `unmarked` function `occuFP`
- Sample level models – detection frequencies (Chambert et al. 2017)
- Next gen models: integrating the classification process with the ecological (occupancy) model

Models with false positive detections

- A basic occupancy model assumes that there are no false positives. A detection is a valid detection (i.e., y = 1 means the species occurs with certainty!)
- This can be incorrect. E.g., observers are highly variable in skill level (e.g., imagine citizen science schemes) and thus errors can be made
- Contemporary context: New technologies that are interpreted automatically (ML/AI) produce errors!
  - ✓ Acoustic monitoring
  - ✓ Camera trapping
  - ✓ eDNA

False positives

Why do we care?

- Even small rates of false positives produce large bias in parameter estimates.
- Unfortunate property of sampling with false positives: $\hat{\psi} \rightarrow 1$ as $nreps$ increases
- Therefore, attempts should be made to address FPs
  - Conservative thinning threshold (e.g., PID in genetics)
  - Expert validation of detections
  - Models that allow false positives!

A basic model

- The traditional occupancy model
$$y_i \sim Bern(p * z_i)$$
  - This implies no false positives. Effective detection probability = 0 if $z = 0$
- Extension to allow false positives:
$$y_i \sim Bern(p * z_i + p_{fp} * (1 - z_i))$$
  - Interpretation: if a site is occupied you detect the species with probability p but if a site is unoccupied you detect the species with probability p_{fp}
  - Royle and Link (Ecology, 2006)

Royle-Link model

- You can estimate both p and p_{fp} from ordinary occupancy data with an important caveat (see next)

- But note: it is a model of “site classification” not a model of “sample classification” so it is not exactly coherent with respect to how surveys are done (which record sample level data and aggregate those up to the site)
  - How do you scale sample level detections up to the site level? (we talk about this later)

The caveat: multi-modality

- This observation model allowing for false positives is precisely a finite mixture model such as the type of model that was made popular in ecological statistics by Norris and Pollock (1996), Pledger (2000), and others for modeling detection heterogeneity in capture-recapture models.

- A well-known feature of such models is that the likelihood is inherently multi-modal (i.e., does not have a unique solution). The likelihood for the parameter values (p, p_{fp}, ψ) is the same as $\left(p_{fp},\ p, 1-\psi\right)$

- This gets really, really complicated in multiple dimensions! (with > 2 classes). Imagine a CT study with 20 species, or acoustic monitoring study with 100 species of birds.

The caveat: multi-modality

- One solution to this is to impose a sensible constraint: $p_{11} > p_{10}$ i.e., the probability of detecting the species at an occupied site is greater than an unoccupied site (embarrassingly we wrote this wrongly in the chapter!). Constraints become complicated when there are > 2 classes!

- As such, it is especially important to control for extraneous heterogeneity in detection when false positives are of direct interest. In other words, unmodeled heterogeneity can "look like" false positives and vice versa. Fitzpatrick et al. (2009) provide an illustration of this phenomenon (heterogeneity due to variable abundance of an invasive insect).

- The other way to deal with multi-modality is to have some "perfect" information (Miller et al. 2011). i.e., validation data.

R template: simulation and model fitting (see script)

```
# Build the unmarkedFrame
summary(umf <- unmarkedFrameOccuFP(y = y, type = type))
umf.occ<- unmarkedFrameOccu(y=y) # Not used

# Using these starting values will find the wrong mode.
largerp10 <- qlogis(c(0.5, 0.1, 0.7))  # Order is psi, p, fp

# These starting values are consistent with our preferred
constraint
largerp11 <- qlogis(c(0.5, 0.7, 0.1))

# Fit the model
(m1 <- occuFP(detformula = ~1,  # model for p_11
       FPformula = ~1,          # model for p_10
       stateformula = ~1,       # model for psi
       data = umf,              # umarkedFrameOccuFP object
       starts = largerp11) )    # add p_10 < p_11 constraint
```

Miller’s multi-state model

A general modeling framework that integrates data of 3 different types:

- Type 1 data: ordinary occupancy data, false negatives but no false positives
- Type 2 data: ordinary occupancy data, but contaminated with random false positives (i.e., Royle-Link)
- Type 3 data: Positive observations are a mix of uncertain positives and confirmed positives. So, there is some confirmation mechanism going on behind the curtain.

