



# Hierarchical spatial modelling for applied population and community ecology

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Jeffrey W. Doser, Marc Kéry,  
Gesa von Hirschheydt

24-27 June 2024







# Multi-species occupancy models (MSOMs)

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# Multi-species detection-nondetection data



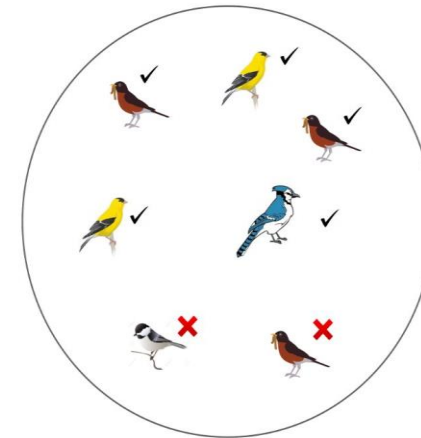
Citizen Science



Acoustic recording units



Camera traps



Point count surveys

# Multi-species data from a single visit

Species	Site 1	Site 2	Site 3	Site 4
A	1	0	0	1
B	0	0	1	0
C	1	1	0	0
D	1	0	0	0
E	0	1	1	1
F	0	0	0	1

# Multi-species data from multiple visits

					Visit 3							
					Species	Site 1	Site 2	Site 3	Site 4			
					Visit 2							
					Species	Site 1	Site 2					
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Visit 1					A	0	NA	C	0	0	0	NA
Species	Site 1	Site 2		B	0	NA	D	0	0	0	0	NA
A	1	0		C	1	NA	E	0	0	1	NA	
B	0	0		D	0	NA	F	0	0	0	NA	
C	1	1		E	0	NA	1	1				
D	1	0		F	0	NA	0	0				
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F	0	0		1	1							
				0	1							

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  - Provide inference at both species and community-levels
  - Use information from other species to improve species-specific estimates

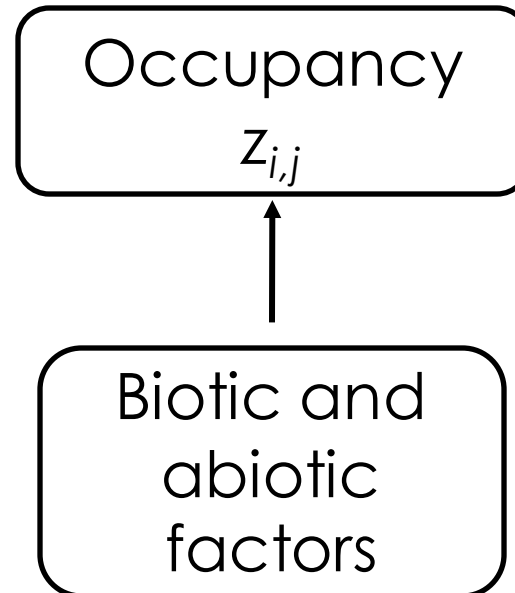
# Ecological Motivation

- Management has historically focused on individual species.
- Increased interest in multi-species management.
- Biodiversity conservation.
- Species are not independent of each other.

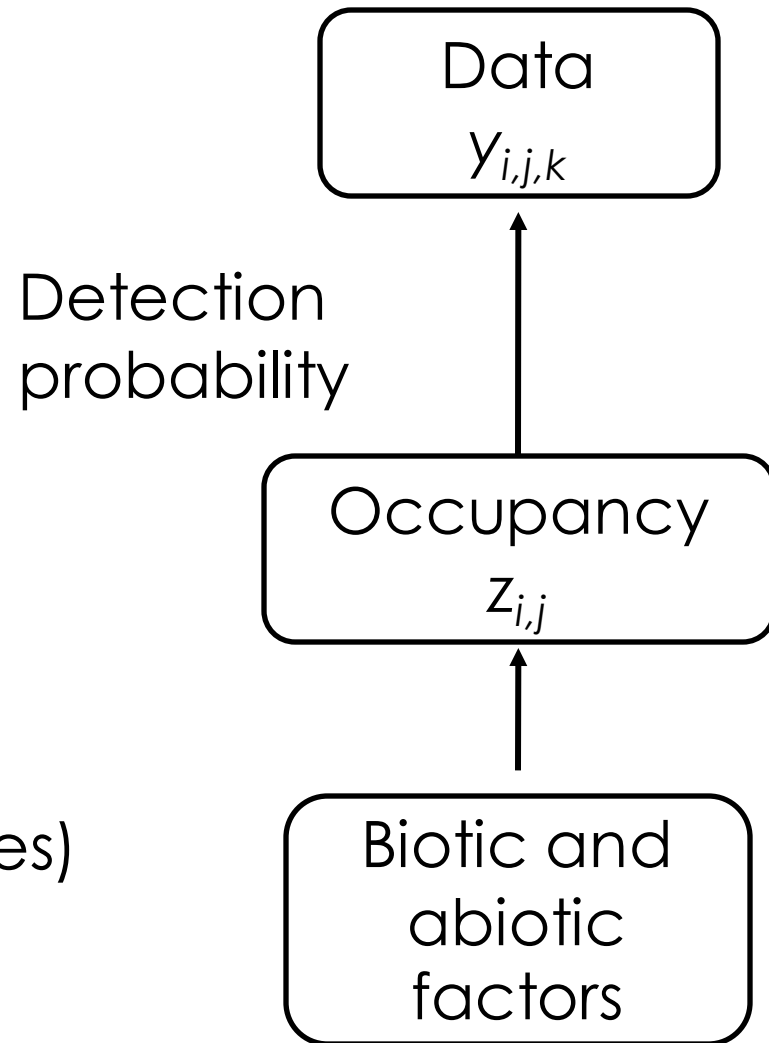


# Multi-species occupancy model

$i = 1, \dots, N$  (species)  
 $j = 1, \dots, J$  (sites)  
 $k = 1, \dots, K$  (replicates)



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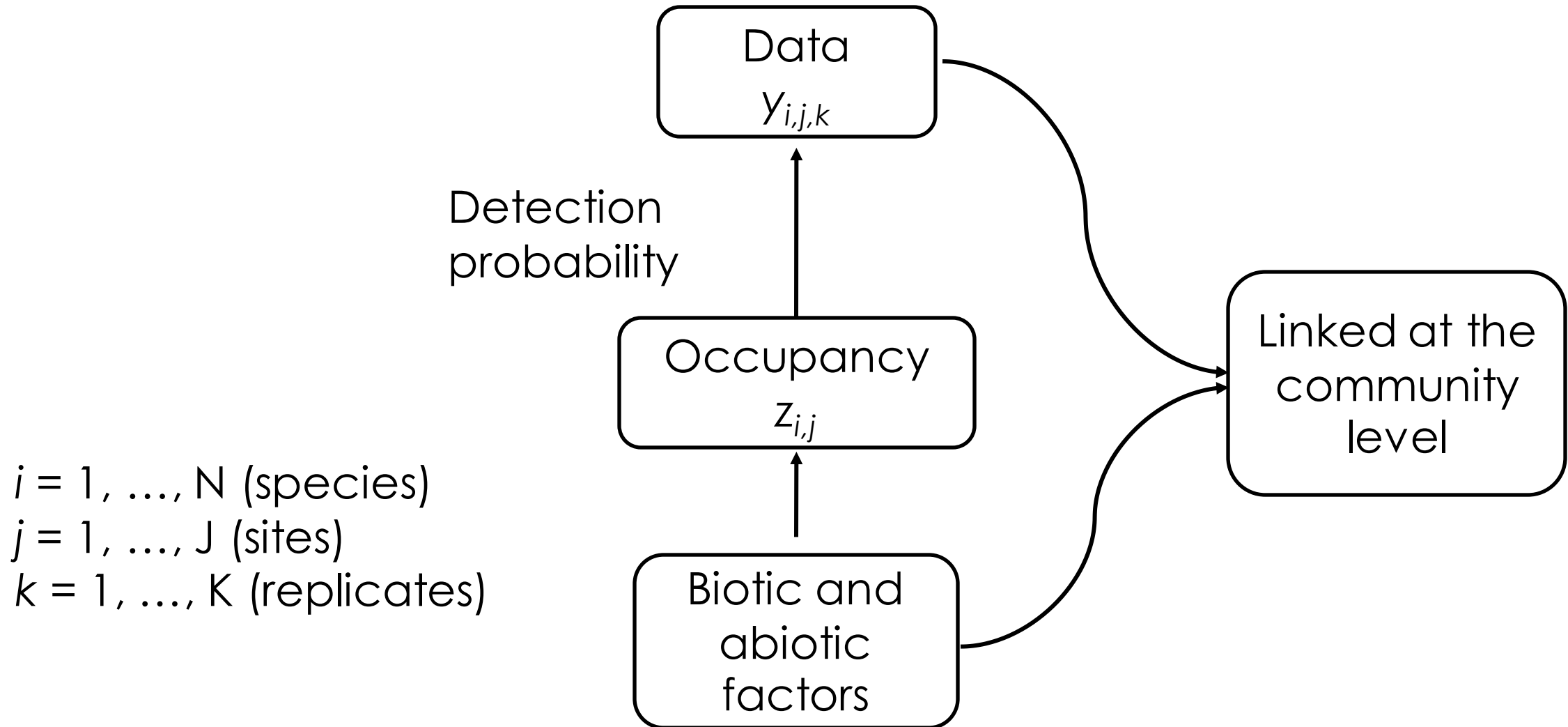


