Southern California Bight 2023
Regional Marine Monitoring Survey
(Bight '23)

Macrobenthic (Infaunal) Sample Analysis Laboratory Manual

Prepared by:
Bight '23 Benthic Committee

Prepared for:
Commission of the Southern California Coastal Water Research Project
3535 Harbor Blvd, Suite. 110
Costa Mesa, CA 92626

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SOUTHERN CALIFORNIA BIGHT
2023 REGIONAL MONITORING PROGRAM

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INTRODUCTION

This document describes laboratory procedures for the analysis of macrobenthic (infaunal) samples collected for the Southern California Bight 2023 Regional Monitoring Program (Bight'23). The procedures represent a continued evolution from the practices of Publicly Owned Treatment Works (POTW) monitoring programs through regional surveys from 1994 to the present. Some modifications have been made to ensure data comparability, facilitate coordination of quality control steps during the Bight '23 infaunal survey, and meet the requirements of the Bight '23 Information Management Plan. It is the responsibility of each participating laboratory's supervisor to assure that:

- The detailed procedures described in this manual are followed during sample processing and analysis,
- All Quality Control (QC) steps are implemented,
- Data submissions conform to the stipulated standards,
- Schedules are met for sample analysis, QC, and data submission
- Copies of all records, forms, and documents generated in the process are securely maintained on file until all aspects of the survey and resulting reports are completed.

Upon receipt in the laboratory of samples from the field, all stages of infaunal sample processing and analysis, including QC and data submission, are described in this manual. In overview, the process consists of the following tasks and activities (Figure 1) which are described in sections as indicated below:

1) Sample Treatment and Storage: The sample is washed free of fixative and transferred to an alcohol solution for processing and/or storage (**Section 1**),
2) Sample Sorting: All organisms are removed from the grunge contained in the sample and sorted into taxa lots to facilitate subsequent taxonomic analysis (**Section 2**)
3) Taxonomic Analysis: All specimens in the samples are identified to the lowest practical level, most often species, and counted (**Section 3**),
4) Data Submission: Resulting data should be kept in an electronic data file compliant with this manual and the Bight'23 Information Management Plan. Data should be submitted via the SCCWRP Bight '23 data submission portal. (**Section 4**).
5) Quality Control: QC is required for steps 2 and 3 (**Section 5**) to ensure data consistency. QC for step 2 involves re-sorting a minimum of 10% of the grunge from each sample. QC for step 3 consists of reanalyzing 10% of the samples processed by each laboratory and required taxonomist participation at Southern California Association of Marine Invertebrate Taxonomists (SCAMIT) workshops that identify and resolve Bight '23 taxonomic problems. Results of this process are used to determine whether the measurement quality objectives (MQOs) established for each step are met.
6) Record Keeping and Procedural Responsibilities are described in **Section 6.** Examples of data forms to be used during processing and QC are presented in **Section 8.**

It is essential that all participating taxonomists have the expertise and experience necessary to assure that Bight'23 macrofaunal data meet standards set during previous regional surveys. Qualification criteria for taxonomists who did not analyze macrofaunal samples for previous Bight surveys are described in **Appendix A**.

In addition, taxonomists are required to participate in the series of workshops jointly sponsored by the Bight'23 benthic committee and the Southern California Association of Marine Invertebrate Taxonomists (SCAMIT) focusing on taxonomic problems arising during analysis of the Bight'23 samples. These workshops culminate in a synoptic review of taxon names in the data set compiled from submissions by all participating laboratories.

Copies of this manual are available on the web site of the Southern California Coastal Water Research Project (SCCWRP) (http://www.sccwrp.org).

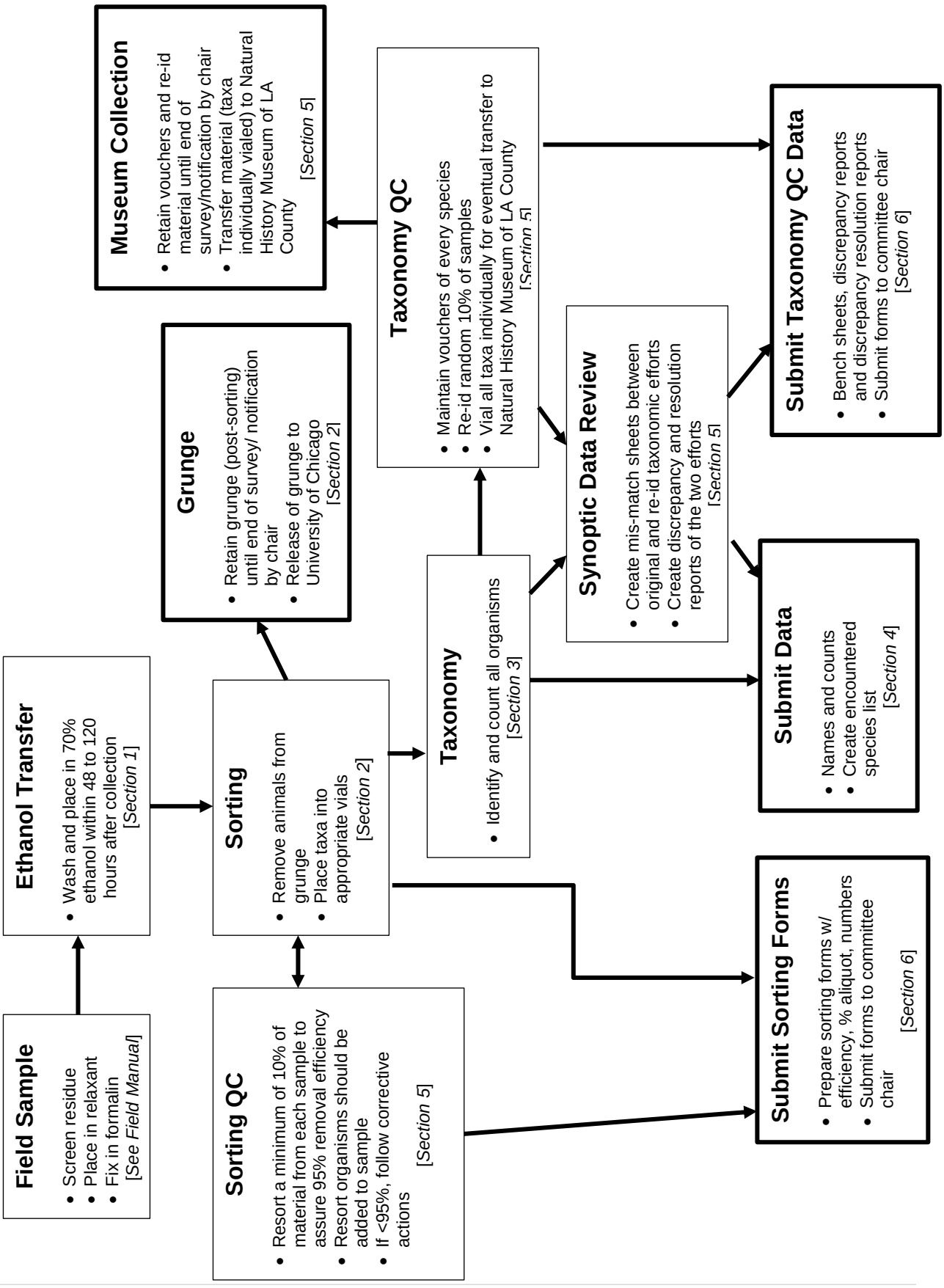

Figure 1. Flow chart of benthic sample processing

1. SAMPLE TREATMENT AND STORAGE

1.1 Upon receipt in the laboratory, samples will be in formalin fixative and must be washed and transferred to a preservative. The removal of formalin is necessary for two reasons. Formaldehyde becomes increasingly acidic over time and prolonged exposure damages organisms with calcareous structures (e.g., shelled mollusks). Also, formaldehyde is a noxious, potentially dangerous chemical; its replacement with ethanol makes subsequent handling of the sample safer. Other benefits of the washing process are the removal of excess silt from mudballs and fecal pellets that may have broken down during storage.

1.2 The samples are to remain in buffered fixative for a minimum of 48 hours. No sample should remain in fixative for longer than 120 hours.

1.3 The preservative to be used for all stages of Bight '23 infaunal samples is a 70% solution of ethanol. **Denatured alcohol is not permitted**. Rose bengal may **not** be used to stain organisms.

1.4 It is recommended that the preservative for mollusk and other calcareous voucher specimens be buffered with marble chips to reduce possible acidity, especially if the ethanol is produced by industrial distillation rather than fermentation.

1.5 Procedure

1.5.1 Select an appropriate 0.5mm or smaller sieve and examine the mesh for holes and adhering organisms. Working under a fume hood with eye protection, decant the fixative through the clean and intact sieve.

1.5.2 After decanting the formalin, refill the sample container with tap or other water, agitate gently by swirling, and wash the entire sample into the sieve.

1.5.3 Gently wash the sample with a low-pressure stream of water to remove any fine silt.

1.5.4 Using a scoopula and wash bottle containing preservative (70% ethanol), transfer the sample back to the sample container, top the sample off with preservative.

1.5.5 Place an internal label in each sample container bearing the station name, sampling date, and split number (if more than one container is used; e.g., 1 of 2). Labels are to be written in pencil or indelible ink on 100% rag-paper, poly- paper, or other paper suitable for permanent wet labels.