They describe an integrated, multi-state model for data that are a mix of these different types.

Type 3 data

- For Type 3 data we code the observations as 0, 1 or 2 (by convention)
  - 0 = not detected
  - 1 = uncertain detection (could be FP). E.g., scat or sign, citizen sighting
  - 2 = certain detection (true positive). E.g., visual or trained expert.
- Values of 2 arise by some confirmation mechanism by which a subset of sites where detections occurred become confirmed positives…

Type 3 data

- Type 3 data have a multinomial likelihood conditional on z

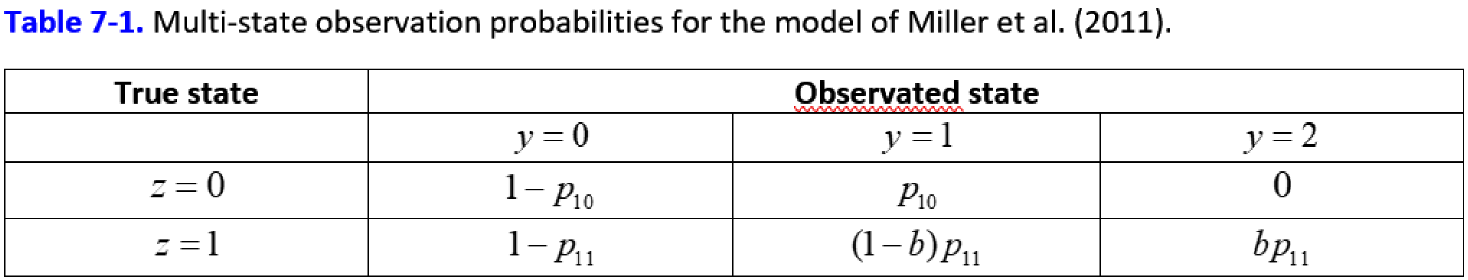


Table 7-1. Multi-state observation probabilities for the model of Miller et al. (2011).

True state	**Observed state**		
	$y=0$	$y=1$	$y=2$
$z=0$	$1-p_{10}$	p_{10}	0
$z=1$	$1-p_{11}$	$(1-b)p_{11}$	bp_{11}

- b = probability an occupied site where detection occurs gets confirmed
- Confirmation is a “site level” process … (more later)

Occupancy models w/false-positives in unmarked

`unmarked` has a very versatile function for fitting these models. It allows for a mix of all 3 types of data:

```
occuFP(detformula = ~1, FPformula = ~1, Bformula = ~1,
stateformula = ~1, data, starts … )
```

`Bformula`: sites may vary in their likelihood of being confirmed. Miller et al. used high calling intensity to define the certain state and related `b` to air temperature. (p was also related to air temperature….)

Note: starts are not in formula order! Starting values order is: psi, p, fp, b (sometimes you have to read the R code to deduce this).

Fitting the Miller et al. model in `unmarked`

You have to declare the ‘type’ of data. The unmarkedFrame constructor function has a ‘type’ argument.

Suppose you just have Type 2 data (occupancy data contaminated with false positives, no confirmation) for $K = 7$ survey occasions

```
    type <- c(0, 7, 0)
    umf <- unmarkedFrameOccuFP(y = y, type = type)
```

Suppose the first 2 periods are Type 1 data (expert listened to all the audio files)

```
    type <- c(2, 5, 0)
```

Suppose the 7th period involved visiting some sites with a human observer to confirm

```
    type <- c(2, 4, 1)
```

Miller et al. model comments

- Confirmation is a site level process, the mechanism by which individual samples within a site are confirmed or not is unspecified. But in practice we know that false positives at the site level happen by making (incorrect) sample-level classifications.
- Model structure is that of a Bernoulli confirmation process for all sites. Implies that all sites have a chance at confirmation. The number confirmed is a random variable.
- *Remember: you can never confirm negatives*: If a site has a detection that may be confirmed, couldn’t it be confirmed negative also? E.g., if you’re using DNA as the confirmation method… NO! Confirmation of a sample is sufficient to confirm presence, but confirmation that the sample is “non target” does not confirm the site is unoccupied.

