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# **Reconciling Ambiguity Resulting From Inconsistent Taxonomic Classification of Marine Fauna Assessed in the Field: Querying a Database to Reclassify by Lowest Accountable Inclusive Taxon (LAIT)**

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**U.S. DEPARTMENT OF COMMERCE**  
National Oceanic and Atmospheric Administration  
National Marine Fisheries Service  
Alaska Fisheries Science Center

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# **Reconciling Ambiguity Resulting From Inconsistent Taxonomic Classification of Marine Fauna Assessed in the Field: Querying a Database to Reclassify by Lowest Accountable Inclusive Taxon (LAIT)**

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October 2016

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## ABSTRACT

Marine areas such as the eastern Bering Sea (EBS) continental shelf contain such significant commercial and ecological resources that it demands our careful stewardship to maintain them. This requires developing a comprehensive knowledge of the ecosystems involved, which in turn requires in-depth, long-term investigations to elucidate and quantify the biotic and abiotic elements, and the relationships among them, that make up these systems and enable their productivity. Accurate assessment of taxonomic diversity and the composition of communities and or biotopes is instrumental. Accordingly, the benthic fauna of the EBS are the subject of annual bottom trawl surveys of the continental shelf conducted by the National Oceanic and Atmospheric Administration (NOAA), Alaska Fisheries Science Center (AFSC), Resource Assessment and Conservation Engineering (RACE) Division. These surveys comprise a time series of data collected from 1982 to 2015, employing standardized gear and sampling methods for consistency over the period.

The region surveyed is an area of the shelf from the Alaska Peninsula and Aleutian archipelago on the south to about 62° N lat., and from the Alaska coast to the shelf break. It comprises roughly 480,187 km<sup>2</sup>, spatially represented by 376 trawl sampling stations distributed throughout. Each station's catch is sorted by taxon, weighed, and individuals counted. Abundance is indexed by catch amount per area swept by the net. The data are entered into an Open Database Connectivity (ODBC) database maintained by RACE. Biomass has averaged 1,429 kg per haul since 1982, with invertebrates constituting roughly 22% of the total. A total of 227 taxa of vertebrates and 624 of invertebrates have been identified and reported. Identifying and classifying catch on a survey of such scope is a formidable task. Certain anomalies and ambiguities occur in the historical data from the survey. Inconsistent resolution in identifying individuals of a given species to the lowest hierarchical level practicable is apparent in the data. To mitigate such problems, this paper presents a query system for objectively transforming the invertebrate catch data from the survey into an unambiguous, consistent, usable form: the reclassification of taxonomic data to lowest accountable inclusive taxon (LAIT). For a given taxon in a dataset, the LAIT is that taxon also reported therein which by definition includes the given taxon and which itself is not defined as a subtaxon of

another reported taxon. When subtaxa are thus consolidated, all LAITs unambiguously account for the invertebrate catch (albeit with possible minor loss of taxonomic resolution), *without the chance of incorrect assessment of the catch of a reported lower-level taxon when the latter is also present among catch identified only to a higher level, inclusive taxon.*

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## INTRODUCTION

The eastern Bering Sea (EBS) continental shelf is an important and productive ecosystem, comprising essential habitat for a number of commercially important fish and invertebrate species (Pereyra et al. 1976, Lauth 2011, Stevenson and Lauth 2012). From the west coast of Alaska south of the Bering Strait and north of the Aleutian Islands, the shelf extends out to the top of the continental slope at a depth of roughly 200 m. Invertebrates are a significant portion of the benthic faunal biomass of the region, and a major element of the food chain supporting substantial stocks of commercially important fish species. In addition some taxa, such as the crab genera *Paralithodes* and *Chionoecetes*, comprise a significant commercial resource in their own right. For example, during the 2011 / 2012 commercial crab fishing season in the eastern Bering Sea, the harvests and estimated exvessel values of red king crab (*P. camtschaticus*), blue king crab (*P. platypus*), and snow crab (*Chionoecetes opilio*) were 7.834 million lbs @ \$7.30/lb, 1.88 million lbs @ \$4.34/lb, and 88.83 million lbs @ \$1.89/lb, respectively (Fitch et al. 2014).

