Bayesian multi-species hierarchical distance sampling: Density estimation of vertebrates in Betampona Madagascar

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Swansea

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Betampona Reserve

Located in the Atsinanana region of eastern Madagascar, roughly 25 km from the coast.

Betampona Reserve is an area of dense rainforest covering 29.29 km^2

Designated an Integral Nature Reserve in 1927.

Reserve supervised by the Madagascar Fauna and Flora Group (MFG).

www.madagascarfaunaflora.org

The Data

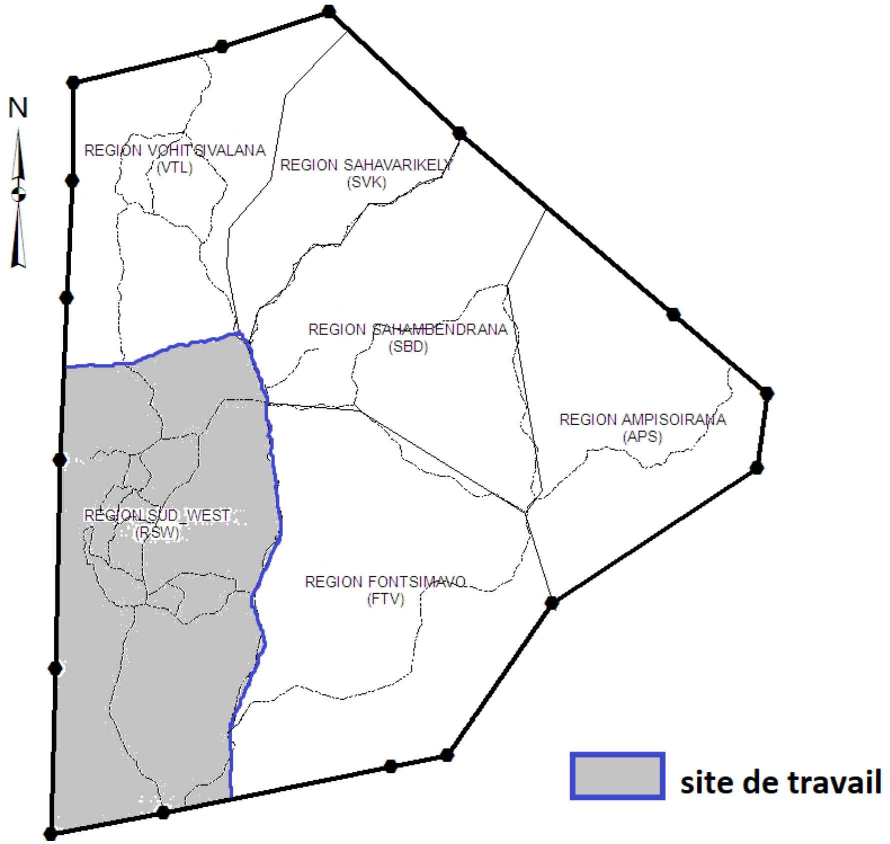
Extensive data set:

- 5 transects: T1, T2, T3, T4, T5
- Multiple sampling occasions each year 2008-2020 (ongoing)

- Vertebrates:
  - Amphibians : 68 species
  - Reptiles : 50 species
  - Mammals : 21 species
  - Birds : 69 species

- Data of interest: distances, x, to detected individuals

- Large number of covariates observed each sampling occasion:
  - Date, Time, Weather, Rain, Sunlight, Location, Age, etc.



The Goals

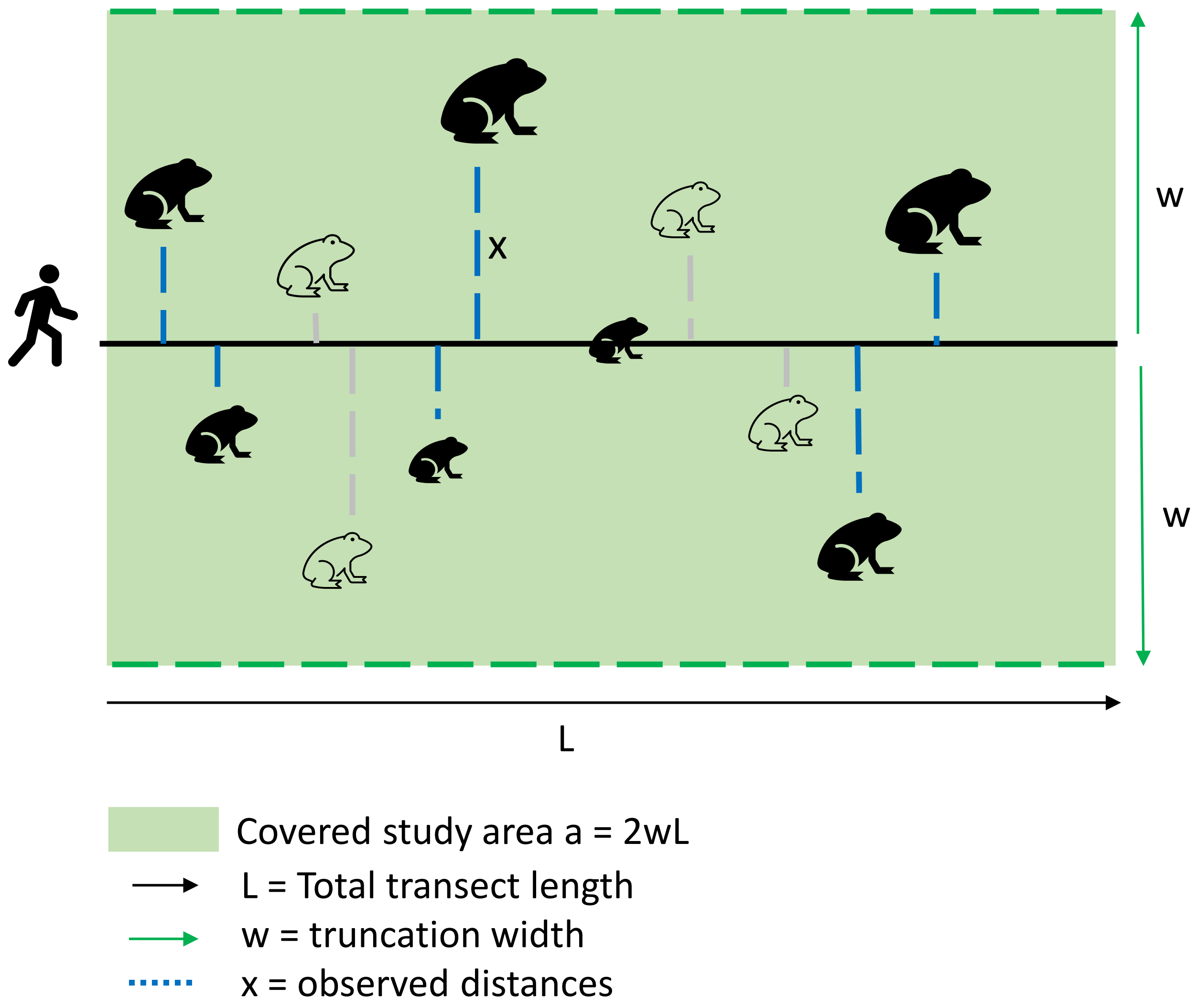
Goals:

