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A Bayesian estimation of daily egg production: Application to sardine in the Bay of Biscay

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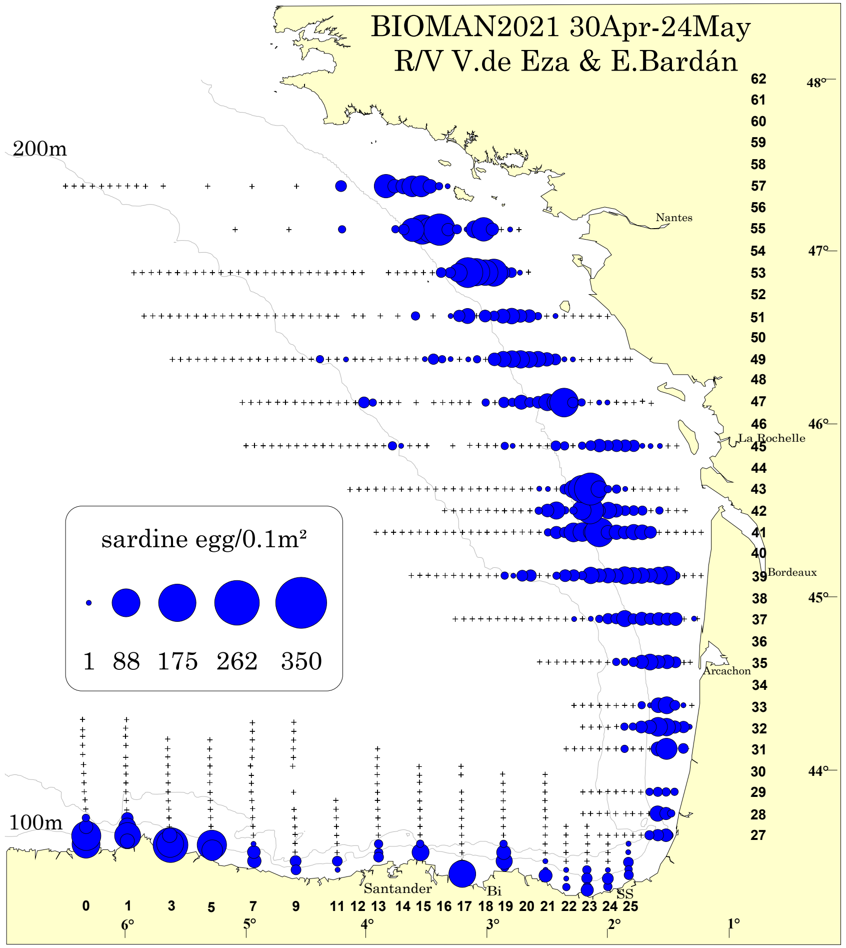
Small Pelagic Fish Symposium 2022

CASE STUDY: BoB sardine

The research survey BIOMAN is conducted yearly for the application of the Daily Egg Production Method (DEPM) in the Bay of Biscay on anchovy and sardine, and obtention of the SSB for each species.

Plankton and adult samples are collected during the survey, covering the whole spawning area of the species.