To assist and inform efforts to preserve and manage these marine resources, the Resource Assessment and Conservation Engineering (RACE) Division, Alaska Fisheries Science Center (AFSC), National Oceanic and Atmospheric Administration (NOAA), conducts annual bottom trawl surveys of the stocks of demersal and benthic fish and invertebrates, encompassing a large portion of the eastern Bering Sea shelf extending from the Alaska Peninsula and Aleutian Islands on the southeast, northwest to approximately 62° N lat. (Fig. 1). These surveys provide an index of the geographical distribution and abundance of each taxon encountered within this area. Methods and gear are generally consistent from year to year. The present configuration of standard sampling stations, methods, and trawl gear design was first adopted in 1982 under the Bering Sea-Aleutian Islands Groundfish Fishery Management Plan (Stauffer 2004, Yeung and McConnaughey 2006, Acuna and Lauth 2008). The annual surveys conducted since then have covered an area divided into a standard grid of 330 squares, each approximately 20 nautical miles (nmi) × 20 nmi (37.04 km × 37.04 km). The standard trawl stations of the survey include 330 located at the respective square centers, plus an additional 16 stations northeast of the Pribilof Islands and 10 stations southwest of St. Matthew Island, at the corners of select grid

squares, added to increase sampling density in areas having significant concentrations of *Paralithodes* species (king crab). An additional 20 squares with center stations were added at the northwest margin of the grid in 1988 to extend the standard survey area northwest and provide further information on the distribution of *Chionoecetes opilio* (snow crab) and *Gadus chalcogrammus* (walleye pollock; Acuna and Lauth 2008). This established the current standard survey design of 376 stations in a grid of 350 squares representing a total area of roughly 480,187 km<sup>2</sup> (Fig. 1).

Abundance of each taxon at each sampling station is indexed by calculating the catch per unit of effort (CPUE: The aggregate weight and the number of viable organisms, divided by the area of bottom swept by the net before hauling). Area swept equals the average width of the net mouth at the footrope times the distance trawled. Station abundance is then extrapolated to represent the taxon over the area of the square. The results are ultimately recorded in a relational ODBC database (RACEBASE) maintained at the AFSC by RACE, listing the data by cruise (indicating survey year), vessel, unique haul identifier, position, and date.

Taxonomic diversity among the benthic fauna of the EBS shelf is considerable. Knowledge and systematics accurately accounting for this variable has been continuously developing over the extensive time series since 1982, with some consequential ambiguity and inconsistency among the data as a whole. This has presented particular challenges for RACE scientists processing the data from a study of such scope. One of these is that of reconciling the desire to retain the greatest amount of taxonomic resolution in identification and classification of catch, with the fact of inconsistencies within the overall data regarding the degree of taxonomic resolution achieved in the identification of a given taxon. This affects the confidence with which identifications specifying a taxon which happens to be a subtaxon of another also reported in the data, can be viewed as unambiguously representing all of the lower-level taxon in the catch. This paper presents a method of mitigating this problem, developing a query system which when run, reclassifies the catch, grouping any subtaxon of a higher-level taxon within the latter, given that catch of the higher-level taxon as originally reported comprises a significant portion of the total of itself and subtaxa also reported.

