

SAN DIEGO BAY BIOACCUMULATION STUDY

Bioaccumulation Database Description

Steven M. Bay

Southern California Coastal Water Research Project

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BACKGROUND

Bioaccumulative contaminants in San Diego Bay sediments have the potential to impact many of the designated beneficial uses for the Bay. Our ability to assess bioaccumulation-related impacts within the Bay is in part limited by the amount and characteristics of available data. Data limitations include a lack of matching sediment and tissue contamination information pertaining to different food web components such as sport fish and wildlife. Such data are needed to develop our understanding of bioaccumulation relationships that will help us to interpret site specific information and to evaluate conditions with respect to the protection of human health and wildlife.

In 2012, the California Regional Water Quality Control Board, San Diego Region (SDRWQCB), the Southern California Coastal Water Research Project (SCCWRP), and the United States Fish and Wildlife Service (USFWS), Carlsbad Fish and Wildlife Office (CFWO) developed a plan to address the bioaccumulation data needs for San Diego Bay. Funding to conduct these studies was received from the Water Board in May 2014 and January 2015. The overall goal of this project was to conduct integrated food web studies within three regions of San Diego Bay. Compilation and analysis of data from multiple studies, as well as additional sampling conducted under this project were used to accomplish three primary study objectives:

- **Describe bioaccumulation among key components of the San Diego Bay food web.** Two major contaminant exposure pathways were evaluated in the study: bioaccumulation related to feeding on sediment-dwelling organisms (benthic pathway) and bioaccumulation related to uptake of contaminants in water column-dwelling organisms (pelagic pathway).
- **Evaluate risk to wildlife from contaminant exposure.** Contaminant concentrations in the eggs and diet of five species of seabirds were examined: California least tern, Caspian tern, double-crested cormorant, western gull, and surf scoter (diet only).
- **Assess potential risk to human health resulting from consumption of San Diego Bay fish.** Tissue contamination data for several popular sport fish, including spotted sand bass, California halibut, and pacific chub mackerel, were compared to consumption advisory levels developed by OEHHA (Office of Environmental Health Hazard Assessment).

Sediment and tissue chemistry data were obtained from three coordinated studies. Data from the 2013 Southern California Bight Regional Monitoring Program (Bight '13) in coordination with the Regional Harbor Monitoring Program (RHMP) included samples of sediment, plankton, benthic invertebrates and fish collected from San Diego Bay. The Bight '13 survey also included seabird eggs from five locations in the Bay. Additional sediment and tissue data were collected in 2014 as part of a shallow water habitat (SWHB) survey designed to complement the 2013 sample collections. The SWHB samples were collected from water depths of 3 m or less in order to provide information on contamination and bioaccumulation patterns in areas frequently used as bird foraging areas and fish nursery grounds. Finally, tissue chemistry data for five species of sport fish were obtained for samples collected in 2014-15 through a combination of targeted fishing and contributions from the public.

The analyses were based on sediment contamination data from 64 stations in San Diego Bay, selected to represent three geographical regions: North, Central, and South. Biota were collected at a subset of these stations. A total of 209 tissue samples were analyzed for a suite of contaminants that included mercury, PCBs, DDTs, chlordanes, dieldrin, and contaminants of emerging concern (PBDE flame retardants and perfluorinated compounds).

A technical report by Bay et al. (2016) contains description of the study and data analysis results. The analytical chemistry upon which the report is based are contained in a Microsoft Access database (SDBayBioaccumulationDatabase_12-3-2016.accdb). This document describes the contents of the database. The location of sediment and tissue samples used in the report are shown in Figures 1 and 2.

The San Diego Bay bioaccumulation database is composed of 16 tables that contain information on sample collection, sediment and water analytical chemistry, and sample compositing. The contents of these tables are described in this document. Table names are denoted by the use of bold italic font (e.g., ***SampleMaster***).