Plausible design scenario for random site confirmation model

- Survey M sites for presence of a species
- Sign are recorded but may be classified with error
- At some sites you also find scat which is analyzed to established species identity with certainty
- It is reasonable to imagine finding scat to be a random event that occurs with probability b

Demonstration

- (see R script)
- I'm going to go over the most general example here, that which involves all 3 data types (this is Part 3 in the script)

```
# Simulation settings
set.seed(2019) # RNG seed
nsites <- 200 # number of sites
nsurveys <- 7 # number of occasions
habitat <- rnorm(nsites) # Some (continuous) habitat descriptor
# Simulate the occupancy states and data
alpha0 <- 0    # Intercept...
alpha1 <- 1    # ... and slope of psi-habitat regression
psi <- plogis(alpha0 + alpha1*habitat) # Occupancy
z <- rbinom(nsites, 1, psi)            # Latent p/a states
y <- matrix(0,nsites, nsurveys)
p <- c(0.7, 0.5)   # method 2 will have a lower p
b <- 0.5           # probability that observed positive is confirmed certain
fp <- 0.05         # False-positive prob.
```

```
# Simulate data of all 3 types. Note p differs between occ 1-2 and 3-7.
# False positives occur in occasions 3-7 but in occasion 7 there are some
confirmed positives

for(i in 1:nsites){
 # Normal occupancy data
 y[i, 1:2] <- rbinom(2, 1, p[1]*z[i])
 # False-positives mixed in
 y[i, 3:6] <- rbinom(4, 1, p[2]*z[i] + fp*(1-z[i]))
 # Type 3 observations are occupancy data contaminated with false positives
but then
 # we identify some of them as true (below)
 y[i, 7] <- rbinom(1, 1, p[2]*z[i] + fp*(1-z[i]))
}

# Here we set some of the detections to confirmed positives
true.positives <- z==1 & y[,7]==1
confirmed <- (rbinom(nsites, 1, b) == 1) & true.positives
y[confirmed, 7] <- 2
```

```
# Make a covariate to distinguish between the two methods
Method <- matrix(c(rep("1", 2), rep("2", 5)), nrow = nsites, ncol = 7, byrow = TRUE)
# Type indicates a mix of all 3 data types
type <- c(2, 4, 1)

# Same covariate structure as before
siteCovs <- data.frame(habitat = habitat)
obsCovs <- list(Method = Method)
summary(umf1 <- unmarkedFrameOccuFP(y, siteCovs = siteCovs, obsCovs = obsCovs, type =
type))

# fp starting value should be small (-1 here).
# Note: last parameter in this model is "Pcertain"
( m3 <- occuFP(detformula = ~ -1 + Method, FPformula = ~1, Bformula = ~1,
stateformula = ~ habitat, data = umf1,  starts=c(0, 0, 0, 0, -1, 0)) )
               # starting values order:   psi parms, p parms, fp parms, b parms.
```

```
Call:
occuFP(detformula = ~-1 + Method, FPformula = ~1, Bformula = ~1,
    stateformula = ~habitat, data = umf1, starts = c(0, 0, 0,
        0, 0, -1))

Occupancy:
            Estimate    SE      z  P(>|z|)
(Intercept)  -0.0813 0.160 -0.509 6.11e-01
habitat       0.9495 0.198  4.791 1.66e-06

Detection:
        Estimate     SE     z  P(>|z|)
Method1   0.9751 0.1802 5.412 6.22e-08
Method2   0.0155 0.0954 0.163 8.71e-01

false positive:
 Estimate    SE     z  P(>|z|)
    -2.86 0.207 -13.8 1.29e-43

Pcertain:
 Estimate    SE     z P(>|z|)
   0.0388 0.292 0.133   0.894

AIC: 1383.091
```