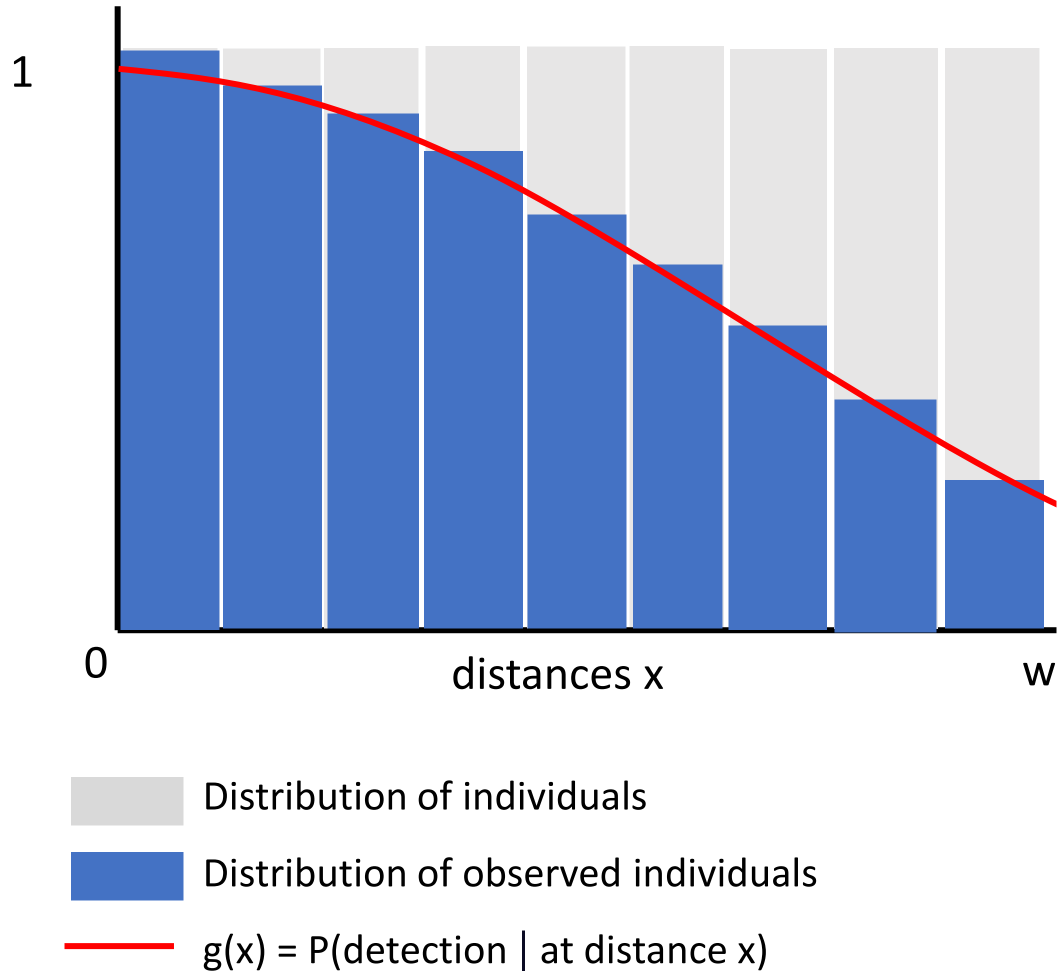
- Study area has pristine (primary) and degraded (secondary) regions:
  - Transects T1 and T5 are in the secondary forest.
- Determine whether forest degradation has a significant impact on species' density.
- Investigate density changes through time.

Problems:

- Most species have very few observations.

