California MLPA Master Plan Science Advisory Team
Responses to Science Questions Posed during MLPA Public Meetings from January 20 to February 11, 2010

Revised March 17, 2010

This document contains science questions posed to the Marine Life Protection Act (MLPA) Master Plan Science Advisory Team (SAT) during its meetings on January 20-21 and February 11, 2010 and at the MLPA North Coast Regional Stakeholder Group (NCRSG) meeting on February 8-9, 2010. Draft responses were developed by SAT work groups with assistance from MLPA Initiative staff. The SAT approved these responses at its meeting on March 16-17, 2010. Additional responses to science questions posed to the SAT were integrated into the *Draft Methods Used to Evaluate Marine Protected Area Proposals in the North Coast Study Region* (draft evaluation methods document) and will be included in presentations to the NCRSG on March 24-25, 2010.

Questions about MPA Size and Spacing

1. ***What are the benefits and limitations of several small MPAs versus fewer larger MPAs? Would fewer large MPAs better meet the goals of the MLPA? Can the distance between MPAs be longer if the MPAs at either end are larger?***

   Draft Response: The MPA size and MPA spacing guidelines described in the *California Marine Life Protection Act Master Plan for Marine Protected Areas* address several goals of the MLPA. The guidelines for MPA size are based on home range sizes of adult fish and invertebrates and are responsive to the goals (1) "to protect the natural diversity and abundance of marine life" and (2) "to help sustain, conserve and protect marine life populations." The guidelines for MPA spacing are based on known dispersal ranges of fishes, invertebrates and seaweeds and are responsive to goal 2 and goal 6, "to ensure that the state's MPAs are designed and managed, to the extent possible, as a network."

   A tradeoff must be made between MPA size and spacing to simultaneously address multiple goals of the MLPA. A few large MPAs (larger than the upper bound of the SAT's preferred size range at 36 square miles) could be designed to meet the MLPA goals 1 and 2. However, if the large MPAs are widely spaced, they may not be connected through exchange of larvae and may not operate as an ecological network (goal 6). Several smaller MPAs could be designed to enhance connectivity between MPAs and thus address a variety of MLPA goals to protect marine life, sustain marine life populations and simultaneously function as an ecological network. The SAT will conduct an evaluation of MPA size so that designers and planners can assess the numbers of MPAs established at sizes within and below the minimum size range (9-18 square miles), and within or above the preferred size range (18-36 square miles).

   Another goal of the MLPA is (4) "to protect marine natural heritage, including protection of representative and unique marine life habitats…" Representation of marine habitats in a network of MPAs will influence their size and spacing. A large MPA may contain a variety of representative habitats if it is established in an area of high habitat diversity. However, if habitats are located in different places throughout the study region, a large MPA may contain fewer habitats than several small MPAs located in places where different habitats occur. The SAT will conduct an evaluation of habitat representation in proposed MPAs so

designers and planners can assess the number of marine habitats are protected and the sizes of protected habitat patches.

Science guidance in the master plan for MPAs states that, "for an objective of lessening negative impact while maintaining value, placement of MPAs should take into account local resource use and stakeholder activities." A very large MPA may have greater potential socioeconomic impacts on single community in the study region while a network of smaller MPAs likely will reduce the potential socioeconomic impacts to any single community and distribute the potential impacts across a greater number of communities. The SAT will conduct evaluations of potential negative economic impacts to commercial and recreational fisheries in the north coast study region. Any fisheries or ports with disproportionate impacts will be noted in the evaluation.

