Hierarchical spatial modelling for applied population and community ecology

Jeffrey W. Doser, Marc Kéry, Gesa von Hirschheydt

24-27 June 2024

Multi-species occupancy models (MSOMs)

Jeffrey W. Doser

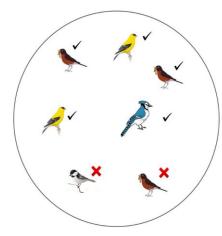24-27 June 2024

Multi-species detection-nondetection data

eBird   iNaturalist

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 1

Species	Site 1	Site 2		
A	1	0		
B	0	0		
C	1	1		
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E	0	1	1	1
F	0	0	0	1

Visit 2

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

Visit 3

Species	Site 1	Site 2	Site 3	Site 4
A	1	0	0	NA
B	0	1	1	NA
C	0	0	0	NA
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(overlapping values) 1 1 / 0 0

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Remember this for when we work with three-dimensional arrays.

Statistical Motivation

- Species of interest (e.g., Species of Greatest Conservation Need) are often the rarest species.
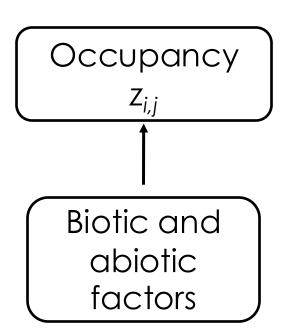
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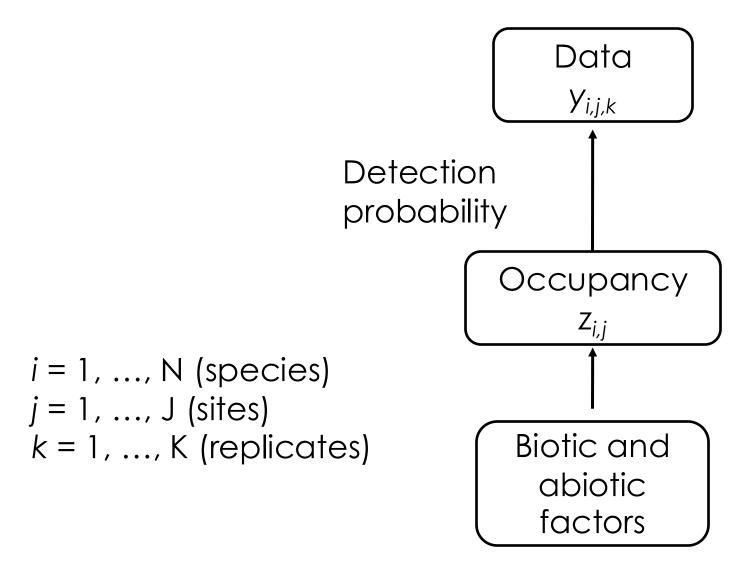
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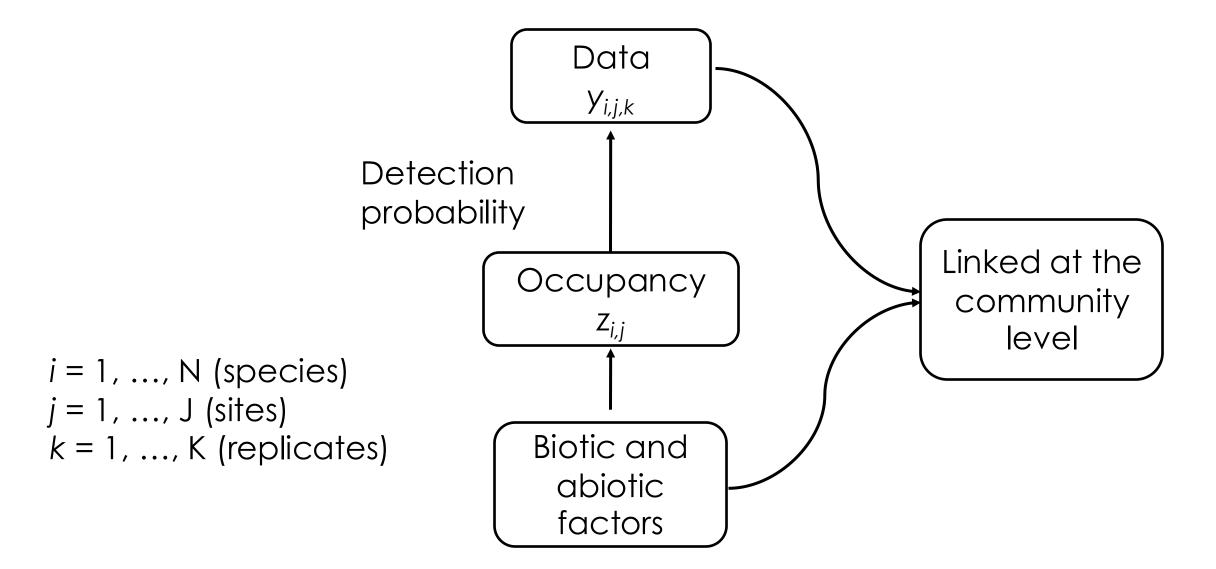 - Use information from other species to improve species-specific estimates