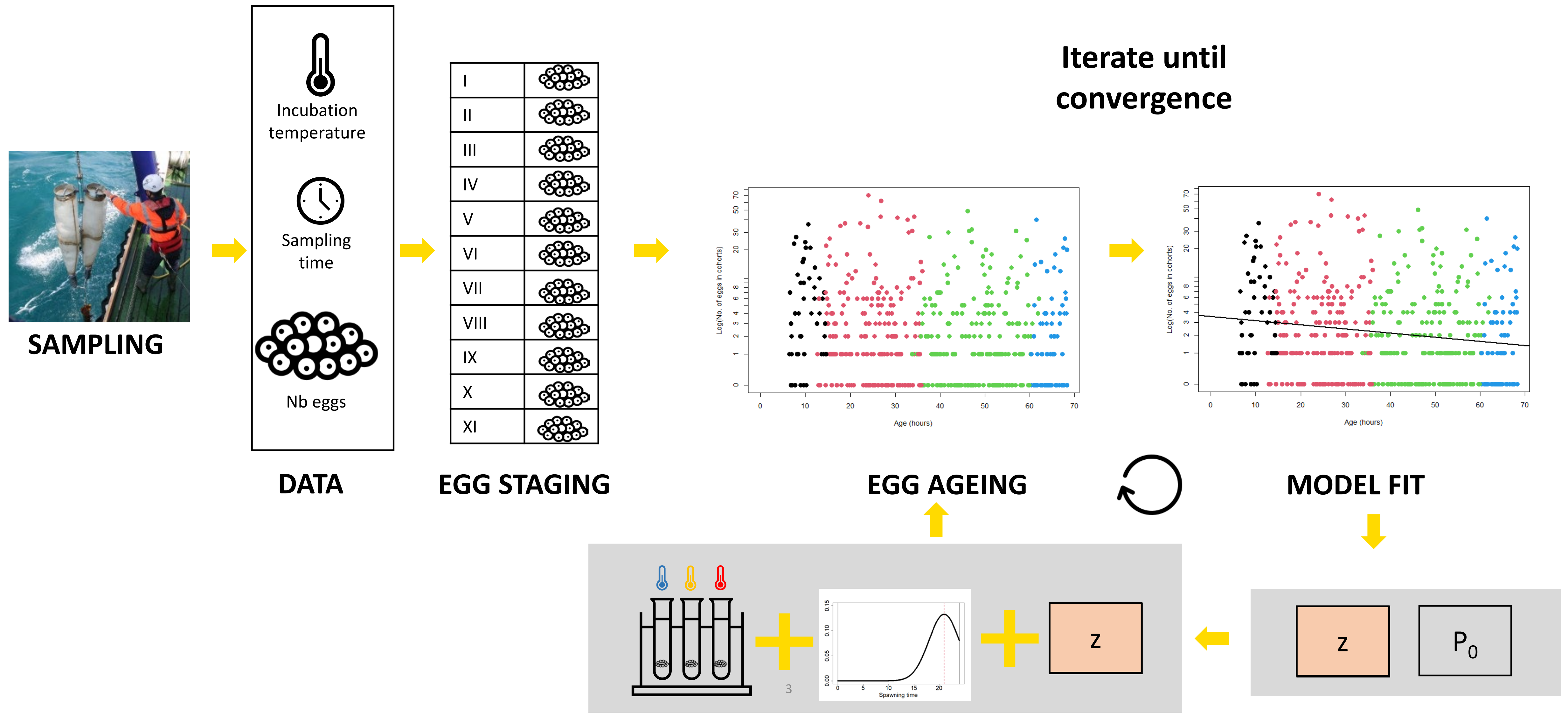


$$SSB = \frac{P_{tot}}{DF}$$

Egg production per unit area

$$P_{tot} = P_0 \cdot SA$$

ESTIMATING P_0 AND z



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ESTIMATION MODEL

$Y_{i,j}$: number of eggs in cohort *j* in station *i*
$a_{i,j}$: mean age of eggs in cohort *j* in station *i*
R_i: effective area sampled in station *i*

$$\log(\mu_{i,j}) = \log(R_i) + \log(P_0) - Z\, a_{i,j}$$

$$Y_{i,j} \sim Negative\ binomial(\mu_{i,j}, \theta)$$

If not, the ecuation will be indicating that the number of eggs increases with time

We know egg mortality (Z) must take a positive value

Frequentist GLM fitting methods don't include prior knowledge and Z can take any value

Iterative process

ASSUME AN INITIAL VALUE FOR Z

CALCULATE DAILY COHORT FREQUENCIES AND MEAN AGE

FIT GLM AND OBTAIN P_0 AND Z ESTIMATES

Repeat until the difference between the old and new Z estimates is small

A Bayesian approach for the fitting of this GLM is proposed, allowing to include prior information (Z>0)

