

## Tuna Forage model

An important component of SEAPODYM is the tuna forage sub-model that explores the dynamics of tuna prey organisms, consisting of macrozooplankton and micronekton, mainly crustaceans, fish and cephalopods from 2cm to 20 cm in size. The SEAPODYM team did not try to develop a detailed explicit food web model for the whole pelagic ecosystem in the Pacific Ocean, instead the tuna forage was considered as a single population. Therefore, we used a simple model for describing the whole forage population  $FO$  dynamics based on recruitment  $S$  and mortality  $\lambda$ :

$$\frac{dFO(t)}{dt} = S - \lambda FO(t); \quad FO(t) = \frac{S}{\lambda} (1 - e^{-\lambda t})$$

The development of a new primary production triggers the development of a new cohort of different organisms that will be recruited in the forage population after a time  $T_r$ . The level energy transferred between these two trophic levels depends on the ecological transfer coefficient, according to Iverson (1990) this transfer is 4%. The equilibrium forage population is  $FO^* = S/\lambda$  and the production is  $FO' = S$ . A single cohort decreases exponentially ( $Se^{-\lambda t}$ ) due to mortality; therefore its mean age can be estimated integrating over time:

$$\int_0^{\infty} t S e^{-\lambda t} dt = \frac{S}{\lambda^2}$$

The mean life span ( $1/\lambda$ ) is calculated by dividing the mean age by the forage equilibrium population. The mean life span since the origin of the cohort can be found if we add the recruitment time ( $1/\lambda + T_r$ ). The maximum life span of organisms within the forage population is determined as the necessary time to reduce the population to certain level (Figure 1), for example for a 99% reduction of the cohort, the maximum life span is given by:  $t_{max} = (1/\lambda) \ln(0.01) + T_r$ . The parameters  $\lambda$  and  $T_r$  can be estimated using biological information of key-species representative of this group.

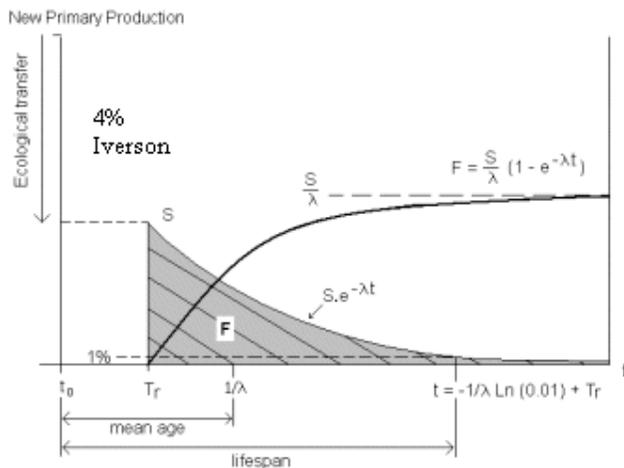


Figure 1. Transfer of primary production to tuna forage and dynamics of this component. Thin curve describes the decay of a cohort, the thick curve describes the dynamics of total forage population.

In SEAPODYM we have improved the forage model presented above by adding migration. The horizontal movement of small forage organisms and tuna larvae and juveniles was described

by advective equations. The advective components in the two horizontal dimensions are oceanic currents, characterized by a diffusion coefficient  $\rho$  that includes water diffusion and organisms' random movement, and  $u, v$  the zonal and meridional components of the current in the euphotic layer:

$$\frac{\partial FO}{\partial t} = \rho \left( \frac{\partial^2 FO}{\partial x^2} + \frac{\partial^2 FO}{\partial y^2} \right) - \frac{\partial}{\partial x} (uFO) - \frac{\partial}{\partial y} (vFO) - \lambda FO + S$$

Tunas are known to be opportunistic predators feeding upon three major groups of prey: fish, squids and crustaceans. Prey sizes range from a few millimeters (euphausiids and amphipods) to several centimeters (squids, small fish, and shrimps). This large spectrum of prey species and prey sizes is difficult to incorporate into an explicit trophic model. Therefore, the integrated tuna forage model described above facilitates modeling tuna forage within a complex model as SEAPODYM.

Regarding the estimation of  $\lambda$ , skipjack and yellowfin tuna regularly feed on the oceanic anchovy, *Encrasicholina punctifer* (Hida, 1973), a species with a short life cycle (less than 1 year), with fast growth and a maturity age of 3–4 months (Dalzell, 1993). Based on this information, a mean age of 120 days was chosen due to the anchovy's maturity age and 60 days were assigned for  $T_r$ . Thus a maximum life span of 336 days was determined. Although these values may need to be refined, they appear to be a reasonable characterization of tuna forage.