Distance sampling: [Buckland et al. 2001], [Buckland et al. 2004]





The model

<u>Hierarchical model (Abundance):</u> [Royle et al. 2004]

Let $N_{i,s,t}$ be the number of individuals of species i $(= 1, \dots, M)$, at site s $(= 1, \dots, S)$, at time t $(= 1, \dots, T)$. The abundance model is then:

$$N_{i,s,t} \sim Pois(\,\lambda_{i,s,t}),$$
$$\log(\lambda_{i,s,t}) = (\alpha_0)_{i,t} + (\alpha_1)_{i,t} \cdot 1_{Secondary}.$$

<u>Community model (Detection):</u> [Sollmann et al. 2016]

Let the $i = 1, \dots, M$ species share a 'similar' detection function. Let $g(x, \vec{z})$ be the probability of detecting an individual at distance x, given covariates $\vec{z}$.

$$\log\big(g(x, \vec{z})\big) = -\frac{1}{2}\left(\frac{x}{\sigma}\right)^2,$$
$$\log(\sigma) = (\beta_0)_i + (\beta_1)_i z_1 + (\beta_2)_i z_2 + \dots.$$

$$\left(\beta_j\right)_i \sim N\left(\mu_j^\beta, \sigma_j^\beta\right).$$

Mantidactylus Chonomantis


(a)


(b)


(c)

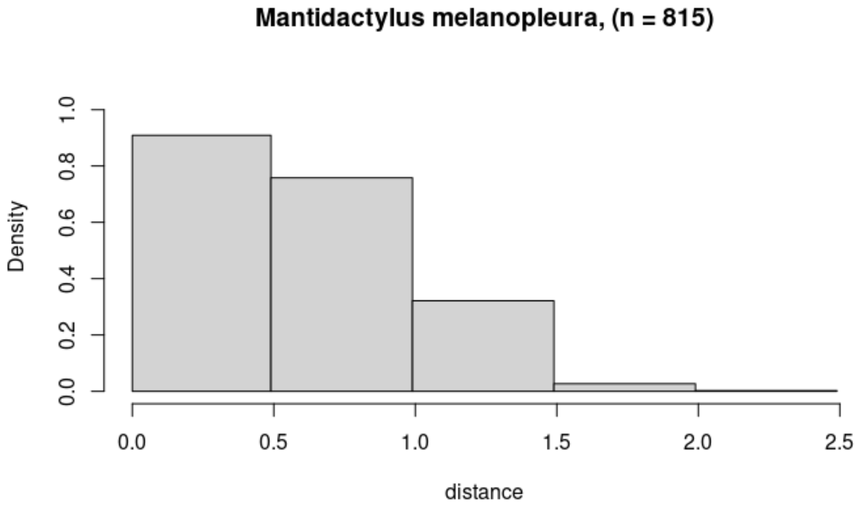

(d)

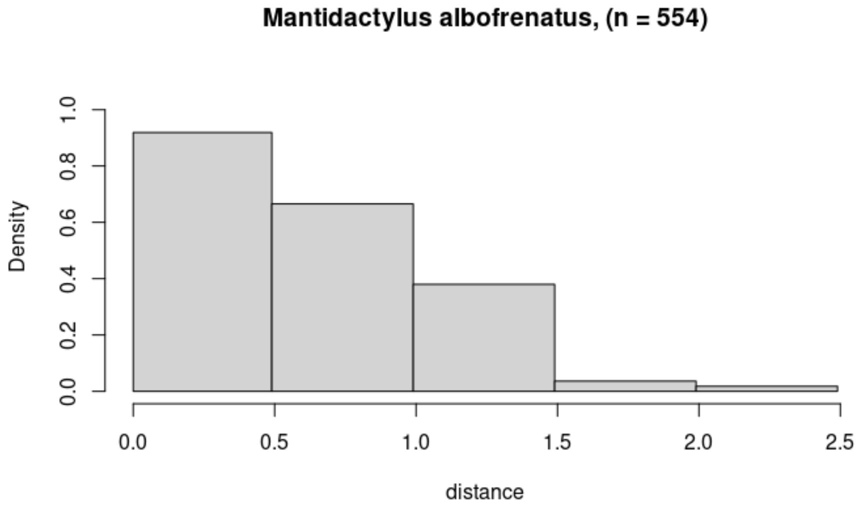

(e)

Species	Conservation Status*	Size	Number of detections
a) M. melanopleura	LC	-	815
b) M. albofrenatus	EN	19mm – 27mm	554
c) M. charlotteae	LC	22mm – 32mm	40
d) M. zipperi	LC	~ 32 mm	14
e) M. opiparis	LC	-	11

