Hierarchical spatial modelling for applied population and community ecology

Jeffrey W. Doser, Marc Kéry, Gesa von Hirschheydt

24-27 June 2024

Spatial Generalized Linear Mixed Models for relative abundance estimation

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- Estimate sustainable yields of harvested populations
- Generate estimates of ecosystem services

Absolute abundance

The total number of individuals in an area.

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Relative abundance

A proxy for the true abundance of a species. An index of true abundance that differs from true abundance by some unknown value.

The term "abundance" is often used to describe both of these terms, but we will use it to describe absolute abundance.
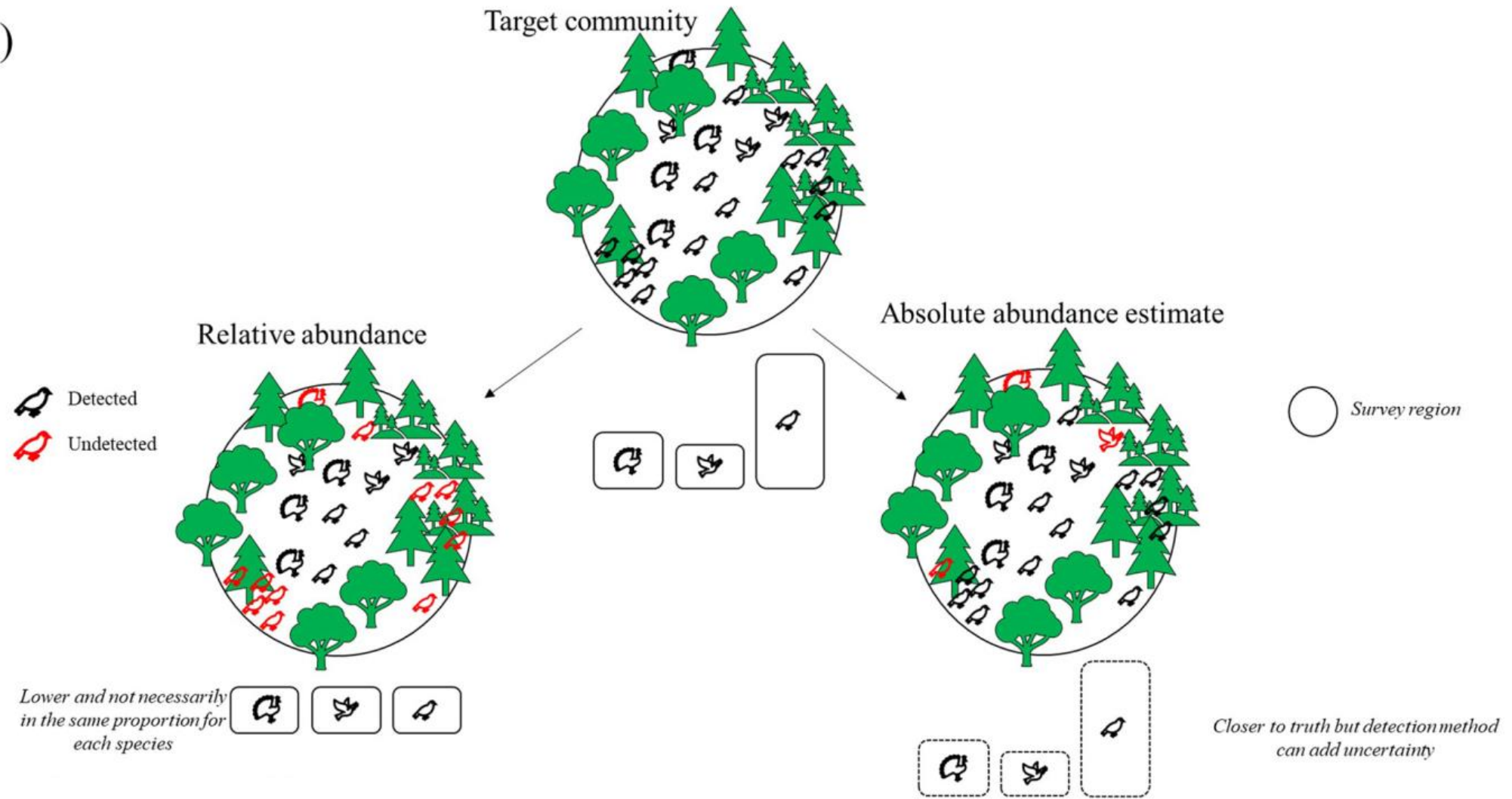
Absolute abundance