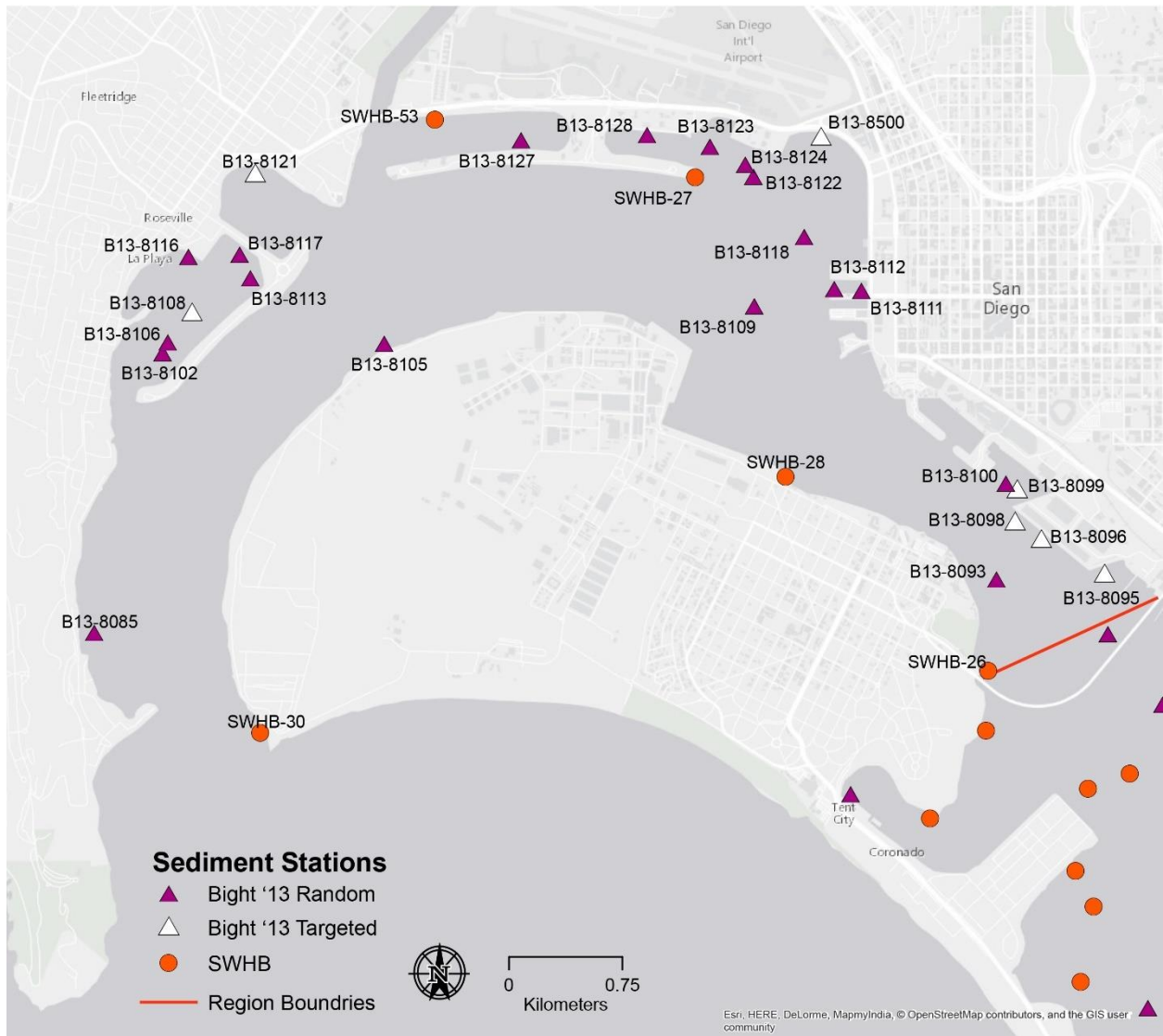


Figure 1a. North Bay sediment sample locations for Bight '13 regional survey and Regional Harbor Monitoring Program (Bight '13) and shallow water habitat survey (SWHB).

