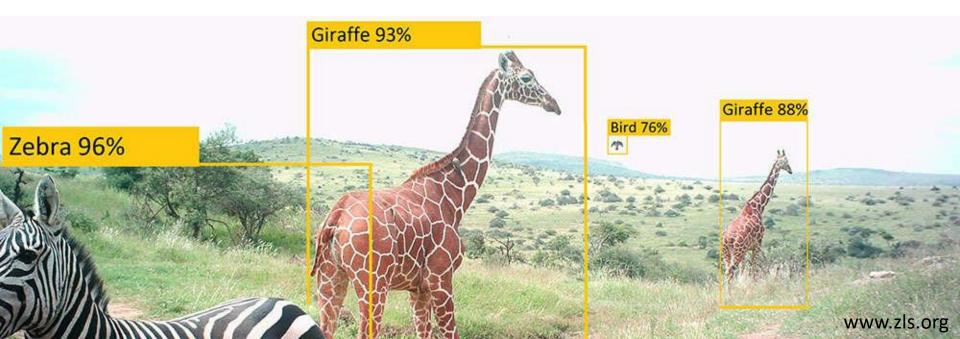
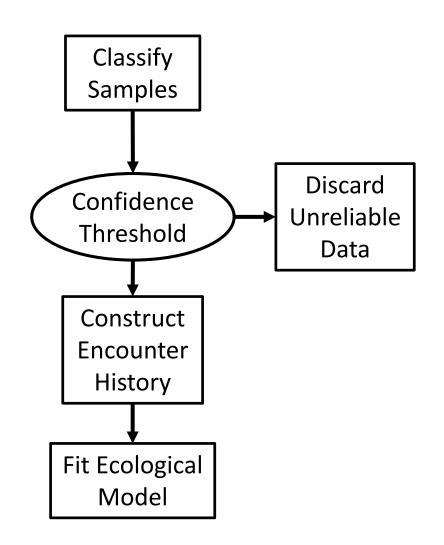




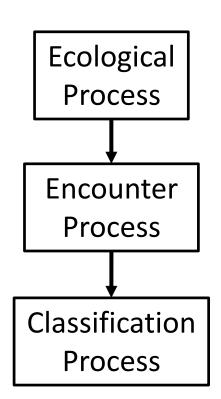
- Many ecological models rely on perfect classification of samples
  - Individual ID
  - Species ID
  - Disease state
  - Etc.



- Typical approach: "uncoupled classification"
- Uncertainty in classification not propagated to ecological parameters
  - Retained data treated as error free
  - Data loss
- Solution: coupled classification in a hierarchical ecological model



- Hierarchical Ecological Models
  - Model the processes that produced our data
- Coupled Classification
  - Classification process determines data we observe
  - Joint estimation of all parameters
- Regard ecological classes in encounter history as variables to be estimated
- Bayesian estimation: sample from joint posterior for encounter history and model parameters via Markov Chain Monte Carlo (MCMC)

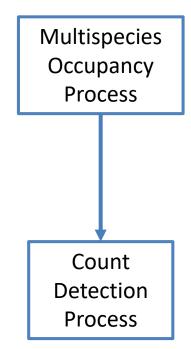


- Base model: multispecies occupancy model with count detections
  - Independent occupancy process (no sps interactions)
  - "species" can be any class, really.
    - Background noise, higher taxonomic orders, disease state, etc.

 $\psi_{i,j}$ : P(site *j* occupied by species *i*)  $z_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$ 

 $\lambda_{i,j,k}$ : Detection rate of species i at site j on occasion k

$$[y_{i,j,k}|z_{i,j}] \sim \text{Poisson}(\lambda_{i,j,k} * z_{i,j})$$





- Unknown species ID extension
  - Observe a species "feature score" instead
  - Correlates with species ID
  - $\gamma_l$ : species ID of sample *l*

$$z_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$$

 $[y_{i,j,k}|z_{i,j}] \sim \text{Poisson}(\lambda_{i,j,k} * z_{i,j})$ 

Disaggregate  $y_{i,j,k}$  to individual detections, index by sample number I

 $[g_l|\gamma_l] \sim \text{Normal}(\mu_{\gamma_l}, \sigma_{\gamma_l})$ 

Multispecies Occupancy **Process** Count Detection **Process Feature** Score Observation **Process** 



