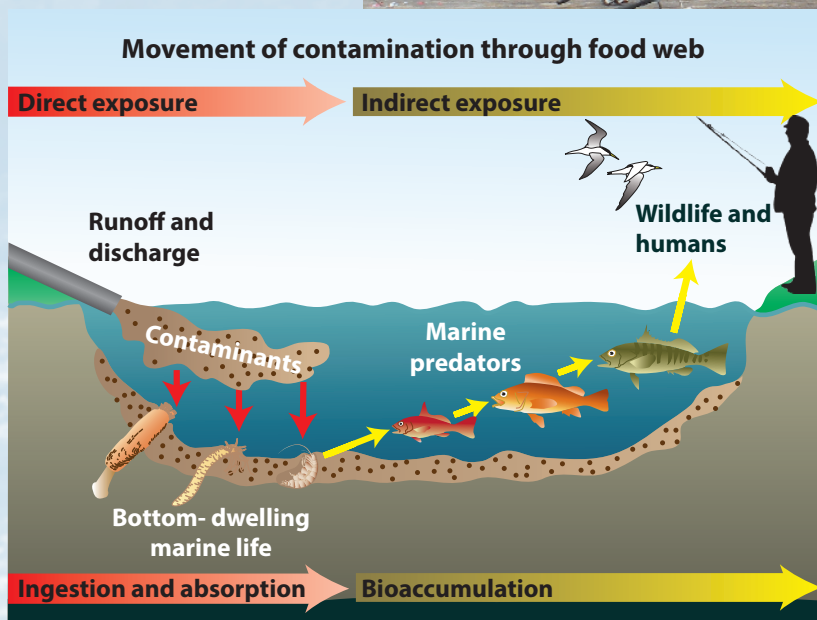


# Development of a Sediment Quality Assessment Framework for Human Health Effects



Steven M. Bay  
Ashley N. Parks  
Aroon R. Melwani  
Ben K. Greenfield

*Southern California Coastal Water Research Project*

SCCWRP Technical Report 1000



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Steven M. Bay<sup>1</sup>, Ashley N. Parks<sup>1</sup>, Aroon R. Melwani<sup>2</sup>, and Ben K. Greenfield<sup>3</sup>

*<sup>1</sup>Southern California Coastal Water Research Project*

*<sup>2</sup>Applied Marine Sciences*

*<sup>3</sup>Southern Illinois University Edwardsville*

## EXECUTIVE SUMMARY

This report describes a proposed assessment framework and tools for assessing the effects of sediment contaminants in enclosed bays and estuaries on human health. This framework was developed to assist the State Water Resources Control Board in implementing California's narrative Sediment Quality Objectives for human health (HHSQO) that states: *Pollutants shall not be present in sediments at levels that will bioaccumulate in aquatic life to levels that are harmful to human health.* This narrative objective focuses on the pathway of humans consuming seafood (fish or shellfish) that have accumulated contaminants from the sediment. The intent of this framework is to provide a standardized assessment approach that is feasible for application to a variety of regulatory and monitoring programs.

The HHSQO assessment framework was developed based on a general conceptual model of sediment-associated contaminant exposure to humans, through the indirect pathway of food web trophic transfer. In this conceptual model, contaminants in sediment and the water column transfer through a food web which includes invertebrates and finfish. Humans are then exposed to these contaminants when they consume the invertebrates or finfish. The assessment framework addresses food web bioaccumulation of contaminants using a mechanistic model of contaminant trophic transfer. To address the complexity of bioaccumulation in food webs, the framework includes eight seafood dietary guilds to address variation in diets of commonly consumed fish. Depending on the exposure dose and toxicity of the contaminant, there is potential for effects to humans.

The focus of the conceptual model establishes the direction of the framework. The conceptual model focuses on the sediment as a potential route of exposure to biota, rather than other potential routes, such as watershed loading, atmospheric deposition, or discharges from upstream water bodies. The HHSQO assessment framework considers spatial scale by requiring a description of the site boundary and forage range of the seafood. Scale is also incorporated into several aspects of the assessment framework, including probability based sampling and analysis of multiple stations within a site, and in later Tiers, explicit consideration of off-site movement by fish.

Evaluation of HHSQO 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: Chemical Exposure and Site Linkage. For the chemical exposure indicator, seafood contamination measurements from the site are compared to advisory tissue levels designed to protect human health. For the site linkage 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.

As with any sediment quality assessment, the first step is the development of a conceptual site model (CSM), which summarizes understanding such features as the site area and boundaries,

seafood species present on the site, and the people that consume seafood captured from the site. The framework includes three tiers, with increasing data requirements, complexity, and sophistication in each tier. Tier 1 is a rapid screening assessment to address the question: *Do the sediments at a site pose a potential human health hazard, warranting further evaluation?* Tier 1 identifies contaminants that do not pose unacceptable hazard to seafood consumers on the site. For contaminants that pose a potential hazard based on Tier I, a Tier 2 evaluation is performed. Tier 2 is a complete site assessment that consists of an evaluation of both tissue data and sediment data to determine potential risk to human health, using available site-specific information. Tier 2 results in site categorization into one of five categories, based on integrating the information from the chemical exposure and site linkage indicators. If a Tier 3 analysis is employed, further site-specific modifications to the approach are employed, based on site characteristics and study objectives.

The approach to addressing uncertainty and variability differs for each tier: Tier 1 addresses uncertainty and variability by making conservative assumptions, Tier 2 includes a Monte Carlo Simulation to generate a cumulative distribution function that describes uncertainty and variability, and in Tier 3 more sophisticated methods may be employed, incorporating site-specific data and methods.

The assessment framework includes data collection and evaluation for contaminant concentrations in sediment and fish, and other site attributes. In Tier 1, only contaminant concentration data and sediment TOC are needed. Frequently this data will already be available from previous monitoring surveys. Tier 2 requires collection of seafood, water column, and sediment contaminant concentrations, seafood lipid content, sediment total organic carbon, and site area and length. Water quality parameters are optional for Tier 2 local data input. If local data are available, the following parameters are used: dissolved and particulate organic carbon, total suspended solids, temperature, dissolved oxygen, and salinity.

To facilitate Tier 2 data analysis and interpretation, a spreadsheet-based analysis tool, referred to as the Decision Support Tool (DST), was developed. It is designed to efficiently perform the complex calculations in the Tier 2 assessment. Available local site data is integrated into the DST calculations. The DST analyzes site information using bioaccumulation and risk models to determine chemical exposure and site linkage. It uses and presents probability-based information, which provides additional information to aid in interpreting the results.

## ACKNOWLEDGMENTS

Greg Pelletier, Washington Department of Ecology, developed the YASAIw Monte Carlo Simulation macro, and provided constructive feedback on the use of the macro. YASAIw was based on the YASAI macro, originally developed by Professor Jonathan Eckstein (Rutgers University) and Steven T. Riedmueller. We thank SFEI staff Michelle Lent, Rachel Allen, Shira Bezalel (SFEI), and LA County Sanitation District staff for technical contributions. Tom Fikslin and Greg Cavallo (Delaware River Basin Commission) provided unpublished data. This report benefitted from technical guidance of the Scientific Steering Committee (Todd Bridges, Peter Landrum, Charlie Menzie, Jim Shine, Donna Vorhees, Rob Burgess, Bruce Hope, and Brock Bernstein), Robert Brodberg (OEHHA), Frank Gobas (Simon Frasier University), Jon Arnot (University of Toronto), Chris Lowe (CSU – Long Beach), and Jim Allen. Many thanks to members of the Sediment Quality Advisory committee for their assistance in reviewing aspects of the framework and providing input on implementation. The Harbor Technical Work Group (Port of Los Angeles, Port of Long Beach, Los Angeles Regional Water Quality Control Board, State Water Board, and Anchor QEA) also made valuable contributions to this report, especially for development of the Tier 3 approach and providing bioaccumulation model validation data. The authors thank SCCWRP staff Darrin Greenstein, Doris Vidal-Dorsch, and Valerie Racor-Rands for assistance with data analysis, report preparation and review. This work was supported by the State Water Resources Control Board Agreements 08-061-250, 11-175-250, and 13-040-250.

# TABLE OF CONTENTS

Executive Summary .....	i
Acknowledgments .....	iii
List of Figures .....	vi
List of Tables .....	vii
Definitions and Abbreviations .....	viii
1 Introduction .....	1
1.1 Scope and Purpose .....	3
1.2 Framework Applications .....	3
1.3 Constraints and Attributes .....	5
1.4 Organization of the Report .....	5
2 Assessment Framework Design .....	6
2.1 Conceptual Approach .....	6
2.2 Treatment of Uncertainty and Variability .....	10
2.3 Dietary Guild Approach .....	10
2.4 Chemical Exposure Evaluation .....	10
2.5 Site Linkage Evaluation .....	11
2.6 Development of a Conceptual Site Model .....	12
3 Tier 1 Screening Evaluation .....	14
3.1 Tissue Evaluation .....	14
3.2 Sediment Evaluation .....	15
3.3 Tier 1 Interpretation .....	18
3.4 Tier 1 Site Assessment Steps .....	18
3.5 Tier 1 Case Study Example .....	19
4 Tier 2 Assessment .....	21
4.1 Chemical Exposure .....	22
4.2 Site Linkage .....	23
4.3 Tier 2 Interpretation .....	26
4.4 Tier 2 Site Assessment Steps .....	26
4.5 Tier 2 Case Study Example .....	27
5 Tier 3 Assessment .....	32
5.1 Tier 3 Objectives .....	32
5.2 Trigger Criteria .....	32
5.3 Assessment Characteristics .....	33
5.4 Results Interpretation .....	34
5.5 Tier 3 Site Assessment Steps .....	34
5.6 Tier 3 Case Study Example .....	35
6 Sampling and Chemical Analysis Recommendations .....	38
6.1 Seafood Sampling and Sample Preparation .....	38
6.2 Sediment Sampling and Sample Preparation .....	46
6.3 Chemical Analytes .....	48
6.4 Data Preparation and Analysis .....	49
7 References .....	50
Appendix 1 – Bioaccumulation Model and Site linkage Calculation .....	68
A1.1 Bioaccumulation Model Equations .....	68
A1.2 Site Linkage Determination .....	80
Appendix 2 - Dietary Guild and Target Species Development .....	82

A2.1 Introduction .....	82
A2.2 Methods .....	83
A2.3 Results .....	85
Appendix 3 - Home Range Parameter Estimation for Fish Species .....	94
A3.1 Introduction .....	94
A3.2 Home Range .....	94
A3.3 Methods .....	95
A3.4 Results .....	96
Appendix 4 - Sensitivity Analysis for Indirect Effects Assessment .....	108
A4.1 Introduction .....	108
A4.2 Methods .....	109
A4.3 Results and Discussion .....	112
Appendix 5 - Analysis of PCB Congeners .....	115
A5.1 Introduction .....	115
A5.2 Methods .....	115
A5.3 Results and Discussion .....	122
Appendix 6 – Application of Assessment Framework .....	126
A6.1 Acknowledgments .....	126
A6.2 Introduction .....	126
A6.3 Methods .....	126
A6.4 Results .....	127
A6.5 Discussion .....	141
A6.6 Supplemental Information .....	142
Appendix 7 – Comparison of Bioaccumulation Model Performance .....	168
A7.1 Introduction .....	168
A7.2 Approach .....	168
A7.3 San Francisco Bay Model Comparison .....	169
A7.4 Independent Model Comparison .....	172
A7.5 Between Site Comparison .....	173
A7.6 Conclusions .....	181



## LIST OF FIGURES

Figure 1.1. Principal sources, fates, and effects of sediment contaminants in enclosed bays and estuaries .....	2
Figure 1.2. Potential role of the HHSQO data assessment framework (shaded region) in sediment quality evaluation and management.....	4
Figure 2.1 Calculation, integration, and interpretation of assessment indicators.....	7
Figure 2.2. Tiered assessment framework. ....	9
Figure 3.1. Tier 1 process using either seafood or sediment contamination data. ....	14
Figure 4.1 Calculation, integration, and interpretation of Tier 2 assessment indicators.....	21
Figure 4.2. Strategy for determining the chemical exposure to seafood consumers. ....	22
Figure 4.3. An example of site sediment linkage distributions for DDTs (red line plot) and PCBs (purple line plot). ....	25
Figure 4.4. Strategy for determining the site linkage to fish bioaccumulation.....	27
Figure 4.5. Cumulative distribution plot of site linkage to observed seafood contaminant concentrations.....	30
Figure 4.6. DST summary of results from the assessment of Los Angeles Outer Harbor for DDTs.....	31
Figure 5.1 Conceptual site model for Los Angeles and Long Beach Harbor.....	35
Figure 5.2. Integrated modeling approach to assess contribution of loadings from multiple sources to fish contamination. ....	36
Figure 6.1. Traits of seafood species for assessing indirect effects. ....	38
Figure 6.2. Recommended minimum sample sizes for Tier 2 assessment of indirect effects....	45

## LIST OF TABLES

Table 2.1. OEHHA Fish Contaminant Goals (FCGs) and Advisory Tissue Levels (ATLs) based on an assessment of human health risk by OEHHA .....	11
Table 3.1. Tier 1 tissue screening thresholds .....	15
Table 3.2. Tier 1 Biota sediment accumulation factors (BSAF) calculated for percent sediment total organic carbon.....	16
Table 3.3. Step 2 calculation results using data from San Francisco Bay.....	19
Table 3.4. Calculation of Tier 1 sediment thresholds for the San Francisco Bay case study.....	20
Table 3.5. Comparison of tissue concentrations (ng/g ww) to the Tier 1 screening thresholds ..	20
Table 4.1. Chemical Exposure thresholds .....	22
Table 4.2. Home range parameters for each sport fish guild. ....	24
Table 4.3. Site sediment linkage categories for Tier 2 evaluation. ....	25
Table 4.4. Site assessment matrix. ....	26
Table 4.5. Seafood input parameters used in the assessment example.....	28
Table 4.6. Sediment DDT concentrations entered into the DST for the assessment example. ..	28
Table 4.7. Additional site-specific parameters entered into the DST for the assessment example. ....	28
Table 6.1. Appropriate species for use in the HHSQO assessment.....	40

## DEFINITIONS AND ABBREVIATIONS

**303(d)** – listing developed by State Water Resource Control Board or USEPA of waterways that are impaired due to aquatic pollution

**ATL** – Advisory Tissue Level

**bioaccumulation** – the accumulation of chemicals in an organism via uptake through all routes of chemical exposure (e.g., dietary and dermal absorption and transport across the respiratory surface)

**bioavailability** – the ability of a contaminant to be transferred from an abiotic matrix, such as sediment, to the tissue of a living organism via ingestion, absorption, or other mechanisms

**biota-sediment accumulation factor (BSAF)** – the ratio of wet weight contaminant concentration in biota to dry weight contaminant concentration in some other matrix; In this report, unless specified otherwise, the term “biota-sediment accumulation factor” refers to wet weight concentration in fish or invertebrate tissue divided by dry weight concentration in sediment

**CDFG** – California Department of Fish and Game

**CDFW** – California Department of Fish and Wildlife

**CERCLA** – Comprehensive Environmental Response, Compensation, and Liability Act

**CFCP** – Coastal Fish Contaminant Program, a program initiated in 1998 to monitor contamination in sport fish and shellfish from California coastal waters

**chlordanes (sum)** – Components of the technical chlordane mixture; for the HHSQO program, five chlordane compounds are analyzed: cis-chlordane, trans-chlordane, cis-nonachlor, trans-nonachlor, and oxychlordane

**CSM** – conceptual site model

**DDTs (sum)** – the combination of DDT (dichlorodiphenyltrichloroethane) and its degradation products, DDD (dichlorodiphenyldichloroethane) and DDE (dichlorodiphenyldichloroethylene)

**direct effects** - impacts of contaminated sediment to aquatic life residing directly in the sediment

**DST** – Decision Support Tool used in Tier 2 of the HHSQO assessment

**dw** – dry weight

**EMAP** – Environmental Monitoring and Assessment Program (USEPA 2006)

**EPA** – US Environmental Protection Agency

**FCG** – Fish Contaminant Goal

**GRTS** – Generalized Random Tesselation Stratified

**indirect effects** - impacts of contaminated sediment to organisms via dietary trophic transfer through the food web (this report focuses on indirect effects to humans, through seafood consumption)

**HHSQO** – Human health sediment quality objective, for protection of human health from sediment contamination impacts resulting from consumption of resident fish and shellfish

**HR** – Home range

**K<sub>ow</sub>**—octanol-water partitioning coefficient

**MCA** – Monte Carlo Simulation

**NOAA** –National Oceanic and Atmospheric Administration

**NPDES** – National Pollutant Discharge Elimination System

**OEHHA** – the Office of Environmental Health Hazard Assessment, an Office within the California Environmental Protection Agency (Cal/EPA) responsible for assessing the risk posed by hazardous substances on human health and the environment and in addition, the development and posting of fish consumption advisories.

**PAH** – polycyclic aromatic hydrocarbons

**PCBs (sum)** – the total concentration of all polychlorinated biphenyl congeners present in a sample

**Regional Water Boards** – Regional Water Quality Control Boards

**RL** – method reporting limit

**RMP** - The Regional Monitoring Program for Water Quality in San Francisco Bay

**SCCWRP** – Southern California Coastal Water Research Project

**SD** – standard deviation

**SE** – standard error of the mean

**SFEI** – The San Francisco Estuary Institute

**SQAC** – Sediment Quality Advisory Committee

**SQO** – Sediment Quality Objective

**SSC** – Scientific Steering Committee

**SUF** – Site use factor

**SWAMP** – Surface Water Ambient Monitoring Program, a California monitoring program coordinated by SWRCB

**State Water Board (SWRCB)** – State Water Resources Control Board of California

**TMDL** – Total Maximum Daily Load, the maximum amount of a pollutant allowed to be discharged into a water body while still meeting water quality standards

**TSMP** – Toxic Substances Monitoring Program, which monitors fish and invertebrate tissues in freshwater and estuarine habitats (Rasmussen 1995)

**TOC** – total organic carbon

**UCL** – Upper Confidence Limit (e.g., the upper limit of the 95% confidence interval of the mean)

**USACE BSAF database** –A web database developed by US Army Corps of Engineers, containing information on lipid content and other parameters for benthic invertebrates (Lutz 2010)

**ww** – wet weight

**Water Boards** – State and Regional Water Boards

# 1 INTRODUCTION

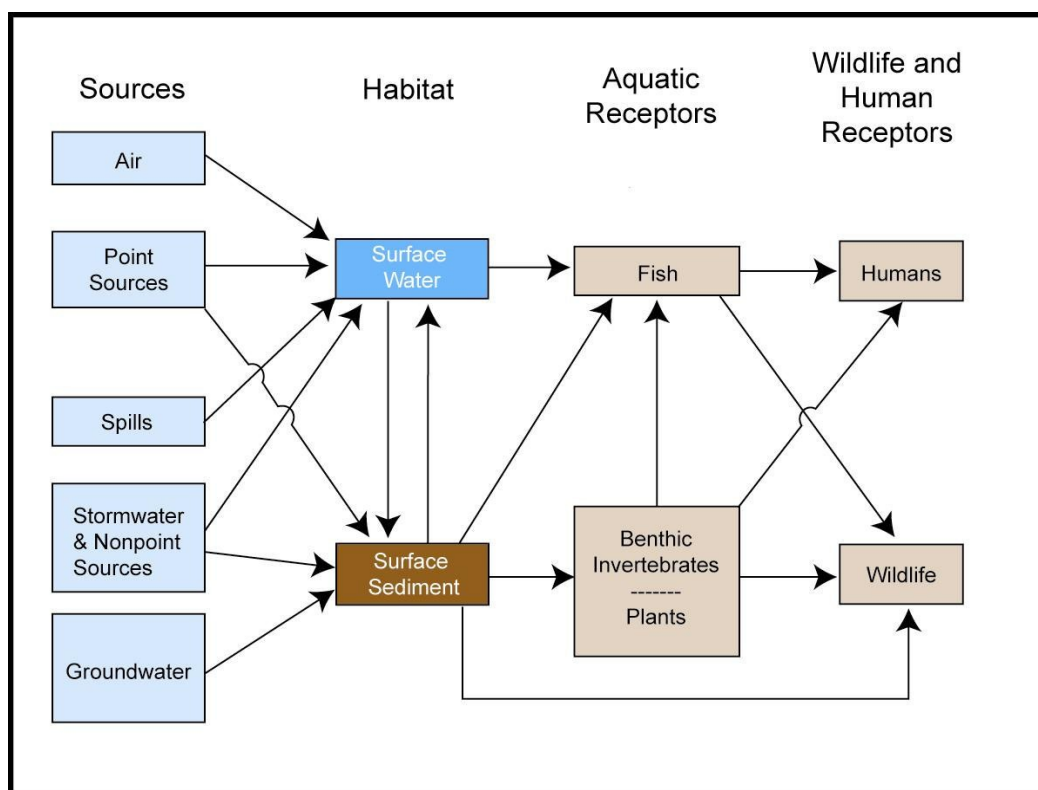
This report describes a proposed assessment framework and tools for assessing the potential of sediment contamination to impact human health from the consumption of contaminated fish or shellfish (seafood). This framework was developed to assist the State Water Resources Control Board (State Water Board) in implementing its narrative Sediment Quality Objective for human health (HHSQO) that states: *Pollutants shall not be present in sediments at levels that will bioaccumulate in aquatic life to levels that are harmful to human health.* This narrative objective focuses on the pathway of humans consuming seafood (fish or shellfish) that have accumulated sediment-associated contaminants through the food web. This objective applies only to enclosed bays and estuaries.

The health of fish, wildlife, and humans can be adversely impacted by contaminated sediment as a result of direct contact with sediment, but more commonly by the indirect pathway of bioaccumulation and food-web trophic transfer (Figure 1.1). It is well established that sediment-associated bioaccumulative compounds, such as dichlorodiphenyltrichloroethane (DDT), polychlorinated biphenyls (PCBs) and methyl mercury, biomagnify and can cause deleterious effects to wildlife and potential health risks to humans at environmentally relevant concentrations (e.g., Anderson *et al.* 1975; Fox *et al.* 1991; Kidd *et al.* 1995; Beyer *et al.* 1996; Huang *et al.* 2006; Schaeffer *et al.* 2006; Wiener and Suchanek 2008; Alava *et al.* 2012). Significant relationships between sediment contamination and fish contamination demonstrate instances where legacy contaminated sediment is the source of risk to wildlife and humans (Wong *et al.* 2001; Zeng and Tran 2002; Melwani *et al.* 2009b; Gehrke *et al.* 2011; Greenfield and Allen 2013), and conceptual and mechanistic models of contaminant bioaccumulation indicate sediment to be an important exposure pathway (Connolly 1991; Thomann *et al.* 1992; Arnot and Gobas 2004; Gobas and Arnot 2010; Parkerton and Connolly 2013).

Despite the importance of sediment as a contaminant reservoir, the relationship between sediment contamination and risk to humans and wildlife exhibits significant variability and uncertainty, affecting assessment and cleanup strategies and cost (Linkov *et al.* 2002; Linkov *et al.* 2005; Gobas and Arnot 2010). In the U.S., federal Comprehensive Environmental Response, Compensation, and Liability Act (CERCLA) risk assessments managed by the Superfund program can cost tens of millions of dollars, and take a decade or more to perform (Hamilton and Viscusi 1999; Gustavson *et al.* 2007). Although such complex and expensive assessments are warranted when costly cleanup efforts may result, there is also a need for more rapid screening-level assessments to evaluate overall ecosystem health and to prioritize among multiple sites. For sediment evaluation, tiered assessment frameworks make good use of limited resources by scaling the effort level to the magnitude and potential cost of the problem (U.S. EPA and U. S. Army Corps of Engineers 1991; 1998; Contaminated Sites Management Working Group 1999; Bridges *et al.* 2005; Chapman and Anderson 2005; Hope 2009; Saloranta *et al.* 2011).

The assessment framework described in this report was developed to address the need for a method to evaluate California's HHSQO. Development of the framework and data analysis tools for application was a collaborative effort involving three groups: SQO Science Team, Scientific Steering Committee (SSC), and Sediment Quality Advisory Committee (SQAC). The Science Team, composed primarily of scientists from SCCWRP and the San Francisco Estuary Institute

(SFEI), developed the conceptual assessment approach, data analysis tools, and model parameters, and conducted pilot testing of the approach. The SSC was composed of scientists with expertise in sediment quality assessment, sediment management, biological effects, risk assessment, chemical fate and exposure, and analytical chemistry. The SSC reviewed technical products from the Science Team and provided guidance for further development. The SQAC was composed of diverse types of stakeholders likely to be affected by implementing the HHSQO framework, including regulatory agencies, water quality managers (e.g., wastewater dischargers, flood control agencies, industry), laboratory managers, legal and environmental consultants, and nongovernmental/conservation agencies (e.g., Sierra Club, California Waterkeepers). Framework development was an iterative process that occurred from 2005 to present and benefited greatly from SSC and SQAC input and technical assistance. Additional information regarding intermediate technical products, and SSC and SQAC input related to the HHSQO framework is available at: <http://www.sccwrp.org/ResearchAreas/Contaminants.aspx>



**Figure 1.1. Principal sources, fates, and effects of sediment contaminants in enclosed bays and estuaries (adapted from Bridges *et al.* 2005)**

## 1.1 Scope and Purpose

The purpose of the HHSQO assessment framework is to provide a means to determine whether sediment within an enclosed bay or estuary meets the narrative SQO protecting the health of human consumers of locally caught seafood. This framework does not address program-specific policy issues, such as regulatory interpretation and application of the results, SQO exceedances, or violations.

This assessment determines whether sediment contamination at a site results in an unacceptable health risk to humans because of the consumption of contaminated fish and shellfish (referred to as seafood in the rest of this document). The flux of pollutants from the site sediment into the water column, as well as the transfer among trophic levels, has an important influence on the resulting seafood contamination. The bioaccumulation modelling used in this assessment considers both routes of exposure, with the relative influence of each route determined by the food web established for target species. The unit of assessment is the site, which is an area of interest within a water body. The size and boundaries of a site are a function of the assessment's purpose and study design, which are identified by developing a conceptual site model. For some applications, a site may be equivalent to an entire bay or estuary, while other programs may require assessment within a portion of the water body.

Risk to wildlife is not included in this assessment. The HHSQO assessment framework is designed to answer two questions:

1. Do pollutant concentrations in fish and shellfish pose unacceptable health risks to human consumers?
2. Is sediment contamination at a site a significant contributor to presence of chemical concentrations of concern in prey tissue?

The technical tools developed for the framework are implemented for legacy organochlorine compounds: PCBs, DDTs, chlordanes, and dieldrin. These compounds were chosen due to well established and validated empirical and mechanistic approaches for characterizing bioaccumulation and human exposure from sediment sources (e.g., Thomann *et al.* 1992; Arnot and Gobas 2004; Gobas and Arnot 2010), and management concern for human exposure to these pollutants in California. The overall assessment conceptual approach (e.g., indicators, data integration strategy, site classification criteria) is applicable to other contaminants if the necessary tools and parameters become available to apply the framework.

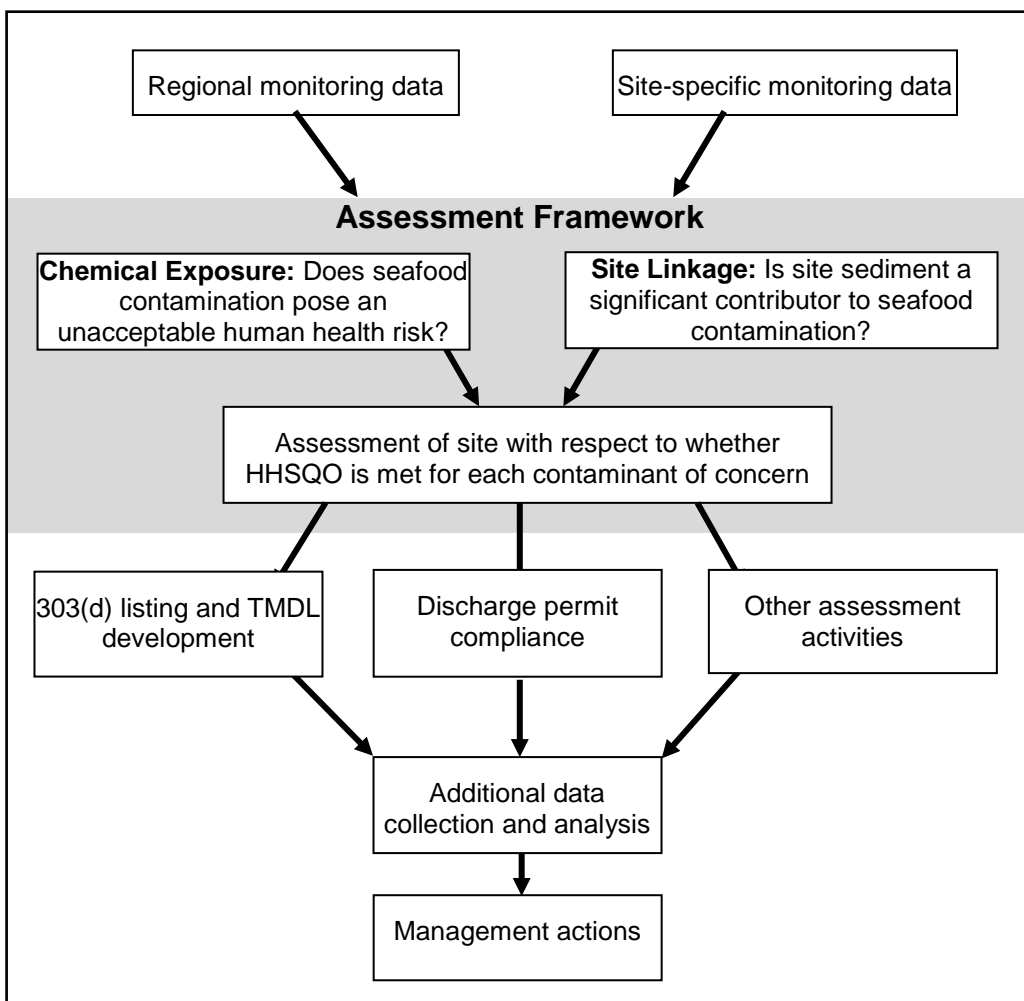
## 1.2 Framework Applications

This framework is intended to be applied in conjunction with a detailed policy of implementation to assess sediment quality for a variety of regulatory and non-regulatory programs including NPDES permit monitoring, site assessment/site cleanup efforts, 303(d) listings, and TMDL development (Figure 1.2). Existing data from prior monitoring activities may be used for an initial site assessment, with additional data collection for a more refined site assessment.

The HHSQO framework and technical tools are intended to provide a consistent method for interpreting monitoring data from several statewide programs. Application of the framework will yield consistent results when used with the same input data, regardless of which agency is using the framework.

The framework and tools described in this document are not intended to address all the needs related to interpreting sediment chemistry and bioaccumulation data for human health risk evaluation, nor are they intended to be the only resource used for guiding regulatory and management activities. For example, the assessment framework does not address other potential contaminant sources (e.g., loading from watershed runoff).

Application of the assessment framework is intended to provide an evaluation of sediment quality that serves to determine the level of compliance with regulatory policies and provide a foundation for determining the need for subsequent activities and research. Other tools, such as contaminant fate/transport models, regional background contamination data, source identification, and temporal trend analysis are needed to select appropriate management actions to achieve or maintain sediment quality that supports beneficial uses related to seafood consumption.



**Figure 1.2. Potential role of the HHSQO data assessment framework (shaded region) in sediment quality evaluation and management.**



### **1.3 Constraints and Attributes**

Several desirable characteristics of the assessment framework were identified by the SSC and SQAC. The design and implementation of the HHSQO assessment framework attempted to incorporate these characteristics, which include:

- The assessment framework should provide results based on sediment contaminant concentrations at the scale of a site. A site represents a region of interest that may be smaller than the water body, but is larger than a single sampling point (station).
- The assessment results should be chemical specific, based on the known attributes (e.g., toxicity, bioaccumulation) of the contaminants of concern. In this phase, the framework was developed for PCBs, DDTs, chlordanes, and dieldrin.
- The overall framework should be adaptable (with modifications to tools or data types) for future use with other contaminants of concern, such as mercury, selenium, and contaminants of emerging concern.
- The data requirements of the framework should be moderate, so that an assessment can be made using existing sediment and tissue monitoring data, or new data requirements can be met at reasonable cost.
- The framework should use methods that reflect current scientific understanding of the factors affecting sediment-biota transfer and risk assessment of sediment contaminants.
- The steps used to integrate and evaluate the data should be transparent, so that stakeholders and regulators can understand the process.
- The products of assessments conducted in separate regions or habitats should be comparable so that comparisons can be made on a statewide basis.
- The product of the assessment should be a measure or ranking of the risk to human health based on sediment contaminant concentrations. This measure should include a range of possible results to aid in prioritizing among sites.

### **1.4 Organization of the Report**

Section 2 of this report provides an overview of the assessment framework conceptual approach and key characteristics. Sections 3-5 describe each tier of the assessment in detail, including examples of calculation and interpretation. Recommendations for study design, sampling and chemical analysis are presented in Section 6. References for the literature citations are included in Section 7.

The remainder of the report includes appendices that provide details and background regarding the bioaccumulation model and selection of parameters for site linkage or chemical exposure calculations. Appendix 6 presents examples of applying the assessment framework to monitoring data sets from multiple water bodies throughout California, and Appendix 7 includes a comparison of bioaccumulation model performance.

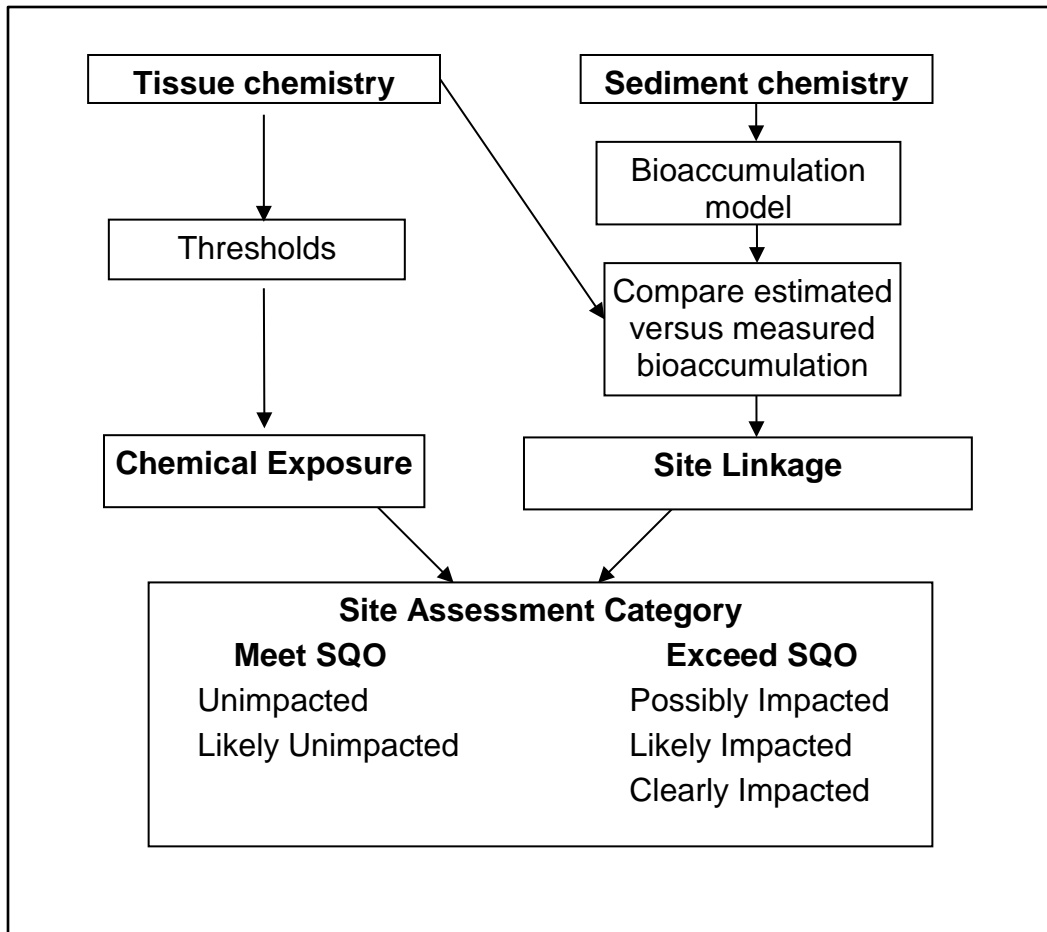
## 2 ASSESSMENT FRAMEWORK DESIGN

### 2.1 Conceptual Approach

Two indicators are evaluated to assess the HHSQO: 1) **Chemical Exposure**, defined as the extent to which pollutant concentrations in seafood pose unacceptable health risks to human consumers, and 2) **Site Linkage**, defined as the relative contribution of sediment contamination at the site to seafood contamination. Chemical exposure is evaluated by comparison of fish tissue contaminant concentrations to seafood consumption advisory levels established by California. Site linkage describes the strength of the association between sediment contamination (including flux into the water column) and seafood contamination. The presence of a strong linkage with site sediment is a critical element in determining whether the HHSQO is attained for the site because it indicates whether health risks are likely due to site conditions (relevant to the SQO) as opposed to off-site factors (e.g., fish movement or watershed loading) that are the focus of other regulatory programs. The degree of site linkage indicates the relative bioaccumulation due to sediment contamination from the site which is estimated using bioaccumulation models.

Integration of the chemical exposure and site linkage indicators produces a categorical site assessment. The categories represent the magnitude of health risk associated with sediment contamination within the site (Figure 2.1). The site assessment category indicates whether the human health SQO is met at the site (e.g., impacted by sediment contamination). These categories range from Unimpacted (best sediment quality) to Clearly Impacted (greatest deviation from the protected condition described in the HHSQO) and are structured similarly to the categories used to assess California's SQO for aquatic life protection (Bay and Weisberg 2012):

- **Unimpacted:** Site sediments have minimal impact, due to very low consumption risk overall
- **Likely Unimpacted:** Low health risk from site sediment contamination is present, or sediments are not responsible for the elevated risk
- **Possibly Impacted:** Unacceptable health risk, but site sediment contamination has a minor influence
- **Likely Impacted:** Unacceptable health risk is present and strongly linked to site sediment contamination
- **Clearly Impacted:** Site sediment contamination is the dominant factor responsible for a high level of health risk to many consumers



**Figure 2.1 Calculation, integration, and interpretation of assessment indicators.**

Application of the assessment framework is organized into three tiers (Figure 2.2). Each tier represents an increasing level of effort and complexity in order to enable the assessment to match variations in data availability, site complexity, and study objectives (U.S. EPA and U. S. Army Corps of Engineers 1991; 1998; Contaminated Sites Management Working Group 1999; Bridges *et al.* 2005; Chapman and Anderson 2005; Hope 2009).

Tier 1 consists of a screening assessment of tissue and/or sediment chemistry data to determine whether there is sufficient potential concern for human health impacts to warrant a complete site assessment. The purpose of Tier 1 is to provide an option for initial site evaluation with relatively low data requirements, thereby enabling rapid identification of areas of low concern (U.S. EPA and U. S. Army Corps of Engineers 1991; 1998; Hope 2009). Sediment or tissue chemical concentration data are interpreted using standardized conservative assumptions to evaluate concern for human consumers of seafood. If Tier 1 indicates potential concern, the analysis proceeds to Tier 2; otherwise, the site is determined to meet the SQO and further assessment is not needed.

Tier 2 represents a complete and standardized site assessment. Both tissue and sediment chemistry data, along with additional site-specific information, are evaluated to determine human health risk. Tier 2 differs from Tier 1 in three important respects. First, some default Tier 1 assumptions and parameters are replaced with site-specific assumptions and parameters, such as seafood forage area, and habitat characteristics. Second, estimates of chemical exposure (from tissue data) and site linkage (from sediment data) are compared to classify the site condition. Finally, the Tier 2 analysis produces a probabilistic output of site linkage to help communicate data variability and uncertainty. If Tier 2 results indicate an acceptable condition, the sediment is classified as meeting the human health SQO.

The Tier 3 assessment may be employed when trigger criteria are met and the Tier 2 results are deemed unreliable due to site-specific conditions such as other sources of contamination, temporal variability, or substantial uncertainty in exposure parameters (e.g., seafood exposure to site sediments, different human consumption rate, or bioavailability of contaminants in site sediments). The specifics of the Tier 3 assessment method are determined on a site-specific basis and might include the collection of additional data or use of alternative data analysis methods. However, final interpretation of the data to determine site conditions follows the same steps as in Tier 2 (Figure 2.1).

The HHSQO assessment approach focuses on the most important processes that govern the indirect effects of sediment contamination to human consumers of seafood. It is simpler than some sediment risk assessment models (e.g., Bridges *et al.* 2005). This model does not address other potential factors that could be important for individual sites. A site-specific Conceptual Site Model (CSM) is needed to address factors such as contaminant transfer between deep sediment and surface sediment; toxicological effects on aquatic plants or invertebrates; or changes over time in contaminant concentrations and transfer pathways. These factors may be important in site-specific evaluations (Davis 2004, Bridges *et al.* 2005, Gobas and Arnot 2005, Greenfield and Davis 2005) and merit use of a Tier 3 assessment. Often these issues are considered when management action or remedial alternatives are being considered, which is outside the scope of the HHSQO assessment. Use of different analytical and modeling approaches may be needed to develop management actions.

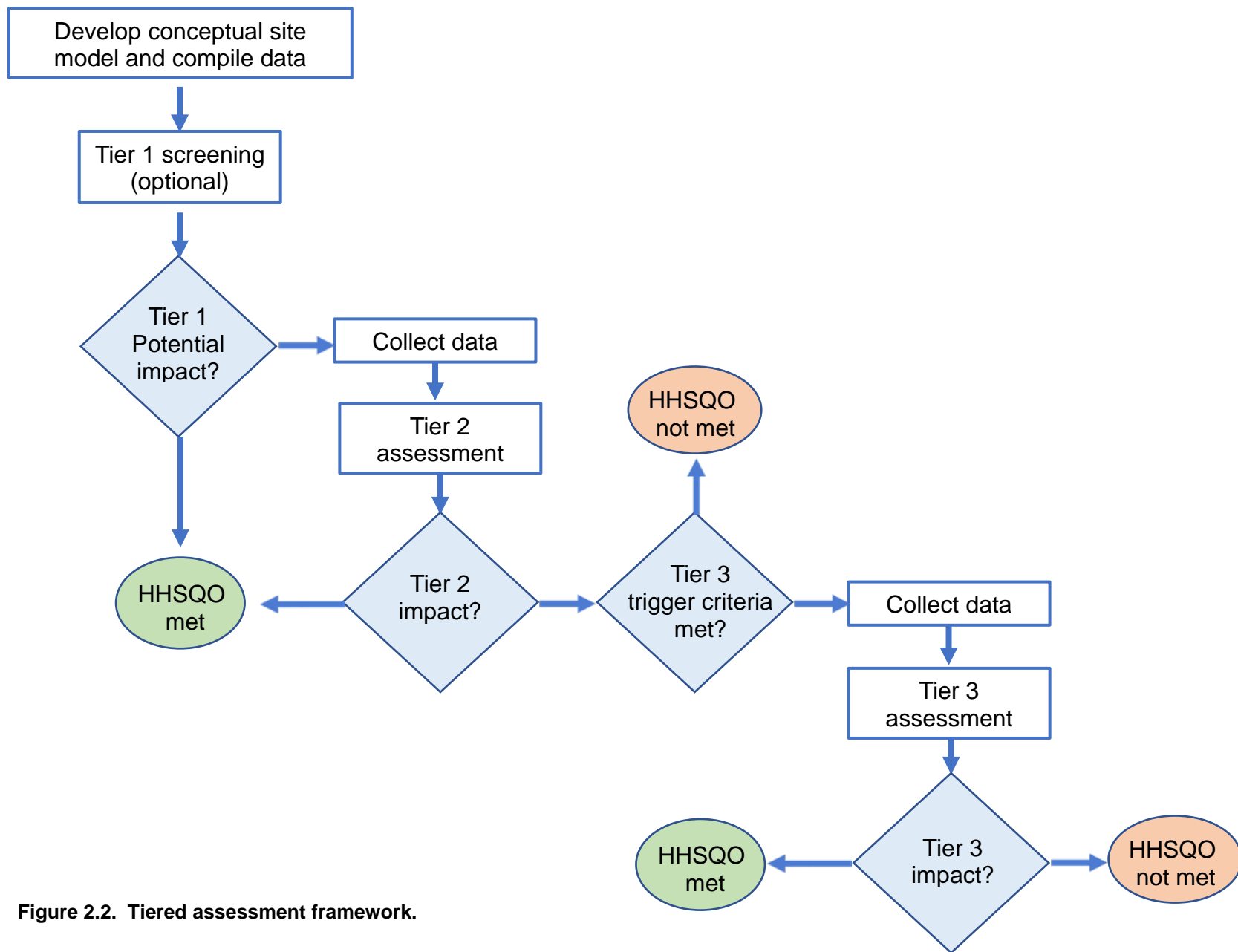


Figure 2.2. Tiered assessment framework.

## **2.2 Treatment of Uncertainty and Variability**

Uncertainty refers to lack of knowledge about specific factors, parameters, or models, while variability refers to observed differences attributable to true heterogeneity or diversity in a population or exposure parameter. The human health risk calculation method is similar between Tier 1 and Tier II, but the approach for incorporating uncertainty and variability differs.

Tier 1 employs a deterministic approach (i.e., based upon calculations that do not include a random element) to provide simplicity and ease of application. The Tier 1 approach addresses uncertainty and variability by employing conservative point estimates of key input parameter values.

Tier 2 employs a stochastic approach (i.e., incorporating a random element into model calculations) to characterize the effects of uncertainty and variability of key parameters related to site linkage calculation. Stochastic approaches have been used to evaluate human health risk in diverse regions, including the Palos Verdes Shelf (Wilson *et al.* 2001), the Housatonic River in New England (Weston Solutions 2005), San Francisco Bay (Gobas and Arnot 2005, 2010), and the New York-New Jersey Bight (Linkov *et al.* 2002). The Tier 2 stochastic analysis is standardized and limited in scope to focus on the uncertainty and variability of a subset of general parameters that will be locally available and are expected to influence the assessment outcome. More sophisticated and complex uncertainty analyses could be performed as part of a Tier 3 evaluation (Section 5).

## **2.3 Dietary Guild Approach**

A dietary guild approach is employed to evaluate health risk and model exposure from the sediment (Appendix 2). For this approach, finfish species in California estuaries and marine embayments are categorized in one of eight dietary guilds, based on trophic position and consumption of benthic prey. The guild approach is intended to provide biological realism, while having reasonable data requirements. The guiding principle is that incorporating information about seafood diet into target species selection and bioaccumulation modeling will provide a more realistic depiction of contaminant exposure than using generic assumptions. Species that consume similar prey types will have similar food web exposure to sediment-associated contaminants.

The guild approach informs the assessment in two aspects. Information regarding guild membership aids in selecting local seafood species for monitoring to assess risk to seafood consumers. Additionally, guild-based diet attributes for selected species are incorporated into the bioaccumulation model to estimate the contribution of site sediments to local seafood exposure.