1.5.6 After each sample is washed, closely examine the sieve to ensure that all organisms have been removed (any organisms found should be reunited

with the sample. Tightly affix the lid of the jar. Finish by thoroughly rinsing the sieve to avoid cross contamination of subsequent samples.

1.5.7 Store infaunal samples in a safe and secure manner protected from environmental extremes. Avoid direct sunlight and temperatures above 30° C as high temperatures will accelerate evaporative loss of preservative.

1.5.8 Routinely inspect all samples to ensure that the container closure is tight and the preservative level adequate. If evaporative loss of preservative is evident, top-off the sample using 95% ethanol and check the lid or rim of the jar for defects and possible replacement. Do not use 70% ethanol for this purpose, as it will lead to dilution of the sample preservative because of the different evaporation rates of ethanol and water.

2. SAMPLE SORTING

2.1 Sorting is the process by which organisms in a benthic sample that were alive at time of collection are removed from the organic and inorganic residues (grunge) that compose the sample and sorted into broad taxonomic categories for subsequent taxonomic analysis. Sorting must be accurate and complete to assure the value of all the subsequent steps in the sample analysis process.

2.2 Procedure

2.2.1 All laboratories participating in the Bight '23 infaunal survey have established sorting procedures that are compatible with the aims of this survey. The following points stipulate those elements essential to the process or unique to Bight '23.

2.2.2 Begin the sorting process by filling out a Bight'23 Macrofauna Sorting Sheet (page 29) with the station name, date, sorter's name + laboratory, and date sorting begins. If the sample consists of more than a single jar, these jars are to be treated together as a single sample. Make sure you have all jars composing the sample.

2.2.2 Sort the sample under a stereo microscope. It is recommended that the sample be sorted in small-volume increments. It has been shown that subsample increments with smaller volumes will not hide small organisms thereby producing better sorting results. Partitioning a sample into large and small size components can also produce better sorting results in the following manner: 2.0mm sieve can be nested above the 0.5mm sieve to partition the sample into large and small sized particle fractions to facilitate the sorting process.

2.2.3 The entire sample is to be sorted. If an unusual sample is encountered for which sorting of an aliquot may be a reasonable alternative, the laboratory supervisor is to contact the Bight '23 Benthic Committee Co-Chairs. The decision whether to allow sorting by aliquot will be made by the Benthic Committee Chair and Co-chair.

2.2.4 ELUTRIATION**.** If a sample is primarily coarse sand, sorting can be greatly facilitated if inorganic material in the sample is separated from the lighter organic grunge and organisms by the following elutriation process.

2.2.4.1 After washing the ethanol from the sample, spread the sample material out in a shallow pan and cover with water.

2.2.4.2 Gently agitate the sample by hand to allow the lighter fraction of grunge and organisms to separate from the heavier material.

2.2.4.3 Decant the water containing the lighter material through the sieve. Repeat the process several times until no more material is observed being carried off in the decanted water.

2.2.4.4 Collect the material retained on the sieve into a small sample container, and top-off with preservative. Return remaining material to the original sample container along with the balance of the sample material. Fill the container with preservative and tightly affix the lid. Be sure that both containers are properly labeled with internal labels.

2.2.5 All sorting must be done in 70% ethanol, except for sorters where health and safety issues exist, with care taken to ensure that the sample being sorted is always fully covered with alcohol. If necessary, sorting may be performed using water, but care must be taken to minimize the time when specimens are not in 70% ethanol. Samples may not be left over night in water, as specimens may degrade. Samples must be placed back into 70% ethanol at the end of each day. For large samples, only placing into water that portion to be sorted in a day's time is advisable.

2.2.6 The organisms removed from the sample are sorted into taxonomic lots for subsequent taxonomic analysis. Each laboratory will determine the taxonomic level of sorting adequate to their needs for subsequent sample analysis by their taxonomists.

2.2.7 Remove all individual organisms and fragments from the sample with the exception of nematodes, foraminiferans and planktonic species, or planktonic life stages of benthic organisms. All fragments, such as decapod chelae and legs, should be placed in their respective taxa lots. Sorters are to be instructed "***If in doubt, pick it out.***"

2.2.8 Note on the Macrofauna Sorting Sheet (page 29) the number and identity of taxa lots composing the sorted sample, the number of containers used if sample is split, and the time (to the nearest ½ hour) required to sort the sample.

2.2.9 Sorters will be required to count animals (head ends) while sorting and note the number on the Macrofauna Sorting Sheet, unless 100% resort of the sample is conducted. This facilitates sorting quality control by providing a number for comparison of QC re-sorting results (Section 5.5).

2.2.10 Sorters are asked to not remove animals from their tubes. At most, the sorter is asked to verify that a tube has an animal inside. That said, it is better to be precautionary and include a tube in the appropriate lot if there is risk in damaging a specimen in the process of verifying the tube is/was occupied. This is the same for shelled molluscs. The sorter should not damage the shell, e.g., snip away at the aperture, to determine whether there is an animal within.

2.2.11 Aggregate the taxa lots into one or more sample containers. Each taxa lot should be internally labeled with the station name, sampling date, station depth, and sorter's initials. Place an internal label in each vial/container with this information and split number (i.e., 1 of 2, 2 of 2) if more than one container is used. Labels are to be written in pencil on 100% rag-paper. Minimally, the material must be segregated into the following taxa lots:

Annelids
Annelid fragments
Arthropods
Echinoderms (non ophiuroid)
Ophiuroids
Ophiuroid arms (optional, but recommended)
Molluscs
Misc. Phyla (*e.g., *Cnidarians, Nemerteans)

Note that if any darkly pigmented echiurans are encountered during sorting, they can be segregated into a separate vial rather than being placed with other annelids. This optional step would prevent the pigments from leaching out and obscuring characters of the other annelids.

3. TAXONOMIC ANALYSIS

3.1 The object of taxonomic analysis is to accurately identify all organisms contained within each sample to the lowest possible taxonomic category and to provide an accurate count of the organisms in each identified taxon.

3.2 The goal of the Bight '23 infaunal survey is to provide species level identifications whenever possible. However, because of difficulties in the taxonomy and the lack of expertise within participating laboratories the following exceptions are made:

Kinorhynchs are identified to Phylum Kinorhyncha
Oligochaete annelids are identified to Subclass Oligochaeta
Hirudinean annelids are identified to Subclass Hirudinea
Podocopid ostracods are identified to Order Podocopida
Harpacticoid copepods are identified to Order Harpacticoida
Insecta arthropods may be identified to Subclass or Order

3.3 The number of organisms reported must account for all organisms in a sample alive at the time of collection. A corollary goal is to not count any individual more than once. Inevitably, samples contain fragments of organisms. Fragments of bilaterally symmetrical organisms will be identified and counted only if the fragment includes the anterior end of the organism. For radially symmetrical organisms (e.g., ophiuroids, anthozoans) only fragments bearing the majority of the oral disk will be identified and counted. Also, care must be taken to avoid reporting empty mollusc shells or crustacean molts in the data.

3.4 The goal of the survey is to describe the macroinvertebrate infauna and epifauna living in soft-bottom habitats. Hard-bottom epifaunal organisms may occur incidentally in samples, particularly in settings where samples are collected immediately adjacent to hard structures (e.g., in harbors near piers). As any records of these incidental contaminants would not be included in the analytical use of the data, these specimens are not to be counted nor included in the submitted survey data. Their presence may be noted on the bench sheets.

3.5 Attached parasites and other epibionts may be noted on the bench sheet as present but are not to be reported in the submitted survey data. Ectoparasites of fish such as cymothid isopods, which may be temporary members of the benthic community, are counted and reported in the submitted survey data.

3.6 Each participating laboratory will use their own taxonomy bench sheets for recording the identifications and counts.

3.7 Nomenclature and orthography follows that used in *A Taxonomic Listing of Benthic Macro- and Megainvertebrates from Infaunal and Epibenthic and Research Monitoring Programs in the Southern California Bight*., Edition 14 (SCAMIT, 2023). This list represents a consensus for standard usage of taxa names in the monitoring programs of the Southern California Bight.

3.8 Taxonomists are to employ three standard notations (*Voucher, Personal Voucher,* and *Exclude*) for the annotation of their bench sheets. While other non-standard notation may also be used, the use of these standard notations is required where applicable. In addition, both the
Voucher and Exclude codes will be included as part of the electronic data record. See the Bight '23 Information Management Plan for the proper form of these fields for data submission.

3.9 Voucher Notation

3.9.1 *Form*: The annotation employed for this purpose on the bench sheet is the letter V followed by the number of specimens removed from the sample. (i.e., V-3)

3.9.2 *Purpose*: To note the removal of specimens from a sample for use as Bight '23 vouchers. Use of this notation on the bench sheet is essential to the process of tracking voucher records and quality control/assessment. Removal of organisms without annotation confuses the resolution of discrepancies during quality control re-analysis and leads to overstatement of error rates. Inclusion in the electronic data submission allows a complete list of Bight '23 vouchers to be extracted from the data.

3.9.3 *Rule of Use*: Removal of any specimens from a sample to the Bight '23 Voucher Collection is clearly noted on the bench sheet by means of the Voucher notation.

3.9.4 In addition to the voucher specimens required for the Bight '23 Voucher Collection (see 5.6 below), individual labs or taxonomists may remove specimens of each taxon for their own voucher collections (note on data entry sheet). The removal of this material must also be clearly noted (by means other than the voucher notation) on the bench sheet in order to account for their effect on quality control re-analysis. The following example would satisfy the requirement for clear notation:

"V-2, HY-1 voucher"

indicating 2 specimens removed to the Bight '23 Voucher Collection and 1 specimen to Hyperion's collection.