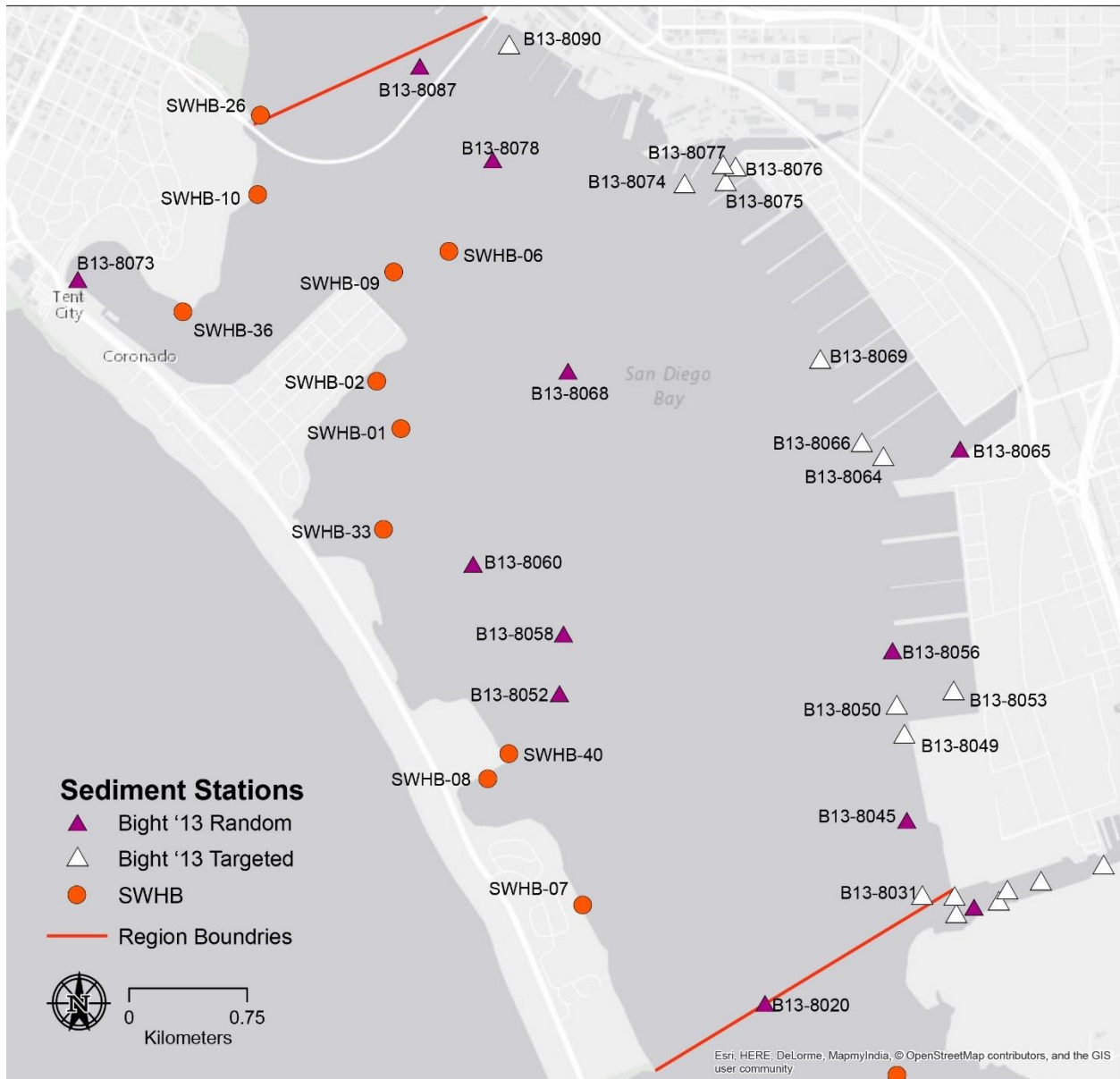


Figure 1b. Central Bay sediment sample locations for Bight '13 regional survey and Regional Harbor Monitoring Program (Bight '13) and shallow water habitat survey (SWHB).