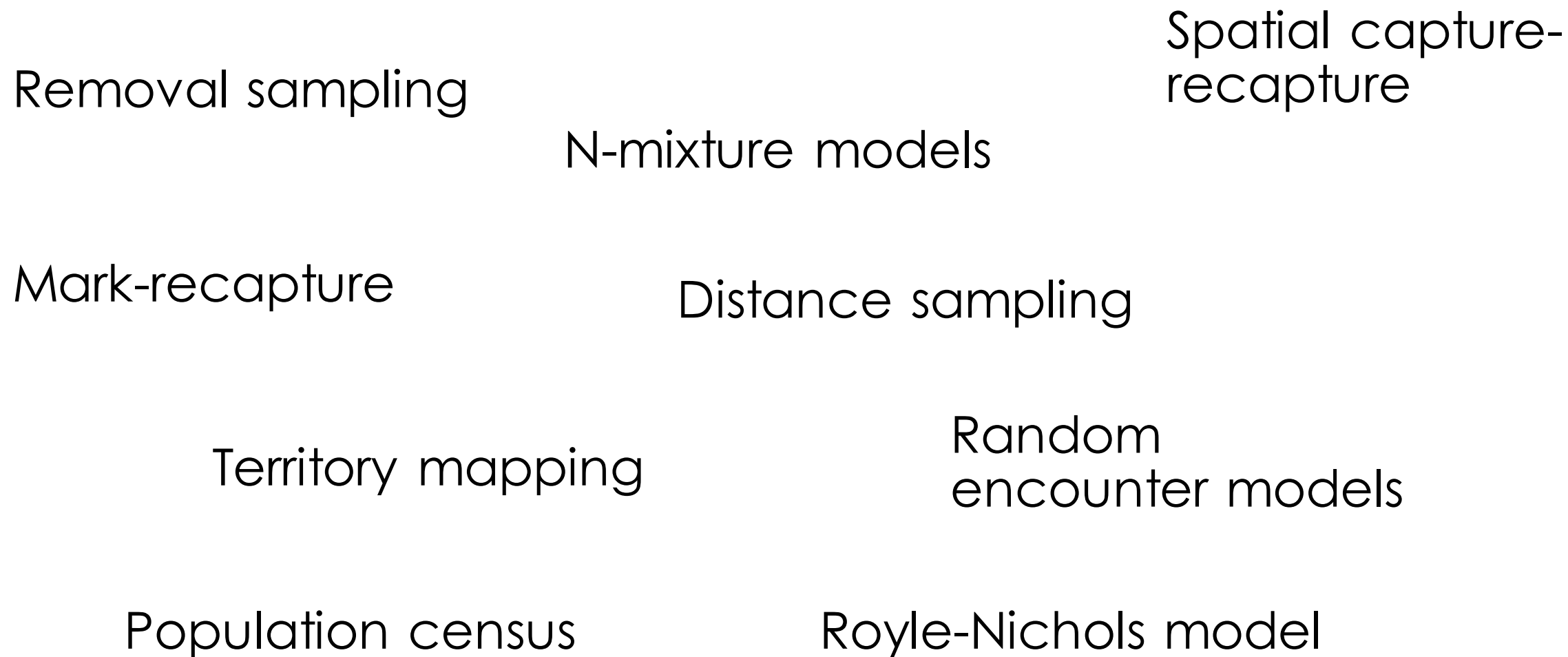The total number of individuals in an area.

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(A)

Target community

Relative abundance

Detected
Undetected

Absolute abundance estimate

Survey region

Lower and not necessarily
in the same proportion for
each species

Closer to truth but detection method
can add uncertainty

Callaghan et al. (2024)

Abundance estimation approaches

Removal sampling

Spatial capture-recapture

N-mixture models

Mark-recapture

Distance sampling

Territory mapping

Random encounter models

Population census

Royle-Nichols model

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- Imperfect detection.
- Harder to collect count data compared to detection-nondetection data.
- Many protocols to account for imperfect detection (e.g., mark-recapture) can be time-consuming and cost-intensive.
- Assumptions of modeling approaches to estimate absolute abundance can be difficult to meet.

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- With standardized survey effort, good design principles, and a few assumptions, we can quantify abundance change over time and/or space in relation to covariates of interest.

- Can use Generalized Linear Mixed Models (GLMMs). GLMMs are (relatively) simple, faster, and easier to fit.