There is a tradeoff between MPA size and MPA spacing, such that smaller MPAs must be closer together and larger MPAs may be spaced further apart to achieve similar conservation outcomes. The SAT will conduct a modeling evaluation for a suite of representative species to assess the biomass produced and fishery yield from all proposed MPA networks. The modeling evaluation takes into account the actual sizes and spacing of all MPA proposals, including proposals with only a few large and widely-spaced MPAs. From previous evaluations using the models in other study regions, the SAT identified three key variables related to the production of biomass: (1), individual MPA size, (2) total area protected in MPAs, and (3) potential for production outside MPAs. The total area protected in MPAs contributes most to biomass production. Fewer large MPA may contribute to high biomass and persistent local populations (goal 2) but without connectivity between MPAs, they may not function as an ecological network (goal 6).

Additionally, for the north coast study region, the SAT will estimate genetic connectivity between MPAs in each proposal, based on numerical models of ocean circulation in the study region. The metric of genetic connectivity takes into account the number of generations required for an allele to move from one side of the study region to the other—and from one MPA to the next. In some places, movement of alleles may be possible across distances longer than the recommended spacing guidelines, while in other places the potential for movement of alleles may be much reduced due to biophysical barriers (such as ocean currents, fronts, eddies, gaps in suitable habitats, etc.).

Science guidance in the master plan for MPAs states that, "for an objective of providing analytical power for management comparisons and to buffer against catastrophic loss of an MPA, at least three to five replicate MPAs should be designed for each habitat type within a biogeographical region." The northern biogeographical region extends from Point Conception to the California-Oregon border. Additionally, the SAT recommended at least one replicate MPA in each bioregion; there are two bioregions in the north coast study region: (1) from the California Oregon border to the mouth of the Mattole River, and (2) from the mouth of the Mattole River to Alder Creek near Point Arena. To incorporate this science guidance, designers must include several MPAs in a network that accounts for the biogeograhical and bioregional differences across the state and the study region. The SAT

will evaluate the number of habitat replicates protected in each bioregion of the north coast study region.

Depending on the frequency and magnitude of disasters and catastrophes in the study region, MPAs may be designed to offset some of the negative impacts of these events (Allison et al., 2003). For example, if oil spill from tankers is a risk in the study region, a network of several smaller MPAs likely will result in continuous protection of a greater area over the long-term than a single large MPA because an oil spill likely would affect only one or a few of the MPAs, while others would continue to sustain, conserve and protect marine life populations. The SAT does not complete a formal evaluation of risk posed by disasters and catastrophes on the MPA proposals.

2. The SAT seems to have two minimum size guidelines: for overall size and for replicate size. How does the SAT evaluate a large MPA that has a very small amount of a particular habitat type?

Draft Response: The science guidance in the master plan for MPAs is to design MPAs that are at least 5-10 kilometers (km) (3-6 miles or 2.5-5.4 nautical miles) and preferably 10-20 km (6-12.5 miles or 5.4-11 nautical miles) alongshore for an objective of protecting adult populations, based on adult neighborhood sizes and movement patterns. Additionally, MPAs should extend from the intertidal zone to deep waters offshore for an objective of protecting the diversity of species that live at different depths and to accommodate the movement of individuals to and from shallow nursery or spawning grounds to adult habitats offshore. The SAT will evaluate the numbers of MPAs and MPA clusters (contiguous MPAs) that have at least a moderate-high level of protection and that are below or within the minimum recommended area of nine to 18 square miles, and within or above the preferred size range of 18 to 36 square miles. The evaluation methods for MPA size are fully described in Chapter 6 of the draft evaluation methods document. The SAT also identified the need for a minimum size for protected patches (or replicate) of each key marine habitat. The minimum size of each replicate is estimated by using a known species-area relationship from empirical data. The SAT determined that at least 90% of the species associated with a particular habitat should be represented in a replicate. The draft minimum replicate sizes for the north coast study region are shown in Table 1.

