Marine Life Protection Act Initiative

Spatial Bioeconomic Model Evaluation for the North Coast

Presentation to the MLPA Master Plan Science Advisory Team
December 17, 2009 • Eureka, CA

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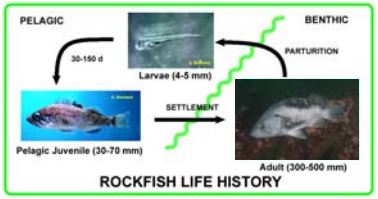
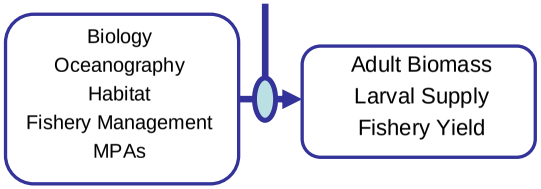
What Bioeconomic Models Do



Spatially Explicit Population Models



Why Models?

- Effective conservation requires MPAs that are
  a) sufficiently large to protect adults from harvest
  b) sufficiently large and close to capture enough larvae to persist
- Size and Spacing Guidelines (SSG): “model-based” threshold criteria focused on conservation benefits
- Spatially explicit models augment SSG by
  a) counting benefits of exceeding SSG (being larger or closer)
  b) evaluating contribution of MPAs that do not satisfy SSG
  c) simultaneously assessing conservation and economic consequences of MPAs
  d) accounting for context (e.g., fishery management, location of habitat within MPAs)

Model Inputs

- Geographic
  – Habitat maps
  – Proposed MPA boundaries and regulations
  – Ocean circulation (ROMS model output)
- Species-specific
  – Life history (growth, natural mortality, fecundity)
  – Adult movement (home range diameter)
  – Larval dispersal (pelagic larval duration, spawning season, some behavior)
  – Egg-recruit or settler-recruit relationship
- Fleet Response

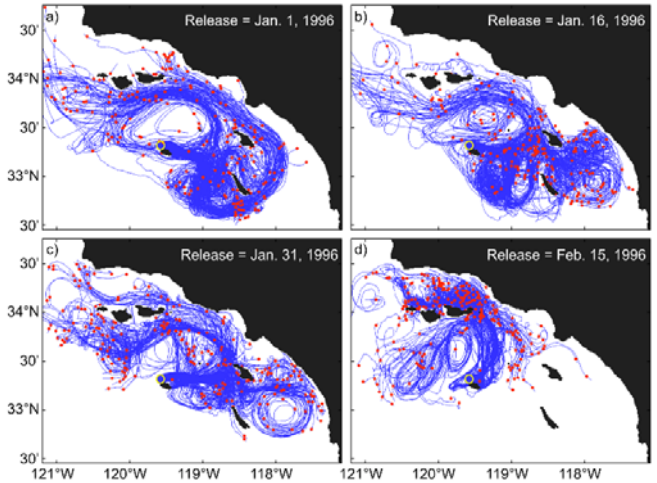
Fishing Fleet Model

- **Original Model:** Fleet responds to spatial abundance of fish
- **Revised Model:** Based on data compiled by EcoTrust where fleet responds to
  - spatial abundance of fish
  - distance from port
  - higher effort further south in south coast study region (UC Davis model only)

Model Species

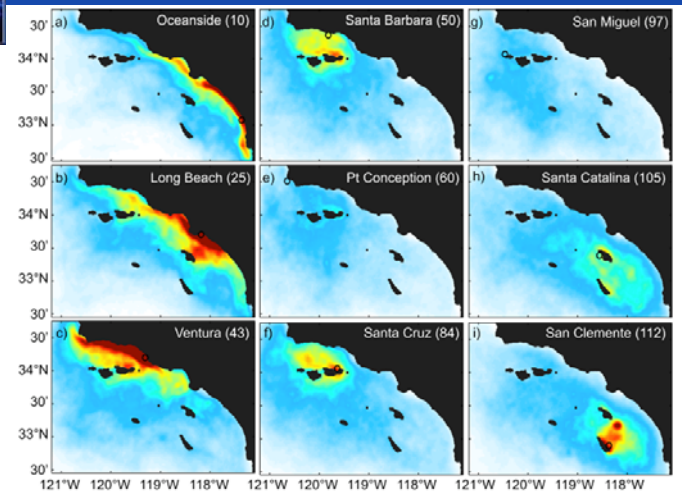
- **North Central Coast**
  - lingcod, black rockfish, canary rockfish, cabezon, California halibut, abalone
- **South Coast**
  - ocean whitefish, black surfperch, opaleye, kelp bass, California sheephead, kelp rockfish, red sea urchin, California halibut
- **Candidates for North Coast**
  - Dungeness crab, cabezon, various rockfishes (e.g., black, brown), red sea urchin, …?