Data for estimating relative abundance

- y_j: count of the number of individuals for the species of interest at site j
- Definition of a site is highly variable across different species/protocols

Swiss MHB: 267 1km^2 quadrats
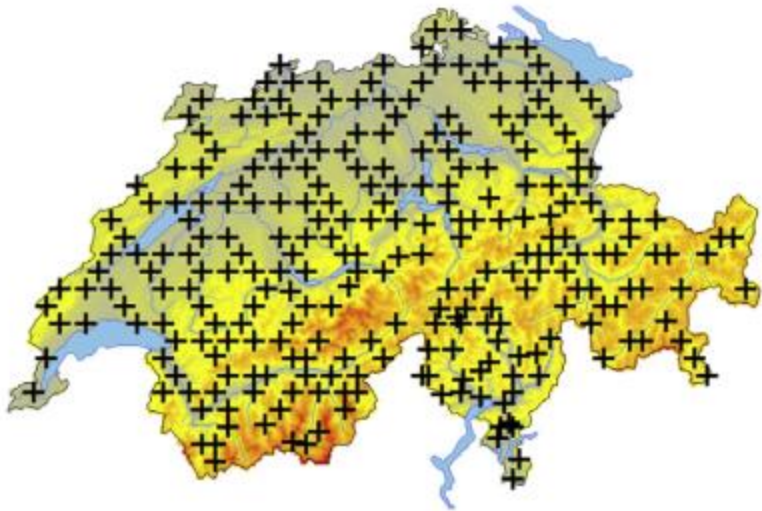
Kéry and Royle (2016)

Butterfly transects

Sevilleja et al. (2019)

Single-species GLMMs for count data

Poisson

$$y_j \sim \text{Poisson}(\mu_j)$$

$$\log(\mu_j) = \beta_1 + \beta_2 \cdot X_{2,j} + \cdots + \beta_r \cdot X_{r,j} + \beta^*_{1,\text{level}_j}$$

$$\beta^*_{1,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

- Remember for Poisson models, the mean is equal to the variance (i.e., no overdispersion).

- Including random effects can account for some overdispersion.

- *May refer to single-species GLMMs as univariate GLMMs*

Single-species GLMMs for count data

Negative Binomial

$$y_j \sim \text{NB}(\mu_j, \kappa)$$

$$\log(\mu_j) = \beta_1 + \beta_2 \cdot X_{2,j} + \cdots + \beta_r \cdot X_{r,j} + \beta^*_{1,\text{level}_j}$$

$$\beta^*_{1,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

- *k* is a positive dispersion parameter. Smaller values (close to 0) indicate overdispersion relative to the Poisson, while higher values indicate minimal overdispersion in abundance.

- As *k* goes to infinity, the NB becomes the Poisson.

Single-species LMMs for abundance-related data

$$y_j \sim \mathrm{Normal}(\mu_j, \tau^2)$$

$$\mu_j = \beta_1 + \beta_2 \cdot X_{2,j} + \cdots + \beta_r \cdot X_{r,j} + \beta^*_{1,\mathrm{level}_j}$$

$$\beta^*_{1,\mathrm{level}_j} \sim \mathrm{Normal}(0, \sigma^2_{\mu,1})$$

- Relevant for continuous abundance-related variables like biomass, or when modelling very large counts (recall from basic stats that the Poisson and Normal distributions become very similar when the count values are very large).
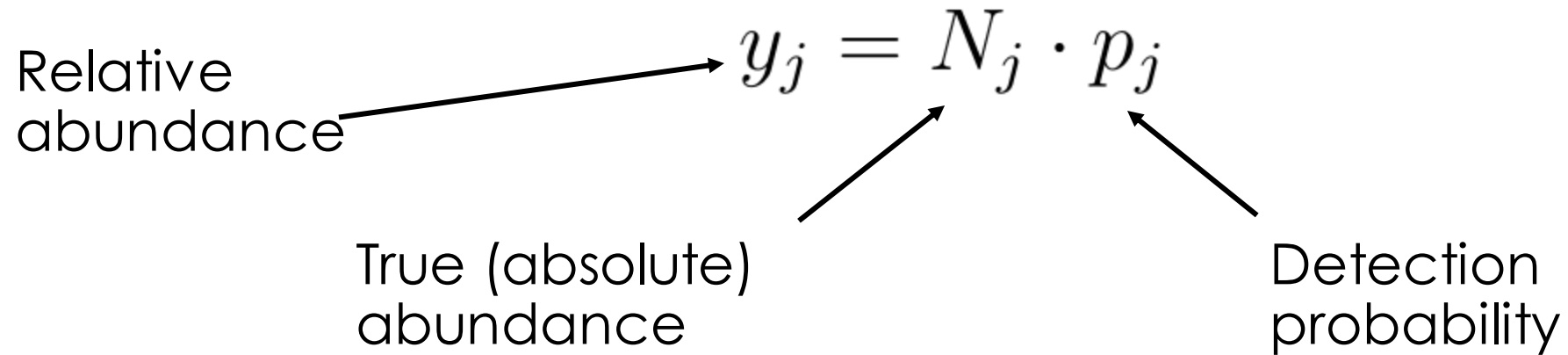
Prior distributions