3.9.5 The voucher notation will be included as part of the electronic data record submitted by each laboratory. See the Bight '23 Information Management Plan for the proper format for its inclusion in the data file. Separate columns will be available to denote whether a specimen was vouchered and the number of organisms in the Bight '23 voucher collection and that of the individual lab or taxonomist's voucher collection.

3.10 Exclude Notation

3.10.1 Form: The letters "EX" written on the row of the bench sheet containing the data record for the taxon to be excluded

3.10.2 Purpose: Provides an aid to data analysis when calculating metrics using the number of taxa present (e.g., diversity, species richness). This field in the final data set represents the taxonomist's recommendation that the reported taxon be excluded from counts of the number of taxa reported in the sample.

3.10.3 Rule of Use: The Exclude annotation is made on the bench sheet whenever a taxon should be excluded from counts of the number of taxa reported in the sample. This annotation is employed when three conditions co-exist:

The identification is not at the species-level (e.g., Pleustidae or *Polydora* sp),
And
The reported taxon is represented in the sample by other members of the same taxon, which have been identified at lower levels,
And
The taxonomist cannot determine if the specimen is distinct from the other members of its taxon represented in the sample.

3.10.4 Examples of Use:

Both *Dipolydora* sp and *Dipolydora socialis* are reported in a sample and the taxonomist cannot determine if the specimen reported as *D.* sp is distinct from *D. socialis*. Exclude (annotate record on bench sheet with **EX**)

An unidentifiable onuphid polychaete is reported as Onuphidae. It is the only member of its family present in the sample. **Do Not** Exclude

Both *Modiolus* sp and *Modiolus capax* are reported in a sample. However, the taxonomist is confident that the specimen identified at the genus-level is not *M. capax*. **Do Not** Exclude

3.10.5 It is necessary that the taxonomists make this evaluation during sample analysis (i.e., by annotation of the bench sheet). It cannot be effectively applied after the fact, as there is no way of determining later whether the third criterion for use was

met.

3.10.6 The Exclude notation will be included as part of the electronic data record submitted by each laboratory. See the Bight '23 Information Management Plan for the proper format for its inclusion in the data file.

3.11 Temporary "in-house" provisional names are erected for those specimens that a taxonomist considers to be distinctive but cannot match with an existing description or other provisional name on the SCAMIT Ed 14 Species List. These provisional names act as markers for these taxa, allowing them to be consistently discriminated in the samples for which the taxonomist is responsible. In-house provisional names are supported by a written differential diagnosis (and figures if necessary) sufficient to allow taxonomists in the other participating laboratories to recognize the species. These diagnoses must be sent to other taxonomists participating in the survey. If provisional descriptions are not circulated among the taxonomists, the provisional name will not be valid for Bight purposes and removed during synoptic data review. The provisional name is formed from the lowest taxon name in which the specimen may be placed with certainty followed by a composite name containing the laboratory's character code (see below) and a number; for example, *Rhachotropis* sp LA2 or Ampharetidae sp SD1. Note there is no space between the agency code and the identifying number.

Lab Name	*Lab Code*
ABC Labs	AB
Weston	WS
CLAEMD	HYP
CSD	SD
LACSD	LA
OCSD	OC
MBC	MB
DCE	DCE
EcoAnalysts	EA

3.12 Timely and frequent communication among the taxonomists analyzing the samples will improve the data produced in the survey. The SCAMIT listserv (general_topics@discussion.list.scamit.org) will be used to facilitate this communication. All taxonomists involved in the Bight '23 survey will be members of the list. If you need help getting on or have problems you can contact Erin Oderlin at erin.oderlin@lacity.org. Messages posted to the list will automatically post to all members, assuring wide and uniform distribution of the contents. Names and e-mail addresses of all taxonomists processing Bight '23 samples will be provided by each participating laboratory to the Bight '23 Benthic Committee Co-Chairs before sample collection begins, or in the case of qualified taxonomists joining after sample processing begins, as soon as possible. List-server messages are archived and available to all list-server members. They will be available for review at least until the Bight '23 Benthic Report is published.

3.13 Appropriate uses of the list server are informing the other members of unusual or newly

encountered species, the erection of in-house provisionals, and requests for information or assistance.

3.14 Messages posted to the list-server should always include in the subject line the critical topic taxon (if any) to which the posting refers followed by a referent higher taxonomic category in parentheses. The subject line should also include phrase "Bight'23" or B'23. For example:

Balanoglossus (Hemichordata); Bight'23
or
Guernea sp MB1 (Gammaridea: Dexaminidae); B'23

3.15 Following identification and enumeration, all the specimens are retained in taxa lots within the sample. Minimally, the material must be segregated into the following taxa lots:

Annelid lots:	***Arthropod lots:***	***Molluscan lots:***
Oligochaeta	Arthropoda	Mollusca
Misc Polychaetes		
Polychaete frags		

Echinoderm lots:	***Misc. Phyla lots:***
Ophiuroidea	Misc Phyla (a collective lot)
Ophiuroidea arms	
Misc Echinoderms	

This level of separation facilitates the quality control process and eases both the burden of re-analysis resulting from failure of a laboratory to meet the measurement quality objective and the recovery of material during the end-of-survey synoptic review. In addition, any taxon subject to specialty taxonomic treatment is to be segregated into a lot for delivery to the designated specialist.

Further segregation of all polychaetes at the family level has been found useful and is recommended.

3.16 All taxa lots within a sample are provided an internal label with the program designation (*i.e.,* B'23), taxa lot name, station name and depth and taxonomists initials. These taxa lots are contained in vials and all of the lots in a sample are aggregated into one or more sample containers. If a taxa lot includes bulky specimens, they may be placed loose in the sample container (accompanied by a loose label) along with the vials containing the remainder of that and other taxa lots. An internal label is placed in each sample container bearing the program designation (*i.e.,* B'23), station name, sampling date, depth, and split number (if more than one container is used; e.g., 1of 2). Labels are written in pencil on 100% rag-paper, for permanent wet labels. Each laboratory will retain bulk taxa sample lots until informed by the Benthic Committee Chair (or designee) that they may be discarded. This will be at a point in time 5 years after completion of the project or 6

months after the final version of the B'23 Benthic Report is released, whichever occurs first.

4. DATA SUBMISSION AND THE FORM OF TAXONOMIC NAMES

4.1 All data submissions must meet the formatting requirements of the Bight'23 Information Management Plan. Data should be submitted electronically to the SCCWRP Bight '23 Benthic Data Portal:
http://bight-sccwrp.opendata.arcgis.com/pages/bight-2023-infauna

4.2 In particular, it is essential that all taxon names be standardized in spelling and form. Because the "taxon" field is one of the key fields for defining a unique record, exactitude is required.

4.3 To minimize the problem of variants, a standard for the spelling and formation of names has been specified prior to the survey. This standard is based on *A Taxonomic Listing of Benthic Macro- and Megainvertebrates from Infaunal and Epibenthic Monitoring and Research Programs in the Southern California Bight*, Edition 14 (SCAMIT, 2023) and the M-AMBI taxa list (after Gillett et al. 2015). The full Edition 14 document will be available at the SCAMIT website (www.SCAMIT.org).

4.4 The name used to represent a taxon should be that listed in the SCAMIT Taxonomic List. If the taxon has not previously been reported in the region and is consequently not on the SCAMIT List, it may still be reported. Taxonomic usage should follow that in WoRMS (http://www.marinespecies.org/) and the primary literature. To facilitate easy upload of the data, provide a file of unlisted name and full details (taxonomic hierarchy, authorship, etc) you plan on submitting to the chair of the Benthic Committee prior to submission of the sample data. This will allow for updating of the datacheckers.

4.5 The following examples of data submission problems from past surveys are included to emphasize the importance of adhering to the Information Management Plan requirements for submission of taxonomy-based data.

4.5.1 The species field is to contain taxon names only. Do not include citation of authorship, comments or other information

As Submitted	***Should Have Been***
Anthozoa, unid.	Anthozoa
Bugula neritina (colonial)	*Bugula neritina*
Enopla sp A SCAMIT 1995	*Enopla* sp A
Heteroserolis n. sp.?	*Heteroserolis* sp
Tubulanus polymorphus/pellucidus	*Tubulanus polymorphus*
frags only	not submitted

4.5.2 The taxon field is to contain formal scientific taxon names only. Do not use common names or anglicized forms

As Submitted	***Should Have Been***
Cirriped	Cirripedia
megalopa	Decapoda (*note the larval stage*)
fish	*a specific fish taxon (at any level)*

4.5.3 The form (spelling, punctuation) of the names are to follow the SCAMIT Taxonomic listing. Note that the SCAMIT list avoids all forms of punctuation (other than parentheses around subgeneric names) within a taxon name.

As Submitted	***Should Have Been***
Scoloplos "*armiger*"	*Scoloplos armiger* Cmplx
Semele sp.	*Semele* sp
Aphelochaeta spp	*Aphelochaeta* sp
Scolelepis texana	*Scolelepis (Parascolelepis) texana*

4.5.4 In forming or using provisional names based upon the agency code, do not include a space between the agency code and the number. When submitting a provisional name, first contact the Benthic Committee Co-Chairs with a list of provisional names to be submitted. They will provide guidance on the suitability of the name(s) and ensure it is added to the data checkers. Doing this prior to submission of data will prevent rejection of the data by the system due to the provisional names not yet being in the data checkers look up list.