BAYESIAN APPROACH

Same GLM model

$$\log(\mu_{i,j}) = \log(R_i) + \log(P_0) - Z\, a_{i,j}$$

$$Y_{i,j} \sim Negative\ binomial(\mu_{i,j}, \theta)$$

Prior distributions

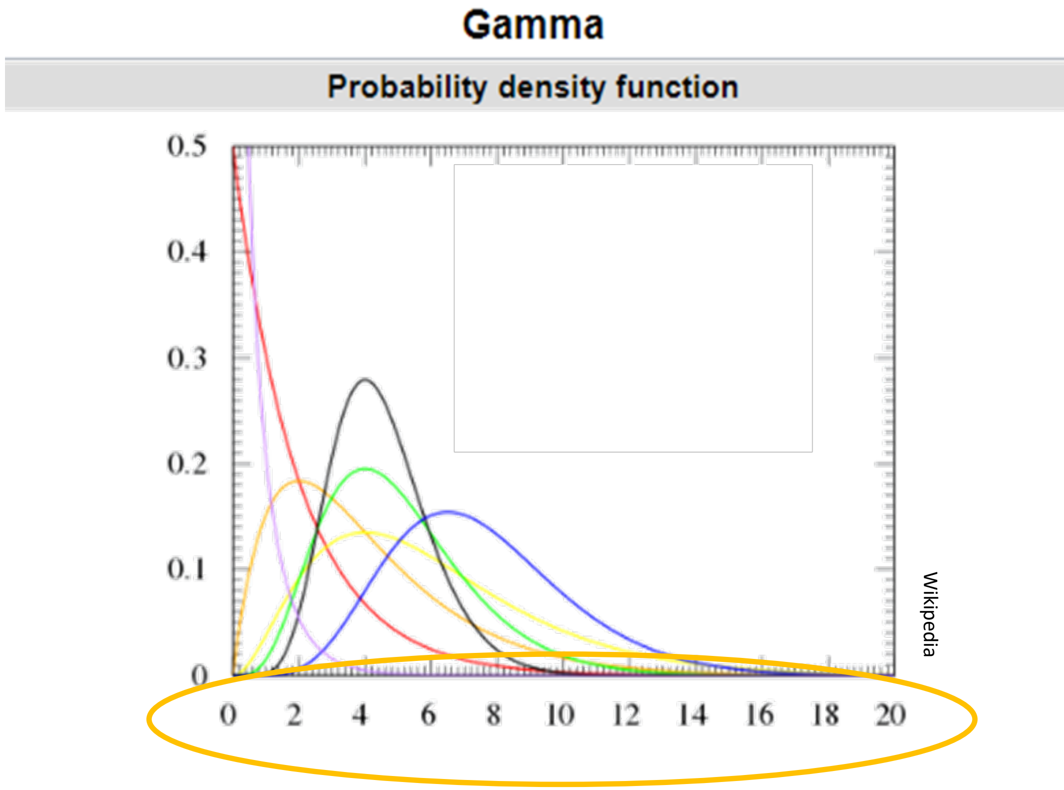
$$\theta \sim Gamma(0.01, 0.01)$$

$$\log(P_0) \sim Student\_t(3, location, scale)$$

Default prior distributions

$$Z \sim Gamma(2.15, 112.56)$$

← Based on literature

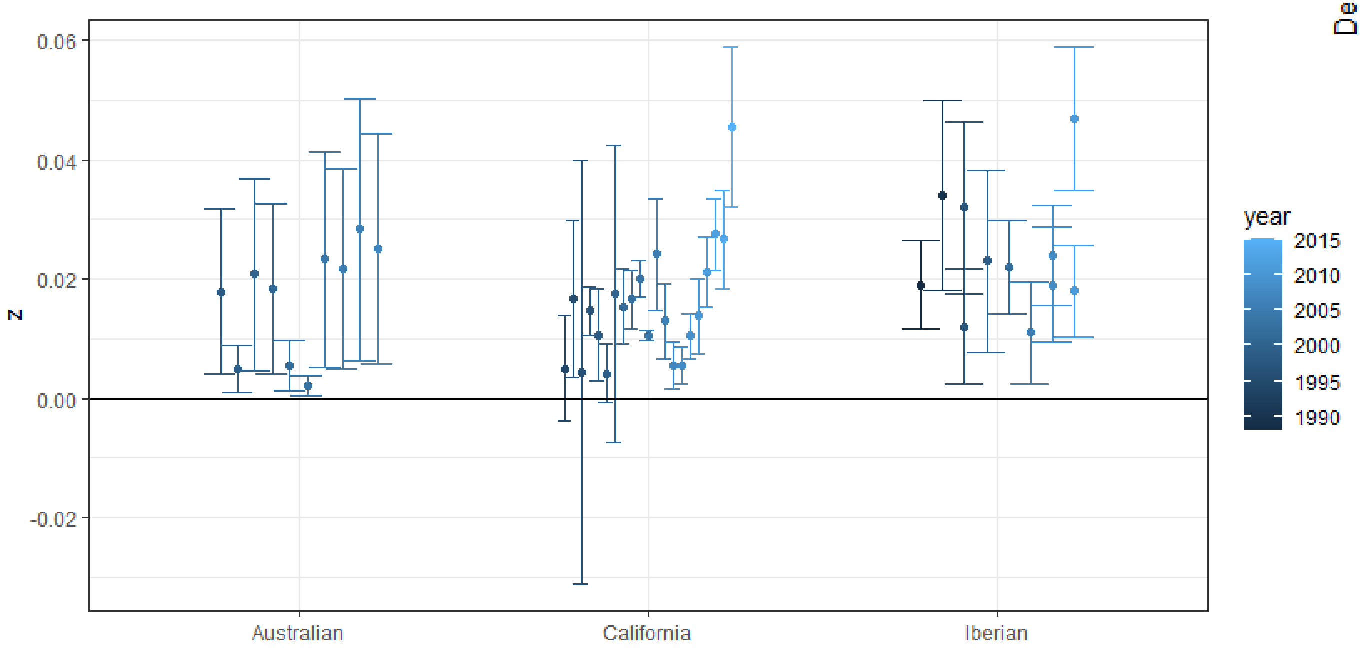


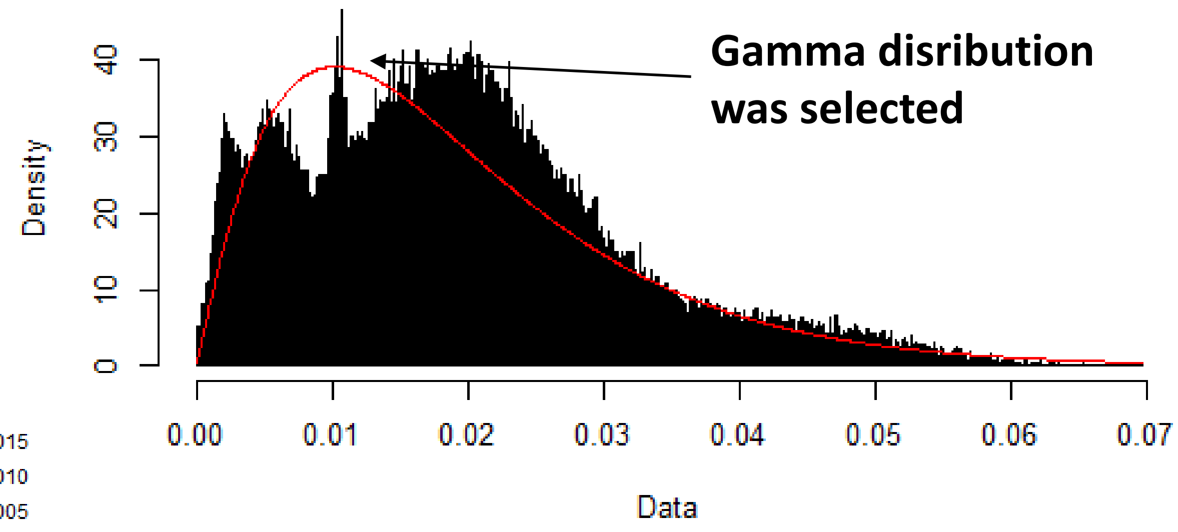
Bayesian inference performed through MCMC methods using the R package “brms” (Bürkner et al. 2017).