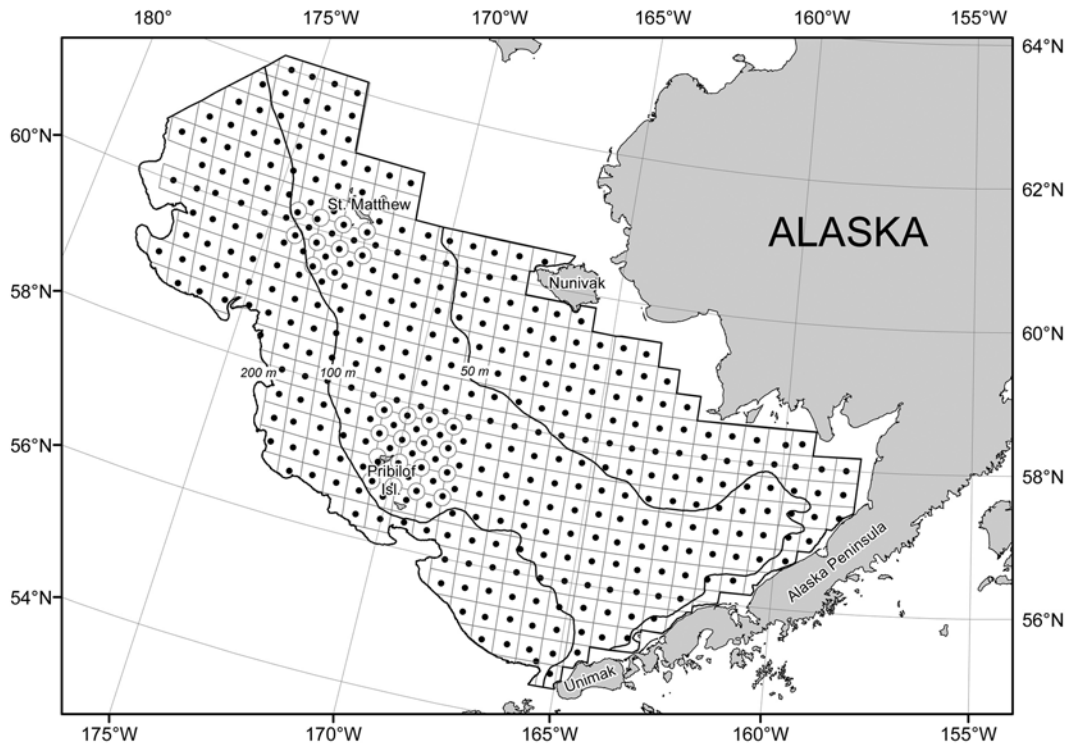


Figure 1. -- Map of survey boundaries and sample station grid for the annual RACE eastern Bering Sea continental shelf groundfish and invertebrate bottom trawl surveys. Dots indicate stations where standardized trawl samples are collected.

## SURVEY PROCEDURES

### Processing Samples at Sea

In the EBS since 1982, RACE has conducted field work of the standard shelf surveys during summer, no earlier in the year than the 23<sup>rd</sup> of May nor later than the 10<sup>th</sup> of September. Trawling is during the hours of daylight. Two or three chartered vessels are typically employed simultaneously on each year's survey, each with a complement of AFSC personnel (typically 5 or 6 individuals). In addition to sorting and weighing catch, these field parties sample biological

data (e.g. frequency distribution of individual weight, size, sex, maturity), and collect tissue samples for age, diet and condition information. Ship crew personnel sometimes assist the field party in sorting or weighing, as overseen by the Field Party Chief. RACE field parties serve 3-week “legs” on a vessel during a given year’s survey, with some or all of the party replaced in port for each succeeding leg. Ships’ crews do not rotate as frequently, often remaining constant on a vessel throughout a 3-leg summer’s survey. With the constraints of contract-allotted time and transit to and from port, vessels must usually average 3+ hauls per day in the survey area for the survey to be completed.

The total catch weight of fauna reported in EBS standard survey hauls from 1982 to 2015 was 17,988,857 kg. Weight per haul averaged 1,429 kg. During this period the yearly proportion of total survey catch weight constituted by invertebrates has averaged 22.4%. Although composition by taxon weight in large hauls was sometimes estimated by weighing the entire catch in the codend, then sorting and weighing a haul subsample by taxa and extrapolating to estimated respective portions of the total haul, processing of each haul has generally required considerable effort by the field party.

Field parties sort all (non-detrital) fauna to the lowest taxonomic hierarchical level distinguishable. Since 1982 in the region, RACE has recorded in catch data 851 taxa whereby organisms have been classified, of which 622 taxa were invertebrates, ranging in levels of the hierarchy from invertebrate unidentified at the highest, most general to (397) species at the lowest, most specific. The 225 supraspecific invertebrate taxa reported included many genera, families, orders, and classes. These higher-level taxa are in some cases defined as encompassing subtaxa otherwise reported in their own right, in the same or other years. Each taxon is represented in the database by a unique numeric code.

The survey is thus an extensive and labor-intensive data time series in both number of sampling stations and the total period to date. Obtaining and recording accurate, useful data on such a large scale, over such an extended period produces major tasks for RACE Division scientists.