Ecological Motivation

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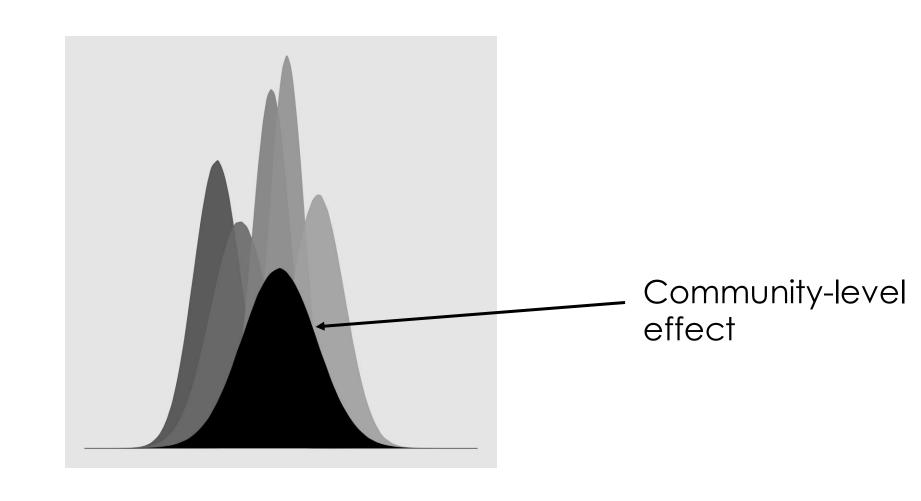- Species are not independent of each other.
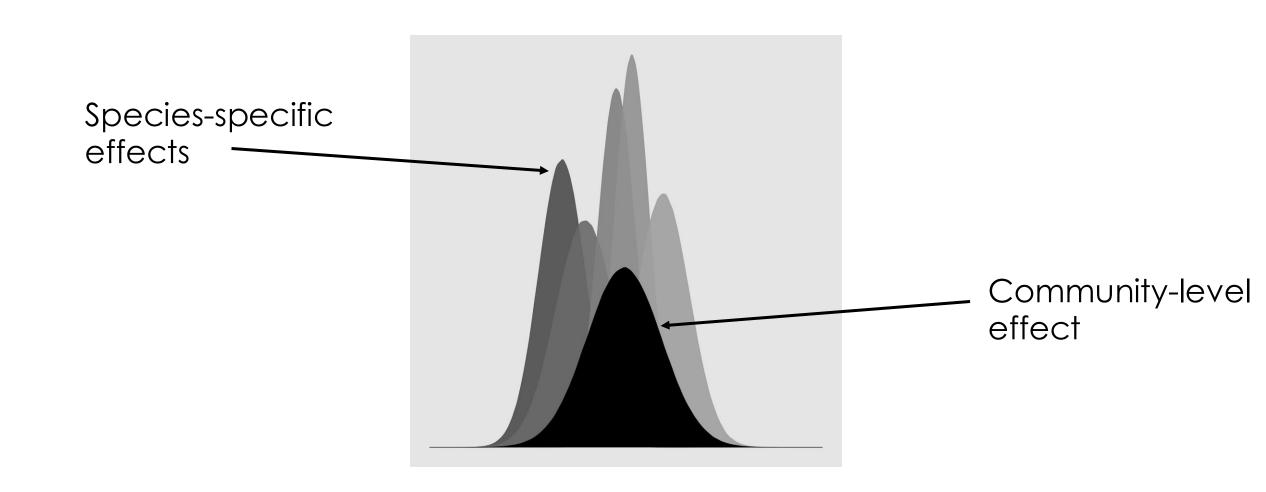
Multi-species occupancy model

