

Depletion modelling for herpetological translocations

Rachel McCrea



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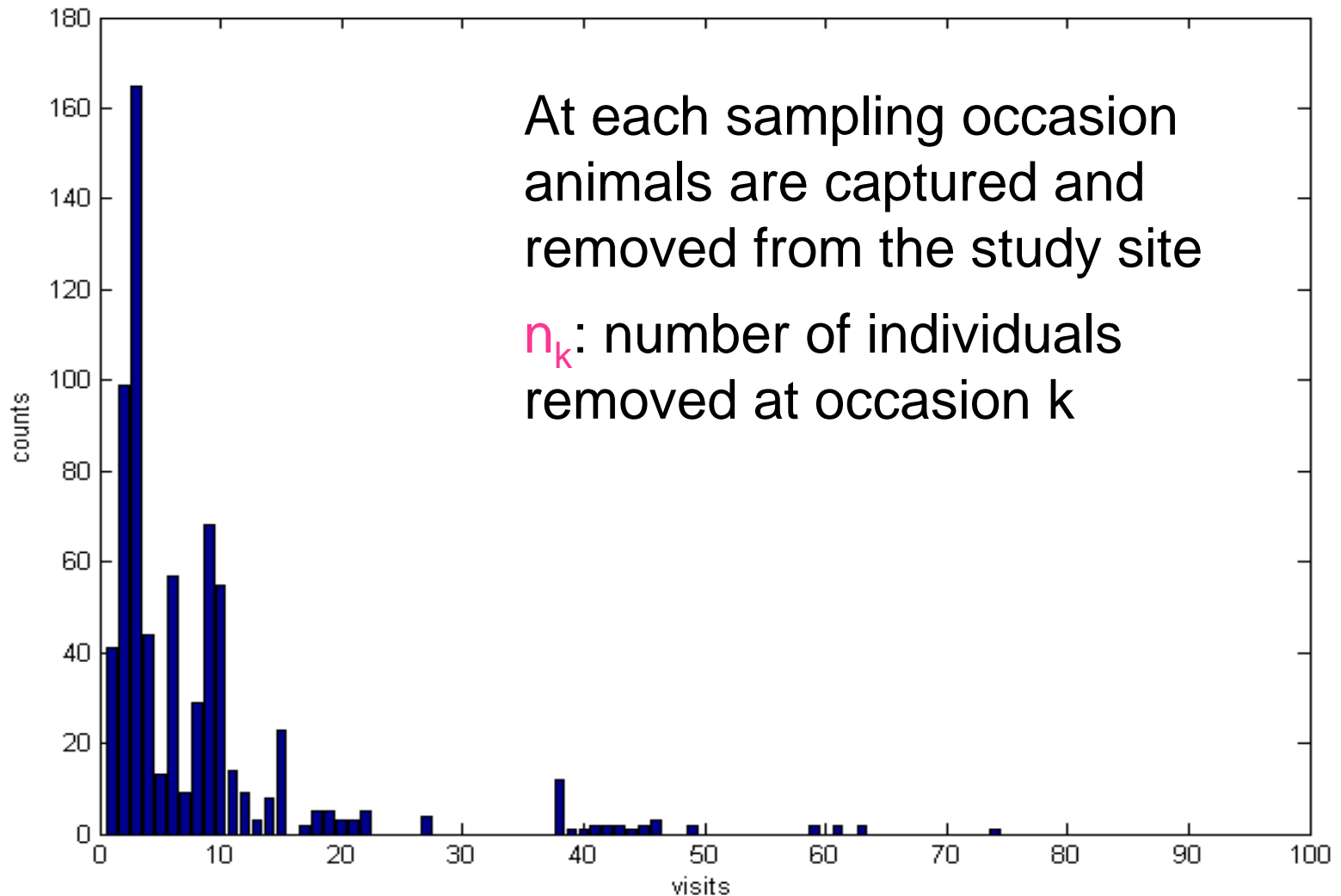


Eleni Matechou, Byron Morgan,
Richard Griffiths, Brett Lewis
and David Sewell

Overview

- Depletion data
- Existing models
- Incorporating weather covariates
- Incorporating “new arrivals”
- New developments
- Future directions