Ocean Currents to Larval Transport



From S. Mitarai et al., (UCSB, UCLA)

Ocean Currents to Larval Transport



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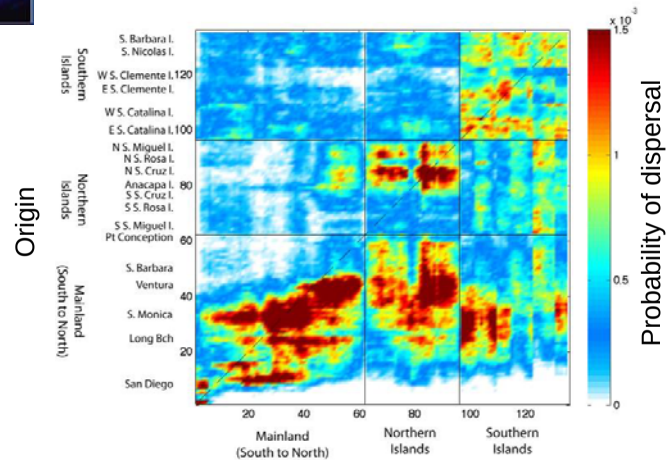
Ocean Currents to Larval Transport



From S. Mitarai et al., (UCSB, UCLA)

Model Outputs

- **Conservation**
  - Spatial distribution of larval settlement and biomass
  - Total settlement and biomass (summed over study region, weighted sum across species)
- **Economic**
  - Spatial distribution of fishery yield
  - Total fishery yield (summed over study region, weighted sum across species)

Model Outputs

- **Other Model Outputs**
  - Spatial distribution of fishing effort
  - Effective connectivity patterns that integrate larval production, dispersal, and settlement
- *All outputs are based on long-term equilibria*
- *Each output is calculated for a range of assumptions about future fishery management outside MPAs*[1]

[1]For complete list of assumptions, see evaluation methods document, Chapter 8, Appendix B.

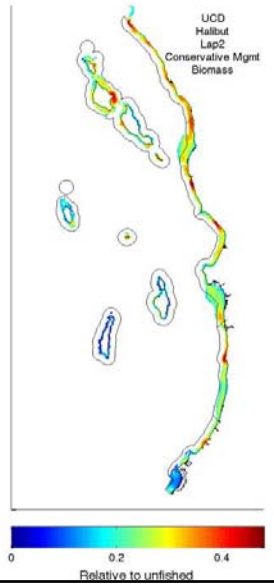
Model Results

Spatial Distribution of Biomass

(Maps also available for recruitment, fishery yield and fishing effort)

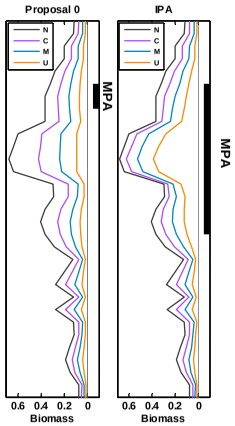
- **Example species**: Halibut
- **Example proposal**: Lapis 2
- **Management assumption***: Conservative management outside MPAs

*Also run for "unsuccessful management" and "Maximum Sustainable Yield" (MSY-type) management

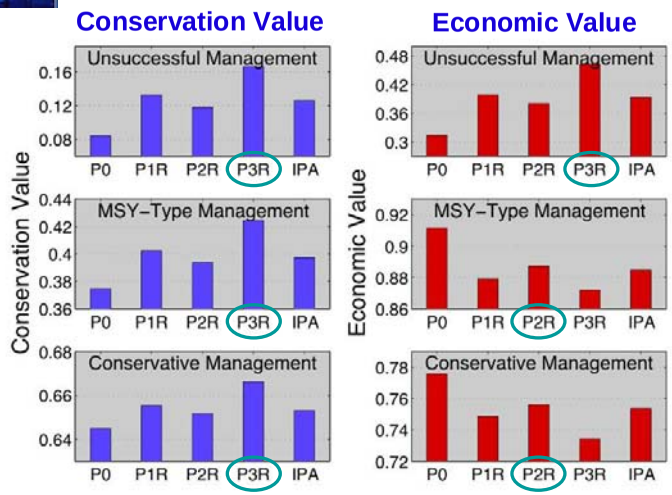


MPA Effects in Context

- Habitat and fishery management strongly influence distribution of biomass
- Fishing affects protected populations
  - Catch of adults near MPA boundary
  - Reduced larval supply from harvested areas
- Fishery likely to have important consequences for community structure within MPAs