As Submitted	***Should Have Been***
Anobothrus sp LA 1	*Anobothrus* sp LA1
Malmgreniella sp SD 3	*Malmgreniella* sp SD3

4.6 **ENCOUNTERED SPECIES LIST:** All submissions are to be accompanied by an encountered species list providing the taxon name and, for species level names (including provisional taxa), authorship citation. These lists will facilitate the recognition of variant forms within the compiled data set and, more importantly, the cases of potential or real homonymy or synonymy. A comments column is provided to submit additional information that may be of value in evaluating the list entries.

4.6.1 The encountered species list should contain every unique taxon name occurring within the data being submitted.

4.6.2 The encountered species list should be in the form of a four column Excel worksheet with the following format (see example below):

Column A = Taxon
Column B = Authority (*for species-level taxa*)
Column C = Lab (*the Bight '23 Information Management Plan Agency code*)
Column D = Comments

4.6.3 The list should be sorted alphabetically by taxon name

Taxon	Authority	Lab	Comment
Acanthina sp		WS	
Acanthomunna tannerensis	Schultz, 1966	WS	
Acanthoptilum sp		WS	
Acila castrensis	Hinds 1843	WS	
Aclis sp		WS	
Acoetes pacifica	Treadwell 1914	WS	
Acontifera sp A	Ljubenkov 2010	WS	
Acrocirridae		WS	
Acteocina cerealis	Gould 1853	WS	
Acteocina culcitella	Gould 1853	WS	
Acteocina harpa	Dall 1871	WS	
Acteocina inculta	Gould 1855	WS	
Actiniaria		WS	
Actiniaria sp 49	Ljubenkov 2003	WS	
Acuminodeutopus heteruropus	J. L. Barnard 1959	WS	
Adontorhina cyclia	Berry 1947	WS	
Adontorhina lynnae	Valentich Scott 2000	WS	
Aeolidioidea		WS	
Aglaophamus erectans	Hartman 1950	WS	
Aglaophamus verrilli	McIntosh 1885	WS	
Alaba sp		WS	
Alderia willowi	Krug, Ellingson, Burton and Valdés 2007	WS	
Alia carinata	Hinds 1844	WS	
Alpheidae		WS	
Alpheus californiensis	Holmes 1900	WS	
Alpheus sp		WS	
Alvania rosana	Bartsch 1911	WS	
Alvania sp		WS	
Amaeana occidentalis	Hartman 1944	WS	
Amage anops	Johnson 1901	WS	
Amakusanthura californiensis	Schultz 1964	WS	
Amathia sp		WS	
Ambidexter panamensis	Abele 1972	WS	
Americhelidium rectipalmum	Mills 1962	WS	
Americhelidium shoemakeri	Mills 1962	WS	
Americhelidium sp		WS	
Americhelidium sp SD1	Pasko 2005 §	WS	
Americhelidium sp SD4	Pasko 2005 §	WS	
Americorophium salmonis	Stimpson 1857	WS	
Ammothea hilgendorfi	Böhm 1879	WS	
Ampelisca agassizi	Judd 1896	WS	
Ampelisca brachycladus	Roney 1990	WS	
Ampelisca brevisimulata	J. L. Barnard 1954	WS	
Ampelisca careyi	Dickinson 1982	WS	
Ampelisca coeca	Holmes 1908	WS	
Ampelisca cristata cristata	Holmes 1908	WS	
Ampelisca cristata microdentata	J. L. Barnard 1954	WS	
Ampelisca hancocki	J. L. Barnard 1954	WS	
Ampelisca indentata	J. L. Barnard 1954	WS	
Ampelisca lobata	Holmes 1908	WS	
Ampelisca milleri	J. L. Barnard 1954	WS	
Ampelisca pacifica	Holmes 1908	WS	
Ampelisca pugetica	Stimpson 1864	WS	
Ampelisca romigi	J. L. Barnard 1954	WS	
Ampelisca sp		WS	
Ampelisca unsocalae	J. L. Barnard 1960	WS	

Example of a partial encountered species list for submission

5. QUALITY CONTROL

5.1 The laboratory analysis of infaunal samples for Bight '23 involves three processes: sample washing and preservation, sample sorting, and organism identification and enumeration. Quality assurance in the form of procedures and standardized reporting requirements are provided in this document for all three processes. Quality control exercises will be implemented at stages for which MQOs have been established (sample sorting, identification and enumeration). These exercises include repeating the procedures at each of these stages for a sub-set of samples. The results will be used to determine achievement of the MQOs established for each stage.

5.2 For the most challenging process, organism identification, additional quality control steps are included in order to foster comparability among the taxonomic data sets produced by the participating laboratories and taxonomists

5.3 Where warranted, the Benthic Committee Co-Chairs (or designee) may conduct audits of each laboratory while sample analysis is underway to assure that the Bight '23 procedures are being followed.

5.3.1 An audit would be invoked in those cases where there was evidence of consistent mistakes or QC failures in sorting or taxonomic identification; indicating that "best practices" are not being followed in a given lab (See sections 2 and 3).

5.3.2 The audit could entail, among other things, a review of documented corrective actions by the internal QC person/lab manager, requests for external re-identification or re-sorting, or demonstration of improvement.

5.4 Sample Sorting

5.4.1 Quality control of sorting is essential to assure the value of all the subsequent steps in the sample analysis process. An accuracy MQO of 95% removal efficiency has been set for this stage of the sample analysis.

5.4.2 A standard sorting form (page 29) is used for tracking the sample. It includes the name of the sorter, time required for sorting, comments, and re- sorting results. Re-sorting of samples is employed for quality control of sorting.

5.4.3 A minimum of 10% of all material in Bight '23 samples will be re-sorted to monitor sorter performance and to determine achievement of the MQO of 95%. In practice, the minimum 10% of all material stipulation will be achieved by the evaluation of each sorter via the aliquot method (sections 5.4.4-6).

5.4.4 Sorting efficiency should be assessed following the ***aliquot method***, wherein a representative aliquot of at least 10% of the sample volume of every sample processed is re-sorted by an experienced sorter who is different than the original sorter. Re-sorting of a higher percentage of a sample may be required or optionally performed to ensure MQO performance.

5.4.5 Aliquots may be obtained by standardizing the sample volumetrically, for example by stirring and then withdrawing 10% of the sample with a Hensen-Stemple pipette. Alternatively, the grid method can be used. This is accomplished by spreading the sample evenly in a gridded shallow pan and selecting a random10% of grids/cells for re-sort. The responsible supervisor of each participating laboratory selects the method of obtaining a sample aliquot.

5.4.6 The re-sorting process is to follow the procedures given in Section 2 of this document.

5.4.7 Percent sorting efficiency is calculated as follows:

$$\%_{Efficiency} = 100 * \{\#_{orig} / [\#_{orig} + (\#_{resort} / \text{aliquot fraction})]\}$$

5.4.8 If sorting efficiency is greater than 95%, no action is required. Sorting efficiencies below 95% will require continuous monitoring (e.g., 100% resorting) of that technician until efficiency is improved.

5.4.9 Organisms found in the re-sort should be given to the appropriate taxonomist for identification and enumeration for inclusion in the results from the sample.

5.4.10 The calculated sorting efficiency is recorded on the Macrofauna Sorting Form for each sample (page 29) for which QC re-sorting is conducted. All sorting sheets should be scanned as a pdf and emailed to the Benthic Committee Co-Chairs.

5.4.11 The laboratory responsible for the sorting must retain sample grunge after sorting. It is to be properly labeled and preserved with 70% ethanol. Upon completion of all quality control and assessment steps for the survey, including taxonomic re-analysis and discrepancy resolution (Section 5.5), the Benthic Committee Co-Chairs (or designee) will notify each participating laboratory that the sample grunge may be prepared for transport to Dr. Susan Kidwell of the University of Chicago.

5.5 Quality Control and Quality Assurance of Taxonomic Analysis

5.5.1 The goal of taxonomic analysis for the Bight '23 infaunal survey is species level identification of all macrobenthic organisms collected and an accurate count of each species. The procedures for sample re-analysis are based upon those developed and employed in previous Bight surveys. This task is complicated by the participation of multiple laboratories and taxonomists in the analysis. Two approaches are taken for providing data quality control. The first is an assessment of each laboratory's accuracy by re-analysis of a subset of samples from each laboratory. The second focuses on ensuring consistent and comparable results among the participating taxonomists through cooperative activities under the aegis of SCAMIT.

5.5.1.1 Participation in SCAMIT involves, but is not limited to, attending monthly meetings and workshops whose topic related to a taxonomist's area of responsibility or expertise (e.g., polychaetes, arthropods, Mollusca, etc.). In addition, participation on ad hoc committees (e.g., Species List Review Committee), while not required, is strongly encouraged. In instances where multiple taxonomists at a laboratory have the same specialty, a single representative may fulfill the SCAMIT meeting attendance requirement for all by transmitting the meeting's contents to the other taxonomists in the laboratory.

5.5.1.2 Failure to comply with these standards (i.e., missing 2 or more meetings covering a taxonomist's area of expertise/responsibility during the Bight '23 taxonomic identification period) can result in disqualification of that taxonomist or taxonomic laboratory from Regional Monitoring Program participation. Any determination will be made by the Benthic Committee Co-Chairs after consultation with the SCAMIT officers. Logs of SCAMIT meeting attendance will be documented in the SCAMIT minutes and newsletter. They will be provided upon request to the Benthic Committee Co-Chairs.