## **Taxonomic Systematics**

Accurately separating samples according to taxa is important in conducting useful studies of the biological resources of a marine region and the ecosystems sustaining them. In many areas, a resource-rich and stable ecology is supported by a multiplicity of taxa, with variation in their relative abundances even among important members of the biocenosis (Piraino et al. 2002). Moreover, over extended periods and in the presence of either temporal variability or stability in overall ecosystem biomass, changes observed in relative abundance among taxa can indicate factors for important further consideration (Bell et al. 2014). Observance of these dynamics requires the ability to consistently assess and monitor taxa involved. Over the EBS survey period from 1982 to the present, RACE scientists have striven to classify sample fauna according to taxon systematics and nomenclature generally established by concurrent acceptance in the scientific community. They have looked to a number of authoritative sources for assistance, such as Turgeon et al. (1998), Cairns et al. (2002), Ruppert et al. (2004), McLaughlin et al. (2005), and Clark (2006a, 2006b, 2006c, 2006d). In recent years, RACE taxonomy has been largely informed by such authorities in systematics as the Integrated Taxonomic Information System (I.T.I.S.; <http://www.itis.gov/>) and the World Register of Marine Species (WoRMS; <http://www.marinespecies.org>). Both sources are upgraded continuously. For accurate identification in the field, RACE has employed field guides providing descriptions, keys, drawings, and or photos conveying the identifying characteristics of these marine species; for example, Wilimovsky (1958), Hitz (1965), Grainger (1966), Hart (1973), Keen and Coan (1974), Kozloff (1974), MacIntosh (1976), Kessler (1985), Lambert et al. (2000), Mecklenburg et al. (2002), Kramer and O'connell (2003), Kramer et al. (2008), and Acuna (2009). These have been provided to field party personnel for orientation and as identification guides at sea. In recent years of the EBS survey, the guide by Clark (2006a, 2006b, 2006c, 2006d), with plasticized color photographs of each species included, has been the most widely used at sea for identifying invertebrates in the catch. Also recently, RACE taxonomists have provided field parties yearly pre-survey orientation seminars describing taxa likely to occur, with definitive characters as well as photographic images of specimens returned from the field surveys.

In addition, over the period of the annual surveys RACE scientists have themselves conducted ongoing taxonomic research on the fauna of the region, especially regarding marine

fish species. Studies based on specimens from the region, including ones collected in the surveys, have brought recognition of previously unrecognized species, for example the fishes *Lepidopsetta polyxystra* (northern rock sole; Orr and Matarese 2000) and *Sebastes melanostictus* (blackspotted rockfish; Orr and Hawkins 2008).

## PROBLEM

### **Ambiguity in Field Identification**

On the RACE bottom-trawl surveys, conditions at sea for collecting and recording data are often demanding due to the scope of the sampling assigned each vessel, relative to the allotted manpower, days at sea, etc. A single haul can contain many species. Work can be required during inclement weather, or days cut short because of the same. The catch itself can be muddy or mangled by the gear. Within a taxon, definitive morphological characteristics separating one subtaxon from another can be subtle, calling for close inspection and possibly recourse to a field guide. This is difficult to manage on a frequent basis due to the usual high tempo of operations. Thus classification often takes place in less-than-ideal circumstances.

In addition to changes in the skill of field personnel in taxon identification over the years, there have also been changes in policy regarding the identification of some species. For example, because of the difficulty in accurately discriminating among species of small shrimps of the genera *Argis* and *Crangon* within the family Crangonidae, survey leaders in the early 2000s advised field parties to restrict classification thereof to the respective genus, without trying to identify the species. Thus survey data for these species cannot be compared across all years on a species level.