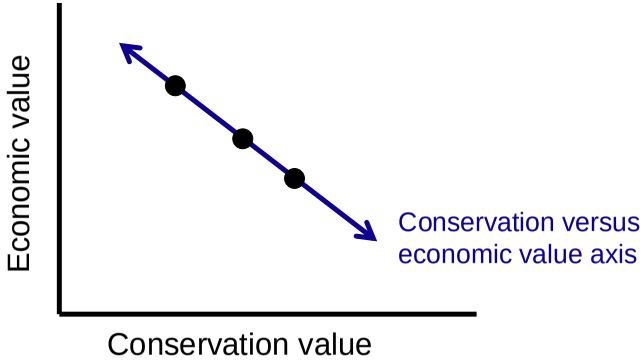


Proposal Rankings



South Coast Study Region UC Davis, Original Fleet Model

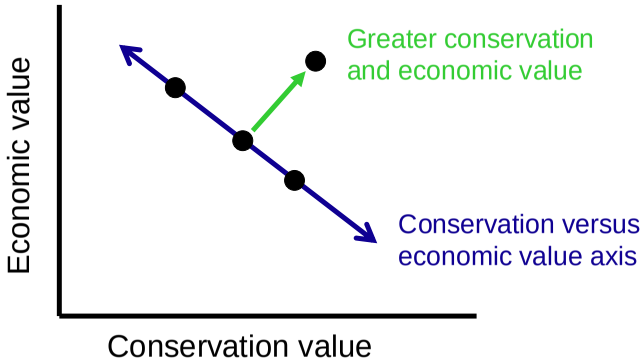
Model Results: Rankings in Context



- Choice along this axis is a matter of policy priorities

- Models can put the options in context

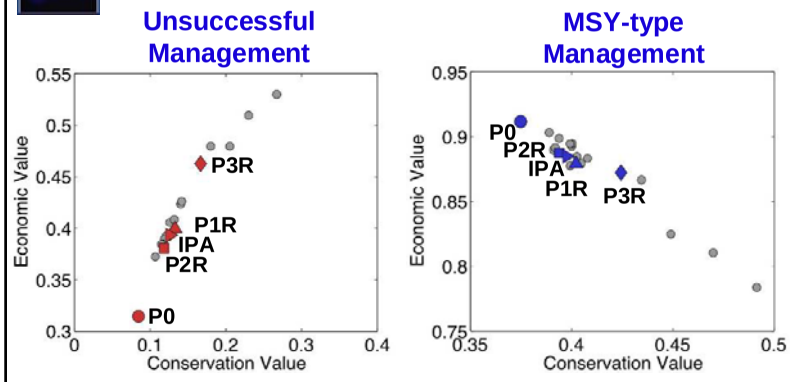
Model Results: Rankings in Context



- Models can reveal where one proposal is superior to another

- Most apparent under assumption of unsuccessful management

South Coast Proposal Rankings

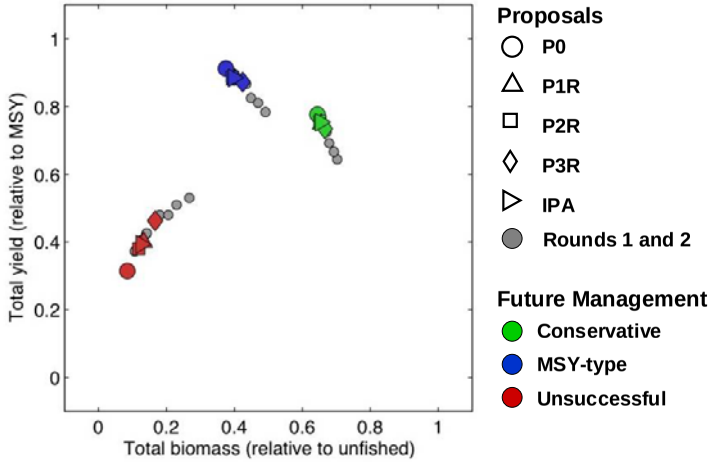


Proposals from Rounds 1 and 2

From South Coast Study Region, UC Davis, original fleet model

Effect of Fishery Management

South Coast Study Region, UC Davis, original fleet model



Proposals
- P0
- P1R
- P2R
- P3R
- IPA
- Rounds 1 and 2

Future Management
- Conservative
- MSY-type
- Unsuccessful

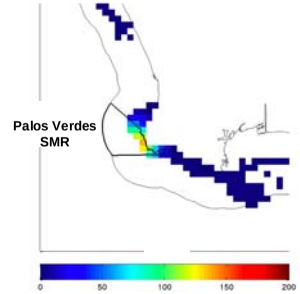
Model Results: Individual MPAs

- **Focus evaluation on role of individual MPAs in the context of their network**
- **Deletion analysis: How does removal of an individual MPA from an MPA network affect the expected consequences of the network?**
  - Spatial distribution of biomass and larval production
  - Overall conservation and economic measures
  - Connectivity