- Unknown species ID extension
  - Observe a species "feature score" instead
  - Correlates with species ID
  - $\gamma_l$ : species ID of sample I

$$z_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$$

#### Example

$$y_{1,3,2} = 2$$
  
 $y_{2,3,2} = 3$ 

$$\gamma_1 = 1$$
, site<sub>1</sub>= 3, occ<sub>1</sub> = 2  
 $\gamma_2 = 1$ , site<sub>2</sub>= 3, occ<sub>2</sub> = 2  
 $\gamma_3 = 2$ , site<sub>3</sub>= 3, occ<sub>3</sub> = 2  
 $\gamma_4 = 2$ , site<sub>4</sub>= 3, occ<sub>4</sub> = 2  
 $\gamma_5 = 2$ , site<sub>5</sub>= 3, occ<sub>5</sub> = 2

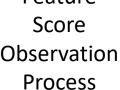
$$[y_{i,j,k}|z_{i,j}] \sim \text{Poisson}(\lambda_{i,j,k} * z_{i,j})$$

Disaggregate  $y_{i,i,k}$  to individual detections, index by sample number I

$$[g_l|\gamma_l] \sim \text{Normal}(\mu_{\gamma_l}, \sigma_{\gamma_l})$$

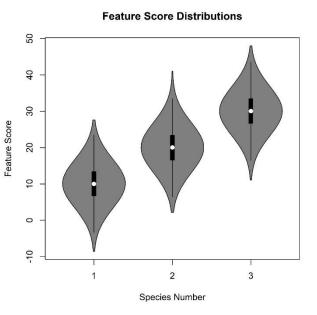
Occupancy **Process** Count Detection **Process Feature** Score Observation

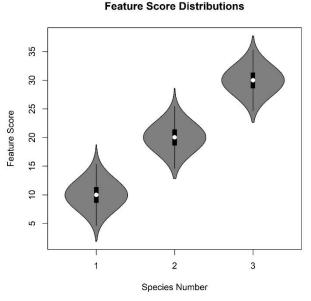
Multispecies

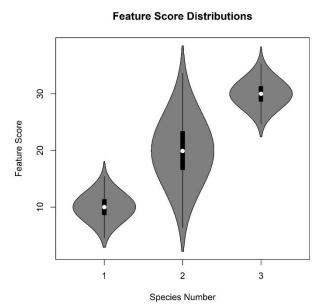




- Hypothetical Feature Score Visualization
  - 3 species, Normal Distribution







$$[g_l|\gamma_l] \sim \text{Normal}(\mu_{\gamma_l}, \sigma_{\gamma_l})$$



- Factor count likelihood to fit model
  - Only works with Poisson count model

$$[y_{i,j,k}|z_{i,j}] \sim \text{Poisson}(\lambda_{i,j,k} * z_{i,j})$$

#### Site by occasion contribution

$$y_{.,j,k} \sim \text{Poisson}(\Lambda_{j,k})$$

$$y_{.,j,k} = \sum_{i} y_{i,j,k}$$

$$\Lambda_{j,k} = \sum_{i} \lambda_{i,j,k} * z_{i,j}$$

#### **Species contribution**

$$\gamma_l \sim \text{Categorical}\left(\frac{\lambda_{1:N,j,k} * z_{1:N,j}}{\sum_i \lambda_{i,j,k} * z_{i,j}}\right)$$

"Ecological Prior" for species ID  $\gamma_l$ 

```
for(l in 1:n.samples){
   gamma[l] ~ dcat(sps.prob[1:N,G.site[l],G.occ[l]])
   g[l] ~ dnorm(mu=mu[gamma[l]],sd=sigma[gamma[l]])
}
```

```
or(j in 1:J){
    for(k in 1:K){
        bigLam[j,k] <- sum(lambda[1:N,j,k]*z[1:N,j])
        y2D[j,k] ~ dpois(bigLam[j,k])
        sps.prob[1:N,j,k] <- (lambda[1:n.species,j,k]*z[1:N,j])/bigLam[j,k]
    }
}</pre>
```