Along with the ongoing development and dissemination over time of taxonomic knowledge necessary to fully classify the many species encountered, these facts have contributed to a particular difficulty which has attended achieving maximum taxonomic resolution in field identifications over the survey time series: Ambiguity due to inconsistent resolution in the identification of individuals of a given taxon. This occurs both between years and within a single year. Historically survey records often only specify a taxon of a higher-level, more inclusive rank than that of species. In some instances this is because the individual(s) observed were of a species within the named taxon but seldom encountered in the area, and for which definitive characteristics were subtle or unfamiliar to RACE personnel at the time. At other times a more common species has been identified at more than one taxonomic level, due to differences in taxonomic knowledge possessed by field personnel between survey years, or even between vessels or vessel-legs of the same year. There also have been differences in the emphasis and

priority given to further resolution of taxon identification within some higher-level taxa, relative to other time constraints. These inconsistencies all likely occurred less frequently over time with increased instruction and familiarity of field personnel in general regarding the full complement of species in the region, but there is no way of accurately refining these historic records in the absence of the specimens themselves. In the event, even in the case of a very common species usually recognized, to assume that any individuals classified to a higher-level taxon in that hierarchy were not of that familiar species risks erroneously quantifying the catch of the species. The assumption means that the higher taxon, when named, becomes in effect an “all the clade except...”, paraphyletic classification. Further, it requires that field personnel all be aware of that distinction when classifying catch. An example might be recording data for the unusually distinctive hermit crab *Pagurus ochotensis*, identifiable in the shell even in muddy conditions due to a unique color-band sharply defined along the inner margin of the larger claw. This species designation might occur in datasets along with other records for “hermit crab unidentified” (generally, Paguridae), but separating them this way risks incorrectly assuming that records for the distinctive subtaxon represent all of the *P. ochotensis* that were caught.

### **Examples**

Examination of RACE EBS survey catch data reveals multiple instances of inconsistency in the degree of taxonomic resolution achieved in classifying a given taxon in the field. In some years of the survey, a parent taxon and alternatively one or more of its subtaxa are both classifications occurring in the data, but tending to be differentially reported depending on the sampling vessel. For example, the class Asteroidea (sea stars) is a significant element of the regions benthos (Yeung and McConnaughey 2006, Smith and Armistead 2014). There is a classification in RACE data for Asteroidea unidentified, but within the taxon are 62 species or genera that have been identified and variously reported in the EBS shelf catch between 1982 and 2015, so pervasive that their combined total catch weight comprised 27.9% of the total for all invertebrate catch. However, data for the 1983 survey show a considerable vessel effect on whether sea stars were classified as being of one of these subtaxa or simply as Asteroidea. Of the two vessels employed, the RV *Chapman* successfully completed 176 standard hauls and the RV *Alaska* completed 177. Geographically the sampling stations over the survey region were fairly



evenly distributed between vessels, usually by alternating north-south “columns” of grid squares assigned to each. This distribution of sampling stations is common, intended to make sampling of different subareas of the survey roughly equal between vessels. As adjacent columns are often traversed by the vessels somewhat concurrently, it also facilitates between-vessel assistance in case of logistical or emergency needs. Figures 2 and 3 show the distribution of catch accorded the two classifications, respectively. For visual discrimination, only the 327 sampled standard stations centered in grid squares are represented. Survey vessels are represented by square color. The vessel effect on classification of catch is obvious, but can be broken down statistically for better overall understanding. Comparing adjacent squares under the assumption that they would be most likely to harbor similar benthic communities, in Figure 2 there are 254 pair combinations of 2 squares sharing a common side separating them by longitude or latitude, but each sampled by a different vessel, and also with one or both samples showing catch of one or more individual subtaxa of Asteroidea. Within these pairs, 148 show that *Chapman* reported such catch (“+”) while *Alaska* reported none (“0”). Conversely, only 28 of the pairs show the reverse; that is, “0” for *Chapman* and “+” for *Alaska*. The remaining 78 pairs show “+” for both vessels. Figure 3 shows the corresponding information for the vessels’ classification of catch as Asteroidea unidentified. Here, pair combinations of adjacent squares sampled by different vessels and with at least one square reporting that classification numbered 189, with 125 pairs showing “0” catch for *Chapman* but “+” for *Alaska*. The reverse, *Chapman* recording catch but *Alaska* showing none, occurred in only 25 of the pairs. For the remaining 39 pairs, both squares showed “+”.