10 000 MCMC iterations from a single chain saved with a burning period of 1000 iterations (more chains were generated to check convergence).

PRIOR FOR z

Prior distribution based on historical data from other sardine case studies



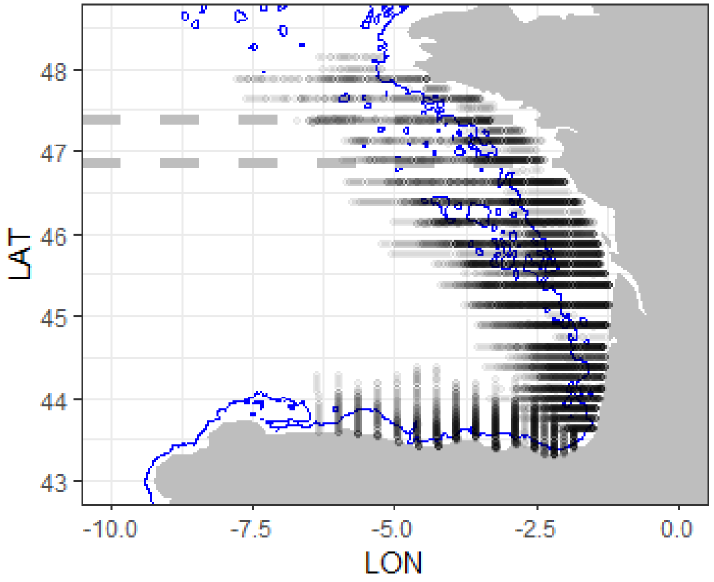


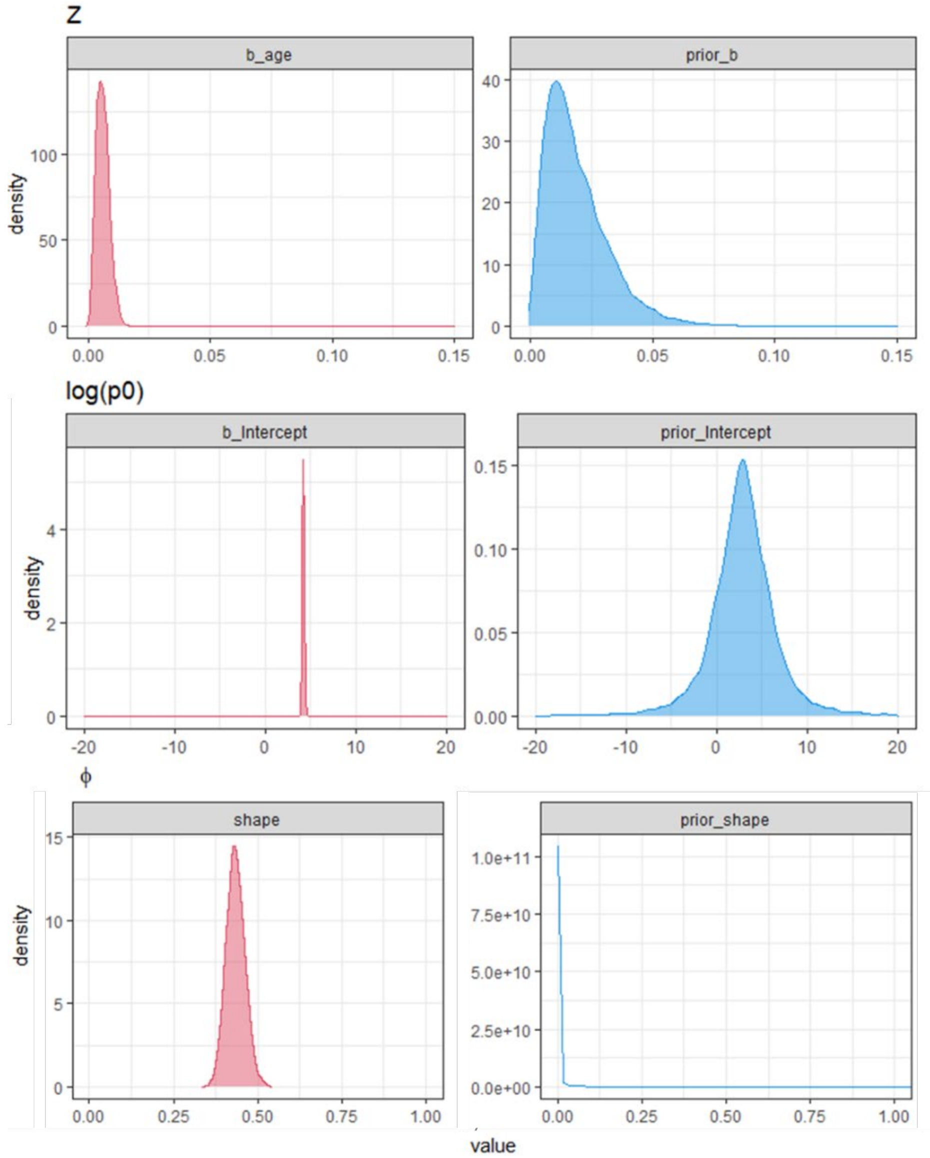
Distr	Q50	Q2.5	Q97.5	mean	sd
Mixture	0.0180	0.048	0.0019	0.019	0.012
Gamma (2.15,112.56)	0.0162	0.052	0.0025	0.019	0.013

The chosen probability distribution is a positive continuous distribution.