## **2.4 Chemical Exposure Evaluation**

Human exposure and health risk associated with consumption of contaminated seafood is typically evaluated by calculating the additional risk of both cancer and noncancer adverse effects. California's Office of Environmental Health Hazard Assessment (OEHHA) has established statewide seafood consumption guidelines that consider both cancer risk and

noncancer hazard, balanced by the health benefits of consuming fish (OEHHA, 2008). These guidelines are in two forms: Fish Contaminant Goal (FCG) that represents a contaminant concentration below which no significant adverse health effects are expected, and Advisory Tissue Level (ATL) a concentration range where no significant health effects are expected at specified consumption rates of 1, 2, or 3 meals per week (Table 2.1).

All tiers of the HHSQO assessment framework use thresholds based on the OEHHA FCG and/or maximum of ATL ranges to determine the chemical exposure category. Use of the OEHHA values has several benefits for SQO assessment:

- Provides comparability with other state programs concerned with preventing adverse impacts from seafood consumption
- Values have been peer-reviewed and adopted by regulatory agencies
- Familiarity of stakeholders and public with use of values.
- Protect humans from both cancer and noncancer adverse impacts

**Table 2.1. OEHHA Fish Contaminant Goals (FCGs) and Advisory Tissue Levels (ATLs) based on an assessment of human health risk by OEHHA (Klasing and Brodberg, 2008). All values given in ng/g (ppb) wet weight. One serving is defined as 8 ounces (227 g) prior to cooking.**

Contaminant	FCG	ATL for 8 oz Serving Size (ng/g)			
		ATL3 3 servings per week	ATL2 2 servings per week	ATL1 1 serving per week	No Consumption
Chlordanes (ng/g)	≤ 5.6	≤ 190	> 190-280	> 280-560	> 560
DDTs (ng/g)	≤ 21	≤ 520	> 520-1000	> 1000-2100	> 2100
Dieldrin (ng/g)	≤ 0.46	≤ 15	> 15-23	> 23-46	> 46
PCBs (ng/g)	≤ 3.6	≤ 21	> 21-42	> 42-120	> 120

## 2.5 Site Linkage Evaluation

Site linkage is evaluated differently in each assessment tier. High site linkage is assumed in Tier 1, in line with the simplified and conservative approach of this tier. Tier 2 evaluates site linkage using a standardized approach and bioaccumulation model (Appendix 1), where the estimated biota concentration resulting from site sediment contamination is compared to observed concentrations for the same species. Evaluation of site linkage in Tier 3 is more flexible and may use alternate methods or models, as long as the conceptual approach and method of classifying linkage strength is comparable to Tier 2.

## 2.6 Development of a Conceptual Site Model

For an end user to apply this indirect effects framework, the first step is to develop a conceptual site model (CSM) much like the general model discussed in Section 2.1 but focused on the specific site or waterbody characteristics, contaminants, receptors, and sources. This is needed to structure the indirect effects assessment. CSM development is flexible; however, CSMs generally include a written description of the specific issues associated with a site, as well as a graphical depiction of contaminant sources, processes, and receptors (i.e., target species). The graphical depiction aids in beginning to identify potential linkages, as well as sources of uncertainty, such as what types of anglers capture and consume fish from the site, how frequently does fishing activity occur, and what seafood species occur in the site.

Several documents provide general recommendations on CSM development (Cura *et al.* 1999; Bridges *et al.* 2005; USEPA 2005, 2008a, 2009). Recommendations include that the CSM should be based on local information and expertise, and developed in a collaborative process that includes local environmental managers, impacted stakeholders, and scientists. The CSM can be informed by prior and ongoing scientific activities, including literature, prior field data collection, anecdotal evidence, and modeling activities. This information should be documented as part of CSM development. Issues to be considered and addressed include: model assumptions; key processes; spatial and temporal scales of interest; system characteristics and behaviors; available data sources and collection programs; and data gaps (USEPA 2008a). The CSM should be written in clear language with a minimum of jargon. Examples of CSMs for PCBs and legacy pesticides in California estuaries and marine embayments include von Stackelberg *et al.* (2003), Connor *et al.* (2004), Anchor Environmental (2005), and Davis *et al.* (2006a).

The CSM should identify water body characteristics, key exposure pathways, and areas of uncertainty (USEPA 2009). For HHSQO assessment, exposure pathways are defined, a priori, as human consumption of contaminated seafood. However, there are site-specific aspects of human seafood consumption that should be addressed in the CSM. Specifically, the CSM should contain information needed to determine the following parameters:

- Site boundaries and site size
- Seafood consumer population characteristics (e.g., consumption rate)
- Seafood species to be monitored
- Food web associated with seafood
- Site-specific modification to other parameters (e.g., seafood movement range or diet) as needed
- Sources
- Fate and transport mechanisms

A definition of the site boundaries and site size is needed to aid in data collection and data reduction, in addition to being a key input for the site linkage indicator. Site boundaries may be defined based on geomorphic and hydrologic boundaries, areas of management concern, previous boundary definitions (e.g., water body segments), and other local considerations.



Selection of the site size can have a large influence on the accuracy and reliability of the assessment. Selection of a small site within a larger water body, such as an individual marina, small basin, or channel is discouraged, as it is likely that overlapping contaminant inputs from offsite sources, currents, and fish movement will substantially under estimate the influence of sediment contamination on the chemical exposure indicator. Several priority species for chemical exposure evaluation have home ranges greater than several km<sup>2</sup> and attempting to conduct an HHSQO assessment at sites smaller than 1 km<sup>2</sup> will tend to minimize the contribution of site-associated sediment contamination. In general, it is preferable to conduct the assessment at the largest scale that is relevant to the project and then consider specific management alternatives at a smaller scale if appropriate.

Another consideration is the spatial distribution of sediment contamination within a site. Some sites may contain specific areas of elevated contamination (“hotspots”), and it may be worthwhile to perform the assessment at multiple scales, including the hotspots, as well as less contaminated areas, to determine whether the assessment outcome would be different. During the CSM development, it would be useful to compile existing data on contamination in seafood and sediment, and plot the results to examine the spatial distribution of contamination. Similarly, journal publications and technical reports describing contaminant sources and spatial patterns should be summarized, and local experts consulted, to identify potential hotspot areas.

The seafood consumer population is chosen based on what is known about fishing practices and consumption rates at the site. Selection of an appropriate consumer population will aid in identifying available information on local consumption rates to give perspective to the consumption rates established for determining the chemical exposure category. Surveys from other California water bodies may be employed to determine consumption rates if local data are not available. Selection of seafood species of interest will be based on the fishing and consumption practices of local consumers, as well as species known to reside in the site, and representing predominant dietary guilds.

Additionally, the CSM can describe the broader environmental processes and pathways that affect human exposure to contaminated seafood at the site. This can include a depiction of the historic and current sources and processes that potentially result in elevated or reduced site sediment contamination (USEPA 2009). Examples of potential sources are legacy contaminated sites, agricultural or urban areas in which the contaminants were historically used. Processes that change site sediment contamination may include erosion or deposition events, or management activities that contribute to or reduce food web exposure to sediment contamination. The CSM may also include a description of other environmental matrices or areas outside the site that could result in food web contaminant exposure (e.g., known hotspots outside the site; ongoing external sources such as tributaries or storm basins). More complex contaminant fate and process information may be incorporated into a Tier 3 assessment, if deemed necessary.

CSM development is a dynamic process. As additional data and information becomes available, they are used to refine the CSM, by adding additional sources, pathways, or targets, or modifying existing linkages. As proposed in this framework, a preliminary CSM should be developed prior to Tier 1 assessment, and CSM refined prior to Tiers 2 or 3 assessment.

### 3 TIER 1 SCREENING EVALUATION

Tier 1 is an optional rapid screening evaluation that uses available data. The outcome of this assessment is binary, either the site is classified as unimpacted (meets SQO) or the site is determined to have sufficient potential for human health impacts and thus a complete assessment is needed (Tier 2 or 3).

Tier 1 utilizes conservative assumptions to address uncertainty and reduce the chance of concluding unacceptable chemical exposure does not exist when in fact it does. High site sediment linkage is assumed for Tier 1, meaning that all the observed fish tissue contamination is assumed to be derived from site sediment contamination. The assessment outcome is therefore based on whether resident fish tissue contamination exceeds a screening threshold. The assessment may be based on either measured sport fish tissue or sediment contaminant concentration, depending upon what data are available (Figure 3.1). If both sediment and tissue contamination data are available, the Tier I assessment is performed using both data types. A separate assessment is conducted for each contaminant group (PCBs, DDTs, chlordanes, or dieldrin).

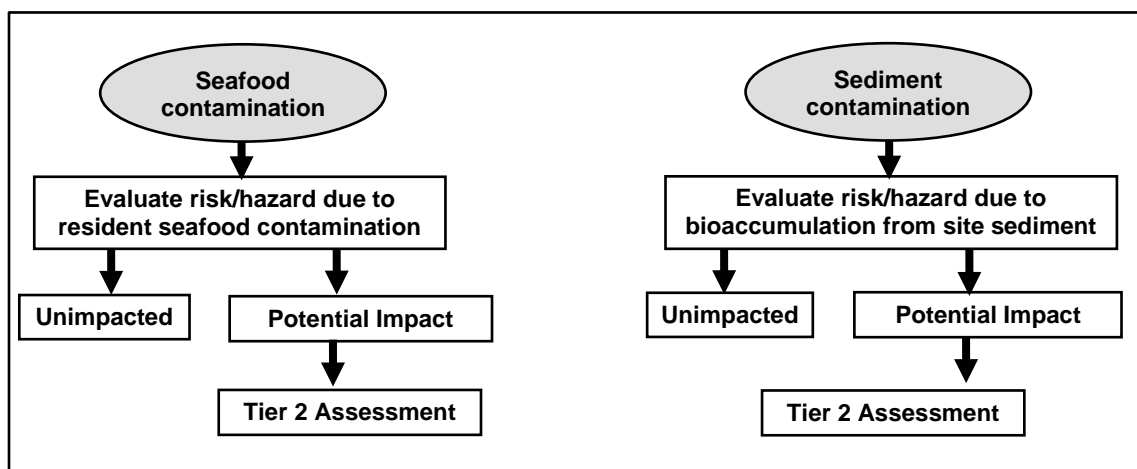


Figure 3.1. Tier 1 process using either seafood or sediment contamination data.

#### 3.1 Tissue Evaluation

The tissue-based chemical exposure evaluation is performed by comparing measured tissue concentration to screening thresholds. This comparison is based on tissue data from all the species identified in the CSM. The 95% upper confidence limit (UCL) of the concentration is used for comparison to provide a safety factor and address data uncertainty.

The Tier 1 tissue evaluation concentration ( $C_{Tis95}$ ) is equal to the mean of the 95% upper confidence limit (UCL) of the mean tissue concentration for each species.

$$C_{Tis95} = [\Sigma C_{Tis95i}]/n$$

Where

$C_{Tis95i}$  = 95%UCL of the mean tissue concentration for sport fish species i (ng/g ww)

$\Sigma$  is the sum across all species, and n is the number of species.

Where the sample size is too low to calculate the UCL for a given species (less than 3), the maximum concentration is used for that species.

Chemical exposure is evaluated by comparison of  $C_{Tis95}$  to thresholds corresponding to the maximum of the OEHHA ATL3 range (Table 3.1). If the tissue concentration is greater than any tissue screening threshold in Table 3.1, there is the potential for unacceptable chemical exposure and a Tier 2 evaluation is required. If the tissue concentration is equal to or less than the tissue screening threshold, the chemical exposure is acceptable and the site is assessed as Unimpacted.

**Table 3.1. Tier 1 tissue screening thresholds (maximum of ATL3).**

DDT (ng/g ww)	PCB (ng/g ww)	Chlordane (ng/g ww)	Dieldrin (ng/g ww)
>520	>21	>190	>15

### 3.2 Sediment Evaluation

Tier 1 sediment evaluation is also based on chemical exposure. The Tier 1 Sediment Evaluation is performed by comparing site sediment concentration to sediment screening thresholds. Sediment screening thresholds are calculated for each contaminant evaluated at the site. To conduct the sediment evaluation, compare the 95% UCL of the mean concentration for site sediment to the threshold. Where the sample size is too low to calculate the UCL, the maximum sediment contaminant concentration is used as the site linkage estimate.

The sediment threshold is calculated as the tissue threshold divided by a biota-sediment accumulation factor (BSAF):

$$T_{Sed} = (T_{Tis})/(BSAF)$$

Where

$T_{Sed}$  = sediment screening threshold (ng/g dw)

$T_{Tis}$  = tissue screening threshold in nanograms per gram wet weight (ng/g ww)

BSAF = biota-sediment accumulation factor (BSAF)

The highest BSAF for the dietary guilds identified in the CSM is used in calculating the sediment screening threshold. Tissue screening thresholds are provided in Table 3.1. The BSAF for each contaminant is determined based on the contaminant, dietary guild, and site total organic carbon (Table 3.2). A site sediment concentration (95% UCL of the mean) that is equal to or less than  $T_{Sed}$  is evaluated as Unimpacted. Concentrations greater than  $T_{Sed}$  are classified as potentially impacted and require Tier 2 evaluation to make an assessment.

**Table 3.2. Tier 1 Biota sediment accumulation factors (BSAF) calculated for percent sediment total organic carbon.**

TOC (%)	1. Piscivore (California Halibut)				2. Benthic with piscivory (Spotted Sand Bass)				3. Benthic and pelagic with piscivory (Queenfish)				4. Benthic without piscivory (White Croaker)			
	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs
0.1	47.8	57.5	23.2	54.6	53.5	67.7	24.8	64.7	68.9	81.5	32.6	76.6	62.3	72.9	39.1	70.1
0.2	24.5	30.2	11.6	29.0	27.9	36.3	12.6	35.0	34.9	41.9	16.4	39.6	32.9	40.3	20.0	39.4
0.3	16.7	21.0	7.8	20.4	19.3	25.7	8.6	25.1	23.6	28.6	11.0	27.2	23.1	29.4	13.6	29.1
0.4	12.8	16.4	5.9	16.0	15.0	20.4	6.5	20.1	17.9	22.0	8.3	21.0	18.2	23.8	10.4	23.8
0.6	8.9	11.8	4.0	11.6	10.7	15.1	4.5	15.0	12.3	15.4	5.5	14.8	13.2	18.1	7.2	18.4
0.8	6.9	9.5	3.0	9.4	8.6	12.4	3.5	12.4	9.4	12.0	4.2	11.7	10.7	15.2	5.6	15.5
1.0	5.7	8.0	2.4	8.0	7.3	10.7	2.9	10.8	7.7	10.0	3.4	9.8	9.2	13.3	4.6	13.7
1.2	4.9	7.0	2.1	7.1	6.4	9.5	2.5	9.7	6.6	8.7	2.8	8.5	8.1	12.0	4.0	12.5
1.4	4.4	6.3	1.8	6.4	5.7	8.7	2.2	8.9	5.8	7.7	2.5	7.6	7.4	11.1	3.5	11.5
1.6	3.9	5.8	1.6	5.9	5.3	8.0	1.9	8.2	5.1	7.0	2.2	6.9	6.8	10.3	3.2	10.7
1.8	3.6	5.4	1.4	5.5	4.9	7.5	1.8	7.7	4.7	6.4	1.9	6.3	6.4	9.7	2.9	10.1
2.0	3.3	5.0	1.3	5.1	4.6	7.1	1.6	7.3	4.3	5.9	1.8	5.9	6.0	9.2	2.7	9.6
2.5	2.8	4.3	1.1	4.5	4.0	6.3	1.4	6.5	3.6	5.1	1.4	5.1	5.3	8.2	2.3	8.5
3.0	2.5	3.9	0.9	4.0	3.6	5.7	1.2	5.9	3.1	4.5	1.2	4.5	4.8	7.4	2.0	7.8
3.5	2.2	3.5	0.8	3.6	3.3	5.3	1.1	5.5	2.8	4.1	1.1	4.1	4.4	6.8	1.8	7.2
4.0	2.1	3.3	0.7	3.4	3.1	4.9	1.0	5.1	2.5	3.7	0.9	3.8	4.1	6.4	1.7	6.7

Chlor – Chlordane      Diel – Dieldrin

**Table 3.2. Continued.**

TOC (%)	5. Benthic and pelagic without piscivory (Shiner perch)				6 Benthic with herbivory (Common Carp)				7. Benthic and pelagic with herbivory (Topsmelt)				8. Pelagic with benthic herbivory (Striped Mullet)			
	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs	Chlor	DDTs	Diel	PCBs
0.1	23.8	27.5	14.7	26.4	52.6	52.8	38.9	49.0	17.8	18.5	12.8	17.4	38.1	31.3	36.4	28.3
0.2	12.3	14.7	7.4	14.3	27.6	28.3	20.2	26.5	9.1	9.6	6.5	9.1	20.0	16.7	18.9	15.3
0.3	8.5	10.4	5.0	10.3	19.3	20.1	13.9	18.9	6.2	6.6	4.3	6.3	13.9	11.9	13.0	10.9
0.4	6.6	8.3	3.8	8.2	15.1	15.9	10.8	15.2	4.7	5.1	3.3	4.9	10.9	9.4	10.1	8.7
0.6	4.7	6.1	2.6	6.1	10.9	11.8	7.7	11.3	3.3	3.6	2.2	3.5	7.9	7.0	7.2	6.5
0.8	3.7	5.0	2.0	5.1	8.8	9.6	6.1	9.3	2.5	2.9	1.7	2.8	6.4	5.7	5.7	5.4
1.0	3.1	4.3	1.6	4.4	7.5	8.3	5.2	8.1	2.1	2.4	1.4	2.4	5.4	5.0	4.8	4.7
1.2	2.7	3.8	1.4	3.9	6.6	7.4	4.5	7.3	1.8	2.1	1.2	2.1	4.8	4.5	4.2	4.3
1.4	2.4	3.5	1.2	3.6	6.0	6.8	4.1	6.7	1.6	1.9	1.0	1.9	4.4	4.1	3.8	3.9
1.6	2.2	3.2	1.1	3.3	5.5	6.3	3.7	6.2	1.4	1.7	0.9	1.7	4.0	3.8	3.5	3.7
1.8	2.1	3.0	1.0	3.1	5.1	5.8	3.4	5.8	1.3	1.6	0.8	1.6	3.7	3.6	3.2	3.5
2.0	1.9	2.8	0.9	2.9	4.8	5.5	3.2	5.5	1.2	1.5	0.7	1.5	3.5	3.4	3.0	3.3
2.5	1.7	2.5	0.8	2.6	4.2	4.9	2.8	4.8	1.0	1.3	0.6	1.3	3.1	3.1	2.6	3.0
3.0	1.5	2.2	0.7	2.4	3.8	4.4	2.5	4.4	0.9	1.2	0.5	1.2	2.8	2.8	2.4	2.7
3.5	1.4	2.1	0.6	2.2	3.4	4.0	2.3	4.0	0.8	1.1	0.5	1.1	2.6	2.6	2.2	2.6
4.0	1.3	1.9	0.5	2.0	3.2	3.7	2.2	3.8	0.8	1.0	0.4	1.0	2.4	2.5	2.0	2.4

Chlor – Chlordane      Diel – Dieldrin

### 3.3 Tier 1 Interpretation

The Tier 1 screening evaluation is only applied to assess whether sediment is unimpacted in relation to the sediment quality objective or if a more detailed analysis is required by conducting a Tier 2 assessment. Possible outcomes of the Tier 1 screening are described below.

If either tissue or sediment is applied in Tier 1 and the result exceeds the threshold for any constituent, Tier 2 is required for those constituents. If both tissue and sediment are applied the possible outcomes are as follows:

- A. If both tissue and sediment results fall below the threshold, the chemical exposure associated with the sediment and tissue is acceptable and the sediment quality is **Unimpacted**.
- B. If tissue results fall below the threshold and sediment equals or exceeds the threshold, the chemical exposure is acceptable and the sediment quality is **Unimpacted**.
- C. If sediment results fall below the threshold and tissue equals or exceeds the threshold, the chemical exposure to consumers is potentially unacceptable and a **Tier 2 assessment is needed**.
- D. If both sediment and tissue results equal or exceed the threshold, the chemical exposure to consumers is potentially unacceptable and a **Tier 2 assessment is needed**.

### 3.4 Tier 1 Site Assessment Steps

The following steps should be followed to conduct a Tier 1 screening assessment:

#### *Step 1: Develop a conceptual site model*

The conceptual site model is needed to define the site boundaries, guide selection of seafood species to evaluate, and identify appropriate sediment contamination data.

#### *Step 2: Calculate contaminant concentration*

For either seafood tissue or sediment data, the contaminant concentration is calculated as the 95% upper confidence limit (UCL) of the arithmetic average (i.e., Mean + 2 \* Standard Error of the Mean). The estimated concentration is obtained using all appropriate data within the site boundaries (defined in Step 1). For sediment data, average total organic carbon (TOC) concentration is also calculated.

#### *Step 3: Calculate sediment threshold for site*

For sediment data evaluation, a sediment threshold is calculated for each contaminant evaluated at the site. The sediment threshold is calculated as the tissue threshold divided by a bioaccumulation factor (BSAF).

$$\text{sediment threshold} = (\text{tissue threshold})/(\text{BSAF}).$$

The BSAF is obtained from a look up table, based on the contaminant, fish guild, and site TOC.

#### ***Step 4: Compare data to thresholds and determine assessment outcome***

The results are interpreted as described in Section 3.3. A Tier 1 assessment results in one of two categorical outcomes, depending on how site concentrations compare to threshold values.

1. **Unimpacted:** Concentrations are below threshold values, indicating low potential risk to sport fish consumers based on the data evaluated. Results should be corroborated with both data types, if available. If only one data type is available, then no further evaluation is needed, and the analysis is complete.
2. **Proceed to Tier II:** Concentrations are above threshold values, indicating potential risk to sport fish consumers based on the tissue or sediment data evaluated. Tier 2 assessment is needed to confirm the results.

### **3.5 Tier 1 Case Study Example**

A case study example from San Francisco Bay illustrates the Tier 1 assessment process.

**Step 1.** The CSM identified three fish species for assessment: leopard shark, white croaker, and shiner perch.

**Step 2.** Measurements of sediment and fish tissue are summarized in Table 3.3.

**Table 3.3. Summary of sediment and fish tissue data from San Francisco Bay case study example. All contaminant results are the 95% UCL of the average. Sediment TOC is the average. Tissue values are reported in ng/g ww and sediment values are reported in ng/g dw.**

Matrix	Species Guild	DDTs	PCBs	Chlordanes	Dieldrin	TOC (%)
Leopard shark	Benthic diet with piscivory	10.5	25.3	1.4	0.7	
White croaker	Benthic and pelagic diet without piscivory	70.4	251	12.1	2.2	
Shiner perch	Benthic diet without piscivory	27.4	122	6.7	1.6	
Three species combined	Average of three species	36.1	133	6.7	1.5	
Sediment		2.6	7.0	0.2	0.1	1.3

**Step 3.** Sediment thresholds were calculated based on Tier 1 tissue thresholds and the highest BSAF corresponding to the three fish guilds sampled (Table 3.2). If the exact TOC is not listed in the table, then either use the value for the next lowest TOC or interpolate. In this example BSAFs corresponding to 1.2 % TOC were used. For all compounds, white croaker (benthic and pelagic diet without piscivory) had the highest BSAF. These BSAFs were used to calculate the sediment thresholds (Table 3.4).

**Table 3.4. Calculation of Tier 1 sediment thresholds for the San Francisco Bay case study.**

Compound	Tissue Threshold	Bioaccumulation Factor	Sediment Threshold Calculation	Sediment Threshold
		White Croaker (Benthic diet without piscivory)		
Chlordane	190	8.1	190/8.1 =	23.5
DDTs	520	12.0	520/12.0 =	43.3
Dieldrin	15	4.0	15/4.0 =	3.8
PCBs	21	12.5	21/12.5 =	1.7

**Step 4.** Tissue and sediment results were directly compared to the Tier 1 threshold for each contaminant (Table 3.5). Examination of the tables illustrates consistent findings for sediment and tissue. Neither sediment nor tissue results exceeded the Tier 1 thresholds for DDTs, chlordanes, or dieldrin. Both sediment and tissue concentrations exceeded their respective thresholds for PCBs. In this example, both sediment and tissue data indicated that the sediment quality is unimpacted for pesticides, and that a Tier 2 evaluation should be employed for PCBs.

**Table 3.5. Comparison of tissue concentrations (ng/g ww) to the Tier 1 screening thresholds. Highlighted results exceed the Tier 1 tissue threshold.**

Parameter	DDT	PCB	Chlordane	Dieldrin
Observed tissue concentration	36.1	133	6.7	1.5
Tissue threshold	520	21	190	15
Observed sediment concentration	2.6	7.0	0.2	0.1
Sediment threshold	43.3	1.7	23.5	3.8



## 4 TIER 2 ASSESSMENT

Tier 2 is a standardized site-specific assessment which utilizes targeted data based on the developed conceptual site model. The possible outcomes of this assessment are Unimpacted, Likely Unimpacted, Possibly Impacted, Likely Impacted, and Clearly Impacted. Results of Possibly, Likely, and Clearly Impacted represent a failure to meet the HHSQO. The overall results from the Tier 2 assessment are a product of both chemical exposure and site linkage (Figure 4.1). Like in Tier 1, a separate assessment is conducted for each contaminant group (PCBs, DDTs, chlordanes, or dieldrin). These calculations can be performed using the provided equations and bioaccumulation model; however, a Decision Support Tool (DST) has been developed to facilitate data analysis and integration. The DST is programmed with the model and indicator calculations necessary to complete the Tier 2 assessment. The DST and user guide is available at:

<http://www.sccwrp.org/Data/DataTools/SedimentQualityAssessment.aspx>

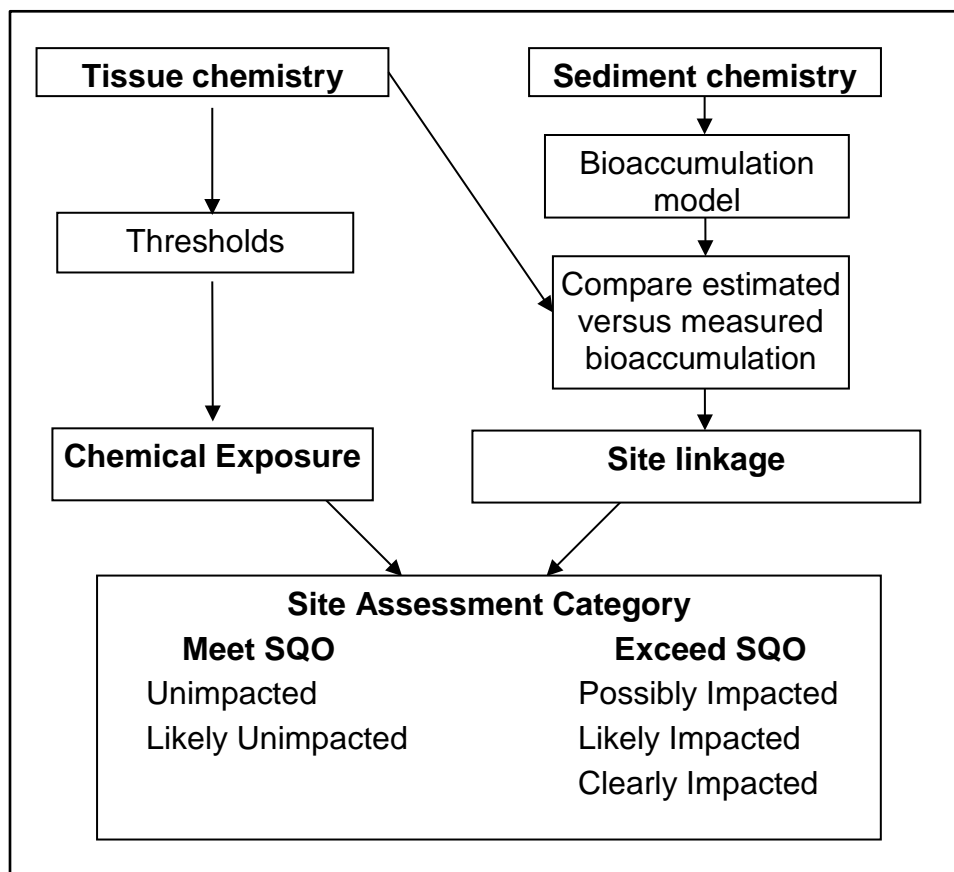
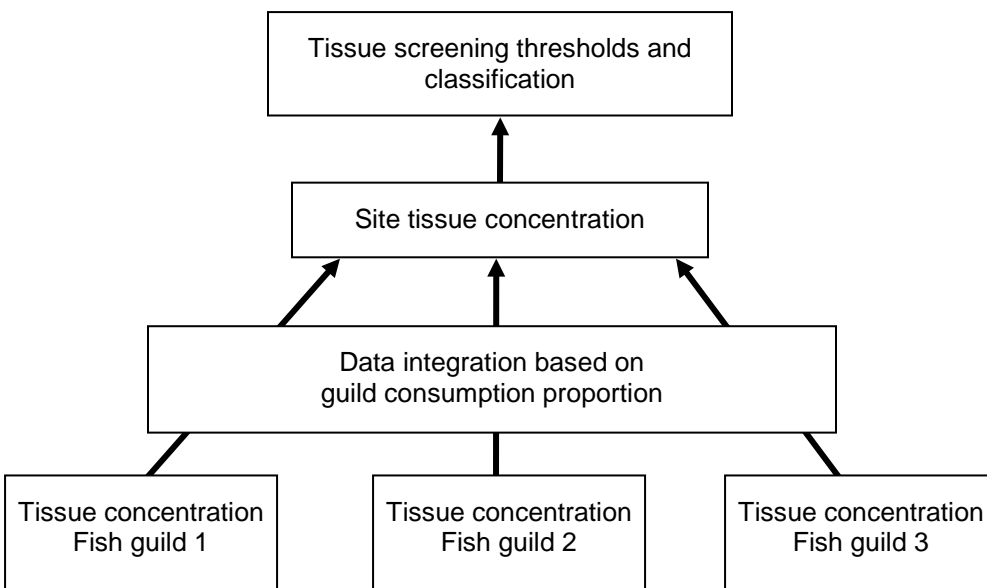


Figure 4.1 Calculation, integration, and interpretation of Tier 2 assessment indicators.

## 4.1 Chemical Exposure

Chemical exposure is determined using the weighted average measured tissue concentration (Figure 4.2). This is calculated for each chemical class based on the diet proportion for each fish species represented and measured tissue concentration. Compare this weighted average to the chemical exposure thresholds (Table 4.1).



**Figure 4.2. Strategy for determining the chemical exposure to seafood consumers. The number of guilds included in the analysis depends of the conceptual site model.**

**Table 4.1. Chemical Exposure thresholds. Based on OEHHA Fish Contaminant Goals (FCGs) and Advisory Tissue Levels (ATLs) (Klasing and Brodberg, 2008). All values given in ng/g (ppb) wet weight.**

Contaminant	FCG	ATL for 8 oz Serving Size (ng/g)			
		ATL3 3 servings per week	ATL2 2 servings per week	ATL1 1 serving per week	No Consumption
Chlordanes (ng/g)	≤ 5.6	≤ 190	> 190-280	> 280-560	> 560
DDTs (ng/g)	≤ 21	≤ 520	> 520-1000	> 1000-2100	> 2100
Dieldrin (ng/g)	≤ 0.46	≤ 15	> 15-23	> 23-46	> 46
PCBs (ng/g)	≤ 3.6	≤ 21	> 21-42	> 42-120	> 120
Score	1	2	3	4	5
Category	Very Low	Low	Moderate	High	Very High

## 4.2 Site Linkage

Tier 2 site linkage is based on the Arnot and Gobas food web model (2004), modified by Gobas and Arnot (2010). This is a mechanistic bioaccumulation model which has limited complexity to increase ease of application while accurately depicting the primary bioaccumulation processes (Burkhard 1998, Arnot and Gobas 2004). The model is structured to depict contaminant concentration in biota as the mass balance of key uptake and loss processes. The model equation structure accounts for uptake by diet and respiration; loss by egestion, metabolism, and respiratory elimination; and growth dilution. More detailed information can be found in Appendix 1.

Biota Concentration ( $C_{\text{Biota}}$ )=  
(Respiratory Uptake\*Water Concentration+ Dietary Uptake\*Prey Concentration) /  
(Elimination + Fecal Egestion + Growth + Metabolism)

This concentration is then converted to BSAF:

$$\text{BSAF} = C_{\text{Biota}}/C_{\text{Sed}}$$

where  $C_{\text{Sed}}$  is the measured concentration in the sediment.

Monte Carlo Simulation (MCS) is used to incorporate the variability of both the measured sediment and tissue concentrations, the fish guild home range (HR), and the estimated BSAF values. For this analysis, a lognormal distribution is used for BSAF and sediment concentrations, and the appropriate distributions for each home range is indicated in Table 4.2. A total of 10,000 iterations should be used for the simulation.

The overall site linkage is calculated as:

$$\text{Site linkage} = C_{\text{Est}}/C_{\text{Tis}}$$

$C_{\text{Est}}$  = weighted average estimated tissue concentration based on the proportion of the human diet for each guild (ng/g).

Calculate the average estimated tissue concentration for each guild, i, and contaminant class (i.e., total DDTs) using the following equation:

$$C_{\text{Est},i} = \Sigma C_{\text{Sed}} \times \text{SUF}_i \times \text{BSAF}_i$$

$\Sigma C_{\text{Sed}}$  = lognormal distribution of sediment concentration using the measured mean and standard error

$\text{SUF}_i$  = HR distribution using the HR mean and HR standard deviation (SD) as found in Table 4.2. If the calculated SUF is less than 1, use the calculated value. If the SUF is greater than 1, use the value of 1.

$\text{BSAF}_i$  = lognormal distribution of the mean BSAF for guild, i, from the model prediction and the calculated BSAF SD.

$$\text{BSAF SD} = \text{CVBSAF} \times \text{BSAF}$$

$$\text{CVBSAF} = 0.782$$

The CVBSAF was estimated from empirical data using the following equations:

$$SD = \sqrt{(m^2)(e^{\sigma^2} - 1)}$$

$$CV = \frac{\sqrt{(m^2)(e^{\sigma^2} - 1)}}{m} = \sqrt{(e^{\sigma^2} - 1)}$$

Where  $\sigma$  = lognormal standard deviation

m = mean (this value cancels out)

CV = coefficient of variation

$C_{Tis}$  = weighted average observed tissue concentration

Use a lognormal distribution for measured mean tissue data and standard error for each guild for total chlordanes, total dieldrin, total DDTs, and total PCBs.

Calculate the weighted average for each contaminant class based on the proportion of the human diet for each guild (ng/g).

**Table 4.2. Home range parameters for each sport fish guild.**

Species	Guild	HR Basis	HR Mean	HR SD	HR Distribution
California halibut	Piscivore	Site length (km)	29.3	60	Lognormal distribution
Spotted sand bass	Benthic diet with piscivory	Site area (km <sup>2</sup> )	0.0071	0.0073	Lognormal distribution
Queenfish	Benthic and pelagic with piscivory	Site area (km <sup>2</sup> )	3	4.689	Lognormal distribution
White croaker	Benthic without piscivory	Site area (km <sup>2</sup> )	3	4.689	Lognormal distribution
Shiner perch	Benthic and pelagic without piscivory	Site area (km <sup>2</sup> )	0.0012	0.000804	Lognormal distribution
Common carp	Benthic with herbivory	Site length*1000 (km)	1.05	9904	Inverse gamma cumulative distribution*
Topsmelt	Benthic and pelagic with herbivory	Site area (km <sup>2</sup> )	0.0012	0.000804	Lognormal distribution
Striped mullet	Pelagic with benthic herbivory	Site length (km)	28.2	80.34	Lognormal distribution

HR mean = mean home range of seafood species under consideration (km or km<sup>2</sup>, depending on taxa).

HR SD = standard deviation of home range of seafood species

\*Inverse gamma cumulative distribution requires 3 terms:

Probability= a random number uniformly distributed over  $0 \leq x < 1$

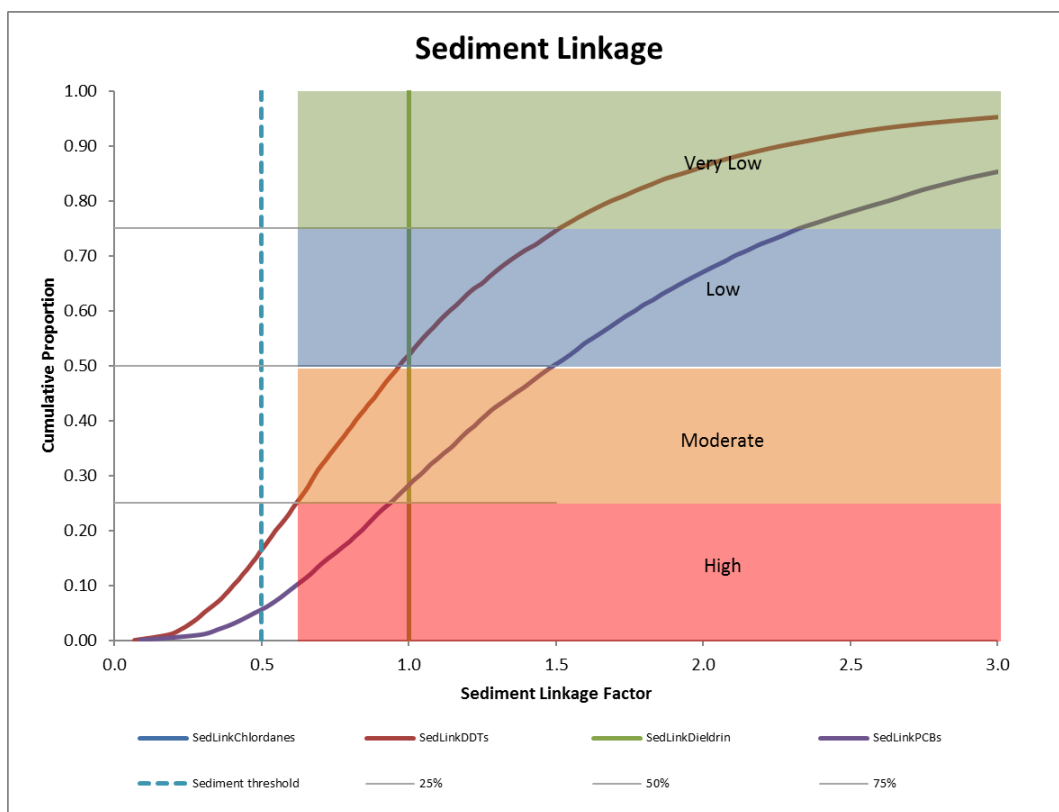
Alpha= HR mean value (shape parameter)

Beta= HR SD value (scale parameter)

Use of the Monte Carlo Simulation for the site linkage calculation results in a distribution of values. A site linkage value of 0.5 was chosen as the threshold. The assessment outcome is based on the cumulative percentage of the distribution which falls above or below that threshold (Table 4.3). An example of this distribution is shown in Figure 4.3.

**Table 4.3. Site sediment linkage categories for Tier 2 evaluation.**

Cumulative % of site linkage distribution	Linkage threshold	Outcome
75%	<0.5	1. Very Low
50%	<0.5	2. Low
25%	<0.5	3. Moderate
25%	≥0.5	4. High



**Figure 4.3. An example of site sediment linkage distributions for DDTs (red line plot) and PCBs (purple line plot). The blue dashed line is the 0.5 threshold and the colored sections (green, blue, orange, and red) denote the various assessment outcome groups.**

### 4.3 Tier 2 Interpretation

A standardized method for integrating and interpreting the indicator results was created to ensure comparability of assessments among different sites. Each indicator is classified into multiple categories (five chemical exposure categories and four site linkage categories) resulting in 20 possible combinations of indicators (Table 4.4).

**Table 4.4. Site assessment matrix.**

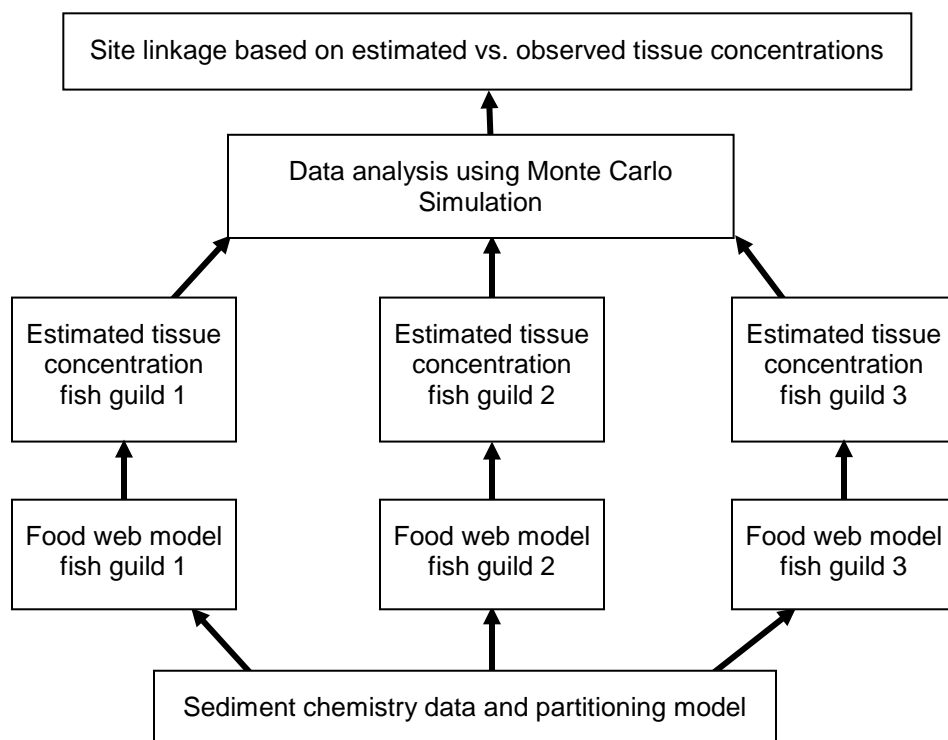
		Chemical Exposure				
		Very Low	Low	Moderate	High	Very High
Site Sediment Linkage	Very Low	Unimpacted	Unimpacted	Likely Unimpacted	Likely Unimpacted	Likely Unimpacted
	Low	Unimpacted	Unimpacted	Likely Unimpacted	Possibly Impacted	Likely Impacted
	Moderate	Unimpacted	Likely Unimpacted	Likely Impacted	Likely Impacted	Clearly Impacted
	High	Unimpacted	Likely Unimpacted	Likely Impacted	Clearly Impacted	Clearly Impacted

### 4.4 Tier 2 Site Assessment Steps

Analyzing data and interpreting the results includes seven steps, which are illustrated in the case study example (Section 4.5). Figures 4.2 and 4.4 provide an overview of the process for calculating chemical exposure and site linkage.

- Step 1: Develop conceptual site model.
- Step 2: Input data for site-specific parameters and chemical concentration.
- Step 3: Run the bioaccumulation model to calculate bioaccumulation factors for use in site linkage calculations.
- Step 4: Perform simulations to generate cumulative probability distributions of site linkage results.
- Step 5: Plot and evaluate results of the simulations.
- Step 6: Categorize results for the chemical exposure and site linkage indicators.
- Step 7: Compare the results for the two indicators to make a site assessment.

This process is conducted for each contaminant group separately. The final site assessment is based on the highest level of risk from site contamination obtained for any compound.



**Figure 4.4. Strategy for determining the site linkage to fish bioaccumulation. The number of guilds included in the analysis depends of the conceptual site model.**

#### 4.5 Tier 2 Case Study Example

A case study is presented using monitoring data to illustrate the Tier 2 assessment approach, and graphical depictions of the output. The example focuses on the Los Angeles Outer Harbor. In this example, DDT concentrations in sport fish and sediment are evaluated and integrated to make a site assessment.

The purpose of this example is to illustrate how the Tier 2 assessment would be performed. The data used in the example have been compiled from multiple studies whose study designs may not be optimal for HHSQO assessment. Also, due to the nature of this example, the conceptual site model is hypothetical.

##### ***Step 1: Develop conceptual site model.***

The CSM identified five fish species for assessment, including the California halibut, queenfish, white croaker, shiner perch, and topsmelt.

##### ***Step 2: Input data for site-specific parameters and chemical concentration.***

In the second step of the analysis, data are summarized and entered into the Decision Support Tool (DST), which performs calculations for Steps 3 and 4. The stochastic approach requires explicit local specification of tissue and sediment concentrations. Based on the conceptual site model, sum DDT concentrations (mean and SE) were calculated for the five finfish species mentioned in Step 1. Average and standard error tissue concentrations for sum DDTs, and

average tissue lipid concentrations for these species (Table 4.5) were calculated and entered into the DST. Because insufficient data are available to establish the relative proportion of each species consumed by individual consumers, an equal relative proportion of consumption was assumed.

**Table 4.5. Seafood input parameters used in the assessment example.**

Species	Dietary Guild	Sum DDTs Mean $\pm$ SE (ng/g)	Lipids (%)	Portion of human seafood
California halibut	Piscivore	24.94 $\pm$ 4.94	0.40	0.2
Queenfish	Benthic and pelagic with piscivory	210.70 $\pm$ 119.62	1.40	0.2
White croaker	Benthic without piscivory	134.30 $\pm$ 38.68	1.00	0.2
Shiner perch	Benthic and pelagic without piscivory	175.10 $\pm$ 0.00	2.36	0.2
Topsmelt	Benthic and pelagic with herbivory	104.01 $\pm$ 14.20	1.80	0.2

A total of 32 tissue samples were collected from three stations. Sediment contaminant data were based on five stations with one sample per station. The average sum DDTs concentration in the sediment was 26.80 ng/g and the standard error of the mean was 10.13. These values are reported in Table 4.6 in addition to the individual congener concentrations. Additional physical-chemical properties of the site such as average sediment TOC, site area, and site length were also determined and entered into the DST (Table 4.7).