Remember: estimates are on the logit scale for probability parameters

Class work session 1

- Eurasian Lynx data (Type 1 and Type 2 data)
  - Status and Conservation of the Alpine Lynx Population (SCALP): a monitoring effort to coordinate and standardize Alpine lynx monitoring (Molinari-Jobin et al. 2012)
  - certain data in which observed presence observations were assumed to be “hard fact” (e.g. a dead lynx), or tracks verified by an expert, or photographs.
  - uncertain data which are unconfirmed data such as direct visual records from nonexperts, which might be contaminated with false positives.
- Create the unmarked data frame using `unmarkedFrameOccuFP`
- Do a likelihood analysis of this data set using `occuFP` to evaluate the magnitude of the false positive probability parameter using just the NULL model
- Trends over time are important since this species is expanding its range. Fit a linear Trend model in each parameter
- Add Cntry as a covariate (additive) to each parameter
- Add the forest covariate to the occupancy sub-model

Loading the lynx data

- Data set shows 3 occasions (2-month periods) but this includes certain (type 2) and uncertain (type 1) records.
- The idea is that in any period there is a chance of getting either type of observation so this is regarded as 6 survey periods

```
data(EurasianLynx)
str(lynx <- EurasianLynx)
```

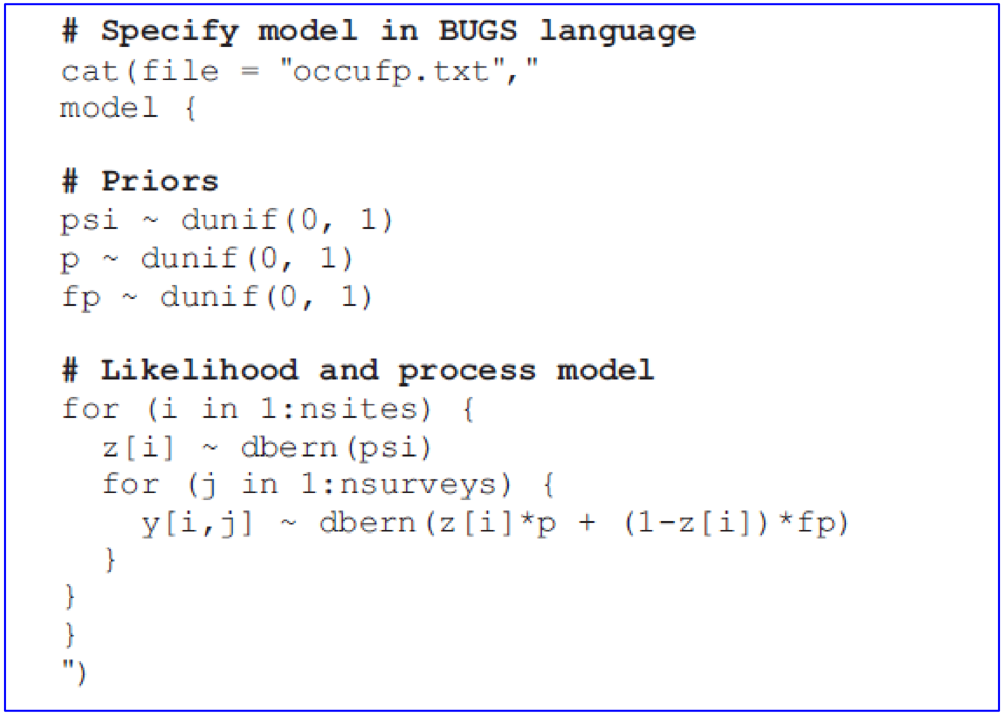
```
 'data.frame':   43332 obs. of  10 variables:
  $ type    : Factor w/ 2 levels "certain","uncertain": 1 1 1 1 1 1 1 1 1 1 ...
  $ site.nr: int  1 2 3 4 5 6 7 8 9 10 ...
  $ y.1     : int  NA NA NA NA NA NA NA NA NA NA ...
  $ y.2     : int  0 0 0 0 0 0 0 0 0 0 ...
  $ y.3     : int  0 0 0 0 0 0 0 0 0 0 ...
  $ Year    : int  1994 1994 1994 1994 1994 1994 1994 1994 1994 1994 ...
  $ Cntry   : Factor w/ 2 levels "Italy","Switzerland": 1 1 1 1 1 1 1 1 1 1 ...
  $ forest : num  78.3 34.1 40.8 68.2 73.5 ...
  $ xcoord : num  4110 4120 4130 4110 4120 4130 4140 4150 4160 4170 ...
  $ ycoord : num  2300 2300 2300 2310 2310 2310 2310 2310 2310 2310 ...
```