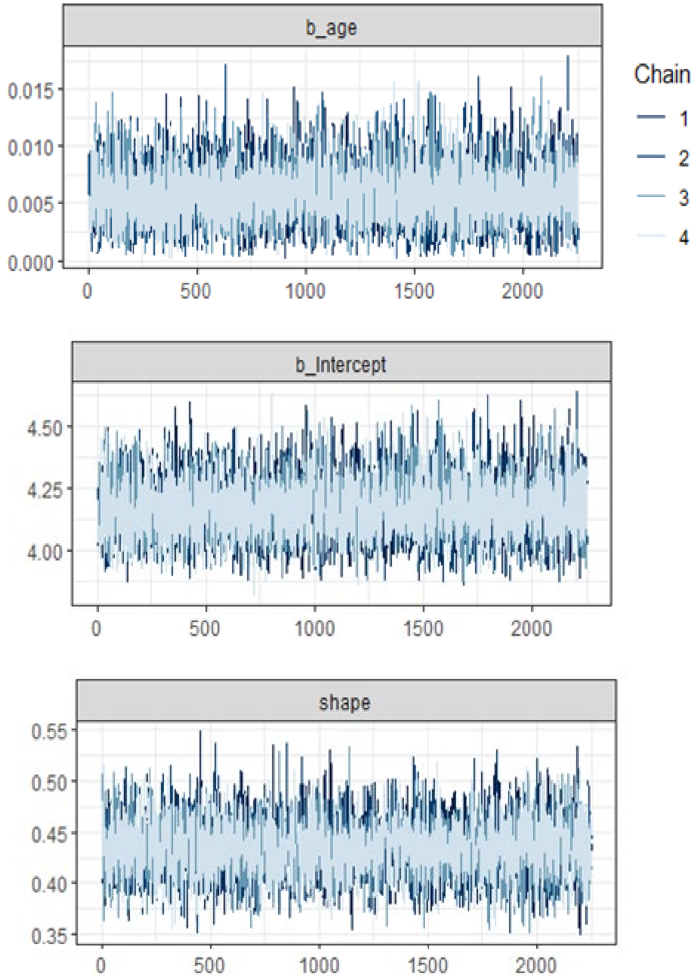
RESULTS- one year

Fitting for a single year (2021)

