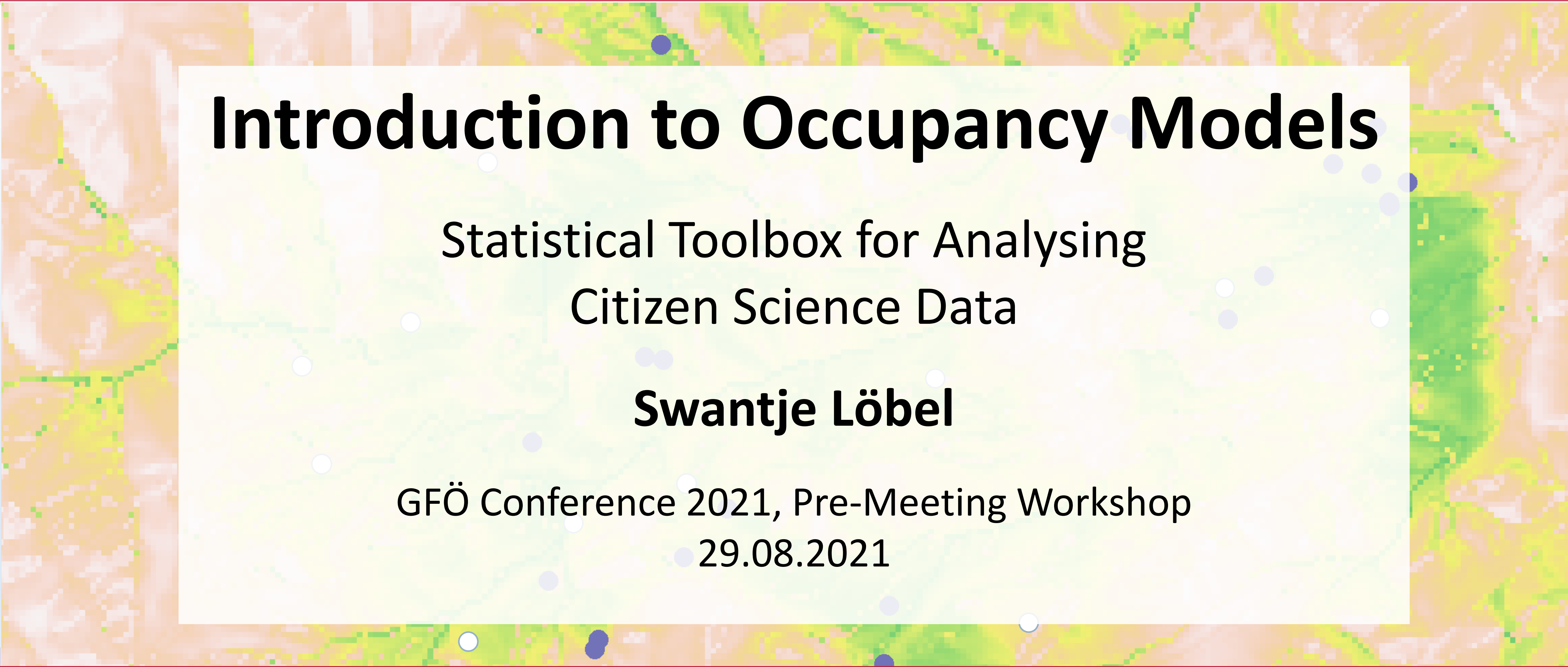


Introduction to Occupancy Models

Statistical Toolbox for Analysing
Citizen Science Data

Swantje Löbel

GFÖ Conference 2021, Pre-Meeting Workshop
29.08.2021

Introduction to Occupancy Models

The **occurrence** of a species at a given location in your data is the result of two processes:

1. The species is actually present

&

2. You detect the species in your survey

The **absence** of a species at a given location in your data is either the result of:

1. The species is actually absent

|

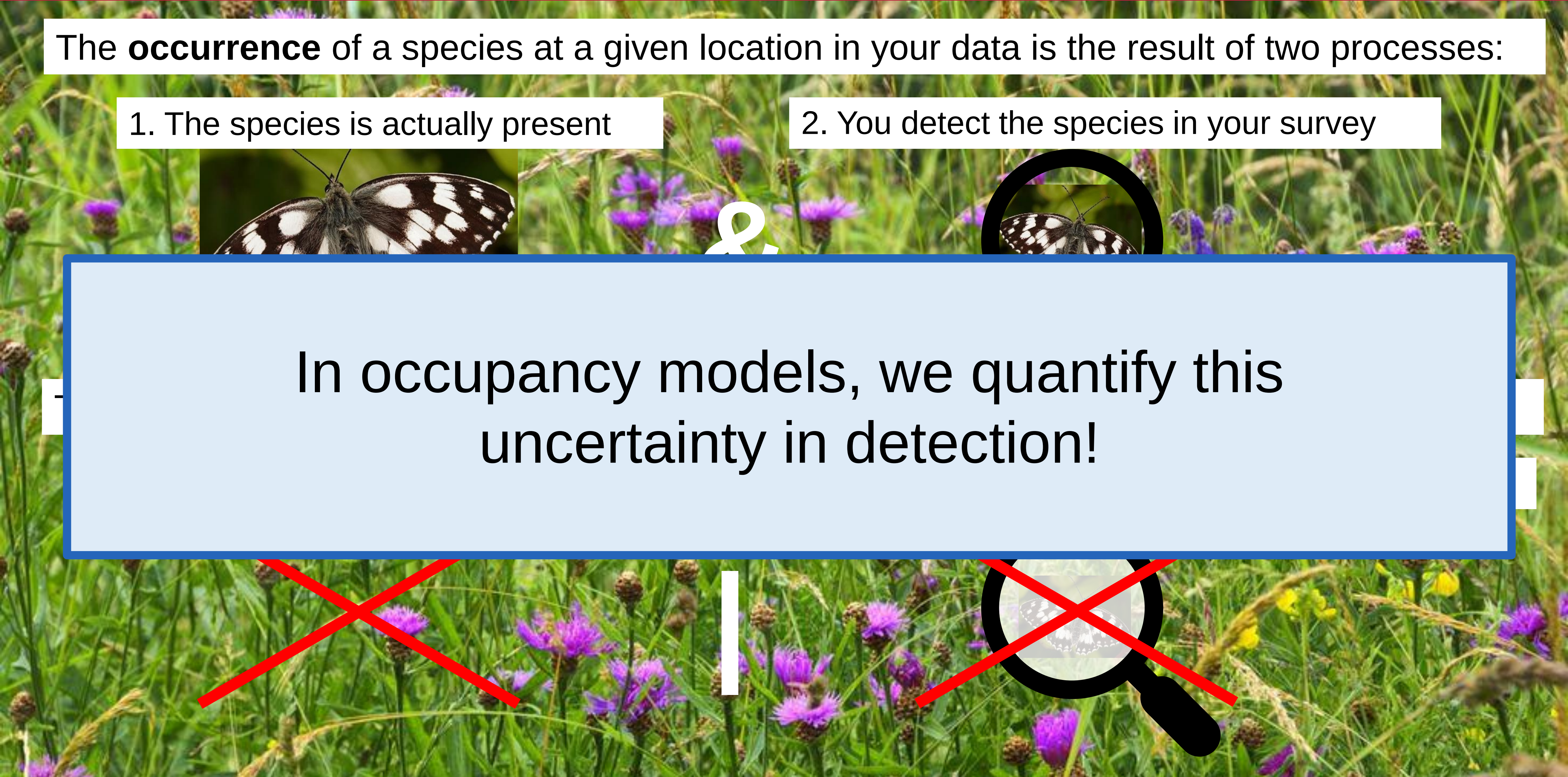
2. You did not detect the species in your survey

Introduction to Occupancy Models

The **occurrence** of a species at a given location in your data is the result of two processes:

