

Introduction to Occupancy Models

Statistical Toolbox for Analysing
Citizen Science Data

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Introduction to Occupancy models

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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



Introduction to Occupancy models

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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

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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



&

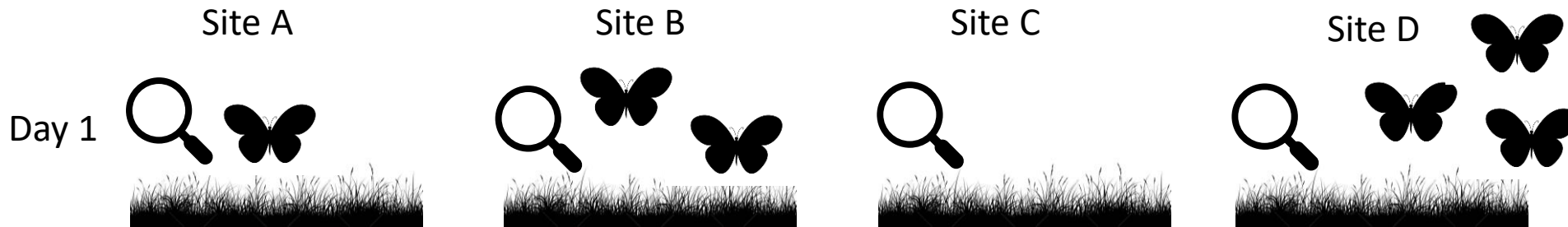


In occupancy models, we quantify this uncertainty in detection!



Study design to estimate detection probability

5

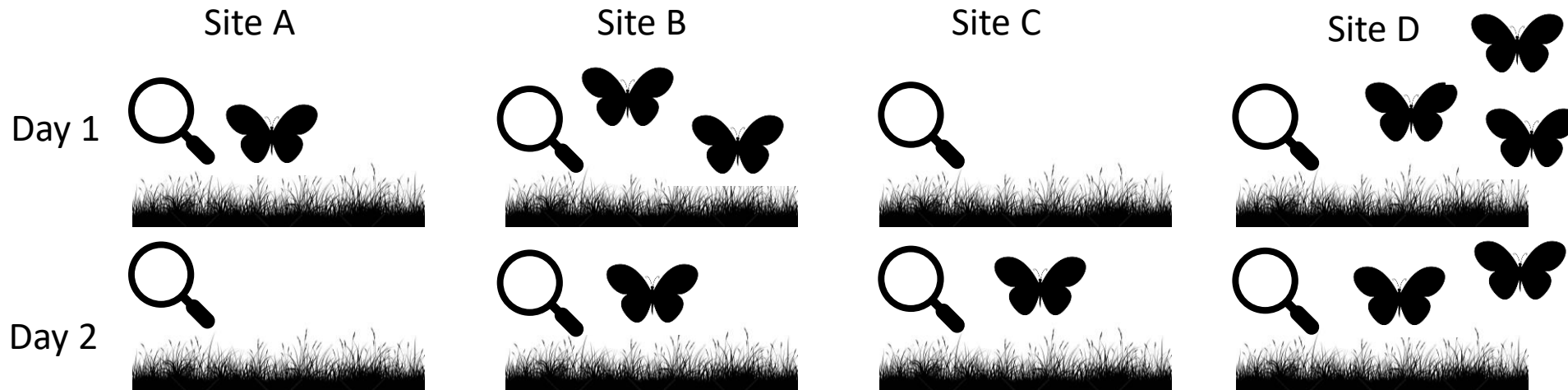


- We visit 4 sites – each site is visited once
- At each site, we count the number of butterflies we see
- Can we separate detection rate from true occurrence rate? **NO !**



Study design to estimate detection probability

6

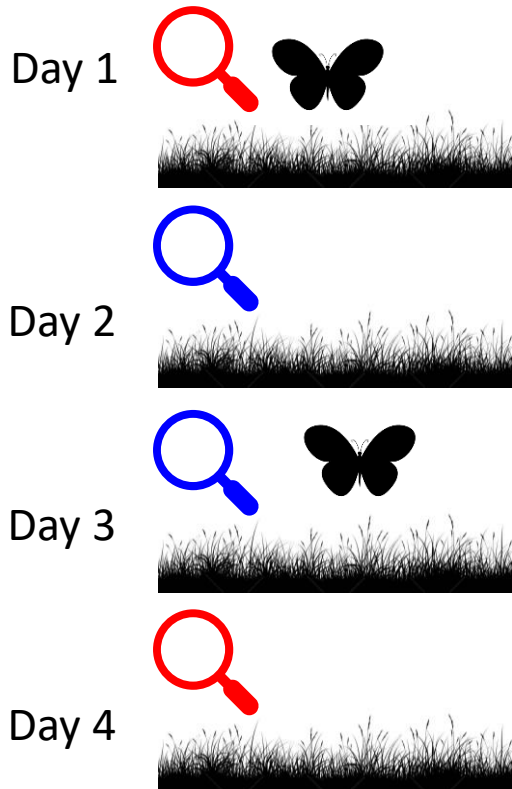


- We visit 4 sites – each site is visited twice on different days
- At each site and on each day, we count the number of butterflies we see
- Can we separate detection rate from true occurrence rate? **YES !**