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

Occupancy
$z_{i,j}$

Biotic and
abiotic
factors

Multi-species occupancy model

Data
$y_{i,j,k}$

Detection probability

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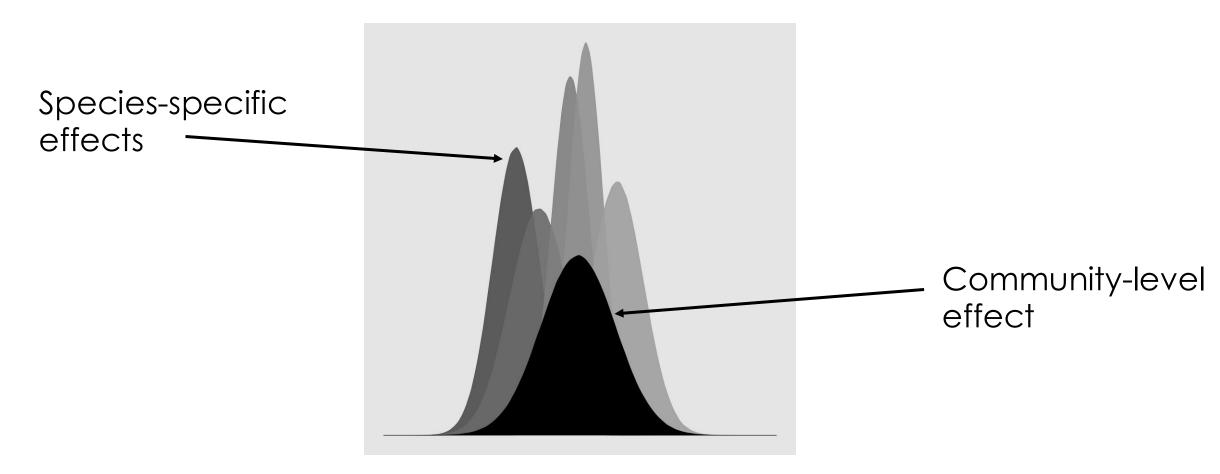# Species-specific and community effects

Community-level effect

Species-specific and community effects

Species-specific effects

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Species-specific and community effects

Species-specific effects

Community-level effect

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

Development of the MSOM

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Occupancy (ecological) sub-model

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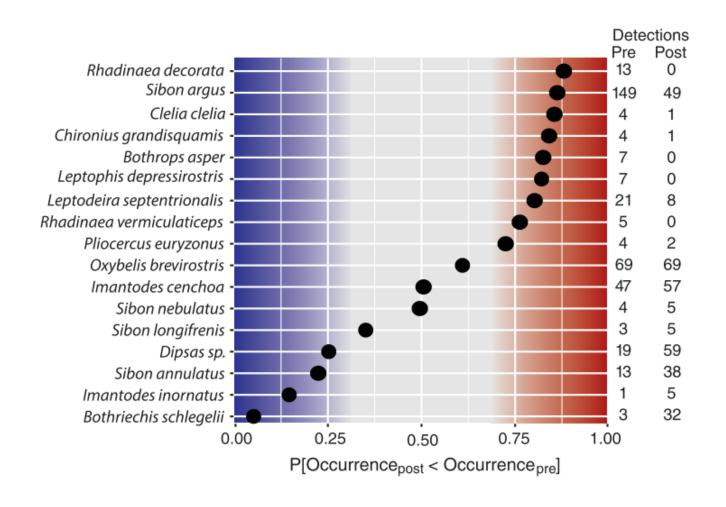
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These are just random slopes and intercepts!!