**Table 4.6. Sediment DDT concentrations entered into the DST for the assessment example.**

Parameter	Value Employed
Sediment sum DDT concentrations $\pm$ SE	26.80 $\pm$ 10.13 ng/g
Sediment DDT congener profile (ng/g)	o,p'-DDD = 0.03 o,p'-DDE = 3.12 o,p'-DDT = 0.54 p,p'-DDD = 2.18 p,p'-DDE = 19.22 p,p'-DDT = 1.74

**Table 4.7. Additional site-specific parameters entered into the DST for the assessment example.**

Parameter	Value Employed
Sediment TOC	0.89 %
Site area	6.80 km <sup>2</sup>
Length of site	4.14 km
Dissolved Organic Carbon Content of water (DOCw) (kg/L)	2.15E-06
Particulate Organic Carbon Content of water (POCw) (kg/L)	1.57E-06
Mean Water Temp (T) (Deg. C)	17.4
Salinity (Sal) (PSU)	25.4
Dissolved Oxygen Concentration (DO) (mg/L)	9
Suspended solid concentration in water column (SSC) (kg/L)	2.27E-05



***Step 3: Run the bioaccumulation model to calculate bioaccumulation factor for the site linkage calculation.***

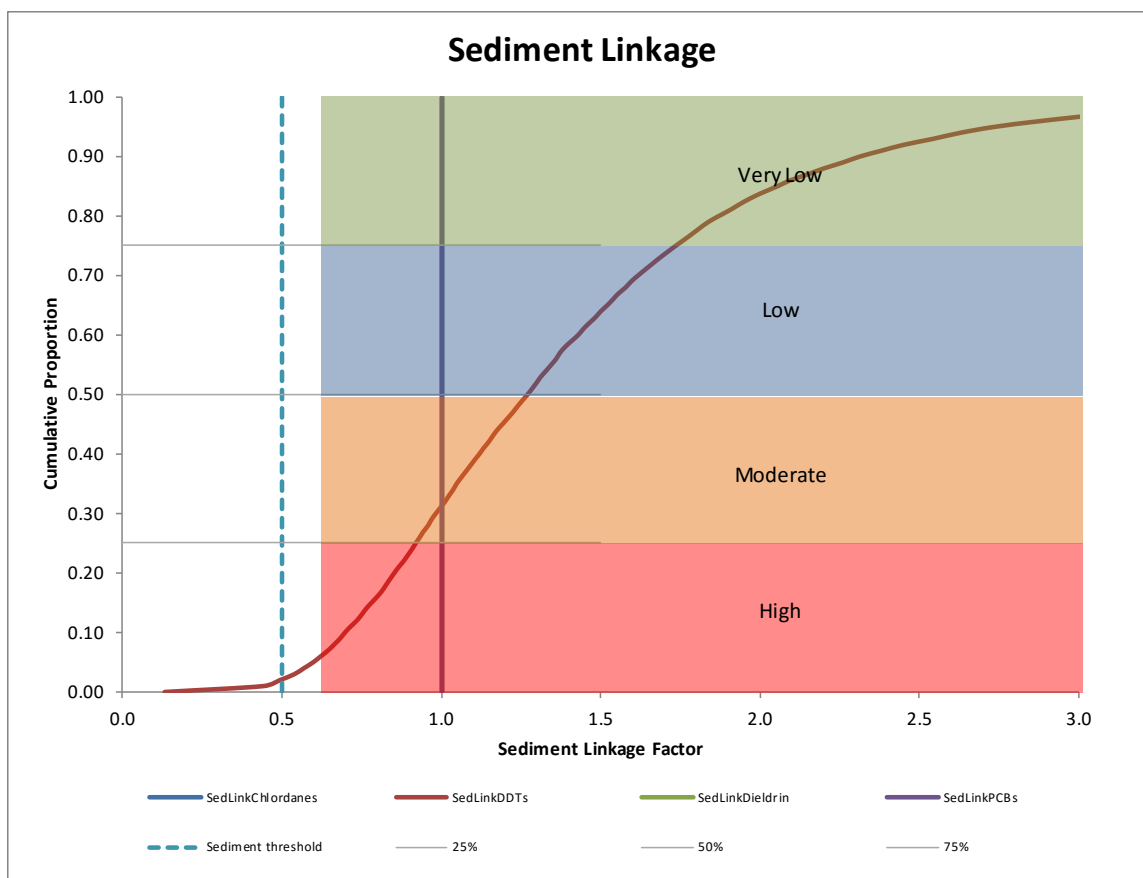
Once data entry is complete, the next step is to calculate the bioaccumulation factor (BSAF) for each fish species included in the assessment. The DST contains a macro that calculates the estimated tissue concentrations for each compound entered (in this case, each of the six DDT congeners) and sums these results to obtain a total concentration (i.e., for sum DDTs). The BSAF is then calculated as the quotient of estimated tissue concentration divided by observed sediment concentration for sum DDTs. The BSAF calculations are performed separately for each dietary guild, with the results applied to the selected finfish species in Step 4.

***Step 4: Perform simulations to generate cumulative probability distributions of results.***

A Monte Carlo Simulation methodology (McKone and Bogen 1991) is employed to obtain cumulative probability distributions for site linkage. This simulation uses the YASAIw add-in Monte Carlo Simulation macro for Excel (Eckstein and Riedmueller 2002, Pelletier 2009), which the user installs prior to using the DST. In the typical application, 10,000 simulations are performed.

***Step 5: Plot and evaluate results of the simulations.***

The stochastic approach lends itself to graphical depiction and interpretation. There are a number of methods to describe the results, and the user can generate graphics to illustrate the findings. The Monte Carlo Simulation macro contains tools for calculating a cumulative distribution function for site linkage. Figure 4.5 indicates the cumulative distribution function for the site linkage to tissue contamination. The x-axis indicates the site linkage to tissue burden, whereas the y-axis indicates the statistical proportion of the population.



**Figure 4.5. Cumulative distribution plot of site linkage to observed seafood contaminant concentrations. Note: linear scale.**

The site linkage threshold of 0.5 is denoted by the blue hashed line. Because the DDT probability distribution (red line) crosses that threshold in the lower portion of the graph, the resulting outcome is High.

***Step 6. Categorize results for the chemical exposure and site linkage.***

The categorical results for each indicator are obtained by comparing the weighted average tissue concentration and the site linkage simulation results to the set threshold values. As was shown in Figure 4.5, the site linkage category is 4, or High. For chemical exposure, the weighted average tissue concentration was 129.81 ng/g. Referring back to Table 4.1, this value is less than the ATL3 (520 ng/g) threshold but larger than the FCG (21 ng/g) threshold, indicating a category of 2, or Low. These results are also reported in a tabular form in the DST (Figure 4.6).

	B	C	D	E	F	G	H
		25th Percentile	50% Percentile or Mean	75th Percentile	95th Percentile	Category Score	Category
8	Indicator						
18	Mean Weighted Observed Tissue Conc. (ng/g)		129.81				
19	Mean Weighted Estimated Tissue Conc. (ng/g)		164.63				
20	Chemical Exposure					2	Low
21	Sediment Linkage	0.917	1.268	1.733		4	High
22	Site Assessment					2	Likely Unimpacted

**Figure 4.6. DST summary of results from the assessment of Los Angeles Outer Harbor for DDTs.**

***Step 7. Integrate the chemical exposure and site linkage results to make a site assessment.***

The categorical scores for the chemical exposure and site linkage categories are combined to obtain a site assessment for indirect effects, following Table 4.4. In this example, the site sediment has a high linkage to the seafood tissue burden. However, most seafood consumers are estimated to be at an acceptable risk from consuming local seafood. This results in a site classification of 2, or Likely Unimpacted.

## 5 TIER 3 ASSESSMENT

Tier 3 represents an alternative assessment of the HHSQO with greater site specificity and more flexibility than Tier 2. This option has been established to address stakeholder concerns that the standardized Tier 2 assessment may not have sufficient sophistication, resolution, or site specificity to accurately evaluate site linkage or potential human health impacts from sediment contamination. More complex models and data analyses are also useful for developing contaminated sediment management or remediation plans (e.g., identify sites for dredging, forecasting changes in sediment quality over time). However, a lower level of complexity may be sufficient for HHSQO assessment, where the objective is solely to determine whether unacceptable human health impacts are associated with current site sediment contamination conditions.

A Tier 3 assessment can take many forms, such as use of different bioaccumulation models/parameters for the site linkage calculation, use of nonstandard seafood species, different thresholds to assess chemical exposure, consideration of other sources of chemical exposure, or consideration of spatial or temporal variability in contamination. The potential benefits of a Tier 3 assessment are countered by several disadvantages. Tier 3 assessment is likely to be more expensive, more time-consuming, and yield results that may not be comparable to assessments based on Tier 2 methods. Thus, the decision to conduct a Tier 3 assessment should be made with the approval of the regulatory agency and be based on evidence that conditions (trigger criteria) exist that indicate a potential for more accurate or useful assessment results.

### 5.1 Tier 3 Objectives

A Tier 3 assessment may be performed to address unique situations or evaluate factors affecting the assessment not considered in Tier 2. The objective of Tier 3 assessment might include:

- Improve accuracy and precision of the assessment
- Evaluate different risk related assumptions associated with chemical exposure determination
- Incorporate spatial and temporal factors into the assessment
- Evaluate specific sub-areas, contaminant gradients or potential hotspots

### 5.2 Trigger Criteria

Before deciding to proceed with a Tier 3 assessment, there should be evidence indicating that the Tier 2 assessment outcome is likely incorrect (e.g., incorrect classification of chemical exposure or site linkage). In general, the site should meet one of the following conditions (trigger criteria):

1. Variation in factors or processes are present that affect contaminant bioaccumulation from sediment, potentially resulting in a difference in site linkage category. Examples include:
  - Differences in the relationship between geochemical characteristics and contaminant bioavailability
  - Differences in physiological processes affecting bioaccumulation model performance, such as growth rate or assimilation efficiency

- Measured sediment concentrations are not representative of actual fish forage area due to spatial or temporal variations in sediment contaminant distribution, fate, or transport
2. Differences in food web or forage range of target species
    - Use of sport fish species other than those listed in Appendix 2
    - Regional differences in fish diet
  3. Changes in exposure factors that are likely to result in a difference in chemical exposure category. Examples include:
    - Consumption rate
    - Proportion of each sport fish species consumed by humans
  4. Presence of spatial or temporal factors likely to affect classification of chemical exposure site linkage; Examples include:
    - Sediment contamination hot spots
    - Temporal change in loading rates
    - Substantial offsite sediment contamination

### **5.3 Assessment Characteristics**

The Tier 3 approach is site-specific, and should be developed based on the conceptual site model, in addition to considerations identified by stakeholders. If a Tier 3 analysis is employed, the specific modifications to the approach will be determined by the information needs for the site in question.

Tier 3 assessments can include a bioaccumulation modeling approach different from that included in the Tier 2 Decision Support Tool. This could include mechanistic models of contaminant fate and transport, in addition to the movement of individual fish or anglers. USEPA (2009) provides useful recommendations regarding how to select a modeling approach in a Tier 3 assessment. The processes included and model complexity should be chosen based on the assessment questions, data availability, and available resources (USEPA 2009).

Tier 3 assessments could incorporate more sophisticated treatments of uncertainty and variability. This may include sensitivity analyses or uncertainty analyses of the calculations of chemical exposure and site linkage. Such analyses could identify local sources of uncertainty, as well as potentially incorrect model assumptions.

Additional data collection may be incorporated into Tier 3 analyses. Examples of local data collection that may be warranted include:

- Seafood consumption surveys to determine local consumption rates
- Development of local parameter values for food web structure and diets of local seafood, to parameterize bioaccumulation models and better characterize site linkage

- Data collection on water column and porewater contaminant concentrations to evaluate the contribution of these matrices to seafood exposure
- Contaminant monitoring in sediment off-site, as well as concentrations in possible sources (e.g., stormwater or creek discharge during runoff events) to determine contribution from off-site sources
- More detailed monitoring of site sediment contamination and organic carbon, to determine potential “hotspot” areas of elevated seafood exposure, and to better characterize the spatial extent of contamination
- Seasonal monitoring of important site sport fish species, to determine seasonal variation in potential exposure to seafood consumers

## 5.4 Results Interpretation

The results of the assessment should be expressed using the same indicators, thresholds, and integration logic described for Tier 2. For example, even though a different type of bioaccumulation model is used in the assessment, site linkage should still be scored as either Very Low, Low, Moderate, or High based on a probability distribution of linkage values. Use of the same indicators and integration relationships will help maintain comparability between Tier 3 and Tier 2 assessments.

## 5.5 Tier 3 Site Assessment Steps

The specific process for conducting a Tier 3 assessment will vary among applications because of variability in the data analysis methods. In general, the process is expected to be similar to that described for Tier 2:

- Step 1: Develop conceptual site model.
- Step 2: Input data for site-specific parameters and chemical concentration.
- Step 3: Run the bioaccumulation model to calculate bioaccumulation factors for use in site linkage calculations.
- Step 4: Perform analyses to generate cumulative probability distributions of site linkage results.
- Step 5: Plot and evaluate results of the simulations.
- Step 6: Categorize results for the chemical exposure and site linkage indicators.
- Step 7: Compare the results for the two indicators to make a site assessment.

This process is conducted for each contaminant group separately. The final site assessment is based on the highest level of risk from site contamination obtained for any compound.

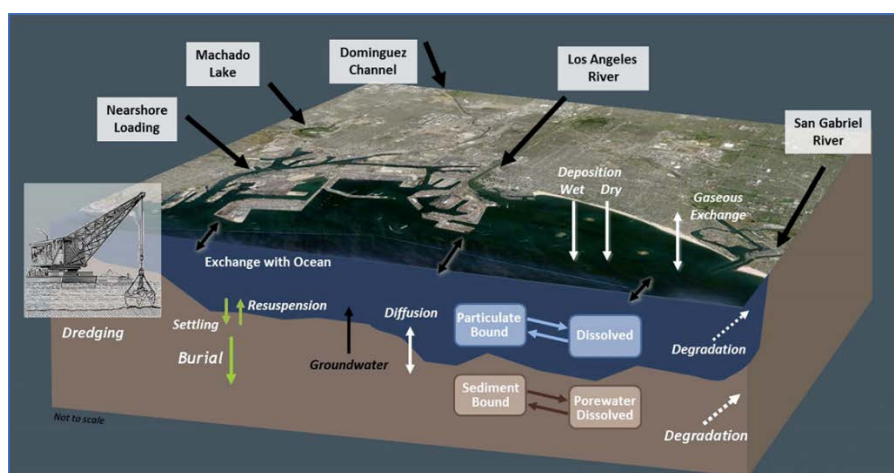
## 5.6 Tier 3 Case Study Example

Few examples of a Tier 3 assessment are currently available, due to the limited implementation of the HHSQO into monitoring and regulatory programs. The following example summarizes use of a Tier 3 assessment for evaluating the HHSQO as part of the Los Angeles and Long Beach Harbor Toxics TMDL. This TMDL includes human health impacts associated with PCB and DDT contamination of sediment and seafood and is one of the first TMDLs to implement the HHSQO as a compliance target. More information about this TMDL is available from: [http://www.waterboards.ca.gov/losangeles/board\\_decisions/basin\\_plan\\_amendments/technical\\_documents/bpa\\_66\\_R11-008\\_td.shtml](http://www.waterboards.ca.gov/losangeles/board_decisions/basin_plan_amendments/technical_documents/bpa_66_R11-008_td.shtml)

Other Tier 3 assessments could vary substantially in scale or complexity from the approach utilized in this example.

### CSM development

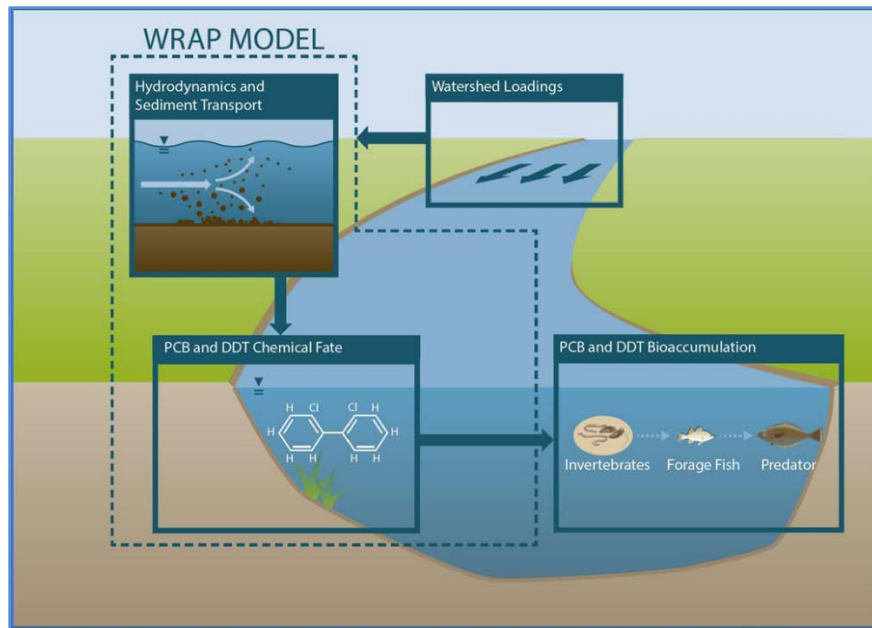
A conceptual site model was developed for toxics loading and fate in the harbor complex (Figure 5.1). The CSM identified watershed loadings, sediment particle transport, and fish movement as potentially important factors to consider in determining site linkage. A Tier 3 assessment approach was determined to be necessary to account for the complexity of fish movement, spatial and temporal variability in contaminant distribution, and influence of watershed loadings. The fish species from the SQO list of primary species were identified for evaluation: California halibut, white croaker, and shiner surfperch.



**Figure 5.1 Conceptual site model for Los Angeles and Long Beach Harbor (adapted from 2015 TMDL stakeholder meeting presentation by the Ports of Los Angeles and Long Beach).**

### Integrated model development

An alternative modeling approach was developed that integrated separate models for watershed loadings, hydrodynamics and sediment transport, chemical fate, and bioaccumulation (Figure 5.2). The bioaccumulation model was based on models used previously to assess bioaccumulation on the nearby Palos Verdes Shelf. The integrated modeling approach was also intended to be applied for evaluating the effectiveness of various sediment management scenarios to attain TMDL targets.



**Figure 5.2. Integrated modeling approach to assess contribution of loadings from multiple sources to fish contamination. (adapted from 2015 TMDL stakeholder meeting presentation by the Ports of Los Angeles and Long Beach).**

### Site specific data generation

Parameterization of the models required a variety of special studies to fill data gaps and reduce model uncertainty. These studies required up to four years to complete. Some of the key study types were:

- **Hydrodynamic/sediment transport**  
Measurements of bathymetry, watershed contaminant loading, currents, sediment resuspension by propwash
- **Chemical fate**  
Sediment and water column measurements of PCBs and DDTs
- **Bioaccumulation**  
Determination of food web structure and contamination, fish movement tracking
- **Natural recovery rate estimation**  
Sediment core analysis
- **Regional background concentrations evaluation**  
Compilation of regional monitoring data

### Site linkage evaluation

A site-specific, calibrated bioaccumulation model based on the AQFDCHN model framework was used to evaluate site linkage. The model accounts for growth rates of organisms, fish movement patterns, spatial variation in sediment contamination, as well as seasonal and annual changes in diet and lipid content. Site linkage was determined by comparing estimated fish tissue contaminant concentrations under two modeling scenarios: baseline (all sources contributing)



and a scenario where sediment contaminant concentrations were set to zero. The difference between these estimates represented the amount of bioaccumulation associated with site sediment. Multiple model runs were conducted at various high and low values for key parameters to generate a probability distribution of linkage values for comparison to standard thresholds (see Section 4).

#### Chemical exposure evaluation and data integration

Evaluation of chemical exposure and integration of both indicators followed the same method described for Tier 2 assessment.

## 6 SAMPLING AND CHEMICAL ANALYSIS RECOMMENDATIONS

For HHSQO assessment, contaminant concentrations and ancillary data are determined in sediment and seafood from the site being evaluated. This section reviews field and analytical methods needed for ensuring quality of data collected for Tier 2 assessment. This section also addresses study design issues, such as what seafood species are appropriate for assessment. The recommendations in this section may also be useful in guiding sampling or data selection for Tier 1 assessment. However, Tier 1 assessment is expected to focus primarily on existing data and have less stringent data requirements; therefore, some of the recommendations described below may not be applicable.

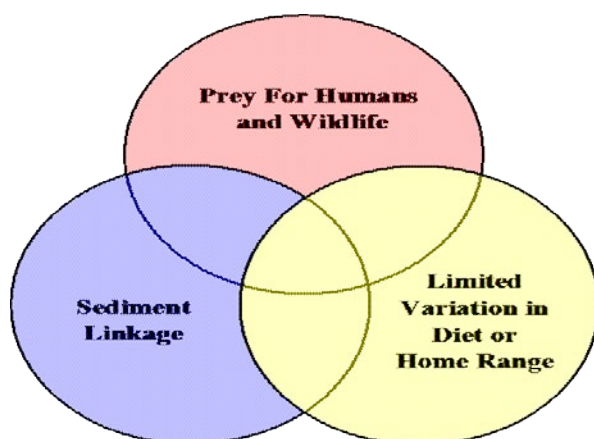
The HHSQO assessment method is based on the analysis of seafood tissue and sediment contamination data. The scope of the technical recommendations for the HHSQO assessment is limited to nonpolar organic contaminants, including polychlorinated biphenyls (PCBs), and legacy pesticides (DDTs, chlordanes, and dieldrin).

### 6.1 Seafood Sampling and Sample Preparation

#### Appropriate seafood species

Seafood monitored for the HHSQO assessment should be indicative of indirect human exposure to local sediment contamination. Therefore, to the extent possible, species chosen for analysis should have the following three attributes (Figure 6.1):

- i. They should be local organisms with limited movement range within the water body (Burkhard 2009).
- ii. Individuals of that species should be commonly consumed by humans from the water body of interest (USEPA 2000).
- iii. They should exhibit a dietary association with sediment, including in their diets either animals that reside in or on the sediment, or animals that consume sediment-associated prey.



**Figure 6.1. Traits of seafood species for assessing indirect effects. The preferred species incorporate all three traits.**

A detailed review of finfish species occurring in estuaries and marine embayments was performed (Appendix 2). Based on this review, and considering the three criteria (Figure 6.1), a listing of appropriate species for inclusion in this HHSQO assessment framework was developed. Table 6.1 lists 41 species appropriate for a HHSQO evaluation. These species were selected based on their fulfillment of the three criteria according to peer reviewed and grey literature (Allen *et al.* 1996, SFEI 2000, Moyle 2002, Silver *et al.* 2007, Jahn 2008, Melwani *et al.* 2009b), and discussions with local experts (M. J. Allen [SCCWRP], G. Cailliet [MLML], Andy Jahn [Port of Oakland], and Kathy Hieb [CDFG], *pers. comm.*).

Species not listed in Table 6.1 may be appropriate for HHSQO analysis depending upon availability within the site location. Additional species should be selected based on available data and knowledge of behavior and life history. Peer-reviewed literature, local experts, and the FishBase website ([www.fishbase.org](http://www.fishbase.org); Froese and Pauly 2009) may be consulted to aid in selection of appropriate target species. To aid in determining whether other species would be appropriate, the three criteria for seafood selection should be considered.

### **Local organisms with limited movement range**

Contaminant levels in seafood tissue used for the HHSQO assessment should indicate the potential hazard to local seafood consumers due to food web exposure of contaminants in site sediment. This evaluation differs from an evaluation of overall human health risk due to seafood consumption because the focus is on contamination from local sources. Animals with relatively small movement ranges should be targeted because they will be more representative of local sediment conditions (Burkhard 2009). Highly migratory sport fish such as Chinook salmon, striped bass, albacore, pacific barracuda, and many shark species (e.g., grey smooth hound, spiny dogfish, and seven-gill shark) would be poor indicators of localized sediment contamination, and are thus not appropriate for HHSQO assessment.

**Table 6.1. Appropriate species for use in the HHSQO assessment. Dietary guild refers to the feeding guild the species is categorized in for modeling site linkage (see Appendix 2).**

Common Name	Scientific Name	Dietary Guild
Barred sand bass	<i>Paralabrax nebulifer</i>	Benthic diet with piscivory
Barred surfperch	<i>Amphistichus argenteus</i>	Benthic diet without piscivory
Bat Ray	<i>Myliobatis californica</i>	Benthic diet with piscivory
Black perch	<i>Embiotoca jacksoni</i>	Benthic and pelagic diet without piscivory
Black rockfish	<i>Sebastes melaops</i>	Benthic and pelagic diet with piscivory
Blue rockfish	<i>Sebastes mystinus</i>	Benthic and pelagic diet with piscivory
Bonefish	<i>Albula vulpes</i>	Benthic diet with piscivory
Brown rockfish	<i>Sebastes auriculatus</i>	Benthic diet with piscivory
Brown smoothhound	<i>Mustelus henlei</i>	Benthic diet with piscivory
Cabezon	<i>Scorpaenichthys marmoratus</i>	Benthic diet with piscivory
California halibut	<i>Paralichthys californicus</i>	Piscivore
Channel catfish	<i>Ictalurus punctatus</i>	Benthic diet with piscivory
Common carp	<i>Cyprinus carpio</i>	Benthic diet with herbivory
Dwarf perch	<i>Micrometrus minimus</i>	Benthic and pelagic diet without piscivory
English sole	<i>Parophrys vetulus</i>	Benthic diet with piscivory
Fantail sole	<i>Xystreurys liolepis</i>	Benthic diet without piscivory
Grass rockfish	<i>Sebastes rastrelliger</i>	Benthic diet with piscivory
Kelp bass	<i>Paralabrax clathratus</i>	Benthic and pelagic diet with piscivory
Leopard Shark	<i>Triakis semifasciata</i>	Benthic diet with piscivory
Lingcod	<i>Ophiodon elongatus</i>	Piscivore
Monkeyface prickleback	<i>Cebidichthys violaceus</i>	Benthic diet with herbivory
Pacific angel shark	<i>Squatina californica</i>	Piscivore
Pacific sanddab	<i>Citharichthys sordidus</i>	Benthic diet with piscivory
Pile perch	<i>Rhacochilus vacca</i>	Benthic diet without piscivory
Queenfish	<i>Seriphus politus</i>	Benthic and pelagic diet with piscivory
Redtail surfperch	<i>Amphistichus rhodoterus</i>	Benthic diet with piscivory
Rubberlip seaperch	<i>Rhacochilus toxotes</i>	Benthic diet without piscivory
Sargo	<i>Anisotremus davidsonii</i>	Benthic diet without piscivory
Señorita	<i>Oxyjulis californica</i>	Benthic diet with herbivory
Shiner perch	<i>Cymatogaster aggregata</i>	Benthic and pelagic diet without piscivory
Spotfin croaker	<i>Roncador stearnsii</i>	Benthic diet without piscivory
Spotted sand bass	<i>Paralabrax maculatofasciatus</i>	Benthic diet with piscivory
Starry flounder	<i>Platichthys stellatus</i>	Benthic diet with piscivory
Striped mullet	<i>Mugil cephalus</i>	Pelagic diet with benthic herbivory
Striped seaperch	<i>Embiotoca lateralis</i>	Benthic diet without piscivory
Topsmelt	<i>Atherinops affinis</i>	Benthic and pelagic diet with herbivory
Walleye surfperch	<i>Hyperprosopon argenteum</i>	Benthic diet without piscivory
White catfish	<i>Ameiurus catus</i>	Benthic diet with piscivory
White croaker	<i>Genyonemus lineatus</i>	Benthic diet without piscivory
White seabass	<i>Atractoscion nobilis</i>	Benthic diet with piscivory
White seaperch	<i>Phanerodon furcatus</i>	Benthic diet without piscivory
Yellowfin croaker	<i>Umbrina roncadore</i>	Benthic diet with piscivory

### **Commonly consumed by humans**

In order to assess human exposure to local contamination, targeted species should be commonly consumed by humans (USEPA 2000). Target species for fishers can be identified from a variety of sources, including local fishing surveys (creel surveys; Gassel and Brodberg 2005), Pacific states marine recreational fishing data (available at [www.recfin.org](http://www.recfin.org)), and local and regional sport fish consumption studies (e.g., Allen *et al.* 1996, SFEI 2000, Silver *et al.* 2007). All 42 recommended species (Table 6.1) were either recorded as captured in the RecFin fishing database or were recorded as a top choice by Delta anglers (Shilling *et al.* 2010).

### **Dietary and life history association with sediment**

A strong relationship between sediment and tissue contamination is needed to indicate chemical exposure to fish consumers from sediment-associated contaminants. To ensure a strong food web linkage, targeted species should prey on animals that live in or on the sediment (Burkhard *et al.* 2003, Melwani *et al.* 2009b). Species with benthic diets often exhibit relatively high lipid and organic contaminant concentrations, and are therefore a protective choice for organic contaminant monitoring (Davis *et al.* 2000, Gassel and Brodberg 2005, de Vlaming 2008, Stahl *et al.* 2009). Piscivores that include in their diet fish which prey on sediment associated animals would also be appropriate. Preference for a dietary association with sediment is not intended to discount the importance of contaminant uptake from the water column, generally through the gills or via consumption of plankton. However, establishing a mechanistic linkage to site sediment contamination is an important feature of the assessment framework and it is difficult to establish a connection to site contamination without the presence of some degree of sediment-related feeding. The species selection step in developing the study design should consider whether bioaccumulation from site-related water column contamination will be adequately represented.

### **Shellfish**

Shellfish monitoring should not be performed in lieu of finfish monitoring. Contaminant concentrations can differ widely between finfish and shellfish. Finfish concentrations are frequently higher than shellfish for chlorinated organic contaminants (Kennish and Ruppel 1996, 1998, Greenfield *et al.* 2003, City and County of San Francisco Natural Resources Division 2006). Additionally, human consumption patterns differ between finfish and shellfish (Sunderland 2007).

### **Field sampling**

Field sampling design for seafood requires professional judgment and understanding of local site conditions, fishing practices, available collection methods, and other factors (Murphy and Willis 1996). Because of these factors, a “one size fits all” sampling program is not specified. Rather, this section describes sampling design recommendations to collect appropriate data in a variety of conditions. Local site conditions, spatial movement of finfish, and temporal variation in contaminant trends influence these recommendations.

### **Sampling methods**

A variety of sampling methods may be employed, depending on what is most suitable for collecting target species (Murphy and Willis 1996). Sampling methods for marine finfish typically include gill or fyke nets, trawling, and hook and line. In low salinity estuarine zones,

electrofishing may also be appropriate. If shellfish monitoring is employed, appropriate methods include crab and crayfish traps, otter trawling, and manual collection.

### **Preservation of sample integrity**

Regardless of method used, effort should be made to not puncture the skin of the fish or otherwise damage the tissue until dissection (Gassel and Brodberg 2005). Sources of extraneous tissue contamination should also be avoided, and cleaning measures should be taken to reduce exposure. Potential contaminant sources include grease from boat winches or cables, engine fuel spills and exhaust, dust, and ice. Wrapping samples in Teflon<sup>®</sup> sheeting or waterproof plastic bags is an appropriate method to minimize contamination (USEPA 2000, Myers *et al.* 2002, Greenfield *et al.* 2003). Dissection and fillet preparation should be performed in a laboratory cleanroom environment, rather than in the field (USEPA 2000).

### **Sampling location selection**

Finfish are mobile and cannot be expected to reside in a fixed location. Therefore, seafood collection need not occur at individual sediment stations. Collection effort should focus on characterizing potential human exposure throughout the site. In consideration of this, sampling location selection should consider where human fishing activity is expected to be high (e.g., public piers) and where target species are likely to be caught.

### **Legal size requirement**

Sampling should target seafood that may be legally caught and consumed by humans. Thus, all samples should be within the legal range for capture and consumption. Fish length should be measured and compared to CDFW legal fishing sizes to determine whether fish samples are appropriate as human prey. Legal fishing size information may be obtained from the CDFW website <http://www.dfg.ca.gov/> (California Department of Fish and Wildlife 2017).

### **Use of data from existing monitoring programs**

Samples obtained in ongoing monitoring programs may be used, provided that samples are appropriate for the evaluation of chemical exposure (e.g., appropriate target species, legal size). Currently, monitoring programs that sample in California estuaries and marine embayments include the Surface Water Ambient Monitoring Program (SWAMP), the Toxic Substances Monitoring Program (TSMP), the Coastal Fish Contaminant Program (CFCP), the Southern California Bight Regional Survey, and the Regional Monitoring Program in San Francisco Bay (RMP). This is not an exhaustive listing, and other local sampling programs may be available.

### **Site placement and spatial scale**

Finfish move and forage across large areas, and therefore will be exposed to contamination at relatively large spatial scales. Finfish sampled at a specific location will indicate contaminant exposure in the region surrounding that location (Moore *et al.* 2005, Burkhard 2009, Melwani *et al.* 2009b). Because of this, it is appropriate to sample a subset of areas over a spatial region.

Sampling site locations for finfish should be considered during the conceptual site model development. Factors to consider in site selection include areas targeted by anglers, sites where sediment-associated species are likely to occur, spatial patterns in sediment contamination, habitat, depth, morphometry (e.g., subembayments, channels, or harbors), and sampling access.

The appropriate number of sampling locations is related to the size of the site being assessed. For large sites (e.g., estuarine or marine embayments greater than 8 km<sup>2</sup> in area), OEHHHA staff recommend that sampling should target multiple locations within the site, to better characterize the range of seafood exposure conditions (Gassel and Brodberg 2005), as well as possible spatial patterns in exposure that may be associated with areas of elevated contamination. For moderately sized sites (e.g., harbors, estuarine subembayments, or small marine embayments, less than 8 km<sup>2</sup> in area), all finfish sampling can be performed in one location. In these situations, pooling of samples across the entire site would be acceptable.

Sampling of small sites (e.g., small harbors or estuarine creeks around 1 km<sup>2</sup> in area) presents greater difficulty, as finfish may not be resident or readily captured within the site. In this situation, seafood sampling could occur at nearby collection locations, where captured fish may be expected to exhibit some exposure to the site. Similarly, data or samples obtained by other studies from locations near the site may be used. Best professional judgment should be used when deciding whether to use tissue samples obtained from outside of small sites. Factors to consider should include number of samples needed to reduce uncertainty, sampling difficulty, and whether the samples are likely to be representative of the site.

### **Seasonal variation**

Timing of fish tissue collection should be considered. Organisms show changes in contaminant content with season, often associated with seasonal changes in lipid content or reproductive activity (Madenjian *et al.* 2000, Stapleton *et al.* 2002, Greenfield *et al.* 2005, Moore *et al.* 2005). Concentrations of chlorinated organic contaminants are generally elevated when tissue lipid contents are highest (Greenfield *et al.* 2005).

Sample design should account for the possibility of seasonal variation in contaminant concentrations. To be protective, if seasonality is known, sampling should occur when lipid content is expected to be highest. This is typically just prior to reproductive activity. If sufficient resources are available, fish should be sampled from multiple seasons.

### **Long term temporal variation**

Tissue samples that represent current conditions should be used in the assessment. Many legacy contaminants, including organochlorine pesticides and PCBs, have shown declining concentrations since monitoring began (Greenfield *et al.* 2005, Davis *et al.* 2006a, O'Connor and Lauenstein 2006, de Vlaming 2008). Thus, use of historical tissue data may not accurately represent current site conditions. Historic data also has limited relevance because of limited lifespans for many species. For example, lifespan is five years for California halibut (Haugen 1990), eight years for shiner perch, (Goals Project 2000), and twelve years for white croaker (Love *et al.* 1984). Therefore, samples collected more than five to twelve years ago may represent different exposure conditions than encountered by current fish.

In general, only data collected in the past five years should be used for assessment. Prior to including data older than five years, graphical or statistical analyses should be performed to evaluate their potential effect on the interpretation of the results.

## Compositing

Assessment of seafood contamination should be based on sampling a statistically representative population of fish, which can be achieved through sufficiently large sample sizes. Using composites of multiple individuals for laboratory analysis can increase the representativeness of chemical concentration exposure. In compositing, fillet samples from multiple individuals of the same species are combined prior to chemical analysis.

Composite samples should meet the following four requirements:

1. Individuals should be from the same fish species
2. Individuals should be from the same general collection location and collection time period
3. Individuals should have similar body sizes
4. Tissue mass should be the same for samples taken from each individual included in the composite

If body size of finfish targeted by seafood consumers varies widely, composites may be size stratified. With respect to size, OEHHHA recommends following USEPA's 75% guideline: that the smallest individual in the sample should be no less than 75% of the total length of the largest individual (USEPA 2000, Gassel and Brodberg 2005).

When composites are prepared, OEHHHA recommends that fillet tissue from each individual should be weighed and subsampled to achieve even mass for each fillet. This preparation method will ensure that each individual of the composite contributes equally to the composite concentration (Gassel and Brodberg 2005).

Analysis of individual fish may be employed as an alternative to compositing. However, individual analysis will not improve the ability to characterize the average tissue concentration, upon which the HHSQO assessment framework is based. To accurately characterize average chemical concentrations in seafood, a larger number of laboratory analyses must be employed when using individual fish samples than when using composites. For example, the accuracy of the average estimate will be the same for three composite analyses of five fish each versus fifteen individual analyses. But analysis of individuals will increase the ability to describe the full range of variability in fish concentrations. Analysis of individuals will also aid in understanding potential factors contributing to elevated concentrations, such as lipid content, size, or sampling location.

## Sample size

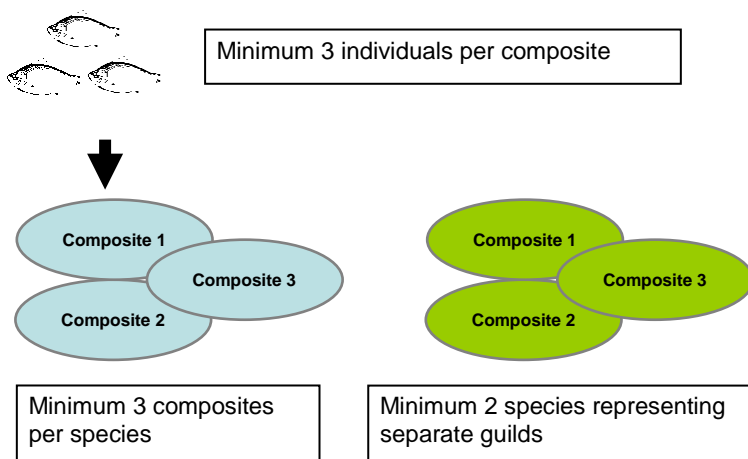
If compositing is employed, OEHHHA recommendations for screening surveys are that a minimum of three composite samples should be collected and analyzed for each target species in each site to be evaluated for HHSQO assessment. Each composite should consist of fillet tissue from a minimum of three individual fish, with five individuals preferred (Gassel and Brodberg 2005; Figure 6.2). If more fish are obtained in field sampling, number of individuals per composite can be much larger. For example, the Regional Monitoring Program for San



Francisco Bay routinely analyzes 20 individuals per shiner perch composite (Greenfield *et al.* 2003).

For the HHSQO evaluation, triplicate composite samples should be obtained from a minimum of two species targeted by human consumers (Figure 6.2). To increase the range of exposure conditions considered, each species should be from a separate feeding guild. Appendix 2 provides supporting information on sample size considerations for seafood tissue sampling.

As an alternative to three composite samples of three individual fish, nine or more individual fish per species may be analyzed separately.



**Figure 6.2. Recommended minimum sample sizes for Tier 2 assessment of indirect effects.**

### Field ancillary data for seafood sampling

At each seafood sampling location, spatial coordinates (e.g., latitude and longitude) should be recorded with a GPS monitoring device. In addition, all finfish samples should be measured in the field for total length (longest length from tip of tail fin to tip of nose/mouth), fork length (longest length from fork of tail fin to tip of nose/mouth), and body mass, to confirm legal capture size. Total length analysis is particularly important, as this is the method of evaluating whether fish meet legal size requirements.

### Seafood sample preparation methods

Preparation of sample fillets, sample compositing, and homogenization should be employed in a laboratory cleanroom environment whenever possible. USEPA (2000) recommended protocols for organic sample preparation should be followed. These include processing samples using stainless steel, anodized aluminum, borosilicate glass, polytetrafluoroethane (PTFE), quartz, or ceramic equipment. Fillet preparation should be performed on PTFE or glass cutting boards using instruments composed of corrosion resistant stainless steel, quartz, titanium, or PTFE. Prepared samples should be stored in borosilicate glass, quartz, or PTFE containers with PTFE-lined lids (USEPA 2000).

### Finfish tissue type (use of fillet tissue)

Tissue type and preparation can significantly influence contaminant concentrations in fish. Concentrations are typically higher for whole body than fillet tissue (e.g., Goldstein *et al.* 1996, Amrhein *et al.* 1999), and for skin-on fillets than skin-off fillets (Davis *et al.* 1999, Davis *et al.* 2011). These factors should be considered in sample preparation and selection.

For HHSQO assessment of risk to human consumers, consistent with OEHHA recommendations (Gassel and Brodberg 2005), all finfish samples should be analyzed as fillet tissue, unless local information indicates that the consumer population regularly consumes additional tissues. Removal of skin from fillet samples (i.e., skin-off fillets) will generally result in lower concentrations of organic contaminants (Davis *et al.* 1999, Davis *et al.* 2011). Although OEHHA recommends consuming fish with skins removed, consumer preparation methods may vary.

## 6.2 Sediment Sampling and Sample Preparation

### Study design

HHSQO assessment differs from the assessment of direct effects to benthic communities in that assessment occurs at a site scale rather than a station scale. Because finfish and anglers move, they are exposed to contamination at multiple locations within a site. In order to accurately characterize this exposure, consideration must be put into choosing an appropriate study design for collection of sediment contamination data. This begins with the conceptual site model (CSM), in which the site boundaries are defined, and an understanding of historic data and sources is summarized. The sediment sampling area should correspond to the site area, based upon the site boundaries as defined in the CSM.

A probabilistic survey design should be employed to characterize the site. The USEPA Office of Research and Development has developed extensive guidance on development of probabilistic survey designs, which should be consulted (USEPA 2002). Additional characteristics of a probabilistic survey design include explicit definition of the population of sites sampled, a known probability of sampling every station within the site, and a random element to sampling (Olsen *et al.* 2009).

Ad hoc, targeted sampling focused on discharge points or “hotspots” is not recommended, as it will not accurately estimate exposure for mobile seafood organisms. Probabilistic sampling enables one to characterize the entire site condition, whereas a targeted design (such as a design of convenience, or a design focused on anticipated hotspots) will only indicate concentrations at the stations chosen. If specific areas expected to contribute disproportionately to exposure, and exhibit higher concentrations and variability, there may be the desire to more accurately sample these areas. In this case, a stratified sampling design is recommended, with probabilistic selection of stations within each stratum, but a higher density of samples collected within the more contaminated strata.

The USEPA has also developed a set of tools to aid in designing probabilistic surveys, and characterizing the variance and other statistical properties of the results, using the Generalized Random Tessellation Stratified (GRTS) methodology (available at [https://archive.epa.gov/nheerl/arm/web/pdf/grts\\_ss.pdf](https://archive.epa.gov/nheerl/arm/web/pdf/grts_ss.pdf)). The GRTS method is an appropriate

method for designing sediment surveys for the HHSQO assessments. In the GRTS method, samples are probabilistically sampled in a more evenly dispersed fashion than simple random sampling, which more efficiently characterizes site condition (Stevens 2004). Starting in 2002, the GRTS survey design was employed to design a sediment sampling scheme for the Regional Monitoring Program for Water Quality in San Francisco Bay (Lowe *et al.* 2004, SFEI 2010). The RMP design is a stratified design, with a higher sampling density in the Lower South Bay to account for the higher concentrations and variability in that site (Melwani *et al.* 2008). A GRTS method is also used in a stratified random sampling design for the Southern California Bight Regional Monitoring Program (Bay *et al.* 2011).

### Use of ongoing monitoring program data

Samples obtained in ongoing monitoring programs may be used, provided that these samples are obtained and analyzed in a fashion that is appropriate for the HHSQO assessment. Examples of programs that employ methods appropriate for the HHSQO assessment include the Southern California Bight Regional Monitoring Program and the RMP.

### Sample collection and ancillary data

To increase the usefulness of sediment contamination data for the framework, several specific recommendations should be followed. Samples should be collected from the sediment surface (i.e., top 5 cm), as these are most representative of potential exposure for seafood and their prey.

Appropriate methods for sediment sampling for the HHSQO assessment are identical to those for the direct effects assessment adopted and implemented by the State Water Board, and are described in Chapter 2 of Bay *et al.* (2013). Briefly, the sampling method must consistently obtain an undisturbed sediment sample at least down to 5 cm, and the sample, once collected, must not be compromised by additional mixing.

At each sediment sampling location, spatial coordinates (e.g., latitude and longitude) should be recorded with a GPS monitoring device at the time the sampling device collects the sediment (i.e., is on the bottom). Care should be taken to ensure that the coordinate system is documented, to enable accurate mapping of spatial position. The following additional ancillary data regarding the sampling event and grab event should also be recorded (Bay *et al.* 2013):

- Station identification
- Date
- Time of arrival
- Collecting agency identification (or code)
- Vessel name
- System used for navigation
- Weather and sea conditions
- Salinity
- Station fail code identifying reason for abandonment (if site is abandoned)
- Time of event (grab on bottom)

- Depth of water (where grab on bottom)
- Depth of penetration of grab in sediment (to nearest 0.5 cm)
- Sediment composition (e.g., coarse sand, fine sand, silt or clay, gravel, or mixed grain size; presence of shell hash)
- Sediment odor and color

After collection, samples should be placed in pre-cleaned certified containers, using precleaned equipment. Samples should be stored immediately on ice or dry ice, and should be analyzed within an appropriate holding time consistent with programmatic QAPPs. A minimum of five composite samples should be collected and analyzed in each site. For stratified sampling, at least five samples should be collected within each strata.

### **6.3 Chemical Analytes**

The HHSQO assessment has established methods for evaluating four classes of organic contaminants: PCBs, DDTs, chlordanes, and dieldrin. Target compounds for legacy pesticides follow USEPA (2000) and Klasing and Brodberg (2008). For PCBs, six target congener lists are available, and a method has been developed to calculate total congener abundance from any of these lists.

#### **DDTs**

Six compounds comprise total DDTs and should be included in all analyses: o,p'-DDD, o,p'-DDE, o,p'-DDT, p,p'-DDD, p,p'-DDE, and p,p'-DDT.

#### **Chlordanes**

Five compounds should be included in all analyses: cis-chlordane, trans-chlordane, cis-nonachlor, trans-nonachlor, and oxychlordane (USEPA 2000).

#### **Dieldrin**

Dieldrin is an individual compound to be evaluated in the indirect effects assessment.

#### **PCBs**

Polychlorinated biphenyls (PCBs) are biphenyl compounds with between one and ten chlorine compounds attached to the phenyl groups in varying positions. There are 209 PCB compounds, individually referred to as congeners (PCB-1 through PCB-209), and each PCB congener has a unique IUPAC number. Total PCB concentration equals the sum of the 209 PCB congeners. Monitoring programs typically measure a subset of the most abundant and biologically active congeners. The specific congeners monitored varies among programs. Appendix 5 provides an analysis of the relationship between common congener subsets and total PCB concentration. Analysis of the current set of PCB congeners measured for SWAMP bioaccumulation studies is recommended for HHSQO assessment. This list provides the most accurate assessment of total PCB concentration (Appendix 5).

## 6.4 Data Preparation and Analysis

Recommendations for data preparation and analysis are presented in the User Guide for the DST, available at: <http://www.sccwrp.org/Data/DataTools/SedimentQualityAssessment.aspx>. Prior to using the Decision Support Tool, the user should compile and organize the data for the site under consideration. The following data should be compiled for input into the DST.

### Sediment contaminant concentrations

For sediment contaminant concentrations, means (average) should be calculated for all parameters. This includes individual compounds in each class (e.g., PCB congeners, DDT and chlordane compounds) and sum of compounds. Standard error of the mean (SE) should also be calculated for sum of PCBs, sum of DDTs, sum of chlordanes, and dieldrin. SE does not need to be calculated for individual compounds.

Sediment data should be converted to ng/g (i.e., µg/kg; parts per billion) dry weight prior to entry into the DST. Sediment results will be highly dependent on how values below detection are treated. This requires careful consideration, particularly in the presence of multiple values below detection.

### Tissue contaminant concentrations

For tissue contaminant concentrations, means (average) should be calculated for all sums of compounds (sum of PCBs, sum of DDTs, sum of chlordanes, and dieldrin). Separate results should be obtained for each seafood guild monitored. Standard error of the mean (SE) should also be calculated each guild. Means and SE do not need to be calculated for individual compounds in each class (e.g., PCB congeners, DDT and chlordane compounds) for tissue data. However, sum of PCB concentrations from individual congener results should be calculated. Tissue data should be converted to ng/g (parts per billion) wet weight prior to entry into the DST.