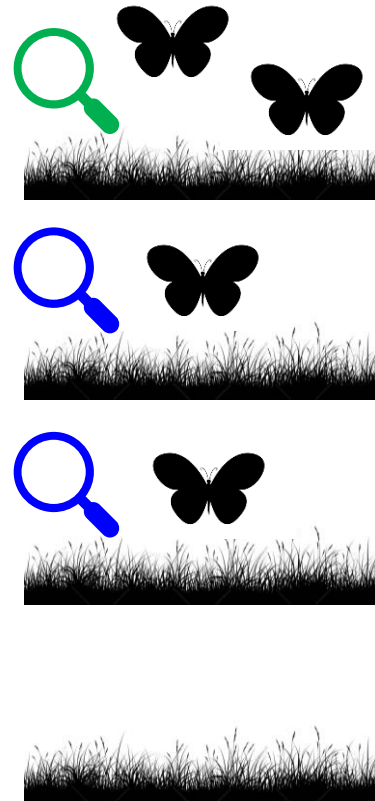
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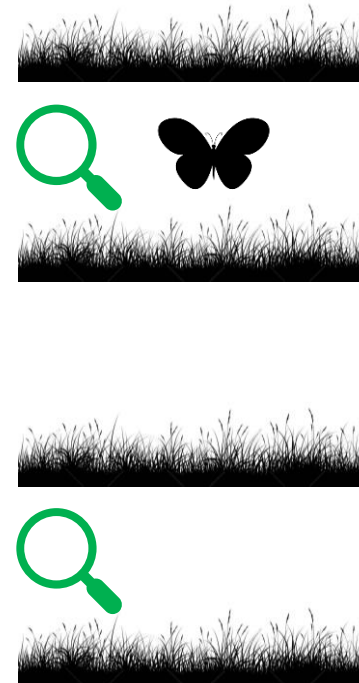
Site A



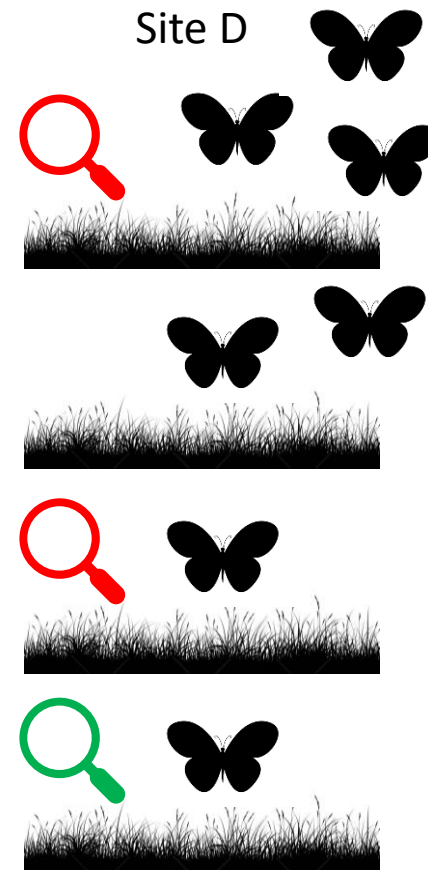
Site B



Site C



Site D



	A	B	C	D
D 1	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



Assumptions:

- Detection probability is constant or explained by covariates.

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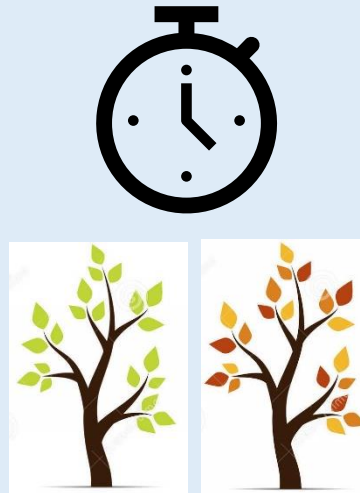
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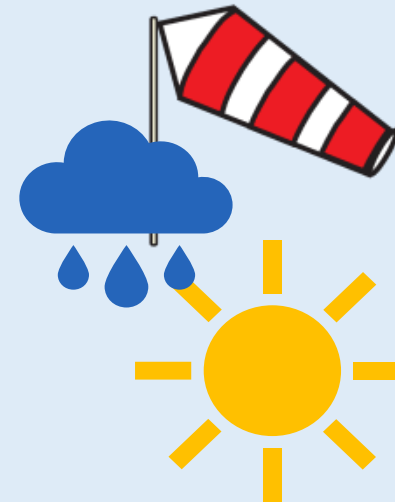
Observer



Sampling effort



Timing



Climate/
Weather



Habitat

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- **Closure:** We require that the (true) presence/absence state of Site i does not change over the course of the study (or one season) !