5.5.2 Quality control is provided by the re-identification of 10% of the samples processed by each laboratory. Samples for re-identification are selected randomly from each lab's assigned set of samples by the Bight '23 Benthic Committee Co-Chairs or designated QC Officer and re-distributed to the QC laboratories.

5.5.3 The re-identification will be conducted at participating QC laboratories or by taxonomists other than those who originally analyzed the samples. The taxonomists conducting the re-identification will not have access to the original results.

5.5.3.1 Some taxonomy labs serve as consortiums of disparate taxonomists working in separate locations rather than a group of taxonomists working together in a single location or laboratory.

5.5.3.2 Under special circumstances to expedite the re-identification procedures, taxonomists from the same taxonomic consortium may be authorized to conduct the re-identification of samples for QC purposes. **This is considered only on a case-by-case basis and may only occur with vocal approval of the entire Bight Benthic Committee**. Re-identification should proceed as detailed from steps 5.5.4 and forward.

5.5.3.3 The laboratories or agencies responsible for the samples to be QC'd must provide assurances that QC taxonomists are truly separated from initial taxonomists. If assurances cannot be maintained, then the agency/laboratory responsible for the samples are obligated to provide QC by a separate lab, in a more traditional fashion.

5.5.3.4 In general, this "within consortium" approach to re-identification is discouraged, as it complicates application of available taxonomic resources for either the initial or QC identification process.

5.5.4 Each laboratory's supervisor will be informed by the Bight '23 Benthic Committee Co-Chairs or designated QC Officer which samples are to be re-identified. The laboratory supervisor is responsible for assuring that these samples are made available to the laboratory responsible for re-identification in a timely manner.

5.5.5 The specimens in each sample will be re-identified and enumerated using the procedures given in Section 4 of this document. Results are reported on the QC laboratory's bench sheet. Upon completion of the re-analysis, the results are submitted to SCCWRP and a match/not match comparison of primary and secondary results will be produced for the reconciliation process.

5.5.6 The taxonomists of the laboratories involved compare the original results to those of the re-analysis. All results are listed on the match / not-match spreadsheet (page 31). A copy of this match / not-match spreadsheet is sent to the laboratory responsible for the original analysis.

5.5.7 The primary and QC labs will reconcile discrepancies and record results on the match / no-match spreadsheets produced by the committee co-chairs (pages 31-32). Columns A-N and X-AE are pre-filled by the Bight Infauna Database. Columns B and C contain the StationID and Replicate information identifying the sample. Columns D-H contain the initial ID information, including records of Bight vouchers and personal vouchers. Columns I and J contain the reID taxonomic information. Columns K-N concern differences between the initial and reID for each taxon, including the abundance (K), the direction of any count difference respective to the initial counts (M), whether the initial and

reID records match in abundance **and** identity (L), and the nature of any disagreement (ID or Count) between the initial and reID data (N). Columns O-T are filled in during the resolution process, recording the lines of data involved in reconciliation (O), the discrepancy classification (P), resolution code (Q),the resolved taxon name (R) the resolved abundance (S), and any pertinent notes (T).

5.5.8 Discrepancies will be discussed and final resolutions determined through meetings between primary and QC laboratories. To facilitate this process, two to four SCAMIT/Bight '23 workshops will be scheduled in which taxonomists will jointly meet for discrepancy resolution. Significant discrepancies in count (±10% of original count) are resolved by a third count performed by the QC lab.

5.5.9 The nature and resolution of discrepancies are recorded on the match / not-match spreadsheets using discrepancy classification and resolution codes detailed on Form B23-3 (page 33). Error types (true, random, non-error), and recommended QC remedial action (training, review best practices) are presented for each resolution code. The naming convention discrepancy code refers to differences in name usage and/or spelling. The variation in level of expertise resolution code notes differences in knowledge or standard practice between taxonomists when addressing especially difficult taxonomic groups or damaged/juvenile specimens.

5.5.10 While completion of this spreadsheet is the responsibility of the QC laboratory, both labs must work together to reach agreement. If agreement cannot be reached, arguments are presented to the Bight'23 Benthic Committee Co-Chairs (or designee) for a decision. The Co-Chairs may seek assistance from SCAMIT members or other experienced taxonomists in reaching a decision.

5.5.11 Once resolution and explanation of all discrepancies has been completed, the Resolution Spreadsheet is emailed to the Bight '23 Benthic Committee Co-Charis or designated QC Officer. Copies of all reports and bench sheets are to be retained by both laboratories for the duration of the survey and final publication of the Benthic Infauna report.

5.5.12 The Bight '23 Benthic Committee Co-Chairs or designated QC Officer reviews the results submitted, discusses with the laboratories any issues needing clarification or arbitration.

5.5.13 The Bight '23 Benthic Committee Co-Chairs or designated QC Officer is responsible for completing the rest of the form, including columns U-W, reviewing the discrepancy classifications and resolution codes, and determining the effect of the resolution (increase, decrease, or no change) on the number of taxa and the organism count reported in the original results.

5.5.14 The tallies in columns U-W are used to calculate the % error of the original laboratory's analysis. Percent error will be calculated for three aspects of sample analysis: 1.) taxa discriminated ($\%Err_{\#\ Tax}$); 2.) count accuracy ($\%Err_{\#\ Orgs}$); and 3.) identification accuracy ($\%Err_{ID}$). Results would be presented on the Infauna QC Report (page 33). The three QC MQO efficiency equations assess taxonomic performance. Efficiency percentages are calculated by individual station, aggregate QC station average, and overall performance and presented on an Infaunal QC Report page (page 33). The Taxa Discriminated equation calculates overall sample speciation accuracy. The Count Accuracy equation addresses abundance accuracy of a sample. The third equation, Identification Accuracy, assesses accuracy errors caused by misidentifications at a station.

5.5.15 The error rates are calculated as follows:

1. Taxa Discriminated = $\{1 - [\ ABS(\#\ Taxa_{\ Resolved} - \#\ Taxa_{\ Original}) / \#\ Taxa_{\ Resolved}]\} * 100$
2. Count Accuracy = $\{1 - [ABS\ (\#\ Individuals_{\ Resolved} - \#\ Individuals_{\ Original}) / \#\ Individuals_{\ Resolved}]\} * 100$
3. Identification Accuracy = $[1 - (\#\ Individuals_{\ Mis\text{-}ID'd} / \#\ Individuals_{\ Resolved})] * 100$

The efficiency target for QC assessment is ≥ 90.0%. A score below 90% will result in corrective actions. Specific problem areas in taxonomy will be identified and reviewed by the original taxonomist to determine why an identification error was made. Training materials will be reviewed and updated as necessary to improve future performance. Likely reasons for counting errors will be determined and solutions for improvement determined through review of best practices and laboratory methods.

Corrective action for samples (laboratory and/or taxonomist) that do not achieve a >90% accuracy for equations #1 and #2 involves a review of best practices.

Equation #3 is the preferred measure of identification accuracy because it accounts for correct species identification weighted for abundance.

In order to determine whether misidentifications highlighted by the QA process was due to taxa being consistently misidentified rather than an isolated incident, a reanalysis is conducted on a minimum of 2 samples containing the highest number of the affected taxa identified by those taxonomists making the errors. If no further errors in identification are uncovered, then the original discrepancy is considered to be an aberration and no additional action is taken. However, if the error(s) is repeated in these subsequent samples, the process continues for all samples containing that taxon and additional, targeted, training is recommended.

Equation #3 is also reported for whole samples with the same 90% threshold. Samples that meet this threshold are considered to have high quality data; while those that do not are identified as being suspect, as are all the samples from the respective laboratory and taxonomist. Moreover, this taxonomist and/or taxonomic laboratory will need to demonstrate corrective action and competency before participation in subsequent Bight Surveys. Corrective actions can be recommended by the Benthic Committee Co-Chairs and appropriate SCAMIT members.

5.5.16 An MQO of 90% has been established as the maximum allowable deviation from the "true" value for taxonomic richness, taxonomic accuracy, and total abundance. These MQOs were empirically derived by systematically

introducing taxonomic and abundance errors into macrobenthic datasets and measuring the response of assessment scores/category and general community structure (Ranasinghe *et al*. unpub.). Acceptable deviations in these benthic response metrics were decided upon by the Benthic Committee and corresponded to 90% accuracy in taxon identity and abundance.

5.5.17 In addition to providing for an assessment of analytical accuracy, this process provides information for the end-of-survey SCAMIT/Bight '23 Synoptic Data Review of the data set compiled from the participating laboratories.

5.5.18 A voucher collection must be created of all species identified in Bight '23 samples either by the laboratory, or by each participating taxonomist. These collections are separate from the laboratories' existing voucher collections and will be the source of material from which is drawn a common Bight '23 voucher collection upon completion of the survey. These collections provide material for review during SCAMIT/Bight'23 workshops and the Synoptic Data Review upon completion of analysis.

5.5.19 The voucher collections are to contain specimen lots of one or more individuals of each reported taxon. The specimens are to be representative of the taxon. At the taxonomist's discretion, more than one specimen lot may be added to the collection. This is particularly appropriate when differences in specimen maturity or within-taxon variability need representation. Only those taxa discriminated to the species-level (or stipulated higher level e.g., Oligochaeta) are to be included in the collection. Species-level identification is considered to include provisional species and conditional taxa. Tentative identifications, as indicated by "?" are not to be represented. See Section 3.10.