Depletion data



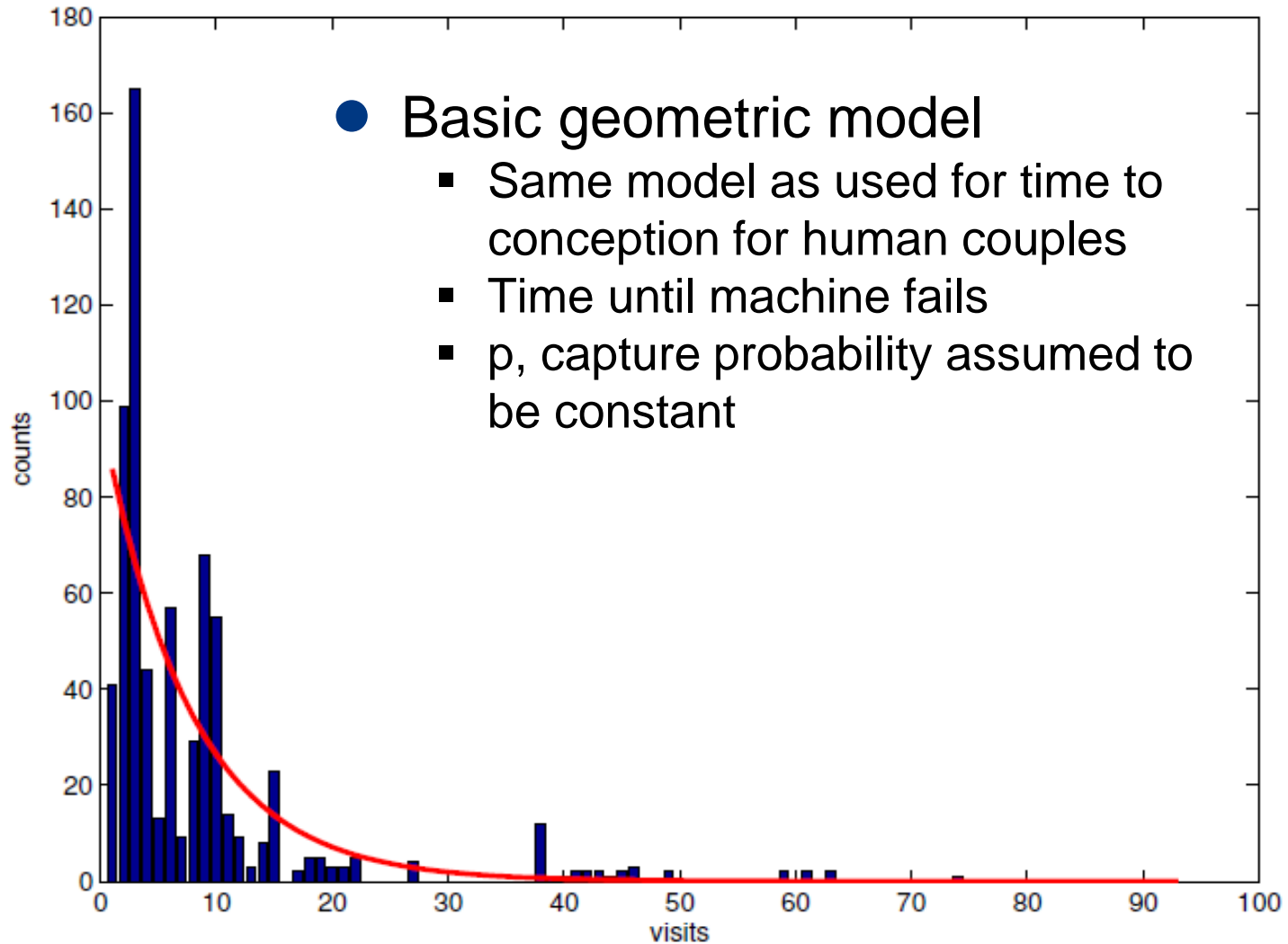
Depletion data

- Capture-recapture data – but with no recaptures!
- 1000
- 0100
- We want to know if there are any individuals who have not been captured by the end of the study....
- ...individuals who have encounter history 0000

Depletion data

- Capture-recapture data – but with no recaptures!
- 1000 p
- 0100 $(1-p)p$
- We want to know if there are any individuals who have not been captured by the end of the study....
- ...individuals who have encounter history 0000
 $(1-p)(1-p)(1-p)(1-p)$

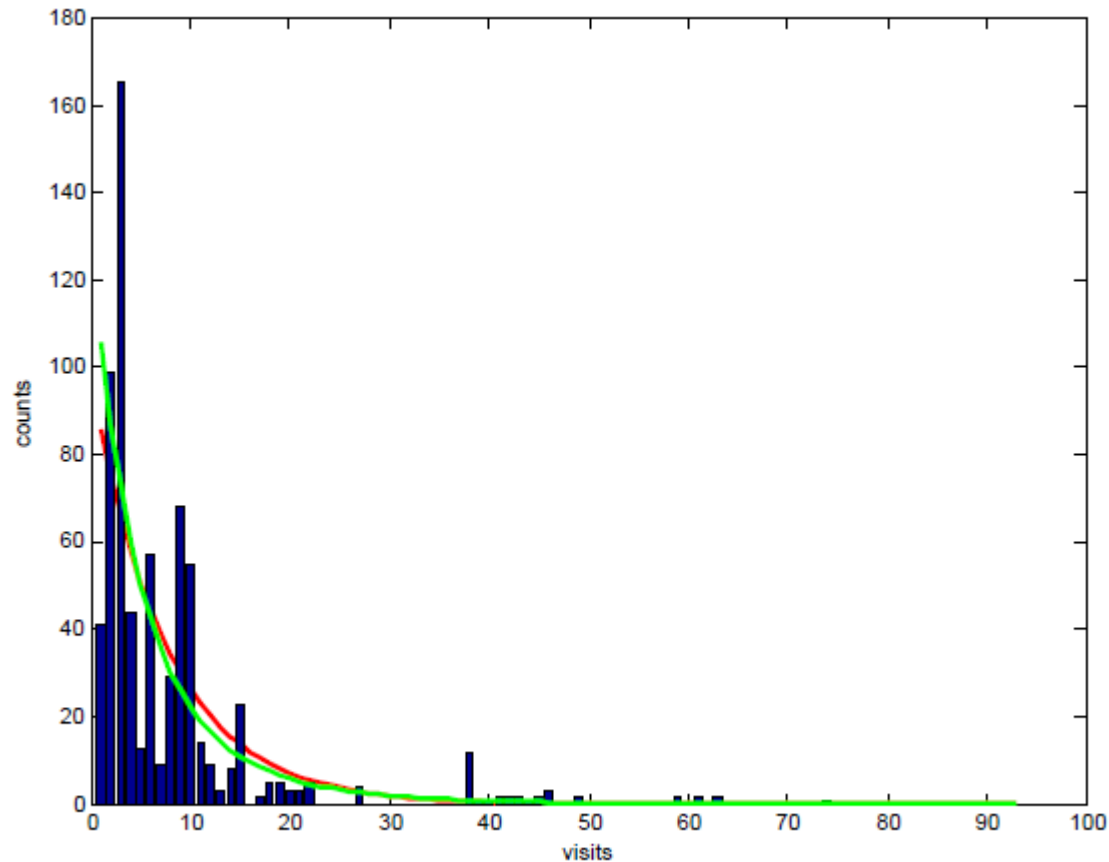
Depletion model



- Basic geometric model
 - Same model as used for time to conception for human couples
 - Time until machine fails
 - p , capture probability assumed to be constant

