Home range parameter estimation for SQO Indicator Fish Species

February 27, 2011

I. Introduction

Background
The Sediment Quality Objectives (SQO) indirect effects assessment determines whether sediments meet California's narrative SQO for human health: ***Pollutants shall not be present in sediments at levels that will bioaccumulate in aquatic life to levels that are harmful to human health***. This program determines whether sediment contamination at a site results in an unacceptable health risk to humans because of the consumption of contaminated fish and shellfish (i.e., seafood). Evaluation of the narrative SQO involves two assessment questions:

- Do pollutant concentrations in seafood pose unacceptable health risks to human consumers?
- Is sediment contamination at a site a significant contributor to the seafood contamination?

These questions are evaluated using two indicators: Consumption Risk and Sediment Contribution. For the consumption risk indicator, seafood contamination measurements from the site are used to determine risk posed to local seafood consumers. For the sediment contribution indicator, the same seafood contamination measurements are compared to estimated seafood concentrations that would result from local site exposure. Estimated site exposure is calculated using a bioaccumulation model. The data collection and bioaccumulation model for the assessment framework are organized based on a dietary guild approach. Eight dietary guilds are defined, and model parameters are developed based on representative species for each dietary guild (SQO Science Team 2010). A Decision Support Tool (DST) has been developed to efficiently perform calculations in the assessment framework.

The sediment contribution indicator determines the contribution of sediments from a particular site to seafood tissue concentrations at that site. This sediment contribution is calculated as the product of sediment chemical concentration, a bioaccumulation factor, and a site use factor. The site use factor is the size of the site divided by the home range of the seafood. If the home range of the seafood species is less than the site area, the site use factor is set to one (Hope 1995; Suter II 2006).

Home range
Home range is defined as follows:

- **Home range:** *the estimated spatial area that an animal covers during its adult lifetime foraging activity*

Sensitivity analyses performed by the SQO Science Team have identified home range as a potentially influential parameter for the sediment contribution evaluation. However, seafood home range is difficult to estimate and local data are typically unavailable. To

facilitate the SQO indirect effects assessment, the home ranges of the indicator species for each dietary guild have been determined based on available information.

The purpose of this document is to describe home ranges that are incorporated into the SQO Decision Support Tool (DST). As with other aspects of the assessment (e.g., consumption rate, food web structure), the user may also incorporate available local data on species home range in lieu of the parameter estimates provided here.

Home ranges were included in the DST as statistical distributions, rather than point estimates. Probability distributions were used to address the uncertainty of home range estimates, and their importance for the assessment outcome. The DST calculates a separate home range probability distribution for each indicator species used in the framework. The use of multiple probability distributions accounts for the wide variability among fish species in movement behavior. Home range was estimated for the nine indicator species developed to depict dietary guilds (SQO Science Team 2010): California halibut, spotted sand bass, white croaker, queenfish, shiner perch, white catfish, common carp, topsmelt, and striped mullet.

Within each species, the probability distribution depicts the variability in movement among individuals, with some individuals remaining in the site, and others moving off site. The distribution for each species was estimated based on differences among individuals within that species. The shape of the distribution was inferred based on patterns in home ranges across estuarine and nearshore marine species.

The home range statistical distributions employed in the DST were selected based on observed variability in home range for the indicator species or similar species, obtained from published literature and technical reports. The remainder of this document describes the home range statistical distributions that were used, and the methods and rationale for their selection.

II. Methods

Several types of date were used to estimate home ranges of guild indicator fish species. These data include direct results of telemetry studies, results from tagging or contamination studies from which home range could be estimated, or home range information for similar California species combined with recommendations provided by local experts. When available, the preferred method for estimating home range is telemetry studies that directly measure and record movement of individual fishes. Acoustic telemetry is appropriate for marine systems, whereas both acoustic and radiotelemetry may be used in freshwaters (Lowe & Bray 2006). Both methods indicate the home range area for a species. In the absence of species specific measurements, home range was estimated based on extrapolation of data for similar species. Telemetry data were used to estimate home range for four guild indicator species: white croaker, queenfish, shiner perch, spotted sand bass, and common carp.

When telemetry-based measurements were unavailable for a species or similar species, home range was estimated based on movement distance information obtained from tag-recapture studies. In these studies, fish are individually marked with numeric tags and released, and the distance traveled by recaptured fish is recorded (Idyll & Sutton 1952; Borgeson & McCammon 1967; Tupen 1990; Domeier & Chun 1995; Lowe & Bray 2006). Tag-recapture studies were used for three guild indicator species: California halibut, striped mullet, and white catfish.

Tag-recapture studies provide information on linear distance traveled, rather than home range area. Determination of a home range area based on linear movement distance would require assumptions regarding the dimensions of the foraging area. Since the shape of the foraging area is unknown, tag-recapture based movement ranges were represented as a distribution of linear movement distances. In the assessment simulations, linear movement distances simulated from this distribution are compared to the distance across the assessment site (i.e., site length), to obtain site use factor. The site length measurement is obtained along the longest axis of the site.

Tag-recapture studies also produce conservative estimates of site use factor because these studies sometimes underestimate movement distance, due to increased sampling of areas nearer the release point (Lowe & Bray 2006). This conservative estimate of site use factor will overestimate rather than underestimate site sediment contribution.