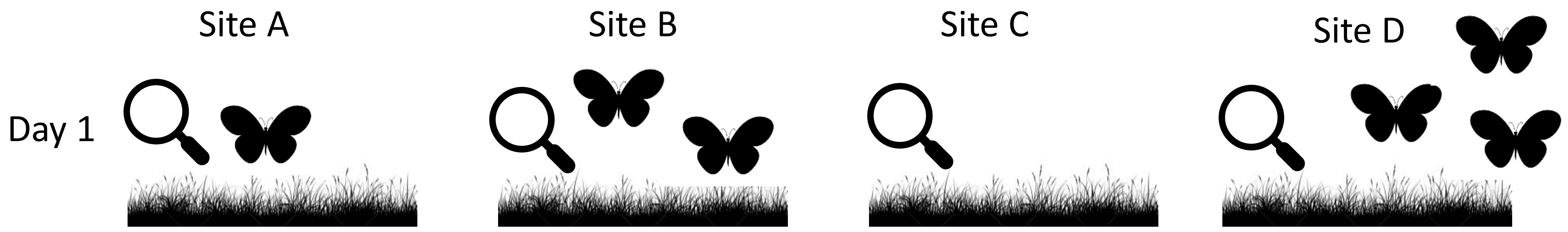
1. The species is actually present

2. You detect the species in your survey



In occupancy models, we quantify this uncertainty in detection!

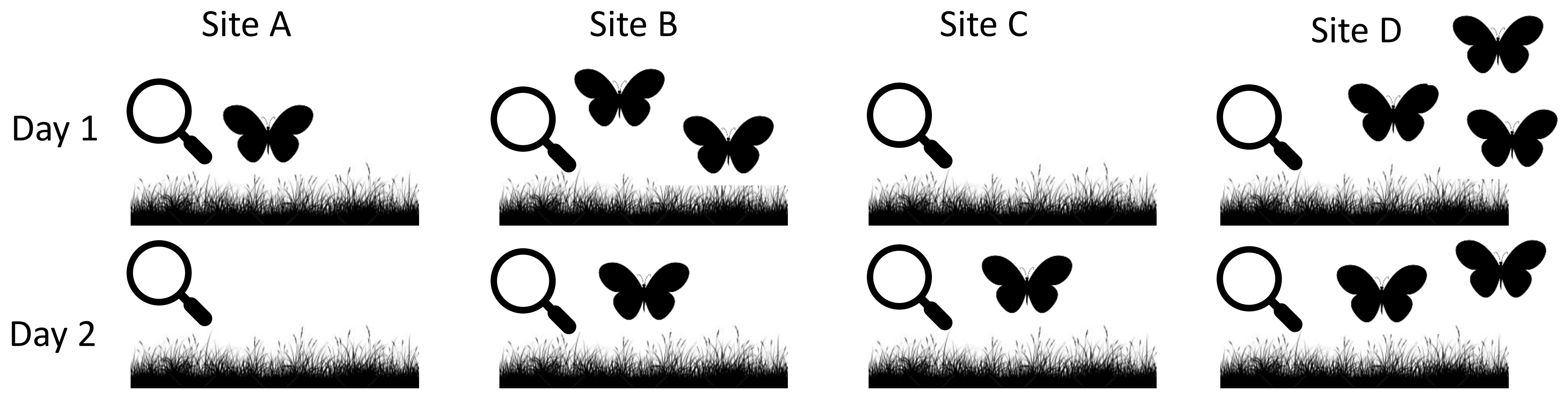
Study design to estimate detection probability



- We visit 4 sites – each site is visited once
- At each site, we count the number of butterflies we see

- Can we separate detection rate from true occurrence rate? NO !

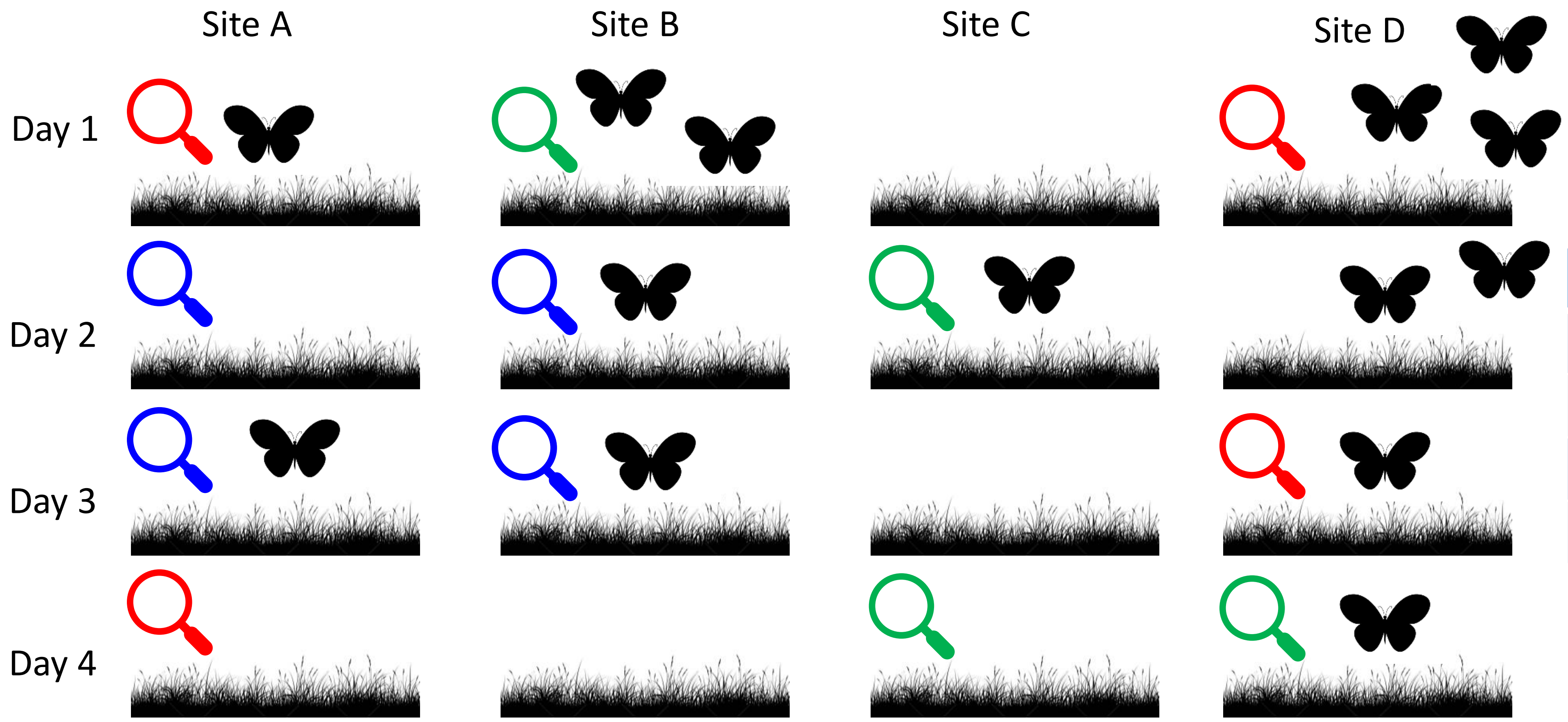
Study design to estimate detection probability



- We visit 4 sites – each site is visited twice on different days
- At each site and on each day, we count the number of butterflies we see

- Can we separate detection rate from true occurrence rate? YES !