Figure 1c. South Bay sediment sample locations for Bight '13 regional survey and Regional Harbor Monitoring Program (Bight '13) and shallow water habitat survey (SWHB).

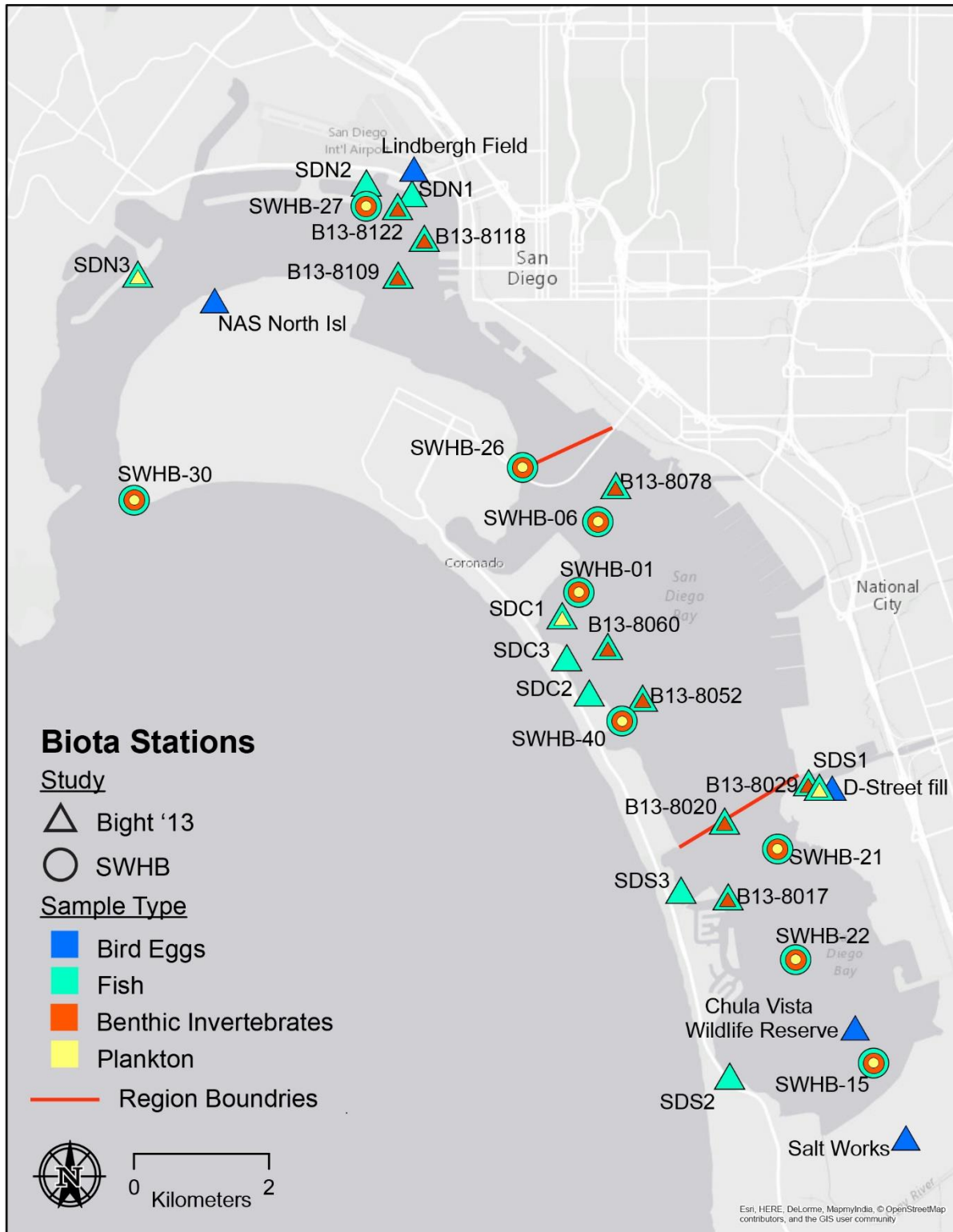


Figure 2. Tissue sample locations for Bight '13 regional survey and Regional Harbor Monitoring Program (Bight '13) and shallow water habitat survey (SWHB).

DATABASE TABLES

AnalysisChemistryData

Contains a subset of the chemistry data provided by the analyzing laboratories (Table 1). This table contains chemistry results and batch information for those individual analytes used in preparing the bioaccumulation study report. The information provided in this table also includes detection limits, data qualifiers and the laboratory that conducted the chemical analysis (Table 1). This table contains data for most of the Bight '13 samples, which includes many samples in locations outside of San Diego Bay. Nondetects are assigned a value of 0 in the results table.

Pay careful attention to the concentration units associated with the data in this table, as they may vary both among and within sample or analyte type. For example, sediment data are expressed on a dry weight basis and tissue data use a wet weight basis. Metals data are reported as ug/g, while trace organics data are reported as ng/g. Units also vary for bird egg mercury; in most cases the data are reported on a wet weight basis, but some samples use a dry weight basis. Percent moisture content data are provided in the database to enable unit conversion from a dry to a wet weight basis. This conversion has already been applied to the San Diego bird egg mercury data in *SDBay Select Chems*.

Sample Master

This table contains general information regarding each sample in the analysis chemistry data tables, such as species names (Table 2). It also contains a field that can be used to link the current sample identifiers with alternate sample identifiers such as those used in the original sample labels. The sample identifiers were modified in some cases in order to make them unique and compatible with other database sample identifiers. A species group field in this table can be used to query different taxonomic groups for the tissue samples. Scientific names for tissue samples are also in this table.

Station