If telemetry and tagging results are not available for a species or similar species, home range can be estimated based on spatial patterns in contaminant concentrations, stable isotope ratios, or other tissue measurements. If large spatial datasets exist on contaminant patterns within individual species, spatial statistics (e.g., kriging) can also be generated to help estimate home range. Previously, general estimates of home range have been developed based on the spatial association between fish and sediment contamination (Burkhard 2009; Melwani *et al.* 2009).

When data were not available for a given species, appropriate surrogate species were selected based on the home range conceptual model developed by Lowe and Bray (2006). According to this conceptual model, five species attributes affect home range: body size, diet (e.g., prey type), foraging strategy, territorial behavior, and habitat. All else being equal, larger fish have larger home ranges (Minns 1995). Foraging strategy will also influence range. Ambush (sit and wait) predators have relatively small home ranges, as they do not actively move in seeking prey. In contrast, active foragers that search for areas of prey availability have larger ranges. Territorial fishes have smaller ranges than non-territorial fishes, as they inhabit and defend a discrete location. Finally, fishes that inhabit structurally complex habitats (e.g., eelgrass, rocky reefs, and human-made piers and other structures) have smaller home ranges than fish that inhabit simpler habitats. Due to higher prey density, more complex habitat areas tend to require less movement to obtain sufficient prey than areas with limited structural complexity (e.g., soft sediments). The Lowe and Bray (2006) conceptual model was used to extrapolate across similar species, based on differences in these factors. For example, for a species with general life history characteristics intermediate between two previously studied species, an

intermediate estimated home range was chosen. Quantitative studies have not been performed on movement range for some of the dietary guild indicator species. Therefore, these kinds of inferences were necessary for estimating home range for the SQO program.

III. Results

Home range statistical distribution
A lognormal distribution was used to depict home range variability within guild indicator species, unless local data indicated otherwise. The lognormal distribution was chosen based on the statistical properties of home range size for estuarine and marine bay finfish species. Across a range of studies and species, the standard deviation is similar in magnitude to or greater than the mean, with most individuals exhibiting relatively small ranges, and a small number of individuals exhibiting much larger ranges (Idyll & Sutton 1952; Borgeson & McCammon 1967; Miller & Geibel 1973; Smith & Abramson 1990; Tupen 1990; Posner & Lavenberg 1999; Lowe *et al.* 2003; Bacheler *et al.* 2005; Topping *et al.* 2005; Stuart & Jones 2006; Parker *et al.* 2007; Jones & Stuart 2009). This type of variability is consistent with the lognormal distribution, which is commonly employed for environmental data (Limpert *et al.* 2001; MacLeod *et al.* 2002). Some fish home range studies indicate more limited variability across individuals (Jorgensen *et al.* 2006; Mason & Lowe 2010), suggesting normally distributed results. However, a lognormal approximation with relatively small variance also fits well to normally distributed data (Limpert *et al.* 2001).

Home range estimates for indicator species

California Halibut

California halibut are common in enclosed bays and the offshore coast of California. California halibut are ambush predators (Haaker 1975) and thus may have relatively small home ranges (Table 1). They are considered to be residential species, spending large time periods in a specific area. However, adult halibut also sometimes exhibit extensive migration, which can complicate home range estimation.

Significant relationships of fish tissue chemistry to sediment contaminant concentrations are found for California halibut. However, these relationships are not as statistically robust as those for other species evaluated. The lack of strong relationships to sediments may reflect the decoupling of halibut from the benthic food web due to the predominantly piscivorous diet of adults (Melwani *et al.* 2009).

California halibut have been the subject of numerous tagging and tracking studies. Acoustically tagged juvenile California halibut in Huntington Beach wetlands had relatively small home ranges of 500 to 800 m^2 over a several week period (Table 2). Movement was somewhat reduced when fish were associated with habitat, such as eelgrass, and fish tended to stay in locations exhibiting high water flow, likely related to

flux of prey organisms within the sites. Fish also tended to favor channels adjacent to marshy regions (C. Lowe, CSU Long Beach, pers. comm.). In Anaheim Bay, Haaker (1975) similarly found that juvenile halibut did not make extensive movements, prior to migration to deeper, offshore waters. However, fish in these studies were juveniles, well below legal capture size (55.8 cm), and therefore of limited relevance for the SQO for human health.

The home range parameters selected for California halibut were linear movement distances, based on results of tag recapture studies of legal capture size adults. Available tag-recapture studies all indicate highly variable movement ranges, with most fish recaptured very close to the release location, but a small subset of fish traveling hundreds of km. Domeier and Chun (1995) found that most individuals were sedentary, being recaptured at or near the release location. Adult halibut movements varied based on size, with higher average travel distance for adults larger than 50 cm compared to fish smaller than 50 cm. Similarly, Tupen (1990) found that 42 halibut tagged off the central California coast from April 1987 through December 1988 exhibited considerable variability in movement distance. Although the largest movement distance was 291 km, 55% of recoveries occurred less than 1 km from the point of original release, indicating sedentary behavior. These two tag-recapture studies on adult halibut were used to determine the linear movement distance mean and standard deviation (Tupen 1990; Domeier & Chun 1995).