5.5.20 Only 1/2, 1, 2, and 4 dram glass shell vials are to be used for the storage of the voucher specimens, unless specimens are inappropriate for wet storage. Larger specimens are put into appropriately sized straight-sided jars with screw cap lids and Teflon liners or equivalent (e.g., Green Thermoset Screw Caps, Fluoropolymer Resin Liner, Qorpak). Shell vials are stoppered with 100% cotton (not rayon or other synthetic fiber), and placed in a larger 4 or 8 dram vial that can accommodate the vial containing the specimen(s). In the larger shell vial containing the smaller vial should be a label with the unique station identifier and the complete taxon name, a count of the number of specimens in the lot, the analytical laboratory's designation (OC, HYP, *etc.*), and the identifying taxonomist's first initial and last name spelled out.

The use of shell vials for all specimens other than large species will facilitate the consolidation of the voucher collections upon completion of the survey. Keeping the specimen(s) separate from the label prevents damage to the specimen and speeds specimen examination. The Natural History Museum of Los Angeles County (NHM) will prepare complete locality and specimen data labels from the Bight '23 database once specimens are received at the NHM and these will be associated with each specimen lot. An example label:

B'23 *Station number*		*Agency Code*
Genus	*species*	count
Taxonomist name (first initial last name)		ID

5.5.21 Labels are written in pencil on 100% rag-paper.

5.5.22 After the vouchering needs of the Bight'23 survey are met, individual labs or taxonomists may remove a reasonable number of specimens for their own voucher collections. This activity is separate from and subordinate to the Bight'23 vouchering requirement. Unique specimens must be reserved for the Bight'23 voucher collection.

5.5.23 After the completion of analyses and publication of reports, vouchers will be transferred to the Benthic Committee Co-Chairs (or designee) at SCCWRP, or directly to the Natural History Museum of Los Angeles with accompanying electronic versions of collecting permits. The vouchers will be incorporated into the Museum's invertebrate holdings. Specimens can be retrieved for further analysis following the standard protocols of the museum. Vouchers of tentatively identified taxa that are not resolved at the time of publication of the Bight reports will also be transferred to the NHM. These specimens will be similarly available for future study. For those taxa determined to be new to science and the discovering taxonomist wishes to publish, in a timely manner, a formal description they may petition the committee to retain the specimen(s) with the understanding that all material including Types will be deposited at NHM.

5.5.24 Taxonomists from the participating laboratories are **required** to participate in special SCAMIT/Bight '23 workshops. Workshops prior to the sampling period focus on the taxonomy of groups identified as potentially problematic to promote uniform treatment in the upcoming survey. The workshops provide training, pooling of regional resources, and designation of the local expert(s) to be called upon for assistance during sample analysis.

5.5.25 After sample analysis has begun, SCAMIT/Bight '23 workshops will be scheduled to address taxonomic problems arising during analysis of the Bight

'23 samples. All taxonomists participating in the survey are required to attend the meetings relevant to the organisms they are tasked with identifying. Furthermore, they are encouraged to attend all of the meetings, regardless of subject, when possible. At these meetings, diagnoses of any "in-house" provisional taxa erected by any of the laboratories will be distributed to the other participants and assistance sought to resolve their identity. Those specimens considered new to SCAMIT will be noted for possible inclusion in the next edition of the species list. Provisional taxa can also be considered for inclusion pending a formal voucher sheet published in the SCAMIT Newsletter (https://www.scamit.org/documents/SCAMIT%20Provisional%20Voucher%20Sheet%20Guidelines_2022.pdf). All decisions about proposed additions to the SCAMIT Species list are the purview of the Species List Review Committee (SLRC). Requirements for inclusion in future lists are outlined in the introductory material found in Edition 14.

5.5.26 The series of SCAMIT/Bight '23 workshops culminates in a Synoptic Data Review of the data set compiled from the submissions of all participating laboratories, and investigation of possible inconsistencies revealed in that process (including examination of voucher specimens or sample lots as needed for resolution). This review also draws upon the results of the quality control re- analysis of 10% of the samples analyzed by each laboratory. All participating taxonomists, including specialty taxonomists, are required to attend the Synoptic Data Review.

6. RECORD KEEPING AND PROCEDURAL RESPONSIBILITY

6.1 Each laboratory is responsible for maintaining thorough and complete records through all stages of the sample analysis and QC procedures. Each laboratory will employ its own bench sheet for taxonomic analysis. For the Bight '23 infaunal survey, certain standard forms of notation are employed with the taxonomist's bench sheet that assures that all labs collect the required information in uniform fashion. Standardized forms are used for sorting and taxonomic identification, as well as all respective QC checks. Each participating laboratory will retain its taxonomic bench sheets and voucher sheets in electronic or paper form. All QC reports are to be submitted to the Benthic Committee Co-Chairs (or designee) upon completion of sample analysis. To insure against loss of documents, copies of all these documents are to be retained by the individual laboratories.

6.2 The laboratory supervisor is responsible for assuring that all steps in the process of analyzing infaunal samples follow Bight '23 procedures and that all QC steps are completed and documented. The laboratory supervisor must implement any specified corrective actions resulting from QC protocols. He or she is also responsible for preparing their data and documents for transmission to the Bight '23 Benthic Committee Co-chairs in the proper form. All data entry must be subject to the established transcription error checking procedures within the originating laboratory. Analytical results are to be transmitted to the Bight '23 Information Management Officer in electronic data files that conform to Bight '23 data submission formats and standards as described in the Information Management Plan. It is the submitting laboratory's responsibility to see that these standards are met.

7. REFERENCES

Gillett, D.J., S.B. Weisberg, T. Grayson, and others. 2015. Effect of ecological group classification schemes on performance of the AMBI benthic index in US coastal waters. Ecological Indicators 50: 99-107.

SCAMIT. 1986. *Protocols and Recommendations for the Use of Open Nomenclature*. SCAMIT Newsletter, May 1986, vol. 5 No. 2.

SCAMIT. 2023. *A Taxonomic Listing of Benthic Macro- and Megainvertebrates from Infaunal & Epifaunal Monitoring and Research Programs in the Southern California Bight*, Edition 14. Barwick, K. L., Cadien, D. B. & Haggin, B. M., eds., San Pedro, CA.

8. DATA FORMS

This section includes examples of the data forms used for the laboratory analysis and QC of Bight'23 infaunal samples.

Form B23-1 Benthic infauna sorting bench and QC sheet – available as pdf from https://bight-sccwrp.opendata.arcgis.com/pages/bight-2023-infauna

Form B23-2 Benthic infauna match / not sheet with pre-filled information comparing initial and ReID taxonomic data and used to record resolved results between initial and QC taxonomists – available as xlsx / csv from committee co-chairs upon submittal of ReID data.

Form B23-3 Benthic infauna taxonomic resolution discrepancy codes – available as pdf from https://bight-sccwrp.opendata.arcgis.com/pages/bight-2023-infauna

Bight 2023 Regional Survey

Form B23-1 *Sorting*

Macrofauna Sorting Sheet

Station: _____ Analytical Laboratory: _____

Sorted by: _____ Sorting Laboratory: _____

Date Sorting Begins: ___/___/___ Total time (hours):