- "Availability" process
  - Optional, but a good idea!
  - Site by occasion-level zero-inflation

$$z_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$$

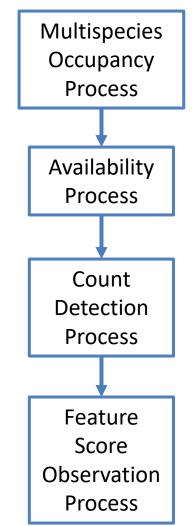
$$[w_{i,j,k}|z_{i,j}] \sim \text{Bernoulli}(\theta_{i,j,k} * z_{i,j})$$

$$[y_{i,j,k}|w_{i,j,k}] \sim \text{Poisson}(\lambda_{i,j,k} * w_{i,j,k})$$

Modified "ecological prior"

$$\gamma_l \sim \text{Categorical}\left(\frac{\lambda_{1:N,j,k} * w_{i:N,j,k}}{\sum_i \lambda_{i,j,k} * w_{i,j,k}}\right)$$

$$[g_l|\gamma_l] \sim \text{Normal}(\mu_{\gamma_l}, \sigma_{\gamma_l})$$



- Ecological "Prior Information"
  - Samples at site j are more likely to belong to
    - Species more likely to occupy site j
    - Species with higher detection rate | occupancy at site j

$$\gamma_l \sim \text{Categorical}\left(\frac{\lambda_{1:N,j,k} * z_{1:N,j}}{\sum_i \lambda_{i,j,k} * z_{i,j}}\right)$$

With Availability Process

$$\gamma_l \sim \text{Categorical}\left(\frac{\lambda_{1:N,j,k} * w_{i:N,j,k}}{\sum_i \lambda_{i,j,k} * w_{i,j,k}}\right)$$

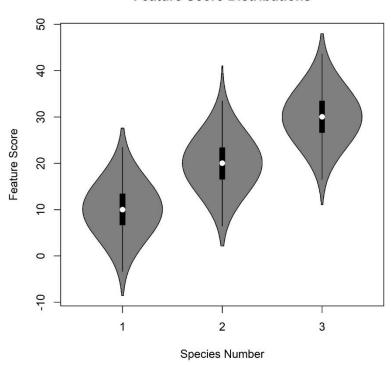
 Function of species-specific occupancy, availability and detection intercepts and possible site and occasion covariate relationships or random effects.

$$logit(\psi_{i,j}) = \beta_{0,i} + \beta_{1,i} * cov_j$$
$$logit(\theta_{i,j,k}) = \alpha_{0,i} + \alpha_{1,i} * cov_j$$
$$log(\lambda_{i,j,k}) = \eta_{0,i} + \eta_{1,i} * cov_j$$

### Validation Data

- Can fit the model without validation data\*
  - Sometimes, not recommended!
  - Limited to most simple models?
  - Multimodality present
    - Like Royle and Link (2016), but better able to tell which species is which?
- Types of validation data
  - Independent: not from focal survey
    - Requires "transferability"
  - Random validation of focal survey detections
    - Bonus: some z and w states known
- Alternatively, can use informative prior

#### **Feature Score Distributions**



- Parameter Estimation via MCMC
  - Default algorithm sometimes will not converge/fully explore posterior
  - Difficulty sampling latent counts conditioned on latent indicator variables
    - Example in AHM book should work fine with default algorithm (background z always 1)
  - Can marginalize likelihood over all latent variables, z, w, γ
    - Marginalize for every parameter update on each iteration (could fit in Stan this way)
    - Sample z, w,  $\gamma$  from marginal distributions (once per iteration)
    - Must calculate the likelihood for all possible combinations of  $z_{ij}$  and  $w_{ijk}$  at each site
    - Number of combinations is 2<sup>N</sup>



```
> 2^(1:15)
[1] 2 4 8 16 32 64 128 256 512 1024 2048 4096 8192 16384 32768
```

- Implemented in Nimble via custom update
  - github.com/benaug/Coupled-Classification-Occupancy