Table 1. Amount of habitat in an MPA necessary to encompass 90% of local biodiversity *(From Evaluation Methods)*

Habitat	Amount of habitat needed to encompass 90% of biodiversity	Data Source
Rocky shores and offshore rocks[a]	0.55 linear miles	PISCO Biodiversity
Nearshore rocky reefs and kelp forest (0-30 m)	1.1 linear miles *including the full 0-30m depth zone*	PISCO Subtidal

Habitat	Amount of habitat needed to encompass 90% of biodiversity	Data Source
Rocky reef 30-100 m	0.13 square miles	Starr Surveys
Rocky reef 100-3000 m	0.13 square miles	Starr Surveys
Beaches	1.1 linear miles	*See below*
Soft bottom 0-3000 m [b] *(includes replicates of 0-30m, 30-100m and >100m soft bottom)*	10 square miles total mapped soft bottom Distributed across depth zones including at least: 1.1 mi 0-30m 5 sq mi 30-100m 1 sq mi >100m	NMFS trawl surveys, 1977-2007
Soft bottom 0-100 m [b] *(includes replicates of 0-30m and 30-100m soft bottom)*	7 square miles total mapped soft bottom Distributed across depth zones including at least: 1.1 mi 0-30m 5 sq mi 30-100m	NMFS trawl surveys 1997-2007
Soft bottom 0-30 m *when not combined with other depth zones*	1.1 linear miles *including the full 0-30m depth zone*	*See below*
Soft bottom 30-100 m [c] *when not combined with other depth zones*	7 square miles	NMFS trawl surveys 1997-2007
Soft bottom >100 m [c] *when not combined with other depth zones*	17 square miles	NMFS trawl surveys 1997-2007
Estuarine Habitats [d]	0.12 square miles (77 acres) total estuarine area Distributed across estuarine habitats including at least: 0.04 sq mi coastal marsh (25 acres) 0.04 sq mi eelgrass (25 acres)	SONGs sampling

[a] *The SAT recommended a minimum replicate size of 0.55 linear miles of either rocky shores, oroffshore rocks, or some combination thereof. The SAT will evaluate the size of each protected patch of both habitats to provide additional information and distinguish the contribution of each.*

[b] *Trawl survey data indicate that large amounts of soft bottom habitat are required to encompass 90% of biodiversity if each depth zone is replicated independently. Since soft bottom associated species tend to utilize multiple depth zones, the SAT recommends that soft bottom habitats across multiple depth zones are included in the same MPA or MPA cluster.*

[c] *During its meeting on March 16-17, 2010, the SAT identified the need to review other datasets that might help to inform the minimum replicate size for soft bottom 30-100 m and 100-3000 m depths. The SAT recognized that the minimum replicate sizes for these habitats may have been overestimated because estimates of minimum replicate sizes were based on National Marine Fisheries Service trawl data, which were comprised entirely of fish species. The SAT will review the analysis of other datasets at its meeting on May 12, 2010 and share at that time any further guidance about the replicate size for soft bottom 30-100 m and 100-3000 m.*

[d] *Estuarine habitat replication thresholds are based upon data from small coastal estuaries in the south and central coast regions and may not be applicable to the large estuarine areas in Humboldt Bay.*

The SAT will conduct an evaluation of the number of replicates of each key habitat type in proposed MPAs in each bioregion of the north coast study region. The evaluation methods for habitat replication are described more fully in Chapter 5 of the draft evaluation methods document. If an MPA or MPA cluster of minimum or preferred size contains a patch of a key habitat that is less than the minimum replicate size, the MPA will not be counted as protecting that key habitat. If the minimum replicate size is met for the key habitat, it will be considered in the evaluation of habitat replication.

Questions about Modeling

3. Is there a way to incorporate the defacto deep water refugia for abalone?

Draft Response: Species that are harvested by hand may effectively be protected from fishing below the depths that can be accessed by divers. For example, in the modeling evaluation for the south coast study region, the SAT modeling team accounted for the limited depth range of urchin divers by assuming sea urchins living below 30 meters (m) depths were protected from fishing. A similar assumption will be applied in the modeling evaluations for the north coast study region.

