New models for reptile and amphibian removal data

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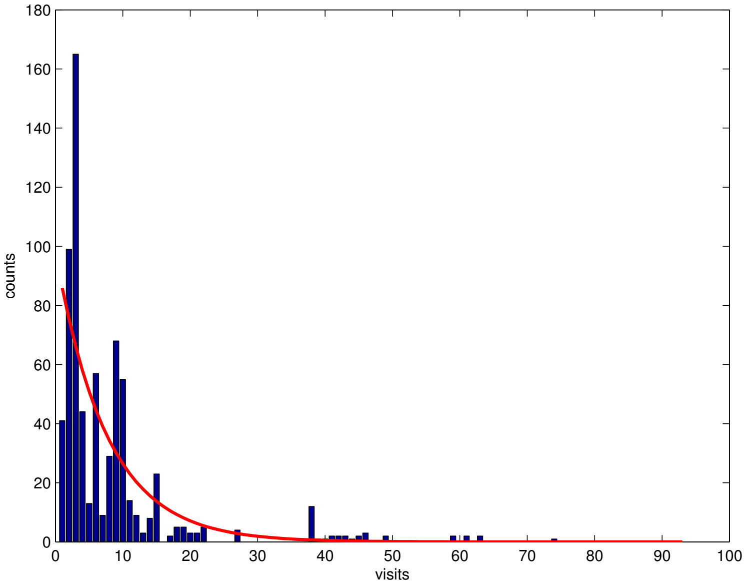
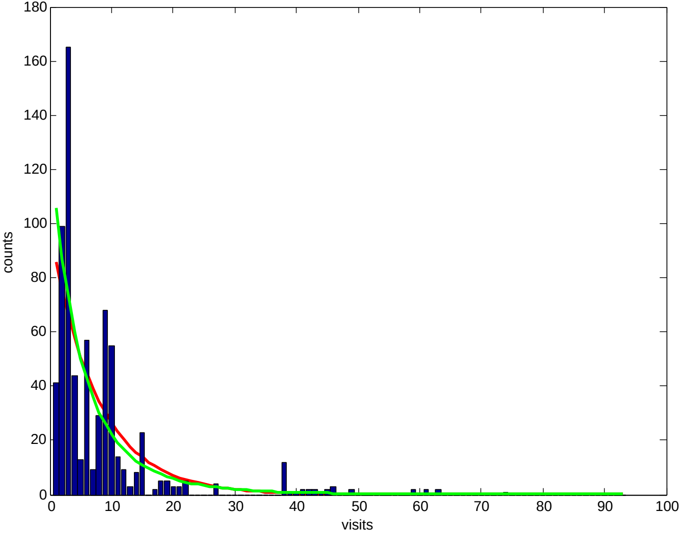
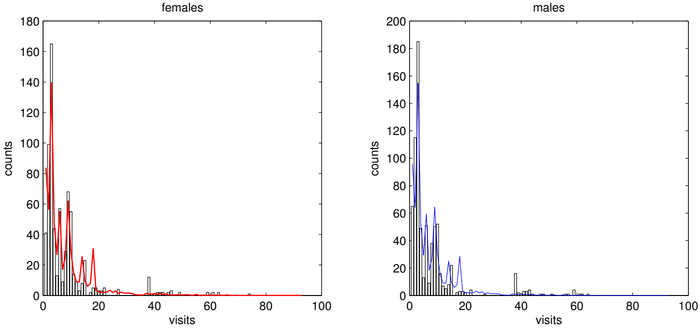
Result of fitting geometric model to GCN data



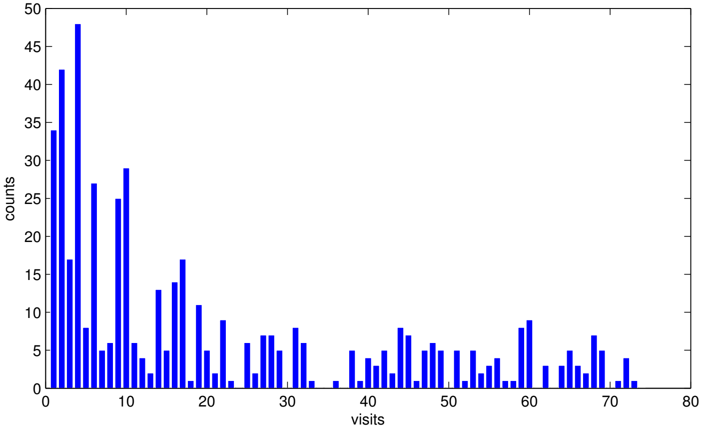
and then adding over dispersion



Geometric removal model with min air temperature



Timed clearance data: mainly slow worms



Model for timed clearences

- For the timed clearance data, at fixed times parts of the study area were cleared.
- This was modelled by assuming a global population of animals of size N, to be estimated.
- Fractions of this number were assumed to be available for capture during each time interval. Cf Stop-over modelling.
- Using maximum likelihood, the fractions were estimated as: 0.45, 0.10, 0.17, 0.28, 0.00.
- The estimated number of animals not observed was $\hat{N}_0 = 51$.