- Normal (Gaussian) priors for the regression coefficients (default mean = 0, variance = 100)

- Inverse-gamma prior for the random effect variances (default shape and scale = 0.1)

- Uniform prior for the NB dispersion parameter (default bounds of 0 to 100)
  - If limited support for NB compared to Poisson in your data set, the estimate of k will likely be very close to the upper bound of this prior.

- Inverse-gamma prior for the Gaussian variance parameter (default shape and scale of 0.01).
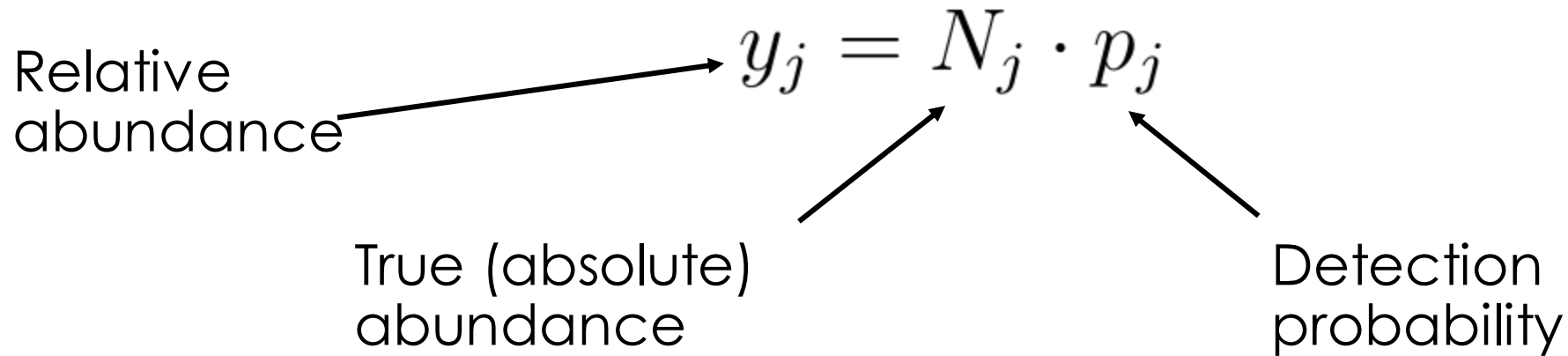
Interpreting relative abundance models

- We do *not* explicitly separate out detection probability from abundance.

- Relative abundance patterns are determined by both true (absolute) abundance and detection probability.

- All interpretations should take this into consideration.

- The reliability of relative abundance as an abundance index is highly dependent on the sampling design, species, and knowledge of the factors potentially influencing detection probability. See Latif et al. (2024) *JWM*
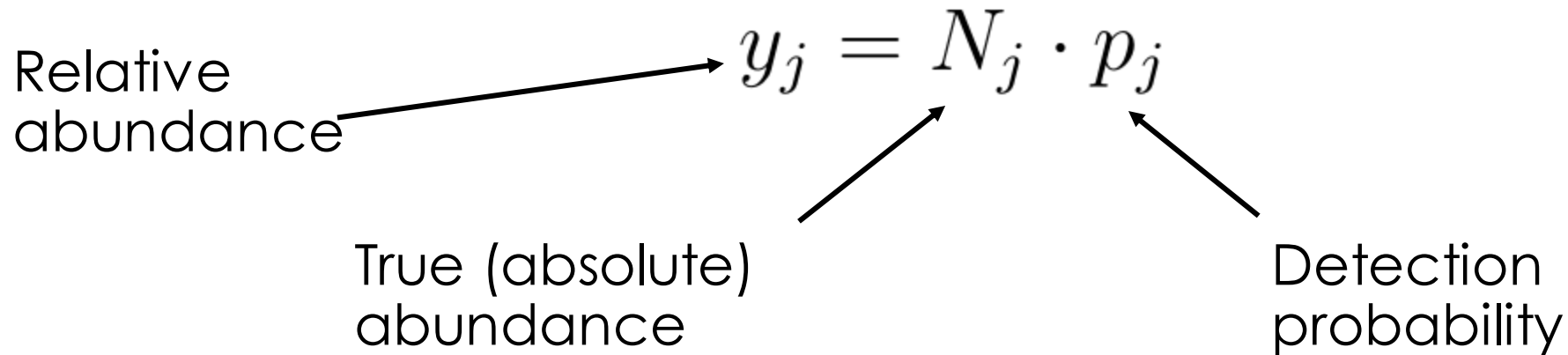
Interpreting relative abundance models