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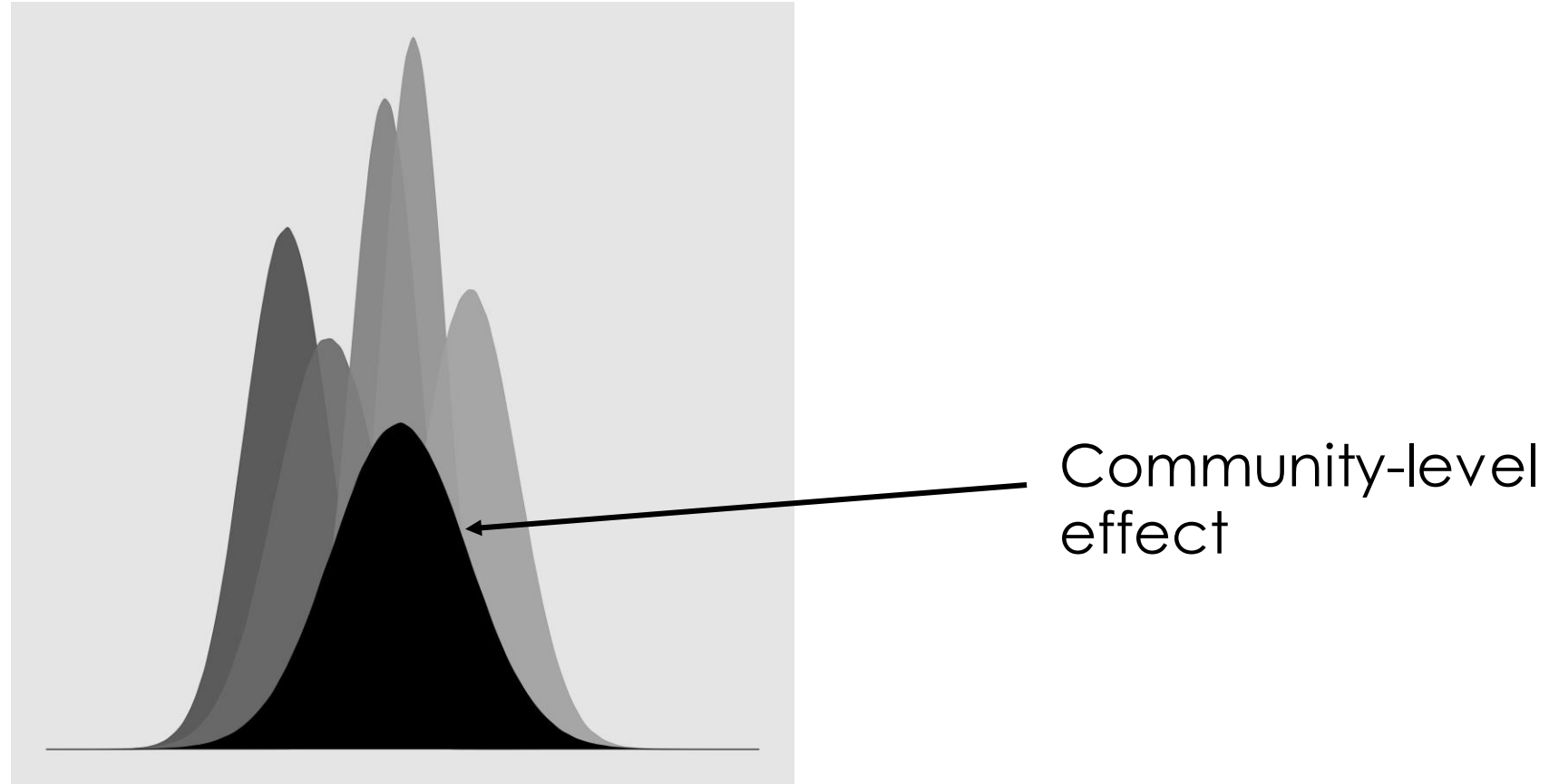
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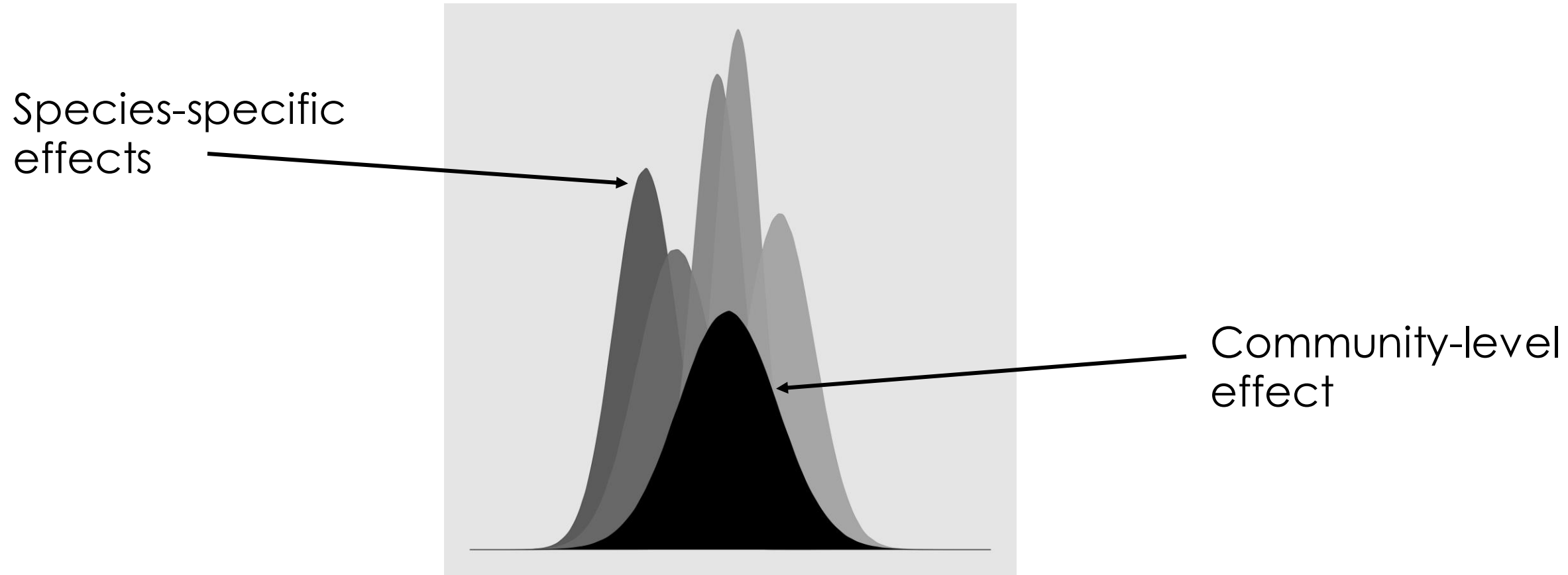