*The IUCN Red List of Threatened Species. Version 2022-2

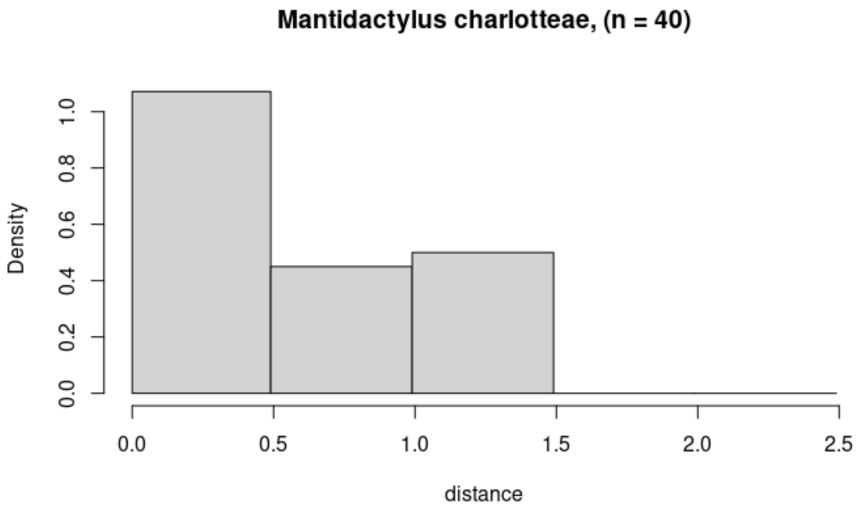
Mantidactylus Chonomantis

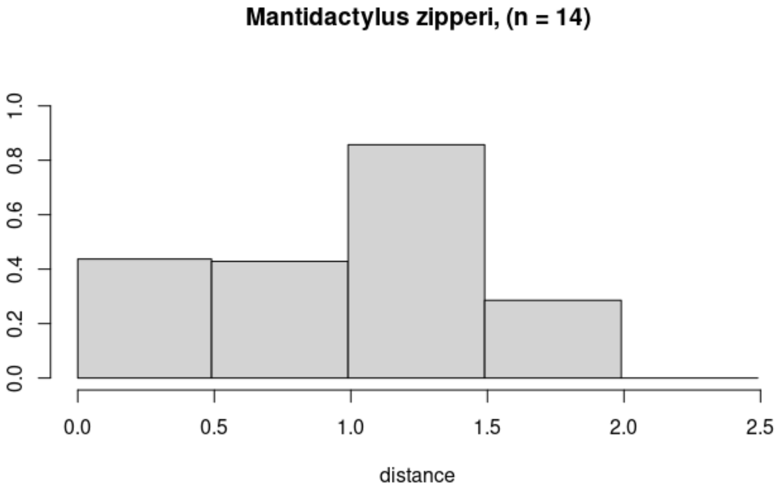


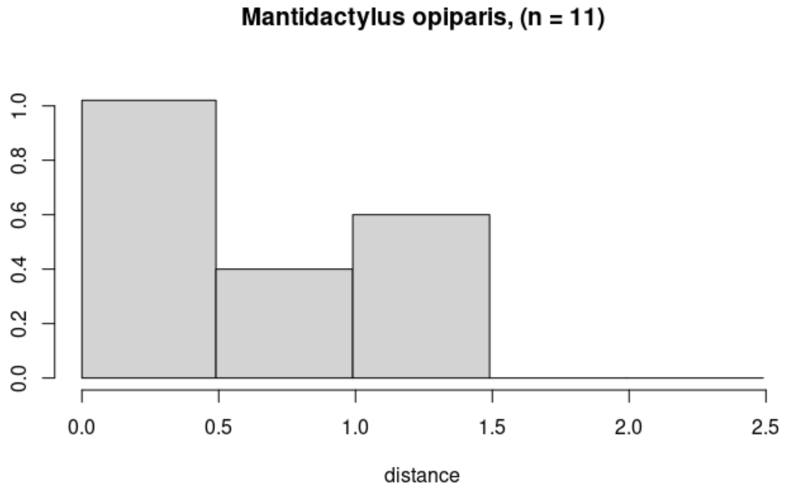


We assume the data are grouped into intervals:
[0, 0.5), [0.5, 1), [1, 1.5), …

Let truncation w = 2.







Details

Pool all detections for a species to get a single detection function shared across all sites and time-points. We have $M = 5$ species, with $S = 2$ sites (primary and secondary forest), and $T = 13$ years.

<u>Detection Covariates:</u>

We let detection vary by amount of sunlight at time of sampling.

There are three sunlight levels, {None, Little, Lots}. Our detection function becomes:

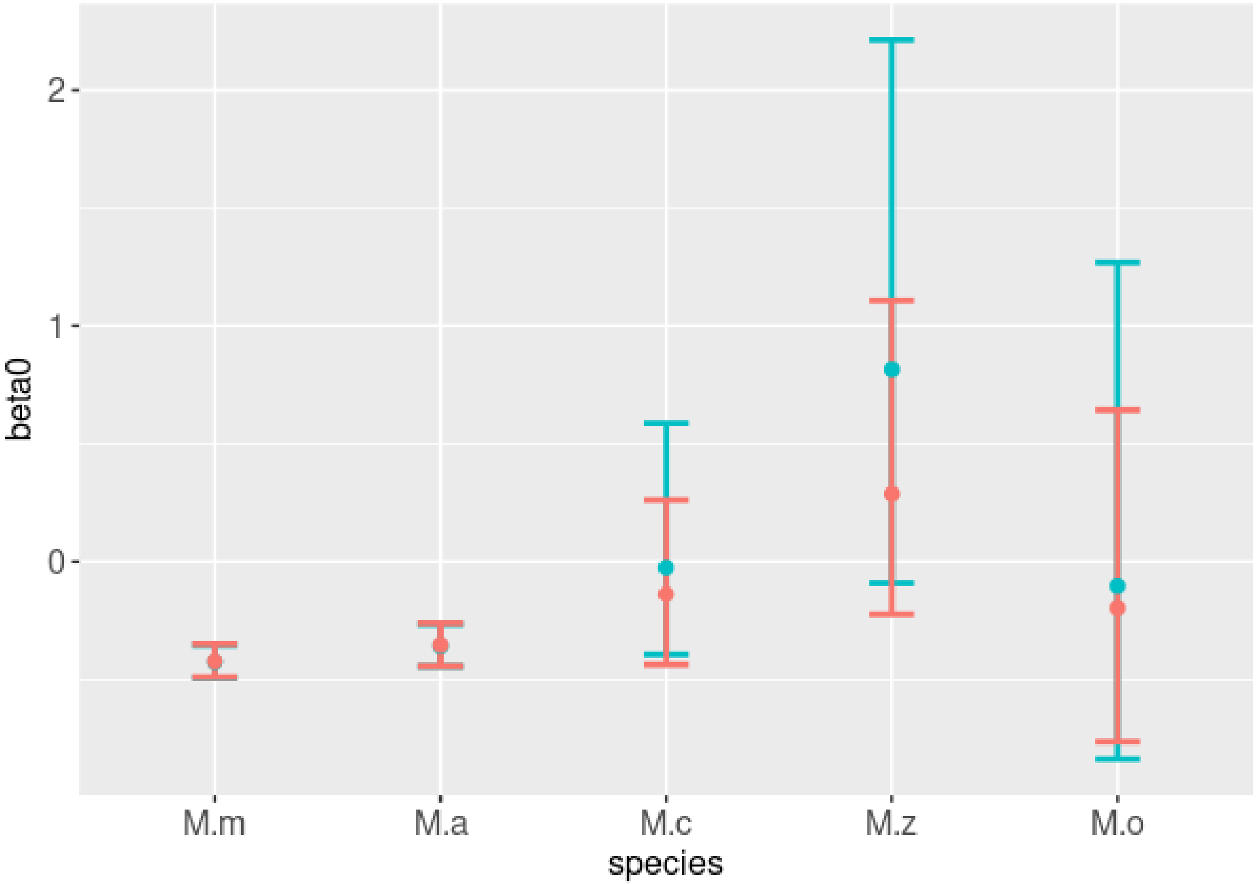
$$\log\big(g(x, \vec{z})\big) = -\frac{1}{2}(x/\sigma)^2$$
$$\log(\sigma) = (\beta_0)_i + (\beta_1)_i \cdot 1_{Little} + (\beta_2)_i \cdot 1_{Lots},$$