$$y_j = N_j \cdot p_j$$

Relative
abundance

True (absolute)
abundance

Detection
probability

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Detection probability

- If changes in abundance across space are large compared to changes in detection probability, changes in relative abundance largely reflect changes in true abundance.

Interpreting relative abundance models

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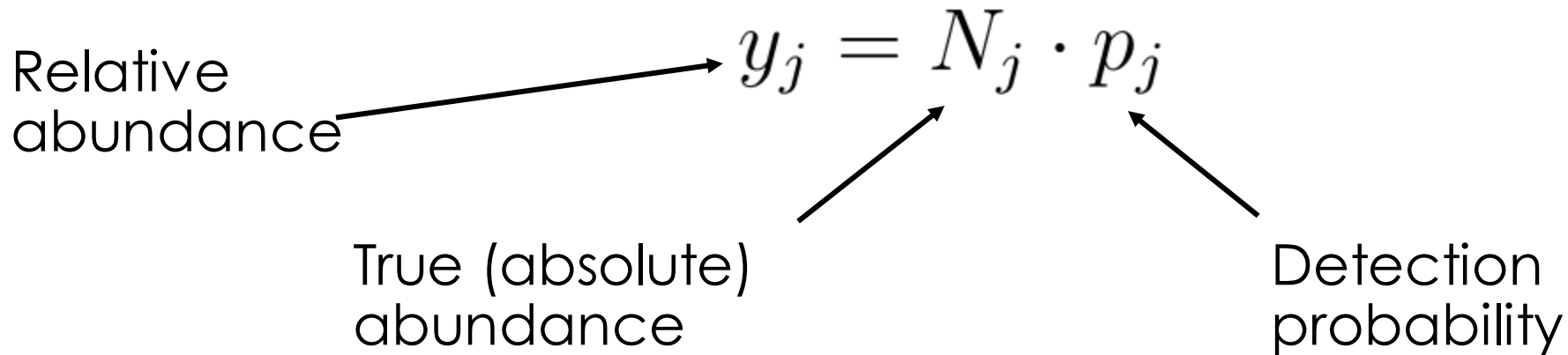
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- In data collection/sampling design, we want to minimize variation in detection probability as much as possible.

Interpreting relative abundance models

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Detection probability

- If changes in abundance across space are large compared to changes in detection probability, changes in relative abundance largely reflect changes in true abundance.

- In data collection/sampling design, we want to minimize variation in detection probability as much as possible.

- We can control for factors influencing detection probability by including them as covariates/random effects in our models (e.g., random observer effect).

Why spatial models for (relative) abundance?

- More accurate predictions

- More accurate uncertainty estimates

- Arguably more important than distribution models to capture fine-scale variation in local population sizes

Spatial GLMMs

- The beauty of hierarchical spatial modelling with Gaussian Processes (or NNGPs) is that the modelling process is extremely similar across different model types.

- There is nothing new in how we go about fitting spatial GLMMs. We add in an NNGP spatial random effect that is governed by a spatial covariance function (i.e., exponential).

Single-species spatial GLMM

$$y_j \sim \text{Poisson}(\mu_j)$$

$$\log(\mu_j) = \beta_1 + \beta_2 \cdot X_{2,j} + \cdots + \beta_r \cdot X_{r,j} + \beta^*_{1,\text{level}_j} + \text{w}_j$$

$$\beta^*_{1,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

$$\mathbf{w} \sim \text{Multivariate Normal}(\mathbf{0}, \tilde{\boldsymbol{C}}(d, \phi, \sigma^2))$$

Spatial random effects vector

NNGP spatial covariance matrix

Spatial decay parameter

Spatial variance parameter

Single-species spatial GLMM

Same approach for NB and Gaussian GLMMs, just switch the likelihood

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spAbundance

- Designed explicitly to fit a variety of spatial Bayesian models to estimate and predict abundance of individual and multiple species.