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- **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
- No residual spatial autocorrelation

- Process or state model

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

Ecological process yields true state (Z)

Latent variable – true species presence or absence

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

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- Observation or detection model

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

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.

- Process or state model

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

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We can add linear predictors to both the occurrence probability (ψ , psi) and detection probability (p)

$$\text{logit}(\psi_i) = \beta_0 + \beta_1 * \text{occupancy.covar}_i + \dots$$

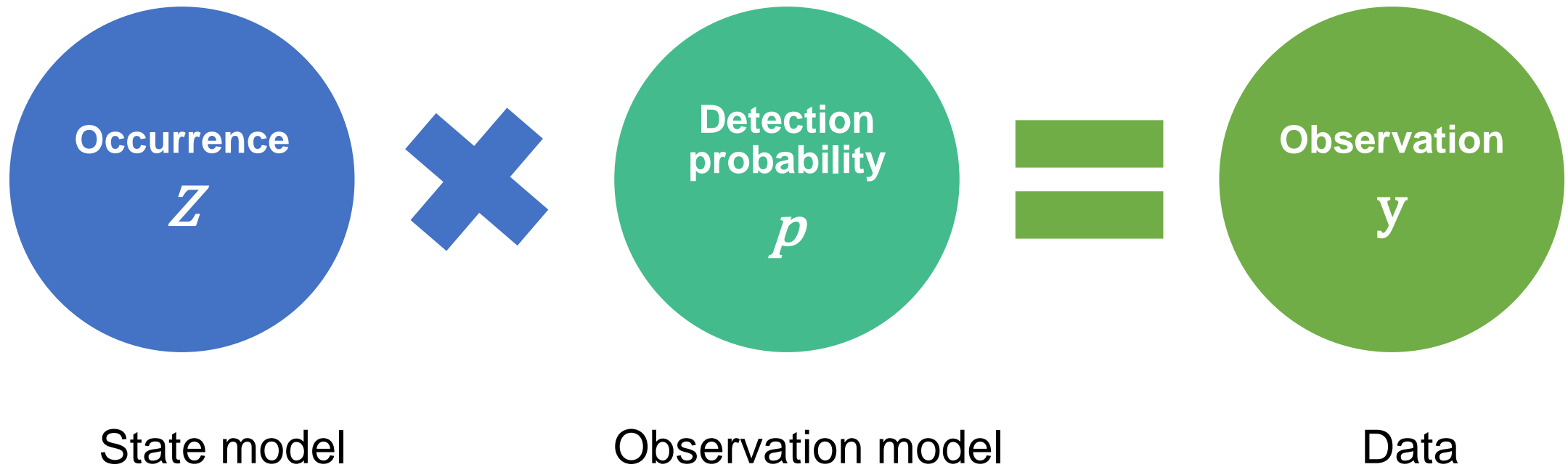
- Observation or detection model

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

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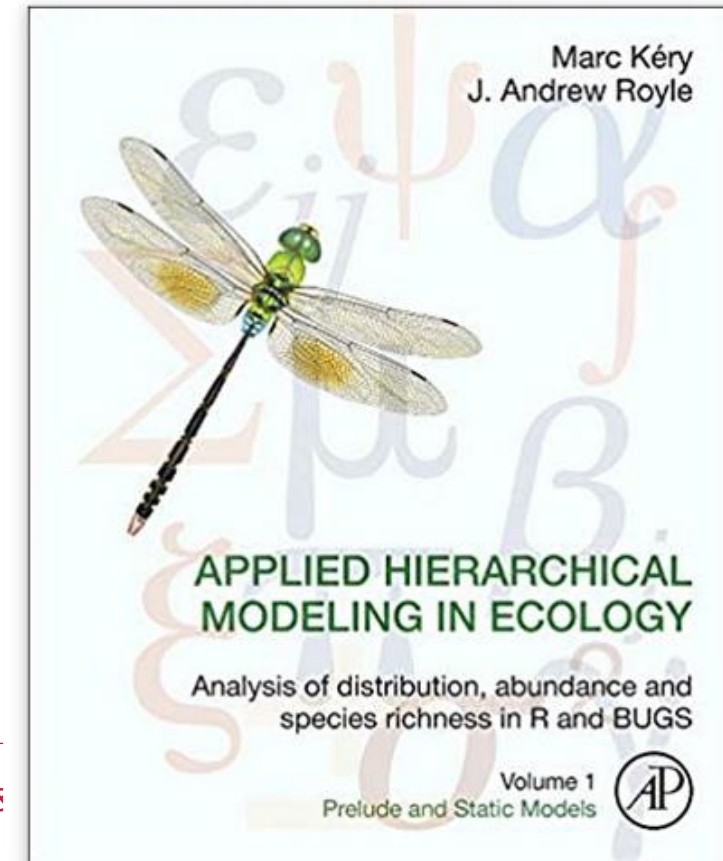
You can include the same or separate covariates in the detection and occupancy components of the model !



