

## Biomass fluxes <sup>1</sup> in SEAPODYM

Let  $B_{a,t,x,y}$  be the biomass density (in mt/km<sup>2</sup>) of tuna population at age  $a = 1, \dots, A+$ , time  $t$  and grid cell  $(x, y)$ . Let's consider two regions,  $r_1$  and  $r_2$ . For a given age  $a$ , we denote

$$\beta_{r_1, r_2} = \sum_{i,j \in r_2} B_{t+\Delta t, x, y} \cdot A_{xy}, \text{ when } B_{t, x, y} \forall x, y \in r_1 \text{ at time } t, \quad (1)$$

where  $A_{xy}$  is the grid cell surface area in km<sup>2</sup>. Hence, we say  $\beta_{r_1, r_2}$  is the total regional biomass moving from region  $r_1$  to region  $r_2$  during time period  $(t, t + \Delta t)$ .

For a given age  $a$  and  $n$  regions we have  $n \times n$  matrix with all elements corresponding to the same time  $t + \Delta t$ :

$$\mathbf{F}_{t,a} = \begin{pmatrix} \beta_{1,1} & \beta_{1,2} & \dots & \beta_{1,n} \\ \beta_{2,1} & \beta_{2,2} & \dots & \beta_{2,n} \\ \vdots & \vdots & \vdots & \vdots \\ \beta_{n,1} & \beta_{n,2} & \dots & \beta_{n,n} \end{pmatrix}, \quad (2)$$

where the  $\sum_j \beta_{i,j}$  is the total biomass that was in region  $i$  before the movement occurred, i.e., at time  $t$ , and the  $\sum_i \beta_{i,j}$  is the biomass in region  $j$  after the movement occurred, i.e., at time  $t + \Delta t$ . In other words,

$\sum_{j \neq i} \beta_{i,j}$  – **outgoing biomass** from region  $i$  to other regions,

$\sum_{i \neq j} \beta_{i,j}$  – **incoming biomass** to region  $j$  from other regions, and

$\beta_{ii}$  – the **resident biomass** that stayed in the region  $i$  during the time period  $(t, t + \Delta t)$ .

As seen from above, the elements of matrix  $\mathbf{F}_{t,a}$  have units of mass flow rate, i.e., mt/ $\Delta t$ . In current SEAPODYM implementation,  $\Delta t$  is set to 3-months period, hence  $\beta_{ij}$  units are mt/qtr.

A simulation with `seapodym_fluxes` application computes  $n_a \times n_t$  of  $n \times n$  matrices, written in  $n_a$  ASCII files and named `sname_FluxesRegion_age[a-1].txt`.

## Converting F to movement probabilities for Multifan-CL

To convert the regional biomass fluxes to probabilities, we first convert the biomass to the number of individuals, which is necessary for the aggregation of several monthly age classes into a coarser Multifan-CL age structure. Simply using the mean weight-at-age  $w(a)$  for each age class with mean age  $a$ , the total number of individuals moving from region  $i$  to  $j$  is  $\nu_{a,i,j} = \frac{\beta_{a,i,j}}{w(a)}$ . Then the probability  $p_{i,j}$  to move from region  $i$  to region  $j$  is computed as

$$p_{i,j} = \frac{\nu_{i,j}}{\sum_j \nu_{i,j}}, \quad (3)$$

where the sum in the denominator is the total number of individuals in region  $i$  before the movement occurred (see above).

Finally, to match the Multifan-CL format, the movement matrices that are provided to the Multifan-CL model are the transpose of SEAPODYM-derived  $\mathbf{P}_{t,a}$  matrices with elements (3) such as:

$$\mathbf{P}_{t,a}^T = \begin{pmatrix} p_{1,1} & p_{2,1} & \dots & p_{n,1} \\ p_{1,2} & p_{2,2} & \dots & p_{n,2} \\ \vdots & \vdots & \vdots & \vdots \\ p_{1,n} & p_{2,n} & \dots & p_{n,n} \end{pmatrix}, \quad (4)$$

so the sum over each column of  $\mathbf{P}_{t,a}^T$  is  $\sum_j p_{i,j} = 1$ .

Note that aggregation to Multifan-CL age classes as well as seasons is done before computing probabilities (3).

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<sup>1</sup>Here in the sense of the mass flow rate