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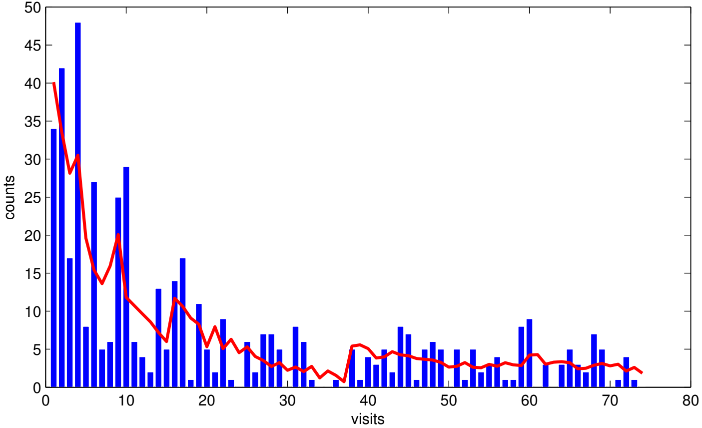
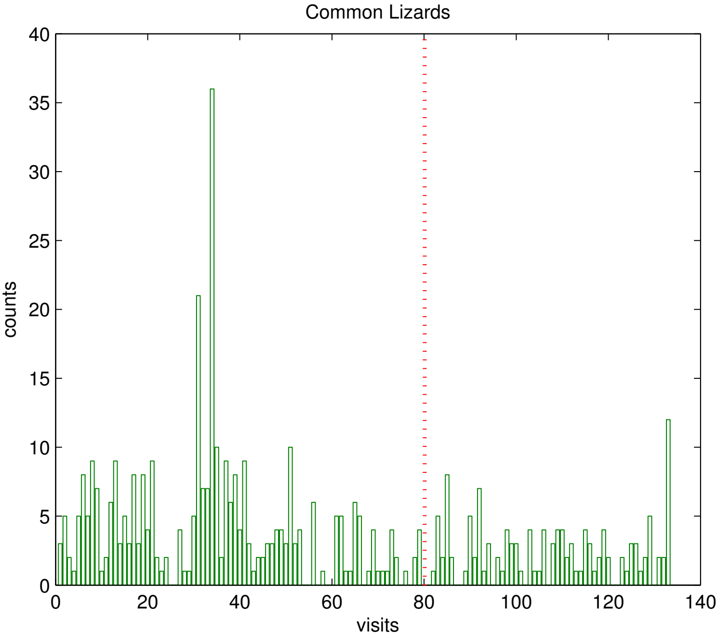



Common Lizards
counts
visits
0
5
10
15
20
25
30
35
40
0
20
40
60
80
100
120
140

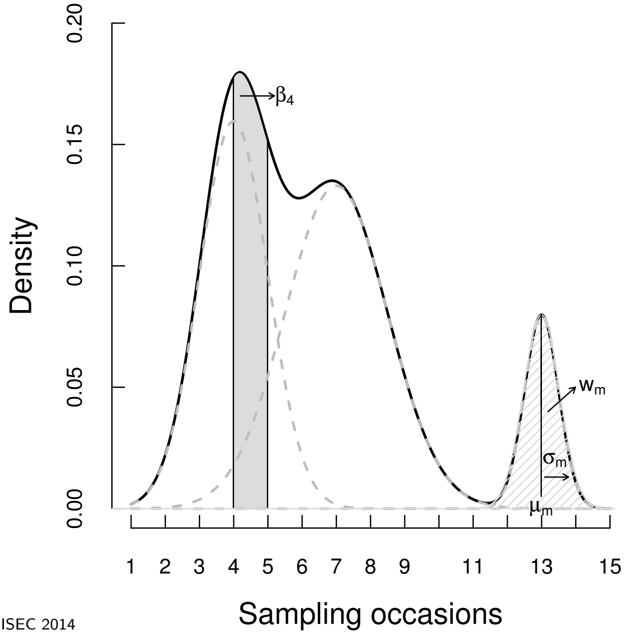
Stop-over model parameters

- N: population size; M: number of arrival groups.
- w_m, μ_m and σ_m, $m = 1, \ldots, M$: The population fractions, mean arrival times and standard deviations of arrival times of the M arrival groups, $\sum_{m=1}^{M} w_m = 1$. The population fraction that arrived between occasions $b-1$ and b is denoted by β_{b-1}. In terms of the mixture components,