This table contains information regarding sample collection and location. Information such as the waterbody, and the latitude and longitude where the samples were collected is also stored in this table (Table 3). The collection methods are also described in this table. This table can be used to create maps and also to provide waterbody and location information. Stations located in San Diego Bay are associated with two waterbody names: San Diego Bay and Sweetwater Marsh. Note that there are multiple records for stations where both sediment grab and trawl samples were collected, because location coordinates differ for each type of collection. A "t" suffix is added to the station code in order to denote the trawl station record (e.g., B13-8017 and B13-8017t). For simplicity and to facilitate data queries, the grab station identifier is associated with all samples, regardless of whether they were collected by grab or trawl.

SDBay Select Chems

This table contains a subset of the chemistry data in *AnalysisChemistryData* combined with identifiers from *Sample Master* and *Station* that are specific for San Diego Bay. These are the raw data used in the bioaccumulation study data analyses. No new data are contained in this table; it is provided as a convenience to the user. Field descriptions are the same as those described previously.

SumChems_All

This table contains the summed chemistry data for common chemical classes, such as PCBs and DDTs. The summation method is described in the appendix. This table contains data for most of the Bight '13 samples, which includes many samples located outside of San Diego Bay. Results for San Diego Bay are associated with two locations: San Diego Bay and Sweetwater Marsh. Field descriptions are the same as those described previously.

OtherChemData

This table contains raw data for analytes not used in the bioaccumulation study report. Fields are the same as for *AnalysisChemistryData*. Note that data for locations outside of San Diego Bay are included in this table.

SedGrainSizeSWHBData

This table contains results of sediment grain size analyses for only the SWHB study. These data were not used in the bioaccumulation study report and are provided as a convenience to the user. Field descriptions are the same as for *AnalysisChemistryData*.