### Water contaminant concentrations

Water column contaminant concentrations should be measured if possible. These data aid in improving accuracy of the bioaccumulation model analyses. If water column data are collected, means (average) should be calculated for all individual compounds in each class (e.g., PCB congeners, DDT and chlordane compounds). SE does not need to be calculated for water concentrations, and sum of compounds is also not needed. Water data should be converted to pg/L prior to entry into the DST. Use of passive sampler devices is recommended for water column sampling for chemical analysis.

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## APPENDIX 1 – BIOACCUMULATION MODEL AND SITE LINKAGE CALCULATION

### A1.1 Bioaccumulation Model Equations

This assessment framework employs the Arnot and Gobas (2004) food web model, modified by Gobas and Arnot (2010), to calculate the biota-sediment accumulation factors (BSAFs) for each of the fish guild species. This is a mechanistic bioaccumulation model which has limited complexity to increase ease of application while accurately depicting the primary bioaccumulation processes (Burkhard 1998, Arnot and Gobas 2004). The Arnot and Gobas model is structured to depict contaminant concentration in biota as the mass balance of key uptake and loss processes. The model equation structure accounts for uptake by diet and respiration; loss by egestion, metabolism, and respiratory elimination; and growth dilution:

$$\text{Biota Concentration (C}_{\text{Biota}}) = \frac{(\text{Respiratory Uptake} * \text{Water Concentration} + \text{Dietary Uptake} * \text{Prey Concentration})}{(\text{Elimination} + \text{Fecal Egestion} + \text{Growth} + \text{Metabolism})}$$

The model equations presented here are used to calculate biota concentration and BSAF for each model species. All model equations and assumptions have been presented in detail elsewhere (Gobas 1993, Arnot and Gobas 2004, Gobas and Arnot 2005, Gobas and Arnot 2010).

A few minor modifications were made to the Gobas and Arnot model equations for this framework. The first change was to modify the list of PCB congeners to match multiple California regional monitoring programs, as well as the addition of three classes of chlorinated pesticides: chlordanes, dieldrin, and DDTs. The second modification consists of basing temperature and salinity corrected  $K_{OW}$  values for each congener on site-specific measurements. Finally, the food-web structure was modified to be more inclusive of the diverse types of sport fish. This included the addition of several sport fish, including the California halibut, spotted sand bass, queenfish, common carp, topsmelt, and striped mullet. Appropriate prey items were also added such as macrophytes and the decapod crab.

This appendix depicts all equations included in the model. Abiotic input parameters and calculations describe key abiotic processes, such as contaminant partitioning between sediment and the water column, and between dissolved and particulate form. This is followed by biotic input parameters and calculations, which are organized separately for primary producers (phytoplankton and macrophytes) and animals (prey organisms and seafood). The primary producer calculations describe net uptake from the water column into phytoplankton and macrophytes at the base of the food web. The animal calculations are performed for each animal taxa, resulting in food web uptake, and ultimately bioaccumulation in the modeled seafood organisms. The model uses a food web structure and dietary proportions specific for each organism (Tables A1.1 and A1.2). For each organism, calculations are performed on a congener-specific basis and later summed to provide total contaminant concentration and BSAF values (i.e., total DDTs).



**Table A1.1. Invertebrate food-web properties. Values indicate the proportion of each diet component.**

		P	M	I1	I2	I3	I4	I5	I6	I7	I8	I9
Diet component	S	---	---	---	0.9	0.9	0.3	0.15	0.1	0.3	0.44	---
	P	---	---	1	0.05	0.05	0.35	0.65	0.45	0.65	0.01	0.3
	M	---	---	---	---	---	---	---	---	---	0.1	---
	I1	---	---	---	0.05	0.05	0.35	0.2	0.45	0.05	0.1	0.3
	I2	---	---	---	---	---	---	---	---	---	---	---
	I3	---	---	---	---	---	---	---	---	---	---	---
	I4	---	---	---	---	---	---	---	---	---	0.2	---
	I5	---	---	---	---	---	---	---	---	---	0.15	---
	I6	---	---	---	---	---	---	---	---	---	---	0.4
	I7	---	---	---	---	---	---	---	---	---	---	---
	I8	---	---	---	---	---	---	---	---	---	---	---
	I9	---	---	---	---	---	---	---	---	---	---	---
	F1	---	---	---	---	---	---	---	---	---	---	---
	F2	---	---	---	---	---	---	---	---	---	---	---
	F3	---	---	---	---	---	---	---	---	---	---	---
	F4	---	---	---	---	---	---	---	---	---	---	---
	F5	---	---	---	---	---	---	---	---	---	---	---
	F6	---	---	---	---	---	---	---	---	---	---	---
Physical properties	PW Respir. (mp)	0	0	0	0.05	0.05	0	0	0	0.05	0.05	0
	Lipid (%)	0.12	0.38	1.00	0.75	0.75	1.00	1.00	1.00	0.86	1.25	2.00
	Mass (kg)	---	---	7.10E-08	1.00E-07	1.10E-04	3.13E-06	5.00E-06	1.50E-05	1.12E-02	5.00E-03	3.72E-04
S-sediment		I4-amphipod		F1-forage fish-herbivore (juvenile jacksmelt)				PW Respir-porewater respiration proportion				
P-phytoplankton		I5-cumacean		F2-forage fish-planktivore (northern anchovy)								
M-macrophytes		I6-mysid		F3-forage fish-primarily benthivore (juvenile white croaker)								
I1-zooplankton		I7-bivalve mollusk		F4-forage fish-benthivore (yellowfin goby)								
I2-small polychaete		I8-decapod crab		F5-forage fish-mixed diet I (juvenile shiner perch)								
I3-large polychaete		I9-crangon shrimp		F6-forage fish-mixed diet ii (plainfin midshipman)								

**Table A1.2. Fish food-web properties. Values indicate the proportion of each diet component.**

		F1	F2	F3	F4	F5	F6	SP1	SP2a	SP2b	SP3	SP4	SP5	SP6	SP7	SP8
Diet component	S	---	---	0.05	---	0.05	0.05	---	---	---	---	0.05	0.05	0.29	0.05	0.3
	P	0.8	0.2	0.05	---	0.1	---	---	0.01	---	---	---	0.1	0.04	0.2	0.1
	M	---	---	---	---	---	---	---	---	---	---	---	---	0.2	0.2	0.35
	I1	0.2	0.35	0.2	---	0.2	---	---	---	---	---	---	0.1	0.11	0.08	0.1
	I2	---	---	0.15	0.2	0.05	0.05	---	---	---	0.06	0.2	0.1	---	---	---
	I3	---	---	0.15	0.2	0.05	0.1	---	---	---	0.05	0.2	0.1	0.01	0.01	---
	I4	---	0.2	0.1	0.15	0.25	0.15	---	0.01	0.2	0.12	0.2	0.2	0.1	0.4	0.03
	I5	---	0.15	0.1	0.15	0.25	0.15	---	---	---	0.02	0.2	0.2	0	0.01	---
	I6	---	0.1	0.1	---	0.05	0.2	0.01	---	0.06	0.24	0.1	0.15	0.06	0.05	0.02
	I7	---	---	---	---	---	---	---	0.28	0.08	---	---	---	0.14	---	0.1
	I8	---	---	---	---	---	---	---	0.35	0.11	---	---	---	0.04	---	---
	I9	---	---	0.1	0.25	---	0.2	0.01	---	---	0.03	0.05	---	---	---	---
	F1	---	---	---	---	---	---	0.08	---	---	---	---	---	---	---	---
	F2	---	---	---	---	---	0.05	0.45	0.1	---	0.48	---	---	---	---	---
	F3	---	---	---	---	---	---	0.25	---	---	---	---	---	---	---	---
	F4	---	---	---	---	---	---	0.1	0.15	0.25	---	---	---	0.01	---	---
	F5	---	---	---	0.05	---	0.05	---	---	0.3	---	---	---	---	---	---
	F6	---	---	---	---	---	---	0.1	0.1	---	---	---	---	---	---	---
Physical properties	PW Respir (mp)	0	0	0	0	0	0.05	0	0	0	0	0	0	0	0	0
	Lipid (%)	1.20	2.50	1.80	3.00	2.00	3.00	m	m	m	m	m	m	m	m	m
	Mass (kg)	4.00E-03	2.15E-02	1.50E-02	3.00E-02	1.31E-03	1.30E-01	1.46	0.60	1.00	0.05	0.37	0.05	2.00	0.02	1.23
S-sediment		I7-bivalve mollusk					SP1-piscivore (California halibut)									
P-phytoplankton		I8-decapod crab					SP2-benthic diet with piscivory (a:Spotted sand bass, b:White catfish)									
M-macrophytes		I9-crangon shrimp					SP3-benthic and pelagic with piscivory (Queenfish)									
I1-zooplankton		F1-forage fish-herbivore (Juvenile jacksmelt)					SP4-benthic without piscivory (White croaker)									
I2-small polychaete		F2-forage fish-planktivore (Northern anchovy)					SP5-benthic and pelagic without piscivory (Shiner perch)									
I3-large polychaete		F3-forage fish-primarily benthivore (Juvenile white croaker)					SP6-benthic with herbivory (Common carp)									
I4-amphipod		F4-forage fish-benthivore (Yellowfin goby)					SP7-benthic and pelagic with herbivory (Topsmelt)									
I5-cumacean		F5-forage fish-mixed diet i (Juvenile shiner perch)					SP8-pelagic with benthic herbivory (Striped mullet)									
I6-mysid		F6-forage fish-mixed diet ii (Plainfin midshipman)					PW Respir-porewater respiration proportion									
		m-measured value														

## Model constants

The Arnot and Gobas model, like other food web models, includes numeric inputs that are site-specific and additional numeric inputs that are generic constants. Site-specific model inputs (e.g., seafood lipid content, sediment organic carbon, and water quality parameters), are obtained locally and modified in each unique application of the model. In contrast, model constants (Table A1.3) are standard constants based on physical principles, not locally available or measured. The model utilizes constants assembled by the model authors (Arnot and Gobas 2004, Gobas and Arnot 2010) based on fitting model equations to datasets developed in global literature reviews. An exception is octanol-water partitioning coefficient ( $K_{OW}$ ) for pesticides and some PCBs, which was not included in prior model documentation. Methods for  $K_{OW}$  development are documented below.

### Octanol-water partitioning coefficient ( $K_{OW}$ )

The octanol-water partitioning coefficient governs compound partitioning between tissue lipids versus water, and between sediment and porewater. PCB  $K_{OW}$  values used in the assessment framework were obtained from Gobas and Arnot (2005). For those PCBs not evaluated in Gobas and Arnot,  $K_{OW}$  values were the median of results combined from five published sources: Li *et al.* (2003), Mackay *et al.* (2000), Beyer *et al.* (2002), Hansen *et al.* (1999), and Hawker and Connell (1988). Pesticide  $K_{OW}$  values were taken from Shen and Wania (2005), or Leatherbarrow *et al.* (2006), which compiled  $K_{OW}$ s from Mackay *et al.* (2000).

Literature  $K_{OW}$ s are generally calculated at temperatures of 25°C, which is higher than many California bays and estuaries. Therefore, PCB  $K_{OW}$ s are temperature corrected to correspond to the water body temperature, based on the site-specific data. Following Gobas and Arnot (2005, 2010), and references cited therein, the  $K_{OW}$  values were temperature corrected using the following equation (Li *et al.* 2003):

$$\log K_{OWE_T} = \log K_{OWD_T} - \frac{\Delta U_{ow}}{\ln(10) \cdot R} \cdot \left( \frac{1}{E_T} - \frac{1}{D_T} \right)$$

Where:

$E_T$  = the environmental temperature (Kelvin)

$D_T$  = the data collection temperature (Kelvin)

$\Delta U_{OW}$  = the internal energy of octanol-water phase transfer

$R$  = the gas law constant (0.0083145 kJ/mol K)

Empirically-derived  $\Delta U_{OW}$  were unavailable for some congeners, and were estimated to be -28 kJ/mol, the median of empirical  $\Delta U_{OW}$  data for other PCB congeners, and -25 kJ/mol for the pesticides.

Following Gobas and Arnot (2005, 2010), and references cited therein,  $K_{OW}$  values are also salinity corrected to correspond to the measured water body average salinity. Salinity corrections followed Xie *et al.* (1997):

$$K_{OWS} = K_{OWT} \times 10^{(SPC \cdot Vh \cdot MCS \cdot Sal / 35)}$$

Where:

SPC = the Setschenow proportionality constant ( $0.0018 \text{ L/cm}^3$ )

Vh = the LeBas molar volume ( $\text{cm}^3/\text{mol}$ ) of the chemical (calculated following Tucker and Nelken 1982)

MCS = the molar concentration of seawater at 35 practical salinity units (0.5)

Sal = the salinity for the system of interest (psu)

Summary tables of the PCB and pesticide physical-chemical parameters (Vh,  $\Delta U_{ow}$ , and  $\text{Log}K_{ow}$  values) are listed in tables A1.4 and A1.5, respectively.

**Table A1.3. Constant values used for bioaccumulation model calculations.**

Bioaccumulation Parameters and Constants	Parameter Name	Value	Units
Density of lipid	dLipid	0.9	kg/L
Disequilibrium factor for particulate organic carbon (POC) partitioning	dPOC	1	unitless
Disequilibrium factor for dissolved organic carbon (DOC) partitioning	dDOC	1	unitless
Proportionality constant describing phase partitioning of POC	alphaPOC	0.35	unitless
Proportionality constant describing phase partitioning of DOC	alphaDOC	0.08	unitless
Non-lipid organic carbon (NLOC) proportionality constant	lipcf	0.35	unitless
Non-lipid organic matter (NLOM) proportionality constant	lipcfp	0.035	unitless
NLOC for plants	NLOC	6.00	%
NLOM for animals	NLOM	20.00	%
NLOM for bivalves	NLOM/2	10.00	%
Metabolic rate constant	kM	0	1/day
Constant for phytoplankton aqueous uptake rate	pA	6.0E-5	1/day
Constant for phytoplankton aqueous uptake rate	pB	5.5	1/day
Growth rate for phytoplankton	kGp	0.080	1/day
Growth rate for macrophytes	kGm	0.125	1/day
Invertebrate Growth Rate Coefficient	IGR	3.5E-4	unitless
Fish Growth Rate Coefficient	FGR	7E-4	unitless
Particle scavenging efficiency for filter feeders	scav	100	%
Invertebrate Lipid Digestion Efficiency (alpha)	alphal	0.75	Unitless
Invertebrate NLOM Digestion Efficiency (beta)	betal	0.75	unitless
Invertebrate Water Digestion Efficiency (chi)	chil	0.55	unitless
Zooplankton Lipid Digestion Efficiency (alpha)	alphaZ	0.72	unitless
Zooplankton NLOM Digestion Efficiency (beta)	betaZ	0.72	unitless
Zooplankton Water Digestion Efficiency (chi)	chiZ	0.55	unitless
Fish Lipid Digestion Efficiency (alpha)	alphaF	0.9	unitless
Fish NLOM Digestion Efficiency (beta)	betaF	0.5	unitless
Fish Water Digestion Efficiency (chi)	chiF	0.55	unitless
Ed - Constant A - Invertebrates and Fish	A	8.50E-8	Unitless
Ed - Constant B - Invertebrates and Fish	B	2	unitless

**Table A1.4. PCB congener list with physical-chemical property values.**

PCB Congener	LeBas molar volume (Mackay 2006)	$\Delta U_{ow}$ at 25 °C (kJ/mol)	Log $K_{ow}$ at 25 °C
PCB 8	226.4	-22.7	5.12
PCB 11	226.4	-28	5.27
PCB 18	247.3	-25	5.3
PCB 27	247.3	-28	5.4
PCB 28	247.3	-26.3	5.66
PCB 29	247.3	-28	5.6
PCB 31	247.3	-25.9	5.78
PCB 33	247.3	-26	5.65
PCB 37	247.3	-28	5.78
PCB 44	268.2	-26	5.82
PCB 49	268.2	-27	5.95
PCB 52	268.2	-27.3	5.91
PCB 56	268.2	-30	6.02
PCB 60	268.2	-30	6.12
PCB 64	268.2	-28	5.79
PCB 66	268.2	-28	6.01
PCB 70	268.2	-28	6.1
PCB 74	268.2	-28	6.11
PCB 77	268.2	-28	6.26
PCB 81	268.2	-28	6.25
PCB 87	289.1	-28	6.35
PCB 95	289.1	-28	6.06
PCB 97	289.1	-28	6.27
PCB 99	289.1	-28	6.36
PCB 101	289.1	-23.8	6.33
PCB 105	289.1	-28.6	6.82
PCB 110	289.1	-28	6.31
PCB 114	289.1	-28	6.65
PCB 118	289.1	-28.5	6.69
PCB 119	289.1	-28	6.4
PCB 123	289.1	-28	6.64
PCB 126	289.1	-28	6.77
PCB 128	310	-28	6.79
PCB 132	310	-25	6.54
PCB 137	310	-28	6.83
PCB 138	310	-25	7.22
PCB 141	310	-25	6.77
PCB 146	310	-28	6.87

**Table A1.4. Continued**

PCB Congener	LeBas molar volume (Mackay 2006)	$\Delta U_{ow}$ at 25 °C (kJ/mol)	Log Kow at 25 °C
PCB 149	310	-25	6.62
PCB 151	310	-25	6.6
PCB 153	310	-31.1	6.87
PCB 156	310	-23	7.01
PCB 157	310	-28	7.18
PCB 158	310	-23	6.87
PCB 167	310	-28	7.28
PCB 168	310	-28	7.11
PCB 169	310	-28	7.42
PCB 170	330.9	-25	7.18
PCB 174	330.9	-28	7.03
PCB 177	330.9	-28	7.01
PCB 180	330.9	-29.1	7.16
PCB 183	330.9	-28	7.12
PCB 187	330.9	-28	7.09
PCB 189	330.9	-28	7.3
PCB 194	351.8	-28	7.76
PCB 195	351.8	-28	7.45
PCB 198	351.8	-28	7.43
PCB 199	351.8	-28	7.2
PCB 200	351.8	-28	7.27
PCB 201	351.8	-28	7.51
PCB 203	351.8	-28	7.53
PCB 206	372.7	-28	7.8
PCB 209	393.6	-28	8.18

**Table A1.5. Pesticide congener list with physical-chemical property values.**

PCB Congener	LeBas molar volume (Mackay 2006)	$\Delta U_{ow}$ at 25 °C (kJ/mol)	Log K <sub>ow</sub> at 25 °C
cis-Chlordane	340.5	-25	6.20
trans-Chlordane	340.5	-25	6.27
cis-Nonachlor	361.4	-25	5.70
trans-Nonachlor	361.4	-25	5.70
Oxychlordane	250	-25	2.60
Dieldrin	332.2	-25	5.48
op-DDD	312.6	-25	5.34
op-DDE	305.2	-25	5.63
op-DDT	333.5	-25	5.70
pp-DDD	312.6	-25	6.33
pp-DDE	305.2	-25	6.93
pp-DDT	333.5	-25	6.39

#### Abiotic site-specific input parameters

TOC = organic carbon proportion in sediment (%)

DOC<sub>w</sub> = DOC concentration in H<sub>2</sub>O (kg/L)

POC<sub>w</sub> = POC concentration in H<sub>2</sub>O (kg/L)

T = mean water temperature (°C)

Sal = water salinity (PSU)

DO = dissolved oxygen concentration (mg O<sub>2</sub>/L)

SSC = concentration of suspended solids (kg/L)

#### Congener-specific abiotic parameters

K<sub>owT</sub> = octanol-water partitioning coefficient (temperature corrected)

K<sub>owS</sub> = octanol-water partitioning coefficient (corrected for temperature and salinity)

K<sub>oc</sub> = octanol-organic carbon partitioning coefficient (uses the K<sub>owS</sub> value)

c<sub>sed</sub> = contaminant concentration in sediment (ng/g dry weight)

c<sub>pw</sub> = dissolved contaminant concentration in porewater (ng/mL)

c<sub>watD</sub> = dissolved contaminant concentration in surface water (ng/mL)

c<sub>wat</sub> = total contaminant concentration in surface water (ng/mL)

phi = ratio of dissolved contaminant concentration to total contaminant concentration in surface water (unitless)



## Congener-specific abiotic calculations

$$\log K_{OWT} = \log K_{OWD_T} - \frac{\Delta U_{ow}}{\ln(10) \cdot R} \cdot \left( \frac{1}{T} - \frac{1}{D_T} \right)$$

Where:

$\log K_{OWD_T} = \log K_{OW}$  at 25 °C or 298K in Tables A1.4 and A1.5.

$\log K_{OWT}$  = temperature corrected  $\log K_{OW}$  at the site-specific temperature (T)

$$K_{OWS} = K_{OWT} \times 10^{(SPC \cdot Vh \cdot MCS \cdot Sal / 35)}$$

$$K_{OC} = 0.35 \cdot K_{OWS}$$

$$cpw = c_{sed} / (TOC \cdot K_{OC})$$

cwatD = measured dissolved water concentration or estimated from total concentration as:

$$cwatD = \phi \cdot c_{wat}$$

$$\phi = 1 / (1 + POC_w \cdot dPOC \cdot \alpha_{poc} \cdot K_{OWS} + DOC_w \cdot dDOC \cdot \alpha_{doc} \cdot K_{OWS})$$

Uptake of dissolved contaminants from the water column into lower trophic levels and across the fish gill is included in the model. Use of measured dissolved contaminant concentrations is recommended, but such values have the potential to be substantially influenced by sources other than site sediment, such as flux from offsite sediment contamination hotspots and watershed runoff. The bioaccumulation model contains a limiting feature to identify and reduce potentially large offsite water column contributions. This feature compares measured surface water concentration for each congener to that estimated to result from the flux associated with site sediment concentration. This estimation uses a standardized fraction of the porewater concentration calculated for the site based on the organic carbon partitioning. Empirical data for several California bays and estuaries were used to calculate the ratio between calculated porewater contaminant concentrations and measured dissolved surface water concentrations. This analysis yielded a median empirical dilution factor of eight, which was used in the equation below to determine the estimated water contaminant concentration associated with site sediment contamination:

$$\text{Estimated } c_{watD} = c_{sed} / (TOC \cdot K_{OC} \cdot 8)$$

The lowest value (measured or estimated) for each congener is used as cwatD in the model calculations.

## Organism-specific parameters

Wb = body weight (kg)

Gv = gill ventilation rate (L/day)

lipid = tissue lipid content (%)

wc = tissue water content (kg water/kg organism ww) = 1-lipid-NLOM (animals), 1-lipid-NLOC (phytoplankton and macrophytes), 1-lipid-(NLOM/2) (bivalves)

Gd = feeding rate (kg food/day)

kG = organism growth rate (1/day)

$vld$  = proportion of diet that is lipid (calculated based on diet proportion of prey and prey lipid content, unitless)  
 $vcd$  = proportion of diet that is non-lipid organic carbon (calculated based on diet proportion of prey and prey NLOC content, unitless)  
 $vnd$  = proportion of diet that is non-lipid organic matter (calculated based on diet proportion of prey and prey NLOM content, unitless)  
 $vwd$  = proportion of diet that is water (calculated based on diet proportion of prey and prey water content, unitless)  
 $vlg$  = lipid fraction of gut (kg lipid/kg organism ww)  
 $vcg$  = NLOC fraction of gut (kg NLOC/kg organism ww)  
 $vng$  = NLOM fraction of gut (kg NLOM/kg organism ww)  
 $vwg$  = water fraction of gut (kg water/kg organism ww)  
 $mp$  = proportion of respiration or transpiration due to porewater (Tables A1.1 and A1.2, unitless)  
 $mo$  = proportion of respiration or transpiration due to overlying water column (unitless)

#### Contaminant-specific model variables

$E_w$  = contaminant-specific gill chemical uptake efficiency (unitless)  
 $E_d$  = contaminant-specific dietary chemical transfer efficiency (also called gut uptake efficiency, unitless)  
 $k_1$  = aqueous uptake rate constant (L/kg·day)  
 $k_{bw}$  = biota-water partition coefficient (i.e., bioconcentration factor, L/kg organism ww)  
 $k_2$  = elimination rate constant (1/day)  
 $k_d$  = dietary uptake rate constant (kg food/kg organism·day)  
 $k_G$  = growth rate (1/day)  
 $G_f$  = fecal egestion rate (kg feces/kg organism·day)  
 $k_{gb}$  = gut-biota partition coefficient (unitless)  
 $k_e$  = fecal egestion rate constant (1/day)  
 $p_i$  = proportion of diet by mass that is prey item  $i$  (unitless)  
 $p_s$  = proportion of diet by mass that is sediment (unitless)  
 $c_D$  = contaminant concentration in diet (weighted average across all prey items, ng/g ww)  
 $c_{biota_i}$  = contaminant concentration in biota organism  $i$  (ng/g organism ww)  
 $BSAF$  = biota-sediment accumulation factor (unitless)

#### Calculations for phytoplankton and aquatic macrophytes

$k_1 = 1/(p_A + p_B/K_{ow}S)$   
 $k_{bw} = (lipid \cdot K_{ow}S / d_{Lipid} + n_{loc} \cdot lipcf \cdot K_{ow}S + wc)$   
 $k_2 = k_1 / k_{bw}$   
 $c_{biota} = k_1 \cdot (c_{wat}D) / (k_2 + k_{Gp}^*)$  [ $k_{Gp}$  for phytoplankton and  $k_{Gm}$  for macrophyte]  
 $BSAF = c_{biota} / c_{sed}$

### Calculations for animals (prey organisms and seafood)

$$E_w = 1/(1.85 + 155/K_{owS})$$

$$E_d = 1/(A * K_{owT} + B)$$

$$G_v = (1400 * W_b^{0.65}) / DO$$

$$k_1 = E_w * G_v / W_b$$

$$k_{bw} = K_{owS} * (\text{lipid}/d\text{Lipid} + n\text{lom} * \text{lipcfp}) + w_c$$

$$k_2 = k_1 / k_{bw}$$

$$G_d = 0.022 * (W_b^{0.85}) * e^{0.06 * T} \quad [\text{For fish and nonfilter feeding invertebrates}]$$

$$G_d = G_v * SSC * \text{scav} \quad [\text{For filter feeding invertebrates}]$$

$$k_d = E_d * G_d / W_b$$

$$k_G = IGR * W_b^{-0.2} \quad [\text{For invertebrates}]$$

$$k_G = FGR * W_b^{-0.2} \quad [\text{For fishes}]$$

$$v_{ld} = \sum_{i=1}^n p_i * \text{lipid}_i ; \quad v_{cd} = \sum_{i=1}^n p_i * n\text{loc}_i ; \quad v_{nd} = \sum_{i=1}^n p_i * n\text{lom}_i ; \quad v_{wd} = \sum_{i=1}^n p_i * \text{water}_i$$

where  $i = [1 \dots n]$  represent individual prey taxa

$$G_f = G_d * ((1 - \alpha) * v_{ld} + (1 - \beta) * (v_{cd} + v_{nd}) + (1 - \chi) * v_{wd})$$

$$v_{lg} = (1 - \alpha) * v_{ld} / ((1 - \alpha) * v_{ld} + (1 - \beta) * (v_{cd} + v_{nd}) + (1 - \chi) * v_{wd})$$

$$v_{cg} = (1 - \beta) * v_{cd} / ((1 - \alpha) * v_{ld} + (1 - \beta) * (v_{cd} + v_{nd}) + (1 - \chi) * v_{wd})$$

$$v_{ng} = (1 - \beta) * v_{nd} / ((1 - \alpha) * v_{ld} + (1 - \beta) * (v_{cd} + v_{nd}) + (1 - \chi) * v_{wd})$$

$$v_{wg} = (1 - \chi) * v_{wd} / ((1 - \alpha) * v_{ld} + (1 - \beta) * (v_{cd} + v_{nd}) + (1 - \chi) * v_{wd})$$

$$k_{gb} = ((v_{lg}/d\text{Lipid} + v_{ng} * \text{lipcf} + v_{cg} * \text{lipcfp}) * K_{owT} + v_{wg}) / ((\text{lipid}/d\text{Lipid} + n\text{lom} * \text{lipcfp}) * K_{owT} + w_c)$$

$$k_e = G_f * E_d * k_{gb} / W_b$$

$$m_o = 1 - m_p$$

$$cD = p_s * c_{sed} + \sum_{i=1}^n (p_i * c_{biota_i})$$

where  $i = [1 \dots n]$  represent individual prey taxa

$$c_{biota} = (k_1 * (m_o * c_{watD} + m_p * c_{pw}) + k_d * cD) / (k_2 + k_e + k_G + k_M)$$

$$BSAF = c_{biota} / c_{sed}$$

## A1.2 Site Linkage Determination

In evaluation of the site linkage, Monte Carlo Simulation (MCS) is used to incorporate the variability of both the measured sediment and tissue concentrations, the fish guild home range (HR), and the estimated BSAF values. For this analysis, a lognormal distribution is used for BSAF and sediment concentrations, and the appropriate distribution for each home range is indicated in Table A1.6. A total of 10,000 iterations should be used for the simulation.

$$\text{Site linkage} = C_{\text{Est}}/C_{\text{Tis}}$$

$C_{\text{Est}}$  = weighted average estimated tissue concentration based on the proportion of the human diet for each guild (ng/g).

The average estimated tissue concentration for each guild, i, and contaminant class (i.e., total DDTs) is calculated using the following equation:

$$C_{\text{Est},i} = \Sigma C_{\text{Sed}} \times \text{SUF}_i \times \text{BSAF}_i$$

$\Sigma C_{\text{Sed}}$  = lognormal distribution of sediment concentration using the measured mean and standard error

$\text{SUF}_i$  = HR distribution using the HR mean and HR standard deviation (SD) as found in Table A1.6. If the calculated SUF is less than 1, use the calculated value. If the SUF is greater than 1, use the value of 1.

$\text{BSAF}_i$  = lognormal distribution of the mean BSAF for guild, i, from the model prediction and the calculated BSAF SD.

$$\text{BSAF SD} = \text{CVBSAF} \times \text{BSAF}$$

$$\text{CVBSAF} = 0.782$$

The CVBSAF was estimated from empirical data using the following equations:

$$SD = \sqrt{(m^2)(e^{\sigma^2} - 1)}$$

$$CV = \frac{\sqrt{(m^2)(e^{\sigma^2} - 1)}}{m} = \sqrt{(e^{\sigma^2} - 1)}$$

Where  $\sigma$  = lognormal standard deviation

m = mean (this value cancels out)

CV = coefficient of variation

$$C_{\text{Tis}} = \text{weighted average observed tissue concentration}$$

A lognormal distribution is assumed for measured mean tissue data and standard error for each guild for total chlordanes, total dieldrin, total DDTs, and total PCBs. The weighted average for each contaminant class is based on the proportion of the human diet for each guild (ng/g).

**Table A1.6. Home range parameters for each sport fish guild.**

Species	Guild	HR Basis	HR Mean	HR SD	HR Distribution
California halibut	Piscivore	Site length (km)	29.3	60	Lognormal distribution
Spotted sand bass	Benthic diet with piscivory	Site area (km <sup>2</sup> )	0.0071	0.0073	Lognormal distribution
Queenfish	Benthic and pelagic with piscivory	Site area (km <sup>2</sup> )	3	4.689	Lognormal distribution
White croaker	Benthic without piscivory	Site area (km <sup>2</sup> )	3	4.689	Lognormal distribution
Shiner perch	Benthic and pelagic without piscivory	Site area (km <sup>2</sup> )	0.0012	0.000804	Lognormal distribution
Common carp	Benthic with herbivory	Site length*1000 (km)	1.05	9904	Inverse gamma cumulative distribution*
Topsmelt	Benthic and pelagic with herbivory	Site area (km <sup>2</sup> )	0.0012	0.000804	Lognormal distribution
Striped mullet	Pelagic with benthic herbivory	Site length (km)	28.2	80.34	Lognormal distribution

HR mean = mean home range of seafood species under consideration (km or km<sup>2</sup>, depending on taxa).

HR SD = standard deviation of home range of seafood species

\*Inverse gamma cumulative distribution requires 3 terms:

Probability= a random number uniformly distributed over  $0 \leq x < 1$

Alpha= HR mean value (shape parameter)

Beta= HR SD value (scale parameter)

## APPENDIX 2 - DIETARY GUILD AND TARGET SPECIES DEVELOPMENT

### A2.1 Introduction

The evaluation of measured and modeled tissue contaminant concentrations is central to the HHSQO assessment framework. Biology of the local seafood organisms will influence contamination because contaminant exposure will vary with organism diet and movement. This variation in contaminant exposure is a technical issue that must be adequately addressed. Careful consideration must be given to the selection of appropriate local seafood species to sample, and how their dietary uptake is depicted. Only finfish were included in the list of species because their higher trophic position (relative to shellfish) provides a greater potential for chemical exposure.

There are a range of possible approaches to indicate local seafood dietary exposure. These include use of a generic fish representative of conditions throughout the state, use of a guild approach in which variation in diet is represented by multiple indicator species, or development of site-specific model parameters for local species. Each approach contains tradeoffs between ease and accuracy. A single “generic” fish may not be adequate to represent local variation. At the same time, detailed dietary and movement characterizations of local seafood species would be impractical in many circumstances. The HHSQO framework includes practical options that are easy to use, while at the same time, incorporating biological realism and local conditions.

The Scientific Steering Committee (SSC) and SQO Advisory Committee recommended the use of a dietary guild approach in the assessment framework. The operational definition of a dietary guild is: *a group of seafood species that consume similar prey types, resulting in similar routes of food web exposure to sediment-associated contaminants.*

The dietary guild approach provides a more realistic indication of seafood exposure to contaminated sediments than using assumptions for a generic seafood organism. At the same time, the use of diets based on representative species within each guild facilitates assessment under circumstances where local species diet data are not available.

Both benthivory and trophic position are important for defining guilds. Dietary linkage to sediment-associated contaminants will be higher for ***benthivores***: consumers of benthic organisms, such as polychaetes, benthic crustaceans, and benthic mollusks (Burkhard *et al.* 2003, Melwani *et al.* 2009b). Trophic position is important because of contaminant biomagnification. Contaminant concentrations, and potential chemical exposure of humans increases for ***piscivores*** (consumers of fish), which are higher on the food web (Vander Zanden and Rasmussen 1996, Kidd *et al.* 1998).

In the assessment framework, dietary guilds are applied to the bioaccumulation model to estimate site linkage to seafood exposure. For each guild, dietary information from a well-characterized primary species is used to provide parameter estimates for the bioaccumulation model. Alternatively (in Tier 3), local dietary information for the monitored species may be input into the model.

This appendix describes the development of appropriate species and dietary guilds for use in the HHSQO framework. Four technical tasks are included:

1. Determine list of appropriate seafood species for HHSQO evaluation
2. Categorize these species into one of several dietary guilds
3. Identify a primary species for each dietary guild
4. Develop representative diet parameters for each primary species

## A2.2 Methods

### Criteria for appropriate HHSQO assessment species

A listing of appropriate species for inclusion in the HHSQO assessment framework was developed based on three criteria:

1. They should be consumed by recreational or subsistence fishers (USEPA 2000).
2. They should be local seafood organisms with limited movement range within the water body (Burkhard 2009).
3. They should exhibit a dietary association with sediment.

For the second criterion, species having extensive offshore, coastal, or inland migration were removed from the list of potential HHSQO species. For the third criterion, fish species were identified as appropriate for inclusion on the list if they were piscivorous or at least partially benthivorous. Benthic prey were defined to include polychaete worms, benthic crustaceans (e.g., crabs, amphipods, isopods), mollusks (e.g., bivalves, gastropods, and cephalopods), and echinoderms (e.g., starfish, brittle stars, sea urchins), as well as benthic detritus and benthic algae. Piscivores were retained on the list of potential target species due to their indirect food web exposure to sediment contamination (Vadeboncoeur *et al.* 2002, Vander Zanden and Vadeboncoeur 2002).

### Development of the HHSQO species list

The first step in developing the species list was to determine species caught and consumed by recreational and subsistence fishers in California estuaries and marine embayments. Species consumed by fishers were identified for marine embayments by querying the Pacific states marine recreational fishing (RecFin) database (available at [www.recfin.org](http://www.recfin.org)). The query included all data collected in California from 2004 to 2009, obtained by the California Recreational Fisheries Survey (CRFS). The query was limited to inland marine waters (i.e., marine embayments), and was separated among six coastal districts organized from North to South (Pacific States Marine Fisheries Commission (PSMFC) 2008). The relative importance of each species in human diets was estimated based on the total mass (metric tonnes) of that species that were caught and not released, relative to the total mass of fish caught (metric tonnes). All species that composed at least 0.1% of the total mass captured were considered. Additionally, species that composed less than 0.1% of the total mass were considered when sufficient information was available to determine their diet and movement range.

The RecFin database does not include landings in the Sacramento-San Joaquin River Delta or other estuarine waters of oligohaline or mesohaline salinity. Therefore, the list of potential

species was augmented to include commonly consumed species in the Delta. Potential species were identified based on the 2005 to 2008 Delta angler survey of Shilling *et al.* (2010), and fishery information described by Moyle (2002).

The second step in developing the species list was to determine which of the potential species exhibited appropriate diet and movement attributes for inclusion in the HHSQO assessment framework. Dietary and movement for marine species was summarized based on [www.fishbase.com](http://www.fishbase.com) (Froese and Pauly 2010), a California database of nearshore marine fishes (Cailliet 2000), a compilation of dietary habits of marine finfish performed to identify appropriate species for statewide monitoring (SFEI and Moss Landing Marine Laboratories 2009), Moyle (2002), expert guidance (M.J. Allen, pers. comm.), and additional journal literature and technical reports. Additional specific dietary information was obtained for indicator species using detailed dietary compilations performed for previous food web modeling exercises in California (Greenfield *et al.* 2007a, Gobas and Arnot 2010).

### Development of dietary guilds and selection of representative indicator species

Based on the compiled dietary information, species were placed into one of several dietary guilds. Dietary guilds were categorized based on two factors: trophic level and degree of benthic association. For trophic position, categories were separated based on whether the predominant prey was plants, invertebrates, or fishes. Species that consume predominantly benthic invertebrates and do not consume fish were categorized as benthivores. Many species consume invertebrates in combination with another taxa, and these intermediate categories were also included (e.g., invertebrates and plants or invertebrates and fish). Species that consume only fish were categorized as piscivores. Some appropriate piscivores included both benthic and pelagic fishes in their diets. For species that consume invertebrates or plants, diets were then categorized as benthic, pelagic, or both benthic and pelagic. Species that only consume pelagic prey (e.g., phytoplankton, zooplankton, or planktivorous fish) were not included in the final species list.

For each dietary guild, one or two primary species were selected to provide statewide parameter estimates for the bioaccumulation model. Primary species were selected based on several criteria. First, these species were important for sport and subsistence fishing, based on proportion of total mass captured in the RecFin database, and reported capture frequency in fish consumption surveys (e.g., SCCWRP and MBC Applied Environmental Sciences 1994, SFEI 2000, Allen *et al.* 2008, Shilling *et al.* 2010). Second, the species were captured in most areas of the state, based on the RecFin database, range information in FishBase, and results of recent statewide contaminant surveys (Gassel *et al.* 2002, Hoenicke *et al.* 2008). Third, these species had available data to estimate diet and foraging range. An emphasis was placed on quantitative diet data, preferably from gut content studies performed in multiple locations and seasons. Acceptable foraging range information included direct results of telemetry studies, results from tagging or contamination studies from which foraging range could be estimated, or foraging range information for similar California species combined with recommendations provided by local experts (C. Lowe, CSU-Long Beach, Pers. comm.). Finally, preference was given to species that are currently targeted in statewide or regional monitoring programs, such as the Coastal Fish Contamination Program, the Surface Water Ambient Monitoring Program, the Regional Monitoring Program in San Francisco Bay, and the Southern California Bight Regional



Monitoring Survey. This criterion aids in creating consistency among programs, and should increase data availability for assessment.

### **A2.3 Results**

#### **Appropriate species for HHSQO evaluation**

Table A2.1 lists appropriate fish species for use in HHSQO assessment and includes 43 species. Although all species in Table A2.1 are targeted by California recreational anglers, the overall importance as prey species in inland marine waters varies widely, as indicated by the RecFin percent of total catch. The most important species by mass were California halibut, spotfin croaker, spotted sand bass, and leopard shark. Table A2.2 lists species that were evaluated and deemed not appropriate for inclusion. Inappropriate species include anadromous species, which migrate between estuarine waters and the offshore coast as part of their life history, and therefore are likely to be exposed to site sediments for extremely limited periods. Examples of anadromous species are white sturgeon, striped bass, and Chinook salmon. Species with pelagic diets and/or wide-ranging movement are also inappropriate (e.g., jacksmelt and chub mackerel). If a local species being considered for use in HHSQO assessment is not listed in Table A2.1 or A2.2, it should be evaluated based on the three criteria above on a case by case basis.

**Table A2.1. Appropriate finfish species for use in HHSQO assessment. RecFin (%) indicates percent of total catch (by mass) in California inland marine waters, from 2004 to 2009, as indicated in RecFin database. NA = data not available for Delta species.**

Common Name	Scientific Name	RecFin (%)
California halibut	<i>Paralichthys californicus</i>	11.83%
Spotfin croaker	<i>Roncador stearnsii</i>	7.71%
Spotted sand bass	<i>Paralabrax maculatofasciatus</i>	5.32%
Leopard Shark	<i>Triakis semifasciata</i>	3.75%
Barred sand bass	<i>Paralabrax nebulifer</i>	2.69%
Bat Ray	<i>Myliobatis californica</i>	2.62%
Sargo	<i>Anisotremus davidsonii</i>	2.55%
Yellowfin croaker	<i>Umbrina roncadore</i>	2.43%
White croaker	<i>Genyonemus lineatus</i>	1.44%
Black perch	<i>Embiotoca jacksoni</i>	1.41%
Striped mullet	<i>Mugil cephalus</i>	1.22%
Bonefish	<i>Albula vulpes</i>	0.90%
Topsmelt	<i>Atherinops affinis</i>	0.85%
Queenfish	<i>Seriphus politus</i>	0.74%
Black rockfish	<i>Sebastes melaops</i>	0.73%
Kelp bass	<i>Paralabrax clathratus</i>	0.61%
White seabass	<i>Atractoscion nobilis</i>	0.36%
Pacific angel shark	<i>Squatina californica</i>	0.35%
Brown rockfish	<i>Sebastes auriculatus</i>	0.34%
Brown smoothhound	<i>Mustelus henlei</i>	0.33%
Striped seaperch	<i>Embiotoca lateralis</i>	0.29%
Lingcod	<i>Ophiodon elongatus</i>	0.27%
Monkeyface pricklyback	<i>Cebidichthys violaceus</i>	0.25%
Redtail surfperch	<i>Amphistichus rhodoterus</i>	0.24%
White seaperch	<i>Phanerodon furcatus</i>	0.21%
Pile perch	<i>Rhacochilus vacca</i>	0.20%
Shiner perch	<i>Cymatogaster aggregata</i>	0.19%
Pacific sanddab	<i>Citharichthys sordidus</i>	0.19%
Walleye surfperch	<i>Hyperprosopon argenteum</i>	0.18%
Grass rockfish	<i>Sebastes rastrelliger</i>	0.17%
Starry flounder	<i>Platichthys stellatus</i>	0.16%
Rubberlip seaperch	<i>Rhacochilus toxotes</i>	0.14%
Barred surfperch	<i>Amphistichus argenteus</i>	0.14%
Cabazon	<i>Scorpaenichthys marmoratus</i>	0.12%
Blue rockfish	<i>Sebastes mystinus</i>	0.09%
Fantail sole	<i>Xystreurus liolepis</i>	0.07%
Señorita	<i>Oxyjulis californica</i>	0.07%
Dwarf perch	<i>Micrometrus minimus</i>	0.00%
English sole	<i>Parophrys vetulus</i>	0.00%
Channel catfish	<i>Ictalurus punctatus</i>	NA
Common carp	<i>Cyprinus carpio</i>	NA
Largemouth bass	<i>Micropterus salmoides</i>	NA
White catfish	<i>Ameiurus catus</i>	NA

**Table A2.2. California finfish species found in inland marine embayments that are not appropriate for HHSQO evaluation. RecFin (%) indicates percent of total catch (by mass) in California inland marine waters, from 2004 to 2009, as indicated in RecFin database.**

<b>Common Name</b>	<b>Reason Species is Inappropriate</b>	<b>RecFin (%)</b>
Albacore	Migratory; does not typically inhabit estuaries or marine embayments	0.14%
American shad	Pelagic planktivore	0.61%
Blacksmith	Pelagic planktivore	0.05%
Bluefin tuna	Does not typically inhabit estuaries or marine embayments; pelagic	0.01%
Bocaccio	Exhibits extensive movement and tends to live far offshore in deep waters	0.26%
California corbina	Primarily surfzone feeder - inappropriate movement characteristics	1.18%
California lizardfish	Insufficient information on diet; reef associated	0.20%
California scorpionfish	Transient - range up to 200 miles	0.38%
California sheephead	Kelp bed/ rock reef resident - inappropriate habitat	0.14%
Chinook salmon	Anadromous	0.33%
Chub (pacific) mackerel	Pelagic diet	3.27%
Coho salmon	Anadromous; not legal to fish in CA	0.01%
Dolphinfish	Highly migratory	0.40%
Giant seabass	Classified as critically endangered; not legal to fish in CA	0.12%
Gopher rockfish	Resides in rocky crevasses of rocky reefs and other hard relief areas (i.e. not sediment associated)	0.04%
Gray smoothhound	Migratory (from Southern to central CA in summer)	0.14%
Green sturgeon	Anadromous species; Classified as endangered; not legal to fish in CA	0.01%
Halfmoon	Pelagic diet	0.21%
Jack mackerel	Pelagic diet	0.08%
Jacksnelt	Large pelagic component in diet	5.10%
Kelp rockfish	Pelagic diet	0.01%
Northern anchovy	Pelagic diet	0.42%
Olive rockfish	Midwater species; very low proportion of catch in marine embayments	0.02%
Opaleye	Diet predominantly kelp bed and other attached and suspended plants (not sediment associated)	1.87%
Pacific barracuda	Migratory	0.36%
Pacific bonito	Migratory	3.43%
Pacific chub mackerel	Pelagic diet	
Pacific hake	Generally occurs offshore	0.00%
Pacific herring	Pelagic diet	0.34%
Pacific sardine	Pelagic diet	0.57%
Plainfin midshipman	Pelagic diet	0.01%
Salema	Pelagic diet	0.04%
Seven gill shark	Extensive migration of great distances	1.06%
Shortfin corvina	Researched extensively on line - can find nothing on movement patterns	0.60%
Shovelnose guitarfish	Primarily surfzone feeder - inappropriate movement characteristics	0.69%
Spiny dogfish (shark)	Extensive migration of great distances	0.06%

**Table A2.2 Continued**

Striped bass	Anadromous	9.39%
Thresher shark	Generally occurs offshore	0.07%
White sturgeon	Anadromous	11.44%
Yellowtail	Migratory and pelagic	0.36%
Zebra perch	Transient	0.30%

### Description of diet guilds

Based on trophic position and benthic versus pelagic diet, fishes appropriate for HHSQO assessment fit into eight dietary guilds. These are organized in Table A2.3 according to trophic position, with higher trophic position guilds listed first. The “benthic diet with piscivory” guild contains the most species (17). The most popular marine species (based on mass landed), California halibut, is a piscivore. Two guilds that contain only one species each are included for completeness.

