Spatial ecological connectivity: what it is, why it's important, how to estimate it, and how to account for it in MPA networks

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What is a Marine Protected Area (MPA) "Network"?

Ecologically speaking...

A collection of MPAs that exchange a sufficient number of individuals to contribute to the persistence of populations, genetic composition, communities and ecosystems across that collection of MPAs

> This exchange of individuals is one form of "connectivity"

"Connectivity"

Spatial Ecological Connectivity

Four forms of connectivity:

1) Population (demographic)

2) Genetic

3) Community

4) Ecosystem

1) Population (demographic) connectivity

The movement of individuals between populations - metapopulations



Propagule (larvae, spores) dispersal is fundamental mechanism of connectivity (contrast with terrestrial and marine mammal populations)

1) Population (demographic) connectivity

The movement of individuals between populations - metapopulations



Propagule (larvae, spores) dispersal fundamental mechanism of connectivity (contrast with marine mammal dispersal)

2) Genetic connectivity

The movement of genes among populations



Propagule (larvae, spores) dispersal fundamental mechanism of connectivity (contrast with terrestrial and marine mammal populations)

3) Community connectivity

Movement of multiple species between communities - metacommunities



3) Community connectivity

Protection of multiple species across MPA networks



Data from Kinlan and Gaines 2003, PISCO 2007

Size:

- 5-10 km, minimum
- 10-20 km, preferred
- Intertidal to deep waters

Spacing:

- 50 100 km apart
- Size and spacing are interrelated
 - smaller MPAs should be closer together
 - larger MPAs may be spaced farther apart

4) Ecosystem connectivity

The movement of nutrients, materials and organisms between ecosystems



Encompass multiple ecosystems within individual MPAs

How do we estimate or measure connectivity?

- 1. Pelagic larval duration
- 2. Genetics: isolation by distance
- 3. Genetics: parentage analysis
- 4. Single or multispecies spatially explicit population models

1) Pelagic larval duration – a proxy for dispersal potential



Shanks et al. 2003 Ecological Applications

1) Pelagic larval duration – a proxy for dispersal potential Time in the larval stage (fish)

Western North American Coastal Fish	Time in Larval Stage midpoint (range)
Aurora Rockfish (Sebastes aurora)	105 (90-120)
Gopher Rockfish (S. carnatus)	75 (60-90)
Yellowtail Rockfish (S. flavidus)	85 (60-110)
Black Rockfish (S. melanops)	145 (110-180)
Blackgill Rockfish (S. melanostomus)	105
Blue Rockfish (S. mystinus)	105 (80-130)
Bocaccio (S. paucispinis)	160 (150 to 170)
Olive Rockfish (S. serranoides)	135 (90-180)
Kelp Bass (Paralabrax clathratus)	30 (25-35)
Spotted Sand Bass (P. maculatofasciatus)	22 (17-27)
White Seabass (Atractoscion nobilis)	32 (29-35)
Halfmoon (Medialuna californiensis)	60
Blacksmith (Chromis punctipinnis)	35 (32-38)
Garibaldi (Hypsypops rubicunda)	20 (18-22)
Rock Wrasse (Halichoeres semicinctus)	30 (26-34)
Senorita (Oxyjulis californica)	39 (36-43)
California Sheephead (Semicossyphus pulcher)	37 (34-52)
Giant Kelpfish (Heterostichus rostratus)	37 (14-60)
Blackeye Goby (Coryphopterus nicholsi)	70
Bluebanded Goby (Lythripnus dalli)	70
California Halibut (Paralichthys californicus)	27
Pacific Sanddab (Citharichthys sordidus)	271
Speckled Sanddab (C. stigmaeus)	219 (113-219)
Petrale Sole (Eopsetta jordani)	180









QJulie Standish

Genetics – Isolation by distance

Geographic distance = genetic difference



2) Genetics: Isolation-by-distance



Dispersal distances generated by estimates of isolation-by-distance



Number of Species

Data from Kinlan and Gaines 2003, PISCO 2007

Different estimates, similar results



Dispersal distances: algae= 0- 5 km; invertebrates = 0-100 km; fishes= 0-100's km

3) Genetics: Parentage analysis

Matching genetic "signatures" of parents, offspring, siblings



Yellow tang, reef fish



Christie et al 2010 Plos One

MPAs sampled for young
 Non- MPAs sampled for young
 MPA seeding unprotected populations

4) Single or multispecies spatially explicit population models

Information needs:

- Distribution of habitat "patches" or subpopulations
- Life history information for particular species spawning time, larval duration, demographic parameters, habitat affinity, etc.
- Larval dispersal from ocean circulation model (ROMS)
- Density-dependent post-settlement mortality
- Fishing fleet model follows ideal free distribution
- Potential MPAs or networks

4) Single or multispecies spatially explicit population models



Distribution of adults based on:

- Habitat
- Fishing (fleet model & MPAS)



Cabezon (Scorpaenichthys marmoratus) PLD = 105 d Spawns Nov-Mar



Brown rockfish (*Sebastes auriculatus*) PLD = 45 d Spawns Dec-Jun

White et al. (2013) Ocean & Coastal Management

Distribution of larval settlement based on:

- Currents and timing
- Suitable habitat

Generate connectivity matrices for each species





Cabezon PLD = 105 d Spawns Nov-Mar





Brown rockfish PLD = 45 d Spawns Dec-Jun



4) Single or multispecies spatially explicit population models

Multiple metrics can be used to evaluate individual MPAs and networks



Calculate response variable: regional population size(s), biodiversity across network **Compare:** alternative networks, impact of adding or removing individual MPAs

Summary

Multitude of approaches for estimating and applying connectivity

- separately or in combination
- depends on available information required for each
- depends on planning process
- different forms of connectivity will influence location, size,
 shape, number, spacing of MPAs
- trade-off between size and spacing
- implications for management inside and outside of MPAs
- evaluate and manage adaptively