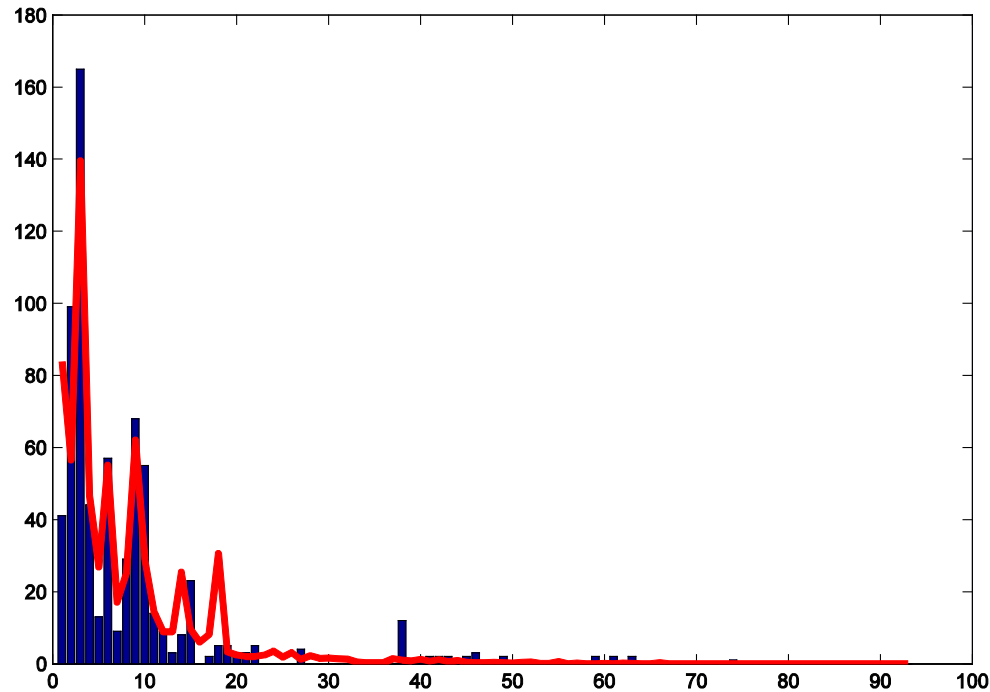
Heterogeneity

- Adding overdispersion – beta-geometric model

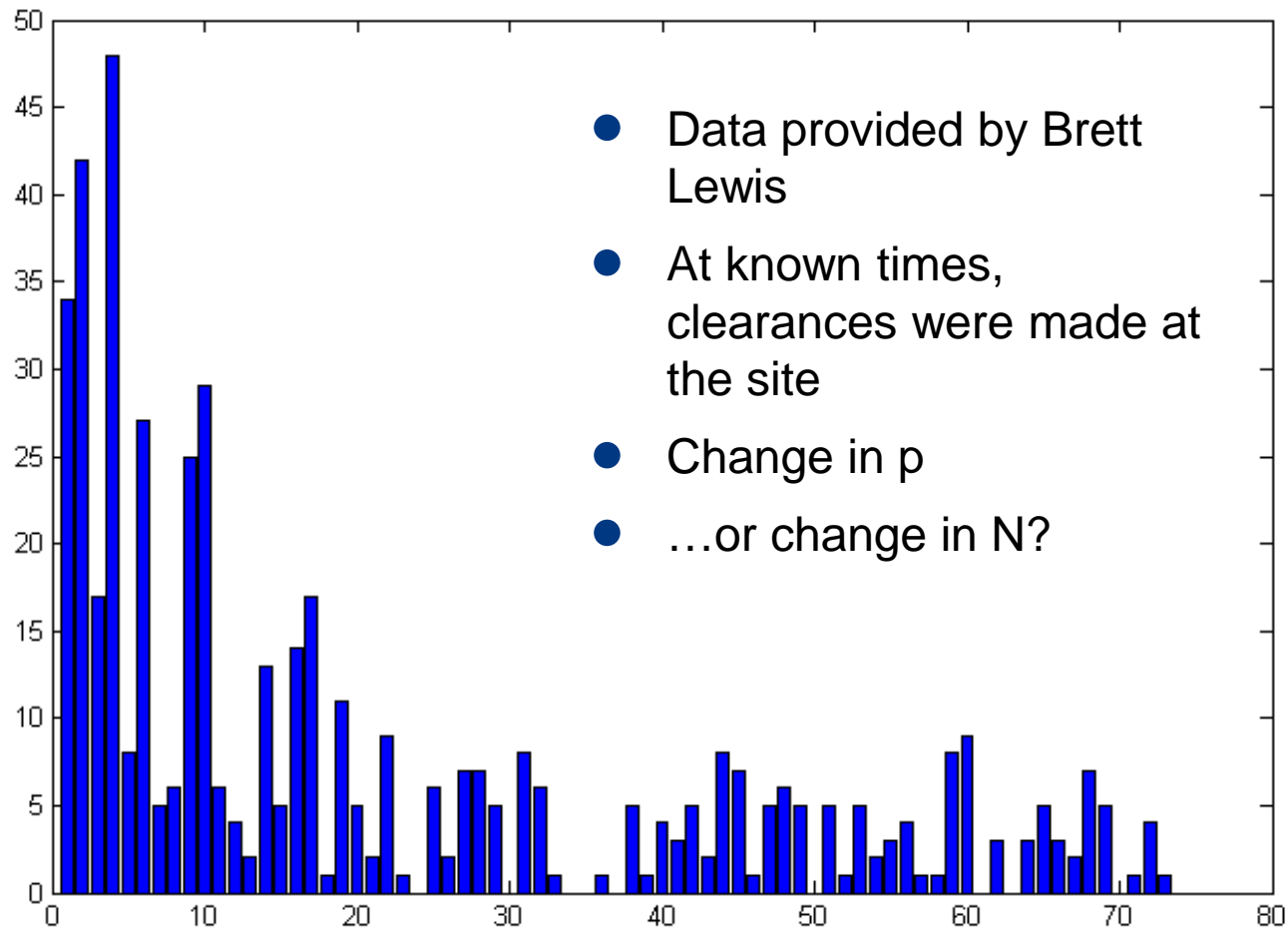


