Hierarchical spatial modelling for applied population and community ecology

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Spatial N-Mixture Models

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Recap: why N-mixture models?

- An *unmarked* protocol for estimating population abundance.
- Only requires repeat counts of individuals, don't need to uniquely mark individuals.
- Conceptually very similar to occupancy models: variation in observed counts during a period of closure allows for estimation of detection probability.

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4. **No individual variation in detection probability**
5. **Parametric modelling assumptions**: do the distributions we choose adequately represent the data-generating process?

N-mixture model

$$
\begin{aligned}
N_j &\sim \text{Poisson}(\mu_j) \\
y_{j,k} &\sim \text{Binomial}(N_j, p_{j,k}) \\
\log(\mu_j) &= \boldsymbol{X}_j^\top \boldsymbol{\beta} \\
\text{logit}(p_{j,k}) &= \boldsymbol{V}_{j,k}^\top \boldsymbol{\alpha}
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Matrix notation

$$\log(\mu_j) = \beta_1 + \beta_2 \cdot X_{2,j} + \cdots + \beta_r \cdot X_{r,j}$$

N-mixture model

Can switch to negative binomial

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Fitting N-mixture models in `spAbundance`

- `NMix()` function
- Family argument can be Poisson or NB (aiming to have zero-inflated Poisson in the future)
- Can include both random intercepts and random slopes (random slopes not yet available in `spOccupancy`). Note that if including both, they are modeled as uncorrelated.
- Will usually need more MCMC iterations to achieve convergence than a comparable occupancy model fit in `spOccupancy`.

Exercise:
Estimating tropical bird abundance across an elevational gradient

`10a-crimson-mantled-woodpecker-nmix.R`

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- Only focusing on spatial autocorrelation in latent abundance, not in detection.
- Count data provide us with potentially MUCH more information for estimating spatial random effects than detection-nondetection data.
- As a result, may often find less uncertainty in spatial random effects in abundance models compared to occupancy models with the same number of spatial locations.

Spatial N-mixture models

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y_{j,k} &\sim \text{Binomial}(N_j, p_{j,k}) \\
\log(\mu_j) &= \boldsymbol{X}_j^\top \boldsymbol{\beta} + \mathrm{w}_j \\
\mathbf{w} &\sim \text{Multivariate Normal}(\mathbf{0}, \tilde{\boldsymbol{C}}(d, \phi, \sigma^2)) \\
\text{logit}(p_{j,k}) &= \boldsymbol{V}_{j,k}^\top \boldsymbol{\alpha}
\end{aligned}
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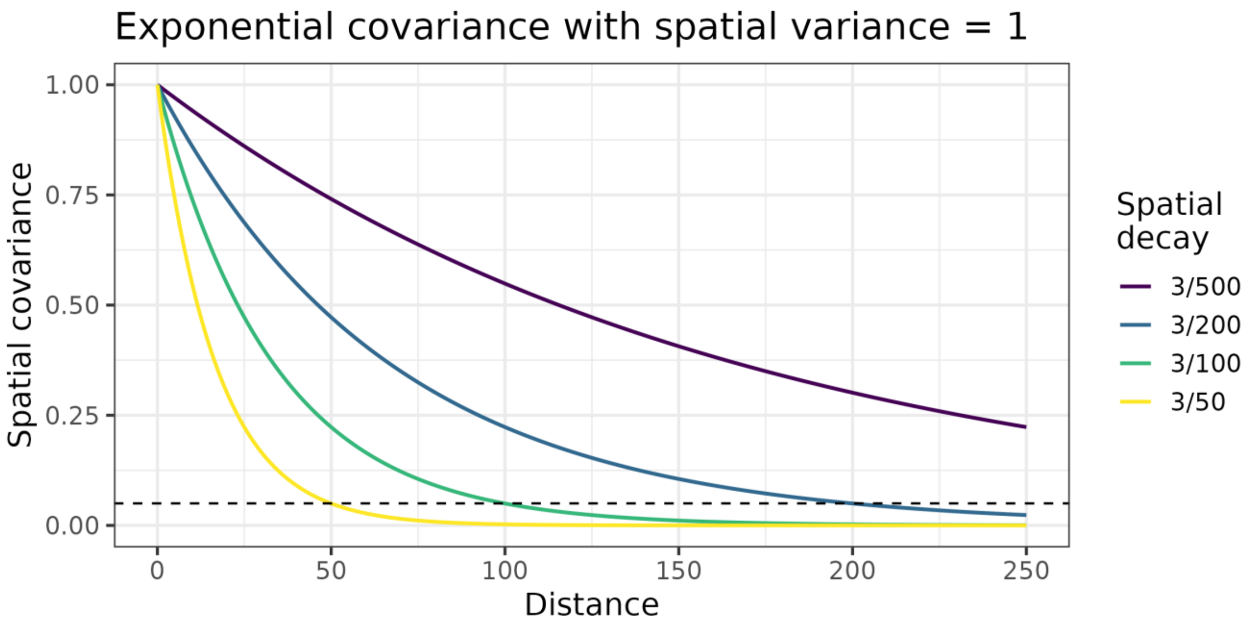