Organizing the lynx data

```
# Add the columns we need for analysis in unmarked
lynx$occ.1 <- 1
lynx$occ.2 <- 2
lynx$occ.3 <- 3
lynx$sYear <- standardize(lynx$Year)

# Extract the type 1 and type 2 data separately and bind them together
lynx1 <- lynx[lynx[,"type"] == "certain", ]
lynx2 <- lynx[lynx[,"type"] == "uncertain", ]
lynx <- cbind(lynx1[,c(2,3:5)], lynx2[,3:5] )
colnames(lynx) <- c("site.nr", "y.1", "y.2", "y.3", "y.4", "y.5", "y.6")

occ <- cbind(lynx1[,c("occ.1","occ.2","occ.3")], lynx2[, c("occ.1", "occ.2", "occ.3")])
colnames(occ) <- c("occ.1", "occ.2", "occ.3", "occ.4", "occ.5", "occ.6")
lynx <- cbind(lynx,lynx1[, c("Year", "sYear", "Cntry")])

# Make the false-positive unmarkedFrame. Be sure to indicate type!
y <- lynx[,paste0("y.", 1:6)]
siteCovs <- lynx[, c("sYear", "Year", "Cntry")]
obsCovs <- list(occ = occ)
```

Bayesian analysis models with false positives

- FP models, including multi-state model, can be written out directly in the BUGS language



```
# Specify model in BUGS language
cat(file = "occufp.txt","
model {

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

# Likelihood and process model
for (i in 1:nsites) {
  z[i] ~ dbern(psi)
  for (j in 1:nsurveys) {
    y[i,j] ~ dbern(z[i]*p + (1-z[i])*fp)
  }
}
}
")
```

Initial values are really important! Try to start p and fp near the correct mode (p > fp)

Bayesian analysis models with false positives

- Data with false positives + ordinary occupancy data (a kind of integrated model)
- You need 2 likelihood bits:
  - For data with false positives

    ```
    for (j in 1:n1) {
        y1[i,j] ~ dbern(z[i]*p + (1-z[i])*fp)
    }
    ```

  - For ordinary occupancy data

    ```
    for (j in (n1+1):(n1+n2) ) {
        y2[i,j] ~ dbern(z[i]*p)
    }
    ```

- You need 2 data objects or one data object with some indexing tricks
- Data could be same or different sites which might affect how you formulate the model (pad the y matrix with NA…)

Example of a multi-method model. Ordinary occupancy data + Site-confirmation data (Type 3)

```
# Specify model in BUGS language
cat(file = "occufp2.txt","
model {
# Priors
psi ~ dunif(0, 1)
fp ~ dunif(0, 1)
b ~ dunif(0, 1)
alpha0 ~ dnorm(0,0.01)
alpha1 ~ dnorm(0,0.01) # Method effect

# Likelihood and process model
for (i in 1:nsites) { # Loop over sites
z[i] ~ dbern(psi) # State model
# Define observation matrix (obsmat)
for(j in 1:(nsurv1+nsurv2)) {
  obsmat[i,j,1,1] <- 1-fp # z = 0 obs probs
  obsmat[i,j,2,1] <- fp
  obsmat[i,j,3,1] <- 0
  obsmat[i,j,1,2] <- 1-p[i,j] # z = 1 obs probs
  obsmat[i,j,2,2] <- (1-b)*p[i,j]
  obsmat[i,j,3,2] <- p[i,j]*b
}
# Observation model: part 1 (for first 3 cols in y)
for(j in 1:nsurv1) { # Loop over replicate surveys
  logit(p[i,j]) <- alpha0
  y[i,j] ~ dbern(z[i]*p[i,j] ) # ordinary occupancy data
}
# Observation model: Type 3 data (for last 4 cols in y)
for (j in (nsurv1+1):(nsurv1+nsurv2)) {
  logit(p[i,j]) <- alpha0 + alpha1
  y[i,j] ~ dcat(obsmat[i,j,1:3,z[i]+1] )
}
}
}
")
```