### Selection and diet description of guild diet indicator species

The site linkage indicator uses a modeling approach to estimate the linkage of contaminants from site sediment. The accuracy of the linkage estimates is enhanced when realistic values for parameters such as trophic status, dietary reliance on benthos, and forage area are used. This section describes the primary species selected for each guild, the basis for selection, and the diet. The primary species’ diets are summarized to form a basis for generating appropriate assumptions for use in the bioaccumulation model. The diets associated with each dietary guild are generalized, and primarily based upon the best available literature for the primary indicator species for each guild. There is substantial uncertainty regarding these dietary relationships because they may be based upon studies conducted in a different habitat, on a different species, and do not reflect regional differences. More recent and site-specific data should be used, when available, and the Tier 3 assessment provides an option for incorporating such information.

#### **Piscivore - California halibut**

Of the three species in the “piscivore” category (Table A2.3), California halibut was selected as the indicator species. California halibut has the largest catch (11.8% of total inland catch in the RecFin query) and is caught statewide. Additionally, there are published diet information (Plummer *et al.* 1983, Wertz and Domeier 1997) and extensive tag-recapture results (Haaker 1975, Tupen 1990, Domeier and Chun 1995, Posner and Lavenberg 1999) to form a basis for feeding and movement parameter development.

**Table A2.3. Dietary guild categories used for HHSQO assessment species. The selected indicator species for categories are highlighted in bold.**

<b>Dietary Guild</b>	<b>Description</b>	<b>Guild Species</b>
Piscivore	The majority of the diet is fish. Large predatory invertebrates (e.g., cephalopods, decapod crustaceans, and echinoderms) are also consumed to some degree. 3 species	<b>California halibut</b> Pacific angel shark Lingcod
Benthic diet with piscivory	Diet regularly includes a mixture of benthic invertebrates forage fish. The most diverse category. 17 species, including two estuarine species: white catfish and channel catfish, each of which is commonly targeted by recreational anglers in the Sacramento-San Joaquin Delta (Shilling <i>et al.</i> 2010).	<b>Spotted sand bass</b> <b>White catfish</b> Leopard shark Barred sand bass Bat Ray Yellowfin croaker Bonfish White seabass Brown rockfish Brown smoothhound Redtail surfperch Pacific sanddab Grass rockfish Starry flounder Cabezon English sole Channel catfish
Benthic and pelagic diet with piscivory	Diet includes a combination of benthic invertebrates, pelagic invertebrates (e.g., zooplankton, shrimp, and mysidae), and forage fish. 4 species	<b>Queenfish</b> Black rockfish Kelp bass Blue rockfish
Benthic diet without piscivory	Diet largely composed of small benthic invertebrates, such as amphipods and other crustaceans, bivalve mollusks, and polychaete worms. 10 species	<b>White croaker</b> Spotfin croaker Sargo Striped seaperch White seaperch Pile perch Walleye surfperch Rubberlip seaperch Barred surfperch Fantail sole
Benthic and pelagic diet without piscivory	Diet includes a mixture of epibenthic and pelagic invertebrates (e.g., zooplankton, shrimp, and mysids). 3 species	<b>Shiner perch</b> Black perch Dwarf perch
Benthic diet with herbivory	Largely consumes benthic invertebrates, benthic algae, and aquatic plants. 3 species, including common carp, an estuarine species captured in the Delta	<b>Common carp</b> Monkeyface prickleback Señorita
Benthic and pelagic diet with herbivory	Diet consists of benthic and pelagic invertebrates and plant material, including benthic algae and phytoplankton. 1 species	<b>Topsmelt</b>
Pelagic diet with benthic herbivory	Diet includes largely pelagic invertebrates and benthic algae. This includes a substantial component of benthic algae and attached plants, likely as floating detritus. These benthic plants constitute a potential dietary association with sediment. 1 species	<b>Striped mullet</b>

Adult California halibut larger than 20 cm are primarily piscivorous, with fish comprising the vast majority of their prey by mass. This includes a combination of pelagic prey species such as northern anchovy, as well as benthic species such as gobies and killifish. (Plummer *et al.* 1983, Wertz and Domeier 1997). Invertebrates that are consumed include large predatory species, such as cephalopods (Wertz and Domeier 1997). Based on this available information, the bioaccumulation model for halibut is parameterized as 98% forage fish, including both benthic and pelagic prey fish (Table A1.2).

#### **Benthic diet with piscivory - spotted sand bass**

Spotted sand bass is the first of two primary species for the “benthic diet with piscivory” category. Spotted sand bass was selected because it is the most important seafood species in the category by mass, and has available diet information (Allen *et al.* 1995, Mendoza-Carranza and Rosales-Casian 2000).

Two studies were available to develop quantitative dietary composition for spotted sand bass (Allen *et al.* 1995, Mendoza-Carranza and Rosales-Casian 2000). Both studies reported decapod crabs as the second most important prey type. Allen *et al.* (1995) indicated mollusks to be the primary prey type, while Mendoza-Carranza and Rosales-Casian (2000) indicated fishes as the most important prey. Based on the average importance in these studies, model input parameters indicated benthic and pelagic fishes (35%), crabs (35%) and mollusks (28%) to be the major prey items. Phytoplankton and amphipods were both present in the diet but only a very minor contribution to total prey mass, and were each included as 1% of total diet (Table A1.2).

#### **Benthic diet with piscivory - white catfish**

White catfish was selected as an additional primary species for the estuarine Sacramento and San Joaquin River Delta. White catfish is a freshwater species, found in inland estuarine waters, such as the Delta. It was selected as an indicator species because is a commonly captured and consumed prey for sport and subsistence anglers (Moyle 2002), second only to striped bass in frequency and amount caught and consumed (Shilling *et al.* 2010). Additionally, white catfish is periodically monitored in Delta contaminant surveys, and has published local diet and movement data (Turner and Kelley 1966, Borgeson and McCammon 1967, Davis *et al.* 2000, Melwani *et al.* 2009a).

Because white catfish resides in the Delta, its dietary composition is based on an estuarine food web. White catfish are carnivorous benthivores, including crayfish and fish in their diets, as well as smaller invertebrates and miscellaneous carrion (Moyle 2002). White catfish prey proportions are based on prey volume composition results of the Delta study performed by Turner (1966). Following this study, model input parameters indicated forage fish to be a substantial prey item (55% of prey), followed by amphipods (20% of prey), crayfish (11%), mollusks (e.g., *Corbicula fluminea*, 8%), and mysids (6%).

### **Benthic and pelagic diet with piscivory - queenfish**

Queenfish was selected as the primary species for this category. It has the greatest mass caught by anglers, and has a greater association with soft bottom sediment than some of the other species (e.g., kelp bass, black rockfish and blue rockfish are more associated with rocky and reef habitat).

Two studies developed quantitative mass or volume based estimates of queenfish diets (Hobson and Chess 1976, DeMartini *et al.* 1985). DeMartini *et al.* (1985) found that approximately 90% of queenfish prey were northern anchovy. In contrast, Hobson and Chess (1976) found that mysids were the predominant prey item (45%), followed by amphipods (22%), annelid worms (22%), with very small contributions of shrimp, isopods, and fish. Prey proportions for the bioaccumulation model, obtained by averaging the results of these two studies, included benthic and pelagic invertebrates and fish, with the following proportions: pelagic forage fish (48%), mysids (24%), amphipod crustaceans (12%), large and small polychaetes (5% and 6%, respectively), crangonid shrimp (3%), and cumacean crustaceans (2%) (Table A1.2).

### **Benthic diet without piscivory - white croaker**

White croaker was selected as the primary species for the “benthic diet without piscivory” category for several reasons. White croaker is captured in all portions of the state, unlike some other heavily caught fish in the category (e.g., sargo and spotfin croaker are only caught in southern California). Among the more commonly targeted species, the best dietary, life history, and contaminant information are available for white croaker (Sigala *et al.* 2002, Gobas and Arnot 2005, Melwani *et al.* 2009b, Gobas and Arnot 2010). Diet parameters developed for white croaker have been validated for PCBs and legacy pesticides in San Francisco Bay, exhibiting low model bias and error (Greenfield *et al.* 2007a, Gobas and Arnot 2010). Finally, white croaker is a target species of current regional and statewide contaminant monitoring programs, so a large data set of contaminant and other parameters is available (Gassel *et al.* 2002, Greenfield *et al.* 2005, Industrial Economics Incorporated 2007).

White croaker is a bottom-dwelling fish that inhabits large bays and shallow near-shore coastlines. White croaker is a bottom feeder, predominantly consuming benthic invertebrates and fishes. The most common food items are polychaetes, crabs, amphipods, mysids, and small fishes. Several dietary studies in San Francisco Bay found gut contents to include bivalves, polychaetes, crangonid shrimp, and small fishes (Sanchez 2001, Sigala *et al.* 2002, Jahn 2008). Likely due to this close association with a benthic food web, white croaker tissue contamination data show statistically significant relationships to sediment contamination for many trace organic contaminants (CH2M HILL 2003, Melwani *et al.* 2009b).

The food web model parameters for white croaker (Table A1.2) are the same as the parameters in previously validated case studies (Greenfield *et al.* 2007a, Gobas and Arnot 2010). The modeled diet largely includes benthic invertebrates: polychaete worms (40%), amphipod crustaceans (20%), and cumacean crustaceans (20% *Nippoleucon hinumensis*). Additional invertebrate prey include benthopelagic mysids (10%) and crangon shrimp (5%). Sediment consumption is also included as 5% of white croaker diets, because croaker are roving benthic grazers that siphon sediment to consume prey (C. Lowe, CSU Long Beach, pers. comm.).

### **Benthic and pelagic diet without piscivory - shiner perch**

Shiner perch was selected as the primary species for this category because its biology and diet is better understood than the other two species (black perch and dwarf perch). As with white croaker, bioaccumulation model application has previously been validated for shiner perch (Greenfield *et al.* 2007a, Gobas and Arnot 2010). Additionally, shiner perch has been the subject of several diet studies (Odenweller 1975, Hobson and Chess 1986, Sigala *et al.* 2002, Jahn 2008), and has received contaminant monitoring in multiple estuaries and marine embayments (Gassel *et al.* 2002, Allen *et al.* 2004, Greenfield *et al.* 2005). Despite its small size, shiner perch is frequently caught by recreational fisherman due to high abundance and ease of capture. Although it comprises a minor component of angler catch by mass, it is distributed statewide and caught in all regions.

Shiner perch exhibit similar life history to other surfperch species, such as silver surfperch (*Hyperprosopon ellipticum*) and walleye surfperch (*Hyperprosopon argenteum*). They are generally epibenthic feeders, primarily feeding off the sediment surface or on epifauna of hard structures. Odenweller (1975) reported that for Anaheim Bay shiner perch, the primary food source was zooplankton and benthic organisms, including bivalves, gastropods, polychaetes, tunicates, and fish eggs. Several dietary studies in San Francisco Bay indicate particular reliance on benthic and epibenthic crustaceans, augmented by polychaetes and clams (Roberts *et al.* 2002, Jahn 2008).

The bioaccumulation model parameters used for shiner perch (Table A1.2) follow those established by Gobas and Arnot (2010): sediment (5%); benthic polychaete worms (20%), amphipod crustaceans (20%), and cumacean crustaceans (20%); benthopelagic mysids (15%); and pelagic phytoplankton (10%) and zooplankton (10%).

### **Benthic diet with herbivory - common carp**

Common carp was selected, along with white catfish, as a primary species for the Delta. Common carp fits into the benthic with herbivory guild. Carp were chosen because there are extensive data available to characterize the diet and movement of this species (Crook 2004, Stuart and Jones 2006, Jones and Stuart 2009, Osborne *et al.* 2009, Froese and Pauly 2010). Common carp is a freshwater and brackish water species, and is found in inland estuarine waters, such as the Delta and the San Gabriel River (Moyle 2002). Though historically regarded as a “rough fish” in the U.S., carp are opportunistically caught and consumed by California sport and subsistence anglers (Chiang 1998, Allen *et al.* 2008, Shilling *et al.* 2010). Monitoring in the Delta and other statewide and national monitoring programs has indicated organic contaminant exposure in carp (Davis *et al.* 2000, de Vlaming 2008, Stahl *et al.* 2009).

Carp are predominantly benthic omnivores, rooting in the benthos for vegetation and benthic invertebrates (Moyle 2002). Although dietary studies have not been performed in the Delta or other California estuaries, Froese and Pauly (2010) summarize studies on common carp diet in eleven separate water bodies, globally (Bisht and Das 1981, Maitland and Campbell 1992, Specziár *et al.* 1997, Specziár *et al.* 1998, Blanco *et al.* 2003, Talde *et al.* 2004). The predominant item consumed is sediment (29%), based on the detritivorous behavior of carp, tendency to take silty sediment into their mouths (Moyle 2002), and frequent reporting of abundant detritus in the gut (Bisht and Das 1981, Maitland and Campbell 1992, Talde *et al.*



2004). Macrophytes (submerged vascular plants) are the second most important item (20%), as carp frequently consume plant material. Benthic invertebrates consumed include amphipods (10%), mollusks (14%), annelids (worms, 1%), and decapod crustaceans (i.e., crayfish, 4%). Carp also consume zooplankton (11%), mysids (6%), and benthic fish (1%).

### **Benthic and pelagic diet with herbivory - topsmelt**

Topsmelt is the only species that fits the selection criteria in this guild. Topsmelt comprised 0.85% of the statewide recreational catch, by mass, suggesting some degree of consumption by anglers. Topsmelt diets include benthic and pelagic invertebrates, benthic algae, and phytoplankton (Marine Biological Consultants Inc. and SCCWRP 1980, Logothetis *et al.* 2001, Horn *et al.* 2006, Visintainer *et al.* 2006, Greenfield and Jahn 2010). Studies in Newport Bay (Allen 1980, Marine Biological Consultants Inc. and SCCWRP 1980) and San Francisco Bay (Visintainer *et al.* 2006, Greenfield and Jahn 2010) provide somewhat contrasting results. The Newport Bay studies indicate substantial contribution of benthic herbivory, and the San Francisco Bay studies indicate a combination of benthic and pelagic invertebrates in the diet. Morphometric analyses by O'Reilly and Horn (2004), and by Horn *et al.* (2006) indicate dietary adaptations for herbivory, suggesting that plant material constitute a primary component of topsmelt diets. Combining the results from these studies, the bioaccumulation model input parameters are set with herbivory constituting a moderate dietary proportion (20% of topsmelt prey as phytoplankton and 20% as submerged plants). Benthic amphipods constitute the other major prey item (40%), with minor contributions from zooplankton (8%), sediment (5%), mysids (5%), polychaetes (1%), and cumaceans (1%) (Table A1.2).

### **Pelagic diet with benthic herbivory - striped mullet**

Like topsmelt, striped mullet are adapted to consume plant material, with most dietary studies indicating sizable contributions of plants and algae, as well as detritus (i.e., sediment). They are unusual among marine fish in California in that sediment and plant material often constitute the majority of their diet (Allen 1980, Marine Biological Consultants Inc. and SCCWRP 1980, Wells 1984, Blanco *et al.* 2003), resulting in their classification in a separate dietary guild. This is reflected in the selected prey proportions for the bioaccumulation model (Table A1.2).

Following the average results of global published diet studies of adults (Marine Biological Consultants Inc. and SCCWRP 1980, Wells 1984, Blanco *et al.* 2003), 75% of the diet is composed of sediment and plant material (30% sediment, 35% benthic macrophytes, and 10% phytoplankton). The remaining diet includes zooplankton (10%) and benthic invertebrates (10% mollusks, 3% amphipods, and 2% mysids).

### **Food web matrix tables**

The food web tables in Appendix 1 indicates the food web structure of the nine primary fish species described above. These diets include fifteen benthic and pelagic animal prey items, in addition to phytoplankton, macrophytes (submerged aquatic plants), and direct consumption of sediment. Dietary proportions for the indicator species vary, representing the range of feeding guilds encountered in California marine embayments. The diets of benthic and pelagic prey items (invertebrates and small forage fishes) are also represented. This includes six different forage fish, to indicate the range of dietary habits among small marine forage fish.

## APPENDIX 3 - HOME RANGE PARAMETER ESTIMATION FOR FISH SPECIES

### A3.1 Introduction

In the Tier 2 assessment, the site linkage indicator determines the linkage of sediment from a site to seafood tissue concentrations at that site. The estimated tissue contaminant concentration due to site linkage 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). Seafood home range is difficult to estimate and local data are typically unavailable. This Appendix determines the home ranges of the indicator species for each dietary guild, as a basis to quantify site linkage to seafood exposure.

The home range information used in the assessment has a high level of uncertainty due to data gaps, regional variation, and species-specific variation. The home range of the primary indicator species (e.g., California halibut for piscivore guild) has been selected to represent the movement patterns for the dietary guild. Use of a different species than the indicator species in the assessment will therefore introduce additional uncertainty into the calculation of the site use factor. For some species, lack of data describing movement patterns in bays required estimating the home range by extrapolating across similar species or using data from a different habitat. There is also a general lack of long-term mark-recapture studies from which to generate estimates of movement range. The variability associated with the following home range estimates has been documented in this section to the extent feasible and this information is incorporated into the site use factor calculations using Monte Carlo Simulations.

### A3.2 Home Range

Home range is defined as: *the estimated spatial area that an animal covers during its adult lifetime foraging activity.*

Sensitivity analyses performed by the Science Team have identified home range as a potentially influential parameter for the site linkage evaluation. However, local home range data are typically unavailable. This appendix determines the home ranges of the primary species for each dietary guild based on available information.

Home ranges are represented in the site linkage calculation 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. A separate home range probability distribution is calculated for each 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 primary species developed to depict dietary guilds: 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 were selected based on observed variability in home range for the primary species or similar species, obtained from published literature and technical reports. The remainder of this section describes the home range statistical distributions that were used, and the methods and rationale for their selection.

### **A3.3 Methods**

Several types of data were used to estimate home ranges of guild primary 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 and 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 and Sutton 1952, Borgeson and McCammon 1967, Tupen 1990, Domeier and Chun 1995, Lowe and 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 and Bray 2006). This conservative estimate of site use factor will overestimate rather than underestimate site linkage.

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.* 2009b).

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 sediment). 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 primary species. Therefore, these kinds of inferences were necessary for estimating home range for HHSQO assessment.

### **A3.4 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 and Sutton 1952, Borgeson and McCammon 1967, Miller and Geibel 1973, Smith and Abramson 1990, Tupen 1990, Posner and Lavenberg 1999, Lowe *et al.* 2003, Bacheler *et al.* 2005, Topping *et al.* 2005, Stuart and Jones 2006, Parker *et al.* 2007, Jones and 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 and 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 primary 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 A3.1). 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.

**Table A3.1. Background information for guild primary 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 primary 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 and 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 sediment
White croaker	15 - 30	Benthic without piscivory	Bays, sand	Roving benthic grazer, including prey on sediment surface as well as within sediment
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 <i>et al.</i> 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

Significant relationships of fish tissue contamination 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 sediment may reflect the decoupling of halibut from the benthic food web due to the predominantly piscivorous diet of adults (Melwani *et al.* 2009b).

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<sup>2</sup> over a several week period (Table A3.2). 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 HHSQO evaluation.

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 and 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 A3.2). 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 A3.2; Figure A3.1) 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.

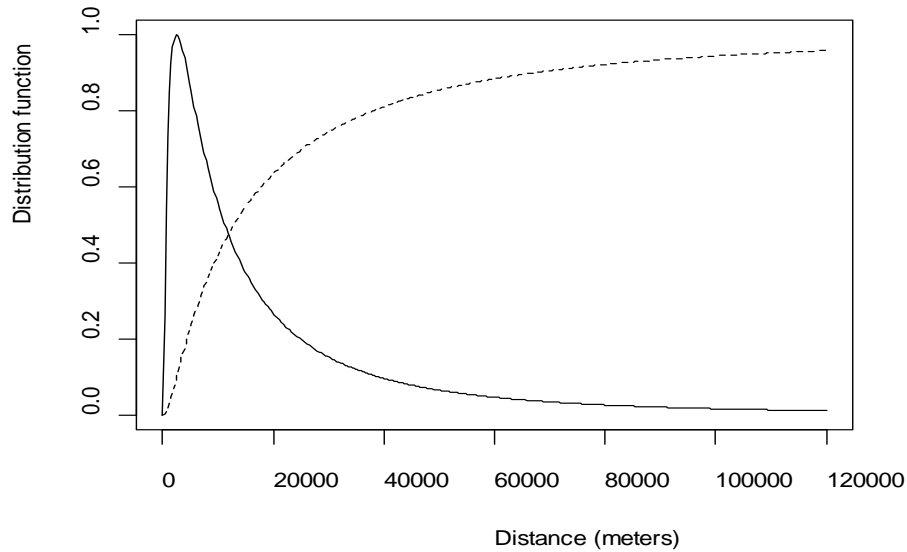
### **Spotted sand bass**

Because spotted sand bass are ambush predators, tending to stay in one location when feeding (Table A3.1), 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 and Lowe 2010) were used to estimate spotted sand bass home range. Like barred sand bass, spotted sand bass feed in soft sediment. However, spotted sand bass will tend to have some degree of association with kelp beds and other benthic structure (Table A3.1), similar to kelp bass.

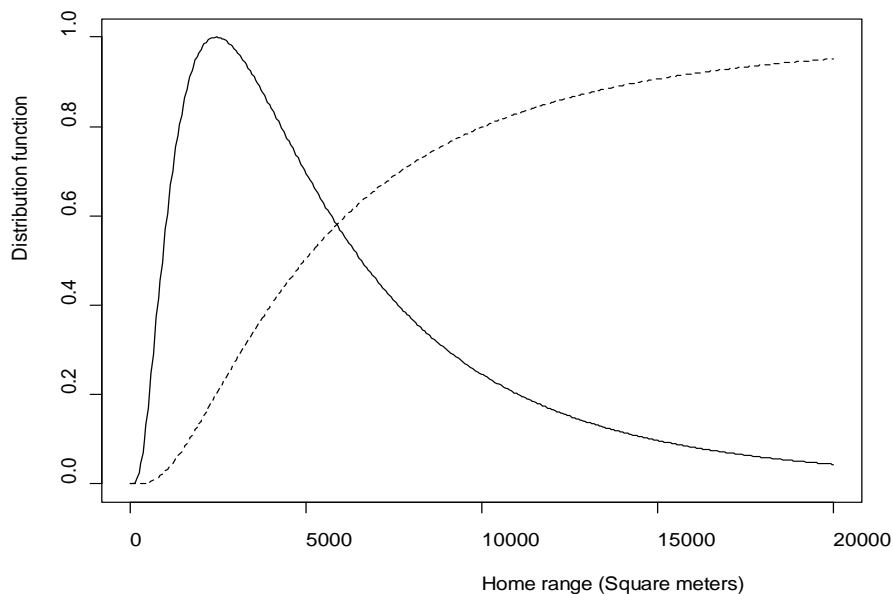
**Table A3.2. Movement range estimates for guild primary species. Parameters are presented assuming a lognormal distribution for each species.**

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 and 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 <sup>2</sup>	4950 m <sup>2</sup>	19,708 m <sup>2</sup>	7100 m <sup>2</sup>	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 and McCammon 1967).
Queenfish	Lognormal	259,600 m <sup>2</sup>	1,617,000 m <sup>2</sup>	10,070,000 m <sup>2</sup>	3,000,000 m <sup>2</sup>	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 <sup>2</sup>	1,617,000 m <sup>2</sup>	10,070,000 m <sup>2</sup>	3,000,000 m <sup>2</sup>	4,689,000	Home range estimate based on telemetry results in Palo Verdes shelf (C. Lowe, unpublished data). Ocean whitefish and California sheephead (Topping <i>et al.</i> 2005, Bellquist <i>et al.</i> 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 <sup>2</sup>	1000 m <sup>2</sup>	2684 m <sup>2</sup>	1200 m <sup>2</sup>	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 and Stuart 2009). Gamma distribution parameters are shape parameter [k] = 1.05; scale parameter [θ, theta] = 9904.
Topsmelt	Lognormal	373 m <sup>2</sup>	1000 m <sup>2</sup>	2684 m <sup>2</sup>	1200 m <sup>2</sup>	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 and Jahn 2010), suggesting limited movement ranges.
Striped mullet	Lognormal	.			28,200 m	80,340	Tag recapture studies on adults (Bacheler <i>et al.</i> 2005). Species likely does not have a home range, but forages nearshore throughout estuary. Offshore migration of great distances sometimes occurs (Idyll and Sutton 1952, Bacheler <i>et al.</i> 2005), supporting use of high coefficient of variation.





**Figure A3.1. 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.**

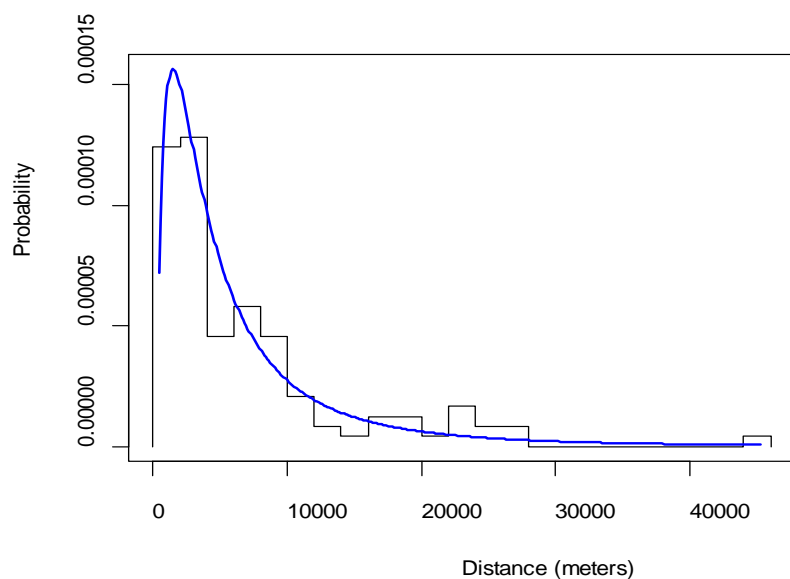


**Figure A3.2. Home range estimate (m<sup>2</sup>) for spotted sand bass. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit the y axis. The probability distribution function indicates the relative probability of a particular home range being selected in the simulations.**

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<sup>2</sup>; Lowe *et al.* 2003) and barred sand bass (mean = 10,003 m<sup>2</sup>; Mason and Lowe 2010). A mean home range of 7100 m<sup>2</sup> 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<sup>2</sup>, 50% (median) = 4950 m<sup>2</sup>; 95% = 19,708 km<sup>2</sup> (Table A3.2; Figure A3.2).

### White catfish

White catfish are carnivorous bottom feeders that inhabit fresh and estuarine waters, including the Sacramento-San Joaquin Delta (Table A3.1). 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 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 A3.3). The percentiles of the distribution are: 5% = 775 m, 50% (median) = 4207 m; 95% = 22,830 m. The parameters selected for HHSQO assessment correspond to the mean of the original data (6920 m) and the standard deviation of the fitted distribution (9600 m; Table A3.2).



**Figure A3.3. 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 sediment, on the sediment surface, and just above the sediment (Table A3.1). Recent 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 to 4000 m of the shelf in an area of 1000 m width (i.e., 3,000,000 - 4,000,000 m<sup>2</sup>; 3 - 4 km<sup>2</sup>) 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.*).

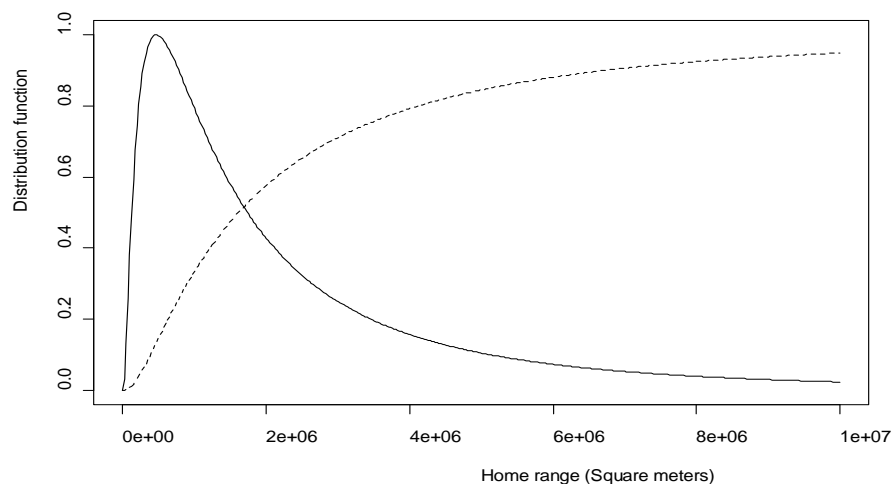
In addition to the croaker studies off Palo Verdes Shelf, examination of similar species may also serve as proxies for white croaker and queenfish (Topping *et al.* 2005, Bellquist *et al.* 2008). In particular, acoustic telemetry studies have been performed on ocean whitefish and California sheephead 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 sediment and limited benthic structure (Table A3.1) (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 contaminant concentrations in white croaker versus sediment have also been performed. Two studies applying these methods estimated exposure area diameters ranging from 2 to 10 km in diameter, depending on the location and trace organic contaminant being evaluated (CH2M HILL 2003, Melwani *et al.* 2009b). These diameters equate to large exposure area<sup>a</sup> estimates of 3 to 79 km<sup>2</sup>.

A distribution for the home range of white croaker and queenfish was developed based on the preliminary home range data provided by Chris Lowe (CSU Long Beach), and the variability exhibited in ocean whitefish and California sheephead. The distribution had the following characteristics: 1) A mean of 3,000,000 m<sup>2</sup> (3 km<sup>2</sup>) 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<sup>2</sup>, 50% (median) = 1,617,000 m<sup>2</sup>; 95% = 10,070,000 m<sup>2</sup> (Figure A3.4; Table A3.2).

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<sup>a</sup> I.e., Area =  $\pi$  (Diameter/2)<sup>2</sup>



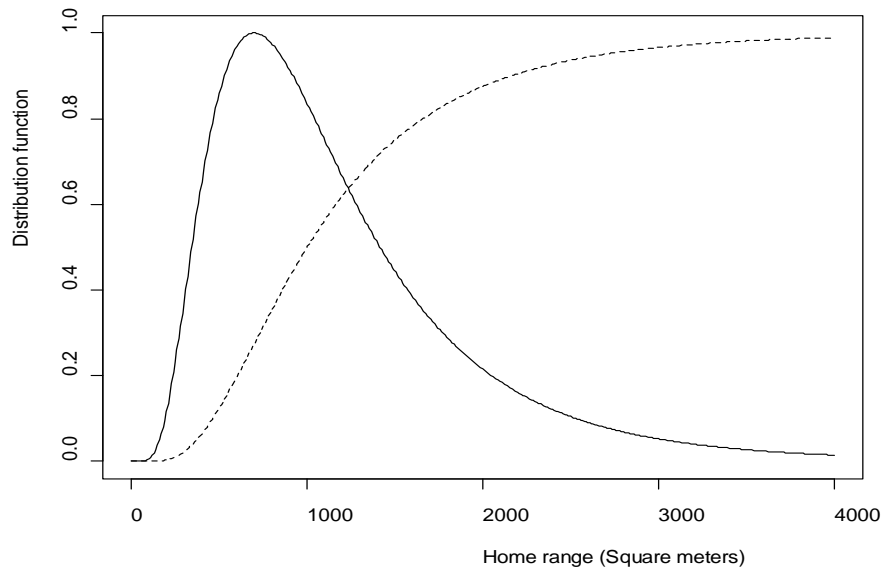
**Figure A3.4. Home range estimate (m<sup>2</sup>) for white croaker and queenfish. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, scaled to fit on the plot. The probability distribution function indicates the relative probability of a 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 A3.1). They frequently reside in 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<sup>2</sup> (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.* 2009b). 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<sup>2</sup> 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<sup>2</sup>, 50% (median) = 1000 m<sup>2</sup>; 95% = 2684 m<sup>2</sup> (Figure A3.5, Table A3.2).

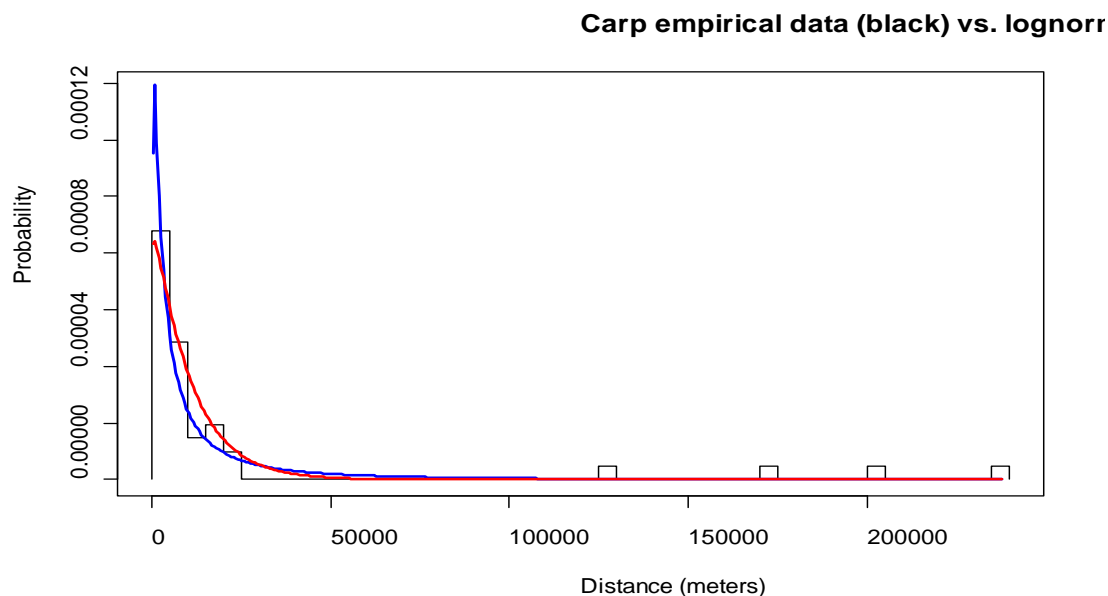


**Figure A3.5. Home range estimate (m<sup>2</sup>) for shiner perch. Dashed line indicates cumulative distribution function. Solid line indicates probability distribution function, indicating relative probability of a particular home range being selected in the simulations.**

### Common carp

Common carp is an omnivorous bottom feeder inhabiting fresh and estuarine waters (Table A3.1). 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 A3.6). For example, in south-eastern Australian forest water streams, 36 recaptured common carp had moved from 0.4 to 238 km (mean  $30 \pm 61$  km) from the point of initial release (Jones and 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).

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 A3.6). 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 A3.2) because it better predicted the proportion of extreme values, with the lognormal distribution tending to overestimate the frequency of very small values (Figure A3.6).



**Figure A3.6. 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 and Stuart 2009).**

### **Topsmelt**

Topsmelt exhibits a different diet and foraging strategy than the other dietary guild primary species. Topsmelt are schooling nearshore fishes, and consume benthic and pelagic plants and invertebrates (Table A3.1). 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 contaminants in topsmelt similarly indicate significant differences in contaminant concentrations among adjacent sampling locations (Battelle *et al.* 2005, Greenfield and Jahn 2010). Topsmelt sampled across different southern California mainland and coastal sites exhibit significant variation in body morphology (O'Reilly and 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.

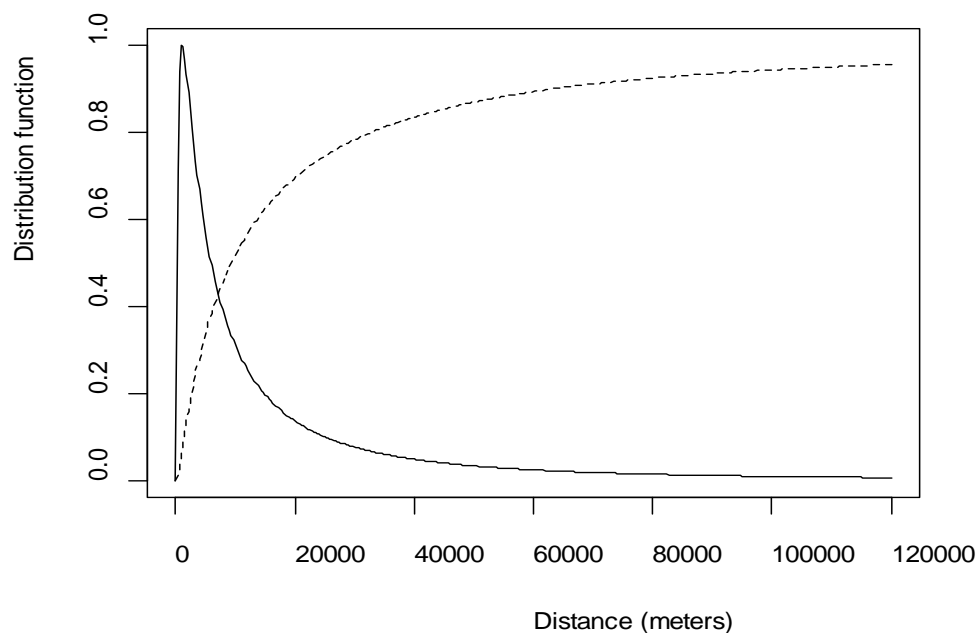
In the absence of specific information on topsmelt movement distance, conservative (small) values were selected based on the small size of the species, and the indirect evidence of limited movement among sampling locations. The relatively small home range estimates for shiner perch were applied to topsmelt. Specifically, a lognormal distribution was selected with percentiles of 5% = 373 m<sup>2</sup>, 50% (median) = 1000 m<sup>2</sup>, and 95% = 2684 m<sup>2</sup> (Figure A3.5; Table A3.2).

### **Striped mullet**

Striped mullet exhibits a different diet and foraging strategy than the other dietary guild primary species. 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 A3.1). 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 A3.2), which was highly skewed, as for California halibut (Figure A3.7).



**Figure A3.7. 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.**

## APPENDIX 4 - SENSITIVITY ANALYSIS FOR INDIRECT EFFECTS ASSESSMENT

### A4.1 Introduction

#### The need to prioritize local data collection

Like most mechanistic models of the food-web exposure and risk of contaminants (e.g., Kitchell *et al.* 1977, Thomann *et al.* 1992, Gobas 1993, Morrison *et al.* 1996), the equations in the HHSQO assessment framework require estimation of multiple input parameters. These parameters pertain to biotic and abiotic attributes, including contaminant concentrations, other chemical properties, physical attributes of the sediment and water column (e.g., temperature), and food web characteristics.

For practical use of this framework, the needs for local input parameters must be prioritized. Sensitivity analyses can help determine which input parameters cause the greatest uncertainty in assessment outcome (USEPA 2001). In addition, the anticipated availability of local site data, the difficulty of additional data collection, and the required accuracy of the assessment will also influence decisions regarding the parameters that require locally collected data.

The expected need for local data collection should differ among assessment tiers. Because Tier 1 is a screening assessment, statewide estimates of parameter values may be used in lieu of local data, to enable a more rapid assessment to be performed. Therefore, Tier 1 would only require inclusion of parameters that have readily available local data and are most important for the assessment outcome. Tier 2 is a site-specific evaluation to provide a complete assessment, based upon the calculated risk at a particular site. Therefore, multiple parameters may be considered in Tier 2 for local data collection.

#### Basis for the sensitivity analysis

Sensitivity analysis employs one of several possible methods to aid in understanding the behavior of a mathematical simulation model. Sensitivity analyses determine how the model responds to variations in individual input parameters, and compare the parameters in terms of relative sensitivity of the model outputs (USEPA 2001, 2005).

The site linkage part of the HHSQO assessment framework uses the Arnot and Gobas (2004) model. This model requires multiple input parameters, many of which are routinely estimated using default values from the literature. Previous sensitivity analyses on the same model characterized the relative sensitivity of model outputs to a range of input parameters, employing a variety of methods and emphases (von Stackelberg *et al.* 2002, Gobas and Arnot 2005, Condon 2007, Gobas and Arnot 2010), which aided in understanding the general behavior of the model.

The sensitivity analyses described in this appendix are specifically intended to help determine which parameters in the HHSQO assessment framework equations should receive the greatest emphasis for local data collection in Tiers 1 and 2. The key question of interest is: *how influential are the combined variability and uncertainty in each input parameter for the potential outcome of the data analysis?* This sensitivity analysis is similar to the analysis by Von Stackelberg *et al.* (2002) in that its inputs are based on observed empirical distributions in parameters. In particular, this analysis uses empirical distributions observed among California



estuaries and marine embayments. By using empirical data on variability, this analysis specifically determines which parameters are likely to be most influential. These influential parameters would be candidates for local data collection in Tiers 1 and 2 to determine site-specific estimates. They would also be considered as parameters to be varied in the Tier 3 analysis.

The sensitivity analysis focused on the parameters that play a role in the site linkage indicator. This analysis aided in developing recommendations for which parameters should be obtained locally. The last section of this appendix summarizes findings and briefly highlights follow-up Science Team activities. The findings of the sensitivity analysis described in this appendix influenced the selection of parameters for local site measurement and probabilistic description of variability, resulting in the data collection requirements for the HHSQO assessment framework.

## **A4.2 Methods**

The site linkage sensitivity analysis was performed with the Arnot and Gobas (2004) bioaccumulation model, which is a component of the HHSQO assessment framework. Parameters expected to influence model predicted tissue contaminant concentration were varied according to distributions observed among California water bodies. Those parameters with high influence on the model outcome are potential candidates for local data collection. Parameter influence on model outcome, in combination with difficulty of local data collection, were used to determine which parameters should be locally obtained (versus statewide estimates) in Tiers 1 and 2.

The bioaccumulation model equations for the site linkage indicator are complex and require a large number of input parameters to be specified (Appendix 1). Due to the high model complexity, two approaches were employed for the site linkage sensitivity analysis, to determine if the results were consistent among approaches. The first approach used a Monte Carlo Simulation methodology and performed using the YASAIw add in for Excel (McKone and Bogen 1991, Eckstein and Riedmueller 2002, Pelletier 2009). Five-thousand simulations were performed, and the contribution to variance relative to other parameters was calculated.

The second approach employed individual parameter perturbation. Individual parameter perturbation determines the potential change in tissue contaminant concentration due to each parameter, in the absence of changes in other parameters (Bartell *et al.* 1986, USEPA 2005). This provides an absolute estimate of the potential variation caused by each parameter.

In the individual parameter perturbation, all parameters were initially set to the 50<sup>th</sup> percentile values, generated in the Monte Carlo Simulation. Each parameter was then individually shifted to the 84<sup>th</sup> percentile. This is equivalent to adding one SD on the linear scale for normally distributed parameters, or adding one SD on a lognormal scale for lognormally distributed parameters. The percent change in predicted tissue contaminant concentration was recorded for each parameter.

This analysis assumed that the compound had the chemical attributes of p,p' - DDE. Analyses based on the attributes of PCB congener 110, PCB congener 194, and dieldrin yielded similar results and are not presented here.

Table A4.1 lists the input parameters that were varied, their selected probability distributions and summary statistics, and the basis for the chosen values. Other parameters were set at fixed values (Appendix 1, Table A1.3), developed in previous applications of the bioaccumulation model to San Francisco Bay (Gobas and Arnot 2010).

The sensitivity analysis evaluated 13 input parameters, including sediment contaminant concentration; sediment organic carbon; water column dissolved and particulate organic carbon, and suspended sediment concentration; water temperature, salinity, and dissolved oxygen; lipid content of seafood and their prey; and seafood body mass. The analysis also included piscivory, here defined as the percent of the diet of seafood that is fish, rather than invertebrates. Percent benthic diet was also included, here defined as the proportion of the dietary pathway of the seafood that is directly or indirectly (via food web trophic transfer) linked to the sediment. The selection of these thirteen parameters for the sensitivity analysis was based on three factors: they were identified as important in previous sensitivity analyses (Gobas and Arnot 2005, 2010); they were known to vary among sites and water bodies; and they were expected to influence contaminant bioaccumulation based on Scientific Steering Committee recommendations and literature review.

For normal and lognormal distributions, the sensitivity analysis used measures of dispersion (i.e., standard deviations) based on variability in parameter distributions among California water bodies (Table A4.1). Empirical variation in California was the focus in order to identify parameters for which local empirical measurements would substantially improve estimates of tissue contaminant concentration. For physical and chemical parameters (sediment contaminant concentration, sediment total organic carbon, and water column chemical properties and temperature), empirical variation was based on observed data distribution statewide for California bays and estuaries. Sediment contamination and TOC data were obtained from the California SQO database (Myre *et al.* 2006), and water quality data were obtained from peer reviewed literature, web queries, and unpublished data (Table A4.1). Average values were calculated for individual water bodies, and these water body averages formed the basis for the modeled distributions listed in Table A4.1.

For biological attributes of seafood and their prey (including lipid and body mass), averages were obtained for multiple seafood species occurring in California. These species averages formed the basis for modeled distributions (Table A4.1). Percent piscivory and percent benthic diet are difficult to obtain due to spatial and temporal variation and inconsistency in study methods, and were assumed to have a uniform distribution, ranging from 0 to 100% for the sediment sensitivity analysis.

