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From discussion

Our sampling on patchy coral reefs was designed for mark-recapture analysis rather than a comprehensive habitat or abundance census, so though we accounted for uneven sampling, we could have missed population declines if the underlying habitat was shifting. We used tagged anemones to account for unvisited patch habitat, but tags with missing anemones are harder to find. If anemones disappeared over time at our patches, we could have overestimated the number of fish and missed population declines indicating lack of persistence even with outside input. These scaling challenges are not unique to our study: few ecological studies are full censuses through time, and marine metapopulations tend to be patchy and heterogeneous (e.g. coral reefs, the intertidal zone, and kelp forests; Saenz-Agudelo et al., 2011; Johnson, 2001; Castorani et al., 2015), where individuals are not well-mixed across space or time. In these cases, carefully considering how sampling interacts with distribution, properly accounting for such uncertainties, and characterizing uncertainty in parameter

estimates, is an important part of persistence estimation.

More random text

Methods

For a population to persist, each individual must on average replace itself (e.g. Hastings and Botsford, 2006; Botsford et al., 2019). In non-spatially structured populations, we use criteria such as the average number of recruiting offspring each individual produces during its life (called R_0 when the population is age-structured and density-independent) or the growth rate of the population (such as the dominant eigenvalue λ of an age-structured Leslie matrix) (Caswell, 2001; Burgess et al., 2014). For spatially-structured populations, we must also consider the spatial spread of offspring, often represented through a dispersal kernel or connectivity matrix (Burgess et al., 2014).

Our equation for SP is a modification of that used in Burgess et al. (2014), which uses LEP to represent offspring produced and uses local retention (the number of surviving recruits that disperse back to the natal patch divided by the number of eggs produced by the natal patch) to capture egg-recruit survival and dispersal combined: $LEP \times \text{local retention} \geq 1$. We modify this to include egg-recruit survival in the offspring term instead, using LRP in place of LEP.

We used an integral projection model (IPM) (Ellner et al., 2016) with size as the continuous structuring trait L to estimate lifetime egg production on each patch i (LEP_i). We initialized the IPM with one recruit-sized individual (recruit defined

in SI ??) at the initial annual time step ($t = 0$), then projected forward for 100 years. We used the size- and site-dependent survival (eqn. ??) and growth (eqn. ??) functions as the probability density functions in the kernel to project the individual into the next time step. The size distribution (v_L) at each time step represents the probability that the individual has survived and grown into each of the possible size categories, ranging from a minimum of $L_s = 0$ cm to a maximum of $U_s = 15$ cm divided into 100 equal size bins.

We then multiplied the size-distribution $v_{L,t}$ at each time by the size-dependent fecundity f_L (eqn. ??) to get the total number of eggs produced at each time step. Integrating across time and size gave the total number of eggs one recruit produced in its lifetime (details in ??, uncertainty details in SI ??):

Discussion

References

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