

California Connectivity Population Model Methods and Results Summary

The following summary of connectivity model methods and results was provided by principal investigators Drs. Peter Raimondi and Mark Carr as supplemental material to include in this report. At the time that this review report becomes available in early 2023, the connectivity model will still be in development. A comprehensive report and more detailed results from the connectivity modeling will become available shortly after the release of this review report in 2023.

California Connectivity Population Model Background

One of the most distinctive attributes of California's system of marine protected areas (MPAs) established by the Marine Life Protection Act (MLPA) is its science-based design as an ecological network. One key feature of a geospatial ecological network is the degree to which locations are connected by the transport of propagules (animal larvae or algal spores) among the MPAs and interspersed populations that constitute the network. For most nearshore marine species, population connectivity is achieved primarily via propagule transport (i.e., dispersal), and such transport is often dictated by the interaction between oceanographic forcing and life history attributes (e.g., planktonic larval duration). Spatial variation in ocean currents and differences among species in propagule duration influence the direction and distance to which a species' propagules are dispersed. As such, the location of an MPA will greatly influence the number and location of MPAs to which propagules produced in that MPA will be transported to.

Over the last decade there have been remarkable advances in modeling oceanographic processes and propagule transport. Such models are typically developed using ROMS (Regional Ocean Modeling System) approaches. These are typically four-dimensional models (three spatial dimensions and time) that track propagules through spatial cells in a temporal series of incremental (time steps) spatial movements (through x, y, z vectors). Random movement via (random) turbulent vertical velocity can be incorporated to simulate small-scale effects not otherwise captured in the grid (cell)-based propagule movement forcing. For the application of ROMS to estimate spatial population connectivity via propagule dispersal, as we did in our analyses, mathematical propagules are "released" in cells and their dispersal is tracked over a period of time. At each time-step in the modeled period the location of the propagule can be assessed. By releasing a similar number of propagules from all of the cells across the spatial domain of the model (i.e., northern Baja California, Mexico to northern Washington state, including California state waters) and matching cell configuration with MPAs, the relative contribution of all locations (MPAs and Non-MPA sites) to the replenishment of other MPAs or reference area can be estimated.

Specifically, by incorporating a metric or proxy (e.g., area of suitable habitat) for spatial variation in propagule production among cells and applying a predetermined pelagic duration of a species' propagules (PLD), the relative contributions of populations as donor or recipient locations can be estimated. PLD categories representative of the diversity of marine species can be applied both to represent the spectrum of durations and dispersal of California marine species, and to assess how PLD influences the distribution of dispersing propagules. These relative contributions of propagule exchange among populations, often referred to as "connectivity", are often characterized by "source" populations

that contribute more propagule replenishment to other populations than they receive from other populations, and “sink” populations, that conversely receive more propagules than they contribute to other populations. While sink populations can be more reliant on connectivity for replenishment and persistence, source populations can contribute disproportionately to the replenishment of other populations across the network. All of this suggests that ensuring that source MPAs support large populations and high levels of propagule production is key to the size and persistence of protected populations across the MPA network. In addition, those populations (or MPAs) that receive disproportionate numbers of propagules (relative to other locations) or that have disproportionate number of links to donor populations (or MPAs) may in fact be more resilient than other populations (or MPAs).

Previously, we developed a population connectivity model for the purpose of identifying source populations and MPAs that was then incorporated into CDFW’s MPA prioritization scheme for the spatial design of the long-term MLPA monitoring program. Since the development of the original model, we have made several updates. These include updating the state’s seafloor database with data produced by more recent mapping studies, making it possible to separate mapped and predicted habitat where habitat types were interpolated across the unmapped nearshore “white zone”, use of high-resolution data to attribute habitat depth zones, new methods and data sources for calculating kelp cover and an important recent update to the ROMS cell/MPA area estimates for individual habitats.

A very important use of these results is to assess the MLPA design attribute of enhanced connectivity for MPA’s, which was included as a design attribute to increase resilience of the MPA network. Through the use of the model and the incorporation of the updates described we have been able to estimate the “connectivity” (which here is defined as the ROMS oceanographic connectivity coupled to estimated propagule production) from all MPA and Reference areas (sites other than MPA’s) in California to all MPA and Reference areas in California for three key habitats: rocky intertidal, Shallow Rock and Kelp habitat (0-30 meters depth) and deeper rocky reef habitats (30-100 meters depth).

