

Documentation

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This document provides a walk-through on the model fitted for the freshRestore project. The document begins with the objectives for the modelling, dataset and covariates used and some results obtained.

1 Objectives

- Fit a population dynamic model (IPMs) with anthropogenic drivers (human driven factors such as climate change, direct exploitation, pollution, biological invasions, sea-use change; Moullec et al., 2021).
- The IPM should be a mechanistic model (plug and play; Frost et al., 2023; Smallegange et al., 2017). The IPMs should describe how the variables affect population.
- IPMs should model temporal trends in human characteristics using variables that indicate catchment state of each year and a continuous time series data.
- Produce prediction maps (of what?)

2 Example dataset received

I have received three files which are located here in the gitHub repository:

- *Example1.csv* : This file contains fish population data across lakes in Norway. The description of the column names in this file can be found here.
- *Example2_vatnLnr.csv* : This file contains a individual fish data of the population harvested. The description of the column names in this file can be found here.
- *model_catchment_vars.csv* : This file contains the catchment variables for all the lakes. The description of the variables can be found here.

23 3 Data format and exploration

24 The individual fish data was formatted into an age at harvest format with their **lake**, **sex** and **year**
25 **growth occurred** as variables to widen the long-format dataset received.

26 3.1 Catchment Variables

- 27 • Easily accessible variables e.g. using remote censored data
- 28 • environmental covariates

29 I first perform a simple exploration of the catchment variables using *GGally* package. This is
30 to help me reduce the number of catchment variables to include in the model. But since the end
31 product expected is a plug and play type, I would have to include these catchment variables of
32 interest even if they are not selected in the pre-screening phase.

```
33 # Not run  
# copy and run if needed  
GGally::ggpairs(dataList$ageAtHarvestData[, c(53:68)])
```

34 The following catchment variables are selected to model the fish survival in the lakes:

- 35 • Coniferous forest
- 36 • Moors and heathland
- 37 • Peat bogs
- 38 • Water bodies
- 39 • Broad-leaved forest
- 40 • Sparsely vegetated areas
- 41 • mean_ndvi

42 3.2 Other covariates

43 The **length at age this year** of the individual fishes was modelled with the following covariates:

- 44 • Mean temperature in June
- 45 • Precipitation in May
- 46 • Precipitation in June
- 47 • Precipitation in July

```

# Not run

# copy and run if needed

GGally::ggpairs(ageAtHarvestData[, c(1:3, 15, 36:45)])

```

48

49 4 Fitted model

50 I fit a Bayesian age-at-harvest population model following Bærum et al. (2021); Skelly et al. (2023).

51 The script to run for the analysis can be found here.

52 Here, I present a brief overview of the model fitted.

53 Let:

- 54 • i = individual
- 55 • a = age under consideration. Here the age is from 0 to 10.
- 56 • L_i = length at age this year for individual i
- 57 • S_{ia} = spawning of individual i at age a
- 58 • F_{ia} = Fecundicity of individual i at age a

59 4.1 Modelling L_i

$$L_i \sim N(\lambda_L, \sigma_L^2)$$

$$\lambda_L = X_L^T \beta_L$$

60 where X_L is a matrix of the covariates: Mean temperature in June, Precipitation in May, Precipita-
61 tion in June and Precipitation in July; and β_L is a vector of covariate effect plus an intercept term
62 and σ_L^2 is the variation of the error term.

63 The prior distributions assumed for β_L and σ_L^2 are $N(0, 10^2)$ and $Uniform(0.1, 10)$ respectively.

64 4.2 Spawning probability

$$S_{ia} \sim Bernouli(\psi_{ia})$$

$$\text{logit}(\psi_{ia}) = X_{sp}^T \beta_{sp} + \Gamma_a + \xi_{sex[i]}$$

$$\Gamma_a \sim N(0, \sigma_a^2)$$

$$\xi_{sex[i]} \sim N(0, \sigma_{sex}^2)$$

65 where X_{sp} is a matrix of covariates: age at year, L_i , age at year * L_i , capture per unit effort; and

66 β_{sp} is a vector of covariate effect plus an intercept term.

67 4.3 Fecundicity

68 The equation for the fecundicity is derived from Bærum et al. (2021).

$$F_{ia} = \exp(\log(L_i * 2.21 - 6.15) \times S_{ia})$$

69 4.4 Survival Probability

$$\text{logit}(\gamma_{ia}) = X_{surv}^T \beta_{surv} + \nu_a + \Xi_{lake[i]}$$

$$\nu_a \sim N(0, \sigma_a^2)$$

$$\xi_{lake[i]} \sim N(0, \sigma_{lake}^2)$$

70 where X_{surv} is a matrix of covariates described in section 3.1; and β_{surv} is a vector of covariate effect
71 plus an intercept term.

72 4.5 Projection Matrix (A)

73 The projection matrix used is the same as described in Bærum et al. (2021). The reader is referred
74 to page 9 of the paper.

75 4.6 Model for observed counts at each age

76 The age at harvest count is modeled using the model described in (Skelly et al., 2023). The change
77 we make is to estimate the stable population λ from the largest eigenvalue of the projection matrix
78 (A) instead of simulating it from an informed prior.

79 5 Results

80 I am currently running the model with 20000 iteration for each of the 2 MCMC chains. It seems to
81 take a while.

82 References

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