

A Quick and Dirty Bayesian Leslie Matrix Model of Norway HarpEast Data

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Population Values

A_t = Number of Nonpups in year t

H_t^A = Harvest of Nonpups in year t

P_t = Number of Pups in year t

H_t^P = Harvest of Pups in year t

$N_t = A_t + P_t$

A Simple Two-age Leslie Matrix Model

Boveng, P.L., Ver Hoef, J.M., Withrow, D.E., and London, J.M. 2018. A Bayesian Analysis of Abundance, Trend and Population Viability for Harbor Seals in Iliamna Lake, Alaska. Risk Analysis 38(9): 1988-209 DOI:10.1111/risa.12988

$$A_t = \delta_{t-1}(A_{t-1} - H_{t-1}^A) + \kappa_{t-1}(P_{t-1} - H_{t-1}^P),$$
$$P_t = c_{t-1}\phi_{t-1}(A_{t-1} - H_{t-1}^A),$$

$$\mathbf{n}_t = \begin{pmatrix} P_t \\ A_t \end{pmatrix}, \mathbf{h}_t = \begin{pmatrix} H_t^A \\ H_t^P \end{pmatrix}, \mathbf{M}_t = \begin{pmatrix} 0 & c_t\phi_t \\ \kappa_t & \delta_t \end{pmatrix}$$

$$\mathbf{n}_t = (\mathbf{n}_{t-1} - \mathbf{h}_{t-1}) \mathbf{M}_{t-1}$$

$$c_t = \exp(-\rho N_t/1000)$$

c_t = Exponential decay in fecundity with increased N_t

Parameters

P_1 : Abundance of Pups in Year $t = 1$

A_1 : Abundance of Nonpups in Year $t = 1$

δ_t : Adult Mortality Rate in Year t

κ_t : Pup Mortality Rate, from Survey to Survey, in Year t

ϕ_t : Fecundity Rate for all Adults, to Survey Time, in Year t

ρ : Controls Exponential Decay in Fecundity as Population \uparrow

Priors

$$[P_1] = \pi(P_1) \sim N(300,000, 50,000^2)$$

$$[A_1] = \pi(A_1) \sim N(1,000,000, 100,000^2)$$

$$[\delta] = \pi(\text{logit}(\delta_t)) \sim N(2.2, 0.5^2) \forall t; \text{logit}^{-1}(2.2) = 0.90$$

$$[\kappa] = \pi(\text{logit}(\kappa_t)) \sim N(1.4, 0.5^2) \forall t; \text{logit}^{-1}(1.4) = 0.80$$

$$[\phi] = \pi(\text{logit}(\phi_t)) \sim N(-0.4, 0.5^2) \forall t; \text{logit}^{-1}(-0.4) = 0.40$$

$$[\rho] = \pi(\log(\rho)) \sim N(-4.0, 0.5^2)$$

Data

H_t^A and H_t^P for all years

p_t an estimate of pup abundance in year $t \in \mathcal{S}$

s_t a standard error of pup abundance in year $t \in \mathcal{S}$

\mathcal{S} is an index set of sampled years from T total years

\mathcal{T} is the index set of years $t = 1, \dots, T$

Likelihood

$$[p_t \mid P_t, s_t, \boldsymbol{\delta}, \boldsymbol{\kappa}, \boldsymbol{\phi}, \rho, P_1, A_1, \{\mathbf{h}_t; t \in \mathcal{T}\}] \sim \text{N}(P_t, s_t)$$

where P_t is obtained from

$$\mathbf{n}_t = (\mathbf{n}_{t-1} - \mathbf{h}_{t-1}) \mathbf{M}_{t-1}; t \in \mathcal{T}$$

where $\{\mathbf{n}_t; t \in \mathcal{T}\}$ depends on $\boldsymbol{\delta}, \boldsymbol{\kappa}, \boldsymbol{\phi}, \rho, P_1, A_1$