- Some possible Feature Score Distributions
  - Any parametric distribution

$$[g_l|\gamma_l] \sim \text{Normal}(\mu_{\gamma_l}, \sigma_{\gamma_l})$$

Feature Score Observation Process

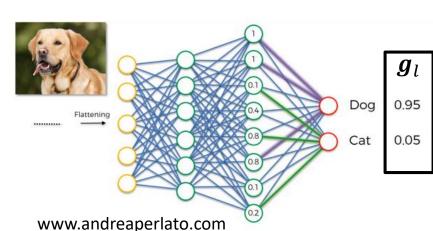
 $[g_l|\gamma_l] \sim \text{Categorical}(\pi_{\gamma_l})$  (Equivalent to Wright et al. 2020)

 $[\boldsymbol{g}_l|\gamma_l] \sim \text{Dirichlet}(\boldsymbol{\pi}_{\gamma_l})$ 



Vectors of length N  $\mathbf{\pi}_{\gamma_I}$  sums to 1

Softmax vector output from CNN



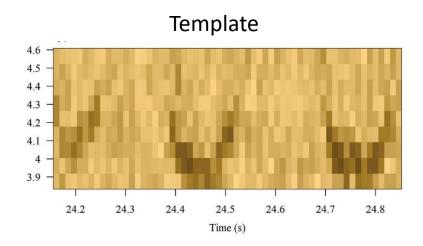
- Northern Spotted Owl (NS0) acoustic occupancy data set
- Collected by Connor Wood, Zach Peery, and others
- 45 sites, 3 weekly occasions
- 2-3 ARUs per site
- Variable Effort: ARU-nights
- Acoustic events identified by correlation with NSO template
- Statistically, owl calls difficult to distinguish from "background noise"



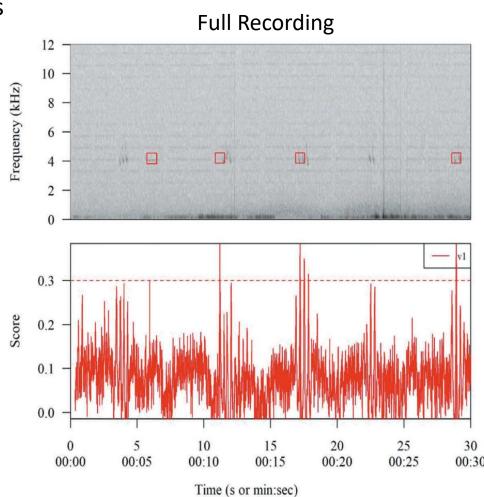




- Acoustic events identified by correlation with NSO template
  - Events with correlation < 0.8 discarded</li>
  - Humans classified 12777 all events
    - Owl vs. background
  - Event "features" measured