# Species-specific and community effects

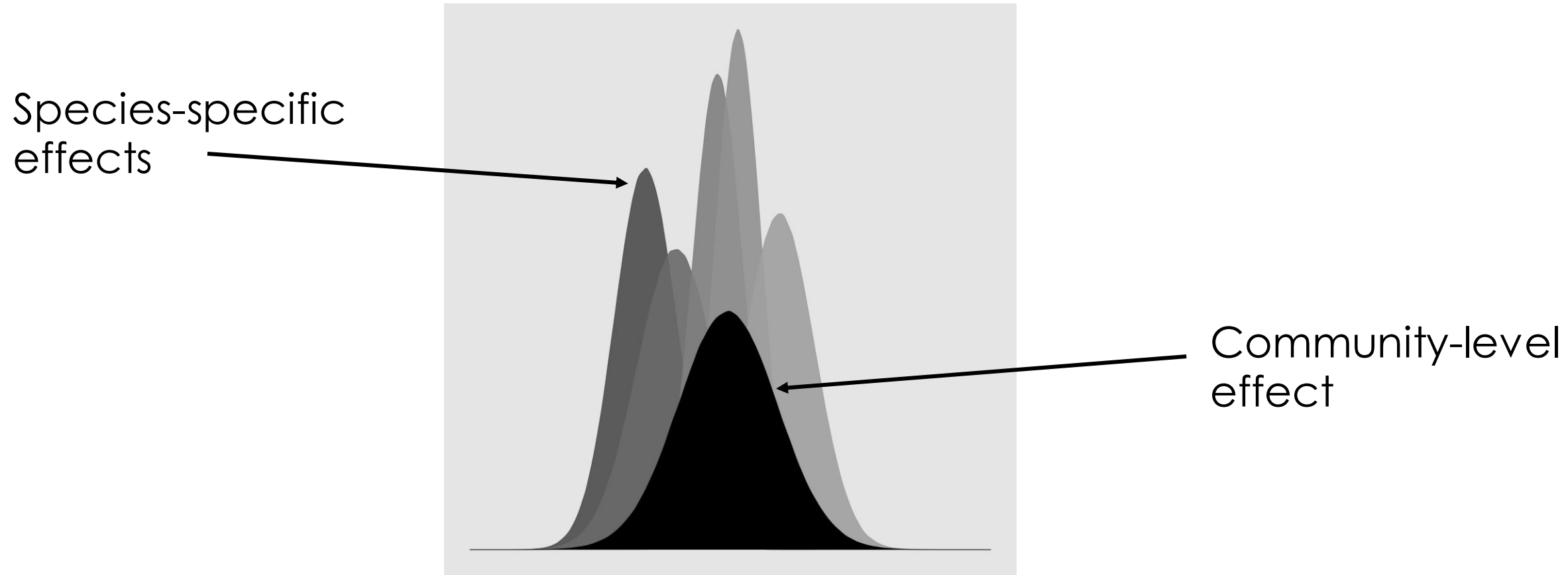




# Species-specific and community effects



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Species-specific effects are drawn from a common, community-level distribution

# Development of the MSOM

JOURNAL ARTICLE

## Modelling Species Diversity Through Species Level Hierarchical Modelling

Alan E. Gelfand, Alexandra M. Schmidt , Shanshan Wu, John A. Silander, Jr, Andrew Latimer, Anthony G. Rebelo

*Journal of the Royal Statistical Society Series C: Applied Statistics*, Volume 54, Issue 1, January 2005, Pages 1–20, <https://doi.org/10.1111/j.1467-9876.2005.00466.x>

**Published:** 22 October 2004    **Article history** ▼

Primary Article

## Estimating Size and Composition of Biological Communities by Modeling the Occurrence of Species

Robert M Dorazio & J. Andrew Royle

Pages 389–398 | Published online: 01 Jan 2012

“ Cite this article    <https://doi.org/10.1198/016214505000000015>

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Occupancy (ecological) sub-model

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$$\beta_{r,i} \sim \text{Normal}(\mu_{\beta_r}, \tau_{\beta,r}^2)$$

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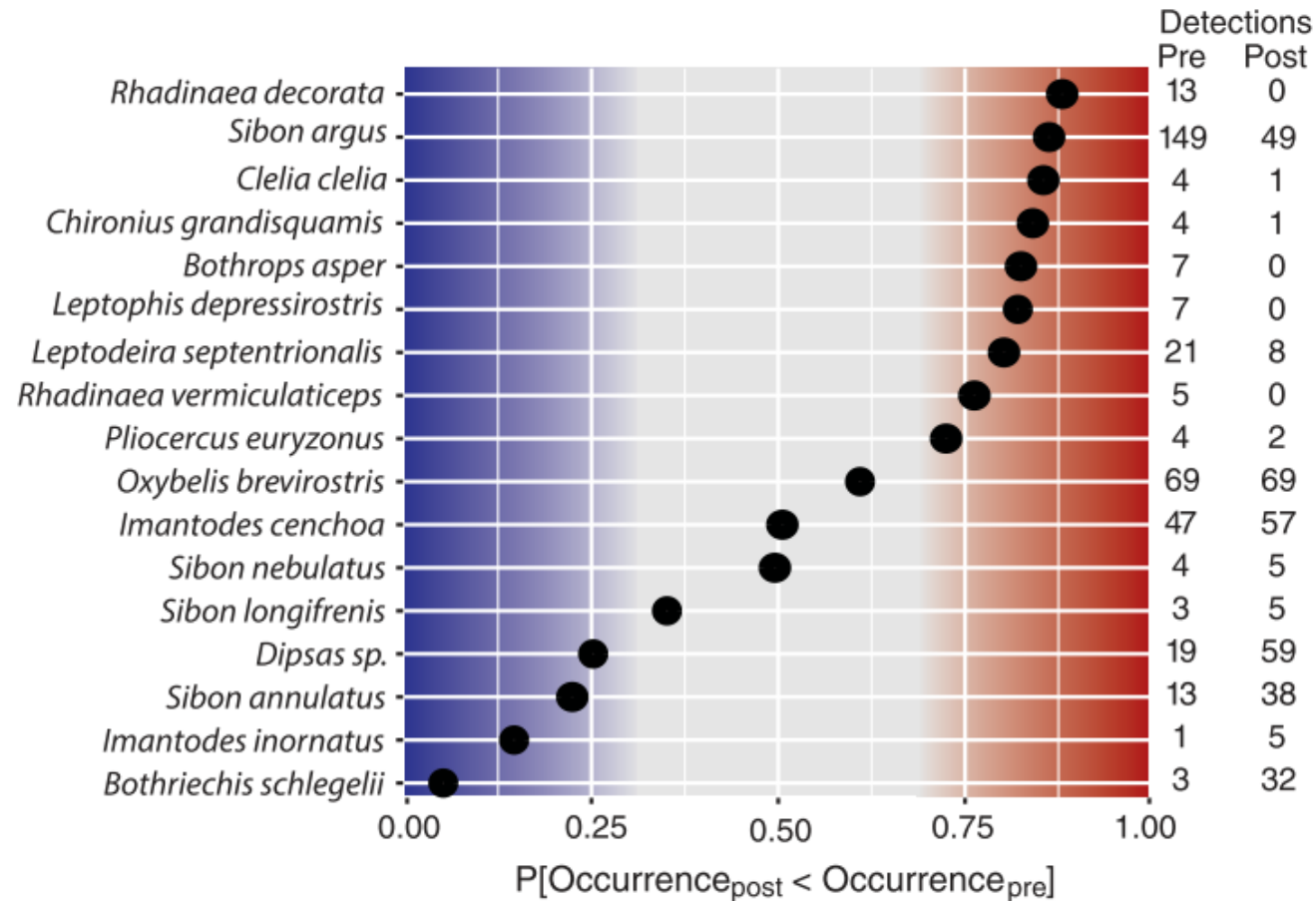
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These are just  
random slopes and  
intercepts!!

