

Hydra Methology

Drafting notes

Using organization of MS_SCAA methodology as a template

Also compare with Vanessa's multiple species state space model: https://github.com/vtrijoulet/Multisp_model_JAE (link to paper) https://github.com/vtrijoulet/MS_SSM (link to up to date model)

Model description

Population dynamics For an individual species i , the number of individuals N in size class j at time $t + 1$ represent the survivors from that cohort from the previous time step (t) that have not grown into a larger size class, plus the number of individuals growing into size class j from smaller size classes during the time interval. We only consider transitions among immediately adjacent size classes. For size classes larger than the recruit (smallest) size class, the model for each species i can be written:

$$N_{i,j,t+1} = \sum_{j'} \phi_{i,j' \rightarrow j,t} S_{i,j',t} N_{i,j',t}$$

The proportion surviving from size class $j - 1$ to size class j for a species at time t is denoted $S_{j',t}$. $\phi_{j' \rightarrow j}$ is the probability of moving from size class $j - 1$ to size class j .

[Lots more here but GF wanted to make progress on the objective function, see Gaichas et al. 2017 supplementary for rest of Hydra specs]

Objective Function

The model can be fitted to multiple data streams

Catch Expected catch is summed over time steps to the fishing/calendar year y .

$$\hat{C}_{y,i,q} = \sum_{t \in y} \sum_j \frac{s_{i,j,q} F_{i,j,q,t}}{M1_{i,j,t} + M2_{i,j,t} + s_{i,j,q} F_{i,j,q,t}} \left[1 - e^{-(M1_{i,j,t} + M2_{i,j,t} + s_{i,j,q} F_{i,j,q,t})} \right] N_{i,j,t} W_{i,j,t}$$

$$\ln(C_{y,i,q}) \sim \mathcal{N}(\ln(\hat{C}_{y,i,q}), \sigma_{q,i,y}^2)$$

Catch length composition

$$\hat{p}_{q,i,y,j} = p_{q,i,y,j}^* / \sum_{j'} p_{q,i,y,j'}^*$$

$$p_{q,i,y,j}^* = \sum_{t \in y} \frac{s_{i,j,q} F_{i,j,q,t}}{M1_{i,j,t} + M2_{i,j,t} + s_{i,j,q} F_{i,j,q,t}} \left[1 - e^{-(M1_{i,j,t} + M2_{i,j,t} + s_{i,j,q} F_{i,j,q,t})} \right] N_{i,j,t}$$

Proportions at length (in numbers) in catch for each gear type - either multinomial, dirichlet, etc.

Survey abundance indices The predicted values for survey abundance rely on the timing of the survey within a year, catchability of the species in the survey, and the (length-based) survey selectivity. Survey g predicted values (in weight) are:

$$\hat{I}_{g,i,t} = q_{i,g,t} \sum_j j s_{i,j,g} N_{i,j,t} l_j W_{i,j,t}$$

The observed annual index values for each species are assumed to be lognormally distributed around the predicted values:

$$\ln(I_{g,i,t}) \sim \mathcal{N}(\ln(\hat{I}_{g,i,t}), \sigma_{g,i,t}^2)$$

Survey length composition

$$\hat{p}_{g,i,t,j} = p_{g,i,t,j}^* / \sum_{j'} p_{g,i,t,j'}^*$$

$$p_{g,i,t,j}^* = s_{i,j,g,t} N_{i,j,t}$$

Proportions at length (in numbers) in the survey - either multinomial, dirichlet, etc.