Weather covariates

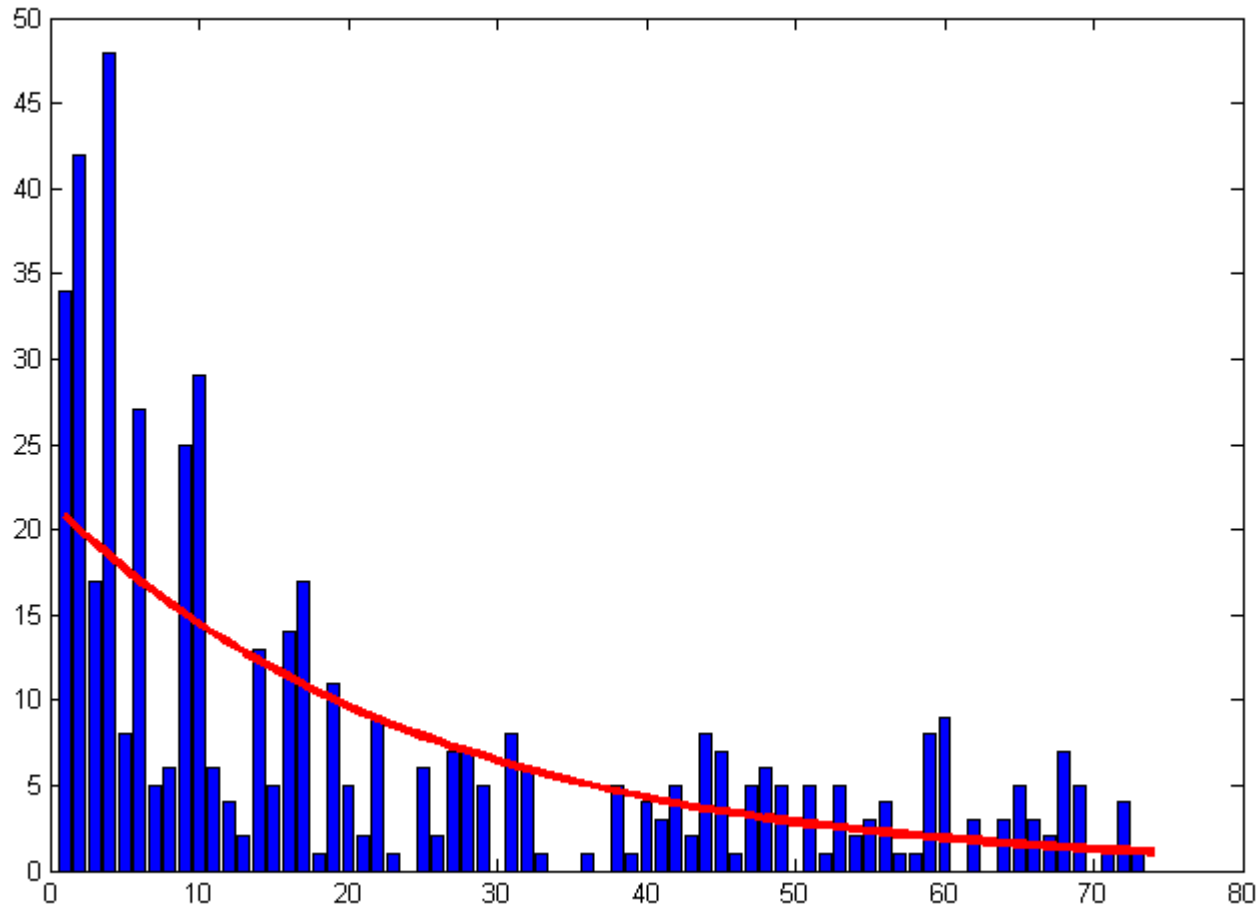
- Temporal variation – weather covariates
- Minimum air temperature