Build the observation state probability matrix here

This is the new part compared to an ordinary occupancy model

Class work session 2

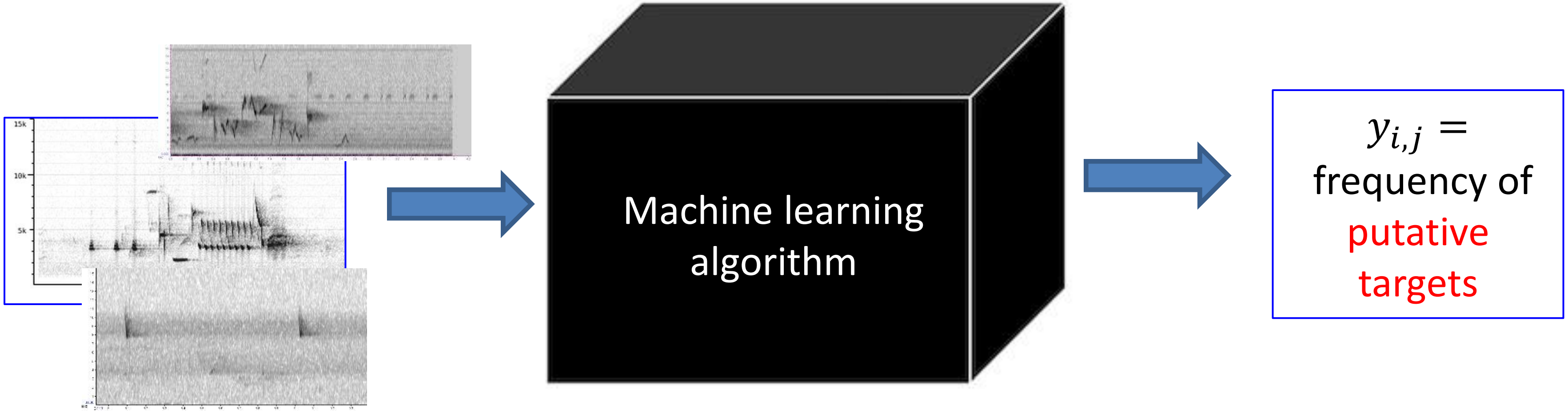
Eurasian Lynx data (Type 1 and Type 2 data)

- Do a Bayesian analysis of this data set to evaluate the magnitude of the false positive probability parameter
- Model Trends over time
- Model Cntry effect
- Add the forest covariate

Sample-level models for false positives

- Site-level classification: Real world doesn’t usually work that way!
- Most methods produce a stochastic number of samples for a site: camera traps, ARUs, human observers. Errors in classification (i.e., false positives) occur at the sample level.
- We would like an occupancy model that accommodates sample level data and misclassification, so that your inference about site classification properly scales with the number and quality of samples produced

Machine learning pipeline

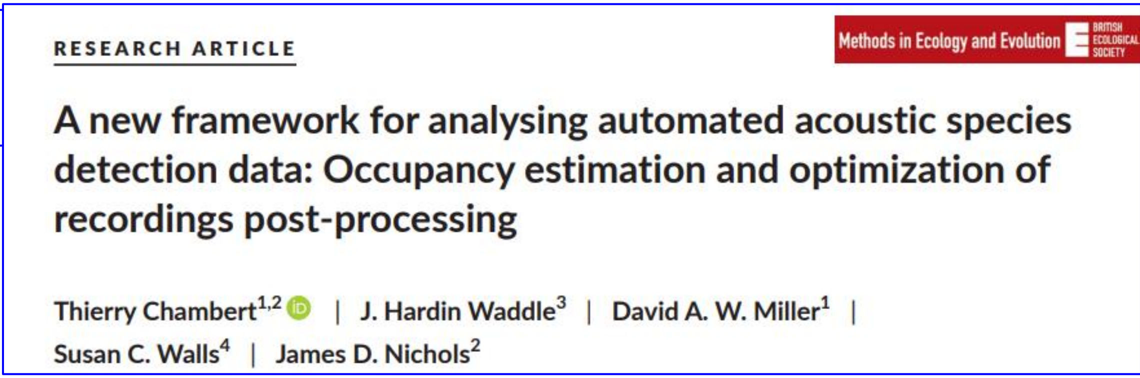


Machine learning algorithm

$y_{i,j} =$ frequency of putative targets

ML/AI methods produce false positives!