Results from the tag-recapture studies, weighted by sample size, were used to generate an overall mean movement range of 29,300 m, and a pooled standard deviation of movement range of 60,000 m (Table 2). These attributes correspond to a lognormal distribution (mean = 9.46, standard deviation = 1.28; both on a natural log scale). Generally, the wide range of this distribution (Table 2, Figure 1) is appropriate given the known pattern of halibut movement, with many fish exhibiting little to no movement, and a few fish exhibiting extremely large movements.
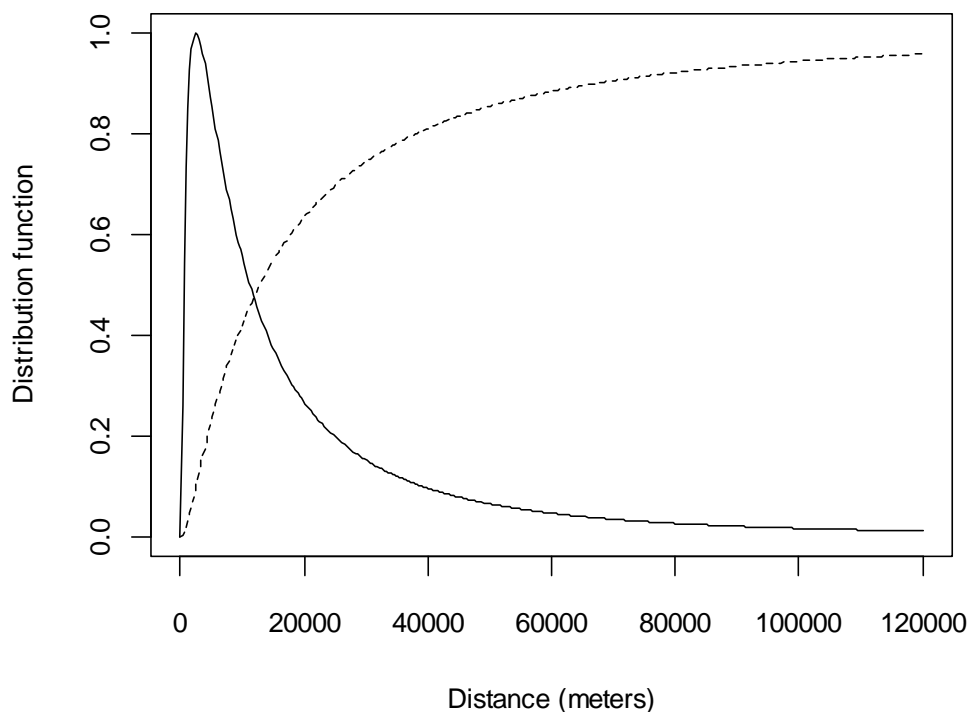
Figure 1. Home range estimate (m) for California halibut. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit the y axis. The probability distribution function indicates the relative probability of a particular home range being selected in the simulations.

Spotted sand bass

Because spotted sand bass are ambush predators, tending to stay in one location when feeding (Table 1), they are expected to exhibit relatively small home ranges. Telemetry or tagging results are not available for spotted sand bass, but telemetry results are available for similar California species. Based on similar foraging strategies, life history, and prey types, home range results for kelp bass and barred sand bass (Lowe *et al.* 2003; Mason & Lowe 2010) were used to estimate spotted sand bass home range. Like barred sand bass, spotted sand bass feed in soft sediments. However, spotted sand bass will tend to have some degree of association with kelp beds and other benthic structure (Table 1), similar to kelp bass.

Table 1. Background information for guild indicator species movement range determination. Habitat and foraging strategy results were compiled from Froese and Pauly (2010), expert guidance (C. Lowe and M.J. Allen, pers. comm.) and other references as indicated. None of the guild indicator species are territorial.

Species	Total length (cm, typical)	Dietary Guild	Habitat	Foraging strategy
California halibut	50 - 100	Piscivore	Sand, benthic	Ambush predator
Spotted sand bass	15 - 35	Benthic diet with piscivory	Bays, shallow coasts, soft bottom; Usually found on sand or mud bottom near rocks and eelgrass, from the coast to a depth of 60 m.	Ambush predator
White catfish	20 - 40	Benthic and pelagic with piscivory	Favor slow current areas, including mud bottomed pools, open channels and backwater sloughs. Found in fresh water and estuarine environments (Moyle 2002).	Carnivorous bottom feeder (Turner 1966; Moyle 2002)
Queenfish (queen croaker)	10 - 20	Benthic and pelagic with piscivory	Sand/mud (Lowe & Bray 2006); Occur inshore, often over sandy bottoms. Common in bays and tidal sloughs, around pilings. Move to deeper water at night.	Roving benthic grazer, including prey on sediment surface as well as within sediments
White croaker	15 - 30	Benthic without piscivory	Bays, sand	Roving benthic grazer, including prey on sediment surface as well as within sediments
Shiner perch	8 - 15	Benthic and pelagic without piscivory	Mixed (often associated with structure)	Roving picker
Common carp	30 - 55	Benthic with herbivory	Inhabit warm, deep, slow-flowing and still waters such as lowland rivers and large, well vegetated lakes. Soft bottom substrates. Found in fresh water and estuarine environments.	Omnivorous bottom feeder. Forages by rooting on silty bottoms, stirring sediment and consuming disturbed prey (Moyle 2002)
Topsmelt	6 - 18	Benthic and pelagic with herbivory	Mixed (often nearshore and pelagic)	Benthic and planktonic grazer, with digestive tract adapted to digesting plant material (Logothetis *et al.* 2001)
Striped mullet	20 - 40	Pelagic with benthic herbivory	Sand/mud bottom; Bays, nearshore surface; school in coastal waters, often near inlets. Usually 0 - 10 m depth.	Grazes on detritus and plant matter at sediment surface. Feeding apparatus and digestive tract adapted to digesting small particles with variable to low nutritional content (Wells 1984, and references therein)