**Table A4.1. Input parameters varied and associated assumptions in the site linkage sensitivity analysis. Values left blank were not needed for those distributions. All parameter values in this table are estimates that were used to perform the sensitivity analyses only. SD = Standard Deviation**

Parameter	Distribution	Min	Max	Mean	SD	Basis for Distribution	Data Source
(Cs) Sediment contaminant concentration, µg/kg	Lognormal			96.5	647	Variability among water body segments of total DDTs for sediment samples collected state wide	CASQO database (Myre <i>et al.</i> 2006) and Delta SQO data (N = 128 water body segments)
Sediment total organic carbon (%)	Lognormal			1.6	1.5	Variability among water body segments for sediment samples collected state wide	CASQO database (Myre <i>et al.</i> 2006) and Delta SQO data (N = 128 water body segments)
Benthic diet (%)	Uniform	0	100			Entire plausible parameter range	
Piscivory (%)	Uniform	0	100			Entire plausible parameter range	
Seafood lipid (%)	Lognormal			1.26	1.23	Variability among species of average fillet tissue contaminant concentrations collected state wide	SWAMP database <sup>a</sup> (Hoenicke <i>et al.</i> 2008) (N = 107 fish species)
Lipid of invertebrate prey (%)	Lognormal			1.55	0.84	Variability among species of average whole body concentrations for marine/estuarine species	USACE BSAF database <sup>b</sup> (Lutz 2010) (N = 14 invertebrate species)
Weight (kg)	Lognormal			0.43	0.56	Variability among species of average body mass for Pacific coast/estuarine fish species	(Rasmussen 1995, Allen <i>et al.</i> 2004, Condon 2007, Greenfield <i>et al.</i> 2007a, Gobas and Arnot 2010) (N = 21 fish species)
Dissolved oxygen concentration (mg/L)	Normal			9.0	1.2	Variability among California estuaries/marine embayments of annual average concentrations	(Kamer and Stein 2003, Kennison <i>et al.</i> 2003, Gobas and Arnot 2010) and web queries (N = 11 water bodies)
Mean water temperature (°C)	Normal			16.8	4.1	Variability among Pacific coast estuaries/marine embayments of reported average concentrations	(Kennison <i>et al.</i> 2003, David <i>et al.</i> 2006, Condon 2007, Greenfield <i>et al.</i> 2007b, Gobas and Arnot 2010) and web queries (N = 14 water bodies)
Salinity (PSU)	Truncated normal <sup>c</sup>	1	35	25.8	9.6	Variability among Pacific coast estuaries/marine embayments of reported average concentrations	(Allen <i>et al.</i> 2002, Kennison <i>et al.</i> 2003, Condon 2007, Greenfield <i>et al.</i> 2007b, Gobas and Arnot 2010) and web queries (N = 14 water bodies)
Suspended solid concentration in water column (kg/L)	Lognormal			2.7E-05	3.4E-05	Variability among Pacific coast estuaries/marine embayments of reported average concentrations	(Zeng <i>et al.</i> 2002, David <i>et al.</i> 2006, Greenfield <i>et al.</i> 2007a, Gobas and Arnot 2010) and unpublished data (N = 6 water bodies)
Particulate organic carbon content of water (kg/L)	Lognormal			1.6E-06	1.6E-06	Variability among Pacific coast estuaries/marine embayments of reported average concentrations	(Condon 2007, Gobas and Arnot 2010) and unpublished data (N = 4 water bodies)
Dissolved organic carbon content of water (kg/L)	Lognormal			2.1E-06	1.5E-06	Variability among Pacific coast estuaries/marine embayments of reported average concentrations	(Condon 2007, Greenfield <i>et al.</i> 2007a, 2007b, Gobas and Arnot 2010) and unpublished data (N = 6 water bodies)

a. Statewide data set including current and recent historic tissue chemistry data maintained by SFEI

b. Available on the web at <http://el.ercd.usace.army.mil/bsafnew/BSAF.html>

c. A normal distribution, with minimum or maximum values established to ensure biological realism

### A4.3 Results and Discussion

Overall, sediment contaminant concentration explained the majority of variation in estimated tissue contaminant concentration for the Monte Carlo Simulation (81.4%; Table A4.2), and the individual parameter perturbation (562%; Table A4.3). Note that the percentages in the Monte Carlo Simulation (MCS) indicate the relative contribution to variance in output, as compared to other parameters. However, the percentages in the individual parameter perturbation (IPP) indicate the total percent change in predicted tissue contaminant concentration when that input parameter is shifted from the 50<sup>th</sup> percentile (median) to the 84<sup>th</sup> percentile (i.e., adding one SD). The IPP results indicate about a six-fold increase in tissue contaminant concentrations, when increasing sediment concentrations across a representative range. These findings in combination indicate the high sensitivity of estimated tissue contaminant concentration to sediment concentration. This indicates that accurate and representative local estimates of sediment contaminant concentration are the greatest data need for evaluating site linkage to seafood tissue contaminant concentrations.

**Table A4.2. Results of Monte Carlo Simulation sensitivity analysis for site linkage. Percentages indicate contribution of parameter to variation in model predicted seafood tissue p,p' – DDE concentrations.**

Parameter	% Contribution to Variance
Sediment contaminant concentration	81.4
Benthic diet %	7.0
Seafood lipid %	4.1
Sediment total organic carbon %	3.1
Piscivory %	1.9
Lipid of invertebrate prey %	0.9
Mean water temperature	0.7
Particulate organic carbon content of water	0.3
Suspended solid concentration in water column	0.2
Dissolved organic carbon content of water	0.1
Dissolved oxygen concentration	0.0
Salinity	0.0
Weight	0.0

Percent benthic diet was an important parameter for predicting tissue contaminant concentration, explaining 7% of the variation for the MCS (Table A4.2), and causing a 57% increase in the individual parameter perturbation (Table A4.3). Other relatively important parameters included seafood tissue lipid, sediment organic carbon, and piscivory, each explaining 2 to 4% of total variation in the MCS, and causing 30 to 57% increase or decrease in the outcome of the IPP (Tables A4.2 and A4.3). Modifying prey lipid caused a 32% change in the IPP outcome.

The remaining parameters explained less than 2% of variation in the MCS, and caused less than a 22% change in the IPP outcome. These included water column parameters (temperature, salinity, suspended sediment concentration, particulate organic carbon, and dissolved organic carbon), as well as body weight of the seafood organism (Tables A4.2 and A4.3).

**Table A4.3. Results of individual parameter perturbation sensitivity analysis for site linkage. Each input parameter was increased from the 50<sup>th</sup> to 84<sup>th</sup> percentile. Values indicate the resulting percent increase or decrease in the model predicted seafood tissue p,p' – DDE concentration.**

Parameter	% Change in Predicted Seafood Contamination
Sediment contaminant concentration	562
Seafood lipid %	60
Benthic diet %	57
Piscivory %	35
Lipid of invertebrate prey %	32
Sediment total organic carbon %	-30
Suspended solid concentration in water column	21
Mean water temp	19
Particulate organic carbon content of water	-7
Salinity	7
Dissolved oxygen concentration	5
Dissolved organic carbon content of water	-2
Weight	2

Table A4.4 presents recommendations for use of statewide values versus local data collection for Tiers 1 and 2. These recommendations are based on the findings of the sensitivity analysis, in combination with the relative difficulty of obtaining defensible local data. Sediment contaminant concentration data must be locally obtained for both Tiers 1 and 2. Additionally, sediment TOC and seafood tissue lipid concentration were important in the IPP (Table A4.3), and should be locally obtained and input for Tier 2 analyses. Local sediment total organic carbon data should also be used for Tier 1 analysis, as it is typically widely available.

Proportion of benthic diet (versus pelagic), and proportion of piscivory (versus invertebrate prey) were both important, but these parameters are very difficult to quantify on a site-specific basis. Therefore, Tier 1 and Tier 2 bioaccumulation model calculations should be based on estimates for benthic diet and piscivory that are representative of local seafood consumed in California bays and estuaries. The Science Team developed these estimates based on available information of the foraging behavior of California seafood. This included development and application of the feeding guild approach, as detailed in Appendix 2. Development of local parameter values for food web structure and diet could be performed as Tier 3 activities, if deemed important in the conceptual site model that is developed by local managers and affected stakeholders.

Remaining parameters that are expected to vary among sites exhibited lower sensitivity in the analysis (Tables A4.2 and A4.3). In consideration of their limited impact, statewide values are sufficient for these parameters. To reduce effort, they need not be emphasized for local data collection in Tier 1 or Tier 2 applications.

The sensitivity analysis described in this section did not include seafood movement, a potentially important influence on site linkage. Separate analyses performed by the Science Team indicated a high potential influence of seafood movement, as well as a high uncertainty in this parameter. Thus, the Science Team summarized best available data on seafood movement in Appendix 3.

**Table A4.4. Proposed treatment of parameters for Tier 1 and Tier 2 assessment. Relative sensitivity is ranked based on results of individual parameter perturbation (Table A4.3). Difficulty = relative difficulty of collecting representative local data. Statewide = statewide default estimate will be developed and should be used in all cases. Local = site-specific estimate should be obtained using local data.**

Parameter	Sensitivity	Difficulty	Tier 1	Tier 2	Rationale
Sediment concentration	Very High (>100%)	Low	Local	Local	Most sensitive parameter with local data available.
Benthic diet	High (50 - 100%)	High	Statewide	Statewide	Sensitive parameter, but difficult to estimate on a local basis. Will be addressed using feeding guilds.
Seafood lipid	High (50 - 100%)	Low	Statewide	Local	Very sensitive parameter with local data available for Tier 2.
Sediment TOC	Moderate (30 - 50%)	Low	Local	Local	Moderately sensitive parameter with local data available for all Tiers.
Piscivory	Moderate (30 - 50%)	High	Statewide	Statewide	Moderately sensitive parameter, but difficult to estimate on a local basis. Will be addressed using feeding guilds
Prey lipid	Moderate (30 - 50%)	Moderate	Statewide	Statewide or optional local	Moderately sensitive parameter. Difficult to estimate and not readily available. Option to include local data, if available.
Temperature	Low (10 - 30%)	Low	Statewide	Statewide or optional local	Low sensitivity, but local data often readily available for Tier 2 inclusion.
Suspended sediment concentration	Low (10 - 30%)	Low	Statewide	Statewide or optional local	Low sensitivity, but local data often readily available for Tier 2 inclusion.
Particulate organic carbon	Very Low (<10%)	Low	Statewide	Statewide or optional local	Very Low sensitivity so no need for local data inclusion.
Salinity	Very Low (<10%)	Low	Statewide	Statewide or optional local	Very Low sensitivity so no need for local data inclusion.
Dissolved oxygen	Very Low (<10%)	Low	Statewide	Statewide or optional local	Very Low sensitivity so no need for local data inclusion.
Dissolved organic carbon	Very Low (<10%)	Low	Statewide	Statewide or optional local	Very Low sensitivity so no need for local data inclusion.
Weight	Very Low (<10%)	Low	Statewide	Statewide	Very Low sensitivity so no need for local data inclusion.

## APPENDIX 5 - ANALYSIS OF PCB CONGENERS

### A5.1 Introduction

PCBs comprise a group of 209 congeners. Measurements of total PCB concentrations in sediment or tissue are commonly based on measurement of a subset of the most prevalent and important congeners, often combined with a statistical method to estimate the total congener concentration (Fikslin and Santoro 2003). California monitoring programs measure a subset of PCB congeners that varies depending upon program or application (Table A5.1). Specification of the list of PCB congeners required for HHSQO assessment has an important influence on the cost and practicality of the analyses. Requirement of analysis of all 209 congeners would give the most complete measurement of total PCB concentration, but would also exclude use of almost all current and past monitoring data (based on a subset of congeners). Selection of a subset of congeners for use in the assessment provides greater feasibility and comparability, but variation in congener lists among monitoring programs creates uncertainty regarding which subset should be used for HHSQO assessment.

With the advent of available data measuring 209 congener concentrations in sport fish from a large nationwide data set in the US (Stahl *et al.* 2009), it is now possible to examine the relationships between various subsets and total exposure. This Appendix examines the level of agreement between the sum of all 209 congeners and estimates of total PCBs based on different congener subsets. The results of these comparisons are used to inform selection of the recommended congener subset for HHSQO assessment.

### A5.2 Methods

USEPA National Fish Tissue Study (NFTS) data were obtained in a CD mailer provided from USEPA (Leanne Stahl). This data set includes fish tissue samples obtained from inland lakes and reservoirs probabilistically sampled throughout the United States (Stahl *et al.* 2009). All samples were analyzed in the laboratory using EPA method 1668A, High Resolution Gas Chromatography/High Resolution Mass Spectrometry. This analytical method produces some coeluting congeners, resulting in 159 individual measurements per sample. However, all 209 congeners are incorporated using this method (CSC Environmental Programs Group 2005, USEPA 2008b, Stahl *et al.* 2009). Samples with >50% non-detect values were excluded from analysis (n = 79). After removal of these samples, the final analysis data set contained 402 tissue samples.

Congener results for these samples with <50% censored values were imputed using the Kaplan-Meier method. The imputation method resulted in mean PCB concentration per sample. To obtain sum of 209 congeners, each mean value was multiplied by the number of PCB congeners included in the analysis (Helsel 2010).

In addition to sum of 209 congeners, summation methods were used for 5 congener subsets commonly measured in California (Table A5.1):

- SWAMP: The congener subset analyzed in Surface Water Ambient Monitoring Program (SWAMP 2008) studies, which include statewide surveys of biota (Hoenicke *et al.* 2008, Davis *et al.* 2010, Davis *et al.* 2011).

- RMP: Congeners analyzed in tissue studies by the Regional Monitoring Program for Water Quality in San Francisco Bay (RMP), including the ongoing RMP sport fish contamination survey (Davis *et al.* 2006b, Hunt *et al.* 2008).
- Bight: Congeners analyzed in the Southern California Bight Regional Survey (Schiff and Allen 2000, Jarvis *et al.* 2008).
- NOAA: The congeners analyzed by National Oceanic and Atmospheric Administration's National Status and Trends Mussel Watch program (Lauenstein and Cantillo 1993, O'Connor and Lauenstein 2006).
- Aquatic Life SQO: Congeners analyzed and interpreted for SQO assessment of potential effects to sediment dwelling invertebrates (SWRCB 2009).
- Most abundant 45 congeners in eight sport fish samples from California lakes surveyed in the National Fish Tissue Survey (Stahl *et al.* 2009), based on analyses performed by OEHHA (Sanborn and Brodberg 2010).

Summary statistics of the summation results were calculated for each subset and compared to the sum of 209 congeners. Linear regression analysis was used to determine regression equations for each summation method. In these models, results from the individual summation method were used to predict Sum of 209 congeners. Data were log-transformed to achieve normally distributed residuals, as required in linear regression (Draper and Smith 1998). In all analyses, the dependent variable was the sum of all 209 PCB congeners. All statistical analyses were performed in R.



**Table A5.1. PCB congeners included in five California monitoring programs, and the most abundant congeners in California finfish.**

CASRN	Congener	IUPAC	RMP	BIGHT	Aquatic Life SQO	NOAA	SWAMP	Most abundant
2051-60-7	1	2-Chlorobiphenyl						
2051-61-8	2	3-Chlorobiphenyl						
2051-62-9	3	4-Chlorobiphenyl						
13029-08-8	4	2,2'-Dichlorobiphenyl						
16605-91-7	5	2,3-Dichlorobiphenyl					✓	
25569-80-6	6	2,3'-Dichlorobiphenyl						
33284-50-3	7	2,4-Dichlorobiphenyl						
34883-43-7	8	2,4'-Dichlorobiphenyl	✓		✓	✓	✓	
34883-39-1	9	2,5-Dichlorobiphenyl						
33146-45-1	10	2,6-Dichlorobiphenyl						
2050-67-1	11	3,3'-Dichlorobiphenyl						
2974-92-7	12	3,4-Dichlorobiphenyl						
2974-90-5	13	3,4'-Dichlorobiphenyl						
34883-41-5	14	3,5-Dichlorobiphenyl						
2050-68-2	15	4,4'-Dichlorobiphenyl					✓	
38444-78-9	16	2,2',3-Trichlorobiphenyl						
37680-66-3	17	2,2',4-Trichlorobiphenyl						
37680-65-2	18	2,2',5-Trichlorobiphenyl	✓	✓	✓	✓	✓	
38444-73-4	19	2,2',6-Trichlorobiphenyl						
38444-84-7	20	2,3,3'-Trichlorobiphenyl						
55702-46-0	21	2,3,4-Trichlorobiphenyl						
38444-85-8	22	2,3,4'-Trichlorobiphenyl						
55720-44-0	23	2,3,5-Trichlorobiphenyl						
55702-45-9	24	2,3,6-Trichlorobiphenyl						
55712-37-3	25	2,3',4-Trichlorobiphenyl						
38444-81-4	26	2,3',5-Trichlorobiphenyl						
38444-76-7	27	2,3',6-Trichlorobiphenyl					✓	
7012-37-5	28	2,4,4'-Trichlorobiphenyl	✓	✓	✓	✓	✓	
15862-07-4	29	2,4,5-Trichlorobiphenyl					✓	
35693-92-6	30	2,4,6-Trichlorobiphenyl						
16606-02-3	31	2,4',5-Trichlorobiphenyl	✓				✓	
38444-77-8	32	2,4',6-Trichlorobiphenyl						
38444-86-9	33	2,3',4'-Trichlorobiphenyl	✓				✓	
37680-68-5	34	2,3',5'-Trichlorobiphenyl						
37680-69-6	35	3,3',4-Trichlorobiphenyl						
38444-87-0	36	3,3',5-Trichlorobiphenyl						
38444-90-5	37	3,4,4'-Trichlorobiphenyl		✓				
53555-66-1	38	3,4,5-Trichlorobiphenyl						
38444-88-1	39	3,4',5-Trichlorobiphenyl						
38444-93-8	40	2,2',3,3'-Tetrachlorobiphenyl						

CASRN	Congener	IUPAC	RMP	BIGHT	Aquatic Life SQO	NOAA	SWAMP	Most abundant
52663-59-9	41	2,2',3,4-Tetrachlorobiphenyl						
36559-22-5	42	2,2',3,4'-Tetrachlorobiphenyl						
70362-46-8	43	2,2',3,5-Tetrachlorobiphenyl						
41464-39-5	44	2,2',3,5'-Tetrachlorobiphenyl	✓	✓	✓	✓	✓	
70362-45-7	45	2,2',3,6-Tetrachlorobiphenyl						
41464-47-5	46	2,2',3,6'-Tetrachlorobiphenyl						
2437-79-8	47	2,2',4,4'-Tetrachlorobiphenyl						
70362-47-9	48	2,2',4,5-Tetrachlorobiphenyl						
41464-40-8	49	2,2',4,5'-Tetrachlorobiphenyl	✓	✓			✓	
62796-65-0	50	2,2',4,6-Tetrachlorobiphenyl						
68194-04-7	51	2,2',4,6'-Tetrachlorobiphenyl						
35693-99-3	52	2,2',5,5'-Tetrachlorobiphenyl	✓	✓	✓	✓	✓	
41464-41-9	53	2,2',5,6'-Tetrachlorobiphenyl						
15968-05-5	54	2,2',6,6'-Tetrachlorobiphenyl						
74338-24-2	55	2,3,3',4-Tetrachlorobiphenyl						
41464-43-1	56	2,3,3',4'-Tetrachlorobiphenyl	✓				✓	
70424-67-8	57	2,3,3',5-Tetrachlorobiphenyl						
41464-49-7	58	2,3,3',5'-Tetrachlorobiphenyl						
74472-33-6	59	2,3,3',6-Tetrachlorobiphenyl						
33025-41-1	60	2,3,4,4'-Tetrachlorobiphenyl	✓				✓	
33284-53-6	61	2,3,4,5-Tetrachlorobiphenyl						
54230-22-7	62	2,3,4,6-Tetrachlorobiphenyl						
74472-34-7	63	2,3,4',5-Tetrachlorobiphenyl						
52663-58-8	64	2,3,4',6-Tetrachlorobiphenyl						
33284-54-7	65	2,3,5,6-Tetrachlorobiphenyl						
32598-10-0	66	2,3',4,4'-Tetrachlorobiphenyl	✓	✓	✓	✓	✓	
73575-53-8	67	2,3',4,5-Tetrachlorobiphenyl						
73575-52-7	68	2,3',4,5'-Tetrachlorobiphenyl						
60233-24-1	69	2,3',4,6-Tetrachlorobiphenyl						
32598-11-1	70	2,3',4',5-Tetrachlorobiphenyl	✓	✓			✓	
41464-46-4	71	2,3',4',6-Tetrachlorobiphenyl						
41464-42-0	72	2,3',5,5'-Tetrachlorobiphenyl						
74338-23-1	73	2,3',5,6-Tetrachlorobiphenyl						
32690-93-0	74	2,4,4',5-Tetrachlorobiphenyl	✓	✓			✓	
32598-12-2	75	2,4,4',6-Tetrachlorobiphenyl						
70362-48-0	76	2,3',4',5'-Tetrachlorobiphenyl						
32598-13-3	77	3,3',4,4'-Tetrachlorobiphenyl		✓				
70362-49-1	78	3,3',4,5-Tetrachlorobiphenyl						
41464-48-6	79	3,3',4,5'-Tetrachlorobiphenyl						
33284-52-5	80	3,3',5,5'-Tetrachlorobiphenyl						
70362-50-4	81	3,4,4',5-Tetrachlorobiphenyl		✓				
52663-62-4	82	2,2',3,3',4-Pentachlorobiphenyl						
60145-20-2	83	2,2',3,3',5-Pentachlorobiphenyl						✓
52663-60-2	84	2,2',3,3',6-Pentachlorobiphenyl						

CASRN	Congener	IUPAC	RMP	BIGHT	Aquatic Life SQO	NOAA	SWAMP	Most abundant
65510-45-4	85	2,2',3,4,4'-Pentachlorobiphenyl						
55312-69-1	86	2,2',3,4,5-Pentachlorobiphenyl						✓
38380-02-8	87	2,2',3,4,5'-Pentachlorobiphenyl	✓	✓			✓	✓
55215-17-3	88	2,2',3,4,6-Pentachlorobiphenyl						
73575-57-2	89	2,2',3,4,6'-Pentachlorobiphenyl						
68194-07-0	90	2,2',3,4',5-Pentachlorobiphenyl						✓
68194-05-8	91	2,2',3,4',6-Pentachlorobiphenyl						
52663-61-3	92	2,2',3,5,5'-Pentachlorobiphenyl						
73575-56-1	93	2,2',3,5,6-Pentachlorobiphenyl						
73575-55-0	94	2,2',3,5,6'-Pentachlorobiphenyl						
38379-99-6	95	2,2',3,5',6-Pentachlorobiphenyl	✓					
73575-54-9	96	2,2',3,6,6'-Pentachlorobiphenyl						
41464-51-1	97	2,2',3,4',5'-Pentachlorobiphenyl	✓				✓	✓
60233-25-2	98	2,2',3,4',6'-Pentachlorobiphenyl						
38380-01-7	99	2,2',4,4',5-Pentachlorobiphenyl	✓	✓			✓	✓
39485-83-1	100	2,2',4,4',6-Pentachlorobiphenyl						
37680-73-2	101	2,2',4,5,5'-Pentachlorobiphenyl	✓	✓	✓	✓	✓	✓
68194-06-9	102	2,2',4,5,6'-Pentachlorobiphenyl						
60145-21-3	103	2,2',4,5',6-Pentachlorobiphenyl						
56558-16-8	104	2,2',4,6,6'-Pentachlorobiphenyl						
32598-14-4	105	2,3,3',4,4'-Pentachlorobiphenyl	✓	✓	✓	✓	✓	✓
70424-69-0	106	2,3,3',4,5-Pentachlorobiphenyl						
70424-68-9	107	2,3,3',4',5-Pentachlorobiphenyl						
70362-41-3	108	2,3,3',4,5'-Pentachlorobiphenyl						✓
74472-35-8	109	2,3,3',4,6-Pentachlorobiphenyl						
38380-03-9	110	2,3,3',4',6-Pentachlorobiphenyl	✓	✓	✓		✓	✓
39635-32-0	111	2,3,3',5,5'-Pentachlorobiphenyl						
74472-36-9	112	2,3,3',5,6-Pentachlorobiphenyl						
68194-10-5	113	2,3,3',5',6-Pentachlorobiphenyl						✓
74472-37-0	114	2,3,4,4',5-Pentachlorobiphenyl		✓			✓	
74472-38-1	115	2,3,4,4',6-Pentachlorobiphenyl						✓
18259-05-7	116	2,3,4,5,6-Pentachlorobiphenyl						
68194-11-6	117	2,3,4',5,6-Pentachlorobiphenyl						
31508-00-6	118	2,3',4,4',5-Pentachlorobiphenyl	✓	✓	✓	✓	✓	✓
56558-17-9	119	2,3',4,4',6-Pentachlorobiphenyl		✓				✓
68194-12-7	120	2,3',4,5,5'-Pentachlorobiphenyl						
56558-18-0	121	2,3',4,5',6-Pentachlorobiphenyl						
76842-07-4	122	2,3,3',4',5'-Pentachlorobiphenyl						
65510-44-3	123	2,3',4,4',5'-Pentachlorobiphenyl		✓				
70424-70-3	124	2,3',4',5,5'-Pentachlorobiphenyl						
74472-39-2	125	2,3',4',5',6-Pentachlorobiphenyl						✓
57465-28-8	126	3,3',4,4',5-Pentachlorobiphenyl		✓				
39635-33-1	127	3,3',4,5,5'-Pentachlorobiphenyl						
38380-07-3	128	2,2',3,3',4,4'-Hexachlorobiphenyl	✓	✓	✓	✓	✓	✓

CASRN	Congener	IUPAC	RMP	BIGHT	Aquatic Life SQO	NOAA	SWAMP	Most abundant
55215-18-4	129	2,2',3,3',4,5-Hexachlorobiphenyl						✓
52663-66-8	130	2,2',3,3',4,5'-Hexachlorobiphenyl						
61798-70-7	131	2,2',3,3',4,6-Hexachlorobiphenyl						
38380-05-1	132	2,2',3,3',4,6'-Hexachlorobiphenyl	✓					
35694-04-3	133	2,2',3,3',5,5'-Hexachlorobiphenyl						
52704-70-8	134	2,2',3,3',5,6-Hexachlorobiphenyl						
52744-13-5	135	2,2',3,3',5,6'-Hexachlorobiphenyl						✓
38411-22-2	136	2,2',3,3',6,6'-Hexachlorobiphenyl						
35694-06-5	137	2,2',3,4,4',5-Hexachlorobiphenyl					✓	
35065-28-2	138	2,2',3,4,4',5'-Hexachlorobiphenyl	✓	✓	✓	✓	✓	✓
56030-56-9	139	2,2',3,4,4',6-Hexachlorobiphenyl						
59291-64-4	140	2,2',3,4,4',6'-Hexachlorobiphenyl						
52712-04-6	141	2,2',3,4,5,5'-Hexachlorobiphenyl	✓				✓	✓
41411-61-4	142	2,2',3,4,5,6-Hexachlorobiphenyl						
68194-15-0	143	2,2',3,4,5,6'-Hexachlorobiphenyl						
68194-14-9	144	2,2',3,4,5',6-Hexachlorobiphenyl						
74472-40-5	145	2,2',3,4,6,6'-Hexachlorobiphenyl						
51908-16-8	146	2,2',3,4',5,5'-Hexachlorobiphenyl						✓
68194-13-8	147	2,2',3,4',5,6-Hexachlorobiphenyl						✓
74472-41-6	148	2,2',3,4',5,6'-Hexachlorobiphenyl						
38380-04-0	149	2,2',3,4',5',6-Hexachlorobiphenyl	✓	✓			✓	✓
68194-08-1	150	2,2',3,4',6,6'-Hexachlorobiphenyl						
52663-63-5	151	2,2',3,5,5',6-Hexachlorobiphenyl	✓	✓			✓	✓
68194-09-2	152	2,2',3,5,6,6'-Hexachlorobiphenyl						
35065-27-1	153	2,2',4,4',5,5'-Hexachlorobiphenyl	✓	✓	✓	✓	✓	✓
60145-22-4	154	2,2',4,4',5,6'-Hexachlorobiphenyl						✓
33979-03-2	155	2,2',4,4',6,6'-Hexachlorobiphenyl						
38380-08-4	156	2,3,3',4,4',5-Hexachlorobiphenyl	✓	✓			✓	✓
69782-90-7	157	2,3,3',4,4',5'-Hexachlorobiphenyl		✓			✓	✓
74472-42-7	158	2,3,3',4,4',6-Hexachlorobiphenyl	✓				✓	✓
39635-35-3	159	2,3,3',4,5,5'-Hexachlorobiphenyl						
41411-62-5	160	2,3,3',4,5,6-Hexachlorobiphenyl						✓
74472-43-8	161	2,3,3',4,5',6-Hexachlorobiphenyl						
39635-34-2	162	2,3,3',4',5,5'-Hexachlorobiphenyl						
74472-44-9	163	2,3,3',4',5,6-Hexachlorobiphenyl						✓
74472-45-0	164	2,3,3',4',5',6-Hexachlorobiphenyl						
74472-46-1	165	2,3,3',5,5',6-Hexachlorobiphenyl						
41411-63-6	166	2,3,4,4',5,6-Hexachlorobiphenyl						✓
52663-72-6	167	2,3',4,4',5,5'-Hexachlorobiphenyl		✓				
59291-65-5	168	2,3',4,4',5',6-Hexachlorobiphenyl		✓				✓
32774-16-6	169	3,3',4,4',5,5'-Hexachlorobiphenyl		✓				
35065-30-6	170	2,2',3,3',4,4',5-Heptachlorobiphenyl	✓	✓		✓	✓	✓
52663-71-5	171	2,2',3,3',4,4',6-Heptachlorobiphenyl						
52663-74-8	172	2,2',3,3',4,5,5'-Heptachlorobiphenyl						

CASRN	Congener	IUPAC	RMP	BIGHT	Aquatic Life SQO	NOAA	SWAMP	Most abundant
68194-16-1	173	2,2',3,3',4,5,6-Heptachlorobiphenyl						
38411-25-5	174	2,2',3,3',4,5,6'-Heptachlorobiphenyl	✓				✓	
40186-70-7	175	2,2',3,3',4,5',6-Heptachlorobiphenyl						
52663-65-7	176	2,2',3,3',4,6,6'-Heptachlorobiphenyl						
52663-70-4	177	2,2',3,3',4,5',6'-Heptachlorobiphenyl	✓	✓			✓	
52663-67-9	178	2,2',3,3',5,5',6-Heptachlorobiphenyl						
52663-64-6	179	2,2',3,3',5,6,6'-Heptachlorobiphenyl						
35065-29-3	180	2,2',3,4,4',5,5'-Heptachlorobiphenyl	✓	✓	✓	✓	✓	✓
74472-47-2	181	2,2',3,4,4',5,6-Heptachlorobiphenyl						
60145-23-5	182	2,2',3,4,4',5,6'-Heptachlorobiphenyl						
52663-69-1	183	2,2',3,4,4',5',6-Heptachlorobiphenyl	✓	✓			✓	✓
74472-48-3	184	2,2',3,4,4',6,6'-Heptachlorobiphenyl						
52712-05-7	185	2,2',3,4,5,5',6-Heptachlorobiphenyl						✓
74472-49-4	186	2,2',3,4,5,6,6'-Heptachlorobiphenyl						
52663-68-0	187	2,2',3,4',5,5',6-Heptachlorobiphenyl	✓	✓	✓	✓	✓	✓
74487-85-7	188	2,2',3,4',5,6,6'-Heptachlorobiphenyl						
39635-31-9	189	2,3,3',4,4',5,5'-Heptachlorobiphenyl		✓			✓	
41411-64-7	190	2,3,3',4,4',5,6-Heptachlorobiphenyl						
74472-50-7	191	2,3,3',4,4',5',6-Heptachlorobiphenyl						
74472-51-8	192	2,3,3',4,5,5',6-Heptachlorobiphenyl						
69782-91-8	193	2,3,3',4',5,5',6-Heptachlorobiphenyl						✓
35694-08-7	194	2,2',3,3',4,4',5,5'-Octachlorobiphenyl	✓	✓			✓	✓
52663-78-2	195	2,2',3,3',4,4',5,6-Octachlorobiphenyl	✓		✓	✓	✓	
42740-50-1	196	2,2',3,3',4,4',5,6'-Octachlorobiphenyl						✓
33091-17-7	197	2,2',3,3',4,4',6,6'-Octachlorobiphenyl						
68194-17-2	198	2,2',3,3',4,5,5',6-Octachlorobiphenyl						✓
52663-75-9	199	2,2',3,3',4,5,5',6'-Octachlorobiphenyl						✓
52663-73-7	200	2,2',3,3',4,5,6,6'-Octachlorobiphenyl					✓	
40186-71-8	201	2,2',3,3',4,5',6,6'-Octachlorobiphenyl	✓	✓			✓	
2136-99-4	202	2,2',3,3',5,5',6,6'-Octachlorobiphenyl						
52663-76-0	203	2,2',3,4,4',5,5',6-Octachlorobiphenyl	✓				✓	✓
74472-52-9	204	2,2',3,4,4',5,6,6'-Octachlorobiphenyl						
74472-53-0	205	2,3,3',4,4',5,5',6-Octachlorobiphenyl						
40186-72-9	206	2,2',3,3',4,4',5,5',6-Nonachlorobiphenyl		✓		✓	✓	✓
52663-79-3	207	2,2',3,3',4,4',5,6,6'-Nonachlorobiphenyl					✓	
52663-77-1	208	2,2',3,3',4,5,5',6,6'-Nonachlorobiphenyl						
2051-24-3	209	Decachlorobiphenyl				✓	✓	

### A5.3 Results and Discussion

Subset methods varied in predicted PCB concentrations, with the median sum concentration ranging from 2.6 ng/g for the CaLRM/CSI sum of 16 PCBs method to 4.4 ng/g for the SWAMP sum of 50 PCBs method (Table A5.2). The median sum of 209 congeners was 5.2, and subset method medians ranged from 51 to 85% of this total. Subsets containing the most congeners provided the closest estimate of the total PCB concentration.

Table A5.3 shows results of the linear regression analysis for each method. All regressions were highly significant ( $p$ -value  $< 0.0001$ ), with a slope generally close to 1 (Table A5.3; Figure A5.1). Intercepts varied across the methods, indicating that they represented different proportions of the total. The NFTS data set included fourteen samples collected in California water bodies; summation relationships for these samples were similar to those for the entire data set (Figure A5.2).

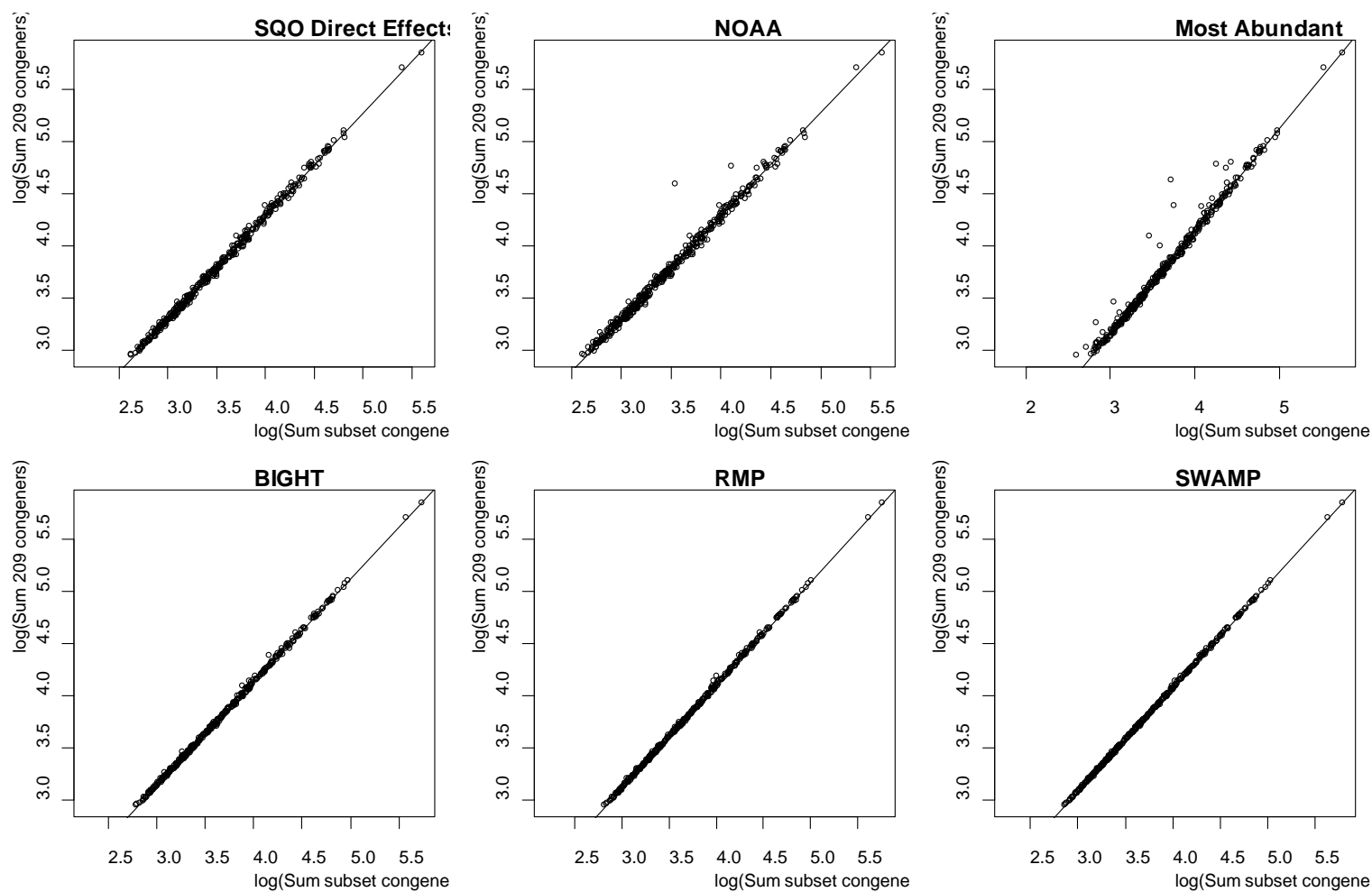
These analyses demonstrate that each congener subset is representative of the prevalence of individual congeners in fish tissue and that regression models can be applied to any of the subsets to provide an estimate of total PCB concentration that is within 1% of the actual value. If a regression model is not applied, then the most accurate estimate of total PCB concentration (85% of actual) is obtained using the SWAMP congener list, which includes the largest number of congeners (50). Simple summation of congeners without use of regression is consistent with the approach typically used by SWAMP, OEHHA, and other agencies to determine total PCB concentration in environmental samples.

**Table A5.2. Summary statistics for tissue samples in NFTS study (N = 402) using different subset summation methods.**

Method	Number of Congeners in Subset	Minimum Sum (ppb)	Maximum Sum (ppb)	Median Sum (ppb)	Median % of Sum 209
SWAMP	50	0.7	604	4.4	85%
RMP	40	0.7	569	4.1	78%
BIGHT	40	0.6	541	3.8	74%
Most Abundant	45	0.4	560	3.7	71%
NOAA	18	0.4	410	2.7	52%
CaLRM/CSI	16	0.4	399	2.6	51%
Sum of 209 PCB congeners	209	0.9	705	5.2	

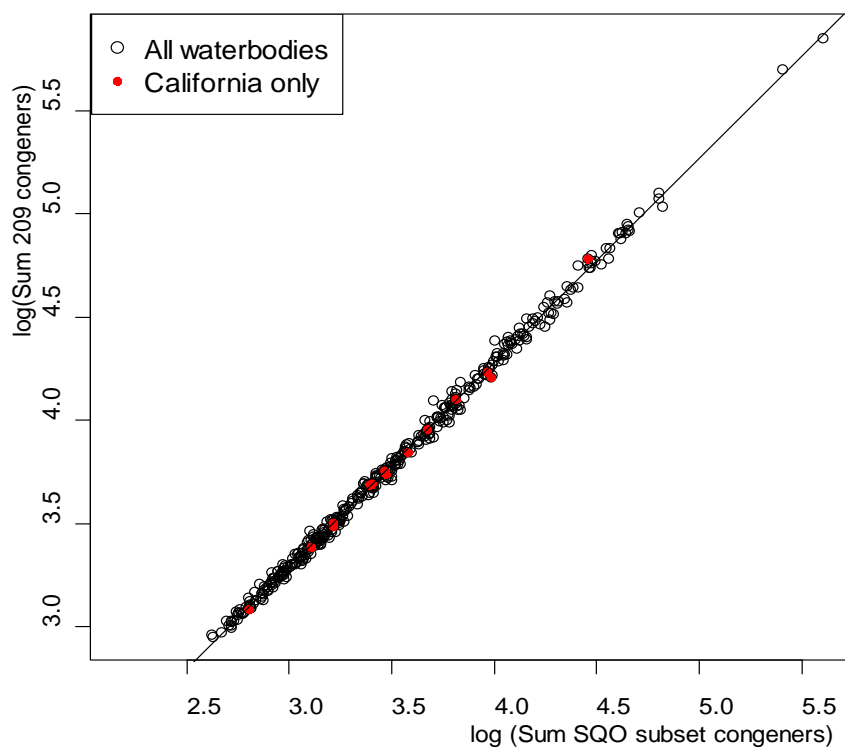
**Table A5.3. Results of regression between  $\log_{10}$  (congener subset method) versus  $\log_{10}$  (sum of 209 PCB congeners). In all cases, the sample size was 402 tissue samples. The last column indicates the equations for converting congener subsets to  $\Sigma$ 209 PCB congeners in seafood tissue samples. S = sum of PCBs in the subset (pg/g).**

Method	Number of Congeners In Subset	R <sup>2</sup>	Slope	Intercept	Calculation for Sum 209
SWAMP	50	0.999	0.9933	0.0981	1.253 S <sup>0.9933</sup>
RMP	37	0.999	0.9869	0.1509	1.415 S <sup>0.9869</sup>
BIGHT	36	0.999	0.9892	0.1697	1.478 S <sup>0.9892</sup>
Most Abundant	24	0.982	0.9780	0.2249	1.678 S <sup>0.9780</sup>
NOAA	18	0.989	0.9915	0.3150	2.065 S <sup>0.9915</sup>
CaLRM/CSI	16	0.997	0.9868	0.3312	2.144 S <sup>0.9868</sup>



**Figure A5.1. Relationships of PCB sums: Sum of 209 PCB congeners for six summation methods applied to the NFTS dataset (n = 402). Note log-10 scale of both axes.**





**Figure A5.2. Relationship of estimated sum of PCBs (based on Aquatic Life SQO congener subset) to Sum of 209 PCB congeners using EPA NFTS dataset.**

## **APPENDIX 6 – APPLICATION OF ASSESSMENT FRAMEWORK**

### **A6.1 Acknowledgments**

The authors wish to acknowledge the efforts of their staff and those of collaborating organizations, which have been instrumental to the success of this project. We particularly thank former SCCWRP staff member Doris Vidal-Dorsch, who conducted most of the initial data selection and analyses for this study, and prepared early drafts of the report. Shelly Moore and Darrin Greenstein also played key roles in data compilation and analysis. Thanks also to former SCCWRP staff Patricia Gonzalez, Fernando Vargas, Mary-Caitlin Jordan and Joanna Chavez for assistance with data compilation and analysis.

### **A6.2 Introduction**

The HHSQO tiered assessment framework described in this report was developed to evaluate the effects of contaminated sediments on seafood consumers. The framework provides a standardized and quantitative evaluation as to whether sediments from a site meet the narrative objective: stated in the water quality control plan “Pollutants shall not be present in sediments at levels that will bioaccumulate in aquatic life to levels that are harmful to human health” (SWRCB 2009). The framework consists of three tiers that correspond to 1) screening evaluation (Tier 1); 2) standardized assessment (Tier 2), and 3) site-specific analysis (Greenfield *et al.*, 2015).

The assessment framework was applied to recent data from several regional monitoring and assessment studies. Our overall goal was to apply the assessment framework to water bodies or portions of water bodies to demonstrate the assessment process using preexisting data at varying spatial scales. Most water bodies were divided into two or three subregions that correspond to site boundaries previously used for monitoring programs. The assessments were conducted using both Tier 1 and Tier 2 methodologies. Comparison of the results between tiers was used to determine whether Tier 1 was effective as a conservative screening tool. The Tier 2 results were also compared to 303(d) listing for the waterbodies, to assess whether the framework outcomes were consistent with other assessments.

### **A6.3 Methods**

Fish tissue and sediment chemistry data were obtained from local studies and regional assessments. The data were collected in electronic formats (e.g., Excel, Access), then screened to target both the primary fish species and four contaminant classes included in the framework. Data were only retained from studies that contained the following information: 1) marine/estuarine sampling stations located within California embayments; 2) fish bioaccumulation data for species of interest from 2003 or later; 3) geographic coordinates for each station available; and 4) chemistry data available for PCBs and chlorinated pesticides. The resulting dataset was additionally screened to select sites having at least three samples (individual fish or composites) for one or more of the primary species recommended by the SQO program. Subsequently, tissue and sediment data were matched to ensure that the information came from similar temporal and spatial distributions. Most waterbodies were subdivided for site assessment to simulate typical applications for TMDLs or 303d evaluation.

## Tier 1

Tier 1 assessments were conducted using both tissue and sediment data. These assessments utilized the same data set as the Tier 2 analyses. Analysis methods, thresholds, and interpretation followed the procedures described in Section 2 of this document. The data used for Tier 1 evaluation of each site are included in the Supplemental Information.

## Tier 2

Tier 2 assessment methods, thresholds and interpretation are described in Section 2 of this document. Data analysis was performed with the Decision Support Tool (DST), an Excel spreadsheet tool developed to calculate evaluate the chemical exposure and site linkage indicators and integrate the indicator categories to determine the Tier 2 site assessment. The DST incorporates the bioaccumulation model and thresholds described previously in this document. The DST tool and instructions for use are available at:

<http://www.sccwrp.org/Data/DataTools/SedimentQualityAssessment.aspx>

In most cases, mean sediment and tissue contaminant concentrations were calculated using Kaplan Meyer (KM) methods to address the presence of nondetect values (Helsel 2010). When the KM method could not be used (e.g., > 75% of sample values were below detection limits) summary statistics were calculated by substituting ½ of the method detection limit (MDL) values. Substitution of zero was used for nondetect congeners when calculating sums for contaminant groups containing multiple components (e.g., total PCBs). The data used for Tier 2 evaluation of each site are included in the Supplemental information.

The bioaccumulation model utilizes water quality characteristics of the site (e.g., temperature, dissolved oxygen concentration, dissolved organic carbon concentration) to adjust  $K_{ow}$  values and estimate water column contaminant concentrations. Information for some of these parameters was not available for some sites; standardized statewide average values for these parameters were used in all site assessment analyses (Table A6.1).

## Comparison of Tier 2 Results to Preexisting Advisory Listings

The Tier 2 assessment results were compared to current 303(d) listings. The listing information was taken from public sites:

[http://www.waterboards.ca.gov/centralcoast/water\\_issues/programs/tmdl/303d\\_list.shtml](http://www.waterboards.ca.gov/centralcoast/water_issues/programs/tmdl/303d_list.shtml)

[http://www.waterboards.ca.gov/water\\_issues/programs/tmdl/](http://www.waterboards.ca.gov/water_issues/programs/tmdl/)

## A6.4 Results

### Data compilation

A total of 547 fish tissue samples were initially compiled for this study from CEDEN and other data sources. Fourteen California waterbodies were represented (Table A6.2). However, data from some areas did not meet minimum criteria for the analysis. Sites such as Anaheim Bay, Dana Point Harbor, Humboldt Bay, Oceanside Harbor and Tomales Bay did not have enough fish tissue samples to conduct the assessment. Only waterbodies with high or good data availability were used to conduct Tier 1 and 2 analyses (Table A6.2).

Final data screening resulted in selection of 5 waterbodies for assessment: San Francisco Bay, San Pedro Bay (including Los Angeles/Long Beach Harbors), Newport Bay, Mission Bay, and San Diego Bay. With the exception of Mission Bay, each waterbody was divided into 2-5 subregions, resulting in a total of 13 sites for Tier 1 and 2 assessment (Figures A6.1 – A6.5). The areas and lengths varied greatly for the 16 sites and ranged from 0.5 – 372.6 km<sup>2</sup> and from 1.9 to 32.9 km, respectively (Table A6.3). The Los Angeles and Long Beach Inner Harbor sites contained the highest number of fish tissue and sediment samples. San Francisco Bay\_Central, Eastern San Pedro Bay, Los Angeles Inner Harbor, Long Beach Outer Harbor, and Long Beach Inner Harbor had the greatest number of tissue samples (52 to 65). And Long Beach Inner Harbor, San Diego Bay\_North, and San Diego Bay\_Central and South had the greatest number of sediment samples (29 to 42).

Data for six fish species belonging to diverse dietary guilds were used for this analysis. The species included: California halibut, queenfish, shiner perch, spotted sand bass, topsmelt, and white croaker. Six feeding guilds were represented, including piscivory, benthic and pelagic with piscivory, benthic and pelagic without piscivory, benthic with piscivory, benthic and pelagic with herbivory, and benthic without piscivory. Of the species used, white croaker (214) and topsmelt (85) had the most numerous samples.