Key model assumptions

To properly interpret model results, it is imperative to recognize and consider several key assumptions of the design and implementation of the model:

- 1) No effect of MPA or other protection was initially included in the modeling. Below we include a general range of MPA effects based on results for kelp forest habitat.
- 2) Propagule production and subsequent settlement is assumed to be directly and linearly related to the amount of Habitat in the donor and recipient MPA or Non-MPA ROMS cell. Here habitat means the general habitat types described above (e.g., rocky intertidal, kelp forest, hard bottom subtidal from 0-30 m). This assumption has the following associated assumptions
 - a) No effect of meso- or micro-habitat features on the abundance, the size structure or the size independent fecundity of species. These will be addressed in future versions of the modeling
 - b) No geographic patterns of abundance, the size structure, or the size independent fecundity of species. These will be addressed in future versions of the modeling

- c) No geographically independent environmental impacts on the abundance, the size structure or the size independent fecundity of species (e.g., local hypoxic events). However, note that projections of change in environmental conditions could be incorporated into modeling. Two scenarios will serve as examples. First, spatially explicit climate related change in temperature, OA or other attributes could be incorporated into connectivity and contribution modeling. Second, sea level rise could also be formally incorporated into connectivity modeling through projected spatially explicit predictions of habitat gain or loss.

Summary of Results

Below we address two questions.

What are the observed (modeled) patterns of contribution from MPAs and Reference areas to MPAs and Reference areas? And are contributions into MPA's greater than expected (a key design attribute)?

The modeled results indicate that contribution of propagules (from any source) into MPA's is greater than what is predicted for Reference areas and also greater than what is expected based on habitat area (Table 1 and Figure 1). For all habitats, the contribution to MPA's from other MPA's is greater than expected (Table 1) and the results also show that contribution from reference locations to MPA's is also higher for rocky intertidal and (30-100m) rocky reef MPA's (Table 1). Recall that these model results do not incorporate an MPA effect (e.g., an increase in propagule production due to reduction of harvest in the MPA). This means the effects described above are due to the location of MPA's with respect to coastal circulation patterns. These results suggest that MPA placement enhances both contributions from and settlement into MPA's. It is very important to note that these were specific design goals during the MPA spatial design process.

Finally, we used a very basic approach to incorporate MPA effects into the contribution models (Figure 2). The results from the kelp forest decadal assessment suggested that biomass in MPA's for harvested species might increase up to 50% relative to reference areas. We used this value as the upper limit of a possible MPA effect for the three habitats and modeled the effect of MPA effect on contribution to reference areas. This is shown as the ratio of expected contribution into reference areas based on different MPA effect levels (10-50%) relative to no MPA effect. Hence, the ratio is an estimate of the enhancement to reference areas due to MPA protections. All habitats showed an increasing enhancement with increasing MPA effect (Figure 2). At 50% effect size the enhancement to the habitats ranged from ~8% (kelp forest) to 15% (rock intertidal and 30-100 m rocky reefs).

These results are from very general, non-spatially explicit modeling that also does not incorporate any feedbacks (i.e. the likely increase in biomass in reference areas due to increased contribution into the areas from MPAs under the MPA effect is not part of this model) or any density-dependent dampening of population growth.