Table 2. Movement range estimates for guild indicator species. Parameters are presented assuming a lognormal distribution for each species.

Species	Distribution	5th %	Median	95th %	Mean	SD	Basis for estimate and additional movement information
California halibut	Lognormal	1559 m	12,858 m	106,020 m	29,300 m	60,000	Tag recapture studies on adults (Tupen 1990; Domeier & Chun 1995), and acoustic telemetry study of juvenile (sublegal) halibut in Huntington Beach wetlands. Fish are associated with eelgrass, high water flow areas, and other areas of high prey abundance (C. Lowe, unpublished data).
Spotted sand bass	Lognormal	1243 m^2	4950 m^2	19,708 m^2	7100 m^2	7300	Home range expected to be larger than for kelp bass and smaller than barred sand bass, based on expert recommendation (C. Lowe, pers. comm.). Data were fit to have SD = mean, similar to barred sand bass.
White catfish	Lognormal	775 m	4200 m	22,800 m	6920 m	9600	Tag recapture studies using angler information from Sacramento-San Joaquin Delta (Borgeson & McCammon 1967).
Queenfish	Lognormal	259,600 m^2	1,617,000 m^2	10,070,000 m^2	3,000,000 m^2	4,689,000	Assumed to be similar to white croaker, given similar life histories and diets (see next entry).
White croaker	Lognormal	259,600 m^2	1,617,000 m^2	10,070,000 m^2	3,000,000 m^2	4,689,000	Home range estimate based on telemetry results in Palo Verdes shelf (C. Lowe, unpublished data). Ocean whitefish and California sheephead (Topping *et al.* 2005; Bellquist *et al.* 2008) were used as proxies to estimate variability (i.e., coefficient of variation), as they are both roving predators like white croaker.
Shiner perch	Lognormal	373 m^2	1000 m^2	2684 m^2	1200 m^2	804	Expected to exhibit limited movement due to diet, association with structure, and avoidance of predation. Average and variation selected based on expert recommendation (C. Lowe, pers. comm.).
Common carp	Gamma	601 m	7347 m	30,625 m	-	-	Telemetry studies of movement in rivers (Crook 2004; Jones & Stuart 2009). Gamma distribution parameters are shape parameter [k] = 1.05; scale parameter [θ, theta] = 9904.
Topsmelt	Lognormal	373 m^2	1000 m^2	2684 m^2	1200 m^2	804	Selected to be same as shiner surfperch. Species likely does not have a home range. Contaminant monitoring results indicate significant differences among adjacent sites (Greenfield & Jahn 2010), suggesting limited movement ranges.

| Striped mullet | Lognormal | . | | | 28,200 m | 80,340 | Tag recapture studies on adults (Bacheler *et al.* 2005). Species likely does not have a home range, but forages nearshore throughout estuary. Offshore migration of great distances sometimes occurs (Idyll & Sutton 1952; Bacheler *et al.* 2005), supporting use of high coefficient of variation. |

Because of similar biology and intermediate habitats, the spotted sand bass home range distribution was estimated to be intermediate between that of kelp bass (mean = 3349 m^2) (Lowe *et al.* 2003) and barred sand bass (mean = 10,003 m^2) (Mason & Lowe 2010). A mean home range of 7100 m^2 was chosen. Variability in spotted sand bass home range was selected such that standard deviation would approximately equal the mean, corresponding to the variability of kelp bass (SD/mean = 1.0). These attributes were obtained with a lognormal distribution (mean = 8.507, standard deviation = 0.84; both on a natural log scale). The percentiles of the distribution are: 5% = 1243 m^2, 50% (median) = 4950 m^2; 95% = 19,708 km^2 (Table 2, Figure 2).
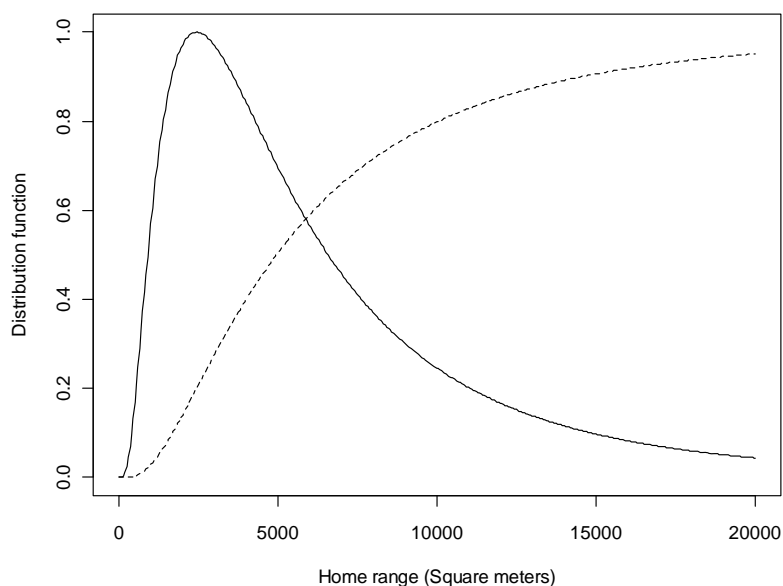