Similar deep water refugia may exist for red abalone in the north coast study region because red abalone occur from the intertidal to about 24 m deep, and few free divers can access abalone at the lower end of that depth distribution. However, we are unable to resolve these potential refugia due to limitations of the available habitat maps. In order to detect these refugia, we would need to be able to identify areas of hard substrate between 15 m (where free diving becomes more difficult) and 24 m. Unfortunately, current habitat maps classify all hard substrate between 0 and 30 m into one category so it is not possible to identify refugia less than 30 m. Additionally, any refugia are likely to be small relative to the 1 square kilometer scale at which the model runs, and so the potential deep water refugia for abalone would be inadequately represented in the modeling evaluation. In contrast, deep water refugia for red urchin are often spatially extensive and can be easily quantified at an appropriate scale in the modeling evaluation.

4. How does the SAT take into account the fishing days available?

Draft Response: The modeling evaluation, described in Chapter 8 of the draft evaluation methods document, does not directly incorporate fishing days available or the number of fishermen. While it is true that there are fewer fishermen and fewer fishing days in the north coast study region relative to other regions of California, what is important to the sustainability of fisheries is not the total number of person hours fished but the total fishing effort *relative to* the level of fishing that the targeted fish or invertebrate population can sustain. Different fisheries can sustain different levels of harvest, so it is more useful for the models to express fishing effort in a relative way. Therefore, the model represents overall fishing effort relative to biological reference points used in traditional fisheries management. That is, fishing effort is represented in terms of being less than, greater than, or nearly equal to the level that would produce maximum sustainable yield (MSY) for that fishery.

Various fisheries in the north coast study region have experienced each of those general conditions in the past, and it is possible that they also could experience them in the future, depending on future management decisions and socioeconomic conditions. By representing fishing in this general way, the models can be used to forecast the effects of the MPAs well into the future under different fishery management regimes, without having to account for possible changes in the number of fishermen or other factors.

5. What are the confidence intervals around the "single point estimates" for conservation value?

Draft Response: The bioeconomic model is a deterministic one, which means that for any given set of inputs, the output is non-stochastic (i.e., it is not a random variable). However, when model inputs change, the outputs also will change. The question raises two important issues: (a) Why do we want a confidence interval around the point estimate and (b) how would the point estimates change with different inputs to the model (i.e., how "certain" are we of the point estimates)? The responses to each of these questions follow.

a. *Why do we want a confidence interval?* The main use of the bioeconomic model is to compare different MPA proposals against each other and against the status quo. The models also allow us to examine tradeoffs (and spatial results), for example, between economic and conservation metrics. However, question 5 focused specifically on "conservation value" results. For comparing conservation outcomes across different MPA proposals, the key question is how the proposals rank in conservation outcome. To conduct a ranking, we do not require confidence intervals over the point estimates; we require a measure of how robust the ranking is to model inputs. Therefore, it is the ranking of proposals that is the focus, rather than the quantitative results. [A possible secondary use of the model (not yet implemented or approved by the SAT) is to generate numerical predictions about what we would expect (for example, in biomass within a particular MPA) over time after an MPA network has been implemented. In this case, confidence intervals over the outcomes would be useful.]

b. *How sensitive are point estimates (and ranking) to model inputs?* The key issue here is: if a different set of input parameters was used (for example, if the pelagic larval duration of a species was actually 40 days instead of 20 days), how would that affect the point estimate of conservation value (biomass) and how would it affect the ranking of MPA proposals. We routinely conduct a rigorous sensitivity analysis on the model. The main mechanism for doing so is to model several (up to 10) "model" species, each with different life-history traits, to assess how each MPA proposal ranks for each model species. The species are chosen, in part, to represent a wide range of life history traits of species that live in the study region. The modelers also conduct similar sensitivity analysis on non-biological inputs, such as fishing pressure outside MPAs and how the fleet responds to spatial closures. All of these results will be provided to the stakeholders and the BRTF so they can assess how sensitive any model outputs (including conservation value) are affected by different model input

assumptions. Our experience in previous rounds is that changing model inputs (within reasonable ranges) typically will affect the quantitative predictions for conservation value, but seldom affects the ranking of proposals for conservation value.