Study design to estimate detection probability



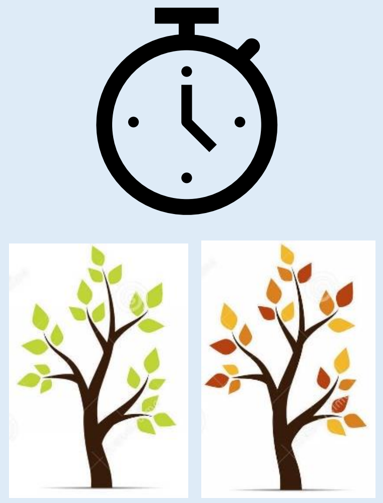
	A	B	C	D
D1	1	2	NA	3
D 2	0	1	1	2
D 3	1	1	NA	1
D 4	0	NA	0	1

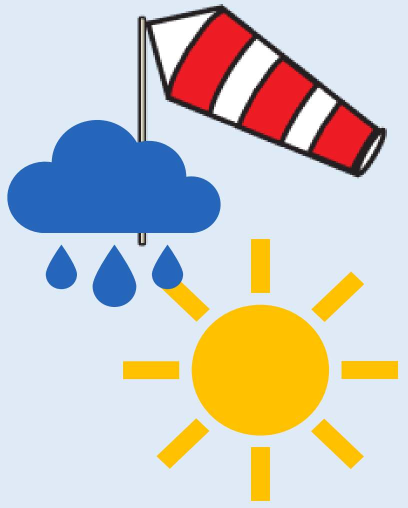
Typical design while working with Citizen Science Data

Occupancy models

Assumptions:

➢ Detection probability is constant or explained by covariates.





Observer

Sampling effort

Timing

Climate/
Weather

Habitat

Occupancy models

Assumptions:

- Detection probability is constant or explained by covariates.
- **Closure:** We require that the (true) presence/absence state of Site i does not change over the course of the study (or one season) !
- No false positive errors
- Independence of occurrence and independence of detection
- No residual spatial autocorrelation

Occupancy model as two connected binomial GLMs

- Process or state model

$$Z_i \sim \mathit{Bernoulli}(\psi_i)$$

Ecological process yields true state (Z)

Latent variable – true species presence or absence

→ simple Bernoulli model with an occurrence probability (ψ).

- Observation or detection model

$$y_{ij} \mid Z_i \sim \mathit{Bernoulli}(Z_i * p_{ij})$$

Observation model links the observations (y = our data) to the state variable (Z).

→ standard observation model is a Bernoulli model. p is the estimated detection probability.

Occupancy model as two connected binomial GLMs

- Process or state model

$$Z_i \sim Bernoulli(\psi_i)$$

We can add linear predictors to both the occurrence probability ($\boldsymbol{\psi}$, psi) and detection probability ($\boldsymbol{p}$)

logit $(\psi_i) = \beta_0 + \beta_1$ * occupancy.covar$_i$ + ...

→ simple Bernoulli model with an occurrence probability ($\boldsymbol{\psi}$).

- Observation or detection model

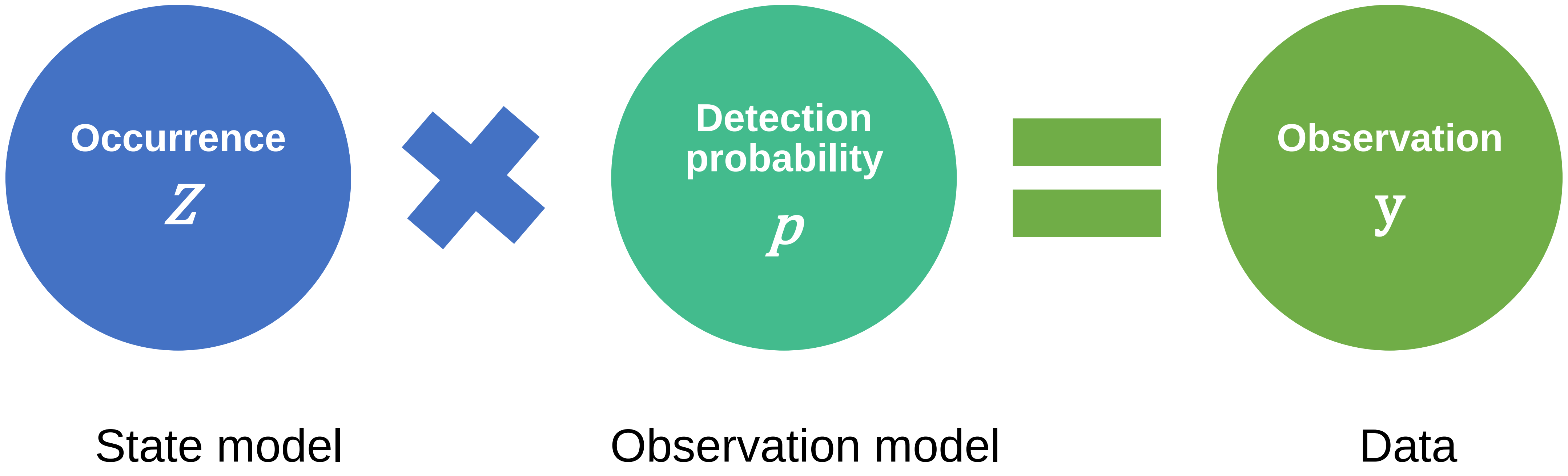
$$y_{ij} \mid Z_i \sim Bernoulli(Z_i * p_{ij})$$

logit $(p_{ij}) = \alpha_0 + \alpha_1$ * detection.covar$_{ij}$ + ...

→ standard observation model is a Bernoulli model. $\boldsymbol{p}$ is the estimated detection probability.

You can include the same or separate covariates in the detection and occupancy components of the model !

Occupancy model as two connected binomial GLMs

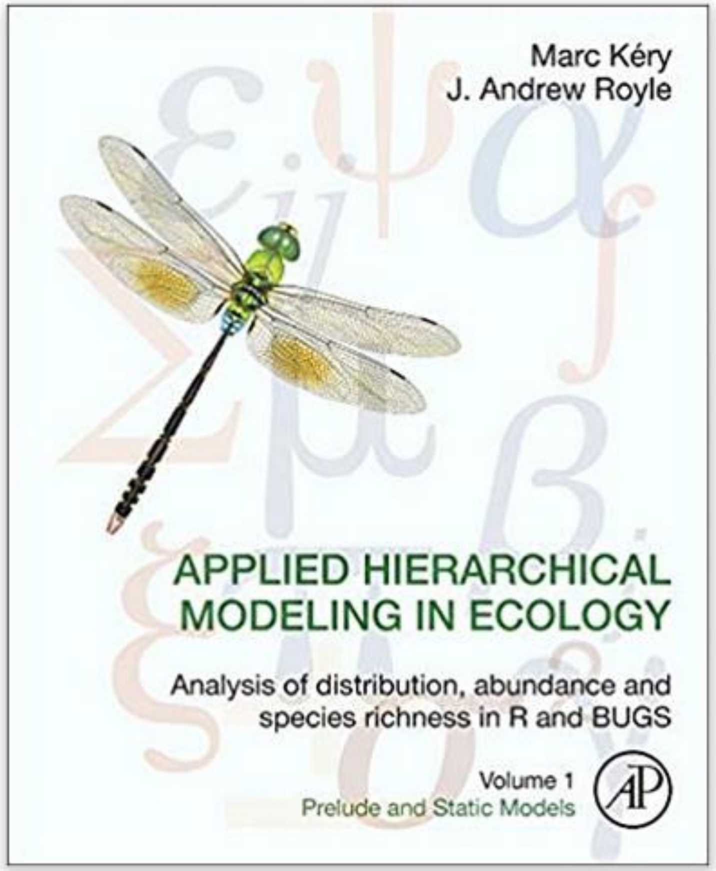


The ***unmarked*** package

Authors: Ian Fiske, Richard Chandler, Andy Royle, Marc Kéry, David Miller, and Rebecca Hutchinson

“Fits hierarchical models of animal abundance and occurrence to data collected using survey methods such as point counts, site occupancy sampling, distance sampling, removal sampling, and double observer sampling. Parameters governing the state and observation processes can be modeled as functions of covariates.”