Model proposed by Chambert et al. 2017:



RESEARCH ARTICLE

Methods in Ecology and Evolution

BRITISH ECOLOGICAL SOCIETY

A new framework for analysing automated acoustic species detection data: Occupancy estimation and optimization of recordings post-processing

Thierry Chambert[1,2] | J. Hardin Waddle[3] | David A. W. Miller[1] | Susan C. Walls[4] | James D. Nichols[2]

Sample-level models for false positives

Conceptual model for observed data:

$y_{i,j}$ = actual targets (true positives) + misclassifications (false positives)

$K_{i,j}$ = true positives

$Q_{i,j}$ = false positives

Statistical representation:

$$y_{i,j} = \underbrace{Poisson(\lambda * z_i)}_{K_{i,j}} + \underbrace{Poisson(\omega)}_{Q_{i,j}}$$

Sample-level models for false positives

Additivity of Poisson rvs (unconditional on K and Q)

$$y_{i,j} \sim Poisson(\lambda * z_i + \omega)$$
$$z_i \sim Bern(\psi_i)$$

- $\lambda =$ mean number of target detections per site
- $z_i =$ occupancy status at site i
- $\omega =$ mean number of false-positives per site

- You observe a count with expected value ω if the species is not present and $\lambda + \omega$ if the species is present.
- This is a natural sample-frequency version of the false positives occupancy model.

Sample-level models for false positives

Integrated models:

Could imagine other data sources provide information about z, independent of the detection frequencies. E.g., suppose detection frequencies are generated by ARUs and machine learning which is producing false positives, and your highly trained field observers are producing normal occupancy data.

Second data source:

$$y_{i,j}^{h} \sim Bern(p \; * z_i)$$

Or even with false positives…

Implementation in JAGS

- This model does not exist in unmarked
  - (but would be easy to do….)

- We show a brief simulation of the integrated model (contaminated occupancy + contaminated detection frequencies)

Detection frequency data subject to false positives + occupancy data also with false positives

```
# Simulation settings
set.seed(2019, kind = "Mersenne")
nsites <- 100 # Number of sites
nsurveys <- 5 # Number of replicates/occasions
psi <- 0.7    # Occupancy
p11 <- 0.5    # Detection probability at an occupied site
p10 <- 0.05   # False detection probability
lam <- 3      # Rate of true positives from ARU
ome <- 0.50   # Rate of false positives from ARU
# Simulate true occupancy states
z <- rbinom(nsites, 1, psi)
# Define detection probability
p <- z * p11 + (1-z) * p10
# Simulate occupancy data and ARU count frequencies
yARU <- y <- K <- Q <- matrix(NA, nsites, nsurveys)
for(i in 1:nsites){
  y[i,] <- rbinom(nsurveys, 1, p[i]) # Detection/nondetection data
  K[i,] <- rpois(nsurveys, lam*z[i]) # True positive detection frequency
  Q[i,] <- rpois(nsurveys, ome)      # False-positive detection frequency
  yARU[i,] <- K[i,] + Q[i,]          # Number of ARU detections
}
# Bundle and summarize data
str( bdata <- list(y = y, yARU = yARU, nsites = nsites, nsurveys = nsurveys ))
```

```
# Specify Model A in BUGS language
cat(file = "modelA.txt","
model {
# Priors
psi ~ dunif(0, 1) # psi = Pr(Occupancy)
p10 ~ dunif(0, 1) # p10 = Pr(y = 1 | z = 0)
p11 ~ dunif(0, 1) # p11 = Pr(y = 1 | z = 1)
lam ~ dunif(0, 1000)
ome ~ dunif(0, 1000)
# Likelihood:process and observation models
for (i in 1:nsites) {
  z[i] ~ dbern(psi) # Occupancy status of site i
  p[i] <- z[i] * p11 + (1-z[i]) * p10 # false-positive detection model
  for(j in 1:nsurveys) {
    y[i,j] ~ dbern(p[i]) # Binary occupancy data
    yARU[i,j] ~ dpois(lam * z[i] + ome) # ARU detection frequency data
 }
}
}
")
# Initial values
inits <- function(){list(z = apply(y, 1, max), psi = runif(1),
p10 = runif(1, 0, 0.05), p11 = runif(1, 0.5, 0.8), lam = runif(1, 1, 2),
ome = runif(1, 0, 0.4) )}
# Parameters monitored
params <- c("psi", "p10", "p11", "lam", "ome")
# MCMC settings
na <- 1000 ; ni <- 2000 ; nt <- 1 ; nb <- 1000 ; nc <- 3
# Call JAGS (tiny ART), gauge convergence and summarize posteriors
out1 <- jags(bdata, inits, params, "modelA.txt", n.adapt = na,
n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
par(mfrow = c(2, 3)) ; traceplot(out1)
print(out1, 3)
```