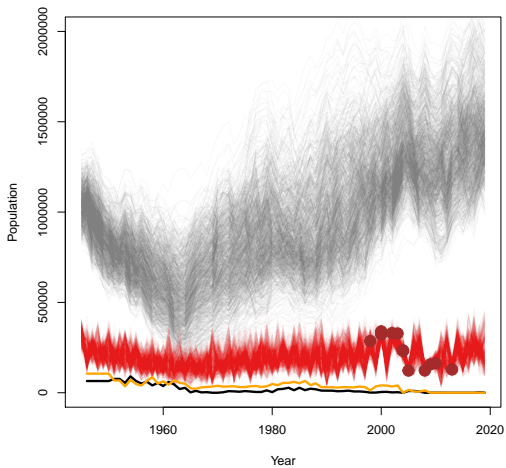
Posterior

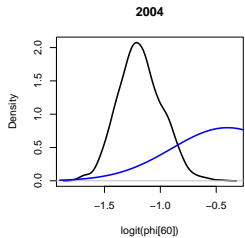
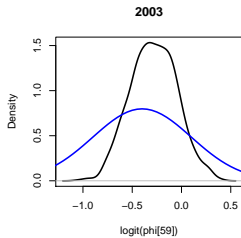
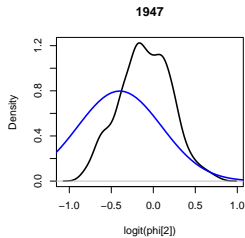
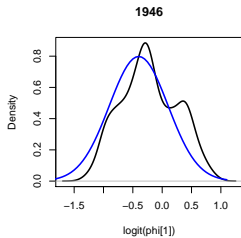
$$[P_1, A_1, \delta, \kappa, \phi, \rho \mid \{(p_t, s_t); t \in \mathcal{S}\}, \{\mathbf{h}_t; t \in \mathcal{T}\}] \propto \prod_{\mathcal{S}} [p_t \mid P_t, s_t, \delta, \kappa, \phi, \rho, P_1, A_1, \{\mathbf{h}_t; t \in \mathcal{T}\}] [P_1] [A_1] [\delta] [\kappa] [\phi] [\rho]$$

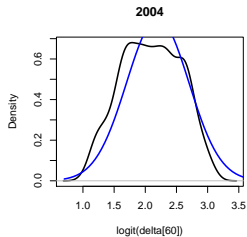
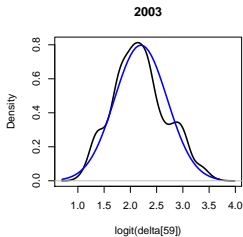
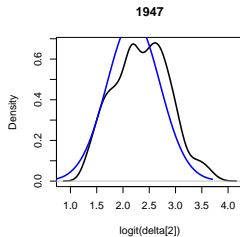
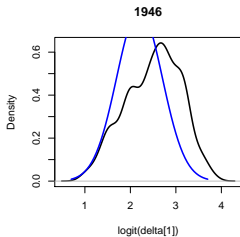
Posterior of $\{\mathbf{n}_t; t \in \mathcal{T}\}$ is constructed from posteriors of $P_1, A_1, \delta, \kappa, \phi$ and ρ .

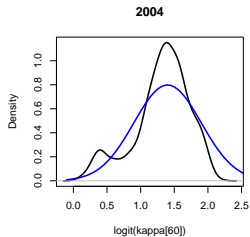
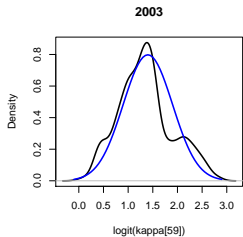
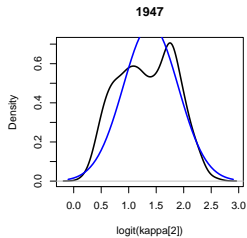
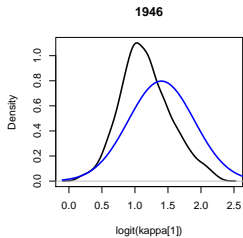
Use MCMC with Metropolis sampling to obtain sample from posterior distribution.

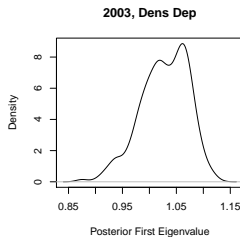
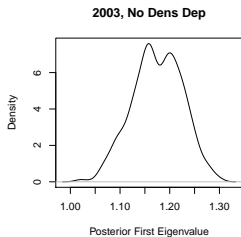
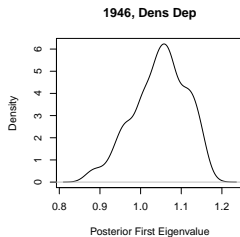
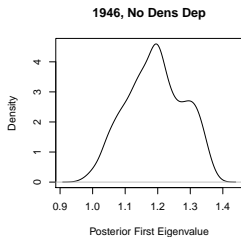
Custom code written in R, uses batch sampling for δ, κ, ϕ , with a burnin of 10,000 samples, followed by 100,000 where only each 100th sample was saved, yielding 1,000 samples from posterior.











Notes

- ▶ The 2-age Leslie matrix model can be obtained from more detailed age- and sex-structured Leslie matrix models if they are collapsed properly. The details can be found in the appendix of Boveng et al. (2018), listed above. The intrinsic growth rate (first eigenvalue) and stable age proportions can be preserved between detailed Leslie matrix and collapsed Leslie matrix. Collapsing the Leslie matrix model matched more closely to the data at hand.
- ▶ This is not a realistic model for harp data, as there are better priors that can be developed from auxilliary data. However, this package shows that it is easy to create custom code.

- ▶ The code runs quickly for such a small data set, even though there are 228 parameters (75 each for δ , κ , and ϕ , along with ρ , P_1 , and A_1), but using batch sampling for δ , κ , and ϕ .
- ▶ There is very little survey data, on pups only. The results of the model depend a lot on the priors.
- ▶ The attraction of a full Bayesian model is that we sample from the full joint posterior distribution. The posterior distribution of pup and nonpup abundance is derived from the Leslie matrix model through the joint distribution of δ , κ , ϕ , ρ , P_1 , and A_1 . Moreover, the posterior distribution of intrinsic growth, obtained from the first eigenvalue of the Leslie matrix model, is easily obtained if we have the joint posterior distribution of Leslie matrix parameters.