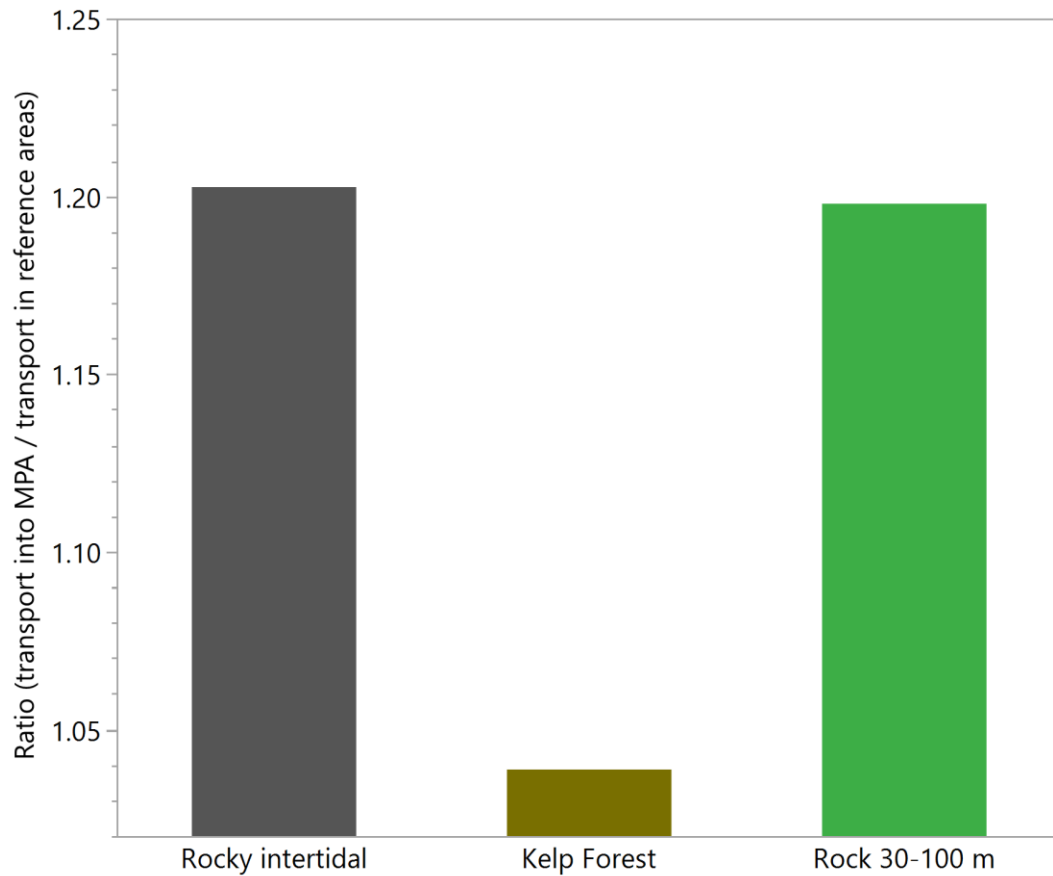


Figure 1: The ratio of transport of propagules into MPA's to that into reference locations on a per unit area of habitat basis.

Table 1: Percent deviation from expected propagule contribution to MPA's (based on habitat area) based on contribution model. For example, 30-100m deep rocky reefs in MPA's are predicted to receive 17% more propagules from Reference areas than would be expected based on area of habitat in the MPAs.

Habitat	Contribution from Reference to MPA	Contribution from MPA to MPA
Rocky Intertidal	20.5%	19.5%
Kelp Forest	-1%	23%
Rocky Reef (30 – 100m)	17%	26%

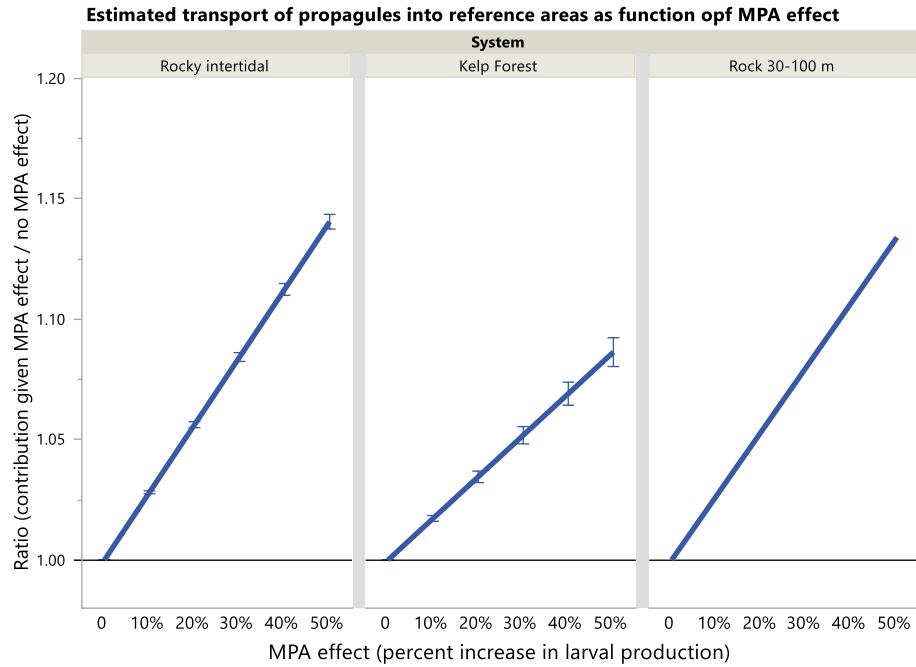


Figure 2: The relationship between MPA effect (percent increase in biomass leading to same percent increase in larval production) and contribution of propagules (from MPAs and reference areas) to reference areas (as a ratio of contribution based on MPA effect / contribution with no MPA effect).