$$\beta_{b-1} = \sum_{m=1}^{M} w_m \left\{F_m(b) - F_m(b-1)\right\}, \; b = 2, \ldots, T-1$$

where $F_m(b) = P(X \leq b)$ when $X \sim N(\mu_m, \sigma_m^2)$. The first and last intervals are open-ended with $\beta_0 = \sum_{m=1}^{M} w_m F_m(1)$ and $\beta_{T-1} = 1 - \sum_{m=1}^{M} w_m F_m(T-1)$, $\forall m$, ensuring that the entry parameters sum to 1 i.e. $\sum_{b=1}^{T} \beta_{b-1} = 1$.

Stop-over model: $M = 3$



Forming the likelihood

If an individual belongs to category t, $t = 1, \ldots, T$, then it was removed on sampling occasion t. The unknown number of individuals that were never detected and therefore never removed belong to category $T + 1$.

The probability of belonging to category t, γ_t, is:

$$\gamma_t = \begin{cases} \sum_{b=1}^{t} \left[\beta_{b-1} \left\{\prod_{k=b}^{t-1} (1 - p_k)\right\}\right] p_t, & t = 1, \ldots, T \\ 1 - \sum_{t=1}^{T} \gamma_t = \sum_{b=1}^{T} \left[\beta_{b-1} \prod_{k=b}^{T} (1 - p_k)\right], & t = T + 1 \end{cases},$$

The likelihood is multinomial with $T + 1$ cells, γ_t, $t = 1, \ldots, T + 1$ probabilities and n_t, $t = 1, \ldots, T + 1$ frequencies.

Stop-over likelihood

The parameters are given by

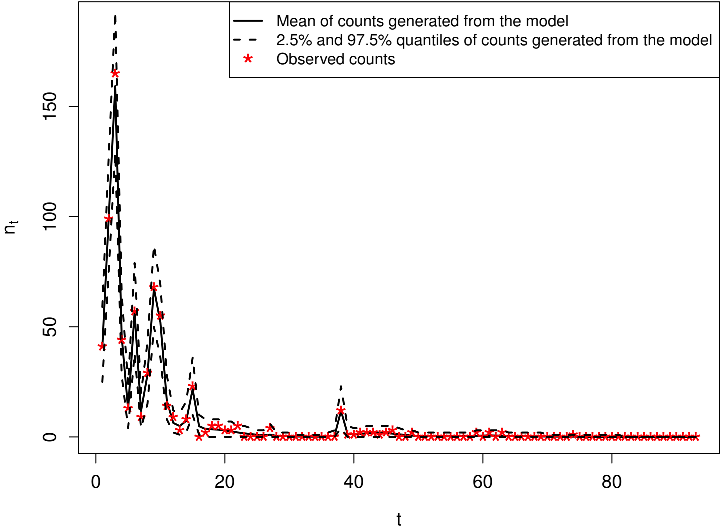
$$\boldsymbol{\theta} = (M, N, (w_m, \mu_m, \sigma_m)_{m=1,\ldots,M}, (p_t)_{t=1\ldots,T})$$

and the likelihood is:

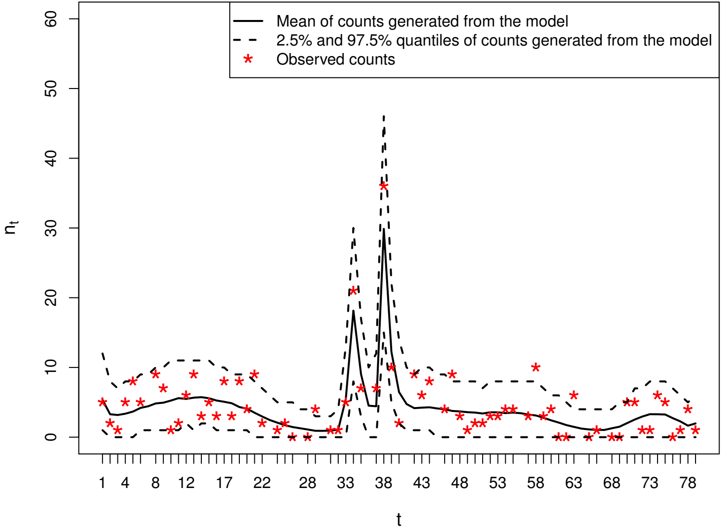
$$p(\mathbf{y}|\boldsymbol{\theta}) = \frac{N!}{\left(\prod_{t=1}^{T} n_t!\right)(N-D)!}\left\{\prod_{t=1}^{T}\gamma_t^{n_t}\right\}\gamma_{T+1}^{N-D},$$

where $D = \sum_{t=1}^{T} n_t$. We assume constant capture in the applications.