FishCompositelInfo

This table describes the components of the fish tissue composites (Table 4).

InvertCompositelInfo

This table describes the components of the benthic macrofauna tissue composites (Table 5).

BirdEggCompositelInfo

This table describes the bird egg characteristics and components of the composite samples (Table 6).

PlanktonCompositelInfo

This table describes the bird egg characteristics and components of the composite samples (Table 7).

LuList AnalyteNames

This look up list table contains the names of all the analytes for which chemistry information is available in the database. It also contains information to help group the analytes, as well as information to determine which analytes were used in sums, such as PCBs or DDTs.

LuList Codes

This look up list contains the description of the qualifier codes associated with the chemistry data.

WaterBight13CLAMData

This table contains concentration data obtained using the CLAM in situ water sampler (Table 8). Data are included for stations in Newport Bay (LNB and UNB StationID) and San Diego Bay, as well as QC samples. Note that the sample type includes dissolved fraction (Result), as well as various QC samples. The SampleIDs for these samples are not included in *Sample Master*. Note that detection limits vary for each sample and are relatively high for many analytes, resulting in an underestimate of dissolved contaminant concentrations.

WaterBight13CLAMSamplInfo

This table contains sampler performance data for the CLAM in situ water sampler (Table 9). Samplers were deployed in both Newport Bay and San Diego Bay. Two sampling events were conducted; event I corresponds to samples with a F1 identifier in ***WaterBight13CLAMData*** and event II corresponds to samples with a F2 identifier in the data table.

WaterRHMPHgData

This table contains total and dissolved mercury data for water samples collected in San Diego Bay. Field descriptions are the same as for ***AnalysisChemistryData***.

QUERYING THE DATA

Retrieval of information for use in statistical analyses usually requires the querying of a combination of the *AnalysisChemistryData*, *Sample Master*, and *Station* tables in order to provide complete information regarding the station location and species name. Note that a StudyID of Bight13 is used to represent samples from both the Bight '13 and RHMP programs; this consolidation was necessary because comingling of samples from these programs resulted in variations in use of the StudyID for the same sample among analytical labs and data reports. Consolidation of the Study ID was needed in order to allow data records for the same sample to be successfully related to each other.

The raw chemistry data table (*AnalysisChemistryData*) should be linked to the *Sample Master* table through the StationID and SampleID fields in order to retrieve data on the organism analyzed. This database contains most of the sediment and biota analytical data for the Bight '13 regional survey, and so contains data for samples located outside of San Diego Bay that were not used in the bioaccumulation study report. Selection of data for a particular waterbody, such as San Diego Bay, is accomplished by linking *AnalysisChemistryData* to *Station* through the StationID and specifying selection criteria for Waterbody and Location. Samples collected in San Diego Bay are associated with two waterbodies: San Diego Bay and Sweetwater Marsh.

A table containing the analytical chemistry data specific to the bioaccumulation study has been provided as an aid to users not familiar with designing data queries: *SDBay Select Chems*. Additional Access queries can be applied this table in order to further refine the data set, or the entire table can be exported as an Excel or text file for analysis outside of Access.

The bird egg chemistry data are generally presented on a wet weight basis. Because the samples represent salvaged eggs with variable levels of desiccation, the wet weight concentration data may not accurately represent the concentration at the time of laying. It is recommended that these data be converted to a fresh weight basis, which better represents the concentration at the time of egg laying. Conversion is accomplished by multiplying the wet weight concentration by a fresh weight adjustment factor. Adjustment factors are provided in *BirdEggCompositeInfo*. Note that adjustment factors are not provided for some samples because the eggs were sampled soon after laying and therefore did not undergo appreciable desiccation; no adjustment of these samples is needed.

This database does not contain sediment chemistry data for nonrandomly selected stations, as these data were not used in the bioaccumulation study report. Analyte concentration data for these samples are contained in a complementary bioaccumulation report by Stransky et al. (2016).