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3. Compute a fit statistic on both the actual data and the model-generated replicate data
4. Compare the fit statistics for the true and replicate data. If they are widely different, this suggests inadequate model fit.

Posterior predictive checks for N-mixture models

- For N-mixture models, there are two ways we can generate the replicate data values
- In `spAbundance`, we refer to the two approaches as *marginal* replicate data values, or *conditional* replicate data values.
- **Conditional replicate data values**: replicate values are generated conditional on the latent abundance N values.
- **Marginal replicate data values**: replicate values are not generated conditional on the latent abundance N values.

Generating conditional fitted values

$$y_{\text{rep},j,k}^{(l)} \sim \text{Binomial}(N_j^{(l)}, p_{j,k}^{(l)})$$

Generating conditional fitted values

MCMC
iteration

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Generating conditional fitted values

MCMC iteration

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- A replicate data value is generated for each MCMC iteration (l).
- The replicate data are conditional on N_j
- What is the minimum value that $N_j^{(l)}$ can take?

Generating marginal fitted values

$$\hat{N}^{(l)}_{\text{rep},j} \sim \text{Poisson}(\mu^{(l)}_j)$$
$$y^{(l)}_{\text{rep},j,k} \sim \text{Binomial}(\hat{N}^{(l)}_j, p^{(l)}_{j,k})$$

- First predict a value of latent abundance at site j for MCMC iteration l.
- Generate the replicate data value using the predicted abundance value
- New predicted latent abundance value not completely dependent on the observed data.

Marginal vs. conditional posterior predictive checks

- See vignette for small simulation study.
- Marginal PPCs may be more sensitive, but need to do more simulation analyses.
- Lots of opportunities to explore GoF assessments and PPCs in N-mixture models and other types of hierarchical models.

Generating replicate values and PPCs

Posterior predictive checks

```
ppcAbund(object, fit.stat, group, type = 'marginal', ...)
```

Generating replicate (fitted) values

```
# S3 method for spNMix
fitted(object, type = 'marginal', ...)
```

Model selection with WAIC

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Expected log pointwise predictive density

Effective number of parameters

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$$\text{WAIC} = -2 \times (\underbrace{\text{elppd}}_{\text{Expected log pointwise predictive density}} - \underbrace{\text{pD}}_{\text{Effective number of parameters}})$$

- Calculating elppd in N-mixture and hierarchical distance sampling models requires integrating out latent abundance
- Calculation of WAIC can be slow, particularly with large counts.

Exercise: Predicting abundance across a simulated landscape

`10b-sim-spatial-nmix.R`

Difficulties with spatial N-mixture models

- When model assumptions are met and overdispersion in counts is reasonable, N-mixture models can work well and give reasonable estimates of abundance (our analysis of the simulated data).

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- Out of all the models in `spOccupancy`/`spAbundance`, spatial N-mixture models (single-species and multi-species) are the trickiest.

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- Why?

Difficulties with spatial N-mixture models

- Recall a key goal of N-mixture models: partition variability in detection probability from variability in abundance.
- N-mixture models are most commonly fit with a Binomial detection sub-model and a Poisson abundance sub-model.
- This works well without any overdispersion.

Difficulties with spatial N-mixture models

- Knape et al. (2018) showed that an N-mixture model with overdispersion in detection (beta-binomial Poisson N-mixture) and a model with overdispersion in abundance (binomial negative binomial N-mixture) are nearly identical.

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RESEARCH ARTICLE

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Sensitivity of binomial N-mixture models to overdispersion: The importance of assessing model fit

Jonas Knape[1] | Debora Arlt[1] | Frédéric Barraquand[2] | Åke Berg[1] | Mathieu Chevalier[1] | Tomas Pärt[1] | Alejandro Ruete[1,3] | Michał Żmihorski[1]

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It is very difficult to distinguish between overdispersion in detection probability and overdispersion in abundance.