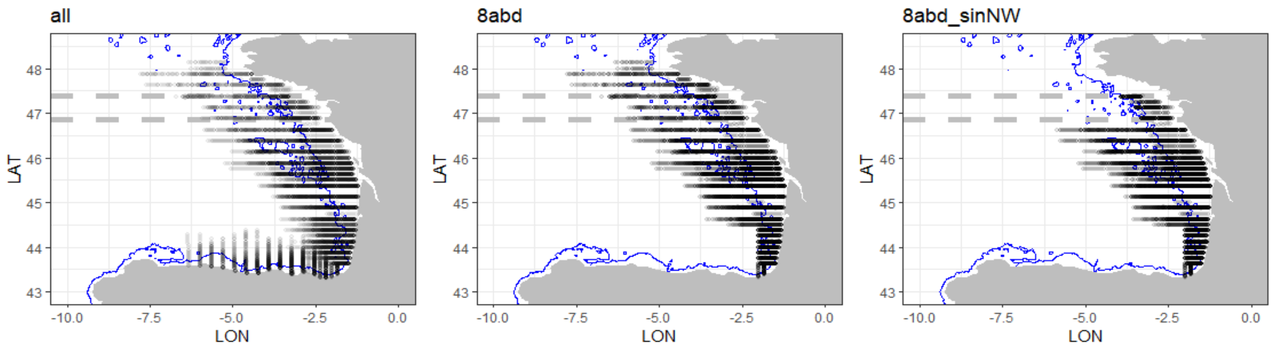


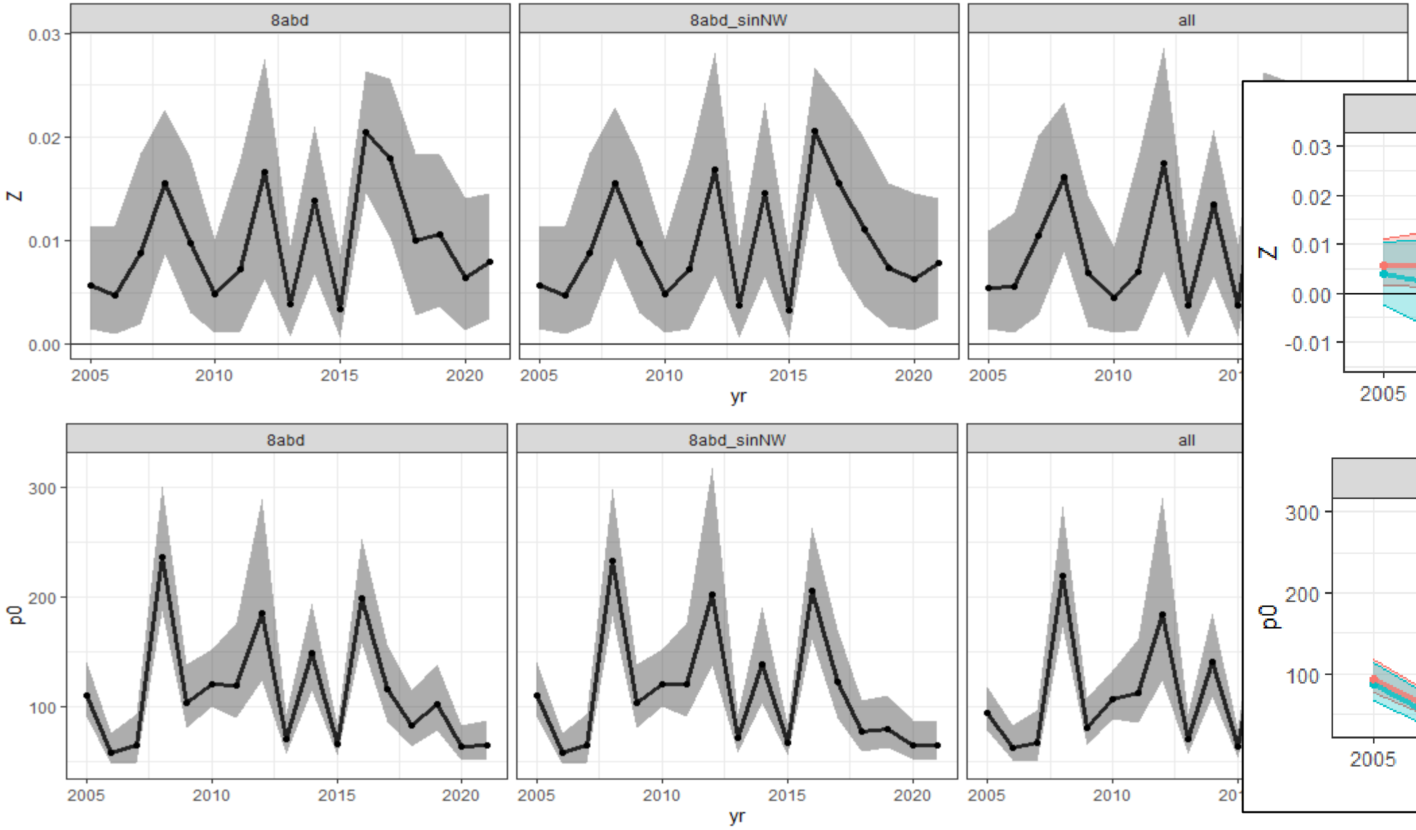


Good convergence

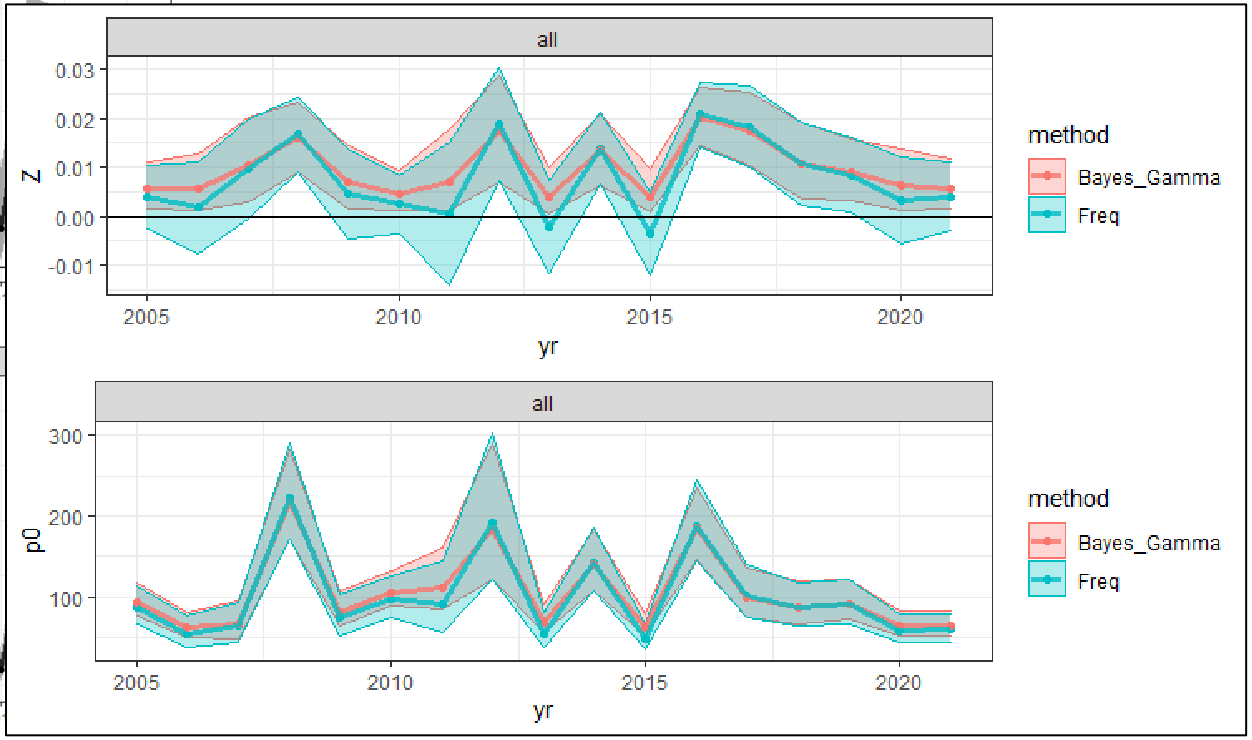


RESULTS – time series (2005-2021)