Figure 2. Home range estimate (m^2) for spotted sand bass. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit the y axis. The probability distribution function indicates the relative probability of a particular home range being selected in the simulations.

White catfish

White catfish are carnivorous bottom feeders that inhabit fresh and estuarine waters, including the Sacramento-San Joaquin Delta (Table 1). Because telemetry based home range studies are not available for white catfish, home range was estimated based on linear movement distance from local tag-recapture studies. Movement data for white catfish were estimated based on the Delta tag-recapture data of Borgeson and McCammon (1967), with linear movement distances manually extracted from Figure 2 using Adobe Illustrator. The mean linear recapture distance was 6921 m and the standard deviation was 7411 m. These data were fitted to a lognormal distribution using the fitdistr distribution fitting procedure in R (v 2.11.1). The resulting lognormal distribution (mean = 8.34, standard deviation = 1.02; both on a natural log scale) corresponded reasonably well to the original data (Figure 3). The percentiles of the distribution are: 5% = 775 m, 50% (median) = 4207 m; 95% = 22,830 m. The parameters selected for the decision

support tool corresponded to the mean of the original data (6920 m) and the standard deviation of the fitted distribution (9600 m; Table 2).
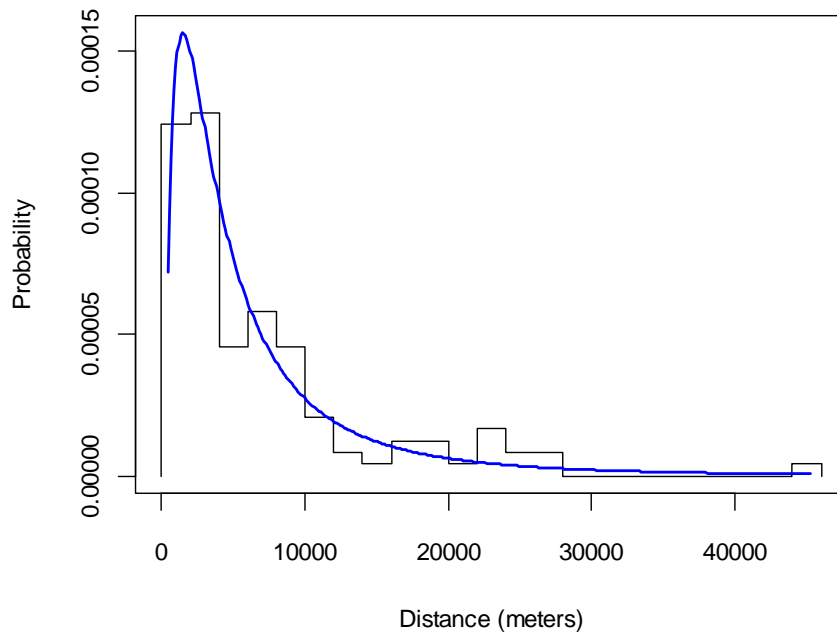

Figure 3. Home range estimate (m) for white catfish. Solid blue line indicates lognormal probability distribution function. Black line indicates histogram of the tag-recapture data extracted from Figure 2 of Borgeson and McCammon (1967).

White Croaker and Queenfish

White croaker and queenfish are both active, roving predators. Both species select invertebrate prey within sediments, on the sediment surface, and just above the sediments (Table 1). Recent and ongoing studies of white croaker have documented their movement patterns on the Palo Verdes Shelf, as well as into and out of the nearby Los Angeles Harbor. These studies indicate the croaker to move broadly across 3000 - 4000 m of the shelf in an area of 1000 m width (i.e., 3,000,000 – 4,000,000 m^2; 3 – 4 km^2) movement range. About 30% of the fish also moved into and out of Los Angeles harbor, spending from a few hours to several weeks within the harbor and then returning to the shelf (C. Lowe, CSU-Long Beach, *pers. comm.*).

In addition to the croaker studies off Palo Verdes Shelf, examination of similar species may also serve as proxies for white croaker and queenfish (Topping *et al.* 2005; Bellquist *et al.* 2008). In particular, acoustic telemetry studies have been performed on ocean whitefish and California sheephead in California marine waters. All four of these species are roving predators, and therefore are expected to exhibit some similarities in life history. However, California sheephead and ocean whitefish exhibit habitat preference for rocky habitat and kelp beds, whereas queenfish and white croaker largely inhabit areas with soft sediments and limited benthic structure (Table 1) (Topping *et al.* 2005; Bellquist *et al.* 2008). Following the conceptual model for influences on home range, croaker and queenfish are expected to have larger home ranges than sheephead and whitefish.