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



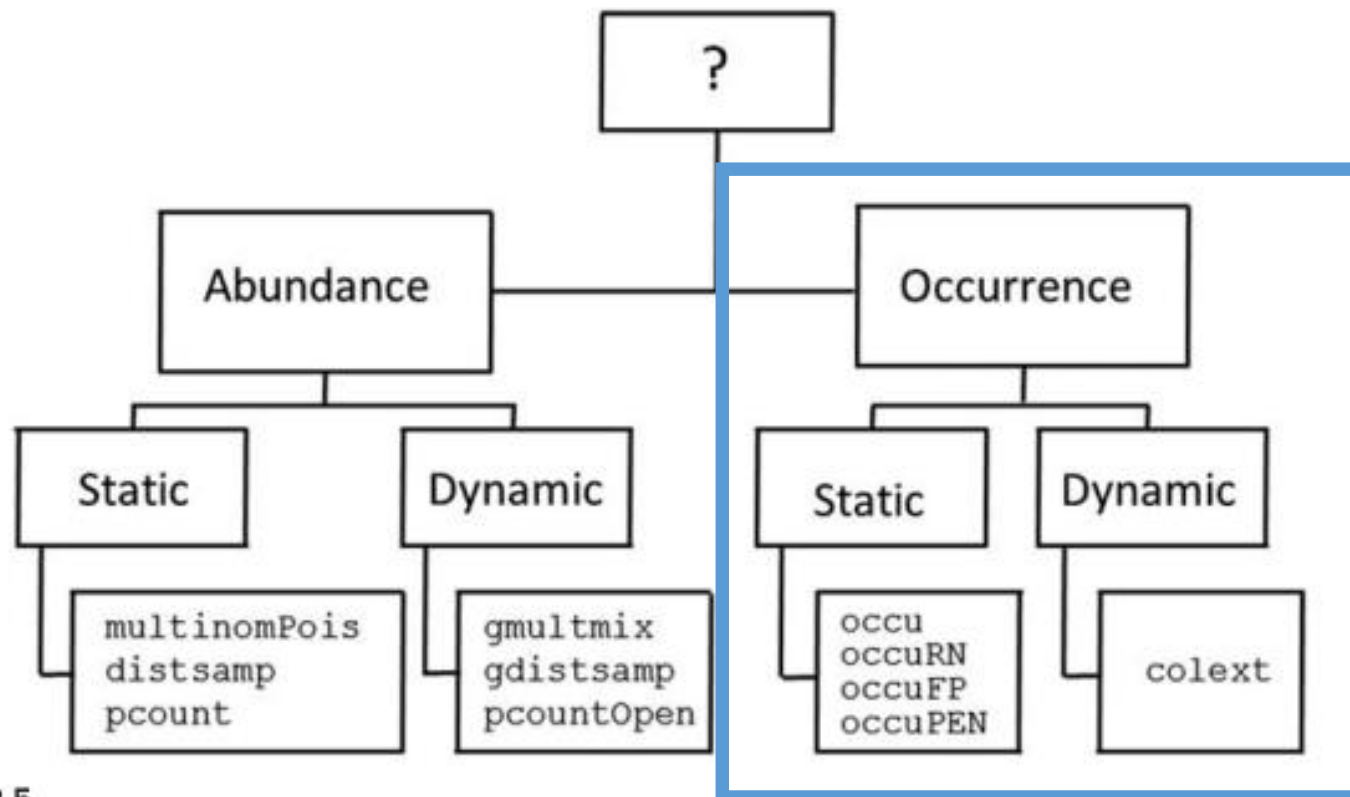


FIGURE 2.5

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)