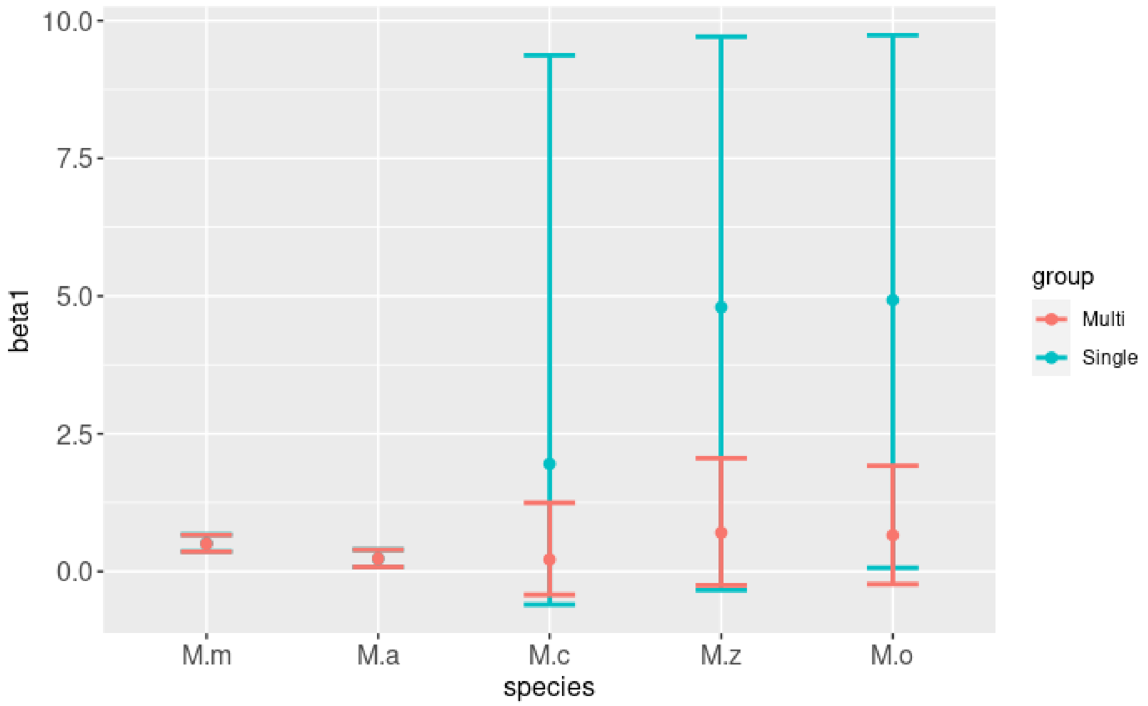
$$\left(\beta_j\right)_i \sim N\left(\mu_j^\beta, \sigma_j^\beta\right), \qquad j = 1,2,3$$
$$\sigma_j^\beta \sim N(1, 0.1), \qquad j = 1,2,3$$