- Current functionality:
  - GLMMs
  - N-mixture models
  - Hierarchical distance sampling models

- Syntax is nearly identical to `spOccupancy`

- Uses NNGPs to work with big spatial data.

Doser et al. (2024) *MEE*

Fitting models in `spAbundance`

- Bayesian algorithms for working with count data (i.e., Poisson and NB distributions) are less efficient than the Pólya-Gamma approach that `spOccupancy` uses (i.e., there are less fully Gibbs updates in the MCMC samplers).

- Often need more MCMC samples for achieving convergence in `spAbundance` than `spOccupancy` for similar model types (e.g., single-species N-mixture model vs. occupancy model).

- All models (both spatial and non-spatial) use an Adaptive Metropolis-Hastings algorithm.

- We specify the number of MCMC batches, the number of samples within each batch, and the initial tuning variance.

Example of Adaptive Metropolis-Hastings

- Set the initial "tuning variance" for all parameters to 0.5 and set the target acceptance rate of newly proposed parameter values to 0.43.

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  - Propose a new value of each parameter (one at a time) from a normal distribution with mean equal to the previous value of the parameter and variance equal to the initial tuning variance (1.5).

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- Repeat for 199 more batches.

Fitting single-species GLMMs in `spAbundance`

- Non-spatial GLMMs: `abund()`

- Spatial GLMMs: `spAbund()`

- Currently supported distributions: Poisson, Negative Binomial, Gaussian, and "zero-inflated Gaussian" (available, but not yet well-documented).
  - Can also fit "Poisson log-normal" models by including random effects in Poisson.

- Not restricted to estimating abundance. These are GLMMs, so they can be used to model pretty much any sort of response!

- Main difference from `spOccupancy`: only one model formula and set of covariates

Structure of the data list


```
> str(data.NOCA)
List of 3
 $ y      : num [1:77] 37 34 40 40 39 30 56 27 50 56 ...
 $ covs   :'data.frame': 77 obs. of  7 variables:
  ..$ obs : num [1:77] 20 44 29 1 4 24 40 10 24 19 ...
  ..$ day : num [1:77] 147 146 146 146 150 152 146 153 153 153 ...
  ..$ tcc : num [1:77] 0 0 19 23 24 70 0 16 0 0 ...
  ..$ elev: num [1:77] 813 319 114 8 95 307 132 679 271 261 ...
  ..$ tmax: num [1:77] 27.7 31.3 32 31.5 32.1 31.4 32.6 28.9 31.5 31.6 ...
  ..$ tmin: num [1:77] -4.6 -2 -1.1 1.5 -2.2 ...
  ..$ ppt : num [1:77] 1165 1187 1166 1363 1134 ...
 $ coords: num [1:77, 1:2] 1190 1303 1528 1716 1576 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : NULL
  .. ..$ : chr [1:2] "X" "Y"
```

A word of caution with spatial NB GLMMs

- Including spatial random effects in an abundance-based GLMM can also be viewed as a form of accounting for overdispersion (where the overdispersion is spatially structured).

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- Thus, a spatially-explicit NB GLMM has two components that account for overdispersion: (1) the spatially structured intercept; and (2) the NB dispersion parameter.

- As a result, there can sometimes be confounding between these two processes, and the model will not converge.

- Advice if encountering convergence issues with spatial NB GLMMs:
  - Prevent the effective spatial range from taking very small values by placing an informative prior on the spatial decay parameter (e.g., set the Uniform upper bound of ϕ to $3 / q_{0.15}$, where $q_{0.15}$ is the 15% quantile of the inter-site distance matrix).

Exercise: Relative abundance of the northern cardinal in North Carolina, USA

`9a-spatial-glmm-birds.R`

Multi-species GLMMs

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- As with occupancy modelling, we can build multi-species GLMMs to estimate species-specific relative abundance simultaneously.

- Other names for multi-species GLMMs:
  o Multivariate GLMMs.
  o Abundance-based Joint Species Distribution Models.

