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Marine Life Protection Act Initiative

Spatial Bioeconomic Model Evaluation for the North Coast

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Model Inputs

- **Geographic**
  - Habitat maps
  - Ocean circulation
  - Proposed MPA boundaries and regulations
- **Species-specific**
  - Life history (growth, natural mortality, fecundity)
  - Adult movement (home range diameter)
  - Larval dispersal (pelagic larval duration, spawning season)
  - Egg-recruit or settler-recruit relationship
- **Fleet response**
  - Spatial abundance of fish
  - Distance from port

North Coast Model Species

Tentative species list, pending availability of necessary parameter values, etc.

- Black rockfish
- Brown rockfish
- Cabezon
- Burrowing shrimp
- Dungeness crab
- Red abalone
- Red sea urchin

Model Outputs

- All outputs are based on long-term steady states—*What will the system look like 30 to 50 or more years from now?*
- Each output is calculated for a range of assumptions about future fishery management outside MPAs:
  - Conservative management
  - Maximum sustainable yield (MSY)-type management
  - Unsuccessful management

Model Outputs

- **Conservation**
  - Maps of larval settlement and biomass
  - Total biomass (summed over study region, weighted sum across species)
- **Economic**
  - Maps of fishery yield
  - Total fishery yield (summed over study region, weighted sum across species)
- **Other Model Outputs**
  - Maps of fishing effort
  - Maps of % change in larval production and successful larval settlement (measures of MPA effectiveness in maintaining larval connectivity)

Model Outputs: Individual MPAs

- **MPA-by-MPA results**
  - Biomass
  - Larval self-recruitment
  - Self-persistence
- **Deletion analysis**
  - How does removal of an individual MPA from an MPA network affect the expected consequences of the network?
  - Change in overall biomass if a given MPA were deleted

Update: Supplemental Connectivity Metrics

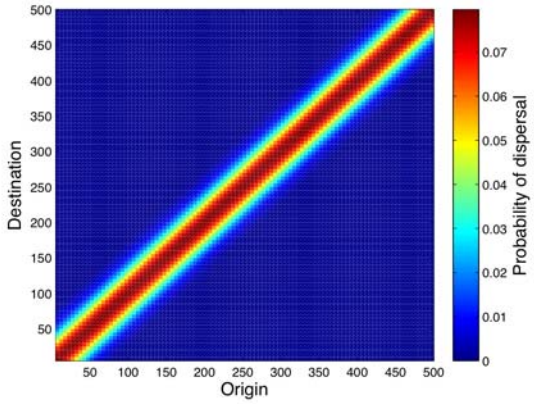
- **Supplemental connectivity metric:**
  - Builds upon existing bio-economic models
  - Measures the rate or consequences of genetic transmission across the network (i.e., movement of a neutral allele across the coastline or implications for genetic structure)
  - Reveals "gaps" between proposed MPAs (Goal 6)
  - Provides 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

Supplemental Connectivity Metric

- **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

Example Connectivity Scenarios

Dispersal kernel

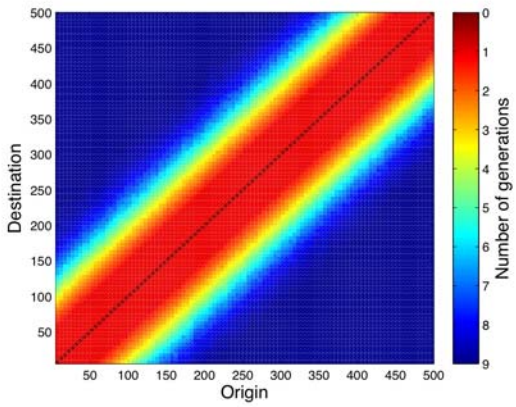


Scenario 1:

- 500 km coastline
- Diffusive larval dispersal (Gaussian)
- 25 km mean dispersal distance

Example Connectivity Scenarios

Genetic connectivity without fishing (# generations)

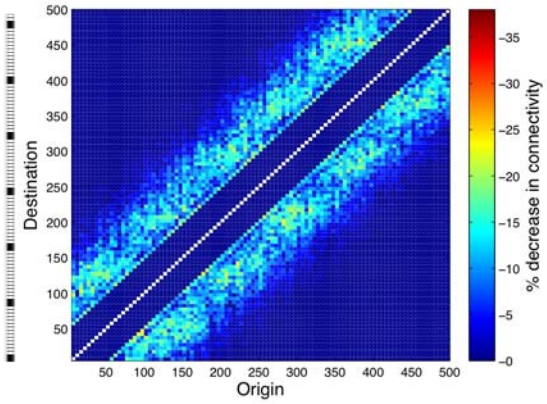


Scenario 1:

- 500 km coastline
- Diffusive larval dispersal (Gaussian)
- Pattern is similar to dispersal matrix

Example Connectivity Scenarios

Example MPA Array 1 (1 cell = 5 km)

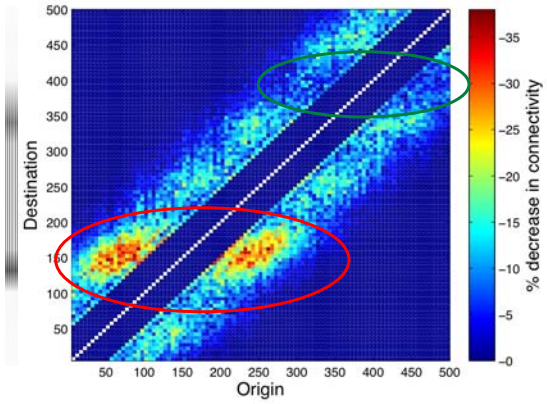


Scenario 1, with MPAs and fishing:

- MPAs have 70 km spacing (within guidelines)
- Dark blue = OK; no change from unfished state
- Warmer colors = decrease in connectivity relative to natural state; MPA configuration has a gap
- For Scenario 1, most values < 20% decrease in connectivity; no big gaps stand out

Example Connectivity Scenarios

Example MPA Array 2 (1 cell = 5 km)

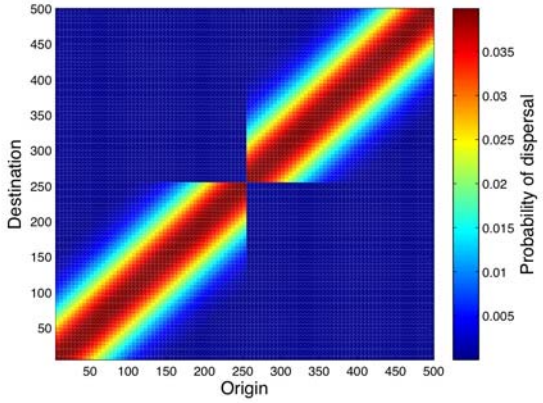


Scenario 1, with MPAs and fishing:

- MPAs have 70 km spacing; except:
  - 1 big gap (120 km)
  - 1 small gap (20 km)
- Dark blue = OK
  - 20 km gap moves system closer to natural connectivity
- Warmer colors = decrease in connectivity
  - 120 km gap produces a connectivity break, relative to unfished state

Example Connectivity Scenarios

Dispersal kernel

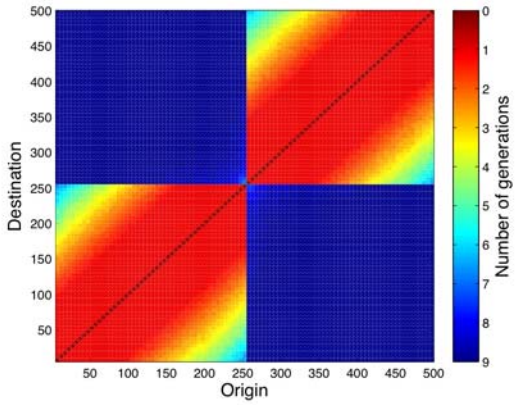


Scenario 2:

- 500 km coastline
- Diffusive larval dispersal (Gaussian)
- Natural break in connectivity

Example Connectivity Scenarios

Genetic connectivity without fishing (# generations)

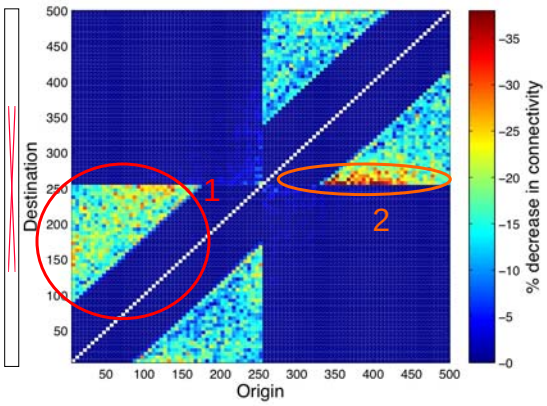


Scenario 2:

- 500 km coastline
- Diffusive larval dispersal (Gaussian)
- Pattern is similar to dispersal matrix
- Two well-connected cells separated by natural gap

Example Connectivity Scenarios

Example MPA Array 3 (1 cell = 5 km)

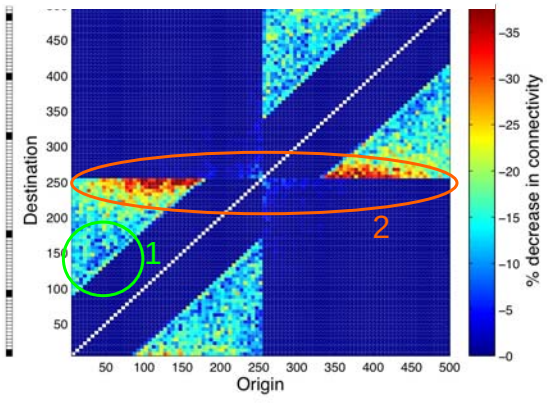


Scenario 2, with MPAs and fishing

- MPAs have 75 km spacing (within guidelines)
  - 1 big gap (130 km)
- Dark blue = OK
- Warmer colors = decrease in connectivity
- Connectivity break in 'southern' region because of big gap between MPAs (1)
- Some decrease in connectivity near natural connectivity break (2)

Example Connectivity Scenarios

Example MPA Array 3 (1 cell = 5 km)



Scenario 2, with MPAs and fishing

- MPAs have 75 km spacing (within guidelines)
  - 1 big gap (130 km) spanning natural break
- Dark blue = OK
- Warmer colors = decrease in connectivity
- Better connectivity within the two regions (1)
- Large decrease in connectivity near natural break. Despite natural break, need closer spacing (2)

Recommendation

- The metric quantifies connectivity in terms of transmission rates.
- The connectivity metric highlights the effect of gaps between MPAs, accounting for natural variations in connectivity.
- Recommendation: Use this evaluation as a supplement to the existing spacing evaluation.
  - Visualize connectivity across entire network, not just maximum gap
  - Accounts for spatial heterogeneity in dispersal (e.g., natural breaks)
  - Useful in revising MPA arrays, but in current form does not lend itself to quantitative ranking