- ➢ easy to use for experienced R-Users
- ➢ Bayesian knowledge is not required (frequentists statistical package !)
- ➢ less flexible than coding in traditional BUGS-Language
- ➢ often less efficient while working with sparse detection-nondetection matrices


Marc Kéry
J. Andrew Royle
APPLIED HIERARCHICAL MODELING IN ECOLOGY
Analysis of distribution, abundance and species richness in R and BUGS
Volume 1
Prelude and Static Models

The *unmarked* package

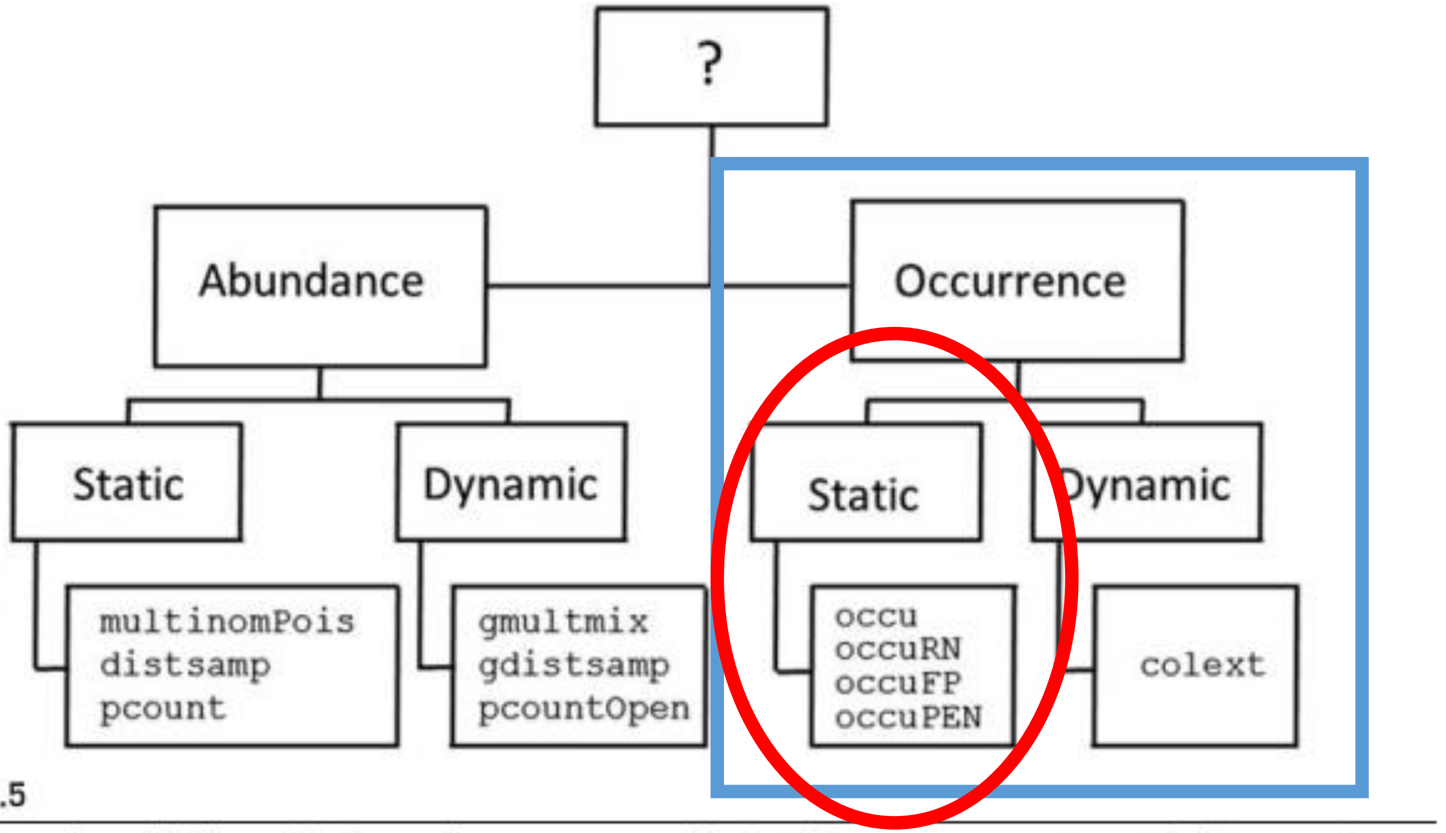


FIGURE 2.5

Decision tree for available models in R package unmarked. A scientific or management question (the question mark in the top square) first suggests a focus on either abundance or occurrence; second, the system is static or dynamic; and third, you use a particular sampling method; all of these determine the appropriate model for your study. *(Figure courtesy of R. Chandler.)*

From: Kéry & Royle (2016)

Using the *unmarked* package

(1) Processing and packaging the data into an "unmarked frame" using standard constructor functions that ensure data are in the proper format (unmarkedFrameOccu()).

```
library(unmarked)
    umf <- unmarkedFrameOccu(
      y = y,                                                 # Pres/Abs measurements
      siteCovs = data.frame(vegHt = vegHt, hab = hab),   # Site covariates
      obsCovs = list(wind = wind, obsID = observerID ))  # Observation covariates
    summary(umf)
```

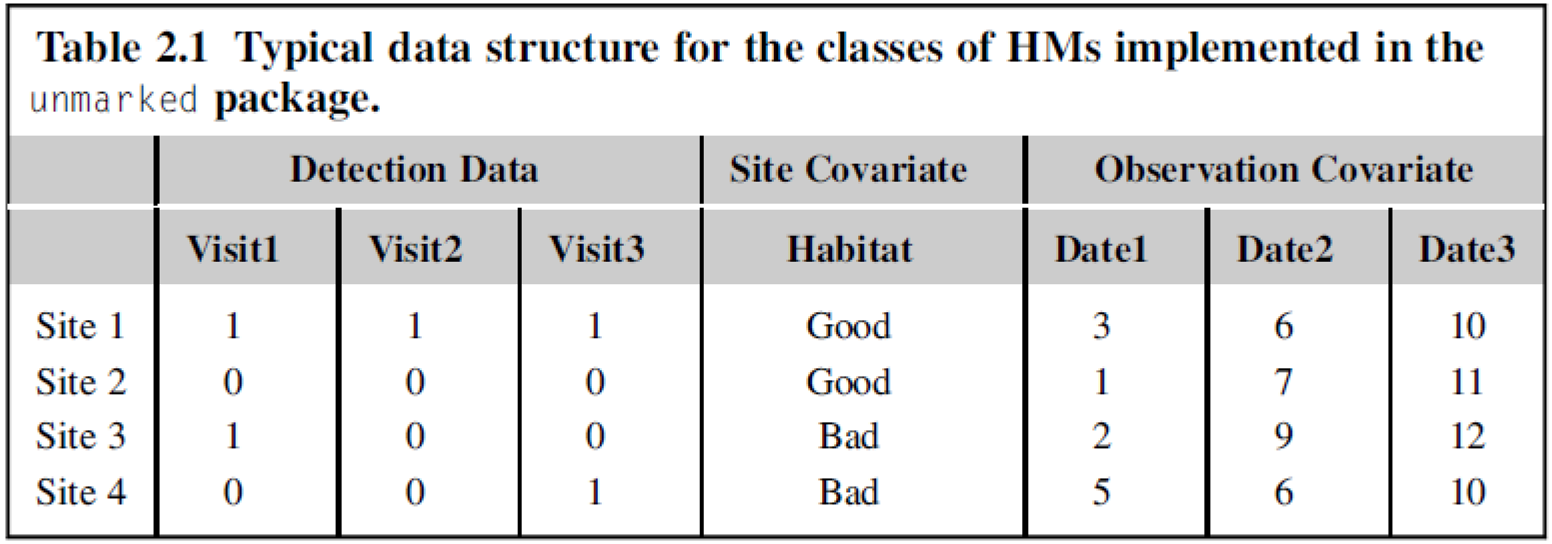


Table 2.1 Typical data structure for the classes of HMs implemented in the unmarked **package.**