Multi-species count data

j = 1, 2, …, J sites

i = 1, 2, …, I species

Species	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8
A	4	0	0	3	8	2	1	1
B	0	1	3	10	2	0	0	2
C	0	0	0	1	1	0	2	0
D	5	3	4	2	2	1	6	7

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D	5	3	4	2	2	1	6	7

Notice the use of I here instead of N as we saw with occupancy models. For abundance models, we use N to represent latent abundance as we will see with N-mixture and distance sampling models

Three types of multi-species GLMMs in `spAbundance`

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   - o Species are modelled hierarchically (as random effects)
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   - Species are modelled hierarchically (as random effects)
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3. Spatial factor multi-species abundance models (`sfMsAbund`)
   - Species are modelled hierarchically (as random effects)
   - Residual species correlations
   - Spatial autocorrelation

Multi-species abundance models (`msAbund`)

$$y_{i,j} \sim \text{Poisson}(\mu_{i,j})$$

$$\log(\mu_{i,j}) = \beta_{1,i} + \beta_{2,i} \cdot X_{2,j} + \cdots + \beta_{r,i} \cdot X_{r,j} + \beta^*_{1,i,\text{level}_j}$$

$$\beta_{1,i} \sim \text{Normal}(\mu_{\beta,1}, \tau^2_{\beta,1})$$

$$\beta^*_{1,i,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

- Species-level effects are modelled as random intercepts/slopes from a community-level distribution
- Often yields improved precision due to "borrowing strength", particularly for rare species

Latent factor multi-species abundance models (`lfMsAbund`)

$$y_{i,j} \sim \text{Poisson}(\mu_{i,j})$$

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$$\beta^*_{1,i,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

$$\text{w}^*_{i,j} = \lambda_{i,1} \cdot \text{w}_{1,j} + \lambda_{i,2} \cdot \text{w}_{2,j} + \cdots + \lambda_{i,q} \cdot \text{w}_{q,j}$$

$$\text{w}_{q,j} \sim \text{Normal}(0, 1)$$

- Account for species correlations through a set of latent factors.
- Latent factors arise from a standard normal distribution.

Spatial factor multi-species abundance models (`sfMsAbund`)

$$y_{i,j} \sim \text{Poisson}(\mu_{i,j})$$

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$$\beta_{1,i} \sim \text{Normal}(\mu_{\beta,1}, \tau^2_{\beta,1})$$

$$\beta^*_{1,i,\text{level}_j} \sim \text{Normal}(0, \sigma^2_{\mu,1})$$

$$\text{w}^*_{i,j} = \lambda_{i,1} \cdot \text{w}_{1,j} + \lambda_{i,2} \cdot \text{w}_{2,j} + \cdots + \lambda_{i,q} \cdot \text{w}_{q,j}$$

$$\mathbf{w}_q \sim \text{Multivariate Normal}(\mathbf{0}, \tilde{\boldsymbol{C}}(d, \phi_q))$$

- Account for species correlations through a set of spatial factors.
- Spatial factors modelled with NNGPs.

Fitting multi-species abundance GLMMs

- All the same prior constraints and convergence guidelines from occupancy models apply here.
- Tons of applications for relevant community ecology questions
  - Model-based ordination.
  - Can derive many different biodiversity metrics like richness, diversity, etc.
  - Assess variation in species-level responses.
  - Quantify residual species correlations.
- These are classic Joint Species Distribution Models.

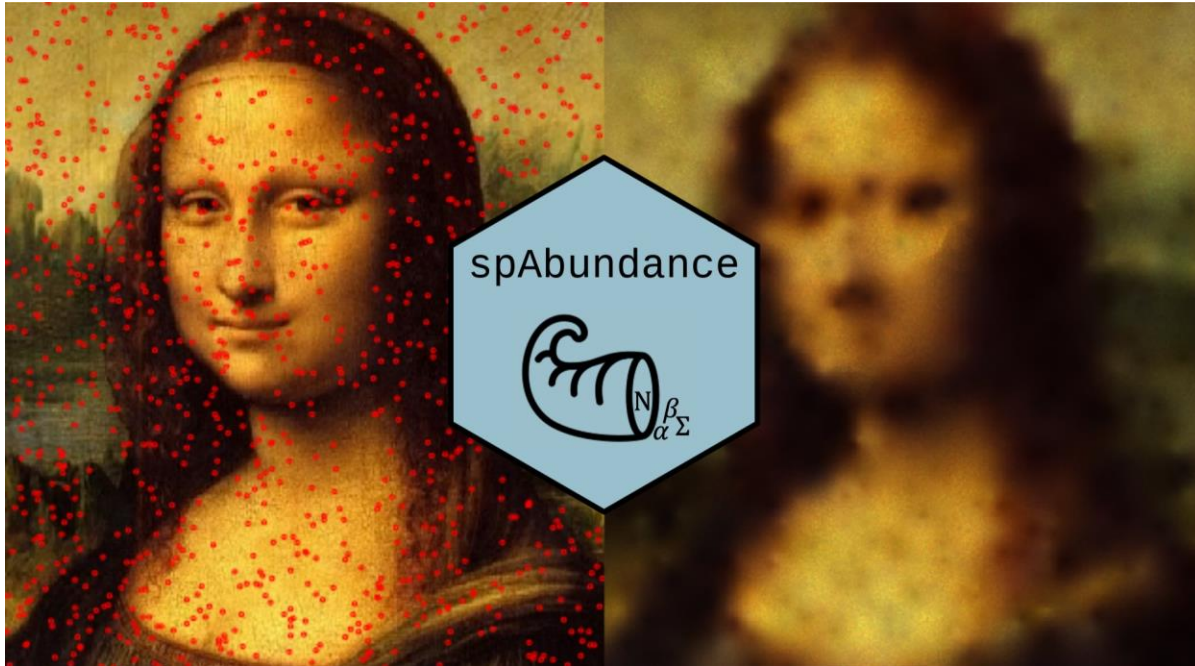# `spAbundance` GLMMs are not just restricted to abundance estimation