This model has contaminated occupancy data and contaminated detection frequency data such as from an ARU

Validation data

- Usually (in a ML workflow) there is some level of expert validation. We would like to use this information to inform model parameters.
- Suppose a batch of detections contains K true positives, Q false positives, you choose n samples to validate of which k turn out to be correctly classified.$\text{Then,}\, k$ has a hypergeometric distribution

$$k \sim dhyper(K, Q, n, 1)$$

Standard model for sampling without replacement.

- In practice we do this by site and so k_i are input as data to JAGS, and the model is expanded to include the hypergeometric likelihood of these data. K and Q are latent variables!

Next gen models

- The detection frequency model assumes that the class of each detection is determined somehow. i.e., a computer algorithm is declaring detected signals to be targets.
- We showed how to allow for the possibility that the classification is incorrect
- In practice there is usually some additional information that the algorithm is using to decide which detections are (most likely) the target. And the amount of information varies from sample to sample. Thus, there is heterogeneity in classification accuracy that is sample-specific
  - E.g., match scores in acoustic data processing
  - Feature score vector produced by a CNN
- How can we use this information in occupancy models?

Next gen models

- Next gen models:
  - Integrate the classification model (and hence the uncertainty) with the ecological models (see Ch. 7 of AHM2)
  - Sample class is itself a latent variable, not data!
  - Hence the classification process should be part of the model

Next Gen models

- How might this work?
- Suppose you have a continuous covariate for each sample say x_i which is informative about the true class of the sample
  - Machine learning output
  - Template correlation
- Model the conditional distribution of $x_k | c_k$
  - $c_k = \text{true class}$

Next Gen models

Suppose 2 groups only – “target” and “non-target”

$$x_k | \, c = 1 \sim Normal(\mu_1, \sigma_1)$$

$$x_k | \, c = 2 \sim Normal(\mu_2, \sigma_2)$$

Need a prior distribution for the latent variable c. Chambert et al. model implies:

Pr(c = 1) = $\frac{\lambda_i z_i}{\lambda_i z_i + \omega_i}$

λ and ω – rates of true positives and false positives are unknown parameters (might depend on habitat, etc..)

Occupancy model: $z_i \sim Bern(\psi_i)$

$$logit(\psi_i) = \alpha_0 + \alpha_1 * cov_i$$

Relevant literature

- Rhinehart, T.A., Turek, D. and Kitzes, J., 2022. A continuous-score occupancy model that incorporates uncertain machine learning output from autonomous biodiversity surveys. *Methods in Ecology and Evolution*, *13*(8), pp.1778-1789.

- Spiers, A.I., Royle, J.A., Torrens, C.L. and Joseph, M.B., 2022. Estimating species misclassification with occupancy dynamics and encounter rates: A semi-supervised, individual-level approach. *Methods in Ecology and Evolution*, *13*(7), pp.1528-1539.

Summary

- False positives are probably more common than we think (or assume)
- Bigger and better hierarchical models accommodate FPs
- The future is dealing with sample level classification errors