6. Does change in alleles in the (connectivity) model translate to actual ecological and/or genetic effects?

Draft Response: The rationale behind developing the genetic connectivity model is to address goal 6 of the MLPA, which requires that MPA arrays be designed as a network. One aspect of biological networks is genetic connectivity. Genetic connectivity typically is assessed by measuring the relative frequency of so-called "neutral alleles" in different locations. Neutral alleles are genetic markers that do not directly affect the survival or fitness of an organism, so they are indicators of a genetic signature that is unaffected by natural selection. Two subpopulations that are not genetically connected typically have very different frequencies of neutral alleles in their gene pool, simply due to the random accumulation of different neutral alleles over time. Well-connected subpopulations will tend to exchange neutral alleles more frequently, and will have similar allele frequencies.

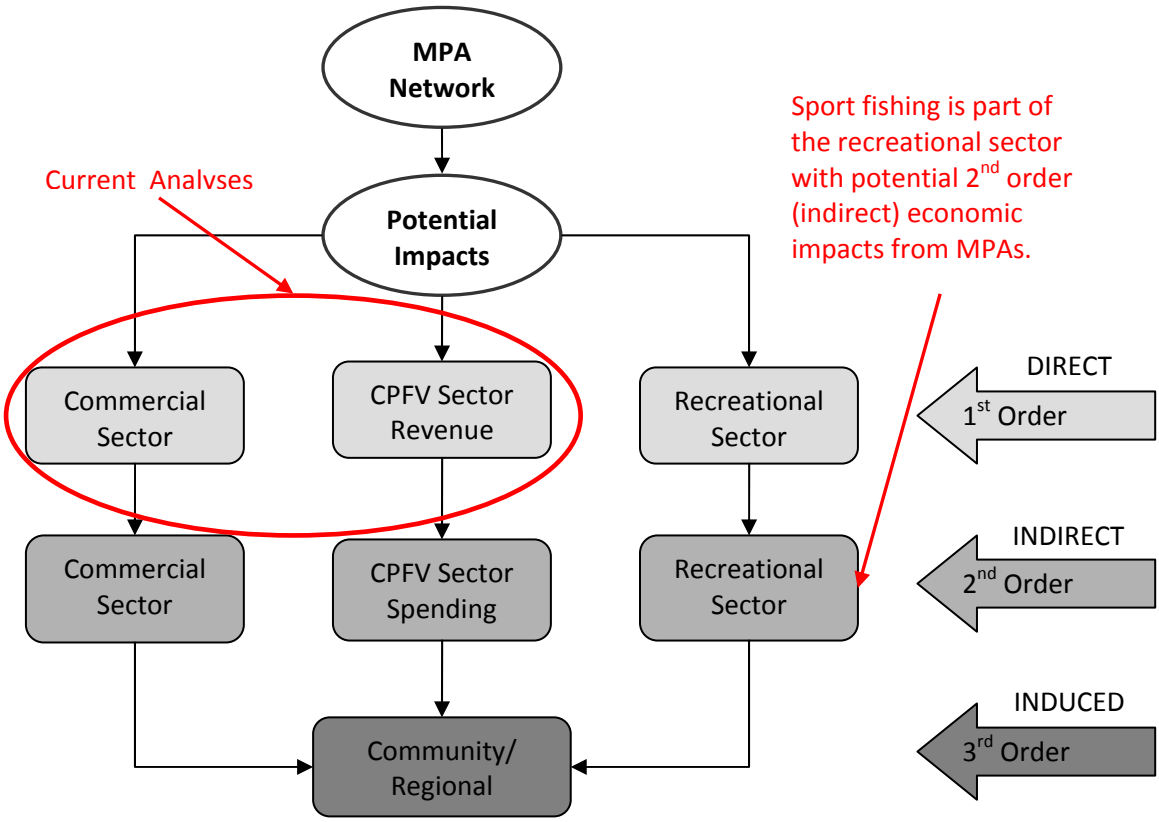
In order to represent this type of genetic connectivity, the genetic model simulates the movement of neutral alleles among locations along the coast. The model determines how many generations it would take for a neutral allele to move between two locations, which is an indication of how similar their allele frequencies would be in the ocean. Thus, the genetic model represents the same type of genetic processes that can be measured in the ocean. However, scientists lack high-resolution estimates of present-day neutral allele frequencies for species in the north coast. Without knowing the starting conditions, it is not possible for a model to produce estimates of allele frequencies that could be compared to real-world estimates. So, while the model gives an indication of how genes move in an MPA array and where barriers to allele transmission might occur, it cannot directly predict what allele frequencies will be in the future. Therefore, the direct answer to question 6 is "no", although in a broader sense the connectivity model does represent our best understanding of real genetic processes.