Relative acoustic activity from ARU data

Kovalenko et al. (2024) *Ecol and Evol*
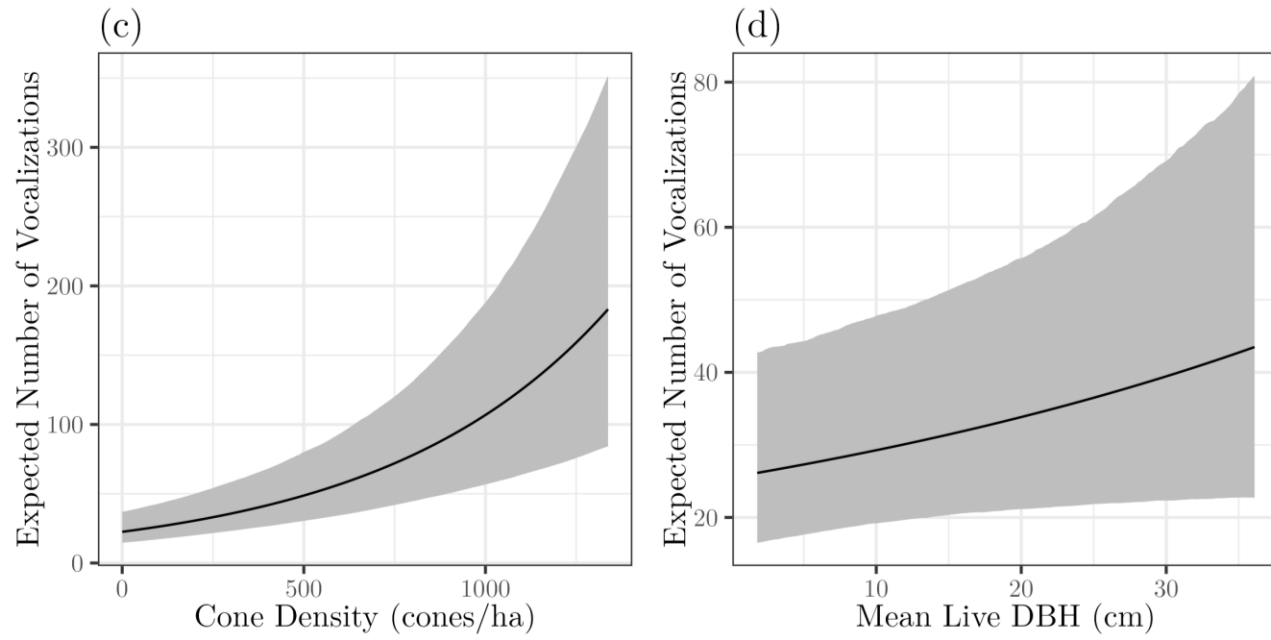
Clark's Nutcracker

`spAbundance` GLMMs are not just restricted to abundance estimation

Javier Fernández-López

https://github.com/jabiologo/nimble/blob/main/monalisa.R

Exercise: Estimating Shannon's diversity of bird communities across North Carolina, USA

`9b-spatial-multi-species-glmm.R`

Exercise: bird communities in North Carolina, USA