	Detection Data			Site Covariate	Observation Covariate		
	Visit1	Visit2	Visit3	Habitat	Date1	Date2	Date3
Site 1	1	1	1	Good	3	6	10
Site 2	0	0	0	Good	1	7	11
Site 3	1	0	0	Bad	2	9	12
Site 4	0	0	1	Bad	5	6	10

Using the *unmarked* package

(1) Processing and packaging the data into an “unmarked frame” using standard constructor functions that ensure data are in the proper format (unmarkedFrameOccu()).

```
library(unmarked)
    umf <- unmarkedFrameOccu(
      y = y,                                               # Pres/Abs measurements
      siteCovs = data.frame(vegHt = vegHt, hab = hab),    # Site covariates
      obsCovs = list(wind = wind, obsID = observerID ))   # Observation covariates
```

(2) Utilization of a standard model fitting function that produces parameter estimates, standard errors, AIC, and other summary statistics.

```
library(unmarked)
    fm1 <- occu( ~ Detection_Covariates   ~ Occupancy_Covariates , data = umf)
```

Detection model

Occupancy model

(3) Summary analyses that include producing model selection tables, goodness-of fit analyses (e.g., using parametric bootstrapping), and plotting predictions or fitted values.

Fitting occupancy models in ***unmarked*** – occu()

```
fm  <- occu( ~ Detection_Covariates ~ Occupancy_Covariates, data = umf)

fm0 <- occu(~ 1 ~ 1, data=umf)                     # intercepts only
fm1 <- occu(~ wind ~ 1, data=umf)                # covariates on detection
fm2 <- occu(~ 1 ~ habitat, data=umf)              # covariates on occupancy
fm3 <- occu(~ wind + observer ~ habitat, data=umf)  # covariates on both

summary(fm3)
```

```
Call:
occu(formula = ~wind ~ habitat, data = umf)

Occupancy (logit-scale):
            Estimate    SE      z  P(>|z|)
(Intercept)   -0.232 0.303 -0.765 4.44e-01
habitat        2.598 0.648  4.012 6.03e-05

Detection (logit-scale):
            Estimate    SE     z  P(>|z|)
(Intercept)    -1.04 0.230 -4.53 5.83e-06
wind           -2.51 0.378 -6.65 3.02e-11
```

Technische Universität Braunschweig

Fitting occupancy models in ***unmarked*** – `occu()`

```
fm  <- occu( ~ Detection_Covariates ~ Occupancy_Covariates, data = umf)

fm0 <- occu(~ 1 ~ 1, data=umf)                    # intercepts only
fm1 <- occu(~ wind ~ 1, data=umf)                # covariates on detection
fm2 <- occu(~ 1 ~ habitat, data=umf)              # covariates on occupancy
fm3 <- occu(~ wind + observer ~ habitat, data=umf)  # covariates on both

summary(fm3)
fm3@AIC
LRT(fm2, fm3)

pred.occ <- predict(fm3, type="state", newdata=newdat)
pred.det <- predict(fm3, type="det", newdata=newdat)
```

Extract latent variable: *Z*

```
ranef(fm3)
```

State process $Z_i \sim Bernoulli(\psi_i)$

```
              Mean Mode 2.5% 97.5%
[1,] 0.015231766    0    0     0
[2,] 0.017820736    0    0     0
[3,] 0.058991790    0    0     1
[4,] 1.000000000    1    1     1
[5,] 0.011251114    0    0     0
[6,] 0.072711276    0    0     1
[7,] 0.015363369    0    0     0
[8,] 0.058627194    0    0     1
[9,] 1.000000000    1    1     1
```

- These random effects are the presence/absence state at each site (*Z*), and their estimates represent our best guess of whether a particular site is occupied or not.
- These predictions of the random effects *Z* are also called **conditional** occupancy probability, where conditional means “given the observed data at that site”.

Extract latent variable: *Z*

```
ranef(fm3)
```

State process $Z_i \sim Bernoulli(\psi_i)$

```
         Mean Mode 2.5% 97.5%
[1,] 0.015231766    0    0     0
[2,] 0.017820736    0    0     0
[3,] 0.058991790    0    0     1
[4,] 1.000000000    1    1     1
[5,] 0.011251114    0    0     0
[6,] 0.072711276    0    0     1
[7,] 0.015363369    0    0     0
[8,] 0.058627194    0    0     1
[9,] 1.000000000    1    1     1
```

- If species was detected at a site, then *Z* is 1 with no uncertainty!!

Extract latent variable: *Z*

```
ranef(fm3)
```

State process $Z_i \sim Bernoulli(\psi_i)$

```
                 Mean Mode 2.5% 97.5%
[1,] 0.015231766     0    0     0
[2,] 0.01782
                         y[1,]        [1] 0 0 0
[3,] 0.05899
[4,] 1.000000000     1    1     1
[5,] 0.011251114     0    0     0
[6,] 0.072711276     0    0     1
[7,] 0.015363369     0    0     0
[8,] 0.058627194     0    0     1
[9,] 1.000000000     1    1     1
```

- Predicting *Z* at a site when species never detected

$$\Pr(z_i = 1 | \{y_i\} = 0) = \frac{\psi(1-p)^J}{(1-\psi)+\psi(1-p)^J}$$

- Model will predict some probability that the species was there

- We have higher confidence in its presence (*Z*=1) despite the negative survey results (*y*=0,0,0) when

1. it is widespread overall (occurrence probability *Ψ* is high),
2. it is elusive (detection probability *p* is small),
3. the number of times we have looked for it (*J*) is small.

Derived parameters: Number of occupied sites

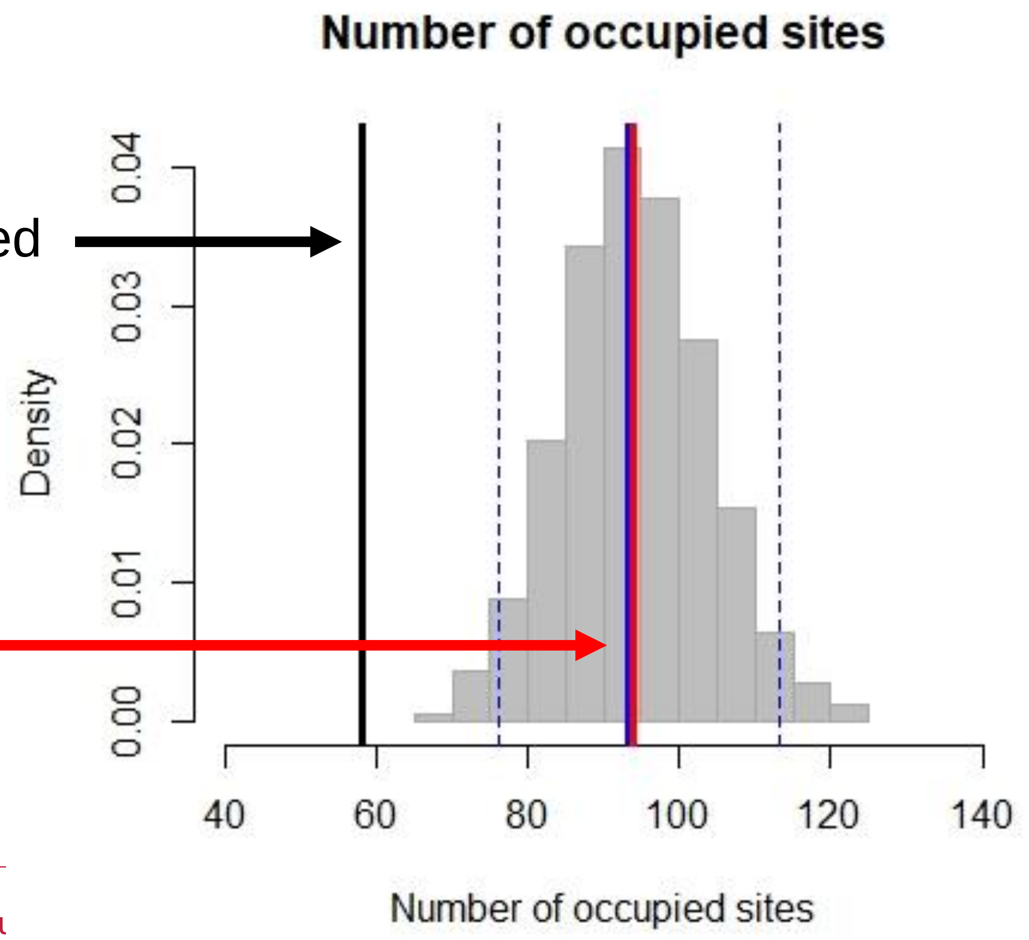
- In **unmarked**, we can obtain the number of occupied sites by summing over the estimates of the random effects *Z*.