Correlation studies between pollutant concentrations in white croaker vs. sediments have also been performed. Two studies applying these methods estimated exposure area diameters ranging from 2 - 10 km in diameter, depending on the location and trace organic pollutant being evaluated (CH2M HILL 2003; Melwani *et al.* 2009). These diameters equate to large exposure area[1] estimates of 3 to 79 km^2.

A distribution for the home range of white croaker and queenfish was developed based on the preliminary home range data provided by Chris Lowe, and the variability exhibited in ocean whitefish and California sheephead. The distribution had the following characteristics: 1. A mean of 3,000,000 m^2 (3 km^2) following C. Lowe's unpublished white croaker telemetry results; 2. A skewed distribution, with variability based on the telemetry studies for California sheephead and ocean whitefish (coefficient of variation = SD/arithmetic mean = 1.56). The selected distribution is a lognormal distribution (mean = 14.296, standard deviation = 1.11; both on a natural log scale). The percentiles of the distribution are: 5% = 259,600 m^2, 50% (median) = 1,617,000 m^2; 95% = 10,070,000 m^2 (Figure 4; Table 2).
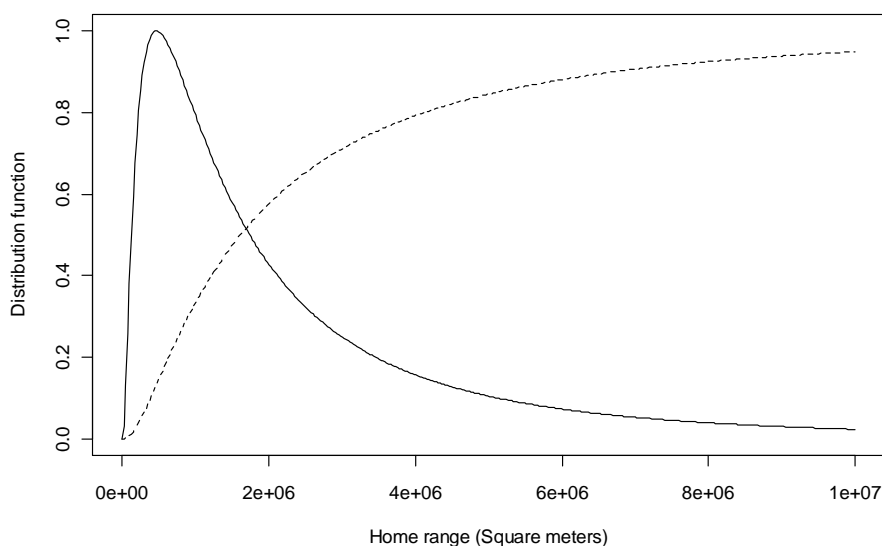

Figure 4. Home range estimate (m^2) for white croaker and queenfish. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit on the plot. The probability distribution function indicates the relative probability of a particular home range being selected in the simulations.

Shiner perch

Tagging or behavioral studies of shiner perch have not been performed to quantify home range. Therefore, inferences were drawn for this species based on contaminant and isotope tracers, results for similar species, and expert guidance. Shiner perch are small roving pickers, selecting zooplankton and epibenthic invertebrates, and epifaunal invertebrates from areas with habitat structure (Table 1). They frequently reside in

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[1] I.e., Area = π (Diameter/2)^2

eelgrass beds and man-made structures such as piers (Goals Project 2000). Because they and other surf perch are small and susceptible to predation they are likely to limit movement to reduce predation exposure.

Expert recommendation based on life history attributes and knowledge of other species indicated that shiner perch home range would vary 10-fold and be centered around 1,000 m^2 (C. Lowe, CSU Long Beach, pers. comm.). This small assumed range is supported by correlation analysis of tissue and sediment contaminant data used to estimate the exposure area. Likely as a result of its dietary mode and predator avoidance, shiner perch has previously shown strong linkages to sediment contamination at relatively small spatial scales (Melwani *et al.* 2009). Consequently, shiner perch exhibits highly significant spatial differences in multiple contaminants among collection locations within San Francisco Bay (Davis *et al.* 2002), and also in nitrogen and carbon stable isotopes (Ben Greenfield, unpublished data).