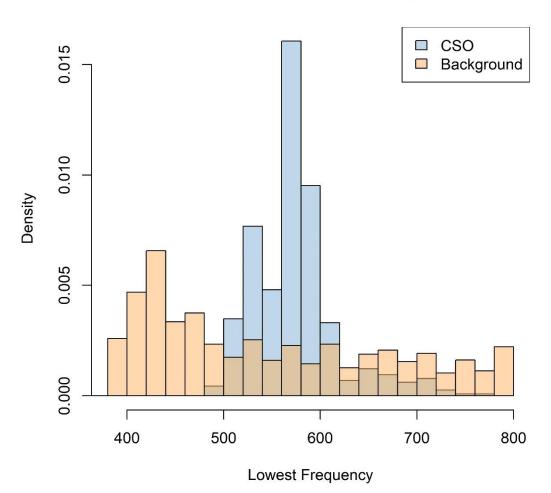
Balantic and Donovan 2020





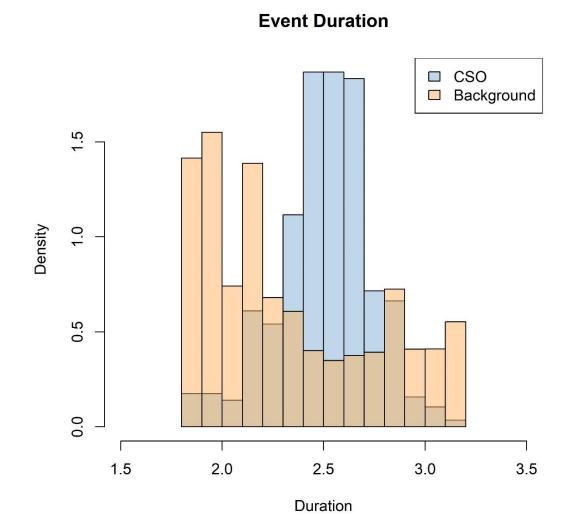
Potential Feature Scores

#### **Event Lowest Frequency**





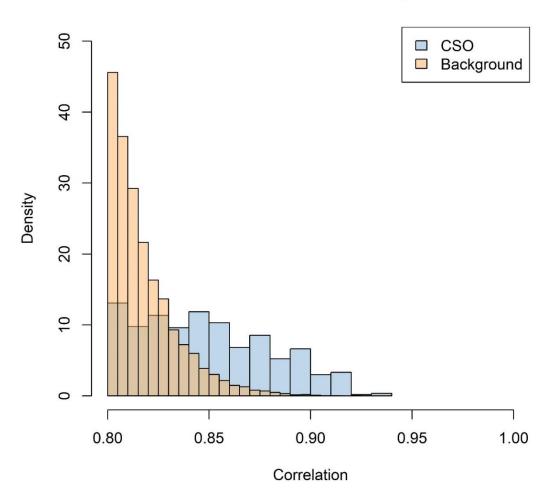
Potential Feature Scores





Potential Feature Scores

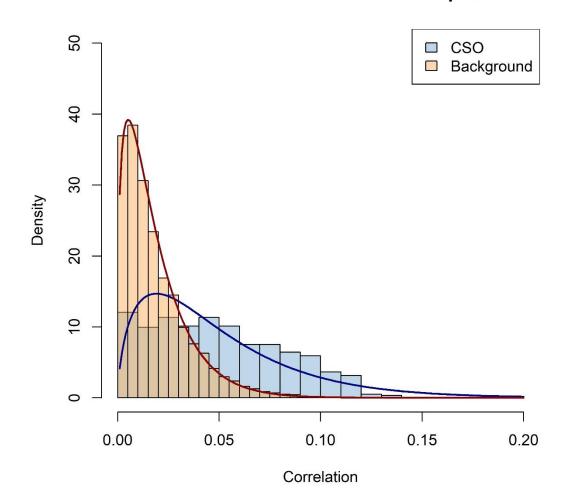
#### **Correlation With CSO Template**





- Potential Feature Scores
  - Treat as Gamma RV
  - Other choices?
    - Truncated Normal?

#### **Shifted Correlation With CSO Template**





#### Model Specification

Occupancy

Availability

#### Detection

 Site by occasion random effect for each species For species *i*, site *j*, occasion *k* 

$$logit(\psi_{i,j}) = \beta_{0,i} + \beta_{1,i} * slope_j$$
$$z_{i,j} \sim Bernoulli(\psi_{i,j})$$

$$logit(\theta_{i,j}) = \alpha_{0,i} + \alpha_{1,i} * slope_j$$
$$[w_{i,j,k}|z_{i,j}] \sim Bernoulli(\psi_{i,j} * z_{i,j})$$

$$\log(\lambda_{i,j,k}) \sim \text{Normal}(\mu_i, \sigma_i)$$

$$[y_{i,j,k}|w_{i,j,k}] \sim \text{Poisson}(\lambda_{i,j,k} * w_{i,j,k} * \text{effort}_{i,j,k})$$