# Why multi-species occupancy modeling?

Improved ability to model rare species



Zipkin et al (2020)

# Deriving community-level metrics

- Recall the Bayesian approach allows us to generate estimates of quantities (with uncertainty) that aren't directly parameters in the model. These are called *Derived Quantities*.
- In an MSOM, we can generate a variety of biodiversity metrics (species richness, composition, diversity) as derived quantities
- Usually involves manipulating the species-specific occupancy estimates at each site  $z_{ij}$  in different ways

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- Defining a "community" is not always straightforward:
  - [Pacifi et al. 2014 Ecology and Evolution](#)
- May not be ideal for the "rarest of the rare" species:
  - [Erickson and Smith, 2023 Ecography](#)

# Fitting the MSOM in `spOccupancy`

- `msPGOcc()` (multi-species Pólya-Gamma occupancy model)
- Same exact arguments as `PGOcc()`
- Detection-nondetection data are now supplied as a three-dimensional array

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spOccupancy 0.7.3   Reference   **Articles**   Changelog

## Formatting data for use in spOccupancy

Jeffrey W. Doser  
2022

Source: [vignettes/dataFormatting.Rmd](#)



See [vignette here](#) for example of formatting data for multi-species occupancy model

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- Could the co-occurrence patterns across different species provide us with improved ecological insights?
- Can we extend the MSOM to account for residual species correlations?



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- Residual correlations can come from
  - Biotic interactions (e.g., competition, facilitation, predation)
  - Missing covariates
- Estimating residual correlations can provide additional insights for hypothesis testing and underlying drivers of community patterns

Historical differences between JSDMs and MSOMs

# Historical differences between JSDMs and MSOMs

## **Joint Species Distribution Models**

- Don't account for imperfect detection
- Account for residual species correlations
- Sometimes treat species-specific effects as random effects
- Key references:
  - Latimer et al. (2009)
  - Ovaskainen et al. (2010)
  - Warton et al. (2015)

## **Multi-species Occupancy Models**

- Account for imperfect detection
- Don't account for residual species correlations
- Treat species specific-effects as random effects
- Key references:
  - Dorazio and Royle (2005)
  - Gelfand et al. (2005)
  - Devarajan et al. (2020)

# Merging JSDMs and MSOMs

*Ecology*, 100(8), 2019, e02754  
© 2019 by the Ecological Society of America

## Joint species distribution models with species correlations and imperfect detection

MATHIAS W. TOBLER <sup>1,5</sup> MARC KÉRY,<sup>2</sup> FRANCIS K. C. HUI,<sup>3</sup> GURUTZETA GUILLERA-ARROITA,<sup>4</sup> PETER KNAUS,<sup>2</sup> AND  
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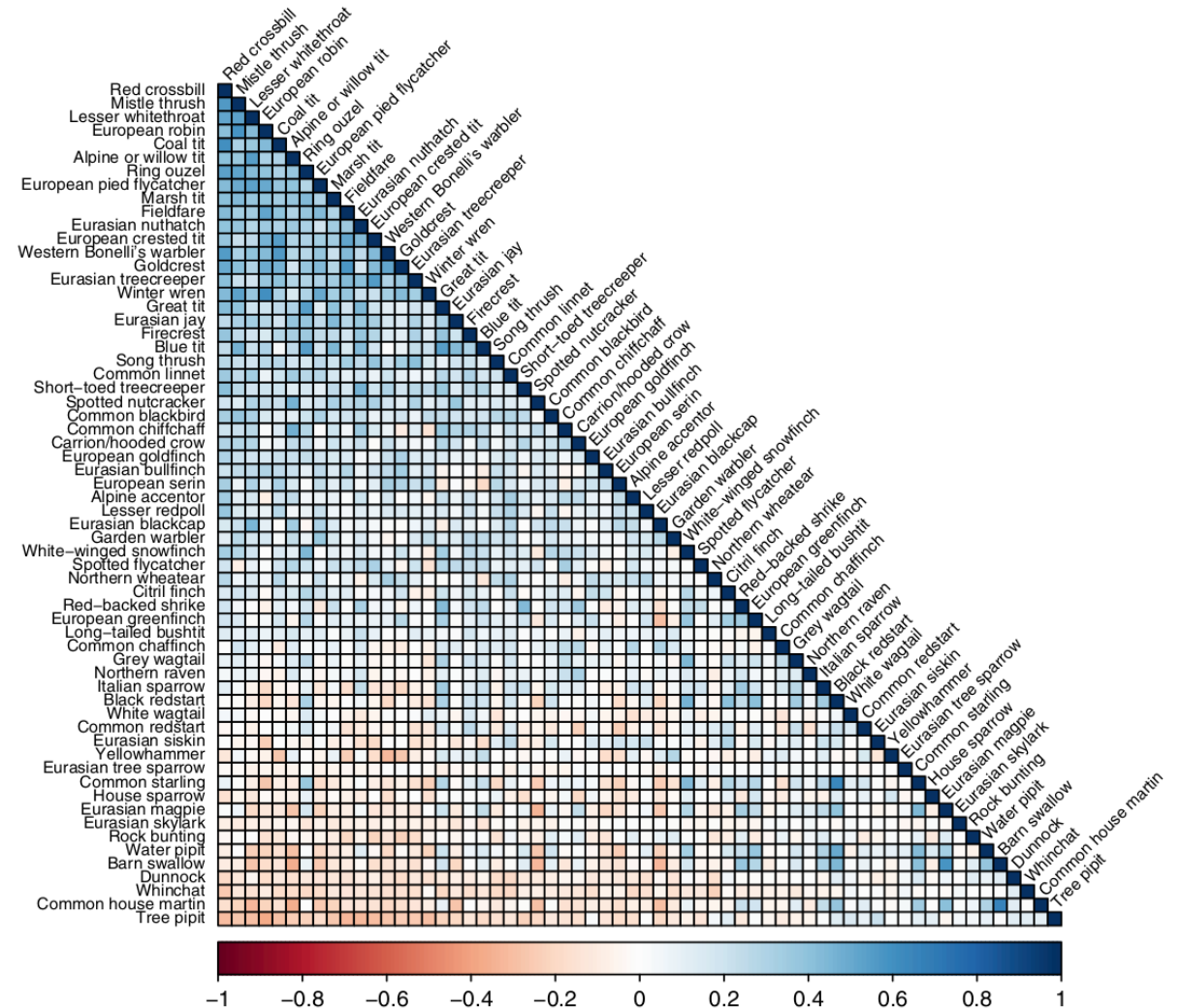
Joint species distribution  
models that account for  
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Multi-species  
occupancy models that  
account for species  
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# JSDMs with imperfect detection