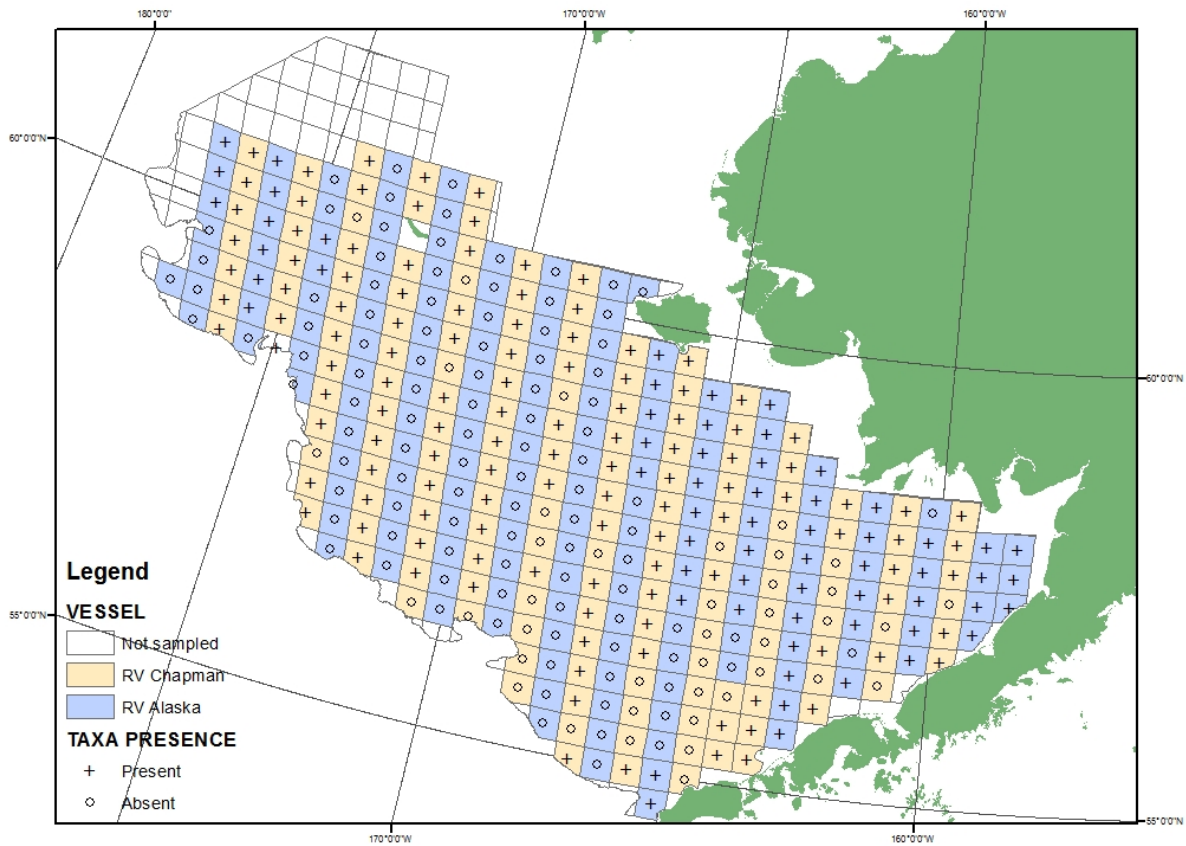


Figure 2. -- Presence or absence of catch classified as one or more subtaxa (species or genus) of the class Asteroidea (sea star) in the eastern Bering Sea groundfish and invertebrate bottom trawl survey, 1983. For clarity, only center-square stations are shown. Color indicates sampling vessel. Blank squares were not sampled.