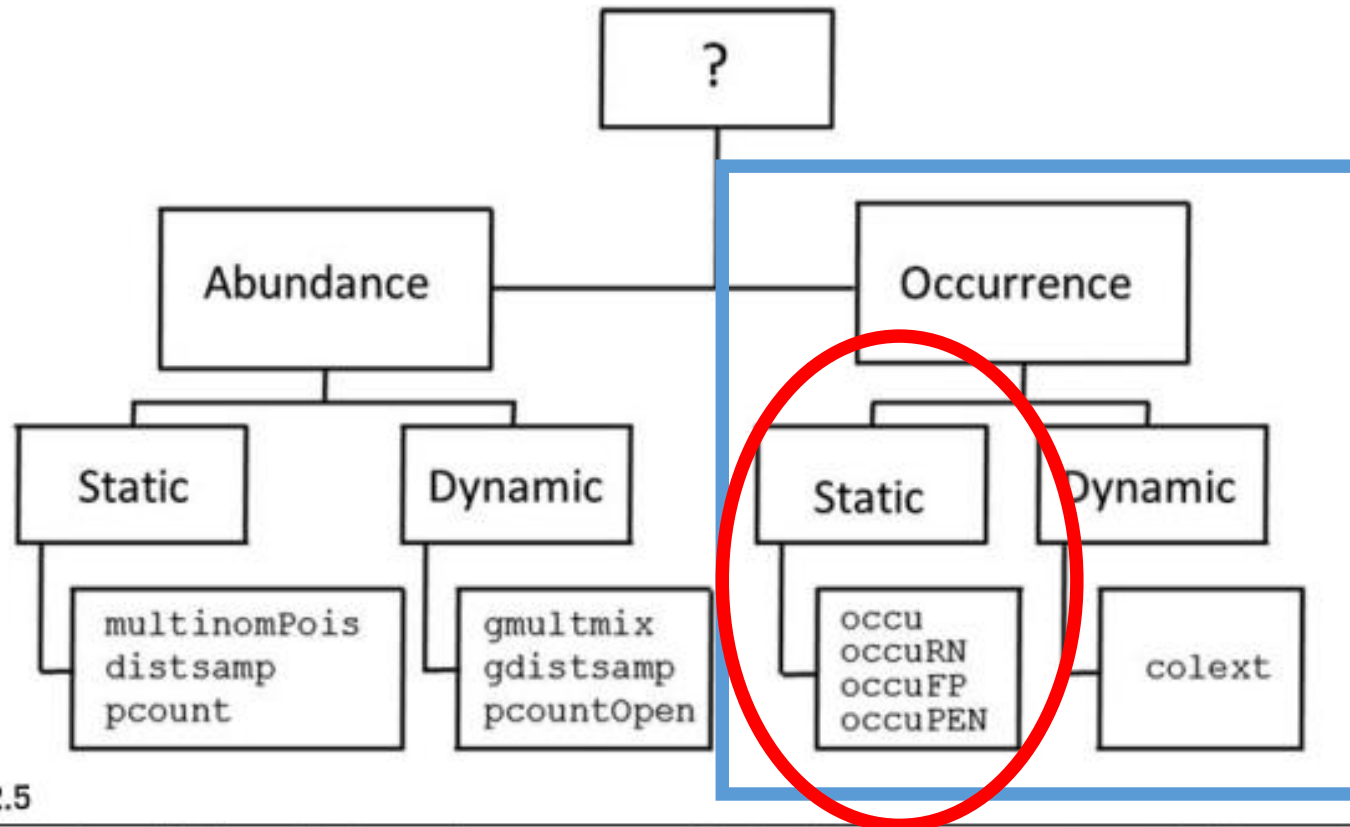


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- (1) Processing and packaging the data into an “unmarked frame” using standard constructor functions that ensure data are in the proper format (`unmarkedFrameOccu()`).

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
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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)
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- (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)
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Detection model Occupancy model



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


```
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 ~ habitat, data=umf)  # covariates on both

summary(fm3)
```

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```

```
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
```

Swan

e

```
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fm3@AIC
LRT(fm2, fm3)
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pred.occ <- predict(fm3, type="state", newdata=newdat)
pred.det <- predict(fm3, type="det", newdata=newdat)
```



ranef(fm3)

State process $Z_i \sim \text{Bernoulli}(\psi_i)$

	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”.

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State process $Z_i \sim \text{Bernoulli}(\psi_i)$

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

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➤ Predicting Z at a site when species never detected

	Mean	Mode	2.5%	97.5%
[1,]	0.015231766	0	0	0
[2,]	0.01782	y[1,]	[1]	0 0 0
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$$\Pr(z_i = 1 | \{y_i\} = 0) = \frac{\psi(1-p)^J}{(1-\psi) + \psi(1-p)^J}$$

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➤ Predicting Z at a site when species never detected

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➤ 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.