mm/dd/yyyy

# of Taxa Lots in Sample: _____ # of Sample Containers _____

Comments: _____

Quality Control Re-Sort

Re-sorted by: _____ Date of re-sort: ___/___/___

mm/dd/yyyy

Percent Sorting Efficiency = {**A** / [**A** + (**B**/**C**)]}*100

A = # of Organisms originally sorted: _____

B = # of Organisms found in resort: _____

C = Fraction of sample re-sorted (i.e., aliquot): _____

% Sorting Efficiency = _____

Quality Control Actions: _____

Note: no action needed if sorting efficiency ≥ 95%

Signed: _____

Responsible Supervisor

Line Number	StationID	Replicate	Taxon Initial	Abundance Initial	Voucher	Personal Voucher	Abundance Initial-Vouchers	Taxon ReID	AbundancReID	Abundance ReID-Initial	Match / Not Match	Direction of Counting Error	Type of Error
1	B18-10212	1	Ampelisca cristata cri	4	0	0	4	Ampelisca cristata cristata	5	-1	NotMatch	Yes - Under	Count
2	B18-10212	1	Cooperella subdiapha	1	0	0	1	Cooperella subdiaphana	3	-2	NotMatch	Yes - Under	Count
3	B18-10212	1	Ampelisca brachyclac	6	0	0	6	Ampelisca brachycladus	5	1	NotMatch	Yes - Over	Count
4	B18-10212	1	Bivalvia	4	0	0	4	Bivalvia	1	3	NotMatch	Yes - Over	Count
5	B18-10212	1	Macoma yoldiformis	5	0	0	5	Macoma yoldiformis	3	2	NotMatch	Yes - Over	Count
6	B18-10212	1	Siliqua lucida	5	1	0	4	Siliqua lucida	3	1	NotMatch	Yes - Over	Count
7	B18-10212	1	Caesia perpinguis	1	1	0	0				NotMatch	No - All Vouchered	
8	B18-10212	1	NEMERTEA	1	1	0	0				NotMatch	No - All Vouchered	
9	B18-10212	1	Pista wui	1	1	0	0				NotMatch	No - All Vouchered	
10	B18-10212	1	Virgulariidae	1	1	0	0				NotMatch	No - All Vouchered	
11	B18-10212	1	Acteocina culcitella	1	0	0	1				NotMatch		ID
12	B18-10212	1	Ampelisca cristata mi	1	0	0	1				NotMatch		ID
13	B18-10212	1	Amphicteis scaphobri	1	0	0	1				NotMatch		ID
14	B18-10212	1	Axiothella rubrocincti	1	0	0	1				NotMatch		ID
15	B18-10212	1	Cumacea	1	0	0	1				NotMatch		ID
16	B18-10212	1	Glycera americana	1	0	0	1				NotMatch		ID
17	B18-10212	1	Kurtiella coani	1	0	0	1				NotMatch		ID
18	B18-10212	1	Lumbrineris cruzensis	1	0	0	1				NotMatch		ID
19	B18-10212	1	Maldanidae	1	0	0	1				NotMatch		ID
20	B18-10212	1	Nuculana taphria	2	0	0	2				NotMatch		ID
21	B18-10212	1	Onuphis sp	1	0	0	1				NotMatch		ID
22	B18-10212	1	Scaphopoda	2	0	0	2				NotMatch		ID
23	B18-10212	1	Scoletoma tetraura C	2	0	0	2				NotMatch		ID
24	B18-10212	1	Solen sp	2	0	0	2				NotMatch		ID
25	B18-10212	1	Turbonilla santarosar	1	0	0	1				NotMatch		ID
26	B18-10212	1	Veneridae	6	0	0	6				NotMatch		ID
27	B18-10212	1						Acteocina cerealis	1		NotMatch		ID
28	B18-10212	1						Amphicteis sp	1		NotMatch		ID
29	B18-10212	1						Euclymeninae	1		NotMatch		ID
30	B18-10212	1						Gadila aberrans	2		NotMatch		ID
31	B18-10212	1						Glycera macrobranchia	1		NotMatch		ID
32	B18-10212	1						Leuconidae	1		NotMatch		ID
33	B18-10212	1						Leukoma staminea	6		NotMatch		ID
34	B18-10212	1						Lumbrineridae	1		NotMatch		ID
35	B18-10212	1						Metasychis disparidentatus	1		NotMatch		ID
36	B18-10212	1						Naaeromya compressa	1		NotMatch		ID
37	B18-10212	1						Nuculana sp A	2		NotMatch		ID
38	B18-10212	1						Onuphis sp A	1		NotMatch		ID
39	B18-10212	1						Scoletoma sp	2		NotMatch		ID
40	B18-10212	1						Solen sicarius	2		NotMatch		ID
41	B18-10212	1						Tellinidae	3		NotMatch		ID
42	B18-10212	1						Turbonilla sp	1		NotMatch		ID
43	B18-10212	1	Amaeana occidentali	2	0	0	2	Amaeana occidentalis	2	0	Match		
44	B18-10212	1	Argissa hamatipes	1	0	0	1	Argissa hamatipes	1	0	Match		
45	B18-10212	1	Chaetozone corona	1	0	0	1	Chaetozone corona	1	0	Match		
46	B18-10212	1	Dialychone veleronis	1	0	0	1	Dialychone veleronis	1	0	Match		
47	B18-10212	1	Diopatra sp	1	0	0	1	Diopatra sp	1	0	Match		
48	B18-10212	1	Ensis myrae	1	0	0	1	Ensis myrae	1	0	Match		
49	B18-10212	1	Euclymeninae sp A	1	0	0	1	Euclymeninae sp A	1	0	Match		

v4_OCSD_B18-10212_HigherTaxa

O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE
Lines in Resolution	Discrepency Class	Resolution Code	Taxon Resolved	Abundance Resolved	Resolution Note	Taxon Changed	# of MiS IDs	# of Mis Counts	Lab Initial	Taxonomist Initial	Lab ReID	Taxonomist ReID	BRI Taxon	SQO Taxon	Stratum	Depth (m)
									OCSD	Tang, D	LACSD	C. McDonald	P029		Inner Shelf	17
									OCSD	Barwick, K	LACSD	T. Petry	P128	SQO	Inner Shelf	17
									OCSD	Tang, D	LACSD	C. McDonald	P026	SQO	Inner Shelf	17
									OCSD	Barwick, K	LACSD	T. Petry		SQO	Inner Shelf	17
									OCSD	Barwick, K	LACSD	T. Petry	P276	SQO	Inner Shelf	17
									OCSD	Barwick, K	LACSD	T. Petry	P466		Inner Shelf	17
									OCSD	Barwick, K			P318		Inner Shelf	17
									OCSD	Ferraro, B					Inner Shelf	17
									OCSD	Ruckman, E			P402	SQO	Inner Shelf	17
									OCSD	Ferraro, B					Inner Shelf	17
									OCSD	Barwick, K			P006	SQO	Inner Shelf	17
									OCSD	Tang, D			P029		Inner Shelf	17
									OCSD	Ruckman, E			P044	SQO	Inner Shelf	17
									OCSD	Ruckman, E					Inner Shelf	17
									OCSD	Tang, D					Inner Shelf	17
									OCSD	Ruckman, E			P206	SQO	Inner Shelf	17
									OCSD	Barwick, K			P313		Inner Shelf	17
									OCSD	Ruckman, E			P270	SQO	Inner Shelf	17
									OCSD	Ruckman, E				SQO	Inner Shelf	17
									OCSD	Barwick, K			P338	SQO	Inner Shelf	17
									OCSD	Ruckman, E			P343		Inner Shelf	17
									OCSD	Barwick, K					Inner Shelf	17
									OCSD	Ruckman, E			P270	SQO	Inner Shelf	17
									OCSD	Barwick, K			P472		Inner Shelf	17
									OCSD	Barwick, K			P512		Inner Shelf	17
									OCSD	Barwick, K				SQO	Inner Shelf	17
											LACSD	T. Petry	P006		Inner Shelf	17
											LACSD	B. Furlong			Inner Shelf	17
											LACSD	B. Furlong		SQO	Inner Shelf	17
											LACSD	T. Petry	P197		Inner Shelf	17
											LACSD	B. Furlong	P207		Inner Shelf	17
											LACSD	C. McDonald			Inner Shelf	17
											LACSD	T. Petry	P432		Inner Shelf	17
											LACSD	B. Furlong			Inner Shelf	17
											LACSD	B. Furlong	P300	SQO	Inner Shelf	17
											LACSD	T. Petry			Inner Shelf	17
											LACSD	T. Petry	P338		Inner Shelf	17
											LACSD	B. Furlong	P343		Inner Shelf	17
											LACSD	B. Furlong			Inner Shelf	17
											LACSD	T. Petry	P472	SQO	Inner Shelf	17
											LACSD	T. Petry			Inner Shelf	17
											LACSD	T. Petry			Inner Shelf	17
											LACSD	T. Petry	P512	SQO	Inner Shelf	17
									OCSD	Ruckman, E	LACSD	B. Furlong	P023	SQO	Inner Shelf	17
									OCSD	Tang, D	LACSD	C. McDonald	P067	SQO	Inner Shelf	17
									OCSD	Ruckman, E	LACSD	B. Furlong	P115	SQO	Inner Shelf	17
									OCSD	Ruckman, E	LACSD	B. Furlong	P119		Inner Shelf	17
									OCSD	Ruckman, E	LACSD	B. Furlong	P153	SQO	Inner Shelf	17
									OCSD	Barwick, K	LACSD	T. Petry	P162	SQO	Inner Shelf	17
									OCSD	Ruckman, E	LACSD	B. Furlong		SQO	Inner Shelf	17

Discrepancy Classifications and Resolution Codes

FormB23-3

Discrepancy Classifications:

E = Error (identification or count)

J = Judgmental difference (difference level of expertise)

N = Nomenclatural difference (naming convention usage)

L = Apparent specimen loss (sample handling)

P = Processing error (data entry, animal from another vial)

Resolution codes:	Error type (* requires data change)	Action
1 = Primary taxonomist misidentification	True*	Training
2 = QC taxonomist misidentification	True	Training
3 = Primary taxonomist miscount	True*	Review best practices
4 = QC taxonomist miscount	True	Review best practices
5 = Primary taxonomist data entry error	Random*	Review best practices
6 = QC taxonomist data entry error	Random	Review best practices
7 = Primary naming convention discrepancy	True*	Review best practices
8 = QC naming convention discrepancy	True	Review best practices
9 = Primary variation in level of expertise	Non Error	Training
10 = QC variation in level of expertise	Non Error	Training
11 = organism added from another vial^{+}(vials other than Annelid fragments and Ophiuroid arms, in which case those would be considered misidentification errors)	Random*	Review best practices
12 = organism lost	Random	Review best practices
13 = specimen vouchered	Non-Error	Data Tracking
14 = specimen damaged during primary ID, not identifiable by QC taxonomist	Non-Error	No Action

APPENDIX A TAXONOMIST

QUALIFICATION FOR BIGHT '23

MACROBENTHIC (INFAUNAL) SAMPLE ANALYSIS

Prepared by:
Bight '23 Benthic Committee

Prepared for:
Commission of the Southern California Coastal Water Research Project
3535 Harbor Blvd, Suite 110
Costa Mesa, CA 92626

INTRODUCTION

The Bight '23 macrobenthic survey is a multi-agency, regional survey of estuary, bay, shelf, slope, and deep basin soft-bottom macrofaunal communities within the Southern California Bight. The survey design, field and laboratory procedures, as well as QA/QC plan, are based upon the experience gained during previous Southern California Bight Regional Monitoring Program infaunal surveys. As in these surveys, the Bight '23 infaunal survey involves the integration of data produced by a large number of taxonomists into a single data set. These taxonomists are employed or contracted by several different agencies participating in the Bight '23 project. As was discovered during the previous surveys, the difficulty of assuring accurate and consistent results in a large scale infaunal survey is compounded by the differences in the expertise, experience and opinion of the participating taxonomists. To minimize the effect of these problems on the survey results, detailed quality assurance plans, including quality control exercises and quality assessments relative to specific quality objectives for taxonomic analysis were established.

