

IWAM_ModelDef

Integrated Watershed-Area Model Objectives

[Insert] overall objective of IWAM model: The integrated watershed are model was developed by the Stock Assessment and Recruitment Team (DFO) for the purpose of estimating population statistics, SMSY and SREP, in low-data use-cases.

Model References

This model was developed by interpreting the models of [Insert] publication references to e.g., Parken et al. 2006, Liermann, etc.

Model Description

The equations and description below will walk you through the hierarchical structure of the IWAM model from raw input to final predictive estimates of spawners for maximum sustainable yield (SMSY) and spawners () (SREP), including a detailed definitions list of all notation used and its corresponding label in the supplied repository code [[carrieholt/Watershed-Area-Model: Watershed Area Model \(github.com\)](https://github.com/carrieholt/Watershed-Area-Model)].

Basic Ricker Model

$$R = S e^{\alpha - \beta S} e^{\tau}$$

Which contains the following terms: R : recruitment per stock [numeric, often scaled], S : Spawners or spawner abundance [numeric, often scaled], α : dimensionless number of recruits per spawner produced at very low spawner density [dimensionless], β : the strength of the density dependence expressed as $1/S_{MAX}$ [$spawners^{-1}$], τ : the normally distributed error. The base Ricker model is written in this form to reflect a stochastic process (time ordered and random) by adding the log-normal error term τ , a normal distributed term often used to account for environmental variability.

Hierarchical Ricker (α) and Linear Form Ricker

This baseline form is then converted into the two following forms of a hierarchical Ricker (1) and a linearized Ricker (2).

$$R_i = S_i \cdot e^{\alpha_i - \beta_i \cdot S_i} \cdot e^{\tau_i}$$

Which is then linearized by log transformation into the form:

$$\log\left(\frac{R_i}{S_i}\right) = \log(\alpha_i) - \beta_i \cdot S_i + \tau_i$$

Where $\tau \sim \text{Normal}(0, \sigma_\tau)$

and $\log(\alpha_i) \sim \text{Normal}(\mu \text{Log}(\alpha), \text{SigmaLog}(\alpha))$,

and $\mu \log(\alpha_i) \sim \text{Normal}(1.5, 5)$,

and $\sigma \log(\alpha_i) \sim \text{InvGamma}(0.01, 0.01)$.

In this regard, α is the intercept and β is the slope of the spawner-recruit relationship. The hyper-priors (incorrect term) on $\log(\alpha)$ are likelihood penalties. In a frequentist model description, the penalizing function is a method for smoothing and to improve the sampling of the estimator - in this case [INSERT SAMPLER].

INSERT PRIOR DISTRIBUTION PLOTS TO ENHANCE ENDING

Watershed Area Model

$$\ln(S_{MSY}) = \ln(\delta_0) + \delta_1 \cdot \ln(WA) + \delta_\epsilon$$

$$\ln(S_{REP}) = \ln(\gamma_0) + \gamma_1 \cdot \ln(WA) + \gamma_\epsilon$$

where,

$$\delta_\epsilon \sim N(0, \sigma_\delta^2)$$

$$\delta_\gamma \sim N(0, \sigma_\gamma^2)$$

Where δ_0 is the intercept and δ_1 is the slope for the relationship between watershed area and either S_{MSY} and S_{REP} . These are then adapted further to separate stream-type and ocean-type fish in the watershed area model. This is done by creating an offset with the baseline as the stream type population.

$$\ln(S_{MSY}) = \ln(\delta_{0,stream}) + \ln(\delta_{0,ocean}) \cdot X + (\delta_{1,stream} + \delta_{1,ocean} \cdot X) \cdot \ln(WA) + \delta_\epsilon$$

where, $\delta_\epsilon \sim Normal(0, \sigma_\epsilon)$ and $X = 0$ for stream type and $X = 1$ is for ocean type populations.

S_{MSY} and S_{REP} Calculation

$$S_{MSY} = \frac{1 - W(e^{1-(\alpha)})}{\beta}$$

$$S_{REP} = \frac{\alpha}{\beta}$$