**Table A6.1. Standardized site parameters used for site linkage analyses with the DST. Values are averages calculated from monitoring programs in multiple California enclosed bays and estuaries.**

Parameter	Statewide Value
Temperature	17.4 °C
Suspended sediment concentration	2.3E-05 kg/L
Particulate organic carbon	1.57E-06 kg/L
Salinity	25.4 PSU
Dissolved oxygen	9.0 mg/L
Dissolved organic carbon	2.15E-06 kg/L

**Table A6.2. Waterbody suitability for analysis, numeric cell values represent the number of samples available for each guild in the area. Highlighted waterbodies were used for tissue Tier 1 and 2 analysis.**

Site	Piscivory (California halibut)	Benthic/ Pelagic/ Piscivory (Queenfish)	Benthic/ Pelagic (Shiner perch)	Benthic/ Piscivory (Spotted sand bass)	Benthic/ Pelagic/ Herbivory (Striped mullet)	Benthic/ Pelagic/ Herbivory (Topsmelt)	Benthic/ without Piscivory (White croaker)	Suitability <sup>a</sup>
Humboldt Bay	1	0	1	0	0	0	0	Poor
Tomales Bay	0	0	1	0	1	0	0	Poor
San Francisco Bay	8	0	27	0	0	12	39	High
Morro Bay	0	0	1	0	0	0	0	Poor
Channel Islands Harbor	1	0	1	0	0	0	0	Poor
Marina Del Rey	2	0	0	0	0	1	0	Poor
Los Angeles/ Long Beach Harbors	43	76	3	0	0	69	175	High
San Gabriel River	0	0	0	0	8	0	0	Fair
Anaheim Bay/ Huntington Harbor	0	1	0	1	0	0	0	Poor
Newport Bay	8	0	3	10	0	4	0	High
Dana Point Harbor	0	0	1	0	0	0	1	Poor
Oceanside Harbor	0	1	0	0	0	0	1	Poor
Mission Bay	0	0	4	5	0	0	0	Good
San Diego Bay	0	0	6	12	0	0	0	Good

<sup>a</sup> Suitability	Species Number	Sample Number
High	≥ 2	> 5
Good	≥ 2	≥ 3
Fair	= 1	≥ 3
Poor	= 1	< 3

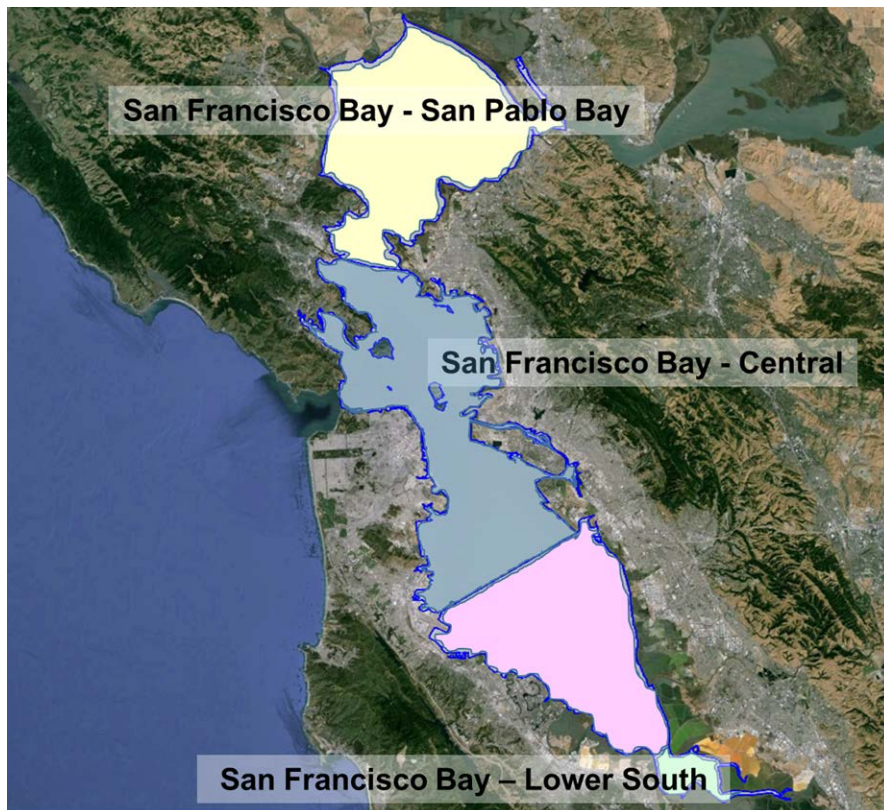
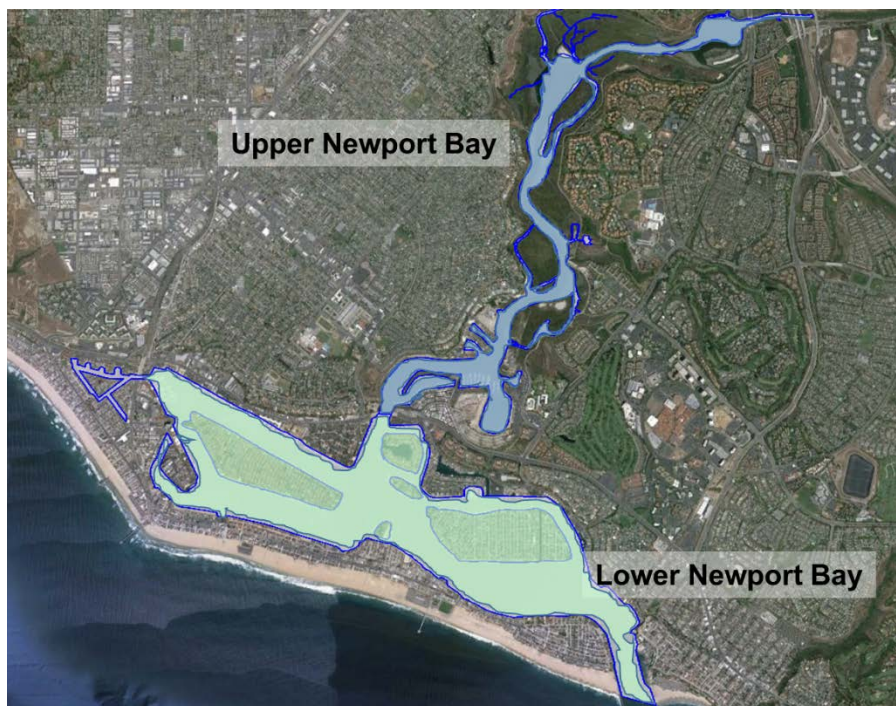


Figure A6.1. San Francisco Bay assessment site boundaries.



Figure A6.2. Los Angeles and Long Beach Harbors assessment site boundaries.

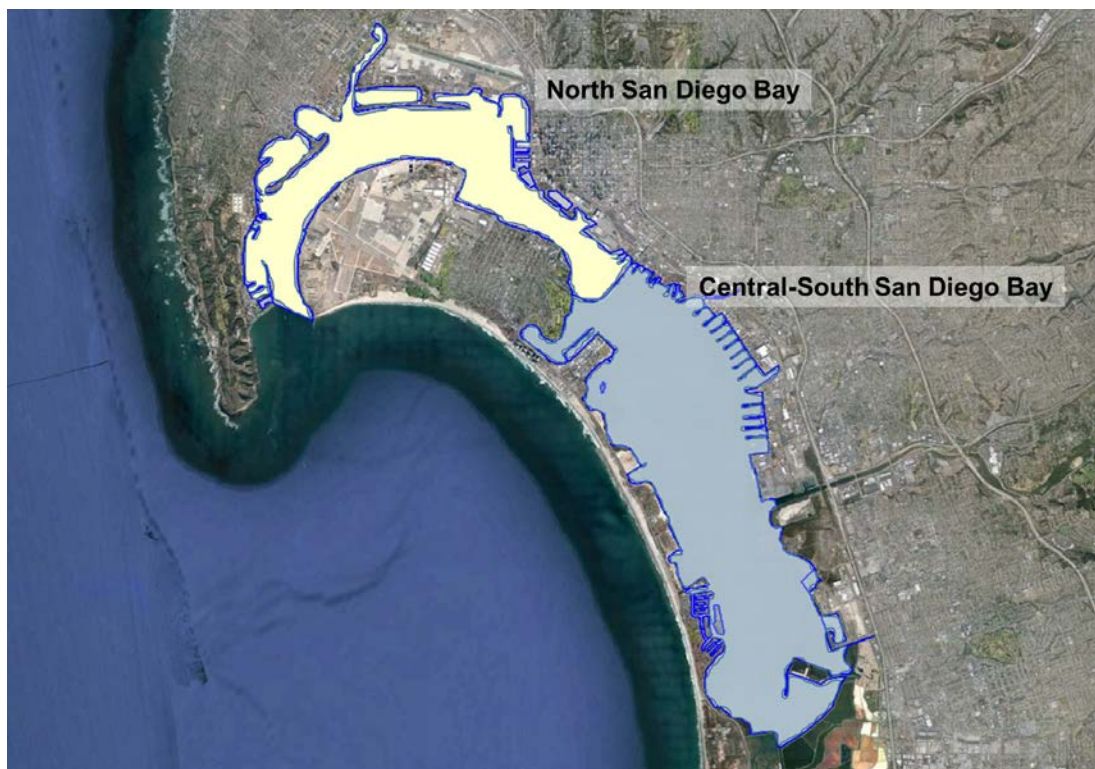




**Figure A6.3. Newport Bay assessment site boundaries.**



**Figure A6.4. Mission Bay assessment site boundary.**



**Figure A6.5. San Diego Bay assessment site boundaries.**



**Table A6.3. Size and boundaries of assessment sites.**

<b>Site</b>	<b>Area km<sup>2</sup></b>	<b>Length (km)</b>	<b>Approximate Boundaries</b>
San Francisco Bay_San Pablo	313.7	23.3	Richmond-San Rafael Bridge northeast to Carquinez Bridge
San Francisco Bay_Central	372.6	32.9	Richmond-San Rafael Bridge south to a dividing line between San Francisco Airport and Oakland Airport
San Francisco Bay_Lower South	26.9	12.6	South end of SFB north to the Dumbarton Bridge
Los Angeles Inner Harbor	5.8	6.6	Pier 400 up channel to boundary
Los Angeles Outer Harbor	6	4.7	Long Beach harbor inside breakwater including the Port of Long Beach
Long Beach Inner Harbor	5.8	4.9	Inner channel areas
Long Beach Outer Harbor	9.9	4.1	Los Angeles harbor inside breakwater and Pier 400 including the Port of Los Angeles
Eastern San Pedro Bay	27	10.5	Mouth of Los Angeles River east to mouth of Anaheim Bay inside breakwater
Newport Bay_Upper	3.1	5.6	Mouth to PCH Bridge
Newport Bay_Lower	1.4	6.8	PCH Bridge north and east to Jamboree Road
Mission Bay	8.1	6	All Mission Bay
San Diego Bay_North	15.8	11.2	Coronado Bridge to mouth of San Diego Bay
San Diego Bay_Central and South	27.5	10.6	Coronado Bridge to south end of San Diego Bay

## Tier 1 Analysis

Tier 1 analysis results showed that 12 of the 13 sites were unimpacted with respect to human health concern for chlordane contamination, while Tier 2 analysis was needed for Eastern San Pedro Bay to evaluate the sediment quality objective (Table A6.4). Chlordane tissue data were not available for Los Angeles and Long Beach Inner Harbors, Los Angeles and Long Beach Outer Harbors, and Eastern San Pedro Bay; hence, Tier 1 assessment for these sites was based on the more conservative analysis of sediment data only.

Twelve of the sites were classified as unimpacted by sediment DDTs. Los Angeles Inner Harbor exceeded both the tissue and sediment screening thresholds for DDT (Table A6.4). None of the sites exceeded Tier 1 screening thresholds for dieldrin, indicating that impacts on human health were unlikely. Tissue dieldrin data were not available for the five sites in San Pedro Bay, so the screening assessment for these sites is based upon sediment data only.

Twelve sites exceeded both the tissue and sediment screening thresholds for PCBs and were classified as needing a complete Tier 2 assessment before a decision regarding attainment of the HHSQO can be made (Table A6.4). Sediment screening thresholds for PCBs were exceeded for the remaining site (Upper Newport Bay), but this site was classified as unimpacted because the tissue threshold was not exceeded. The tissue screening result is given priority when there is a disagreement with sediment screening result, because the tissue data are more representative of potential chemical exposure to humans.

**Table A6.4. Tier 1 analysis results by site. Tiss = Tissue; Sed = Sediment; U = Unimpacted; P = Proceed to Tier 2 analysis; NA = Not available.**

Site	Screening Tier 1											
	Chlordanes			DDTs			Dieldrin			PCBs		
	Tiss	Sed	Final	Tiss	Sed	Final	Tiss	Sed	Final	Tiss	Sed	Final
San Francisco Bay_San Pablo	U	U	U	U	U	U	U	U	U	P	P	P
San Francisco Bay_Central	U	U	U	U	U	U	U	U	U	P	P	P
San Francisco Bay_Lower South	U	U	U	U	U	U	U	U	U	P	P	P
Los Angeles Inner Harbor	NA	U	U	P	P	P	NA	U	U	P	P	P
Los Angeles Outer Harbor	NA	U	U	U	P	U	NA	U	U	P	P	P
Long Beach Inner Harbor	NA	U	U	U	U	U	NA	U	U	P	P	P
Long Beach Outer Harbor	NA	U	U	U	U	U	NA	U	U	P	P	P
Eastern San Pedro Bay	NA	P	P	U	U	U	NA	U	U	P	P	P
Newport Bay_Upper	U	U	U	U	P	U	U	U	U	U	P	U
Newport Bay_Lower	U	U	U	U	U	U	U	U	U	P	P	P
Mission Bay	U	U	U	U	U	U	U	U	U	P	P	P
San Diego Bay_North	U	U	U	U	U	U	U	U	U	P	P	P
San Diego Bay_Central and South	U	U	U	U	U	U	U	U	U	P	P	P

## Tier 2 Analysis

Tier 2 analysis demonstrated that all the sites for which data were available were Unimpacted by sediment chlordane (Table A6.5). Tissue data for chlordanes were not available for the sites located in San Pedro Bay, thus Tier 2 assessments were not conducted for those sites. The data and numeric assessment results for Tier 2 are listed in the Supplemental Information.

The average fish tissue chlordane concentrations for all sites were below the ATL3, indicating low chemical exposure. High site linkage for chlordane was present for most sites, except for the Central and South sites in San Francisco Bay.

All sites for which data were available were assessed as Unimpacted or Likely Unimpacted by sediment DDTs and dieldrin under Tier 2 (Table A6.5). Tissue concentrations did not exceed the ATL3 at any site, indicating low or very low chemical exposure. Site linkage for DDTs was high at all sites, except for Long Beach Inner Harbor; whereas site linkage was high for dieldrin at all sites except Central and South San Francisco Bay.

As indicated by the Tier 1 screening results, most sites were classified by Tier 2 as being impacted by PCBs (Table A6.5). Nine sites were classified as Likely Impacted or Clearly Impacted, representing at least one site in three of the five water bodies investigated. The Mission Bay and Newport Bay sites had low chemical exposure scores and were classified as Likely Unimpacted by PCBs. High site linkage was present at most sites. Most of the variation in the PCB assessment results was related to chemical exposure. All categories of chemical exposure were encountered in the analyses, with one site (Newport Bay\_Lower) classified as having Very Low chemical exposure (tissue concentration less than OEHHA FCG). Low chemical exposure was present at the Newport Bay\_Upper and Mission Bay sites. The highest levels of chemical exposure (greater than ATL1) were present at two sites in San Francisco Bay (Central and South) and San Diego Bay\_Central and South.

**Table A6.5. Tier 2 assessment results by site. CE = chemical exposure; SL = site linkage; U = Unimpacted; LU = Likely Unimpacted; LI = Likely Impacted; CI = Clearly Impacted; NA = Not Available (no tissue data, Tier II analysis was not conducted).**

Site	Chlordanes				DDTs				Dieldrin				PCBs		
	CE	SL	Assessment		CE	SL	Assessment		CE	SL	Assessment		CE	SL	Assessment
San Francisco Bay_San Pablo	1	1	U		2	4	LU		2	1	U		4	2	PI
San Francisco Bay_Central	1	1	U		1	4	U		2	2	U		5	2	LI
San Francisco Bay_Lower South	2	4	U		1	4	U		2	1	U		4	4	CI
Los Angeles Inner Harbor			NA		2	4	LU				NA		4	4	CI
Los Angeles Outer Harbor			NA		2	4	LU				NA		3	4	LI
Long Beach Inner Harbor			NA		2	2	U				NA		4	4	CI
Long Beach Outer Harbor			NA		2	4	LU				NA		3	4	LI
Eastern San Pedro Bay			NA		2	4	LU				NA		4	4	CI
Newport Bay_Upper	1	4	U		2	4	LU		1	4	U		2	4	LU
Newport Bay_Lower	1	4	U		1	4	U		1	3	U		2	4	LU
Mission Bay	1	4	U		1	4	U		2	4	LU		2	4	LU
San Diego Bay_North	1	4	U		1	4	U		1	4	U		4	4	CI
San Diego Bay_Central and South	1	4	U		1	4	U		1	4	U		5	4	CI

There was a high degree of agreement between the outcomes of Tier 1 screening and Tier 2 assessments; the Tier 1 screening result was confirmed for 39 of 42 cases (93%) where both assessments were conducted. All three cases where the assessment differed were the result of the Tier 1 result indicating a potential impact, but Tier 2 classified the site as Likely Unimpacted (Table A6.6). There were no cases where an impact in Tier 2 was not identified by Tier 1 screening.

### Comparison to 303(d) listings

California's 303(d) list of impaired water bodies provides a point of comparison for the HHSQO assessment framework results. Both types of assessment have a similar goal: to identify water body segments where sediment contamination by bioaccumulative chemicals poses a potential threat to human health. However, the two programs are not strictly comparable because different data, thresholds and data analysis methods were used.

Except for Mission Bay, there are bioaccumulation-related 303(d) listings for each of the sites evaluated with the HHSQO Tier 2 assessment framework (Table A6.7). Similar results for PCBs were obtained using Tier 2 analysis, PCB impacts were identified at all sites, except Mission Bay and Newport Bay. Multiple differences between the 303(d) listings and SQO assessments were identified for DDT, chlordane, and dieldrin. The HHSQO Tier 2 assessment did not identify impacts for these chlorinated pesticides at any of the assessment sites, while there were 303(d) listings for DDT at most sites (except for Mission Bay and San Diego Bay) and listings for chlordane and dieldrin in San Francisco Bay, Newport Bay, and at some sites in San Pedro Bay (Table A6.7). No cases were identified where the SQO framework identified an impact that was not consistent with a current 303(d) listing. Most of the differences between site assessments appeared to be related to use of a lower tissue screening threshold for 303(d) listing

**Table A6.6. Comparison of Tier 1 and Tier 2 results. P = Proceed to Tier 2 Analysis; U = Unimpacted; LU = Likely Unimpacted; LI = Likely Impacted; CI = Clearly Impacted; NA = Not Available.**

Assessment											
Site	Chlordanes			DDTS			Dieldrin			PCBs	
	Tier 1	Tier 2		Tier 1	Tier 2		Tier 1	Tier 2		Tier 1	Tier 2
San Francisco Bay_San Pablo	U	U		U	LU		U	U		P	PI
San Francisco Bay_Central	U	U		U	U		U	U		P	LI
San Francisco Bay_Lower South	U	U		U	U		U	U		P	CI
Los Angeles Inner Harbor	U	NA		P	LU		U	NA		P	CI
Los Angeles Outer Harbor	U	NA		U	LU		U	NA		P	LI
Long Beach Inner Harbor	U	NA		U	U		U	NA		P	CI
Long Beach Outer Harbor	U	NA		U	LU		U	NA		P	LI
Eastern San Pedro Bay	P	NA		U	LU		U	NA		P	CI
Newport Bay_Upper	U	U		U	LU		U	U		U	LU
Newport Bay_Lower	U	U		U	U		U	U		P	LU
Mission Bay	U	U		U	U		U	LU		P	LU
San Diego Bay_North	U	U		U	U		U	U		P	CI
San Diego Bay_Central and South	U	U		U	U		U	U		P	CI

**Table A6.7. Comparison of Tier 2 assessment results and California 303(d) listing. NA = No data available.**

Site	Site Impacted by Contaminant?				303(d) Listing?			
	Chlordane	DDTs	Dieldrin	PCBs	Chlordane	DDTs	Dieldrin	PCBs
San Francisco Bay_San Pablo	No	No	No	Yes	Yes	Yes	Yes	Yes
San Francisco Bay_Central	No	No	No	Yes	Yes	Yes	Yes	Yes
San Francisco Bay_Lower South	No	No	No	Yes	Yes	Yes	Yes	Yes
Los Angeles Inner Harbor	NA	No	NA	Yes	Yes	Yes	Yes	Yes
Los Angeles Outer Harbor	NA	No	NA	Yes	No	Yes	No	Yes
Long Beach Inner Harbor	NA	No	NA	Yes	No	Yes	No	Yes
Long Beach Outer Harbor	NA	No	NA	Yes	No	Yes	No	Yes
Eastern San Pedro Bay	NA	No	NA	Yes	Yes	Yes	No	Yes
Newport Bay_Upper	No	No	No	No	Yes	Yes	Yes	Yes
Newport Bay_Lower	No	No	No	No	Yes	Yes	Yes	Yes
Mission Bay	No	No	No	No	No	No	No	No
San Diego Bay_North	No	No	No	Yes	No	No	No	Yes
San Diego Bay_Central and South	No	No	No	Yes	No	No	No	Yes

Listing information from:

[http://www.waterboards.ca.gov/sanfranciscobay/water\\_issues/programs/TMDLs/](http://www.waterboards.ca.gov/sanfranciscobay/water_issues/programs/TMDLs/)

[http://www.waterboards.ca.gov/losangeles/water\\_issues/programs/tmdl/tmdl\\_list.shtml](http://www.waterboards.ca.gov/losangeles/water_issues/programs/tmdl/tmdl_list.shtml)

[http://www.waterboards.ca.gov/santaana/water\\_issues/programs/tmdl/index.shtml#projects](http://www.waterboards.ca.gov/santaana/water_issues/programs/tmdl/index.shtml#projects)

[http://www.waterboards.ca.gov/rwqcb9/water\\_issues/programs/303d\\_list/docs/Staff\\_Report\\_101216.pdf](http://www.waterboards.ca.gov/rwqcb9/water_issues/programs/303d_list/docs/Staff_Report_101216.pdf)



## A6.5 Discussion

This statewide application of the HHSQO assessment framework demonstrated that the framework is generally feasible for use with data from ongoing monitoring programs. Current regional and TMDL monitoring programs measure all the key chemical and general analytes necessary to conduct Tier 1 screening and Tier 2 assessments. However, some of the ancillary water quality characteristics needed for greater accuracy in the Tier 2 assessment, such as dissolved organic carbon content and salinity, were not readily available from the same datasets containing the tissue and sediment chemical data. This data gap was resolved in this study using generalized values for these parameters (based on regional monitoring programs). However, it is recommended that monitoring programs measure these water quality parameters in combination with chemical sampling and make the results readily available in the same databases used to distribute the chemistry data.

The assessment results identified impacts associated with sediment PCB contamination at most of the study sites (10 of 13). These findings were consistent with current 303(d) listings for the sites. No HHSQO impacts were identified for DDTs, chlordane, or dieldrin, whereas several sites had 303(d) listings for these compounds. These differences were due to a combination of factors, especially the use of different data sets, species, and interpretation thresholds. Such differences underscore a potential benefit of conducting standardized Tier 2 assessments with the HHSQO framework, that assessments will be more comparable among locations and over time.

A high level of agreement between Tier 1 screening and Tier 2 assessment outcomes, with 93% of comparisons yielding the same outcome. There were no instances where an impacted site was not identified by Tier 1. These results indicate that the Tier 1 screening method is effective at identifying sites of potential impact and is not overly conservative.

Although we determined that the framework is feasible to conduct assessments, we also acknowledge that it is limited in scope and has areas for future improvement. For example, the approach currently focuses on legacy organochlorine compounds (PCBs and legacy pesticides), but additional analytes could be incorporated for evaluation such as mercury and contaminants of emerging concern.

The statewide scope of this demonstration study was limited to five water bodies. Assessments could not be conducted with existing data for several other embayments due to lack of sufficient data. In most cases, this was due to low sample numbers (minimum of three) for fish tissue chemistry. In other cases, the fish species analyzed did not match the requirements of the study (e.g., not a primary species for the feeding guild). It is recommended that ongoing monitoring programs consider modest study design changes in frequency, species, or number of samples to facilitate application of the HHSQO Tier 2 assessment framework. Greater standardization of study design among regions will result in improved ability to identify spatial and temporal changes in sediment quality among sites and assist in prioritizing management actions.

## A6.6 Supplemental Information

**Table S1. Summary statistics for San Pablo Bay.**

Species	Analyte	N	Mean (ng/g)	Std Error (ng/g)	95% UCL (ng/g)
White croaker	Chlordanes	3	3.67	1.16	6.20
Shiner perch	Chlordanes	6	1.20	0.22	1.64
White croaker	DDTs	3	65.90	22.69	121.80
Shiner perch	DDTs	5	7.87	4.12	16.66
White croaker	Dieldrin	3	1.54	0.12	1.83
Shiner perch	Dieldrin	0			
White croaker	PCBs	3	207.57	69.55	374.50
Shiner perch	PCBs	5	17.72	8.42	35.67
Sediment	Chlordanes	14	0.12	0.02	0.16
Sediment	DDTs	16	3.31	0.36	3.95
Sediment	Dieldrin	16	0.08	0.01	0.09
Sediment	PCBs	15	3.63	0.30	4.16

**Table S2. Lipids and total organic carbon (TOC) average values, and portion of human seafood for San Pablo Bay.**

Average of Lipid Samples Shiner perch (%)	1.10
Average of Lipid Samples White croaker (%)	5.10
Portion of Human Seafood Shiner perch (%)	50
Portion of Human Seafood White croaker (%)	50 (100 for dieldrin)
Sediment TOC (%)	1.10

**Table S3. Tier 1 assessment summary for San Pablo Bay.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S4. Tier 2 assessment summary for San Pablo Bay.**

Compound	Indicator	25%	50%	75%	95%	Category Outcome
Chlordanes	Chemical Exposure		2.43			1
Chlordanes	Site Linkage	0.188	0.280	0.425		1
Chlordanes	Site Assessment Outcome					Unimpacted
DDTs	Chemical Exposure		36.89			2
DDTs	Site Linkage	0.509	0.778	1.227		4
DDTs	Site Assessment Outcome					Likely Unimpacted
Dieldrin	Chemical Exposure		1.54			2
Dieldrin	Site Linkage	0.129	0.208	0.330		1
Dieldrin	Site Assessment Outcome					Unimpacted
PCBs	Chemical Exposure		112.64			4
PCBs	Site Linkage	0.199	0.304	0.481		2
PCBs	Site Assessment Outcome					Possibly Impacted

**Table S5. Summary statistics for San Francisco Bay\_Central.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	Chlordanes	6	0.39	0.05	0.49
Shiner perch	Chlordanes	18	5.95	1.59	8.71
Topsmelt	Chlordanes	0			
White croaker	Chlordanes	28	3.01	0.44	3.77
California halibut	DDTs	6	0.27	0.10	0.47
Shiner perch	DDTs	18	18.23	2.55	22.67
Topsmelt	DDTs	0			
White croaker	DDTs	29	12.51	2.37	16.57
California halibut	Dieldrin	4	0.21	0.00	0.21
Shiner perch	Dieldrin	0			
Topsmelt	Dieldrin	0			
White croaker	Dieldrin	15	0.89	0.10	1.07
California halibut	PCBs	8	3.78	0.82	5.44
Shiner perch	PCBs	18	98.35	16.65	127.32
Topsmelt	PCBs	10	380.92	108.89	580.53
White croaker	PCBs	29	61.29	13.39	84.16
Sediment	Chlordanes	11	0.15	0.02	0.19
Sediment	DDTs	13	3.86	0.54	4.83
Sediment	Dieldrin	11	0.12	0.01	0.14
Sediment	PCBs	11	7.58	0.81	9.05

**Table S6. Lipids and total organic carbon (TOC) average values, and portion of human seafood for San Francisco Bay\_Central.**

<b>Average of Lipid Samples California halibut (%)</b>	0.40
<b>Average of Lipid Samples Shiner perch (%)</b>	1.10
<b>Average of Lipid Samples Topsmelt (%)</b>	3.30
<b>Average of Lipid Samples White croaker (%)</b>	1.90
<b>Portion of Human Seafood California halibut (%)</b>	25 (PCB), 33 (Chlordane, DDT), 50 (Dieldrin)
<b>Portion of Human Seafood Shiner perch (%)</b>	25 (PCB), 33 (Chlordane, DDT)
<b>Portion of Human Seafood Topsmelt (%)</b>	25 (PCB)
<b>Portion of Human Seafood White croaker (%)</b>	25 (PCB), 33 (Chlordane, DDT), 50 (Dieldrin)
<b>Average TOC (%)</b>	1.06

**Table S7. Tier 1 assessment summary for Francisco Bay\_Central.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S8. Tier 2 assessment summary for San Francisco Bay\_Central.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		3.09			1
Chlordanes	Site Linkage	0.134	0.187	0.259		1
Chlordanes	Site Assessment Outcome					<b>Unimpacted</b>
DDTs	Chemical Exposure		10.24			1
DDTs	Site Linkage	1.483	2.015	2.761		4
DDTs	Site Assessment Outcome					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		0.55			2
Dieldrin	Site Linkage	0.276	0.402	0.578		2
Dieldrin	Site Assessment Outcome					<b>Unimpacted</b>
PCBs	Chemical Exposure		136.09			5
PCBs	Site Linkage	0.250	0.337	0.453		2
PCBs	Site Assessment Outcome					<b>Likely Impacted</b>

**Table S9. Summary statistics for San Francisco Bay\_ Lower South.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
Shiner perch	Chlordanes	3	8.95	1.27	11.75
White croaker	Chlordanes	0			
Shiner perch	DDTs	6	12.73	5.08	22.97
White croaker	DDTs	10	19.51	8.71	35.48
Shiner perch	Dieldrin	3	1.66	0.38	2.61
White croaker	Dieldrin	5	1.26	0.38	2.07
Shiner perch	PCBs	6	58.41	24.06	106.88
White croaker	PCBs	10	96.54	44.26	177.67
Sediment	Chlordanes	16	0.28	0.03	0.33
Sediment	DDTs	18	2.89	0.40	3.59
Sediment	Dieldrin	15	0.10	0.01	0.11
Sediment	PCBs	15	8.60	0.68	9.80

**Table S10. Lipids and total organic carbon (TOC) average values, and portion of human seafood for San Francisco Bay\_ Lower South.**

<b>Average of Lipid Samples Shiner perch (%)</b>	2.0
<b>Average of Lipid Samples White croaker (%)</b>	3.9
<b>Portion of Human Seafood Shiner perch (%)</b>	50 (100% chlordanes)
<b>Portion of Human Seafood White croaker (%)</b>	50
<b>TOC (%)</b>	1.12

**Table S11. Tier 1 assessment summary for Francisco Bay\_ Lower South.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S12. Tier 2 assessment summary for Francisco Bay\_ Lower South.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		8.95			2
Chlordanes	Site Linkage	0.056	0.090	0.147		1
Chlordanes	Site Assessment Outcome					<b>Unimpacted</b>
DDTs	Chemical Exposure		16.12			1
DDTs	Site Linkage	1.010	1.530	2.340		4
DDTs	Site Assessment Outcome					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		1.46			2
Dieldrin	Site Linkage	0.120	0.176	0.259		1
Dieldrin	Site Assessment Outcome					<b>Unimpacted</b>
PCBs	Chemical Exposure		77.47			4
PCBs	Site Linkage	0.665	1.000	1.515		4
PCBs	Site Assessment Outcome					<b>Clearly Impacted</b>

**Table S13. Summary statistics for Los Angeles Inner Harbor.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	DDTs	7	37.76	9.69	56.60
Queenfish	DDTs	15	104.94	48.21	189.85
Topsmelt	DDTs	11	101.61	22.00	141.47
White croaker	DDTs	26	800.53	260.83	1246.07
California halibut	PCBs	7	26.96	7.09	40.73
Queenfish	PCBs	16	34.09	9.84	51.50
Topsmelt	PCBs	11	33.60	6.00	44.48
White croaker	PCBs	28	103.24	27.04	149.30
Sediment	Chlordanes	17	7.19	5.74	17.21
Sediment	DDTs	17	58.02	23.83	98.67
Sediment	Dieldrin	18	0.86	0.55	1.82
Sediment	PCBs	18	208.93	148.38	467.06

**Table S14. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Los Angeles Inner Harbor.**

<b>Average of Lipid Samples California halibut (%)</b>	0.40
<b>Average of Lipid Samples Queenfish (%)</b>	1.40
<b>Average of Lipid Samples Topsmelt (%)</b>	1.10
<b>Average of Lipid Samples White croaker (%)</b>	1.69
<b>Portion of Human Seafood California halibut (%)</b>	25
<b>Portion of Human Seafood Queenfish (%)</b>	25
<b>Portion of Human Seafood Topsmelt (%)</b>	25
<b>Portion of Human Seafood White croaker (%)</b>	25
<b>TOC (%)</b>	2.07



**Table S15. Tier 1 assessment summary for Los Angeles Inner Harbor.**

Analyte(s)	Tissue Evaluation Outcome	Sediment Evaluation Outcome	Final Outcome
Chlordanes	Not Evaluated	Unimpacted	<b>Unimpacted</b>
DDTs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>
Dieldrin	Not Evaluated	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S16. Tier 2 assessment summary for Los Angeles Inner Harbor.**

Compound	Indicator	25%	50%	75%	95%	Category Outcome
Chlordanes	Chemical Exposure		No Data			NA
Chlordanes	Site Linkage	No Data	No Data	No Data		NA
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
DDTs	Chemical Exposure		261.21			2
DDTs	Site Linkage	0.499	0.731	1.072		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Likely unimpacted</b>
Dieldrin	Chemical Exposure		No Data			NA
Dieldrin	Site Linkage	No Data	No Data	No Data		NA
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
PCBs	Chemical Exposure		49.47			4
PCBs	Site Linkage	9.028	13.623	20.914		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Clearly impacted</b>

**Table S17. Summary statistics for Los Angeles Outer Harbor.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	DDTs	5	24.94	4.94	35.5
California halibut	PCBs	5	5.85	1.18	8.6
Queenfish	DDTs	7	210.70	119.62	443.1
Queenfish	PCBs	7	17.35	7.86	32.6
Shiner perch	DDTs	3	175.10	0.00	175.1
Shiner perch	PCBs	3	72.13	14.87	111.0
Topsmelt	DDTs	5	104.01	14.20	134.3
Topsmelt	PCBs	5	0.05	0.00	0.05
White croaker	DDTs	10	134.30	38.68	205.2
White croaker	PCBs	11	16.55	2.90	21.81
Sediment	Chlordanes	5	0.84	0.49	1.88
Sediment	DDTs	5	26.80	10.13	48.39
Sediment	Dieldrin	5	0.25	0	0.25
Sediment	PCBs	5	33.16	23.56	83.39

**Table S18. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Los Angeles Outer Harbor.**

<b>Average of Lipid Samples California halibut (%)</b>	0.40
<b>Average of Lipid Samples Queenfish (%)</b>	1.40
<b>Average of Lipid Samples Shiner perch (%)</b>	2.36
<b>Average of Lipid Samples Topsmelt (%)</b>	1.00
<b>Average of Lipid Samples White croaker (%)</b>	1.80
<b>Portion of Human Seafood California halibut (%)</b>	20
<b>Portion of Human Seafood Queenfish (%)</b>	20
<b>Portion of Human Seafood Shiner perch (%)</b>	20
<b>Portion of Human Seafood Topsmelt (%)</b>	20
<b>Portion of Human Seafood White croaker (%)</b>	20
<b>TOC (%)</b>	0.89

**Table S19. Tier 1 assessment summary for Los Angeles Outer Harbor.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Not Evaluated	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Proceed to Tier 2	<b>Unimpacted</b>
Dieldrin	Not Evaluated	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S20. Tier 2 assessment summary for Los Angeles Outer Harbor.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		No Data			NA
Chlordanes	Site Linkage	No Data	No Data	No Data		NA
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
DDTs	Chemical Exposure		129.81			2
DDTs	Site Linkage	0.933	1.275	1.738		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>
Dieldrin	Chemical Exposure		No Data			NA
Dieldrin	Site Linkage	No Data	No Data	No Data		NA
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
PCBs	Chemical Exposure		22.38			3
PCBs	Site Linkage	5.284	7.557	10.879		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Likely Impacted</b>

**Table S21. Summary statistics for Long Beach Inner Harbor.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	DDTs	4	52.20	13.52	84.01
Queenfish	DDTs	16	181.59	47.65	265.13
Topsmelt	DDTs	13	59.45	11.66	80.24
White croaker	DDTs	23	269.49	50.21	355.71
California halibut	PCBs	4	23.83	5.24	36.16
Queenfish	PCBs	16	49.59	11.39	69.56
Topsmelt	PCBs	13	28.77	5.86	39.30
White croaker	PCBs	26	80.98	16.70	109.55
Sediment	Chlordanes	23	2.75	1.27	4.94
Sediment	DDTs	29	8.57	1.00	10.26
Sediment	Dieldrin	24	0.72	0.2	1.06
Sediment	PCBs	24	95.43	41.68	166.86

**Table S22. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Long Beach Inner Harbor.**

<b>Average of Lipid Samples California halibut (%)</b>	0.40
<b>Average of Lipid Samples Queenfish (%)</b>	1.40
<b>Average of Lipid Samples Topsmelt (%)</b>	1.08
<b>Average of Lipid Samples White croaker (%)</b>	1.70
<b>Portion of Human Seafood California halibut (%)</b>	25
<b>Portion of Human Seafood Queenfish (%)</b>	25
<b>Portion of Human Seafood Topsmelt (%)</b>	25
<b>Portion of Human Seafood White croaker (%)</b>	25
<b>TOC (%)</b>	0.76

**Table S23. Tier 1 assessment summary for Long Beach Inner Harbor.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Not Evaluated	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Not Evaluated	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S24. Tier 2 assessment summary for Long Beach Inner Harbor.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		No Data			NA
Chlordanes	Site Linkage	No Data	No Data	No Data		NA
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
DDTs	Chemical Exposure		140.68			2
DDTs	Site Linkage	0.298	0.406	0.554		2
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		No Data			NA
Dieldrin	Site Linkage	No Data	No Data	No Data		NA
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
PCBs	Chemical Exposure		45.79			4
PCBs	Site Linkage	9.008	12.642	18.184		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Clearly Impacted</b>

**Table S25. Summary statistics for Long Beach Outer Harbor tissue.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	DDTs	6	40.72	10.22	61.30
Queenfish	DDTs	10	50.10	5.34	59.89
Topsmelt	DDTs	18	92.68	13.16	115.58
White croaker	DDTs	24	188.52	54.16	281.35
California halibut	PCBs	6	8.72	1.55	11.84
Queenfish	PCBs	11	35.12	18.57	68.77
Topsmelt	PCBs	18	39.39	6.34	50.51
White croaker	PCBs	27	42.72	10.86	61.27
Sediment	Chlordanes	16	0.22	0.04	0.29
Sediment	DDTs	15	14.33	1.46	16.89
Sediment	Dieldrin	15	0.25	0	0.25
Sediment	PCBs	15	4.07	0.66	5.24

**Table S26. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Long Beach Outer Harbor.**

<b>Average of Lipid Samples California halibut (%)</b>	0.40
<b>Average of Lipid Samples Queenfish (%)</b>	1.40
<b>Average of Lipid Samples Topsmelt (%)</b>	1.08
<b>Average of Lipid Samples White croaker (%)</b>	1.00
<b>Portion of Human Seafood California halibut (%)</b>	25
<b>Portion of Human Seafood Queenfish (%)</b>	25
<b>Portion of Human Seafood Topsmelt (%)</b>	25
<b>Portion of Human Seafood White croaker (%)</b>	25
<b>TOC (%)</b>	0.76

**Table S27. Tier 1 assessment summary for Long Beach Outer Harbor.**

Analyte(s)	Tissue Evaluation Outcome	Sediment Evaluation Outcome	Final Outcome
Chlordanes	Not Evaluated	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Not Evaluated	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S28. Tier 2 assessment summary for Long Beach Outer Harbor.**

Compound	Indicator	25%	50%	75%	95%	Category Outcome
Chlordanes	Chemical Exposure		No Data			NA
Chlordanes	Site Linkage	No Data	No Data	No Data		NA
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
DDTs	Chemical Exposure		93.01			2
DDTs	Site Linkage	0.704	0.963	1.323		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>
Dieldrin	Chemical Exposure		No Data			NA
Dieldrin	Site Linkage	No Data	No Data	No Data		NA
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
PCBs	Chemical Exposure		31.49			3
PCBs	Site Linkage	0.568	0.787	1.086		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Likely Impacted</b>

**Table S29. Summary statistics for Eastern San Pedro Bay.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	DDTs	10	162.35	66.31	283.9
California halibut	PCBs	10	58.87	17.41	90.8
White croaker	DDTs	42	91.60	7.87	104.8
White croaker	PCBs	40	70.23	7.74	83.3
Sediment	Chlordanes	4	11.10	5.75	24.63
Sediment	DDTs	10	19.54	6.61	31.66
Sediment	Dieldrin	4	0.05	0.00	0.05
Sediment	PCBs	14	20.01	9.26	36.41

**Table S30. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Eastern San Pedro Bay.**

<b>Average of Lipid California halibut (%)</b>	0.40
<b>Average of Lipid White croaker (%)</b>	2.10
<b>Portion of Human Seafood California halibut (%)</b>	50
<b>Portion of Human Seafood White croaker (%)</b>	50
<b>TOC (%)</b>	1.20



**Table S31. Tier 1 assessment summary for Eastern San Pedro Bay.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Not Evaluated	Proceed to Tier 2	<b>Unimpacted</b>
DDTs	Proceed to Tier 2	Unimpacted	<b>Proceed to Tier 2</b>
Dieldrin	Not Evaluated	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S32. Tier 2 assessment summary for Eastern San Pedro Bay.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		No Data			NA
Chlordanes	Site Linkage	No Data	No Data	No Data		NA
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
DDTs	Chemical Exposure		126.98			2
DDTs	Site Linkage	0.619	0.969	1.512		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>
Dieldrin	Chemical Exposure		No Data			NA
Dieldrin	Site Linkage	No Data	No Data	No Data		NA
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Not enough data</b>
PCBs	Chemical Exposure		64.55			4
PCBs	Site Linkage	0.936	1.491	2.327		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Clearly Impacted</b>

**Table S33. Summary statistics for Newport Bay\_Upper.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	Chlordanes	3	0.63	0.20	1.48
Spotted sand bass	Chlordanes	4	1.65	0.32	3.67
Topsmelt	Chlordanes	3	4.57	2.02	7.43
California halibut	DDTs	4	0.30	0.28	0.94
Spotted sand bass	DDTs	5	19.93	6.32	34.80
Topsmelt	DDTs	3	52.25	34.26	100.70
California halibut	Dieldrin	0			
Spotted sand bass	Dieldrin	3	0.21	0.00	0.22
Topsmelt	Dieldrin	3	0.25	0.02	0.34
California halibut	PCBs	4	0.54	0.17	1.05
Spotted sand bass	PCBs	3	9.64	5.06	22.40
Topsmelt	PCBs	3	5.29	1.94	9.78
Sediment	Chlordanes	11	5.33	1.65	8.46
Sediment	DDTs	14	39.30	10.17	57.73
Sediment	Dieldrin	8	0.53	0.12	0.82
Sediment	PCBs	17	6.48	2.87	11.68

**Table S34. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Newport Bay\_Upper.**

<b>Average of Lipid Samples California halibut (%)</b>	0.43
<b>Average of Lipid Samples Spotted sand bass (%)</b>	0.47
<b>Average of Lipid Samples Topsmelt (%)</b>	1.39
<b>Portion of Human Seafood California halibut (%)</b>	33 (0 dieldrin)
<b>Portion of Human Seafood Spotted sand bass (%)</b>	33 (50 dieldrin)
<b>Portion of Human Seafood Topsmelt (%)</b>	33 (50 dieldrin)
<b>TOC (%)</b>	0.99

**Table S35. Tier 1 assessment summary for Newport Bay\_Upper.**

Analyte(s)	Tissue Evaluation Outcome	Sediment Evaluation Outcome	Final Outcome
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Proceed to Tier 2	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Unimpacted	Proceed to Tier 2	<b>Unimpacted</b>

**Table S36. Tier 2 assessment summary for Newport Bay\_Upper.**

Compound	Indicator	25%	50%	75%	95%	Category Outcome
<b>Chlordanes</b>	Chemical Exposure		2.26			1
<b>Chlordanes</b>	Site Linkage	4.976	7.470	11.322		4
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
<b>DDTs</b>	Chemical Exposure		23.92			2
<b>DDTs</b>	Site Linkage	6.008	9.497	14.918		4
<b>DDTs</b>						<b>Likely Unimpacted</b>
<b>Dieldrin</b>	Chemical Exposure		0.229			1
<b>Dieldrin</b>	Site Linkage	2.356	3.374	4.835		4
<b>Dieldrin</b>						<b>Unimpacted</b>
<b>PCBs</b>	Chemical Exposure		5.11			2
<b>PCBs</b>	Site Linkage	3.525	5.540	8.611		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>

**Table S37. Summary statistics for Newport Bay\_ Lower.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
California halibut	Chlordanes	3	5.19	2.31	7.50
Shiner perch	Chlordanes	4	3.34	0.89	5.44
Spotted sand bass	Chlordanes	3	7.07	1.59	9.32
California halibut	DDTs	3	4.14	4.13	21.90
Shiner perch	DDTs	3	17.57	8.43	26.00
Spotted sand bass	DDTs	3	18.28	9.42	31.60
California halibut	Dieldrin	3	0.21	0.00	0.21
Shiner perch	Dieldrin	0			
Spotted sand bass	Dieldrin	0			
California halibut	PCBs	3	13.09	12.78	68.08
Shiner perch	PCBs	3	10.71	4.00	20.26
Spotted sand bass	PCBs	3	26.02	9.48	41.10
Sediment	Chlordanes	6	5.75	1.49	8.76
Sediment	DDTs	10	35.36	6.17	46.67
Sediment	Dieldrin	4	0.46	0.26	1.23
Sediment	PCBs	12	31.49	7.78	45.46

**Table S38. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Newport Bay\_ Lower.**

<b>Average of Lipid Samples California halibut (%)</b>	0.35
<b>Average of Lipid Samples Shiner perch (%)</b>	2.36
<b>Average of Lipid Samples Spotted sand bass (%)</b>	0.74
<b>Portion of Human Seafood California halibut</b>	33 (0 dieldrin)
<b>Portion of Human Seafood Shiner perch</b>	33 (50 dieldrin)
<b>Portion of Human Seafood Spotted sand bass</b>	33 (50 dieldrin)
<b>TOC (%)</b>	1.49