Table 1. Description of fields found in database table: *AnalysisChemistryData*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
SampleID	Sample identifier; unique identifier
SampleDate	Date when sample was collected
PreparationBatchID	Preparation batch identifier as provided by the analyzing laboratory
AnalysisBatchID	Analysis batch ID as provided by the analyzing laboratory
AnalysisDate	Date when sample was analyzed by the lab
SampleType	Codes described in <i>LuList Codes</i>
SampleType2	Additional descriptor.
Matrix	Matrix type: sediment, seawater, tissue, QA sample
AnalysisMethod	Analysis method as provided by analyzing laboratory
AnalyteClass	Analyte class to use in analyte grouping
AnalyteName	Also provided in <i>LuList AnalyteNames</i>
Units	Concentration units. Laboratory-supplied data were transformed from a dry weight to a wet weight basis in some cases for standardization.
Qualifier	Information for the qualifier codes can be found in <i>LuList Codes</i>
Result	Concentration value used for reporting and analysis.
LabReplicate	Laboratory replicate
LabSampleID	Sample ID assigned by analyzing lab
TrueValue	Value used for QA sample evaluation, not included in this version of database.
MDL	Method detection limit
RL	Reporting limit
LabCode	Lab conducting the chemical analysis
QACode	Codes described in <i>LuList Codes</i>
QualityControl	Codes described in <i>LuList Codes</i>
Comments	Comments provided by analyzing laboratory or added during dataset creation.

Table 2. Description of fields found in database table: *SampleMaster*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
OldSampleID	Old sample identifier, kept in table to link it to the original sample labels but not used in any other table
SampleID	Sample identifier; unique identifier
SampleDate	Date when sample was collected
CommonName	Common name of organism. NA is used for sediment or water
ScientificName	Scientific name of organism. NA is used for sediment or water
SpeciesGroup	Species group for tissue samples. NA is used for sediment or water
Matrix	Matrix type: tissue, sediment, seawater.

Table 3. Description of fields found in database table: *Station*.

Field	Description
Waterbody	Waterbody were sample was collected
Location	Location were sample was collected
StudyID	Study identifier
StationID	Station identifier
Latitude	Collection latitude
Longitude	Collection longitude
CollectionMethods	Method for collecting sample
Comments	Comments provided by analyzing laboratory or revision notes added during dataset creation

Table 4. Description of fields found in database table: *FishCompositeInfo*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
SampleID	Sample identifier; unique identifier
CommonName	Common name of organism.
SampleDate	Date when sample was collected
ItemNumber	Sequential number to identify each fish contained in a composite
StandardLength	Length of fish from tip of nose to base of tail.
StandardLengthUnits	
Weight	Wet weight of organism
WeightUnits	
FishFraction	Describes the portion of the fish included in the analysis sample.
MultiOrganismComposite	Indicates whether analysis sample is composed of multiple fish (Yes) or a single fish (No).
Comments	Comments provided by analyzing laboratory or revision notes added during dataset creation

Table 5. Description of fields found in database table: *InvertCompositeInfo*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
SampleID	Sample identifier; unique identifier
SampleDate	Date when sample was collected
Taxon	Phylogenetic group to which the organisms belong
Count	Number of organisms used for composite if available
TotalWeight	TotalWet weight of analysis sample
TotalWeightUnits	
MultiOrganismComposite	Indicates whether analysis sample is composed of multiple individuals (Yes) or a single organism (No).
Comments	Comments provided by laboratory or revision notes added during dataset creation

Table 6. Description of fields found in database table: *BirdEggCompositeInfo*.