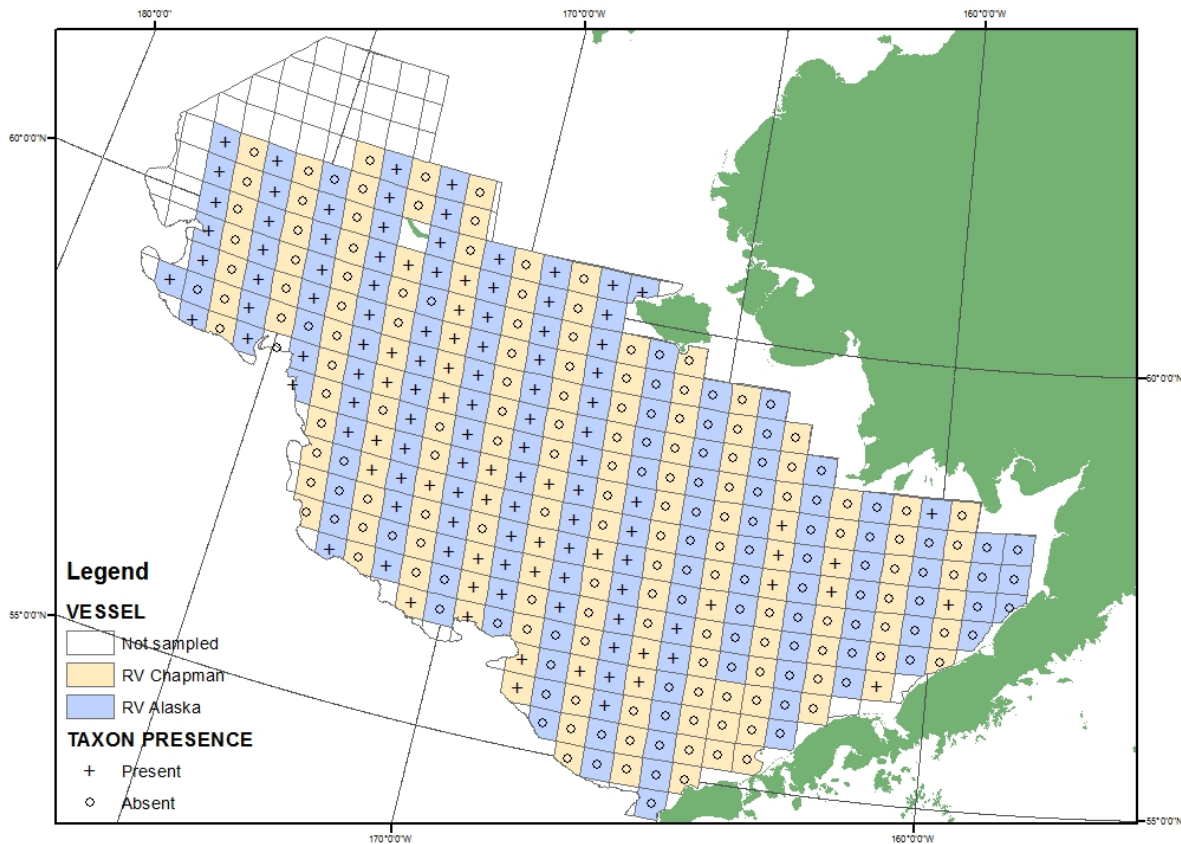


Figure 3. -- Presence or absence of catch classified as Asteroidea (sea star) unidentified at center-of-square stations in the eastern Bering Sea groundfish and invertebrate bottom trawl survey, 1983. Color indicates sampling vessel. Blank squares were not sampled.

Figures 2 and 3 show that this overall difference between vessels regarding resolution of identification of Asteroidea is not consistent throughout the survey. Rather, it is most pronounced in the central and western areas of the survey, and hardly evidenced in the northeast. This may be due to changes in personnel with concomitant changes in areas of expertise in taxon identification within field parties, that occurred on one or both vessels between survey legs, and or to changes in the species of Asteroidea encountered in different areas of the survey. However, the results of the comparison indicate that one would not want to include 1983 in a study of abundance of individual species and or genera of Asteroidea, in the region.

Another example of inconsistent resolution in classification of EBS invertebrates is the reported catch of marine snails of the genus *Buccinum* in the 1990 survey. The genus is easy to recognize and distinguish from other marine snails of the region due to its ovoid operculum with growth ring striations generally concentric about a central nucleus (MacIntosh 1976, Clark 2006b). In contrast, it is more difficult to differentiate among species of *Buccinum*, as the definitive characters for this are more subtle. The genus is fairly common in parts of the EBS survey area, with 11 species variously reported therein since 1982, in addition to catch identified only as unidentified species of *Buccinum* (*Buccinum* sp.). The 1990 survey comprised 187 stations trawled by FV *Ocean Hope 3* and 184 by RV *Alaska*. As in the previous example, maps of the distributions of catch identified as being of one or more particular species of *Buccinum* or as simply *Buccinum* sp. (Figs. 4 and 5, respectively) show a vessel effect. Of 167 pairs of adjacent squares sharing a common border but with center stations sampled by different vessels, and wherein one or both report the presence of one or more individual species of *Buccinum* (Fig. 4), 108 pairs showed *Ocean Hope 3* catch = “+”, *Alaska* catch = “0”. Only 5 pairs showed the reverse, *Ocean Hope 3* = “0” and *Alaska* = “+”. The remaining 54 pairs showed “+” for both vessels.