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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- 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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  - Missing covariates
- Estimating residual correlations can provide additional insights for hypothesis testing and underlying drivers of community patterns

Historical differences between JSDMs and MSOMs

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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

Joint species distribution models with species correlations and imperfect detection

MATHIAS W. TOBLER [iD],[1,5] MARC KÉRY,[2] FRANCIS K. C. HUI,[3] GURUTZETA GUILLERA-ARROITA,[4] PETER KNAUS,[2] AND THOMAS SATTLER[2]

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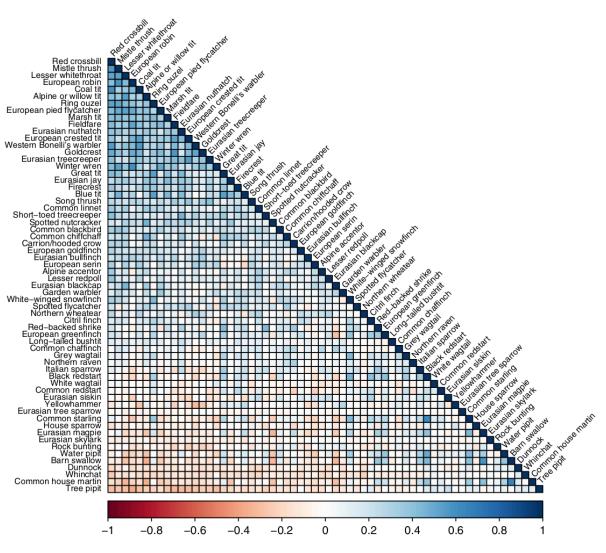
Joint species distribution models that account for imperfect detection **=** Multi-species occupancy models that account for species correlations
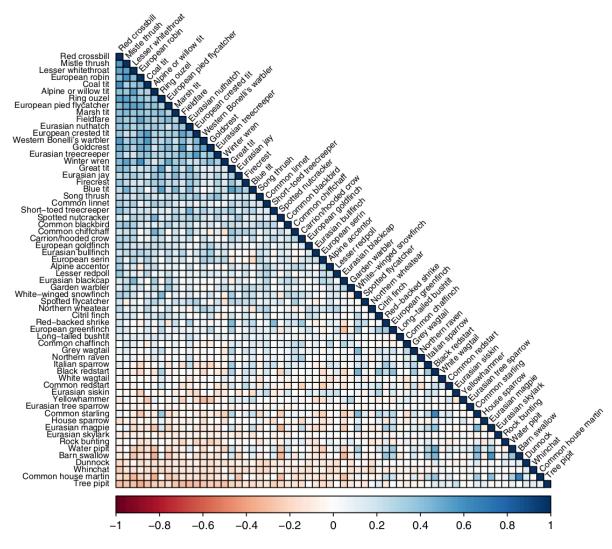
JSDMs with imperfect detection

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Tobler et al. (2019)

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- We could try to explicitly estimate every single correlation between each pair of species in the community.