- Parametric bootstrapping can be used to obtain a confidence interval.

Observed

Species was only seen at 58 sites but was estimated to be present at ~ 93 sites by the model

True number of occupied sites = 94



Why Bootstrapping ?

- For complicated functions, we often compute standard errors and confidence intervals using the method of bootstrapping.
- Parametric bootstrapping - we simulate data sets under the assumed model with parameters equal to the MLEs obtained from our observed data.
- For each simulated data set, we refit the model and obtain the (new) MLEs for the simulated data set. Each set of MLEs thus obtained is called a bootstrap sample, and together they form the bootstrap distribution.
- We can summarize to obtain quantities of interest. For example, the variance of the bootstrap samples is an estimate of the sampling variance. The 0.025 and 0.975 percentiles of the bootstrap distribution form a 95% confidence interval.

Fitting occupancy models in ***JAGS***

What is JAGS?

- JAGS is ‘Just Another Gibbs Sampler’: a software package for performing Bayesian inference Using Gibbs Sampling
- Using a dialect of the BUGS language (WinBUGS, OpenBUGS, STAN)
- It estimates parameter posterior distributions for Bayesian statistical models, of (almost) arbitrary complexity, defined by the relationships between variables.
- JAGS uses MCMC simulation to converge on the posterior distribution of our parameters.

We will access the **JAGS** functionalities within **R**. The package **`rjags`** provides an interface that allows us to handle pre-processing of data, the model estimation and the post-processing of results all together in one R session.

Fitting occupancy models in *JAGS*

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

Model specification in the BUGS syntax

- A BUGS model basically describes relationships between some variables in terms of conditional probability distributions.
- BUGS uses a syntax looking quite similar to R. But be aware: the model description is nothing like a run-able script but just describes the relations between variables in the model!
- Most important elements of the syntax include:

  `x <-` ... '**logical node**' describes x as a deterministic function of some other variables

  `x ~` ... '**stochastic node**' describes a probability distribution of x conditional on some other variables

- Variety of in-build probability distributions: `dnorm(mu,tau)`, `dbin(p,n)`, `dbern(p)`, …
- The BUGS language is not really vectorized - we need loops to define the model for every element in vectors or multidimensional arrays.

Some notes on priors …

10 basic steps of a Bayesian model analysis with JAGS

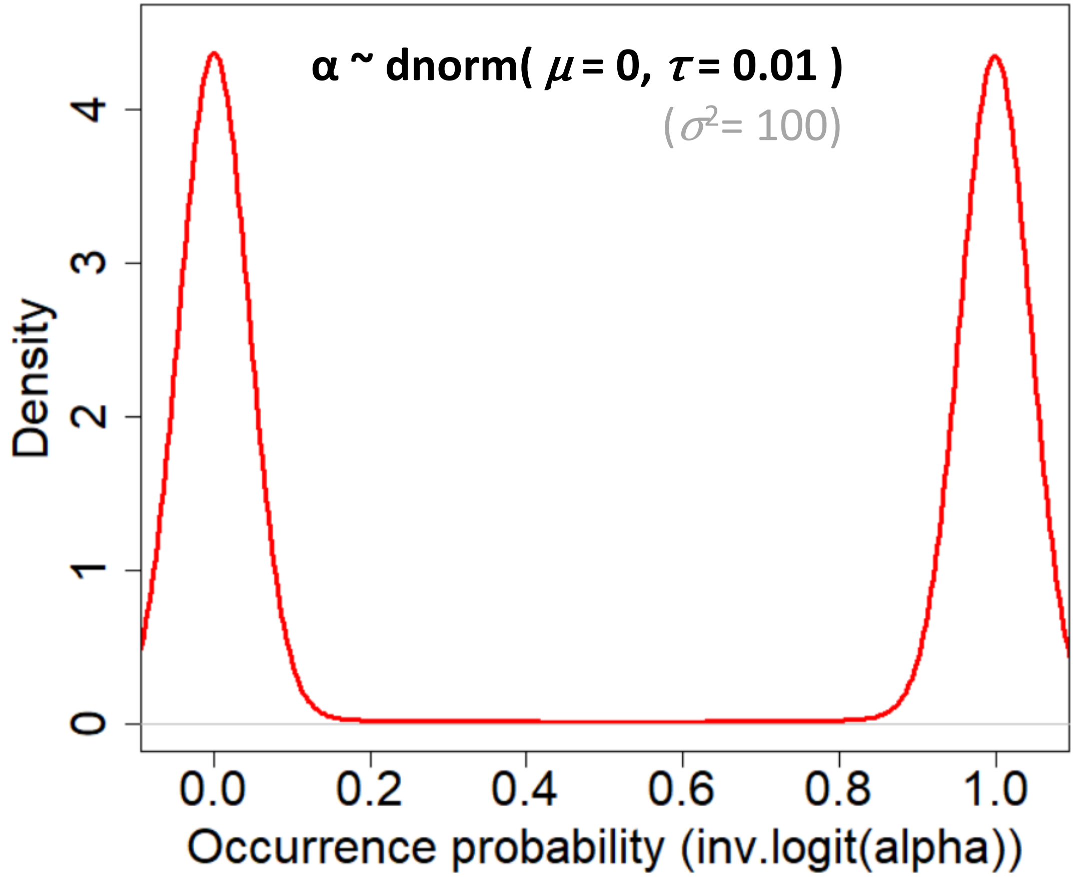
(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

(3) Think about the necessary prior distributions

Most ecologists use vague or uninformative priors, but be careful… priors might not always be as uninformative as you think !

Probability distributions in BUGS are defined by μ and precision τ (= $1/\sigma^2$) !



Some notes on priors …

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

(3) Think about the necessary prior distributions

Most ecologists use vague or uninformative priors, but be careful… priors might not always be as uninformative as you think !

≈ flat priors at probability scale
(e.g., for intercept parameters in logistic models)

```
α ~ dlogis(0, 1)        Northrup & Gerber (2018)

mean.p ~ dunif(0, 1)    Kéry & Royle (2016)
α <- logit(mean.p)

α ~ dnorm(0, 0.5)       Hobbs & Hooten (2015)
```

Choice of priors for slope parameters is often less problematic, typical priors are

```
β ~ dnorm(0, 0.1)     → σ² = 10
β ~ dnorm(0, 0.01)    → σ² = 100

β ~ dunif(-10, 10)
β ~ dunif(-20, 20)
```

The less information your data contains, the more impact has the choice of prior!

Recommendation: Perform a sensitivity analysis with different priors. If your posterior samples differ much – you should think further about your choice of prior.