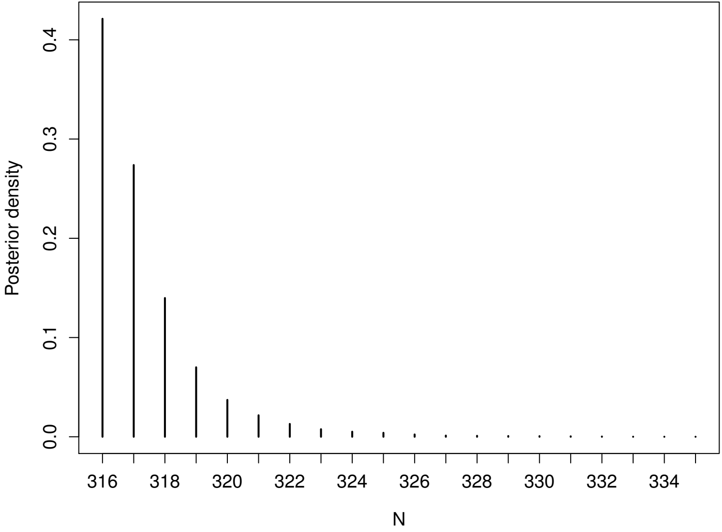
Stop-over, RJMCMC, model averaged, GCN



Stop-over, RJMCMC, model averaged, lizard



Posterior distribution for N for lizard



References

1. Dorazio, Jelks and Jordan (2005)*Biometrics*, **61**, 1093–1101.
2. Matechou, E., Nicholls, G., Morgan, B.J.T., Collazo, J.A. and Lyons, J.E. (2014). Bayesian mixture models for stopover data. Submitted for publication.
3. Moran (1951) *Biometrika*, **38**, 307–311.
4. Ridout and Morgan (1991) *Biometrics*, **47**, 1423–1433.
5. Zippin (1958) *J. Wildlife Management*, **22**, 82–90.

Covariates

- In practice we can expect the capture probability to vary
- for fecundability, conception might vary with age and parity
- for animals capture might vary with temperature. For GCN, minimum air temperature was used
- We may have a logistic transformation, for a covariate w:

$$p = \frac{1}{1 + \exp(\alpha + \beta w)}.$$

- It is often necessary to choose the best covariate(s) from a relevant set.
- Overdispersion may also be included, eg., using a beta-geometric distribution.

Modelling

- The simple removal model dates from papers by Moran (1951) and Zippin (1958)
- It assumes a constant capture probability, p.
- The other parameter is the desired population size, N.
- The same model applies to fecundability data, which record months to conception for human couples.
- 100 Smokers: 29 16 17 4 3 9 4 5 1 1 1 3 7; $\hat{N} = 95$.
- 486 Non-smokers: 198 107 55 38 18 22 7 9 5 3 6 6 12; $\hat{N} = 476$.

Notation and likelihood for geometric model

- N: initial population size
- n_k: size of the k^{th} sample removed from the population, $k = 1, 2, \dots, T$
- $x_k = \sum_{j=1}^{k-1} n_j$, $k = 2, 3, \dots, T+1; x_1 = 0$.

For example: $\mathbf{n} = (65, 115, 185, \dots)$

$$\mathbf{x} = (0, 65, 180, 365, \dots).$$

We then form the likelihood:

$$\mathrm{L}(N, p; \mathbf{n}) = \frac{N!}{(\prod_{k=1}^{T} n_k!)(N - x_{T+1})!} \left[\prod_{k=1}^{T} \{p(1-p)^{k-1}\}^{n_k} \right] (1-p)^{T(N - x_{T+1})}$$

Maximum-likelihood estimates

The likelihood simplifies to give

$$\mathrm{L}(N, p; \mathbf{n}) = \frac{N!}{(\prod_{k=1}^{T} n_k!)(N - x_{T+1})!} p^{x_{T+1}} (1-p)^{TN - \sum_{k=1}^{T+1} x_k}$$

Maximum-likelihood estimates of the two parameters are given by the solutions to the equations:

$$\hat{N} = \frac{x_{T+1}}{1 - (1-\hat{p})^T}$$

$$\frac{\hat{p}}{1-\hat{p}} - \frac{T(1-\hat{p})^T}{1-(1-\hat{p})^T} = \frac{\sum_{k=1}^{T}(k-1)n_k}{x_{T+1}}$$