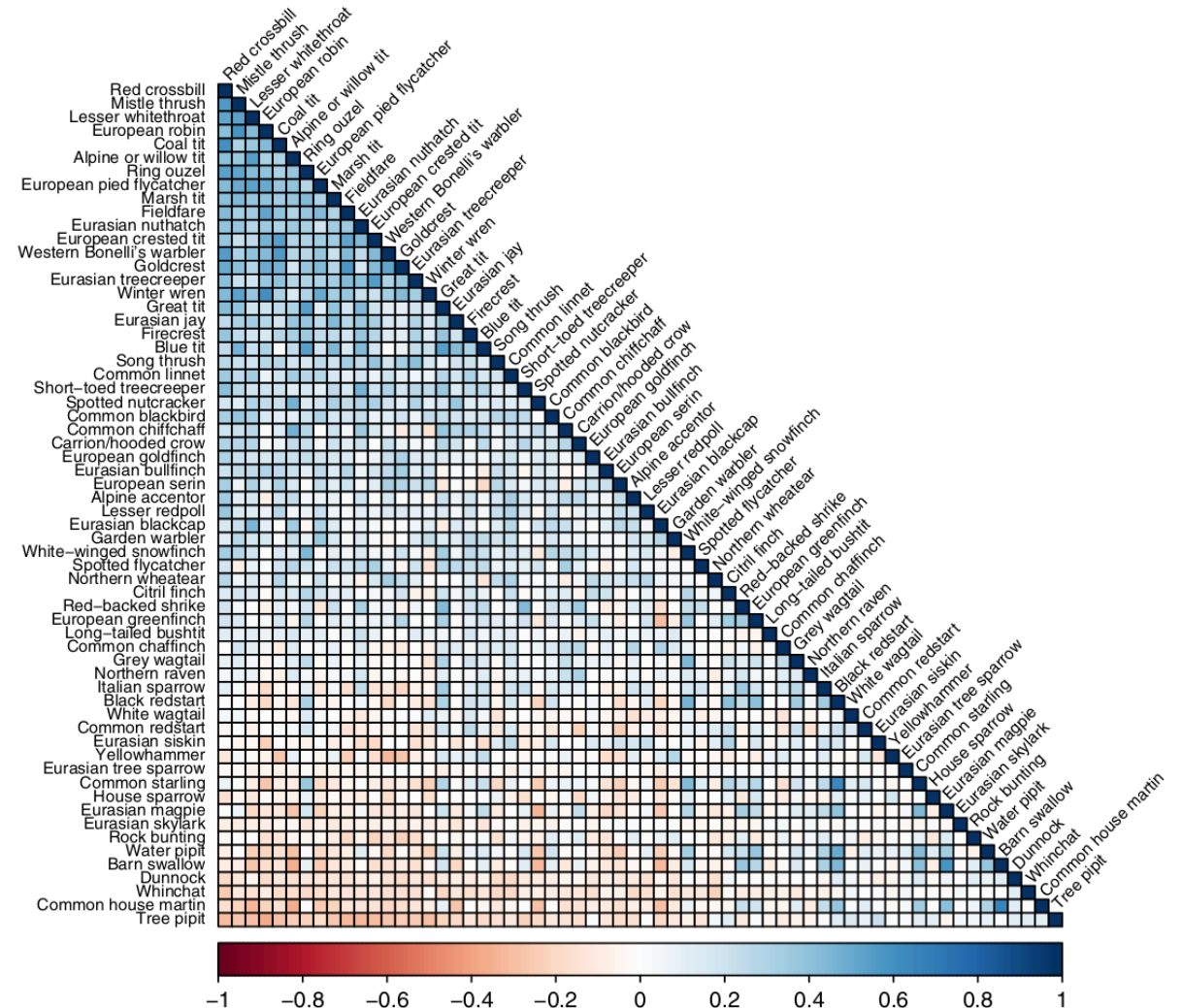
- Residual correlation matrices of occupancy probability can provide insights on underlying biotic/abiotic factors



Tobler et al. (2019)

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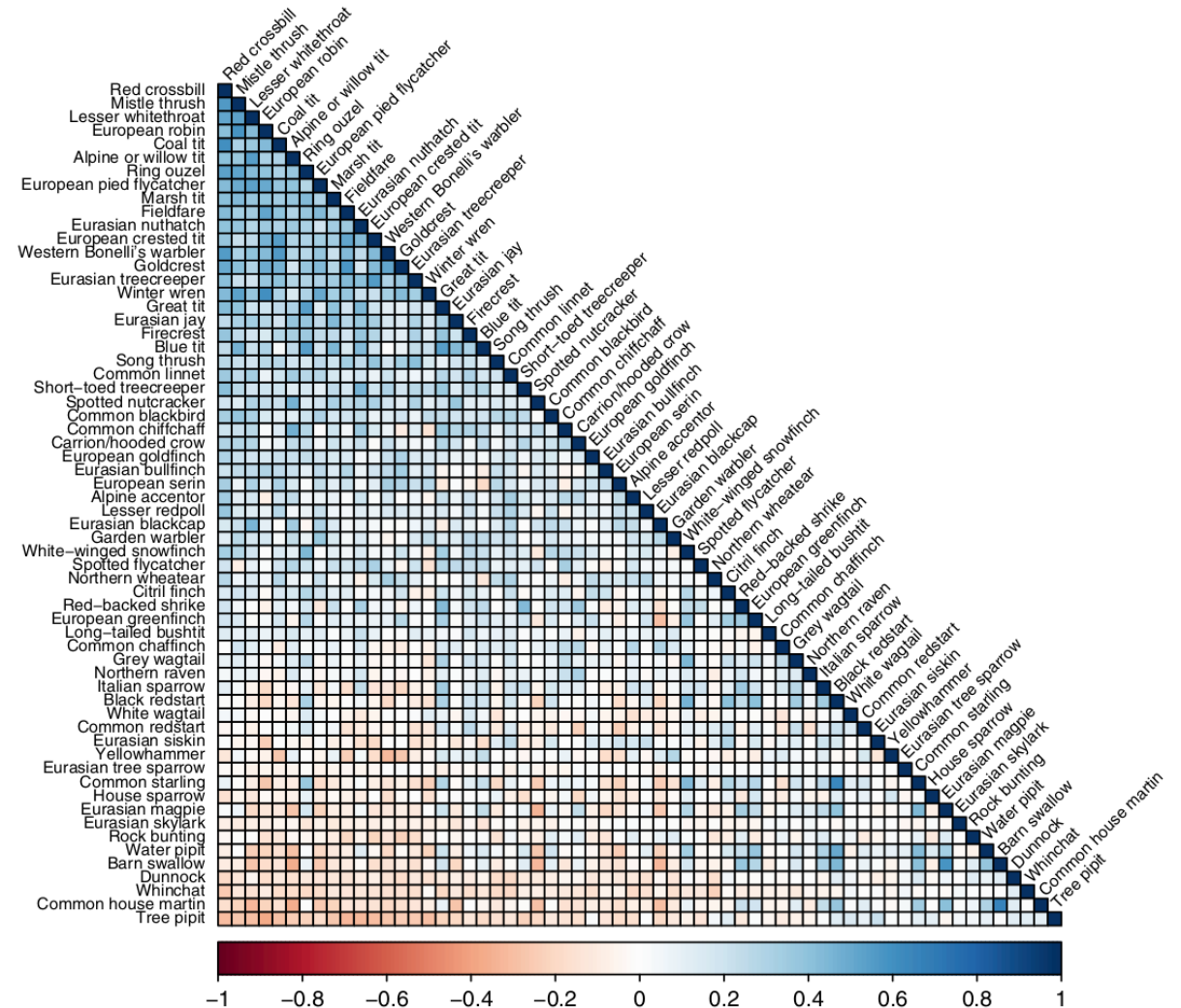
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# JSDMs with imperfect detection

- Residual correlation matrices of occupancy probability can provide insights on underlying biotic/abiotic factors
- We could try to explicitly estimate every single correlation between each pair of species in the community.
- Quickly becomes a lot of parameters and very difficult to estimate.
- Instead, we will use a dimension reduction approach called **Factor Modelling**.



Tobler et al. (2019)

# Latent factor multi-species occupancy model

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- This is a form of factor analysis (similar to PCA)

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Example: one occupancy covariate and two latent factors

Occupancy (ecological) sub-model

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"Missing covariates" that  
account for residual  
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Effects of the missing covariates

# Factor loadings matrix

- $N \times q$  matrix.
- Note that  $N$  is typically much bigger than  $q$ , resulting in a "tall and skinny" matrix.
- Example: 10 species and 3 factors

$N = 10$  species (rows)

$q = 3$  factors (columns)

$$\mathbf{\Lambda} = \begin{bmatrix} \lambda_{1,1} & \lambda_{1,2} & \lambda_{1,3} \\ \lambda_{2,1} & \lambda_{2,2} & \lambda_{2,3} \\ \lambda_{3,1} & \lambda_{3,2} & \lambda_{3,3} \\ \lambda_{4,1} & \lambda_{4,2} & \lambda_{4,3} \\ \lambda_{5,1} & \lambda_{5,2} & \lambda_{5,3} \\ \lambda_{6,1} & \lambda_{6,2} & \lambda_{6,3} \\ \lambda_{7,1} & \lambda_{7,2} & \lambda_{7,3} \\ \lambda_{8,1} & \lambda_{8,2} & \lambda_{8,3} \\ \lambda_{9,1} & \lambda_{9,2} & \lambda_{9,3} \\ \lambda_{10,1} & \lambda_{10,2} & \lambda_{10,3} \end{bmatrix}$$