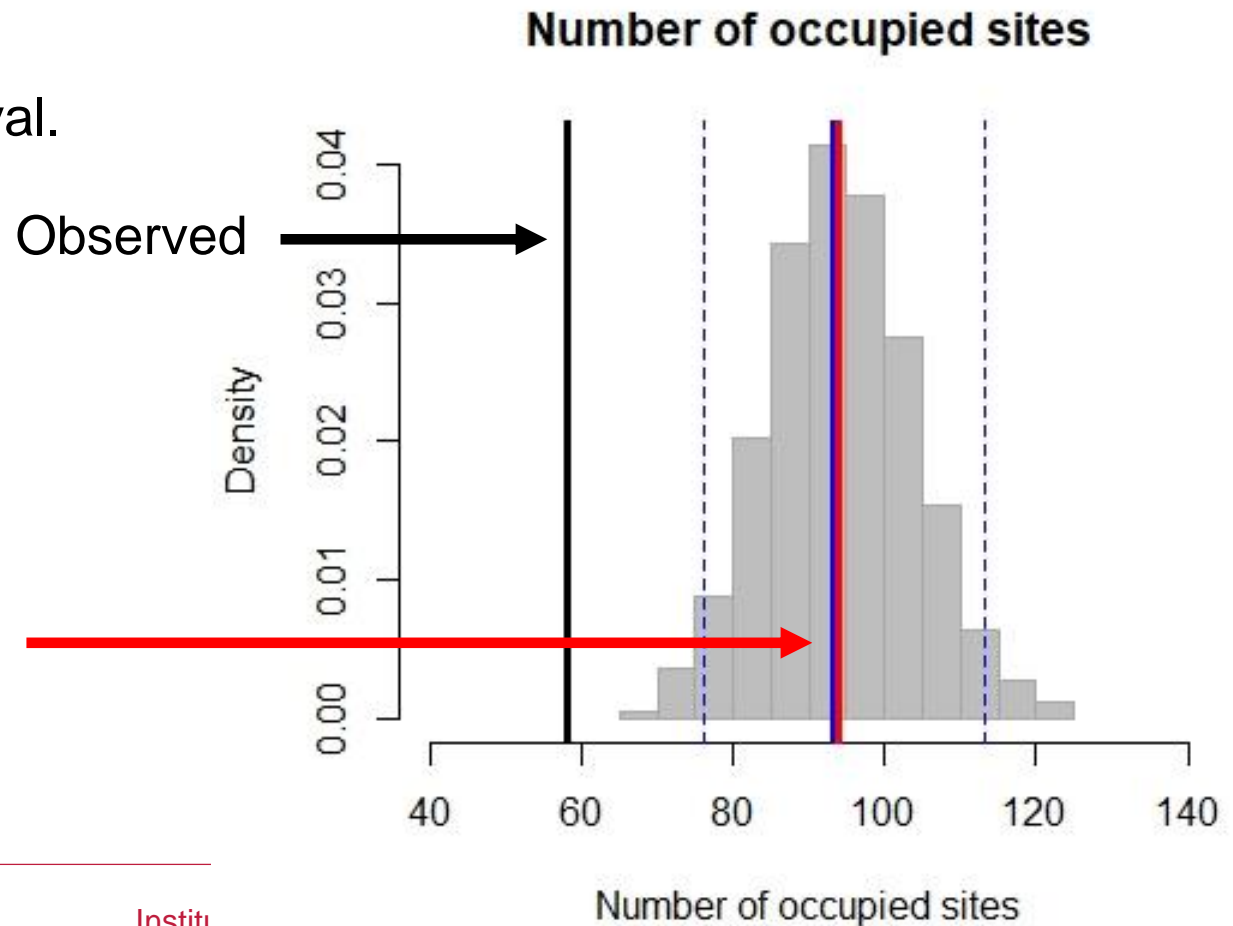
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- Parametric bootstrapping can be used to obtain a confidence interval.

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



- 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.



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.
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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.

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



- A BUGS model basically describes relationships between some variables in terms of conditional probability distributions.
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- Variety of in-build probability distributions: $\text{dnorm}(\mu, \tau)$, $\text{dbin}(p, n)$, $\text{dbern}(p)$, ...
- The BUGS language is not really vectorized - we need loops to define the model for every element in vectors or multidimensional arrays.



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- (3) Think about the necessary prior distributions