In order to assure that the data produced by the Bight '23 macrofaunal survey meets the standards set during the previous two regional surveys, it is essential that all participating taxonomists have the expertise and experience necessary to produce data of comparable quality. Qualification criteria have been established to assure that the taxonomists participating in the Bight '23 are capable of meeting that standard. Agencies or their contractors employing taxonomists who did not perform analysis of macrofaunal samples for the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 are required to assure that their taxonomists meet one of the qualifying criteria prior to participation in the Bight '23 macrofaunal survey. The two criteria are:

> Candidate taxonomists who will be working under the direct oversight and guidance, or mentorship of an experienced taxonomist who analyzed samples in the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 are considered to meet the standard for Bight '23.

or

> Candidate taxonomists who will not be working under the direct supervision and guidance, or mentorship of an experienced taxonomist who analyzed samples in the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 must complete and pass a qualification exercise prior to acceptance as a taxonomist for Bight '23.

The exercise is based upon that used as quality control and assessment in previous Bight Surveys (Montagne & Bergen 1997, Ranasinghe *et al*. 2003, Ranasinghe *et al*. 2007, Ranasinghe *et al* 2012, Gillett et al. 2016). All exercises will be coordinated by the CO-Chairs of the Benthic Committee. Based upon the performance of the candidate taxonomist, the Benthic Committee Co-Chairs and a group of Southern California taxonomists will evaluate the ability of the candidate to participate in the forthcoming Bight Survey

The candidate taxonomist will identify one or two lots of specimens from samples collected

during the most recent Bight Survey (e.g., Bight '18 samples for new taxonomists participating in Bight '23) or a similar survey from the Southern California Bight. Candidate taxonomists will identify and count all organisms in the samples to the appropriate, targeted taxonomic level for the survey they originated from (Sections 3.1-3.8).

The results of the analysis are compared to those of the original taxonomist. Discrepancies will be addressed in a reconciliation meeting between the original taxonomist(s) and the candidate taxonomist(s). Discrepancies found to be the result of error on the part of the candidate taxonomist will be tallied and percent error rates for the number of taxa, organism count, and the accuracy of identification will be calculated using the taxonomic QA/QC equations described in 5.5.14. The candidate taxonomist must be able to meet the measurement quality objective (MQO) of 90% for each of the parameters.

Depending upon performance results, a candidate taxonomist may have no restrictions, may be limited to identifying taxa only from certain strata, or may not be asked to participate in the forthcoming survey at all. Opportunity should be provided to the candidate taxonomist to undertake corrective action(s) to improve any deficiencies and a subsequent re-testing, if all parties are willing to do so.

TAXONOMIST QUALIFICATION CRITERIA

A1. Each Agency or its contractor will provide the Co-Chairs of the Bight '23 Benthic Committee a list of the taxonomists who will be employed for sample analysis, along with the taxonomic group(s) for which each will be responsible.

A2. Those taxonomists who provided macrofaunal sample analysis in the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 surveys are qualified to participate in Bight '23 sample analysis

A3. Any proposed taxonomist who did not participate in the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 infaunal sample analysis will be considered a candidate taxonomist and must meet either of two criteria to be allowed to provide sample analysis for Bight '23.

A4. Criteria

A4.1 Candidate taxonomists who will be working under the direct oversight and guidance of an experienced taxonomist who analyzed samples in the SCBPP, Bight '98, Bight '03, Bight '08, Bight '13, or Bight '18 surveys are considered to meet the standard for Bight '23.

A4.1.1 In this context, direct oversight and guidance means they are either physically co-located or meet regularly to review specimens or vouchers and are actively engaged with the taxonomist providing oversight and guidance.

A4.1.2 Oversight and guidance shall include interactive training and review of identifications, vouchered specimens, and sample processing procedures.

A4.2 Candidate taxonomists who will not be working under the direct oversight and guidance, or mentorship of an experienced taxonomist as defined above must complete and pass a qualification exercise prior to acceptance as a taxonomist for Bight '23.

A5 Qualification Exercise Procedure

A5.1 The exercise will be coordinated by the chair of the Benthic Committee. The purpose of the exercise is to demonstrate the candidate taxonomist's familiarity with estuary, bay, shelf, slope, deep basin, and submarine canyon macrofauna of the Southern California Bight and ability to produce results compatible with those of the other taxonomists who will be performing sample analysis for the Bight '23 macrofaunal survey.

A5.2 Each candidate is required to analyze (identify and enumerate) one to two taxa lots for each taxonomic group from each stratum for which they will be responsible.

A5.3 The taxa lots will come from macrofaunal samples collected from the Southern California Bight by methods to be used in the most recent Bight Survey. For instance, a candidate to perform polychaete identifications will be provided polychaete lots from different strata (e.g., estuary, shelf, or slope), each containing all polychaetes from a single 0.1 sq. meter Van Veen grab, screened on a 1.0 mm mesh sieve.

A5.4 These samples will have been previously analyzed by taxonomists who participated in previous Bight surveys.

A5.5 Selection and dissemination of samples will be coordinated by the Benthic Committee Chair. The samples will be provided to the candidates through their employer by the Bight '23 Benthic Committee. The analysis must be completed and the results returned in a timely manner.

A5.5.1 Samples will be selected at random from previously collected samples from the most recent Bight Survey, or, secondarily, a sampling program from within the Southern California Bight that use the same gear and methodology (i.e., $0.1m^2$ Van Veen Grab sieved on a 1-mm screen).

A5.5.2 Only samples that have not already been re-identified should be used to minimize damage to the individual specimens.

A5.5.3 Samples should have species richness and abundance values between the 5^{th} and 95^{th} percentile of all samples from the appropriate stratum observed in the previous Bight Survey.

A5.5.4 Before being given to the candidate taxonomist, all taxa lots in the samples should be re-labeled with station depth, region of collection (i.e., stratum/county), and a "dummy" station ID.

A5.6 In conducting the analysis the candidate taxonomist is to follow the conventions below:

A5.6.1 Identify all specimens to the lowest practicable level and provide an accurate count of each identified taxon. Species-level identifications following the nomenclature and orthography of the most current SCAMIT species list are expected. Discrepancies in names between current SCAMIT list and names assigned during the previous Bight survey will be rectified by the Benthic Committee Chair and Co-Chair during review of the results.

A5.6.2 Fragments of bilaterally symmetrical organisms are to be identified and counted only if the fragment includes the anterior end of the organism. For radially symmetrical organisms (e.g., ophiuroids, anthozoans) only fragments bearing the majority of the oral disk are to be identified and counted.

A5.6.3 Report results on the standard taxonomy data sheets used in the laboratory for recording of identifications and counts.

A5.6.4 For each name reported in the results, create a taxa lot containing all specimens represented by that name. (e.g., all *Photis brevipes* in a sample are to be aggregated into a single lot). These taxa lots are to contain an internal label providing the sample name and the taxon contained in the lot. Non-countable fragments may be aggregated into a fragments lot.

A5.6.5 Aggregate all taxa lots from a single sample site (sample name) into a single container provided with an internal label identifying the sample.

A5.6.6 All specimens are to be maintained in a preservative solution of 70% non-denatured ethanol.

A5.6.7 Labels are to be written in pencil on 100% rag-paper or other paper suitable for permanent wet labels.

A5.6.8 Upon completion of analysis, return the results and all sample material (sorted into taxa lots) to the Benthic Committee Co-Chairs (or designee) who will review the results, comparing them to the results of the original analysis.

A5.7 Identifications from the candidate taxonomist will be compared to the original identification list by the Benthic Committee Chair or designee; noting any discrepancies. Each discrepancy will be addressed in a reconciliation meeting between the original taxonomist(s) and the candidate taxonomist(s) where possible and practical. Genuine taxonomic differences discovered in the reconciliation process should be settled by a review of the disputed taxa by a qualified anonymous third taxonomist. This meeting should be facilitated by someone with the appropriate taxonomic background and familiarity with Southern California Bight taxa (ideally someone who is neither the Benthic Committee Chair nor one of the original taxonomists for the test samples).

A5.8 Discrepancies found to be the result of error on the part of the candidate taxonomist will be tallied and percent error rates for the number of taxa, organism count, and the accuracy of identification will be calculated using the taxonomic QA/QA equations described in 5.6.13. The candidate taxonomist must be able to meet the measurement quality objective (MQO) of 90% for each of the parameters.

A5.9 The results of the exercise will be assessed by an *ad hoc* committee made up of the Co-Chairs of the Bight '23 Benthic Committee and selected members of SCAMIT with previous experience conducting multi-laboratory taxonomic analysis. This committee will determine whether a candidate taxonomist is capable of meeting the data quality objectives of the Bight '23 infaunal survey. Members selected for the *ad hoc* committee should not be in a position to benefit from the conclusions of the committee.

A5.10 Based upon this assessment, the committee will provide a report to the Bight '23 Sediment Quality Planning Committee recommending the acceptance or rejection of the candidate taxonomist. A negative recommendation will be accompanied by the reasons for that judgment and what steps, if any, should be taken to remedy the deficiency.

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