

N-mixture models

Emily Dennis, Byron Morgan and Martin Ridout

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What the N-mixture model does

- N-mixture models can estimate **animal abundance from a set of counts** with both spatial and temporal replication whilst accounting for **imperfect detection**.
- A benefit of the N-mixture model is the **reasonably low cost and effort** required for data collection compared to alternative sampling methods.
 - Applies for many **citizen-science** based monitoring programs.
 - Highly cited paper: Royle(2004, *Biometrics*).
- Many extensions exist, including
 - The use of **covariates** to examine spatial patterns in abundance and detection.
 - The creation of **maps of spatial abundance**.

Point count data for **American redstart**

Site	Sample									
	1	2	3	4	5	6	7	8	9	10
1	0	0	0	1	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0
3	1	0	0	0	0	0	0	0	0	0
4	0	1	1	3	1	2	2	1	0	1
5	2	0	1	1	0	0	1	0	0	0

Results in an **estimated expected number of 2.81**, when 50 sites are sampled.

Forming the likelihood

Emily Dennis,
Byron Morgan
and Martin
Ridout

The N-mixture
model

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Application

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References

A set of counts is made during $t = 1, \dots, T$ sampling occasions at $i = 1, \dots, R$ sites of a **closed** population.

- Each individual has the same detection probability, p .
- The counts n_{it} at site i and time t are

$$n_{it} \sim \text{Bin}(N_i, p),$$

where N_i is the unknown population size **at site i** .

- Assuming N_i to be independent random variables with probability function $f(N; \theta)$, such as Poisson or negative binomial, the **likelihood** is

$$L(p, \theta; \{n_{it}\}) = \prod_{i=1}^R \left\{ \sum_{N=\max_t n_{it}}^{\infty} \left(\prod_{t=1}^T \text{Bin}(n_{it}; N, p) \right) f(N; \theta) \right\}$$

To infinity and beyond

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$$L(p, \theta; \{n_{it}\}) = \prod_{i=1}^R \left\{ \sum_{N=\max_t n_{it}}^K \left(\prod_{t=1}^T \text{Bin}(n_{it}; N, p) \right) f(N; \theta) \right\}$$

- **Requires selection of a value, K , for ∞ .**

- PRESENCE
- unmarked

Both of these have a **default value** for K . As we shall see, this can be **dangerous**. It would be nice to **avoid having to choose K** , and we now show how this can be done.

Equivalence with the multivariate Poisson model

- The N-mixture model is equivalent to the **multivariate Poisson** with a particular covariance structure.
- The equivalence can be illustrated via comparison of probability generating functions.
- Here we illustrate the bivariate Poisson model ($T = 2$).

The bivariate Poisson

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- Consider $T = 2$ and counts n_1 and n_2 for a particular site written as

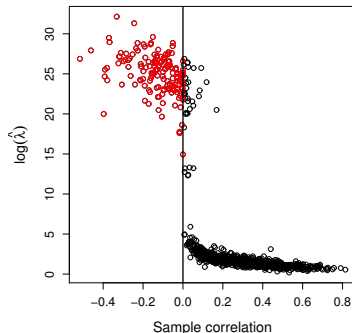
$$n_1 = X_1 + X_{12} \quad \text{and} \quad n_2 = X_2 + X_{12}$$

- $X_1, X_2 \sim \text{Pois}(\theta_1)$, where $\theta_1 = \lambda p(1 - p)$, and $X_{12} \sim \text{Pois}(\theta_0)$, where $\theta_0 = \lambda p^2$.
- All values are independent.
- Note relationship with **capture-recapture**: Cormack (1989)
- Then (n_1, n_2) follow a **bivariate Poisson distribution**, with $\text{corr}(n_1, n_2) = p$, and the likelihood is

$$L(p, \lambda; \{n_{it}\}) = e^{-(2\theta_1 + \theta_0)} \prod_{i=1}^R \left\{ \frac{\theta_1^{n_{i1} + n_{i2}}}{n_{i1}! n_{i2}!} \sum_{m=0}^{\min(n_{i1}, n_{i2})} \binom{n_{i1}}{m} \binom{n_{i2}}{m} m! \left(\frac{\theta_0}{\theta_1^2} \right)^m \right\}$$