Model Results: Individual MPAs

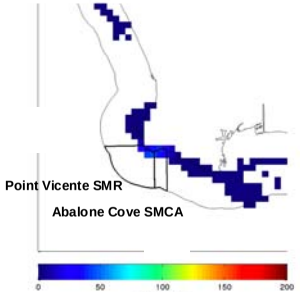
Does the MPA cause more larvae to be produced?

Proposal: P3R



Percent change in larval production (P3R compared to P0)

Proposal: IPA and P2R



Percent change in larval production (IPA and P2R compared to P0)

South Coast Study Region, UC Davis, original fleet model

Update: Supplemental Connectivity Metrics

- **Supplemental connectivity metric would:**
  - Build upon existing bio-economic models
  - Measure the rate or consequences of genetic transmission across the network (i.e., movement of a neutral allele across the coastline or implications for genetic structure)
  - Reveal "gaps" between proposed MPAs (Goal 6)
  - Provide useful information for MPA design
- **A connectivity metric would only be used to evaluate proposed MPA network components**
  - MPA spacing guidelines remain essential for initial design phase

Update: Supplemental Connectivity Metrics

Two approaches under development:

A) Neutral allele model with finite population size

B) Neutral alleles model with infinite population size

Both approaches:

- Perform calculation with and without fishing
- Comparison to unfished state accounts for natural barriers to gene flow
- Rationale: Can MPA network preserve natural levels of genetic connectivity?

Supplemental Connectivity Metric: A

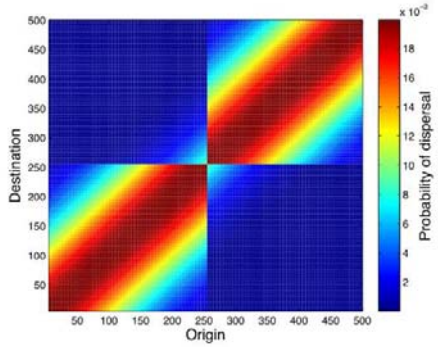
Two approaches under development:

A) Neutral allele model with finite population size

- Introduce new allele at patch *i*, calculate average number of generations for allele to spread to every other patch
- Transmission occurs by movement of finite individuals (stochastic)
- Metric: Percent increase in transmission time from unfished state

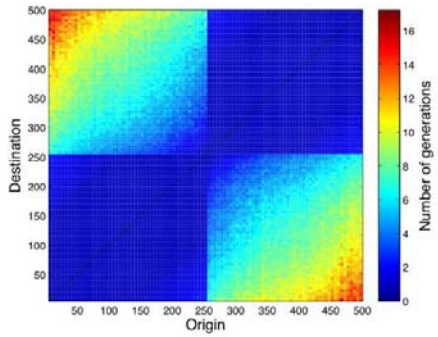
B) Neutral alleles model with infinite population size

Example Connectivity Scenario: Metric A



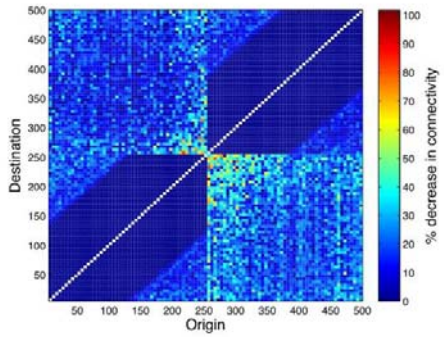
- 500 km coastline
- Diffusive larval dispersal (Gaussian)
- Connectivity break in the middle
- Simple scenario to examine usefulness of connectivity metrics

Results: Connectivity Metric A



- Unfished scenario
- Number of generations required for novel allele to move between each location

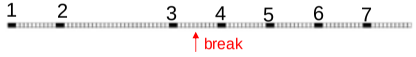
Results: Connectivity Metric A



- Change in connectivity from unfished
- Low values: MPAs preserve 'natural' connectivity
- High values: Connectivity is lower than in unfished state
- Large gap is very noticeable
- Note: No theoretical maximum on this scale, it just happens to go up to ~100% in this example