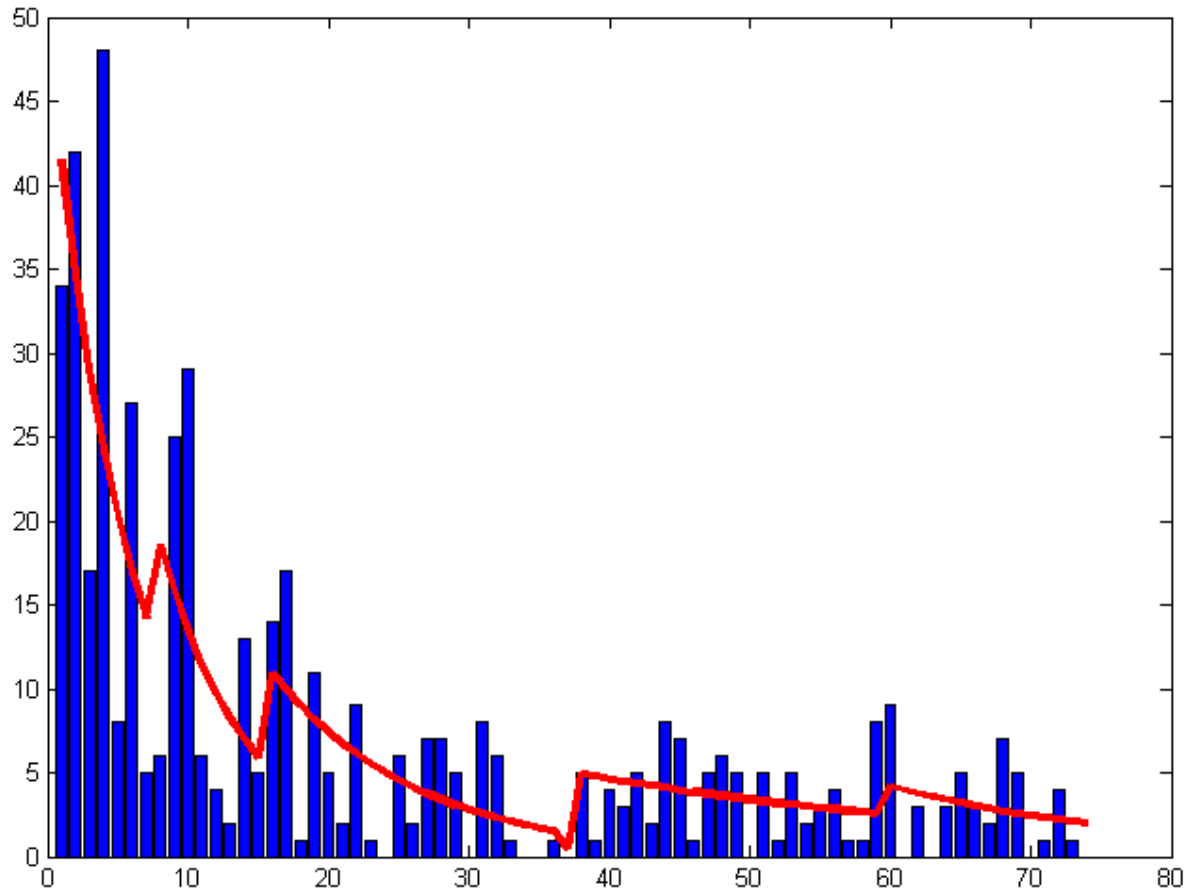
Timed clearances



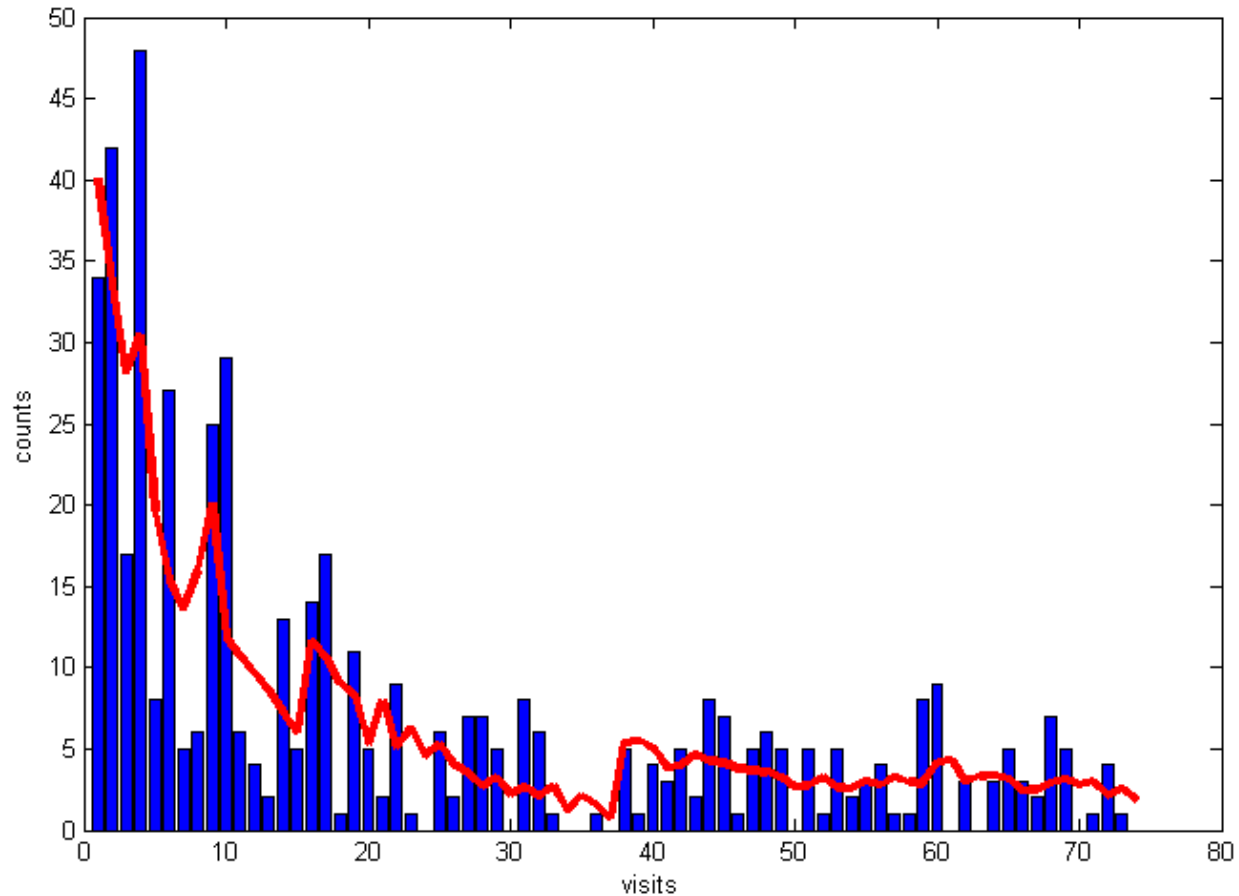
Fitting basic geometric model



Modelling known clearance times

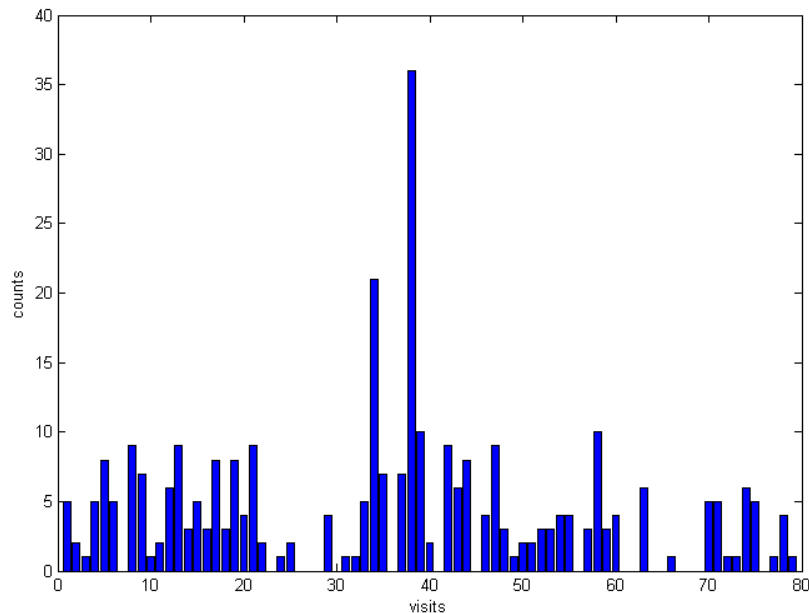


Modelling known clearance times & covariate



Times of population change

- What if times are unknown?



- Borrow an idea from capture-mark-recapture modelling, called **stopover models**

Returning to capture-mark-recapture models

- Studied population might not be closed, but still want to be able to estimate population size
- Jolly-Seber model
 - POPAN/Schwarz-Arnason formulation

0 0 1 0 0



- Entry time into the study population ↗

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- Departure time out of the study population 

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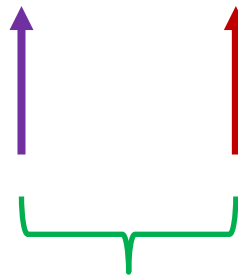
Jolly-Seber model

- If you assume the population is closed when it is not, the parameter estimates will be biased.
- Parameters for the Jolly-Seber model
 - N: **population size**
 - β_t : **proportion of individuals first available for capture at occasion t+1, $\sum_{j=0}^{T-1} \beta_j=1$**
 - p_t : probability an individual is **captured** at occasion t
 - ϕ_t : probability an individual present in the study area at occasion t **remains in the study area** until occasion t+1

Stopover model

- Generalised version of the Jolly-Seber model
- Parameters are defined to be age-dependent
 - **age** corresponds to the time spent in the study area
 - arrival times and departure times are not independent

