

Persistence metrics and data connections

1 Terms

- recruit: fish in the 3.5-6.0cm size class (able to be fin-clipped but not tagged), which preliminary growth analyses suggest settled the previous year and are about one year old (will refine growth analyses to confirm/check)
- LEP (lifetime egg production): the expected reproductive output in terms of eggs of one individual, considering only reproduction as a female
- LR (local retention): recruits returning home over total output of recruits from the patch

$$\begin{aligned} LR &= \frac{\# \text{ arrivals returning home}}{\text{output from patch}} \\ &= \frac{\# \text{ recruits arriving home}}{\# \text{ recruits produced by patch}} \\ &= \frac{p_{i,i} \times \# \text{ recruits from site}}{\frac{\text{recruits}}{\text{egg}} \times \# \text{ eggs produced by site}} \end{aligned} \tag{1}$$

- $p_{i,j}$: of recruits from patch i that recruited somewhere, the probability of dispersing from patch i to patch j
- p_{hab} : proportion of habitat sampled (estimated as number of anemones visited over estimated total number of anemones at site)
- p_{cap} : probability of sampling a fish, given that we visited its anemone (estimated using mark-recapture within a sampling season)

2 Network persistence: demographic connectivity matrix

A group of patches are network persistent if the largest eigenvalue of the demographic connectivity matrix (C) is > 1 (Burgess et al. (2014); Garavelli et al. (2018))

$$C_{ij} = LEP_i \times \frac{\text{recruits}}{\text{egg}} \times p_{ij}. \quad (2)$$

Calculate this metric for both the overall population and smaller groups of patches within the network, to see at what scale persistence might occur.

3 Self-persistence

A patch is self-persistent (Burgess et al. (2014)) if

$$LEP \times LR \geq 1, \quad (3)$$

where both LEP and LR consider the same life stage, essentially seeing whether an individual will be able to replace itself, considering its total lifetime reproductive output, the survival of that output to recruitment, and the probability that recruitment returns to the natal patch.

So, for recruits as the starting age and fecundity and LEP in terms of eggs, you get:

$$SP_i = LEP_i \times \frac{\text{recruits}}{\text{egg}} \times \frac{p_{i,i} \times \# \text{ recruits from site } i}{\frac{\text{recruits}}{\text{egg}} \times \# \text{ eggs produced by patch } i} \geq 1, \quad (4)$$

which simplifies to

$$SP_i = LEP_i \times \frac{\text{recruits}}{\text{egg}} \times p_{i,i} \geq 1, \quad (5)$$

(and is the diagonal entries of C).

Or, alternately, could write it as:

$$SP_i = LEP_i \times \frac{\text{recruits}}{\text{egg}} \times \frac{\# \text{ recruits arriving home to patch } i}{\frac{\text{recruits}}{\text{egg}} \times \# \text{ eggs produced by patch } i} \geq 1, \quad (6)$$

which simplifies to be

$$SP_i = LEP_i \times \frac{\# \text{ recruits arriving home to patch } i}{\# \text{ eggs produced by patch } i} \geq 1. \quad (7)$$

4 Connections with data

- LEP: use survival-by-size estimates from mark-recapture, growth estimates from mark-recapture, fecundity estimates from egg photos (preliminary numbers and relationship with size in progress by Adam) to estimate LEP with an integral projection model
- output in eggs from each site: $N_{\text{eggs},i} = \# \text{females} \times p_{\text{hab}} \times p_{\text{cap}} \times \text{fecundity}$, with fecundity estimates from photos (might be related to size, depending on relationship) and clutches-per-year data from Holtswarth et al. (2017).
- $p_{i,j}$, version 1: integrate the dispersal kernel estimated with the Bode et al. (2018) method (kernel-fitting being done by Katrina using parentage data and proportion habitat sampled) over the distances between sites
 - kernel is a Laplacian kernel with parameters k (scale parameter) and θ (exponent) and depends on distance x : $f(x, k, \theta)$
 - after normalization, the kernel gives the probability of recruiting distance x away from origin, given that you recruited somewhere
 - $d1$: distance between the mid-point of site i and the closest edge of site j
 - $d2$: distance between the mid-point of site i and the farthest edge of site j
 - integrate to get probability of recruiting at site j from site i , given that you recruited somewhere

$$p_{i,j} = \int_{d1}^{d2} f(x, k, \theta) dx. \quad (8)$$

- $p_{i,j}$, version 2: estimate from the proportion-of-recruitment connectivity matrix generated by the Wang (2014) (MigEst) method (migration estimates being done by Katrina using the parentage and data and proportion habitat sampled)
 - the output of MigEst is an s (destination) by t (source) matrix M , where s is the number of sampled patches and there is an additional column for unsampled ghost populations ($t = s + 1$)
 - the matrix entries $m_{s,t}$ are the proportion of recruits at site s that come from site t (the row sums - recruits coming to site s - are 1)

- N_{r_s} : vector of the number of recruits arriving at each site s , found by scaling up the number of sampled recruits by the proportion of habitat sampled
- $N_{o_t} = N_{\text{eggs produced}_t} \times \frac{\text{recruits}}{\text{egg}}$: vector of number of recruits produced by each source site t
- convert migration estimates ($m_{s,t}$) from MigEst to proportion of recruits from site i settling at site j :

$$p_{i,j} = \frac{m_{s,t} \times N_{r_s}}{N_{o_t}}. \quad (9)$$

- $\frac{\text{recruits}}{\text{eggs}}$: relationship between $\frac{\text{eggs}}{m^2}$ and $\frac{\text{recruits}}{m^2}$ the following year, estimated at a site level and where estimates of both egg production and recruits have been scaled up to account for the proportion of habitat sampled in each year and the probability of sampling a fish given that we covered its anemone
- #recruits arriving home to patch i : take raw number of parentage matches matched from site i to i and scale up by proportion habitat sampled (will be an underestimate of self-persistence but could be worth doing as a comparison)

References

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