Results: Connectivity Metric A

Example MPA Array 1



Transmission from:

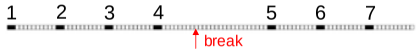
Transmission to:	1	2	3	4	5	6	7
7	0.21	0.21	0.13	0.11	0	0	0
6	0.21	0.13	0.30	0	0	0	0
5	0.18	0.26	0.30	0	0	0	0.01
4	0.30	0.24	**0.26**	0	0	0	0.17
3	0.17	**0.18**	0	**0.26**	0.19	0.16	0.16
2	0	0	**0.19**	0.11	0.15	0.11	0.09
1	0	0	0.25	0.12	0.12	0.08	0.19

Example MPA Array 1
MPA-by-MPA results

- Percent decrease in connectivity from unfished state
- Diagonal = self-connectivity
- Values just off diagonal = nearest neighbor
- Large gap produces large losses in connectivity

Results: Connectivity Metric A

Example MPA Array 2



Transmission from:

Transmission to:	1	2	3	4	5	6	7
7	0.16	0.20	0.18	0.10	0	0	0
6	0.22	0.13	0.14	0.21	0	0	0
5	0.16	0.20	0.19	**0.17**	0	0	0
4	0.14	0	0	0	**0.16**	0.13	0.15
3	0.01	0	0	0	0.18	0.14	0.18
2	0	0	0	0	0.18	0.08	0.14
1	0	0	0	0.14	0.19	0.21	0.29

Example MPA Array 2

- Large gap is now spanning natural connectivity break
- Decrease in connectivity (relative to unfished) less than in previous scenario
- Values just off diagonal = nearest neighbor

Supplemental Connectivity Metric: B

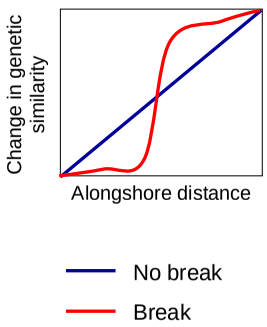
Two approaches under development:

A) Neutral allele model with finite population size

B) Neutral allele model with infinite population size

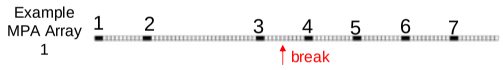
- Introduce different novel allele at each patch, allow new alleles to spread to other patches over fixed number of generations
- Measure allele frequencies after spread
- Metric: Similarity of locations
- Rationale: Can MPA network preserve natural patterns of genetic structure?

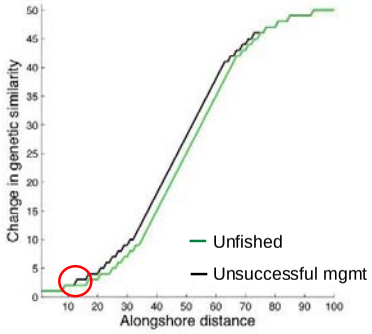
Premise: Connectivity Metric B



- Cluster locations by genetic similarity 50 generations after novel alleles are introduced
- Plot of change in similarity over space reveals genetic breaks
- No breaks: Similarity changes evenly across space ("isolation by distance")
- Breaks: Abrupt changes in similarity across break

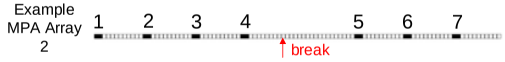
Results: Connectivity Metric B

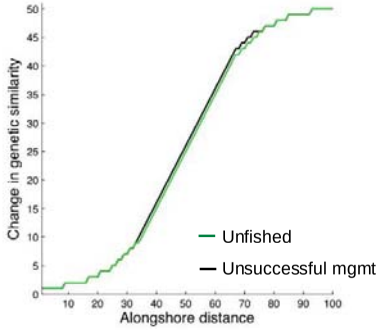




- Same dispersal scenario and Example MPA Array 1
- Metric B reveals natural break and deviation from natural connectivity due to MPA spacing in MPA Array 1
- Similar to Metric A result

Results: Connectivity Metric B





- Same dispersal scenario and Example MPA Array 2
- Metric B reveals natural break; wider MPA spacing over natural break does not change natural pattern
- Similar to Metric A result

Recommendation

- Both metrics show promise and are potentially complementary:
  - Metric A quantifies connectivity in terms of transmission rates
  - Metric B quantifies effect of connectivity in terms of genetic structure using graphical interpretation
  - Both metrics illustrate gaps between MPAs, accounting for natural variations in connectivity
- Recommendation: Continue developing both measures for review during next SAT meeting