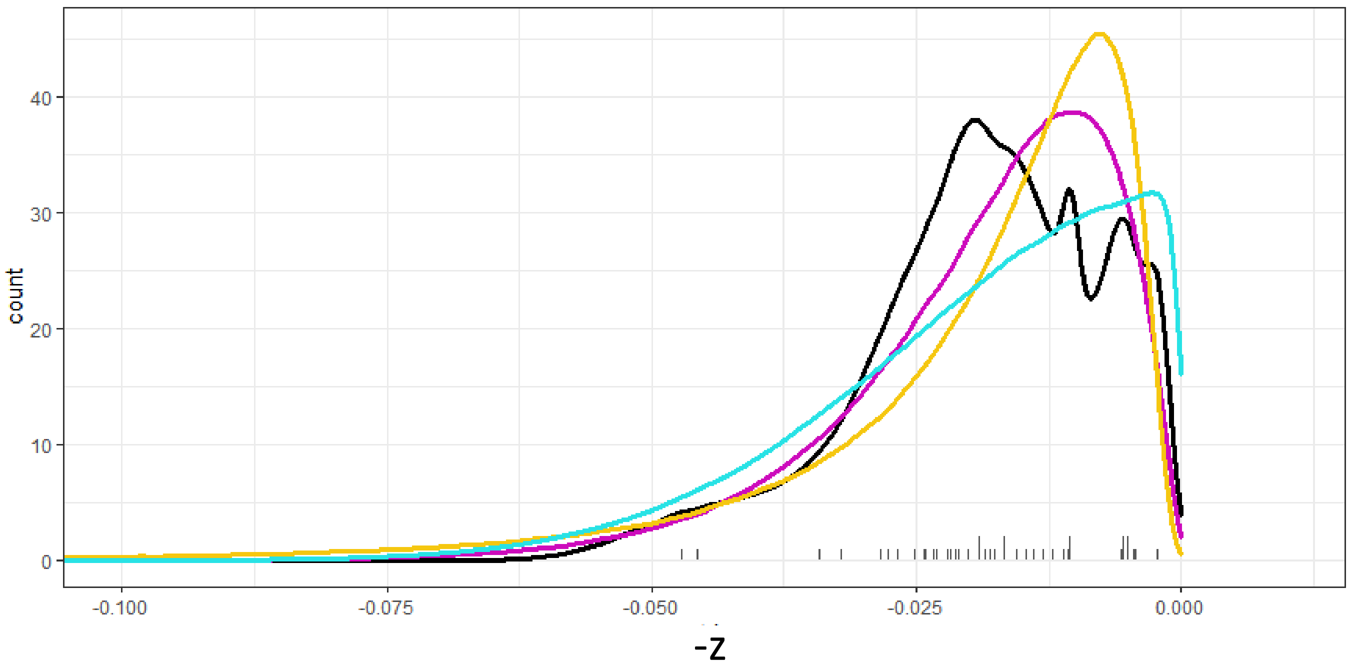


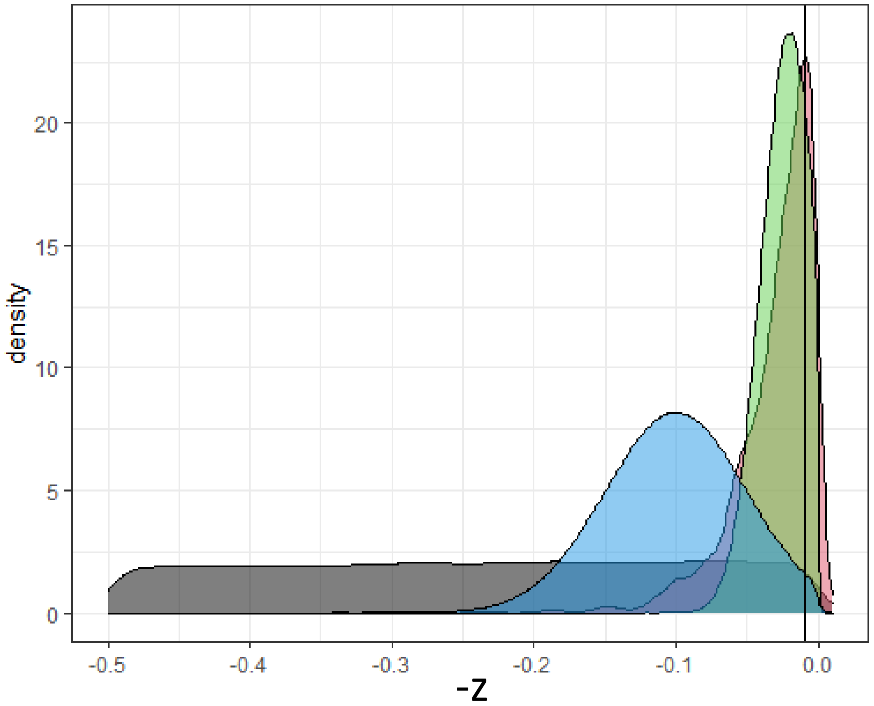
Comparison with the frequentist approach



SENSITIVITY ANALYSIS to z priors

Tested alternative priors for z:





Distr	Q50	Q2.5	Q97.5	mean	sd
-Mixture	-0.0180	-0.048	-0.0019	-0.019	0.012
-Gamma (2.15,112.56)	-0.0162	-0.052	-0.0025	-0.019	0.013
-Lognormal (-4.2,0.82)	-0.0149	-0.075	-0.0029	-0.021	0.021
TruncNorm(0,0.025)	-0.0169	-0.056	-0.0008	-0.020	0.015