Difficulties with spatial N-mixture models

- As a result, spatial N-mixture models can be extremely slow to converge and may require heavily informative prior distributions.
- Further, overdispersed models (i.e., NB N-mixture models and spatial N-mixture models) can yield very high and unreasonable estimates of abundance
  - Often happens in situations where the closure assumption may be violated
  - Kéry (2010) Ecology
- **What should we do with heavily overdispersed repeated count data?**

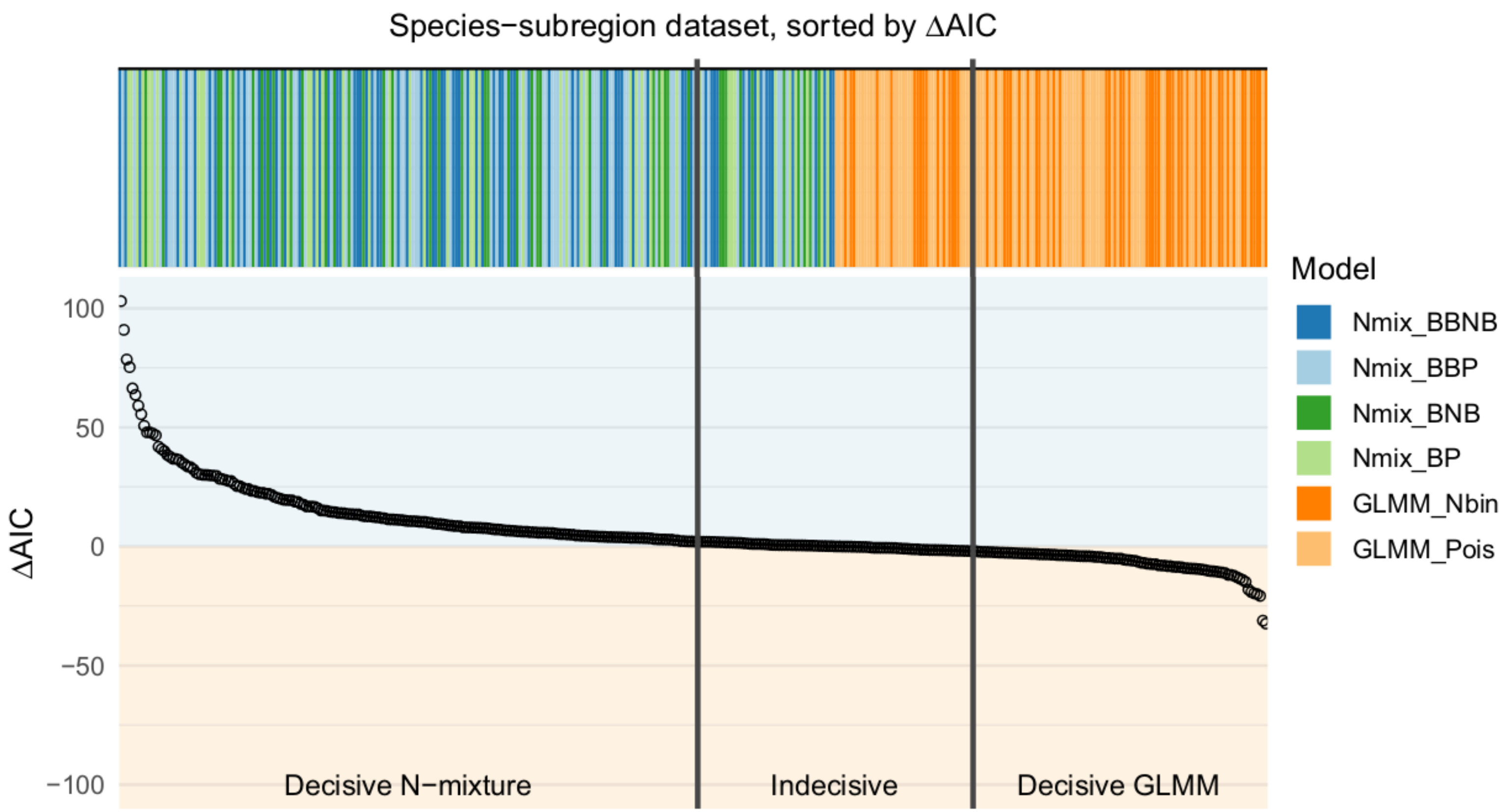
Solutions

1. Explore the use of more informative prior distributions on spatial parameters or the NB dispersion parameter.
2. Consider using GLMMs and estimating relative abundance.

