

Persistence metrics and data connections

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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 of one individual in terms of eggs, considering only reproduction as a female
- LR (local retention): recruits returning home over total output of recruits from the patch

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

- $p_{i,j}$: probability of dispersing from patch i to patch j, given that you recruit somewhere
- p_{hab} : proportion of habitat sampled (estimated as number of anemones visited over 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))

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

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:

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

which simplifies to

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

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)
- $p_{i,j}$, version 1: estimate from the dispersal kernel estimated from parentage and proportion sampled data with the Bode et al. (2018) method (kernel-fitting being done by Katrina)
 - kernel is a Laplacian kernel with parameters k (scale parameter) and θ (exponent) and depends on distance d : $f(x, k, \theta)$
 - 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 Wang (2014) (MigEst) methods with the parentage data and proportion population sampled (migration estimates being done by Katrina)
 - 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

- Michael Bode, David H Williamson, Hugo B Harrison, Nick Outram, and Geoffrey P Jones. Estimating dispersal kernels using genetic parentage data. *Methods in Ecology and Evolution*, 9(3):490–501, 2018.
- Scott C Burgess, Kerry J Nickols, Chris D Griesemer, Lewis AK Barnett, Allison G Dedrick, Erin V Satterthwaite, Lauren Yamane, Steven G Morgan, J Wilson White, and Louis W Botsford. Beyond connectivity: how empirical methods can quantify population persistence to improve marine protected-area design. *Ecological Applications*, 24(2):257–270, 2014.
- Lysel Garavelli, J. Wilson White, Iliana Chollett, and Laurent Marcel Chérubin. Population models reveal unexpected patterns of local persistence despite widespread larval dispersal in a highly exploited species. *Conservation Letters*, page e12567, 2018.
- Jinliang Wang. Estimation of migration rates from marker-based parentage analysis. *Molecular ecology*, 23(13):3191–3213, 2014.