A lognormal distribution for shiner perch home range was developed that was centered at 1000 m^2 and exhibited a 10-fold range for the majority (95%) of results. The selected lognormal distribution (mean = 6.908, standard deviation = 0.6; both on a natural log scale) has percentiles of: 5% = 373 m^2, 50% (median) = 1000 m^2; 95% = 2684 m^2 (Figure 5, Table 2).
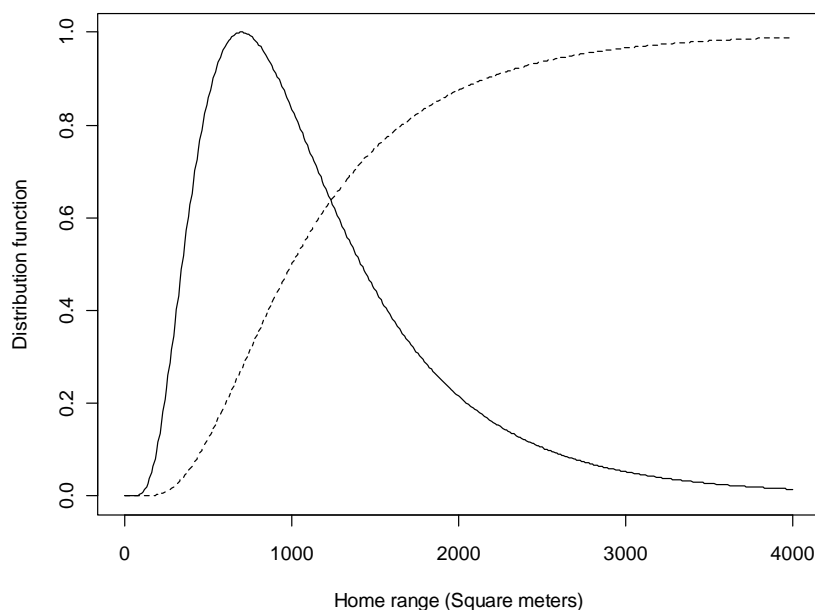

Figure 5. Home range estimate (m^2) for shiner perch. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, indicating relative probability of a particular home range being selected in the simulations.

Common carp

Common carp is an omnivorous bottom feeder inhabiting fresh and estuarine waters (Table 1). Movements of common carp have been extensively studied in Australian and New Zealand rivers and lakes, with results reported as linear movement distance rather than home range area. Common carp tend to move farther distances than white catfish, being more similar to California halibut. Like halibut, the majority of individual carp exhibit small movement distances and a small number of individuals move more than 100 km (Figure 6). For example, in south-eastern Australian forest water streams, thirty-six recaptured common carp had moved from 0.4 – 238 km (mean 30 ± 61 km) from the point of initial release (Jones & Stuart 2009). Of these fish, 38% were recaptured less than 5 km from point of release and 63% were within 10 km. Five fish (12.5%) moved farther than 127 km upstream. Similarly, of 76 tagged carp from the Waikato River in New Zealand, the majority were recaptured within 1 km of the release point, with a median distance traveled < 1 km and 84% of the fish moving less than 5 km (Osborne *et al.* 2009).
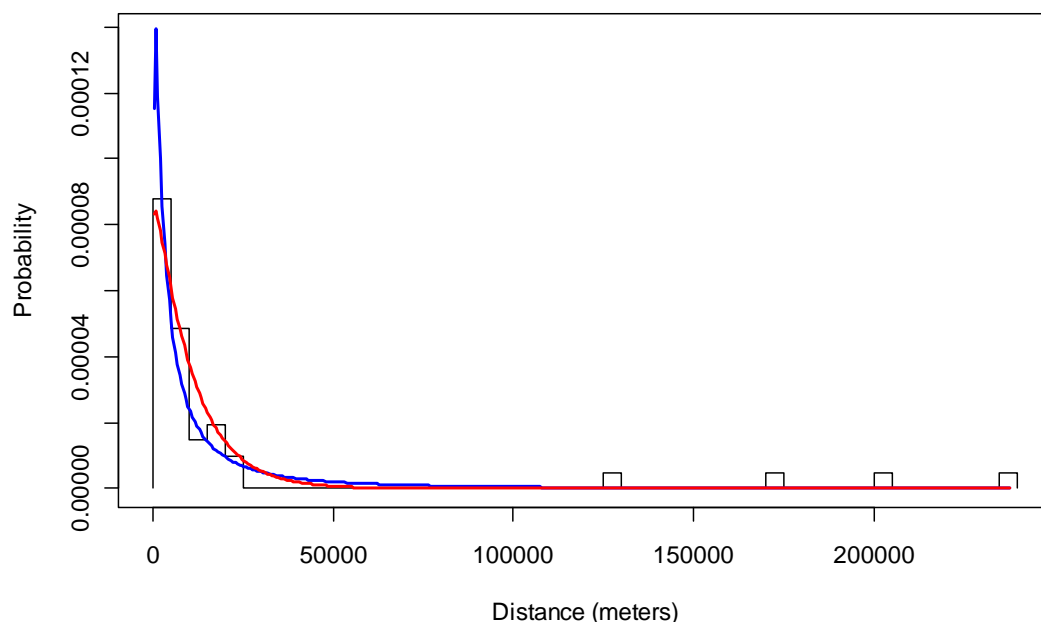

Figure 6. Home range estimate (m) for common carp. The colored lines indicate lognormal (blue) and gamma (red) probability distribution functions. The black line indicates a histogram of telemetry-based movement range data from two studies (Crook 2004; Jones & Stuart 2009).

The carp movement distance (m) distribution was obtained using the telemetry based on linear movement data from two studies that reported individual movement distances: Jones and Stuart (2009) (N = 37) and Crook (2004) (N = 4 fish). After evaluating multiple distribution forms, these data were determined to fit better to a gamma distribution (shape parameter = 1.05; scale parameter = 9904), than a lognormal distribution (mean = 8.702, standard deviation = 1.55; both on a natural log scale) (Figure 6). For the gamma and lognormal distributions respectively, the percentiles (in meters) are: 5% = [601, 457], 50% (median) = [7347, 6021]; 95% = [30,625, 79,358].