Most ecologists use vague or uninformative priors,
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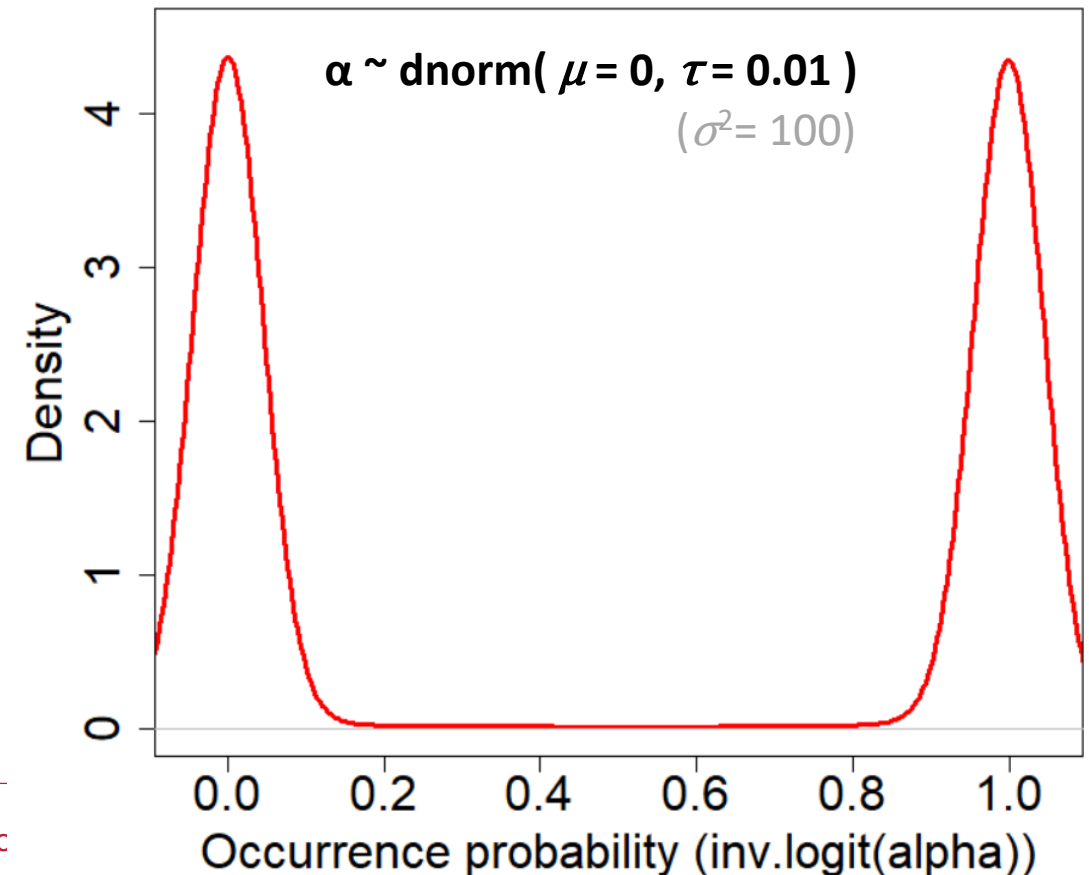


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≈ flat priors at probability scale
(for intercept parameter in logistic models)

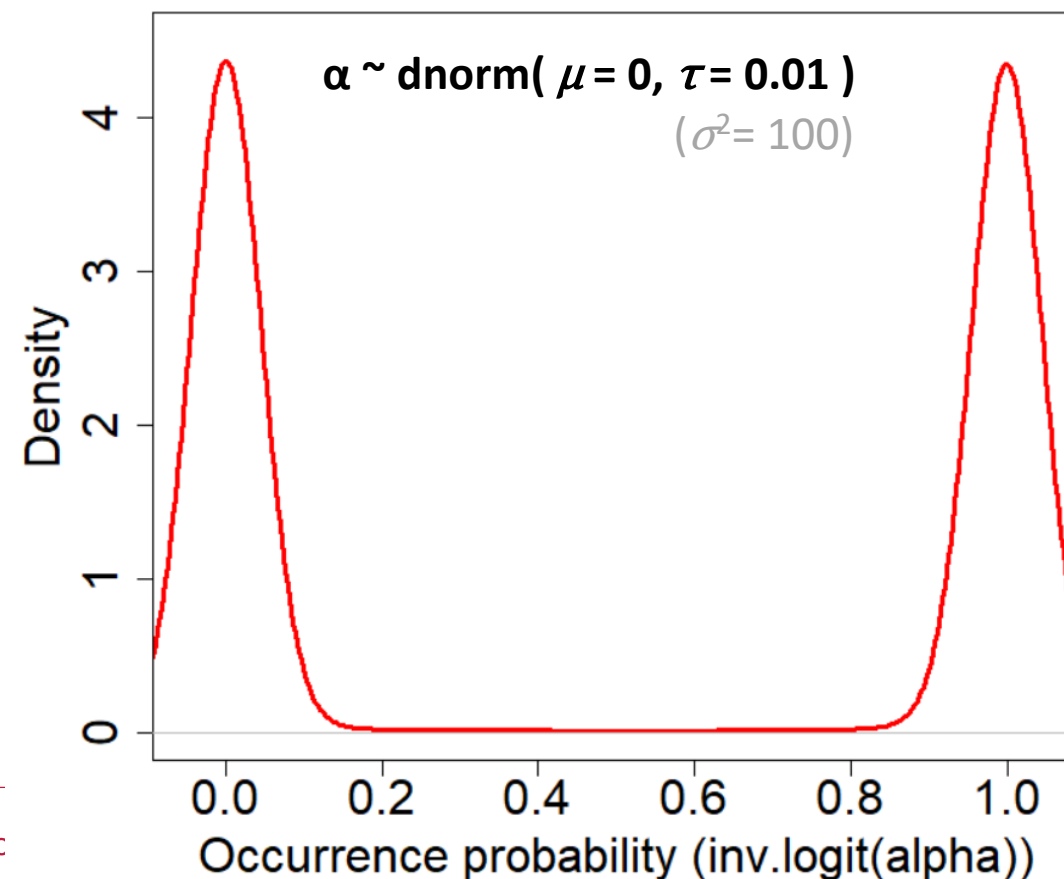
$\alpha \sim \text{dlogis}(0, 1)$ Northrup & Gerber (2018)

$\text{mean.p} \sim \text{dunif}(0, 1)$ Kéry & Royle (2016)

$\alpha \leftarrow \text{ilogit}(\text{mean.p})$

$\alpha \sim \text{dnorm}(0, 0.5)$ Hobbs & Hooten (2015)

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

$\beta \sim \text{dnorm}(0, 0.1) \quad \rightarrow \sigma^2 = 10$
 $\beta \sim \text{dnorm}(0, 0.01) \quad \rightarrow \sigma^2 = 100$

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$\beta \sim \text{dnorm}(0, 0.1) \rightarrow \sigma^2 = 10$
 $\beta \sim \text{dnorm}(0, 0.01) \rightarrow \sigma^2 = 100$

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.