Field	Description
Species	Common name
Date collected	Date of sample collection
Egg ID	Egg unique identifier; assigned in field
Location (general)	Description of collection site and nest location
Lat	Collection latitude
Long	Collection longitude
Shell thickness-digital	Measured with a Starrett electronic digital micrometer, which was fitted with ball attachments, and was accurate to 0.01 mm.
Shell thickness-analog	Measured with a Starrett 1010 M dial micrometer fitted with rounded ball contacts to enable measurements of eggshell thickness without denting membranes
Thickness units	
Egg fw adjustment factor	Adjustment factor calculated from individual egg measurements
Adj factor units	Number of organisms used for composite if available
Ratcliffe Index qualifier	
Ratcliffe Index	Alternate index for evidence of eggshell thinning
Embryo status	Help determine reasons for why an egg did not hatch
Chemical Sample ID	ID of sample submitted for chemical analyses; May be a composite of 2 or more individual eggs (reflected in ID) or a single egg
SampleID	Sample identifier used in database to provide linkage among database tables. ID differs in some cases from Chemical Sample ID due to modifications made during sample processing.
Sample fw adjustment factor	Fresh weight adjustment factor; used to adjust analytical results (wet weight-based) for moisture loss between the time the egg was laid and when it was collected

Table 7. Description of fields found in database table: *PlanktonCompositeInfo*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
SampleID	Sample identifier; unique identifier
SampleDate	Date when sample was collected
SampleDryWeight	Dry weight of sample
DryWeightUnits	

Table8. Description of fields found in *WaterBight13CLAMData*.

Field	Description
StudyID	Study identifier
StationID	Station identifier
SampleID	Sample identifier; unique identifier for field samples
SampleType	Type of QC sample
SampleType2	Either a field sample or QC sample
Sample Info	Sample identifier provided in original file
Units	Concentration units for sample type.
BDE 15 – BDE 183	Concentration of PBDE congener
Chlordene - p,p'-DDT	Concentration of trace organic analyte
PCB74 – PCB206	Concentration of PCB congener
Comments	Comments provided by analyzing laboratory or judged necessary during the dataset creation

Table 9. Description of fields found in *WaterBight13CLAMSampleInfo*.

Field	Description
Sampling event	First or second sampling event
Location	Station identifier
Replicate	Denotes a replicate sample
SampleType	Type of QC sample
Deploy Date	Date of sampler deployment
Deploy Time (h)	Time of day at deployment
Deploy Flow (mL/Min)	Sampler flow rate at start of deployment
Retrieve Date	Date of sampler retrieval
Retrieve Time	Time of day at retrieval
Retrieve Flow (mL/Min)	Sampler flow rate at end of deployment
Average Flow Rate (mL/Min)	Average of deployment and retrieval flow rate.
Total Time	Hours of deployment, incomplete records as provided
Extraction Total (ml)	Volume of water filtered by sampler, in ml
Extraction Total (L)	Volume of water filtered by sampler, in L
Sample Deployed	Person who deployed sampler
Sample Retrieved	Person who retrieved sampler

REFERENCES

Bay, S.M., D.J. Greenstein, A.N. Parks, and C.Q.T. Zeeman. 2016. Assessment of Bioaccumulation in San Diego Bay. Final Report. Southern California Coastal Water Research Project, Costa Mesa, CA. 277 pp.

Stransky, C. K. Tait, C. Sheredy, R. Schottle, R. Kolb, and B. Bernstein. 2016. Aquatic Food Web Bioaccumulation Study of San Diego Bay. Final Report, prepared for the City of San Diego. Amec Foster Wheeler Environment & Infrastructure, Inc., San Diego, CA. 156 pp.

APPENDIX

Analyte Summation Method

1. Define the list of analytes for summation (e.g., Bight '13 PCB congener list)
2. The summation method depends on the presence of nondetect values:
 - a. When all analytes are detected, sum all the values
 - b. If some analytes are below detection, only sum the detected analytes and set the analytes below detection as 0.
 - c. When all the analytes are below detection, use the highest detection limit of the analytes on the list to represent the sum.
3. A conversion factor is not used to correct for partial lists of analytes (e.g., less than 209 PCB congeners measured).