Model specification in the BUGS syntax

```
cat(file = "StaticOccupancyModel.txt","
model{

    ## Specify priors
    beta0.occ ~  dlogis(0,1)               ## prior on occupancy intercept
    beta1.occ ~  dnorm(0,0.01)             ## prior on slope occupancy covariate
    alpha0.det ~ dlogis(0,1)               ## prior on detection intercept
    alpha1.det ~ dnorm(0,0.01)             ## prior on slope detection covariate

    for (i in 1:nSites) {                  ## Loop over Sites
     #--- True state model for the partially observed true state ---#
      z[i] ~ dbern(psi[i])                 ## True occupancy z at site i
      logit(psi[i]) <- beta0.occ + beta1.occ * occ.cov[i]

       for (j in 1:nVisits) {               ## Loop over Visits
         #--- Observation model for the actual observations ---#
          y[i,j] ~ dbern(muy[i,j])          ## Detection-nondetection at i and j
          muy[i,j] <- z[i] * p[i,j]
          logit(p[i,j]) <- alpha0.det + alpha1.det * det.cov[i,j]

         } #j
    } #i
}
")
```

Fitting occupancy models in *JAGS*

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

(3) Think about the necessary prior distributions

(4) Assemble your data

- ➢ format your data as a named list

```
BugsData <- list(y=y, nSites=dim(y)[1], nVisits=dim(y)[2],
                 occ.cov=VegHeight, det.cov=Wind)
```

Fitting occupancy models in *JAGS*

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

(3) Think about the necessary prior distributions

(4) Assemble your data

(5) Generate (overdispersed) initial parameter values

```
## Inits function
zst <- apply(y, 1, max)    ## Starting values for latent states
inits.fn <- function() {list(z = zst, beta0.occ=runif(1, -5, 5),
                             alpha0.det = runif(1, -5, 5)), …}
```

Fitting occupancy models in *JAGS*

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

(2) Formulate a model and code it in the BUGS syntax

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(4) Assemble your data

(5) Generate (overdispersed) initial parameter values

(6) Set the MCMC parameters (n.chains, n.iter, thin, …)

```
n.chains = 3          # Number of chains (typically 3)
n.iter = 5000         # Total number of iterations (start with few)
n.burnin = 2500       # Burnin-length (Samples before will be discarded)
n.thin = 1            # e.g., thin = 1 → All samples are kept, thin = 10
                        → every 10th sample will be kept
parameters.to.save = c(beta0.occ, alpha0.det, … )
                      # Which parameters should be saved?
```

Fitting occupancy models in *JAGS*

10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question

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(4) Assemble your data

(5) Generate (overdispersed) initial parameter values

(6) Set the MCMC parameters (n.chains, n.iter, thin, …)

(7) Call and run JAGS

```
jagsModel <- jags(model.file="StaticOccupancyModel.txt",
                  data=BugsData, inits = inits.fn, n.chains = 3,
                  n.iter=5000, n.burnin=2500,n.thin=1,
                  parameters.to.save=para.names, DIC=T)
```

Fitting occupancy models in ***JAGS***

10 basic steps of a Bayesian model analysis with JAGS

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(4) Assemble your data

(5) Generate (overdispersed) initial parameter values

(6) Set the MCMC parameters (n.chains, n.iter, thin, …)

(7) Call and run JAGS

(8) Check your obtained posterior samples for convergence (traceplot, R-hat < 1.1)

```
print(jagsModel)
traceplot(jagsModel)
gelman.plot(jagsModel)
```

Fitting occupancy models in *JAGS*

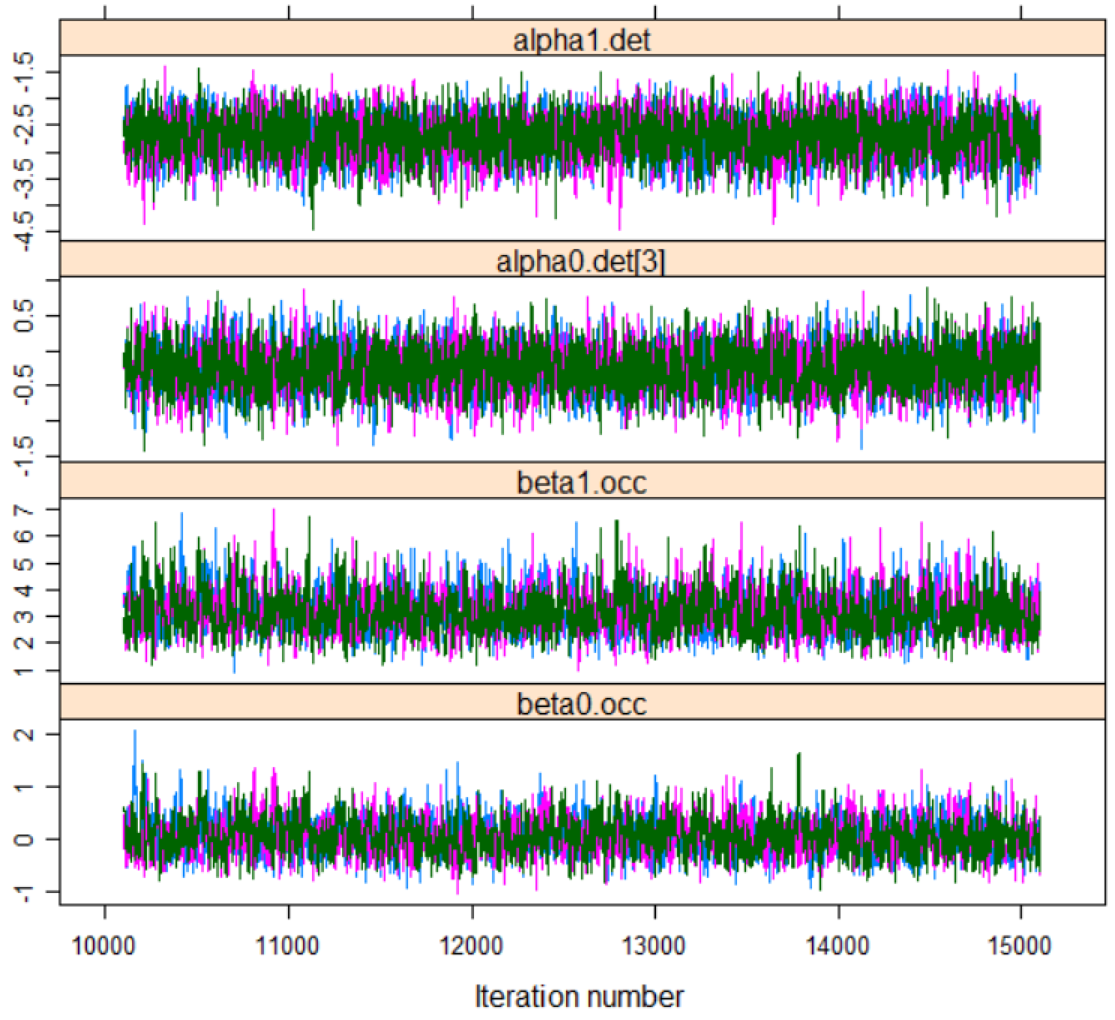
```r
print(jagsModel)
```

```
JAGS output for model 'StaticOcc_Veg_WindObsID.txt', generated by jagsUI.
Estimates based on 3 chains of 5000 iterations, …

                 mean     sd    2.5%     50%   97.5% overlap0     f  Rhat n.eff
beta0.occ       0.033  0.327  -0.564   0.013   0.724     TRUE 0.517 1.001  3609
beta1.occ       3.116  0.769   1.792   3.057   4.821    FALSE 1.000 1.002  1215
alpha0.det     -2.213  0.420  -3.042  -2.219  -1.393    FALSE 1.000 1.001  7500
alpha1.det     -2.715  0.390  -3.503  -2.697  -1.992    FALSE 1.000 1.003  1528
occ.fs         92.491  7.249  79.000  92.000 107.000    FALSE 1.000 1.000  7500
deviance      237.745 15.012 209.222 237.347 267.742    FALSE 1.000 1.000  7500

Successful convergence based on Rhat values (all < 1.1).
Rhat is the potential scale reduction factor (at convergence, Rhat=1).
For each parameter, n.eff is a crude measure of effective sample size.
…
pD = 112.7 and DIC = 350.432
```