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

```
cat(file = "StaticOcc_InterceptsOnly.txt", "  
model{  
  
  ## Specify priors  
  beta0.occ ~ dlogis(0,1)      ## prior on occupancy intercept  
  alpha0.det ~ dlogis(0,1)     ## prior on detection intercept  
  
}
```



```
cat(file = "StaticOcc_InterceptsOnly.txt", "  
model{  
  
  ## Specify priors  
  beta0.occ ~ dlogis(0,1)          ## prior on occupancy intercept  
  alpha0.det ~ dlogis(0,1)        ## prior on detection intercept  
  
  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  
  
  } #i  
}  
")
```



```
cat(file = "StaticOcc_InterceptsOnly.txt", "  
model{  
  
  ## Specify priors  
  beta0.occ ~ dlogis(0,1)          ## prior on occupancy intercept  
  alpha0.det ~ dlogis(0,1)        ## prior on detection intercept  
  
  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  
  
    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  
    } #j  
  } #i  
}
```



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])
```



10 basic steps of a Bayesian model analysis with JAGS

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- (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))}
```



10 basic steps of a Bayesian model analysis with JAGS

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- (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?
```



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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- (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

```
jagsModel <- jags(model.file="StaticOcc_InterceptsOnly.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)
```



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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- (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, $R\text{-hat} < 1.1$)

`traceplot(jagsModel)`

`gelman.plot(jagsModel)`

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, $R\text{-hat} < 1.1$)
- (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** !

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CodingSession_StaticOccupancyModels_SL.R



CodingSession_StaticOccupancyModels_SL.R

Truth

180 sites

1	2	3	...	180
<input checked="" type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>	...	<input checked="" type="radio"/>
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	...	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>	...	<input checked="" type="radio"/>
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	...	<input type="radio"/>

3 repeated
visits to
each site

CodingSession_StaticOccupancyModels_SL.R

Truth

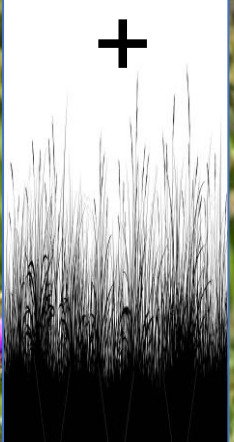
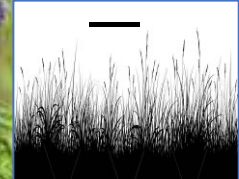


180 sites

1	2	3	...	180
<input checked="" type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>	...	<input checked="" type="radio"/>
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	...	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>	...	<input checked="" type="radio"/>
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	...	<input type="radio"/>

3 repeated
visits to
each site

True state is affected
by vegetation height



















CodingSession_StaticOccupancyModels_SL.R

Truth

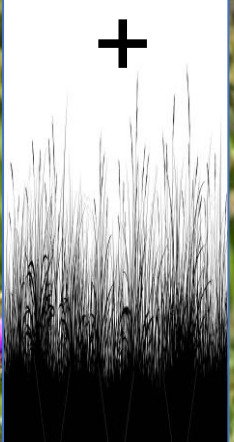


180 sites

1	2	3	...	180
			...	
			...	
			...	
			...	

3 repeated
visits to
each site

True state is affected
by vegetation height



















Variation in detections
used to estimate detection
probability, affected by

CodingSession_StaticOccupancyModels_SL.R

Truth

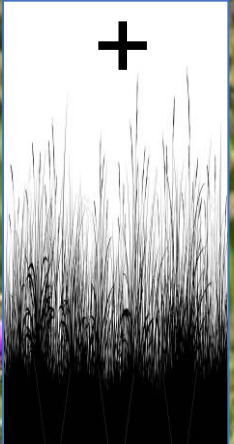


180 sites

1	2	3	...	180
			...	
			...	
			...	
			...	

3 repeated
visits to
each site

True state is affected
by vegetation height



















Variation in detections
used to estimate detection
probability, affected by



CodingSession_StaticOccupancyModels_SL.R

Truth

180 sites

1	2	3	...	180
			...	
			...	
			...	
			...	

3 repeated
visits to
each site

True state is affected
by vegetation height

Variation in detections
used to estimate detection
probability, affected by

+

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