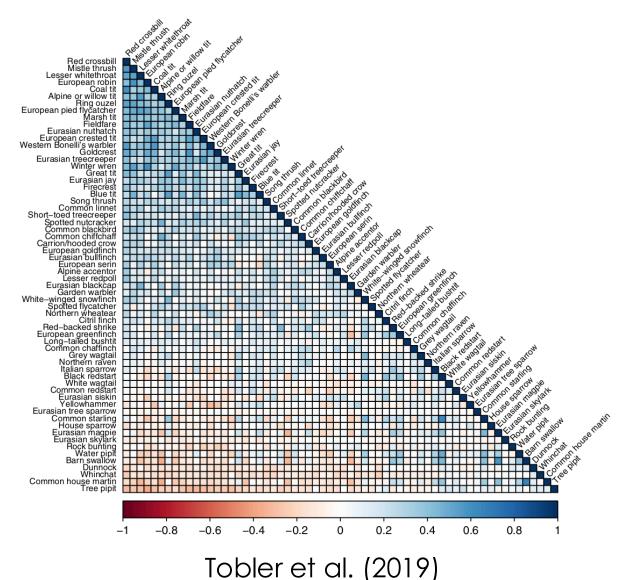

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JSDMs with imperfect detection

- 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)

Latent factor multi-species occupancy model

Example: one occupancy covariate and two latent factors

Occupancy (ecological) sub-model

$$z_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$$
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"Missing covariates" that account for residual species correlations

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Effects of the missing covariates

Factor loadings matrix

q= 3 factors (columns)

- N x 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)

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

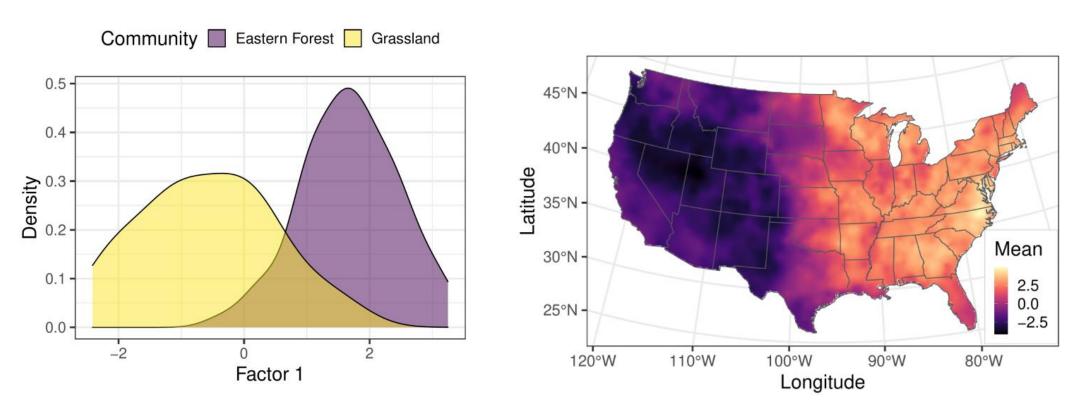# Deriving an interspecies covariance matrix

$$\boldsymbol{\Sigma} = \boldsymbol{\Lambda}\boldsymbol{\Lambda}^{\top}$$

$$
\begin{bmatrix}
\lambda_{1,1} & \lambda_{1,2} & \lambda_{1,3} \\
\lambda_{2,1} & \lambda_{2,2} & \lambda_{2,3} \\
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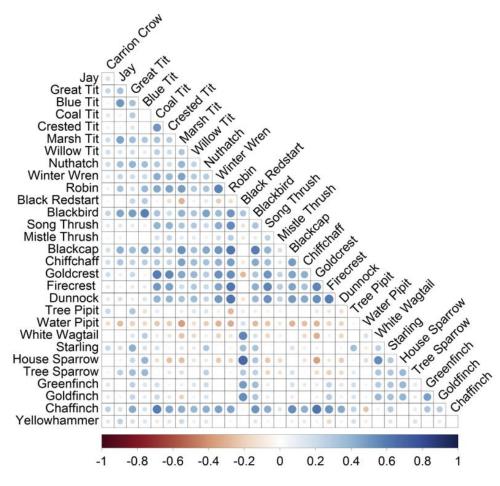\end{bmatrix}
$$