Additionally, it is important to point out that the type of genetic connectivity considered here does not translate into ecological effects on short timescales (within a human lifetime). That is, locations with poor connectivity will not have noticeably different populations of a particular species. Rather, over much longer time scales (evolutionary time), disconnected populations of a single species may diverge into genetically distinct units and eventually become different species.

Questions about Socioeconomics

7. Does the SAT consider potential economic impacts to sport fishing?

Draft Response: The survey conducted by Ecotrust included commercial fisheries and commercial passenger fishing vessel (CPFV) sector in the north coast study region. Ecotrust did not survey private vessels engaged in sport fishing. By definition, individual private recreational activities are not businesses, so therefore there are no direct impacts to profits. The graphic below illustrates the distinction between potential direct and indirect or induced impacts of MPAs on consumptive uses.



Questions about Tribal Uses

8. How will the SAT do an analysis of tribal uses if it is not known what is going on where?

Draft response: If no information on proposed or current tribal uses is available, the SAT may rely on best available information on traditional tribal uses from the scientific literature to conduct socioeconomic and ecological evaluations when possible. The SAT Tribal Work

Group would like to be able to incorporate information about tribal uses into its evaluations and, with input from members of tribes and tribal communities, is developing "guidelines for sharing information about tribal uses." These guidelines can be used by tribes and tribal community members and other knowledge holders, and by SAT members, their students and MLPA staff who may be engaged in documenting information about tribal uses in the north coast.

Information on tribal uses may be shared in a variety of ways, including sharing knowledge at SAT Tribal Work Group meetings, with individual SAT members, through the SAT Tribal Work Group listserv (MLPA_TribalSAT@lists.resources.ca.gov), with MLPA staff, and through the MLPA public comments email address (MLPAcomments@resources.ca.gov). The SAT Tribal Work Group also will compile historical data on tribal uses documented in the scientific literature to achieve a greater understanding of and perspective on current and historical tribal practices. If possible, the work group would like to connect the information about tribal uses to the geography of the north coast in order to identify any locations where there are gaps in knowledge.

The MLPA Initiative and MLPA North Coast Regional Stakeholder Group (NCRSG) already are beginning the second round of a three-round planning process for the north coast study region. As information about tribal uses becomes available, the NCRSG can begin integrating it into the design of MPAs for the north coast study region while the SAT and MLPA staff will work toward integrating it into evaluations of MPAs. The SAT will continue to evaluate habitat representation, habitat replication, MPA size, MPA spacing, biomass and fishery yield from bioeconomic models, birds and mammals, potential negative impacts to commercial and recreational fisheries, and water quality in proposed MPAs for rounds 1, 2 and 3. Information on tribal uses may be integrated into the process of MPA design by the NCRSG and/or SAT evaluations, accounting for any potential limitations due to the availability, format, spatial and temporal extent, or confidentiality of the data.