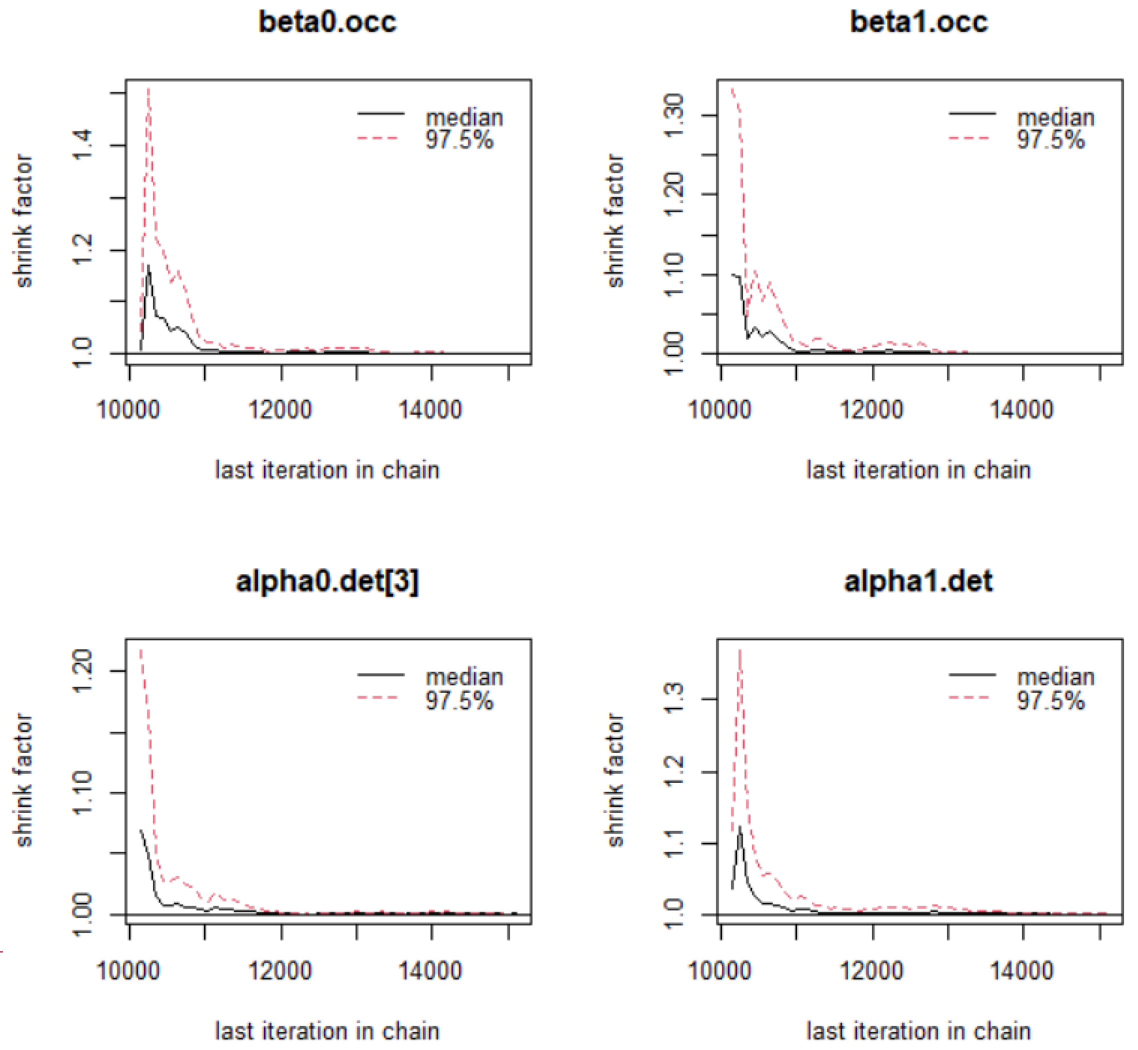
R-hat = Gelman and Rubin's shrink factor
→ Should be < 1.1 for all parameters

Fitting occupancy models in *JAGS*

```
traceplot(jagsModel)  #or
xyplot(jagsModel$samples)
```



```
gelman.plot(jagsModel$samples)
#Gelman and Rubin's shrink factor (R-hat)
```



Fitting occupancy models in ***JAGS***

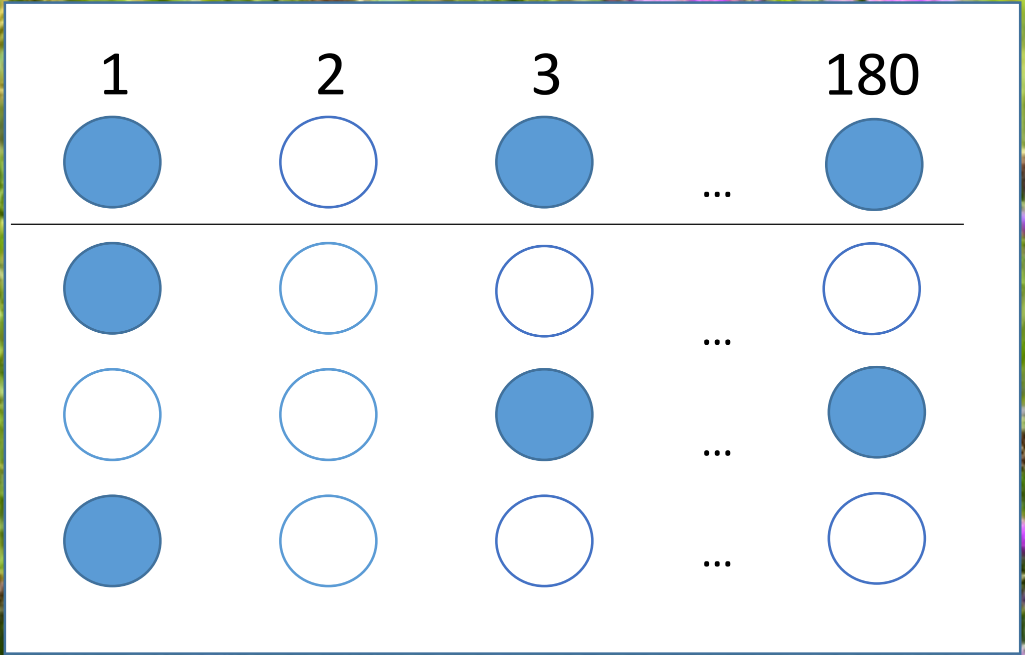
10 basic steps of a Bayesian model analysis with JAGS

(1) Get an idea of your data and your research question
(2) Formulate a model and code it in the BUGS syntax
(3) Think about the necessary prior distributions
(4) Assemble your data
(5) Generate (overdispersed) initial parameter values
(6) Set the MCMC parameters (n.chains, n.iter, thin, …)
(7) Call and run JAGS
(8) Check your obtained posterior samples for convergence (traceplot, R-hat < 1.1)
(9) If necessary, continue with further iterations until convergence
(10) Inspect the posterior sample and analyse it with respect to your research question 1

Lets have fun with **unmarked** and **JAGS !**

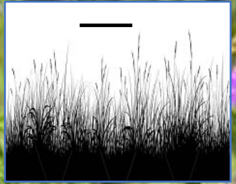
CodingSession_StaticOccupancyModels_SL.R

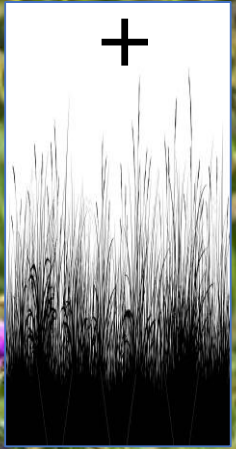
180 sites



3 repeated visits to each site

True state is affected by vegetation height





Variation in detections is used to estimate detection probability, affected by