Performance of the bivariate Poisson model

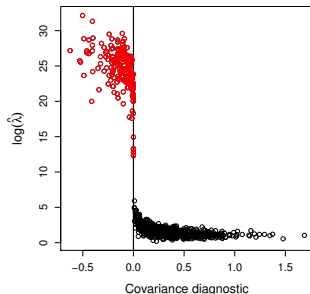
- Investigate model performance via simulation.
 - 1000 simulations for $\lambda = 5$, $\rho = 0.25$ and $R = 20$.
- In some cases estimates for λ were very large.
- Associated with small or negative values of the product moment sample correlation.



A covariance diagnostic for $T = 2$

- Negative values of an estimate of the covariance diagnose high estimates of λ .

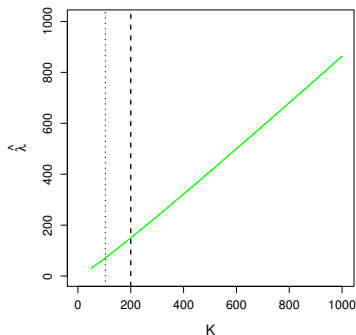
$$\text{cov}^*(n_1, n_2) = \text{mean}(n_1 * n_2) - \{\text{mean}(n_1 + n_2)/2\}^2$$



- Hence in these instances $\hat{\lambda}$ is actually infinite (and $\hat{p} = 0$) and high estimates are obtained as an artefact of the **optimisation routine stopping prematurely** when the likelihood is flat.
- Simulations suggest that the diagnostic extends for $T > 2$.

The effect of the choice of K on fitting the N-mixture model

- The infinite values of $\hat{\lambda}$ for the bivariate Poisson are **limited by the value of K** in the N-mixture model.
- unmarked
 $K = \max(\text{count}) + 100$
(dotted)
- PRESENCE $K = 200$
(dashed)
- **The model should always be fitted for multiple values of K .**



covariance diagnostic ≤ 0

Application to Hermann's tortoise data

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- Analyse data from a study of the threatened Hermann's tortoise *Testudo hermanni* in southeastern France.
- **R=118 sites** were each surveyed **T=3** times.
- Sample covariance diagnostic suggests stable estimates from the N-mixture model (1.052).
- From the N-mixture model with Poisson mixing distribution $\hat{\lambda} = 4.70$ and $\hat{p} = 0.28$, and were stable for $K \geq 30$.
- But the **negative binomial model is better**, and estimates using the negative binomial distribution do not stabilise for increasing values of K .
 - Hence results presented for the negative binomial **will vary with K** .

Hermann's tortoise



Discussion

- The N-mixture model can produce **infinite estimates of abundance**.
 - Particularly when the number of sampling occasions and/or sites is limited and detection probability low.
- The equivalence with the multivariate Poisson was used to understand and diagnose this behaviour.
 - Avoids the requirement to select an upper bound K .
- Is there a suitable diagnostic for the Negative Binomial distribution?
- Use **R package**.
- Note the **use of N-mixture for fitting Multivariate Poisson** (EM and composite likelihood currently used).

- **Peter Jupp**, proving results regarding the diagnostic criterion.
- **Takis Besbeas**, using Hidden Markov Models to fit N-mixture models, including the Open case. These are fast, but still require specification of K, and multiple such values in the open case.
- **Linda Haines**, writing the likelihood in terms of a hypergeometric function, and then using recent work on the numerical evaluation of such functions. Speed is comparable to fixing K and using the binomial mixture, but does not require a value for K. A concentrated likelihood allows analytical advance, and investigation of the test criterion.
- Relationship with **parameter redundancy**.

References

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