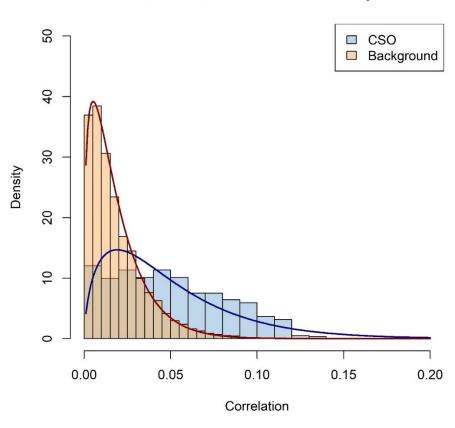
#### Model Specification

 Feature Score for sample/detection /

 $g_l \sim \text{Gamma(shape}_1, \text{rate}_1) \text{ if } \gamma_l = 1$ 

 $g_l \sim \text{Gamma(shape}_2, \text{ rate}_2) \text{ if } \gamma_l = 2$ 

#### **Shifted Correlation With CSO Template**



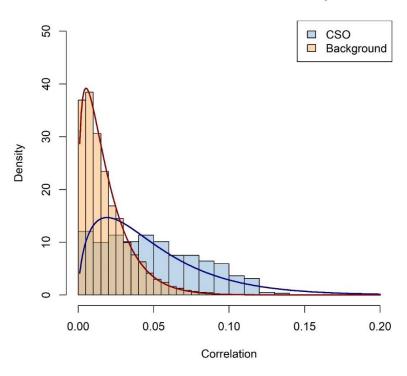
```
for(l in 1:n.samples){
   g[l] ~ dgamma(shape=G.shape[gamma[l]],rate=G.rate[gamma[l]])
}
```



#### Modeling Exercise

- How do model estimates vary as more species IDs are provided?
- Fit models with variable % known ID
  - 100% (regular occupancy model)
  - 50%
  - 25%
  - 10%
- n=1 randomization of known ID samples
  - Better to try many possible ways to select X% to ID

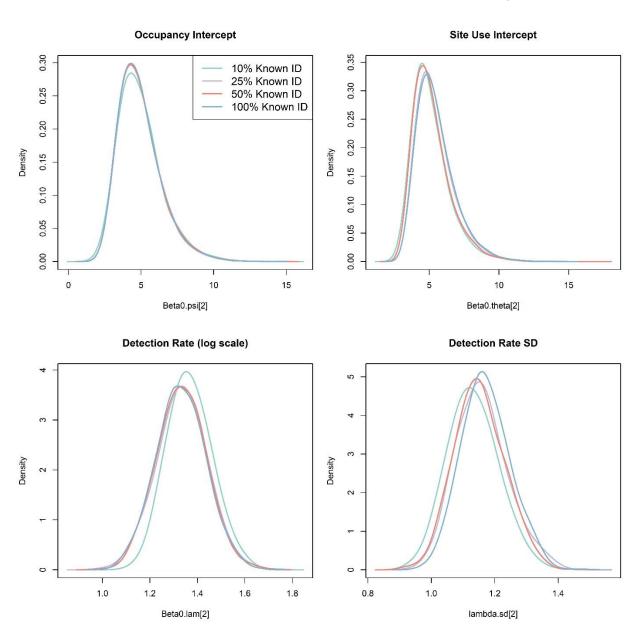
#### **Shifted Correlation With CSO Template**



```
for(l in 1:n.samples){
   g[l] ~ dgamma(shape=G.shape[gamma[l]],rate=G.rate[gamma[l]])
}
```