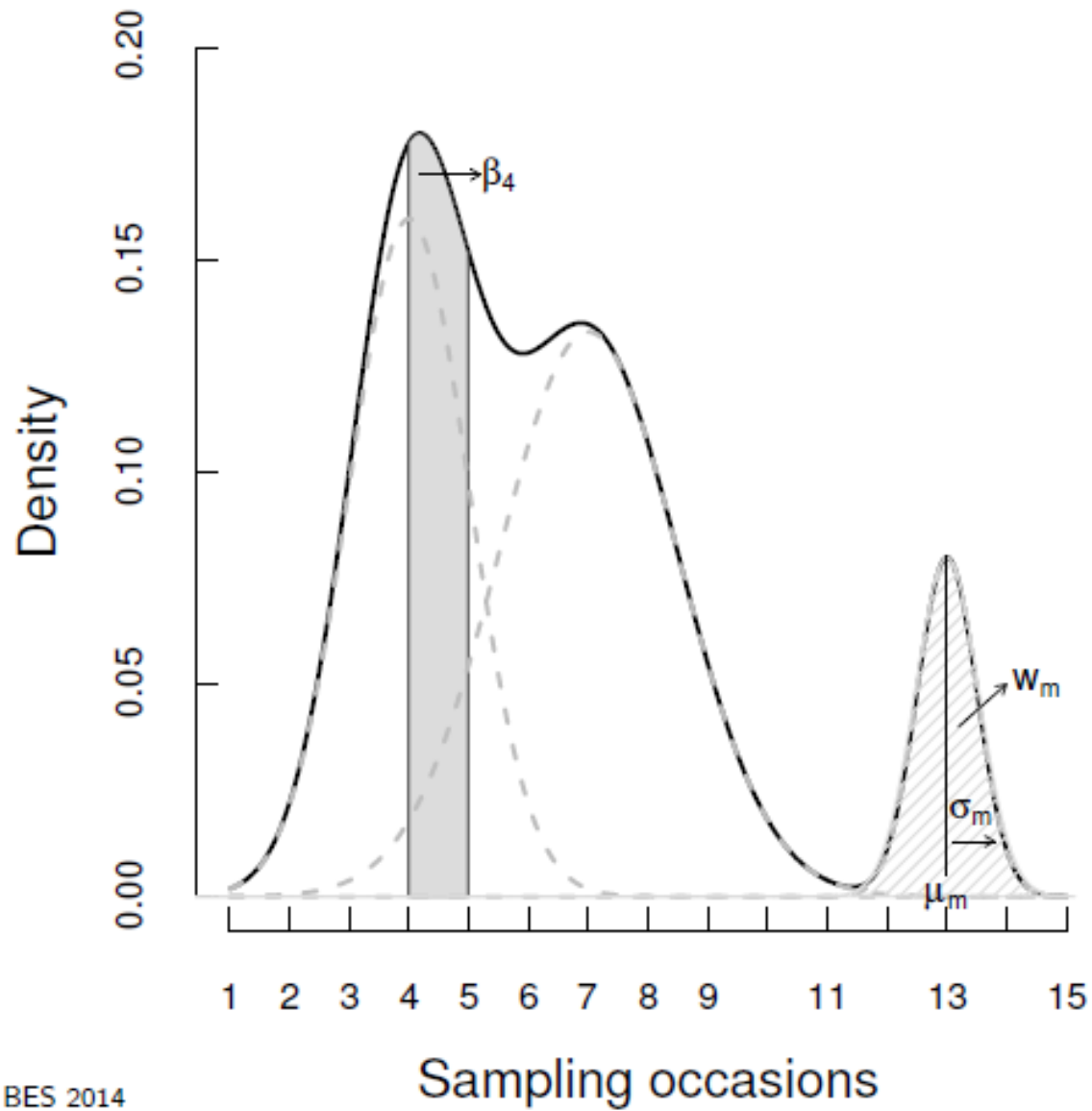
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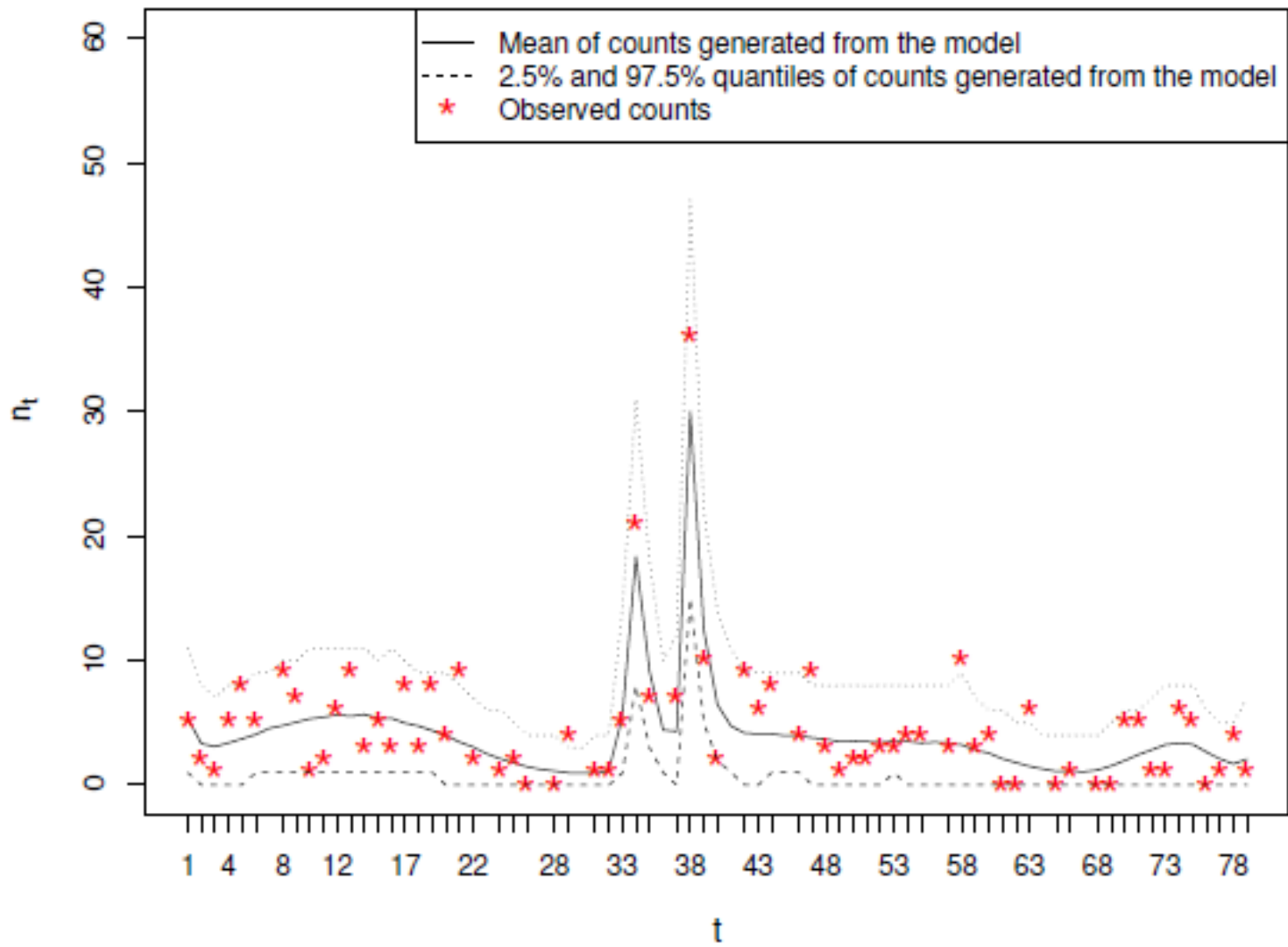
Combining unknown arrivals with removals