0 Truncated values:	Q50	Q2.5	Q97.5	mean	sd
N(0,1)	-0.674	-2.241	-0.031	-0.798	0.602
N(0.3,0.1)	-0.021	-0.098	-0.001	-0.028	0.026
N(-0.02,0.02)	-0.024	-0.061	-0.002	-0.025	0.016
N(-0.1,0.05)	-0.101	-0.198	-0.016	-0.102	0.047

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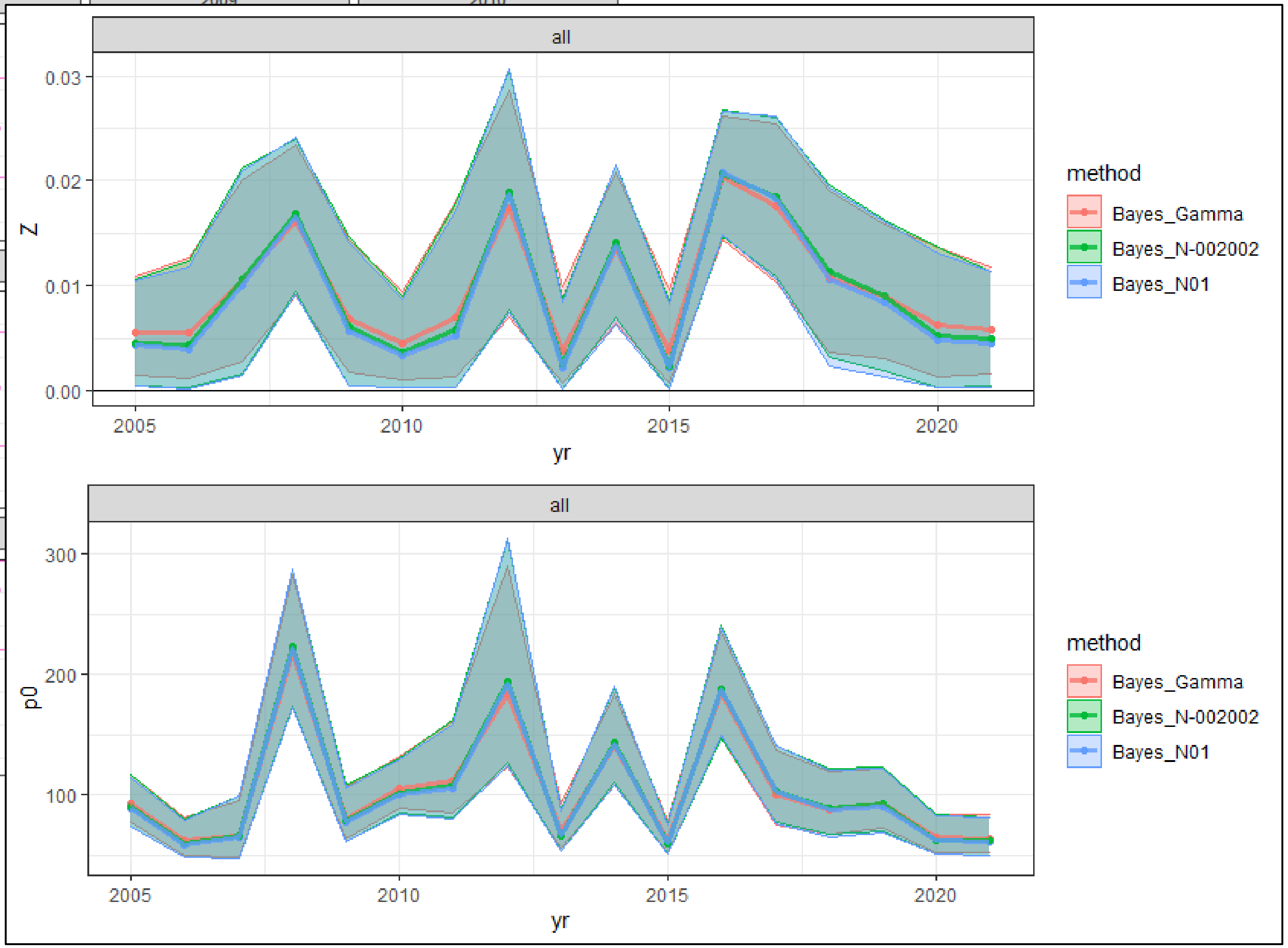
SENSITIVITY ANALYSIS to z priors

Resulting -z estimates:



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CONCLUSIONS

- A Bayesian approach for the estimation of the egg production per unit area was proposed, ensuring that the mortality that is estimated within the model is in the proper domain.
- The proposed methodology was applied to the Bay of Biscay sardine case study from 2005 to 2021, obtaining yearly estimates of egg production per unit area and mortality.
- A sensitivity analysis to the priors for the mortality parameter was carried out comparing the selected Gamma prior distribution based on literature to other alternatives, obtaining that posterior distributions are very similar in all cases.
- The proposed Bayesian approach was also compared to the frequentist approach, showing that the Bayesian approach provided mortality point estimates and credible intervals in the proper domain while the frequentist approach resulted in point estimates and confidence intervals partly incurring in incorrect sign for some years.
- Obtained P_0 estimates with the Bayesian approach are in agreement with the estimates from the previous frequentist approach.
- The proposed method could be used for other species data.

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THANK YOU! OBRIGADA!

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