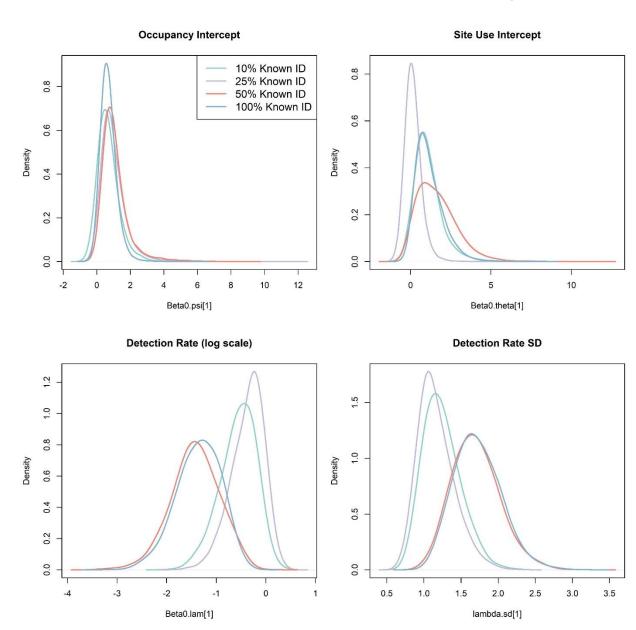


- Compare (some)
   parameter estimates
  - Background



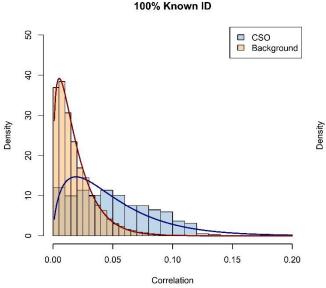


- Compare (some) parameter estimates
  - Owl

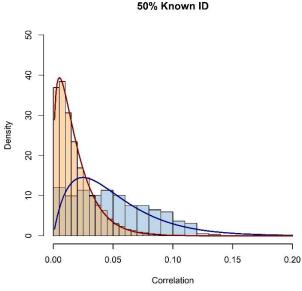


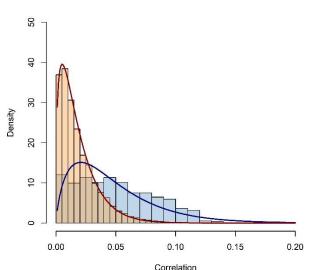


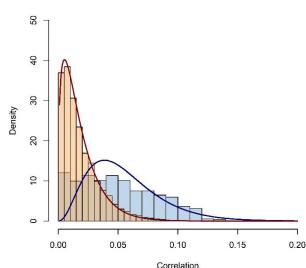
- Compare (some)
   parameter estimates
  - Gamma fit
  - Background fit deviates more with fewer known ID
  - Mostly in area of overlap
  - Not quite gamma?
  - Feature covariate doesn't separate classes well?
  - Site Heterogeneity?



25% Known ID





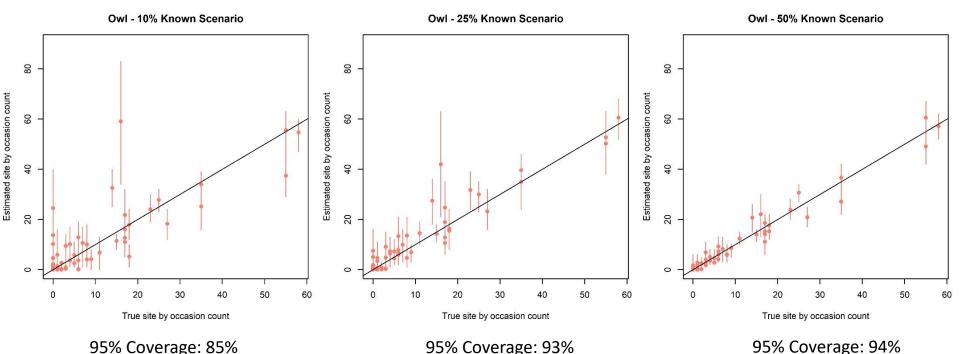


10% Known ID



- How do the models do estimating the true site by occasion detection counts?
  - Owl
  - -y[1,j,k]

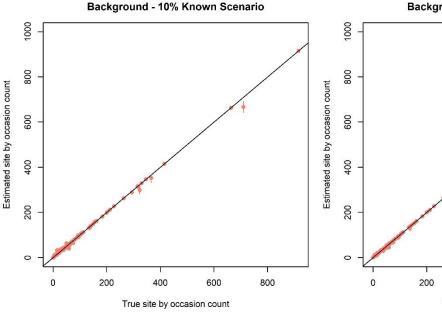
64/573 Known

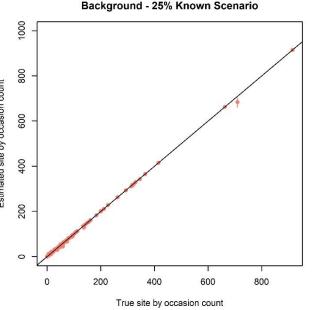


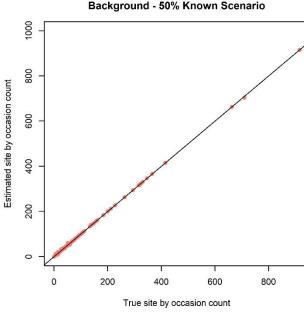
147/573 Known

286/12204 Known

- How do the models do estimating the true site by occasion detection counts?
  - Background
  - -y[2,j,k]