The gamma distribution was selected (Table 2) because it better predicted the proportion of extreme values, with the lognormal distribution tending to overestimate the frequency of very small values (Figure 6).

Topsmelt

Topsmelt exhibits a different diet and foraging strategy than the other dietary guild indicator species (SQO Science Team 2010). Topsmelt are schooling nearshore fishes, and consume benthic and pelagic plants and invertebrates (Table 1). Tag recapture or telemetry studies of movement distance are not available for topsmelt or similar California species. Although topsmelt are not expected to exhibit any kind of fidelity to a specific site or region, their small relative size and nearshore habitat would suggest relatively small home ranges. Studies of Hg and organic pollutants in topsmelt similarly indicate significant differences in pollutant concentrations among adjacent sampling locations (Battelle *et al.* 2005; Greenfield & Jahn 2010). Topsmelt sampled across different southern California mainland and coastal sites exhibit significant variation in body morphology (O'Reilly & Horn 2004). These findings of differences in contaminant concentrations and morphology suggest that topsmelt populations are spatially distinct among regions, and that the species has a limited movement range.

In the absence of specific information on topsmelt movement distance, conservative (small) value were selected based on the small size of the species, and the indirect evidence of limited movement among sampling locations. The relatively small home range estimates for shiner perch were applied to topsmelt. Specifically, a lognormal distribution was selected with percentiles of 5% = 373 m^2, 50% (median) = 1000 m^2, and 95% = 2684 m^2 (Figure 5, Table 2).

Striped Mullet

Striped mullet exhibits a different diet and foraging strategy than the other dietary guild indicator species (SQO Science Team 2010). Striped mullet are schooling benthic and pelagic coastal detritivores and are not expected to exhibit any kind of fidelity to a specific site or region (Table 1). As a result, striped mullet generally move widely. Tagging studies of this species indicate movement distributions even more skewed than California halibut, with some individuals exhibiting extensive movement from the original capture location. Bacheler et al. (2005) and Idyll and Sutton (1952) each report the majority of individuals within several km of the tagging location, but a small subset of captures (~1%) traveling hundreds of km.

Because striped mullet are not expected to have site fidelity, their movement was described based on linear distance travelled, rather than home range area. As for California halibut and channel catfish, tag-recapture studies were used to estimate the distribution of linear movement distance for striped mullet. Bacheler et al. (2005) report a mean movement distance of 28.2 km, and a standard error of 4.1 km, corresponding to a standard deviation of 80.34 km (N = 384 recaptured fish). These results were selected for

a lognormal movement distribution for striped mullet (Table 2), which was highly skewed, as for California halibut (Figure 7).
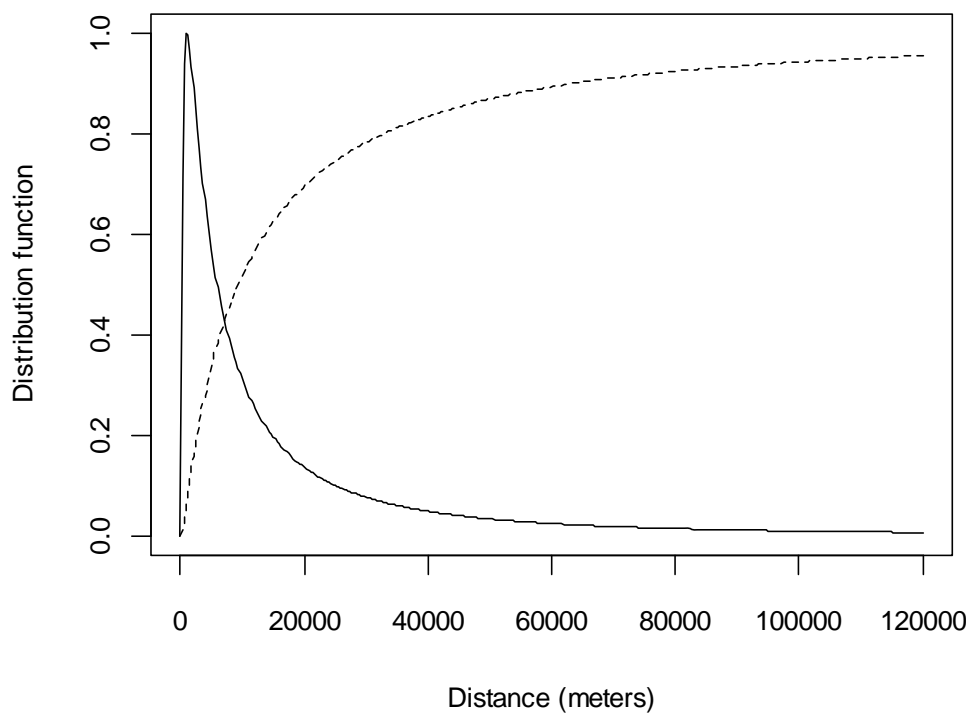

Figure 7. Home range estimate (m) for striped mullet. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit the y axis. The probability distribution function indicates the relative probability of a particular home range being selected in the simulations.

IV. References

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