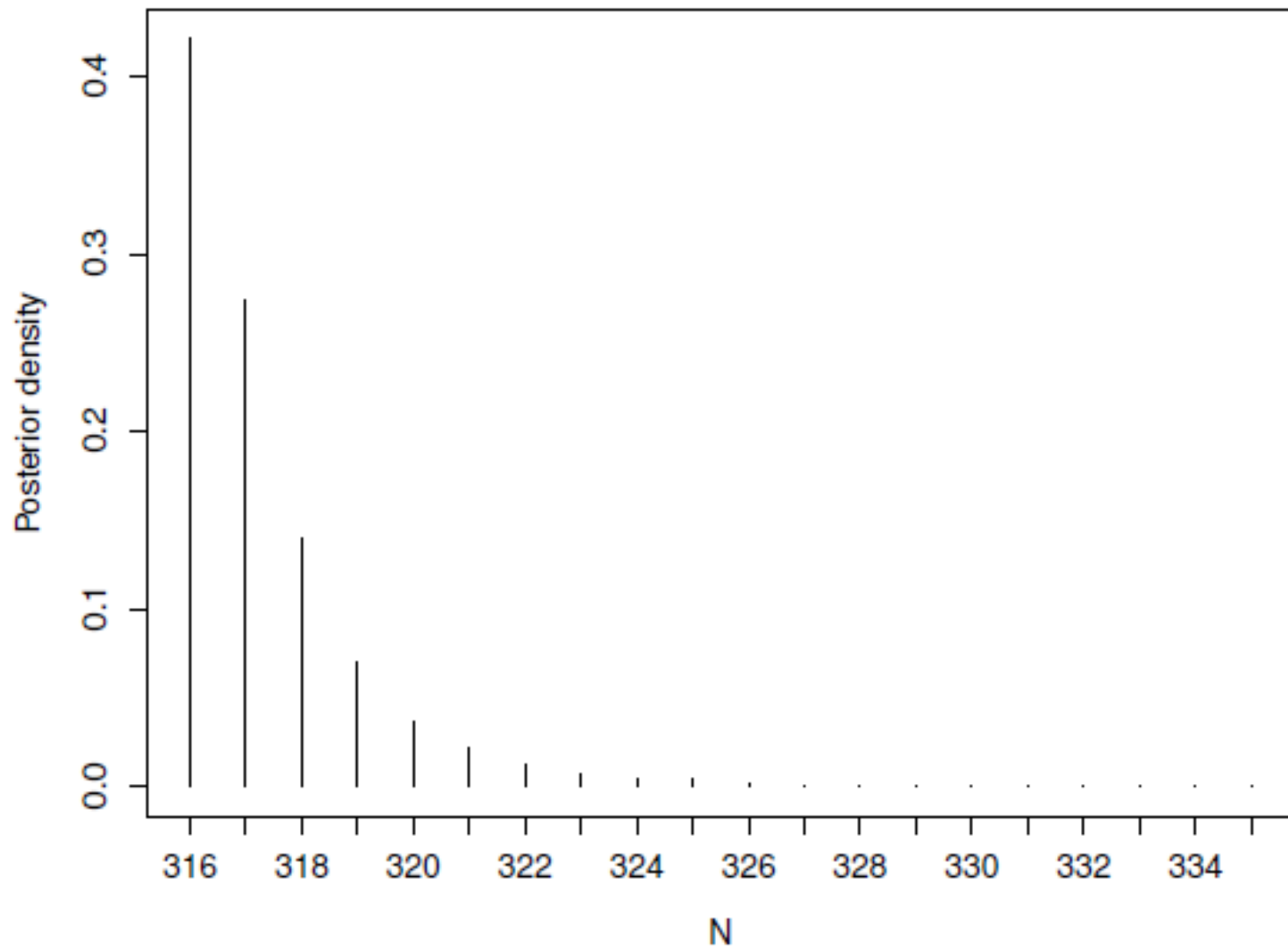
- N: population size
- M: number of arrival groups
- Model arrivals using mixture of normal distributions



Technical aspects

- Use Bayesian modelling approach
- Reversible jump Markov chain Monte Carlo (RJMCMC)
 - Model selection
- Tuning of the RJMCMC is complex





Conclusions

- It is easy to fit a simple geometric model to depletion data but it is not always sensible
- Use extra information within the modelling
- Advanced approaches to account for unknowns

Future directions

- Statistics PhD student
- Development motivated by real case studies
- How sensible are current guidelines for site clearance?
- Release of R package to allow non-statisticians to fit new complex models

Useful References

- Seber (1982) *The estimation of animal abundance and related parameters*. Griffin. 2nd Edition.
- Dorazio, Jelks and Jordan (2005) Improving removal-based estimates of abundance by sampling a population of spatially distinct subpopulations. *Biometrics*. **61**, 1093-1101.
- Matechou, E., McCrea, R.S., Morgan, B.J.T., Sewell, D. and Griffiths, R.A. (2014) Removal models accounting for unknown arrival times of individuals. In prep.