Further complications with N-mixture models

- N-mixture models are powerful, but very sensitive to model assumptions
  - "With great power comes great responsibility."
- Closure violations can lead to biased abundance estimates (i.e., estimates will be biased high).
- Lots of discussion: Duarte et al. (2018), Knape et al. (2018), Bellier et al. (2016), Link et al. (2018), Barker et al. (2018), and many others.
- In cases where assumptions may be violated, abundance estimates from N-mixture models may best be viewed as relative abundance.

N-mixture models vs. GLMMs for relative abundance estimation



Goldstein and de Valpine (2022) *Sci Reports*

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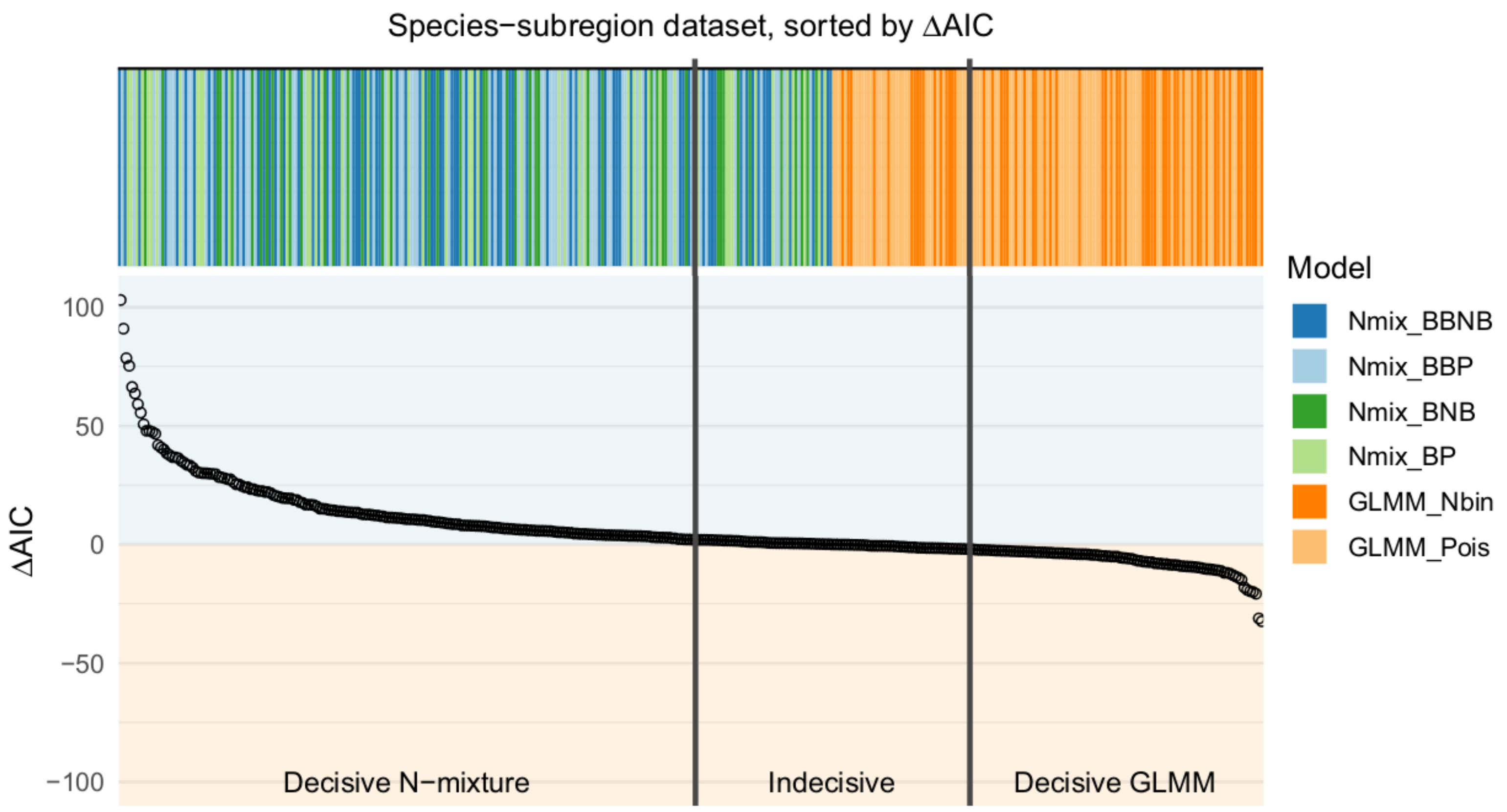

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Lots of outstanding questions to understand performance of N-mixture models for relative abundance estimation

Exercise: Exploring difficulties with spatial N-mixture models

10c-european-goldfinch-spatial-nmix.R