Interpretation of the latent factors and factor loadings

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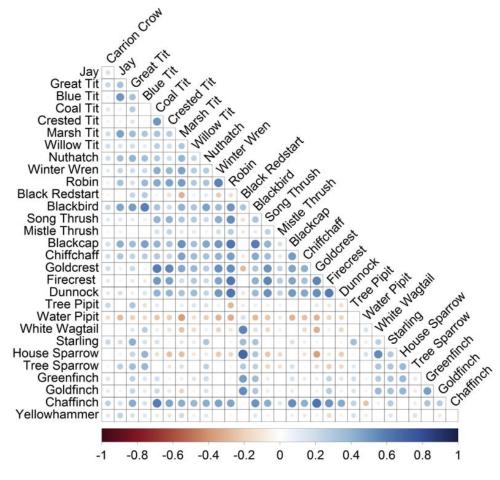

Doser, Finley, Banerjee (2023) Ecology

Interpretation of residual correlation matrix

- Can provide insights on missing covariates and/or biological processes driving co-occurrence patterns
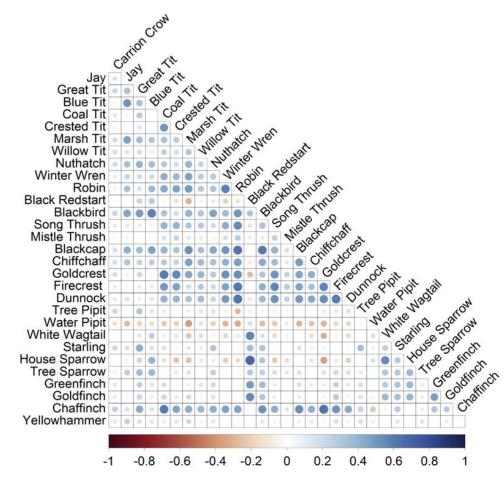

Kéry and Royle (2021) Chapter 8

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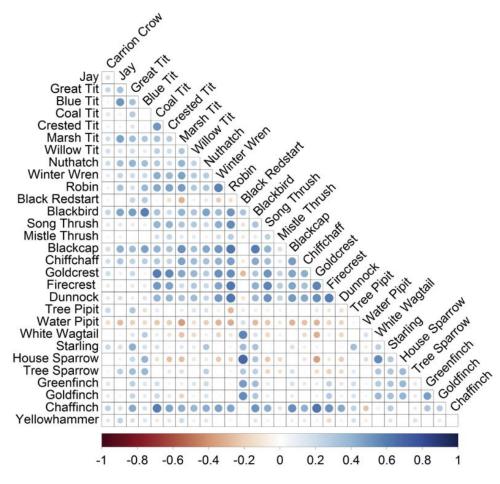
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- See Poggiato et al. (2021) *TREE* and Chapter 8 Kéry and Royle (2021)

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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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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  - Size of community and how much variation you expect across species.
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  - Size of data set and rarity of species in data set.

How to choose the number of factors (q)?

- Similar to performing a PCA and choosing the number of components to look at.
- More factors means more parameters to estimate.
- I often start out with between 5-10 depending on size of community.
- Things to consider:
    - Size of community and how much variation you expect across species.
    - Amount of computational power/time.
    - Size of data set and rarity of species in data set.
- 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
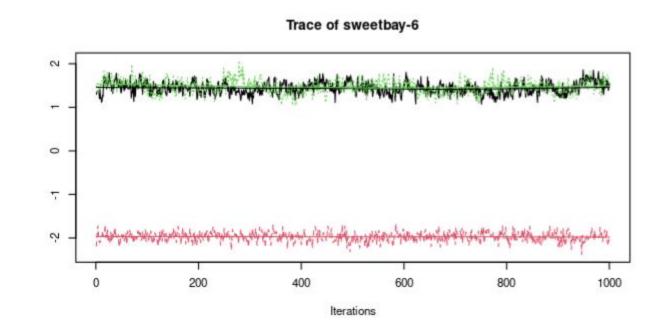
Jeffrey W. Doser

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](#).

Trace of sweetbay-6

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

`06-amphibian-multi-species-occ.R`