# Deriving an interspecies covariance matrix

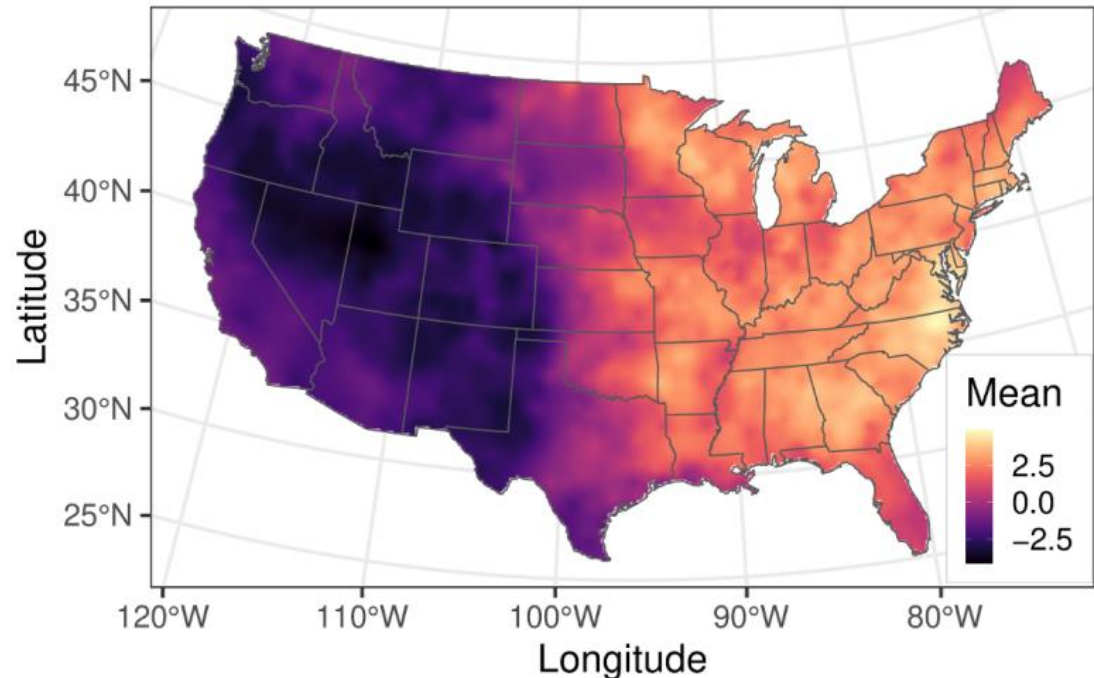
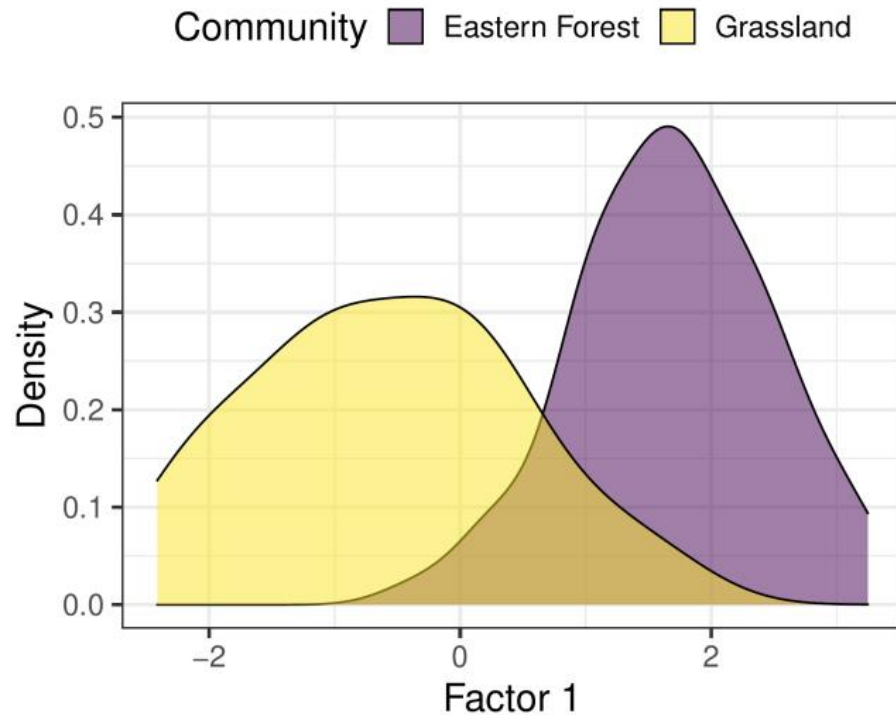
$$\Sigma = \Lambda \Lambda^\top$$

$$\begin{bmatrix} \lambda_{1,1} & \lambda_{1,2} & \lambda_{1,3} \\ \lambda_{2,1} & \lambda_{2,2} & \lambda_{2,3} \\ \lambda_{3,1} & \lambda_{3,2} & \lambda_{3,3} \\ \lambda_{4,1} & \lambda_{4,2} & \lambda_{4,3} \\ \lambda_{5,1} & \lambda_{5,2} & \lambda_{5,3} \\ \lambda_{6,1} & \lambda_{6,2} & \lambda_{6,3} \\ \lambda_{7,1} & \lambda_{7,2} & \lambda_{7,3} \\ \lambda_{8,1} & \lambda_{8,2} & \lambda_{8,3} \\ \lambda_{9,1} & \lambda_{9,2} & \lambda_{9,3} \\ \lambda_{10,1} & \lambda_{10,2} & \lambda_{10,3} \end{bmatrix}$$

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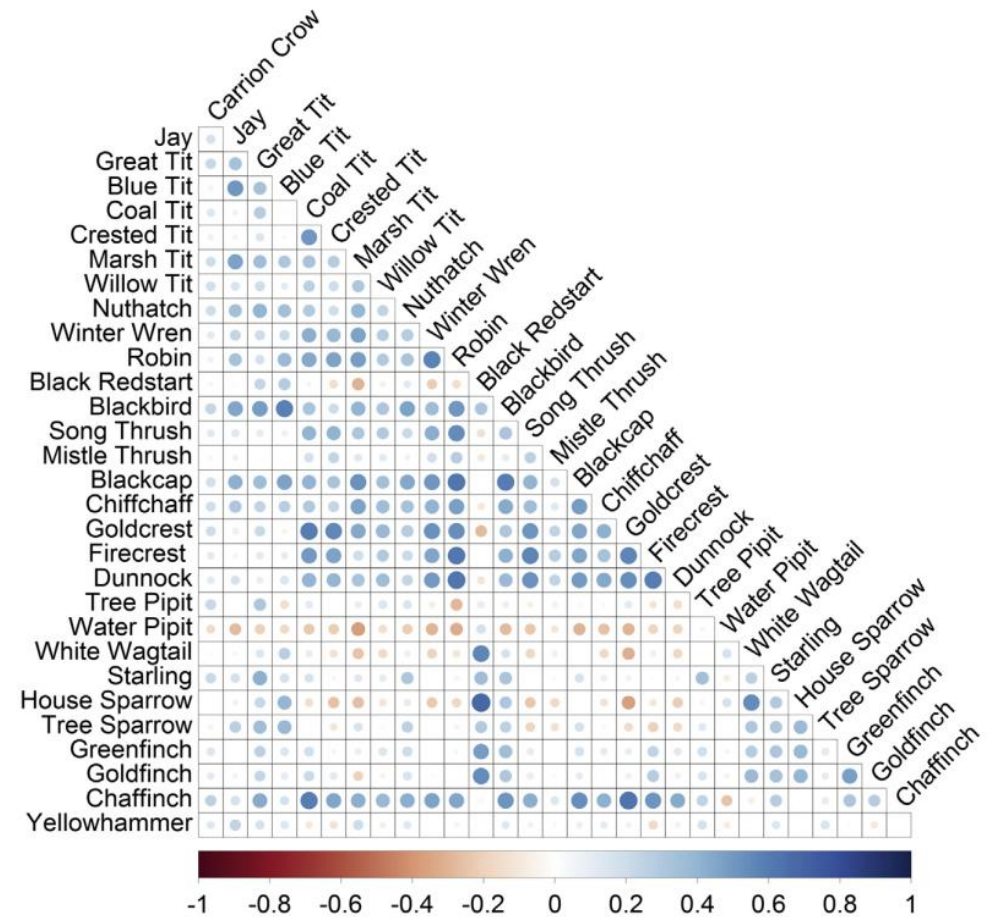
# Interpretation of the latent factors and factor loadings