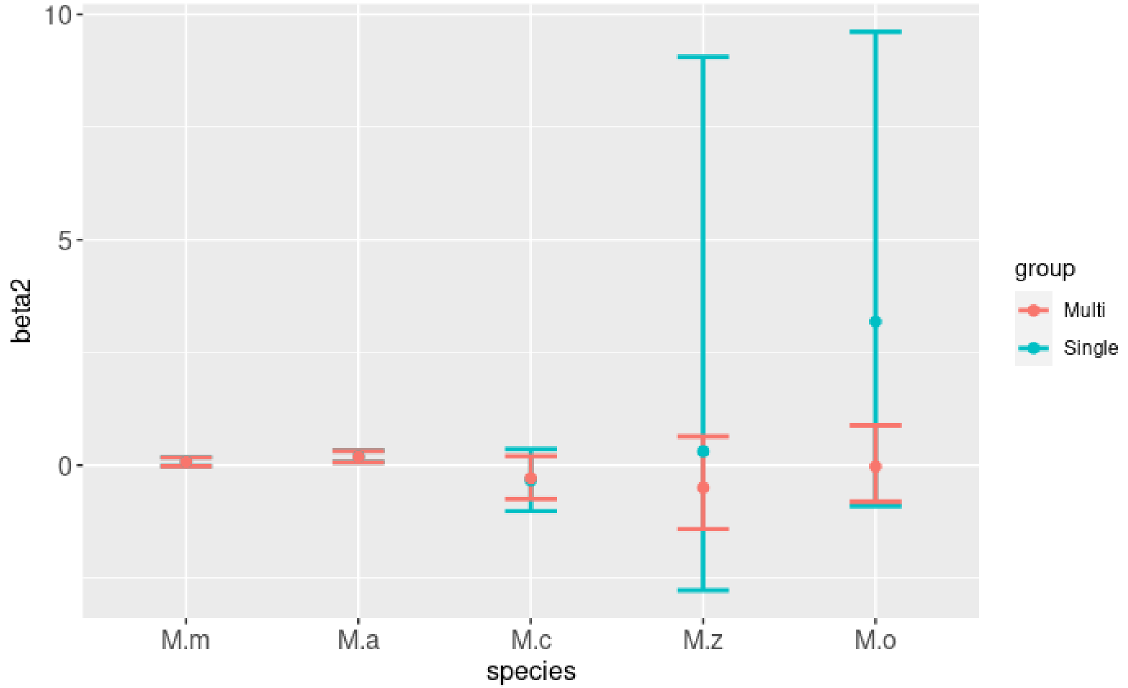
Results:

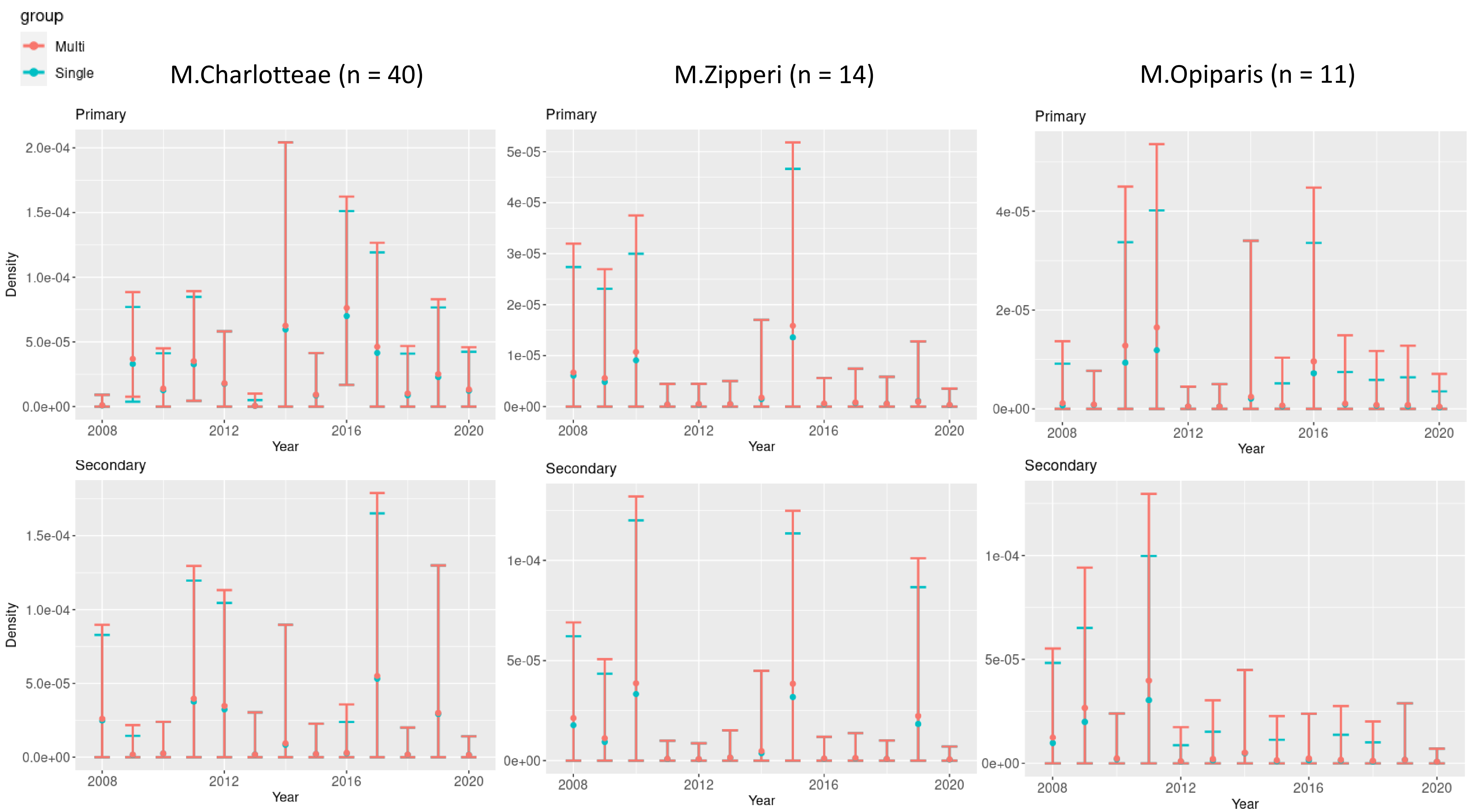
Posterior means and their 95% credible intervals for the multi-species model (pink).