As mentioned for the forage vertical migration six functional groups linked to the ocean-biogeochemical models were defined (Figs. 2 and 3). All these groups are assumed to be influenced by the general circulation. Many forage species have optimized their behavior for finding food, while avoiding predators; migrating into the upper layers at sunset and leaving them during the sunrise structuring the pelagic food web. A forage component is redistributed by currents during the time spent in a layer. The time spent in a particular layer depends on the day length  $DL$  (Figure 4) that varies depending on the latitude  $\phi$  and the Julian day  $J$  of the year (365 days):

$$DL = \frac{24}{\pi} \cos(-\tan \phi \tan \delta)$$

Where  $\delta$  is the solar declination angle:

$$\delta = 23.45 \cos\left(\frac{2\pi}{365(J-172)}\right)$$

The redistribution of converted biomass from the primary production (4% energy transfer) among the six forage classes is achieved using six energy coefficients (Figure 3).

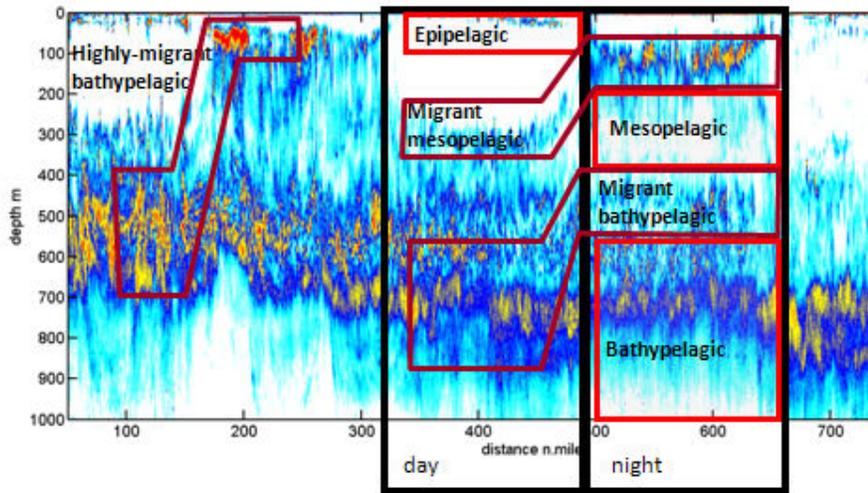


Figure 2. Acoustic backscatter showing the six groups defined for the epipelagic, mesopelagic and bathypelagic layers.

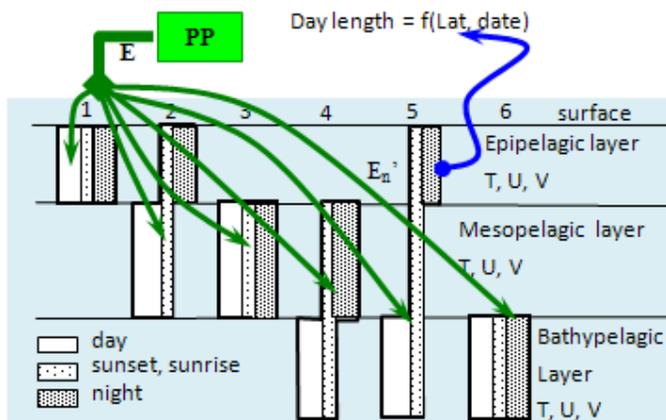


Figure 3. Daily vertical distribution patterns of micronekton in the epipelagic system. 1, epipelagic; 2, migrant mesopelagic; 3, non-migrant mesopelagic; 4, migrant bathypelagic; 5, highly-migrant bathypelagic; 6, non-migrant bathypelagic. Also shown, the distribution of the energy (E) transferred from primary production (PP) to intermediate trophic levels ( $E_n'$ ) through the different components.

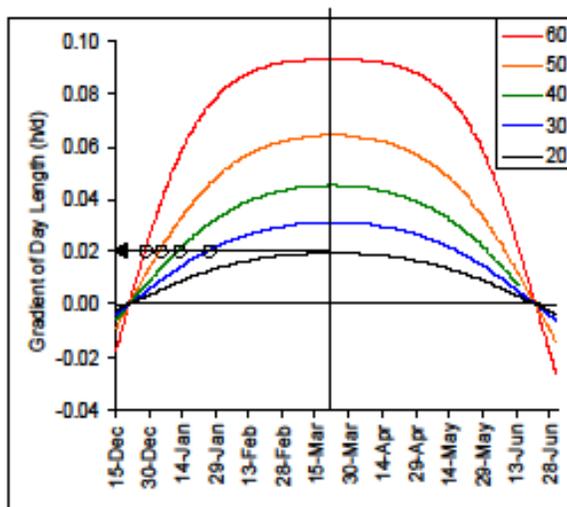


Figure 4. Example of seasonal cycles of the gradient of the day length at different latitudes in the north hemisphere (Threshold of 0.02 hours per day)

The forage sub-model is able to take in account recruitment, ageing, mortality, passive transport with horizontal currents and the vertical behavior of the mid-trophic level organisms to provide essential information for the SEAPODYM [tuna model](#) (Link: [Tuna\\_model\\_html.doc](#)).

## References

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