Can be used as a model-based ordination technique by assessing species with similar factor loadings



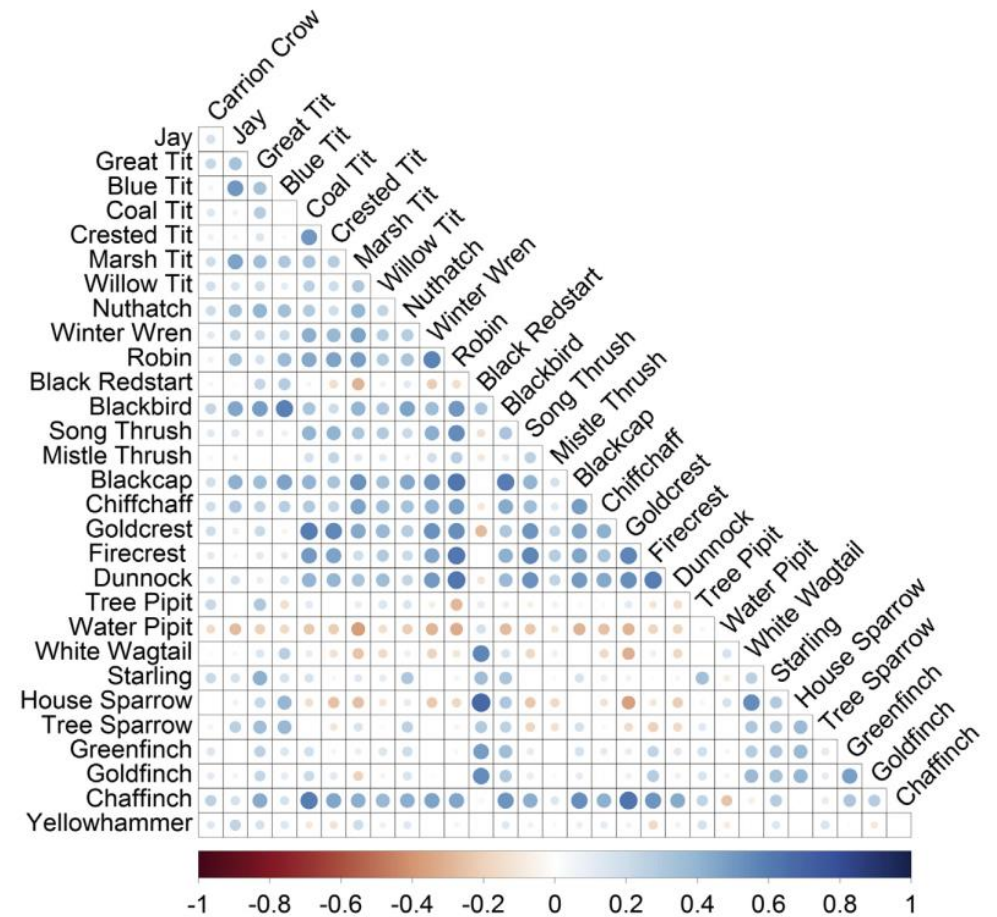
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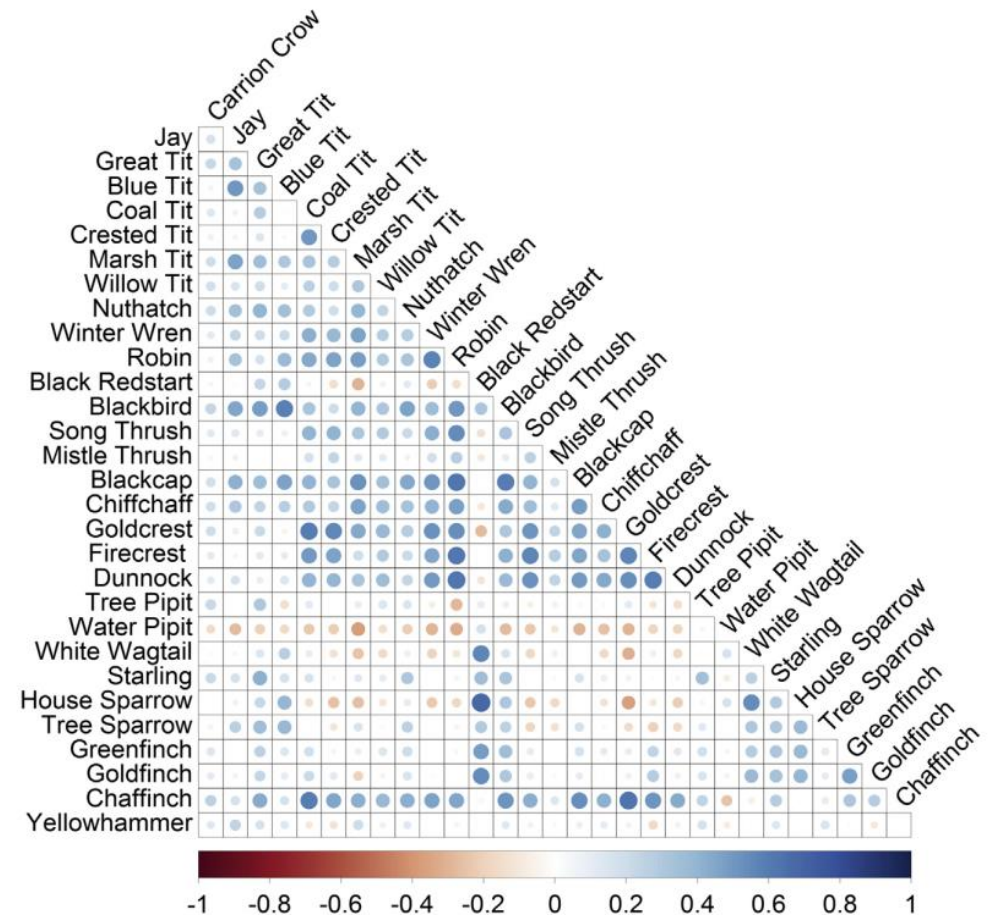
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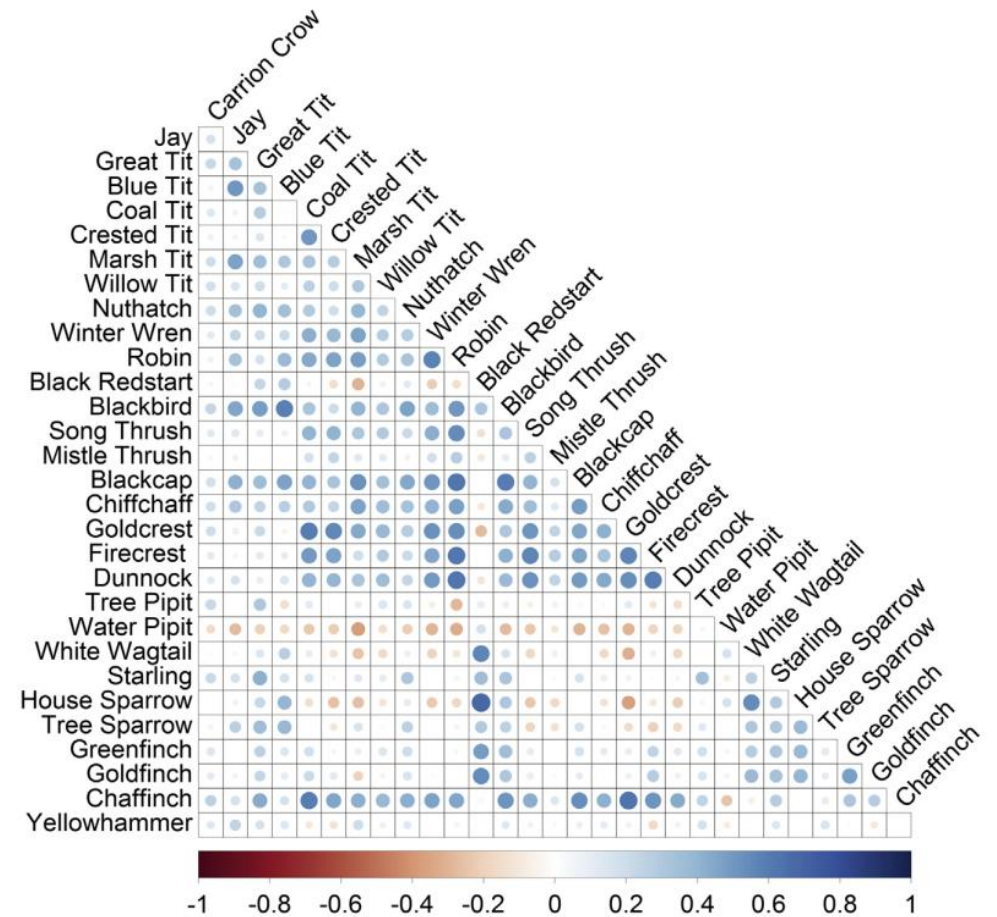
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- Interpretation depends on scale
- See Poggiato et al. (2021) *TREE* and Chapter 8 Kéry and Royle (2021)