**Table S39. Tier 1 assessment summary for Newport Bay\_ Lower.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S40. Tier 2 assessment summary for Newport Bay\_ Lower.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		5.15			1
Chlordanes	Site Linkage	2.461	3.531	5.088		4
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
DDTs	Chemical Exposure		13.19			1
DDTs	Site Linkage	10.820	16.105	23.691		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		0.214			1
Dieldrin	Site Linkage	0.292	0.789	1.827		3
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
PCBs	Chemical Exposure		16.44			2
PCBs	Site Linkage	6.552	9.735	14.447		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>

**Table S41. Summary statistics for Mission Bay.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
Shiner perch	Chlordanes	3	1.00	0.45	1.90
Spotted sand bass	Chlordanes	4	0.52	0.16	0.91
Shiner perch	DDTs	3	3.04	3.09	8.39
Spotted sand bass	DDTs	4	1.06	1.30	5.03
Shiner perch	Dieldrin	3	0.50	0.00	0.50
Spotted sand bass	Dieldrin	4	0.50	0.00	0.50
Shiner perch	PCBs	3	6.77	5.08	15.02
Spotted sand bass	PCBs	4	2.50	1.87	6.89
Sediment	Chlordanes	4	0.50	0	0.05
Sediment	DDTs	16	1.19	0.77	2.57
Sediment	Dieldrin	4	0.5	0	0.05
Sediment	PCBs	15	1.33	1.60	4.16

**Table S42. Lipids and total organic carbon (TOC) average values, and portion of human seafood for Mission Bay.**

<b>Average of Lipid Samples Shiner perch (%)</b>	1.25
<b>Average of Lipid Samples Spotted sand bass (%)</b>	0.44
<b>Portion of Human Seafood Shiner perch (%)</b>	50
<b>Portion of Human Seafood Spotted sand bass (%)</b>	50
<b>TOC (%)</b>	1.63

**Table S43. Tier 1 assessment summary for Mission Bay.**

Analyte(s)	Tissue Evaluation Outcome	Sediment Evaluation Outcome	Final Outcome
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S44. Tier 2 assessment summary for Mission Bay.**

Compound	Indicator	25%	50%	75%	95%	Category Outcome
Chlordanes	Chemical Exposure		0.76			1
Chlordanes	Site Linkage	1.209	1.801	2.674		4
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
DDTs	Chemical Exposure		2.05			1
DDTs	Site Linkage	0.964	1.832	3.516		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		0.50			2
Dieldrin	Site Linkage	0.710	1.006	1.416		4
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>
PCBs	Chemical Exposure		4.64			2
PCBs	Site Linkage	0.532	1.065	2.141		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Likely Unimpacted</b>

**Table S45. Summary statistics for San Diego Bay\_North.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
Shiner perch	Chlordanes	5	2.53	0.42	3.51
Spotted sand bass	Chlordanes	6	1.52	0.93	3.71
Shiner perch	DDTs	5	6.23	2.72	12.62
Spotted sand bass	DDTs	6	1.21	0.62	2.54
Shiner perch	Dieldrin	4	0.38	0.17	2.52
Spotted sand bass	Dieldrin	7	0.22	0.00	0.22
Shiner perch	PCBs	3	1.92	0.98	3.30
Spotted sand bass	PCBs	7	113.21	66.45	283.20
Sediment	Chlordanes	19	0.81	0.64	1.93
Sediment	DDTs	30	1.88	1.30	4.08
Sediment	Dieldrin	28	0.44	0.03	0.49
Sediment	PCBs	31	38.89	22.58	77.22

**Table S46. Lipids and total organic carbon (TOC) average values, and portion of human seafood for San Diego Bay\_North.**

<b>Average of Lipid Samples Shiner perch (%)</b>	1.25
<b>Average of Lipid Samples Spotted sand bass (%)</b>	0.44
<b>Portion of Human Seafood Shiner perch</b>	50
<b>Portion of Human Seafood Spotted sand bass</b>	50
<b>TOC (%)</b>	0.99



**Table S47. Tier 1 assessment summary for San Diego Bay\_North.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S48. Tier 2 assessment summary for San Diego Bay\_North.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		2.02			1
Chlordanes	Site Linkage	0.952	1.605	2.685		4
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
DDTs	Chemical Exposure		3.72			1
DDTs	Site Linkage	1.222	2.114	3.623		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		0.296			1
Dieldrin	Site Linkage	1.609	2.376	3.479		4
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
PCBs	Chemical Exposure		57.57			4
PCBs	Site Linkage	2.262	4.017	7.166		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Clearly Impacted</b>

**Table S49. Summary statistics for San Diego Bay\_ Central and South.**

<b>Species</b>	<b>Analyte</b>	<b>N</b>	<b>Mean (ng/g)</b>	<b>Std Error (ng/g)</b>	<b>95% UCL (ng/g)</b>
Spotted sand bass	Chlordanes	5	3.35	0.55	4.53
Spotted sand bass	DDTs	6	10.57	1.05	12.81
Spotted sand bass	Dieldrin	5	0.24	0.06	0.41
Spotted sand bass	PCBs	5	273.44	43.91	367.05
Sediment	Chlordanes	30	1.69	0.90	3.22
Sediment	DDTs	42	13.02	12.87	34.68
Sediment	Dieldrin	42	0.46	0.02	0.49
Sediment	PCBs	42	40.94	23.30	80.15

**Table S50. Lipids and total organic carbon (TOC) average values, and portion of human seafood for San Diego Bay\_ Central and South.**

<b>Average of Lipid Samples Spotted sand bass (%)</b>	0.44
<b>Portion of Human Seafood Spotted sand bass (%)</b>	100
<b>TOC (%)</b>	1.02

**Table S51. Tier 1 assessment summary for San Diego Bay\_ Central and South.**

<b>Analyte(s)</b>	<b>Tissue Evaluation Outcome</b>	<b>Sediment Evaluation Outcome</b>	<b>Final Outcome</b>
Chlordanes	Unimpacted	Unimpacted	<b>Unimpacted</b>
DDTs	Unimpacted	Unimpacted	<b>Unimpacted</b>
Dieldrin	Unimpacted	Unimpacted	<b>Unimpacted</b>
PCBs	Proceed to Tier 2	Proceed to Tier 2	<b>Proceed to Tier 2</b>

**Table S52. Tier 2 assessment summary for San Diego Bay\_ Central and South.**

<b>Compound</b>	<b>Indicator</b>	<b>25%</b>	<b>50%</b>	<b>75%</b>	<b>95%</b>	<b>Category Outcome</b>
Chlordanes	Chemical Exposure		3.35			1
Chlordanes	Site Linkage	1.283	2.317	4.170		4
<b>Chlordanes</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
DDTs	Chemical Exposure		10.57			1
DDTs	Site Linkage	2.494	5.034	10.422		4
<b>DDTs</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
Dieldrin	Chemical Exposure		0.2442			1
Dieldrin	Site Linkage	1.743	2.870	4.701		4
<b>Dieldrin</b>	<b>Site Assessment Outcome</b>					<b>Unimpacted</b>
PCBs	Chemical Exposure		273.44			5
PCBs	Site Linkage	0.538	0.983	1.778		4
<b>PCBs</b>	<b>Site Assessment Outcome</b>					<b>Clearly Impacted</b>

## **APPENDIX 7 – COMPARISON OF BIOACCUMULATION MODEL PERFORMANCE**

### **A7.1 Introduction**

The Human Health Sediment Quality Objective (HHSQO) assessment framework uses a bioaccumulation model to determine the site linkage of sportfish tissue contamination. The ability of this model to accurately predict bioaccumulation through the food web is one of several factors affecting the accuracy of the site linkage evaluation. This bioaccumulation model uses a number of biotic and abiotic parameters to predict the fate of contaminants in a food web (Appendix 1), and uncertainty or errors in these parameters can lead to either low or high estimates of contaminant bioaccumulation and potentially alter the accuracy of the HHSQO site assessment. Other factors can also impact the linkage calculations, such as accuracy and precision of the chemistry data, representativeness of the sediment and tissue sample locations, site size, spatial contamination gradients, and fish movement/feeding outside of the assessment site. Uncertainty in many of these site-related factors can be minimized through use of an appropriate study design and adequate sample size. The accuracy of the bioaccumulation modeling approach used in the HHSQO framework is difficult to determine, as there is no “gold standard” against which to compare. However, the performance of the model can be described through comparison to other approaches and to data from field studies. This appendix describes relative performance of the HHSQO bioaccumulation modeling approach through three types of analyses: comparison to the source model, comparison to an independently derived model, and comparison to data from multiple sites and species.

### **A7.2 Approach**

Three independent data sets and comparisons were used to characterize performance of the bioaccumulation model used in the HHSQO assessment framework. The first analysis evaluated the comparative ability of the SQO model to predict PCB bioaccumulation in fish, in comparison to the source model from which it was developed: the Gobas and Arnot food web model for San Francisco Bay (Arnot and Gobas 2004, Gobas and Arnot 2010). Data used in this comparison were the same regional monitoring data for white croaker from San Francisco Bay that were used for the original calibration and validation of the Gobas and Arnot model. The objective of this comparison was to document the impact of modifications to the source model made to extend the applicability of the model to additional waterbodies, contaminants and fish species. The analyses included calculation of model bias with respect to measured values of individual PCB congeners. Estimates of total PCB concentration were also compared between the two model versions.

The second analysis of model performance was based on comparison of the HHSQO model approach to an independently derived bioaccumulation model. The bioaccumulation model used for comparison was a site-specific dynamic bioaccumulation model developed and calibrated for use in Los Angeles and Long Beach Harbors as part of a Tier 3 assessment for a TMDL monitoring program. This evaluation compared bioaccumulation estimates for total DDTs and PCBs from the SQO site linkage evaluation approach (e.g., bioaccumulation model combined with Monte Carlo Simulation to include data uncertainty and variability) to those from the Tier 3 model.

The third comparison of bioaccumulation model performance utilized the same datasets used for the framework application study described in Appendix 6. The objective of this comparison was to examine the correspondence between predicted and measured tissue concentrations among multiple site and species combinations. The analysis was conducted for the four contaminant groups included in the HHSQO assessment framework (i.e., chlordanes, Dieldrin, DDTs, and PCBs). This comparison also provides an indication of the variability in results due to multiple factors, including species type, location, and data representativeness.

### A7.3 San Francisco Bay Model Comparison

Since the HHSQO bioaccumulation model was based on the food web PCB bioaccumulation model developed for San Francisco Bay (Gobas and Arnot, 2010), the model outputs should be similar when using the same site characteristics and sediment and water input data. This comparison was limited to PCBs, as the SF Bay model did not include DDTs, chlordanes, or Dieldrin. The sediment and fish tissue data used for this comparison were from the San Francisco Bay Regional Monitoring Program (RMP) from 1999-2001, and were the same data used for model calibration as described by Gobas and Arnot (2010) and contained in the associated model workbook. Sediment data and tissue data for white croaker and shiner perch were used for the comparison. Analyses were conducted for individual congeners as well as for total PCBs (sum of congeners). Estimated tissue concentrations from the SQO model were based on the food web relationships; Monte-Carlo Simulation, which helps to represent uncertainty and variability, was not used in this comparison in order to focus the analysis solely on the relative performance of the two models.

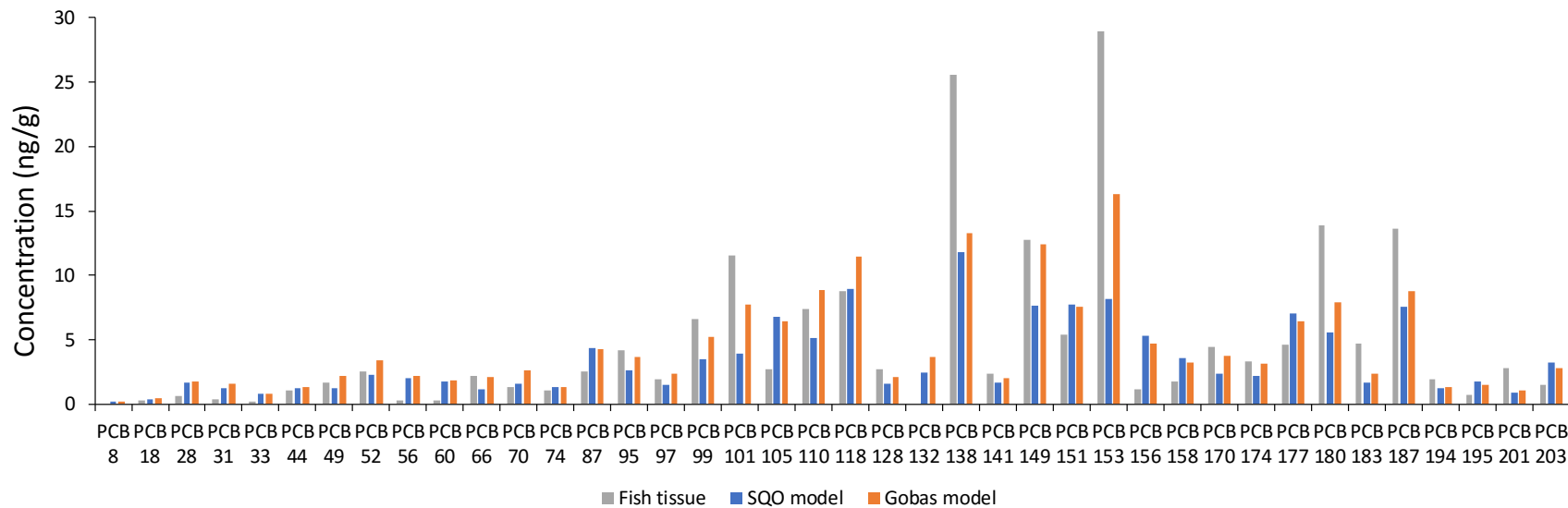
The congener specific comparison for white croaker is shown in Figure A7.1. The two models produced similar results for most congeners and showed similar patterns with respect to over or underprediction relative to the measured values in fish tissue. The SQO model outputs ranged from 28% (PCB 153) to 661% (PCB 156) of the measured white croaker tissue concentration, while the SF Bay model ranged from 50% (PCB 183) to 702% (PCB 156). In most cases, predicted congener concentrations were similar to measured values; estimates for 22 of the 38 measured congeners were within a factor of two for the SQO model, while 29 of 38 estimates were within a factor of two for the SF Bay model.

The mean model bias was also calculated to quantitatively determine the overall difference between model output and measured tissue concentrations using the method described by Gobas and Arnot (2010):

$$MB_j = 10^{\left( \frac{\sum_i^n [\log(\text{Conc}_{P,i} / \text{Conc}_{O,i})]}{n} \right)}$$

Where model bias ( $MB_j$ ) of species  $j$  is a function of the ratio of the predicted ( $\text{Conc}_{P,i}$ ) and observed ( $\text{Conc}_{O,i}$ ) tissue concentrations of PCB congener  $i$ , for the total number of congeners  $n$ .

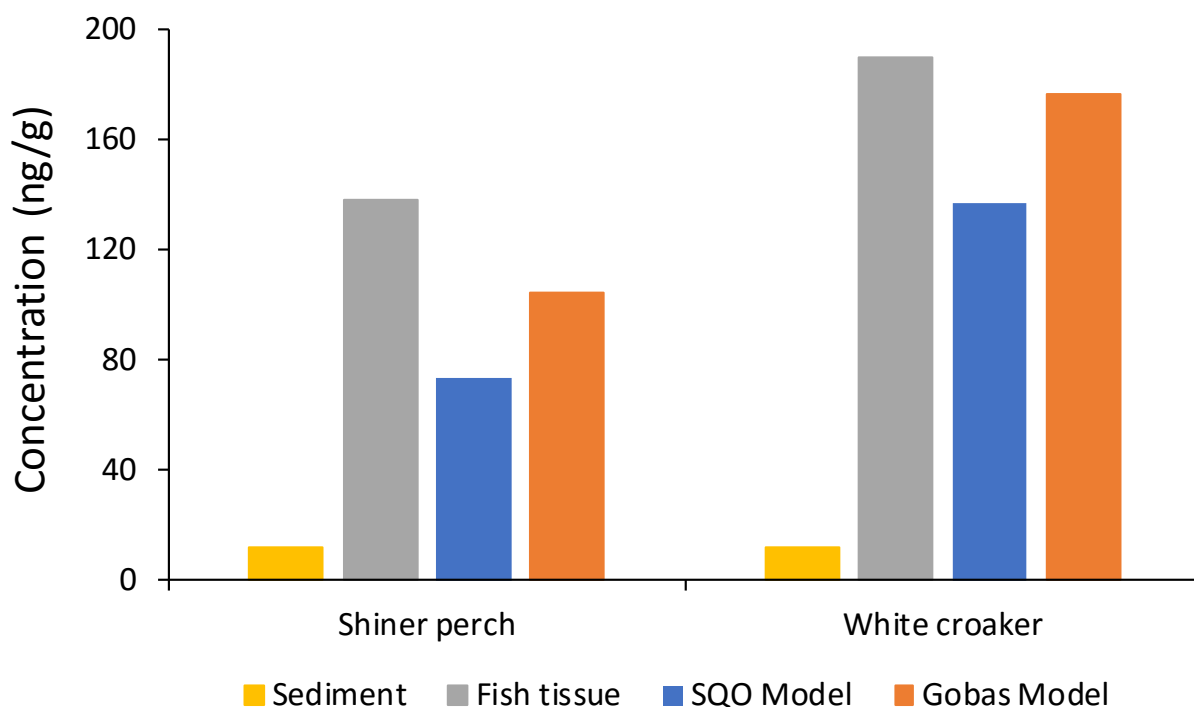
A mean model bias value of 1.0 indicates that, on average, the model accurately predicts the measured tissue concentration. The SQO model mean MB and 95% confidence interval for white croaker was 1.05 (0.20 – 5.47). For comparison, the SF Bay model mean MB and 95% confidence interval was 1.31 (0.33 – 5.18; Gobas and Arnot 2010). Both models performed well,



**Figure A7.1. Comparison of congener-specific concentrations in white croaker tissue (grey) and concentration estimates for the SQO model (blue) and Gobas SF Bay model (orange).**

with the SQO model being somewhat more accurate for this data set; but the large confidence interval indicates that there was no significant difference in model performance.

Relative performance of the two models in an assessment application is illustrated by comparison of predicted total tissue PCB concentration to measured values. Results for the SQO and SF Bay models, run using the same site parameters and RMP PCB data, are shown in Figure A7.2. Both models produced similar results, yielding underestimates of tissue PCB concentration for both shiner perch and white croaker (ranging from 53-93% of measured). The SQO model output was 78% and 71% of the SF Bay model output for white croaker and shiner perch, respectively.



**Figure A7.2. Comparison of total PCB concentration in sediments and fish tissues (shiner perch and white croaker) from San Francisco Bay to the SQO and SF Bay (Gobas model) outputs.**

The differences between the two models can be accounted for by the modifications made to the SF Bay model for SQO framework application. The main adjustment to the SQO model was how the water column concentrations are used in the bioaccumulation calculations. The SF Bay model uses measured water concentration values directly in the calculations. In the SQO model, a comparison between measured water column values and values estimated from pore water diffusive flux is used to select the water column value used, potentially reducing the concentrations of individual congeners used in model calculations. This feature was added to minimize the potential effects of non-sediment related PCB contamination in the water column. As such, the estimated water column concentration (described in Appendix 1) is compared to the measured concentration, and the lowest value is used. In the example here, some of the measured PCB congener concentrations in the water were higher than the estimated values, resulting in use of the lower estimated value which reduced the overall SQO model relative to the SF Bay model.

When this difference in handling of the water column data is accounted for, the two model results are comparable, with SQO model output approximately 105% and 101% of the SF Bay model output for white croaker and shiner perch, respectively.

#### **A7.4 Independent Model Comparison**

The SQO bioaccumulation modeling approach was compared to a site-specific bioaccumulation model for DDTs and PCBs developed for the Los Angeles/Long Beach Harbor complex (Site-Specific model). This bioaccumulation model is based on AQFDCHN, which is a bioenergetic, mechanistic, dynamic model developed by Thomann and Connolly (1984). Some of the inputs to the Site-Specific model are obtained from linked hydrodynamic and fate and transport models, with the integrated set of three models termed the Water Resources Action Plan (WRAP) model (Everest et al., 2009). A more detailed description of the model and its application is provided in conference proceedings from the 2016 WODCON XXI (Curtis et al., 2016). Data for this comparison represent samples from Los Angeles Outer Harbor and were compiled from multiple monitoring programs from 2002-2014, consisting of 49 sediment samples, 3 water column samples, 26 white croaker samples, 18 California halibut samples, and 3 shiner perch samples (Anchor QEA, personal communication).

The objective of this comparison was to compare performance of the standardized SQO model to a model calibrated to site-specific conditions in the harbor complex. The analysis also provides an independent comparison of model performance since development of the Site-Specific model occurred independent of the SF Bay model and uses a different conceptual approach with regards to spatial and temporal variation and includes different abiotic and biotic parameters. Comparisons of estimated and measured tissue contaminant concentrations were conducted for three fish species (California halibut, white croaker, and shiner perch).

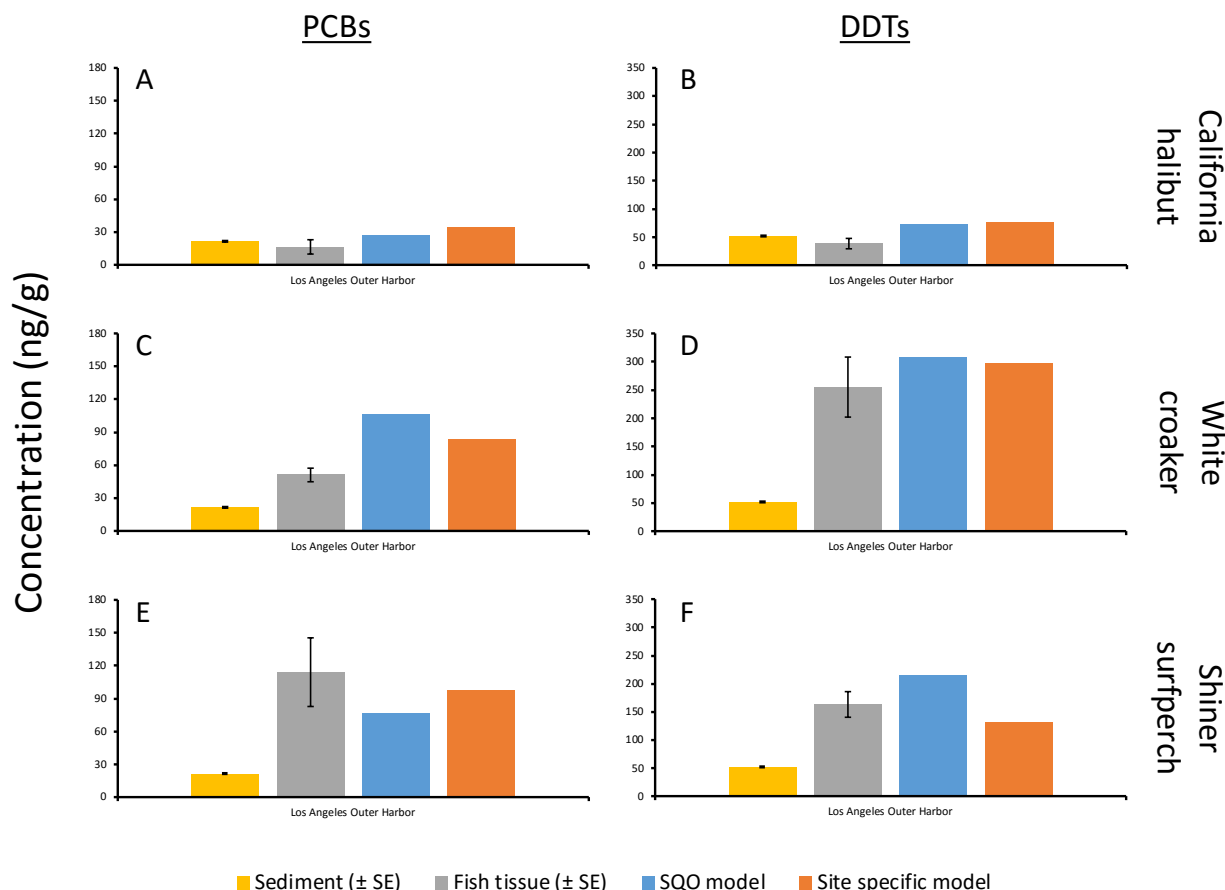
SQO model tissue contamination estimates were based on the site linkage calculation approach, which used Monte Carlo Simulation of uncertainty in measured sediment and tissue concentrations, fish movement, and bioaccumulation model parameters, to produce a probability distribution of estimated values. The tissue contaminant concentration corresponding to the 50<sup>th</sup> percentile of the distribution was used for comparison to the tissue estimate supplied by Anchor QEA for the same data set. Estimated tissue concentrations from both modeling approaches were compared to each other as well as to the measured fish tissue data.

Estimates of total DDTs and PCBs tissue concentrations were similar between the SQO and Site-Specific models (Figure A7.3). Model predictions for DDTs in California halibut and white croaker were nearly identical for both models, and there was no consistent bias (i.e., one model overpredicting in every case). In general, both models slightly overpredicted for PCBs and DDTs in California halibut and white croaker, while both underpredicted PCBs in the shiner perch. The average model agreement for PCBs (estimated concentration divided by measured) for all species was 1.5 for each model. The average model agreement for total DDTs was 1.5 and 1.3 for the SQO and Site-Specific models, respectively.

Overprediction for California halibut and white croaker could be due to the forage areas for those species being larger than the site size. If fish spend part of their lives in a less contaminated area



outside Los Angeles Outer Harbor then their overall tissue concentrations may be lower than expected based on the site sediment contaminant concentrations.



**Figure A7.3. Comparison of SQO model results (blue) to the measured site sediments (yellow), measured fish tissues (grey), and site-specific model results (orange). Results for total PCBs and DDTs in California halibut (A, B), white croaker (C, D), and shiner perch (E, F) are shown.**

## A7.5 Between Site Comparison

In this third evaluation, the HHSQO site linkage-based predicted tissue concentrations were again used for comparison to measured fish tissue concentrations. This comparison encompassed data over a wide range of contaminants, fish species, and locations in California. The objective of this analysis was to gain perspective on the range of results likely to occur in future monitoring applications.

The datasets referenced for the Appendix 6 framework application study were used to compare measured fish tissue concentrations to model-predicted values. These data were produced from multiple monitoring programs and reflected a range of sample sizes, study designs, and data precision. In some cases, tissue and sediment data for a given water body were obtained from separate studies, with the use of different station locations. The bioaccumulation model analyses differed from those conducted in Appendix 6, in that a separate model run was conducted for each species, rather than a combination of two or more species. Water column contaminant

concentration data were not available, so dissolved concentrations were estimated based on diffusion from pore water. Results for total chlordanes and Dieldrin are summarized by species and location in Table A7.1. Results for PCBs and DDTs are summarized in Table A7.2. Fewer comparisons are available for chlordanes and Dieldrin, either because these constituents were not included in the dataset or because sediment concentrations were below analytical detection limits.

The relationship between field tissue contaminant concentration and sediment was highly variable for all contaminant types. The empirical Biota Sediment Accumulation Factor (BSAF), based on field data varied from a high of 57 (PCBs in white croaker from San Pablo Bay) to a low of 0.002 (PCBs in topsmelt from outer LA Harbor). Numerous cases where tissue concentrations were below those reported for sediment were observed for all contaminant types and most sites. For example, 50% of tissue PCB concentrations were lower than sediment values (Table A7.2). DDTs, PCBs, Dieldrin, and chlordane are known to bioaccumulate relative to sediment in biota, so the occurrence of BSAFs < 1 indicate either inaccurate analytical data or non-representative samples (e.g., sampled fish did not receive majority of body burden from contamination associated with site sediment). The cause of these data discrepancies could not be determined for these historical datasets and these data were excluded from subsequent comparisons between model-estimated and field tissue contaminant data. The number of excluded sample combinations were 5, 8, 11, and 19 for chlordanes, Dieldrin, DDTs, and PCB, respectively.

Overall, the model estimates were similar to measured fish tissue data (within a factor of 2) for 48% of all sample comparisons. The frequency of under prediction (34%) was greater than over prediction (18%) for all sample comparisons. Few consistent species- or contaminant-specific biases were observed. The most consistent trend was for Dieldrin, where four of five comparisons indicated model under prediction; on average, the model estimate was 32% of the field tissue. There was much less consistent bias for the other contaminant groups, with the average model estimate corresponding to 119%, 99%, and 117% for the field samples for chlordanes, DDTs, and PCBs, respectively. Within species, over prediction of chlordanes and PCBs was usually present in spotted sand bass; no evaluation was feasible for Dieldrin or DDTs due to a lack of representative field data. Under prediction was frequently observed for white croaker. Instances of both over prediction and under prediction were encountered for most other species evaluated.

Several factors in addition to bioaccumulation model parameters are likely responsible for the variations in relative model estimate accuracy observed. Results for shiner perch illustrate the potential effect of some of these factors, such as lack of representative sediment contaminant concentration data. Field tissue contaminant concentrations for shiner perch are less than sediment values for Newport Bay and north San Diego Bay (Figure A7.4). In contrast, San Francisco Bay shiner perch tissue PCB contamination is much higher than would be expected based on sediment concentrations in San Pablo Bay (when compared to sediment PCB data from other sites). Recent studies by SFEI have documented strong spatial gradients in San Francisco Bay sediment PCB contamination, with the highest concentrations located in the bay margins where shiner perch frequently forage. However, the San Francisco Bay sediment data were

obtained from locations away from the margins, where contaminant concentrations were much lower.

The shiner perch data for DDTs illustrate the potential influence of biological and/or analytical variability. Reported sediment DDT concentrations for outer Los Angeles Harbor and lower Newport Bay are similar, however measured tissue DDTs vary 10-fold (Figure A7.4). Sediment DDT concentrations are not expected to have strong spatial gradients due to the lack of local sources, and shiner perch have a small home range that is estimated to be less than 1% of the site area (Table A7.3). Factors that might be responsible for the tissue differences include extreme variations in diet between sites, seasonal changes in tissue contamination (e.g., reproductive cycles), or inaccurate analytical chemistry. Data were not available to evaluate the likelihood of these, or other factors.

Fish home range may also have influenced the accuracy of bioaccumulation model estimates for some site and species combinations. The estimated fish home ranges and site dimensions (area or length) for these analyses are reported in Table A7.3. The home range of some species, such as spotted sand bass, shiner perch, and topsmelt, are much smaller than the size of all sites examined, indicating that these species have high site fidelity and should be reliable indicators of site contamination. Alternately, the estimated home range of California halibut (33 km) is larger than all sites studied and may not provide representative data for many locations.

The potential influence of poor site fidelity is illustrated by the results for California halibut (Figure A7.5). Field tissue contaminant concentrations were frequently less than sediment levels for all four contaminant groups. This species does not have good site fidelity, and as such, may spend time in locations with different contaminant levels, thereby increasing or decreasing their body burden compared to bioaccumulation model estimates.

**Table A7.1. Chlordane and Dieldrin concentrations measured in sediment and fish tissues, and predicted tissue concentrations in several fish species from California embayment sites. Asterisks indicate sediment-tissue combinations excluded from comparison due to BSAF <1.**

Sites*	Chlordanes					Dieldrin				
	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)
<b>California halibut</b>										
NewpBay low	5.75*	1.49	5.19	2.31	7.16	0.46*	0.26	0.21	0.00	0.17
NewpBay up	5.33*	1.65	0.63	0.20	10.37					
SFB central	0.15	0.02	0.39	0.05	0.53	0.12	0.01	0.21	0.00	0.16
<b>Spotted sand bass</b>										
Mission Bay	0.50*	0.00	0.52	0.16	1.57	0.50*	0.00	0.50	0.00	0.50
NewpBay low	5.75	1.49	7.07	1.59	23.87					
NewpBay up	5.33*	1.65	1.65	0.32	21.95	0.53*	0.12	0.21	0.00	0.80
SD north	0.81	0.64	1.52	0.93	3.89	0.44*	0.03	0.22	0.00	0.67
SD southcentral	1.69	0.90	3.35	0.55	7.77	0.46*	0.02	0.24	0.06	0.70
<b>White croaker</b>										
SFB central	0.15	0.02	3.01	0.44	0.64	0.12	0.01	0.89	0.10	0.24
SFB lowersouth						0.10	0.01	1.26	0.38	0.33
SFB San Pablo	0.12	0.02	3.67	1.16	1.05	0.08	0.01	1.54	0.12	0.32
<b>Shiner perch</b>										
Mission Bay	0.50	0.00	1.00	0.45	0.95	0.50*	0.00	0.50	0.00	0.41
NewpBay low	5.75*	1.49	3.34	0.89	16.40					
SD north	0.81	0.64	2.53	0.42	1.88	0.44*	0.03	0.38	0.17	0.60
SFB central	0.15	0.02	5.95	1.59	0.33					
SFB lowersouth	0.28	0.03	8.95	1.27	0.80	0.10	0.01	1.66	0.38	0.15
SFB San Pablo	0.12	0.02	1.20	0.22	0.25					
<b>Topsmelt</b>										
NewpBay up	5.33	1.65	4.57	2.02	9.59	0.53*	0.12	0.25	0.02	0.57

\*SITE NAMES AND ABBREVIATIONS:

San Francisco Bay San Pablo Bay (SFB San Pablo)  
 Los Angeles Outer Harbor (LA outer)  
 Newport Bay upper (NewpBay up)  
 San Diego Bay North (SD north)

San Francisco Bay Central (SFB central)  
 Eastern San Pedro Bay (ESP Bay)  
 Long Beach Inner Harbor (LB inner)  
 Newport Bay lower (NewpBay low)  
 San Diego Bay South and Central (SD southcentral)

San Francisco Bay Lower South (SFB lowersouth)  
 Los Angeles Inner Harbor (LA inner)  
 Long Beach Outer Harbor (LB outer)  
 Mission Bay (Mission Bay)

**Table A7.2 DDT and PCB concentrations measured in sediment and fish tissues, and predicted tissue concentrations in several fish species from California embayment sites. Asterisks indicate sediment-tissue combinations excluded from comparison due to BSAF <1.**

Sites*	DDTs					PCBs				
	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)
<b>California halibut</b>										
ESP Bay	19.54	6.61	162.35	66.31	72.96	20.01	9.26	58.87	17.41	54.93
LA inner	58.02*	23.83	37.76	9.69	94.62	208.93*	148.38	26.96	7.09	316.85
LA outer	26.80*	10.13	24.94	4.94	59.86	33.16*	23.56	5.85	1.18	54.50
LB inner	8.57	1.00	52.20	13.52	26.29	95.43*	41.68	23.83	5.24	253.61
LB outer	14.33	1.46	40.72	10.22	38.23	4.07	0.66	8.72	1.55	10.27
NewpBay low	35.36*	6.17	4.14	4.13	101.01	31.49*	7.78	13.09	12.78	75.37
NewpBay up	39.30*	10.17	0.30	0.28	163.97	6.48*	2.87	0.54	0.17	17.26
SFB central	3.86*	0.54	0.27	0.10	19.93	7.58*	0.81	3.78	0.82	43.26
<b>Spotted sand bass</b>										
Mission Bay	1.19*	0.77	1.06	1.30	5.13	1.33	1.60	2.50	1.87	5.50
NewpBay low	35.36*	6.17	18.28	9.42	302.17	31.49*	7.78	26.02	9.48	215.73
NewpBay up	39.30*	10.17	19.93	6.32	316.74	6.48	2.87	9.64	5.06	41.85
SD north	1.88*	1.30	1.21	0.62	8.99	38.89	22.58	113.21	66.45	267.26
SD southcentral	13.02*	12.87	10.57	1.05	54.16	40.94	23.30	273.44	43.91	265.88
<b>Queenfish</b>										
LA inner	58.02	23.83	104.94	48.21	231.09	208.93*	148.38	34.09	9.84	690.93
LA outer	26.80	10.13	210.70	119.62	228.49	33.16*	23.56	17.35	7.86	203.14
LB inner	8.57	1.00	181.59	47.65	78.92	95.43*	41.68	49.59	11.39	715.77
LB outer	14.33	1.46	50.10	5.34	133.93	4.07	0.66	35.12	18.57	42.28

Table A7.2 Continued.

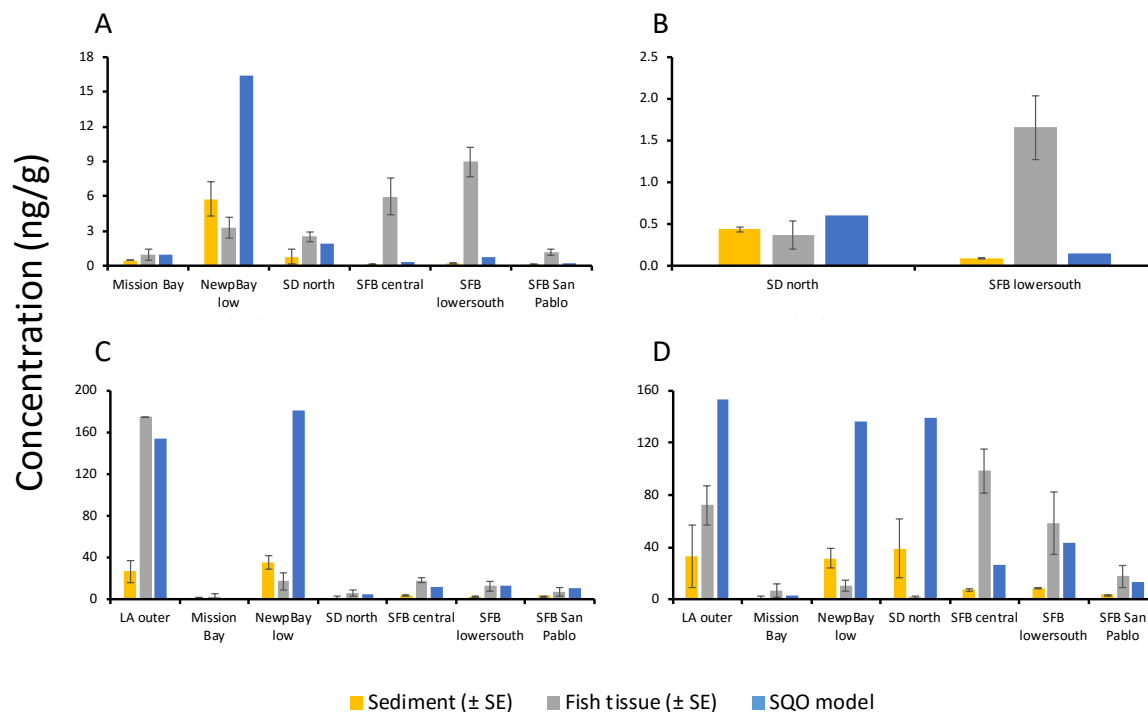
Sites*	DDTs					PCBs				
	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)	Sediment (ng/g)	Standard error (ng/g)	Fish tissue (ng/g)	Standard error (ng/g)	SQO Model prediction (ng/g)
<b>White croaker</b>										
ESP Bay	19.54	6.61	91.60	7.87	140.69	20.01	9.26	70.23	7.74	113.44
LA inner	58.02	23.83	800.53	260.83	233.54	208.93*	148.38	103.24	27.04	829.88
LA outer	26.80	10.13	134.30	38.68	140.94	33.16*	23.56	16.55	2.90	129.18
LB inner	8.57	1.00	269.49	50.21	67.10	95.43*	41.68	80.98	16.70	705.93
LB outer	14.33	1.46	188.52	54.16	90.86	4.07	0.66	42.72	10.86	24.06
SFB central	3.86	0.54	12.51	2.37	24.17	7.58	0.81	61.29	13.39	58.86
SFB lowersouth	2.89	0.40	19.51	8.71	33.16	8.60	0.68	96.54	44.26	106.58
SFB San Pablo	3.31	0.36	65.90	22.69	44.19	3.63	0.30	207.57	69.55	52.94
<b>Shiner perch</b>										
LA outer	26.80	10.13	175.10	0.00	153.47	33.16	23.56	72.13	14.87	153.12
Mission Bay	1.19	0.77	3.04	3.09	2.63	1.33	1.60	6.77	5.08	2.84
NewpBay low	35.36*	6.17	17.57	8.43	180.68	31.49*	7.78	10.71	4.00	136.03
SD north	1.88	1.30	6.23	2.72	4.77	38.89*	22.58	1.92	0.98	139.45
SFB central	3.86	0.54	18.23	2.55	11.49	7.58	0.81	98.35	16.65	26.50
SFB lowersouth	2.89	0.40	12.73	5.08	13.64	8.60	0.68	58.41	24.06	43.64
SFB San Pablo	3.31	0.36	7.87	4.12	11.29	3.63	0.30	17.72	8.42	13.50
<b>Topsmelt</b>										
LA inner	58.02	23.83	101.61	22.00	58.84	208.93*	148.38	33.60	6.00	195.45
LA outer	26.80	10.13	104.01	14.20	71.07	33.16*	23.56	0.05	0.00	71.02
LB inner	8.57	1.00	59.45	11.66	19.83	95.43*	41.68	28.77	5.86	188.31
LB outer	14.33	1.46	92.68	13.16	33.65	4.07	0.66	39.39	6.34	9.27
NewpBay up	39.30	10.17	52.25	34.26	105.70	6.48*	2.87	5.29	1.94	12.70
SFB central						7.58	0.81	380.92	108.89	27.44

**Table A7.3. Home range parameter comparison for each sport fish and site.**

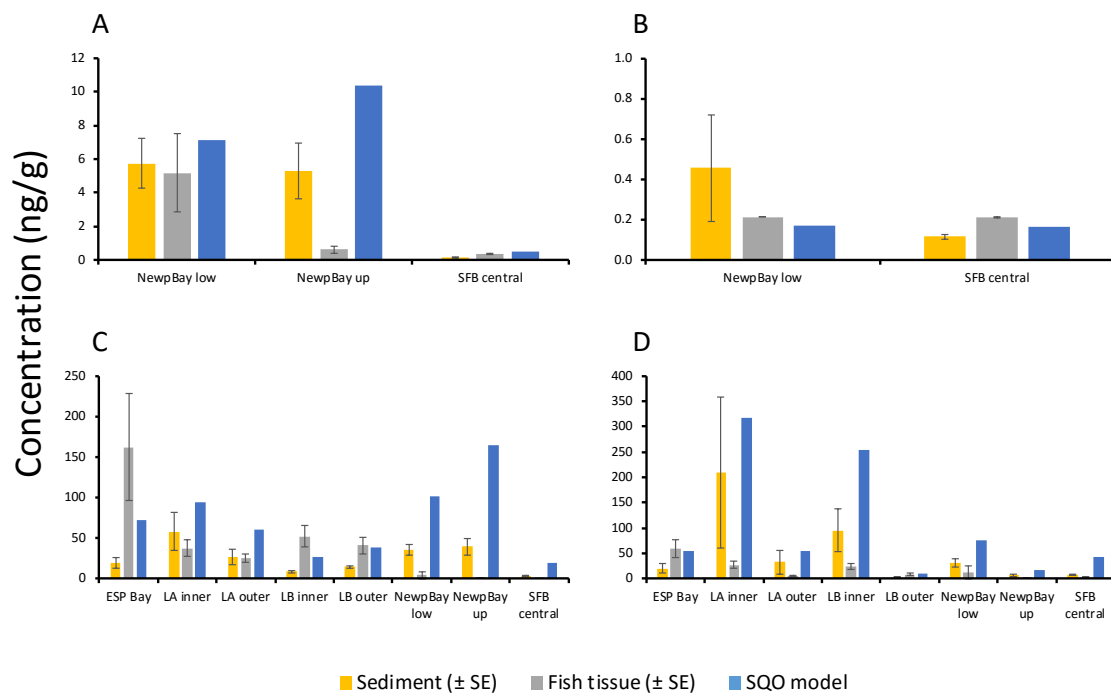
Species	HR Basis	HR Mean	HR SD	SFB Central	SFB Lower South	SFB San Pablo Bay	LA inner	LA outer	LB inner	LB outer	Eastern San Pedro Bay	Newport Bay upper	Newport Bay lower	Mission Bay	SD North	SD South Central
California halibut	Site length (km)	29	60	32.9	12.6	23.3	6.6	4.1	4.9	4.1	10.5	6.8	5.6	6.0	11.2	10.6
Spotted sand bass	Site area (km <sup>2</sup> )	0.0071	0.0073	373	26.9	314	5.8	6.8	5.8	9.9	27.0	1.4	3.1	8.1	15.8	27.5
Queenfish	Site area (km <sup>2</sup> )	3.0	4.7	373	26.9	314	5.8	6.8	5.8	9.9	27.0	1.4	3.1	8.1	15.8	27.5
White croaker	Site area (km <sup>2</sup> )	3.0	4.7	373	26.9	314	5.8	6.8	5.8	9.9	27.0	1.4	3.1	8.1	15.8	27.5
Shiner perch	Site area (km <sup>2</sup> )	0.0012	0.0008	373	26.9	314	5.8	6.8	5.8	9.9	27.0	1.4	3.1	8.1	15.8	27.5
Topsmelt	Site area (km <sup>2</sup> )	0.0012	0.0008	373	26.9	314	5.8	6.8	5.8	9.9	27.0	1.4	3.1	8.1	15.8	27.5

HR mean = mean home range of seafood species under consideration (km or km<sup>2</sup>, depending on taxa).

HR SD = standard deviation of home range of seafood species



**Figure A7.4. Shiner perch, chlordanes (A), Dieldrin (B), DDTs (C), and PCBs (D). Note, y-axes are scaled for each contaminant. SE=standard error.**



**Figure A7.5. California halibut, chlordanes (A), Dieldrin (B), DDTs (C), and PCBs (D). Note, y-axes are scaled for each contaminant. SE=standard error.**



## **A7.6 Conclusions**

The three comparisons conducted for this study each evaluated a different component of the performance of the SQO bioaccumulation model. In total, these comparisons indicate that the modifications of the Gobas and Arnot San Francisco Bay PCB model made to adapt it for use for SQO assessment have not significantly impacted the accuracy of the model, as documented in the literature (Gobas and Arnot 2010). This conclusion is based on the comparison of the SQO version of the model to the PCB model developed for use in San Francisco Bay. Results of this comparison demonstrated that both models have similar accuracy with regards to predicting both congener-specific and total PCB bioaccumulation.

Comparison to an independently-developed bioaccumulation model (Anchor QEA model) also demonstrated that the SQO modeling approach is based on sound science. Results obtained using the standardized SQO model were similar to those from the dynamic and highly site-specific Anchor QEA model, indicating that the SQO approach is likely to yield reliable results for many applications.

Application of the SQO modeling approach to a diversity of monitoring data illustrated that there are many potential sources of error in estimating contaminant bioaccumulation from sediment. Estimates of contaminant bioaccumulation from sediment relative to that measured in the field varied by up to two orders of magnitude, but much of the variation was likely due to factors unrelated to the modeling approach. Variability and uncertainty in factors such as fish movement, station location/representativeness, spatial contamination gradients, analytical accuracy, and life history (e.g., diet) can be just as influential on the accuracy of bioaccumulation estimates as the model conceptual approach. The influence of some of these factors (e.g., fish movement, station location) can be minimized through use of a study design that considers important site-specific factors. Development of an accurate conceptual site model as part of the study design, and collection of a sufficient number of samples to describe variability, can assist in the attainment of accurate bioaccumulation model predictions.