These are compared to the estimates obtained if considering each species individually (blue).





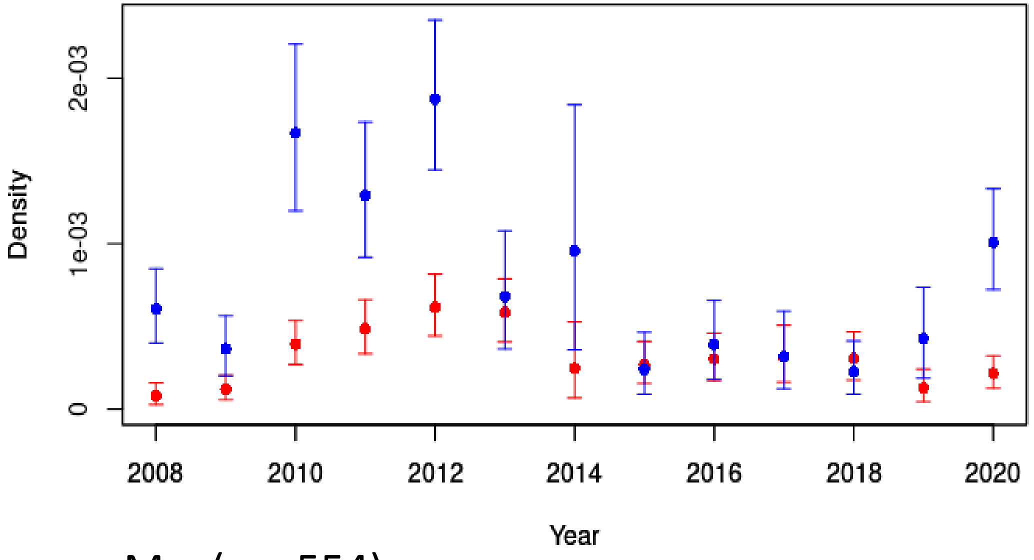



group
Multi
Single
M.Charlotteae (n = 40)
M.Zipperi (n = 14)
M.Opiparis (n = 11)
Primary
Secondary
Density
Year
2008
2012
2016
2020
0.0e+00
5.0e-05
1.0e-04
1.5e-04
2.0e-04
0e+00
1e-05
2e-05
3e-05
4e-05
5e-05
5e-05
1e-04

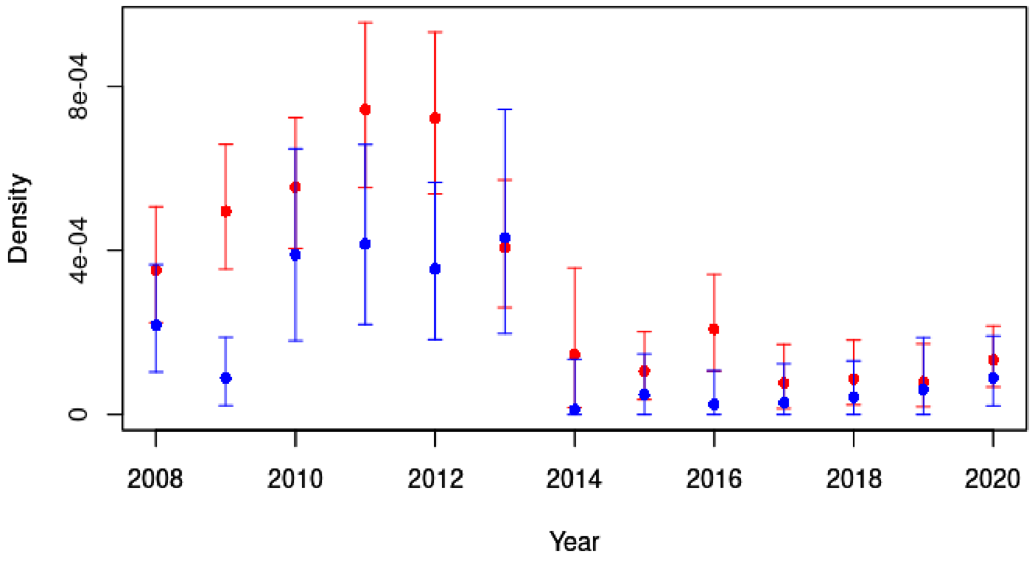
Densities

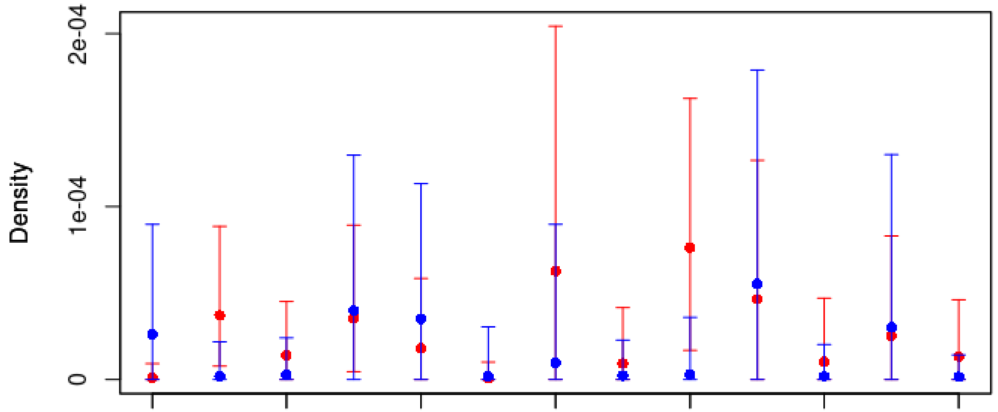
Primary / Secondary

M.m (n = 815)