95% Coverage: 87% 1231/12204 Known

2998/12204 Known

95% Coverage: 92%

95% Coverage: 95%

6074/12204 Known



- Can estimate recall and precision
  - Point estimates
  - Uncertainty estimates
  - Excluding known-ID samples
  - Recall: P(classify as owl|true owl), related to detection
  - Precision" P(true owl|classified as true owl), related to classification error

#### Recall

% Known	Owl	Background
10	0.56	0.99
25	0.62	0.99
50	0.56	0.99

#### Precision

% Known	Owl	Background
10	0.67	0.98
25	0.71	0.98
50	0.76	0.98



### Some Concluding Remarks

- A "more mechanistic" false positive model
  - Greater understanding of false positive sources
- Greater ability to model heterogeneity in false positive rates across sites
  - Depends on how frequently each species is confused with focal and their ecological parameters determining how frequently they are detected in space and time
- More likely that feature score distributions more similar across sites/studies that false positive probabilities
  - Still likely to be unmodeled heterogeneity in feature score distributions
- All (?) FP models lean more heavily on parametric assumptions than when no FPs
  - Definitely CC occupancy models



### False Positive Model Landscape

- Species number
- Detection vs. count observations

Wright et al. (2020), Spiers et al. (2022)

> Two-species, count detections

>1 species

Analyze data for

species 1 only, assume  $\psi_2 = 1$ 

Single-species, count detections

Summarize to binary observations,  $D_{ii\cdot k'} = I(C_{ii\cdot k'} > 0)$ 

 $D_{ij \cdot k'} = I(C_{ij \cdot k'} > 0)$ 

Summarize to

binary observations,

Two-species, binary detections Chambert, Campbell Grant, et al. (2018)

Analyze data for species 1 only, assume  $\psi_2 = 1$ 

"non-focal occupies every site"

 $O_{ij\cdot k'} = I(O_{ij\cdot k'} > 0)$ 

Single-species, binary detections

Royle and Link (2006), Chambert et al. (2011), Chambert et al. (2015)

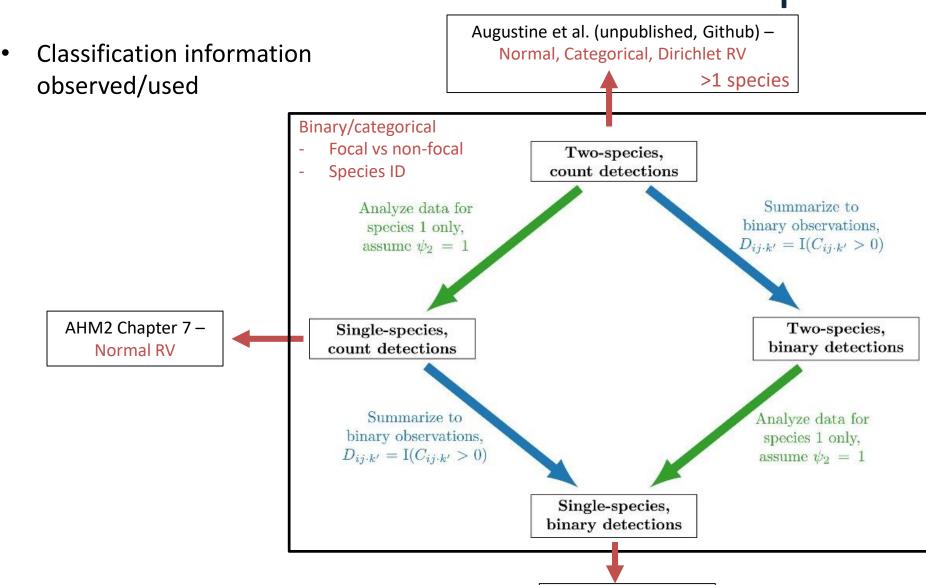


Chambert,

Waddle, et al.

(2018)

# False Positive Model Landscape





Rhinehart et al. (2022) - Normal RV