Kéry and Royle (2021) Chapter 8

# Pros and cons of latent factor MSOM vs. Regular MSOM

## **Pros**

- Often improves model fit, predictive performance, and sometimes even precision of estimates.
- Arguably more biologically realistic since we know species are not independent of each other.
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- Helps generate hypotheses.

## Cons

- Usually requires more data.
- Need to choose the number of factors to include.
- Potential for overinterpretation of residual covariance matrix
- Convergence and model fitting can be very tricky. Need to place restrictions on the factor loadings



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- See [guidance here](#).

# Priors and constraints for the factor loadings

- Without any restrictions, there are infinitely many possible values for the factor loadings and factors.
- We fix the factor loadings on the diagonal to 1 and all values in the "upper triangle" to 0.
- All others have a Normal(0, 1) prior distribution.
- All other priors same as before.

$$\mathbf{\Lambda} = \begin{bmatrix} \lambda_{1,1} & \lambda_{1,2} & \lambda_{1,3} \\ \lambda_{2,1} & \lambda_{2,2} & \lambda_{2,3} \\ \lambda_{3,1} & \lambda_{3,2} & \lambda_{3,3} \\ \lambda_{4,1} & \lambda_{4,2} & \lambda_{4,3} \\ \lambda_{5,1} & \lambda_{5,2} & \lambda_{5,3} \\ \lambda_{6,1} & \lambda_{6,2} & \lambda_{6,3} \\ \lambda_{7,1} & \lambda_{7,2} & \lambda_{7,3} \\ \lambda_{8,1} & \lambda_{8,2} & \lambda_{8,3} \\ \lambda_{9,1} & \lambda_{9,2} & \lambda_{9,3} \\ \lambda_{10,1} & \lambda_{10,2} & \lambda_{10,3} \end{bmatrix}$$



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# Ordering of species in the data set

- Notice the first  $q$  species (rows) have constraints in their factor loadings.
- This means the order of species in our data set could impact how well our model converges/fits.
- In particular, we may need to carefully choose the first  $q$  species.

$$\Lambda = \begin{bmatrix} 1 & 0 & 0 \\ \lambda_{2,1} & 1 & 0 \\ \lambda_{3,1} & \lambda_{3,2} & 1 \\ \lambda_{4,1} & \lambda_{4,2} & \lambda_{4,3} \\ \lambda_{5,1} & \lambda_{5,2} & \lambda_{5,3} \\ \lambda_{6,1} & \lambda_{6,2} & \lambda_{6,3} \\ \lambda_{7,1} & \lambda_{7,2} & \lambda_{7,3} \\ \lambda_{8,1} & \lambda_{8,2} & \lambda_{8,3} \\ \lambda_{9,1} & \lambda_{9,2} & \lambda_{9,3} \\ \lambda_{10,1} & \lambda_{10,2} & \lambda_{10,3} \end{bmatrix}$$

# Choosing the first q species

- Put a common species first
- For the remaining  $q - 1$  factors, place species that you a priori believe may have different occurrence patterns than the first species, as well as the other species placed before it.
- Adjust species ordering after an initial model fit.

Convergence diagnostics and other considerations when fitting spatial occupancy models

Jeffrey W. Doser

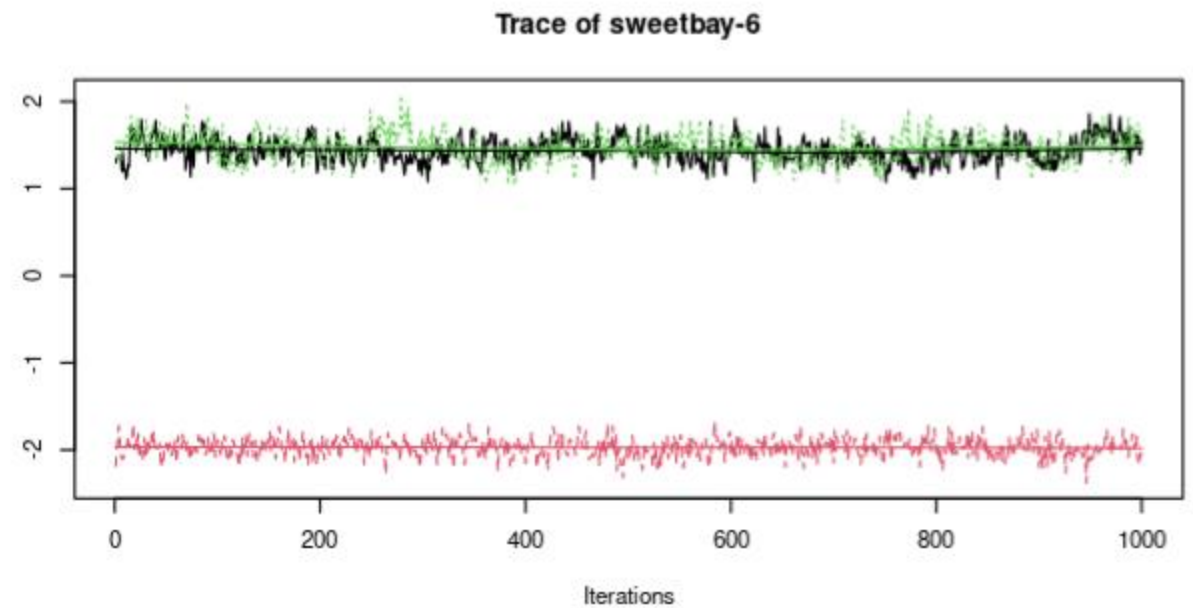
2023 (last update: March 25, 2024)

Source: [vignettes/modelConsiderations.Rmd](#)



# Initial values can be very important!!

- In general, the more complex the model, the more important the initial values can be.
- Drastically different initial values in latent factor models can lead to chain "flip-flopping", where any individual chain looks converged, but across chains there are drastically different values.
- May need to manually set initial values or only run a single chain. See [guidance here](#).



# Fitting the latent factor MSOM in `spOccupancy`

- Function `lfMsPGOcc()` (latent factor multi-species Pólya-Gamma occupancy model)
- Fits the model developed by Tobler et al. (2019) with some adaptations to make it faster
- Same arguments as `msPGOcc()` with the addition of `n.factors` to specify the number of latent factors to use.

# Exercise: Landscape scale effects on occupancy of tropical amphibians

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5-amphibian-multi-species-occ.R