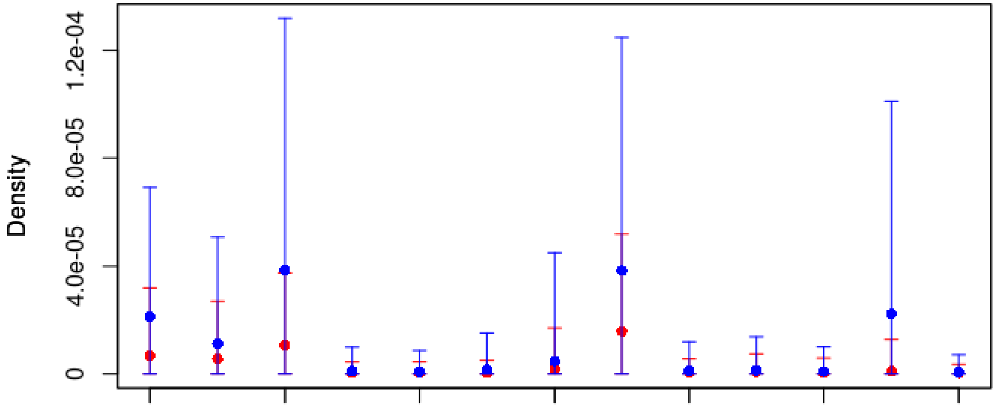


M.a (n = 554)

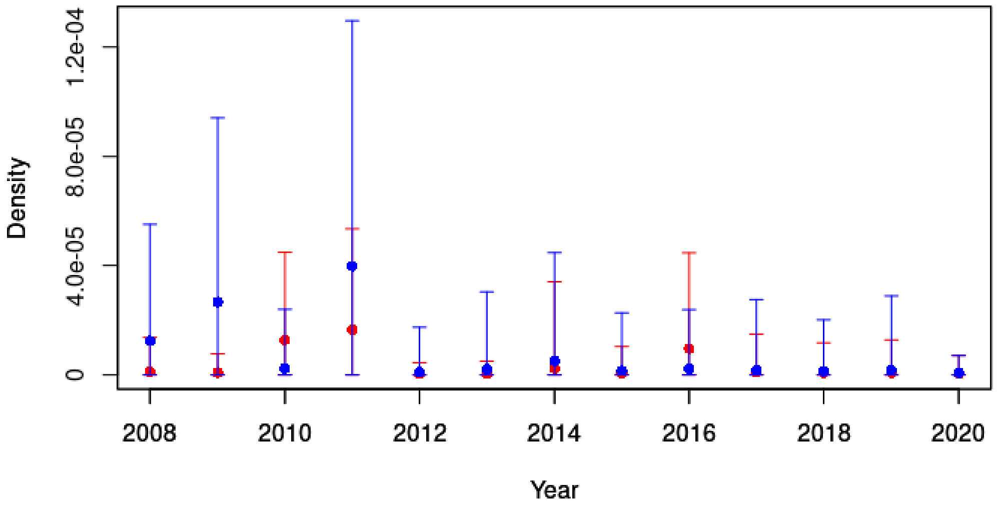




M.c (n = 40)



M.z (n = 14)



M.o (n = 11)

Where next:

Extensive weather data has been collected in the region over the same period as the surveys.

- Want to investigate potential link between density changes and climate changes in the region
- In particular investigate effect of tropical monsoons.

Spatial and temporal analysis.

- Currently not accounting for dependence between time points.
- Have access to rough locations of detections, investigate relationship between density and environmental features such as rivers and invasive plants.

References

Buckland, S. T. Anderson, D. R. Burnham, K. P. Laake, J. L.. Borchers, D. L. Thomas, L. Introductions to Distance Sampling (2001) Oxford University Press

Buckland, S, T. Anderson, D. R, Burnham, K. P. Laake, J. L. Borchers, D. L. Thomas, L. Advanced Distance Sampling (2004) Oxford University Press

Sollmann, R. Gardner, B. Williams, K. A. Gilbert, A. T. Veit, R. R (2016), A hierarchical distance sampling model to estimate abundance and covariate associations of species and communities. Methods in Ecology and Evolution 7, 529–537

Royle, A. J. Dawson, D. K. Bates, S. (2004) Modeling Abundance Effects in Distance Sampling. Ecology, 85 (6), 1591-1597

Full Priors

Detection Covariates:

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$$\left(\beta_j\right)_i \sim N\left(\mu_j^\beta, \sigma_j^\beta\right), \qquad j = 1,2,3$$
$$\mu_0^\beta \sim N(-0.2, 0.1),$$
$$\mu_j^\beta \sim U(-10, 10), \qquad j = 2,3$$
$$\sigma_j^\beta \sim N(1, 0.1) \qquad j = 1,2,3$$

The priors for the single-species analysis:

$$\beta_0 \sim N(-0.2, 1),$$
$$\beta_1, \beta_2 \sim U(-10, 10).$$

Priors (Abundance):

The priors on abundance parameters across each time point for each species are:

$$(\alpha_0)_{i,t} \sim U(-10, 10)$$
$$(\alpha_1)_{i,t} \sim U(-10, 10)$$