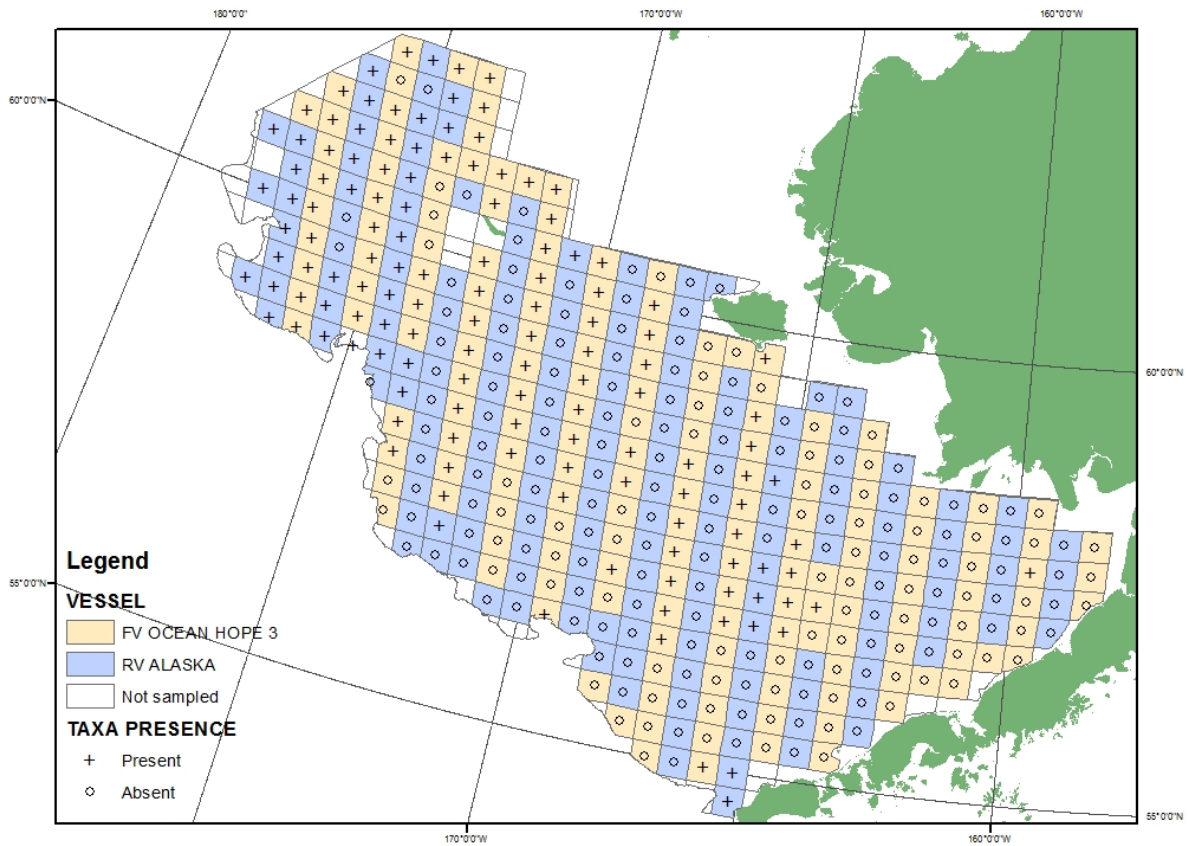


Figure 4. -- Presence or absence of catch identified to one or more individual *Buccinum* species of marine snails, at center-of-square stations in the eastern Bering Sea groundfish and invertebrate bottom trawl survey, 1990. Color indicates sampling vessel. Blank squares were not sampled.

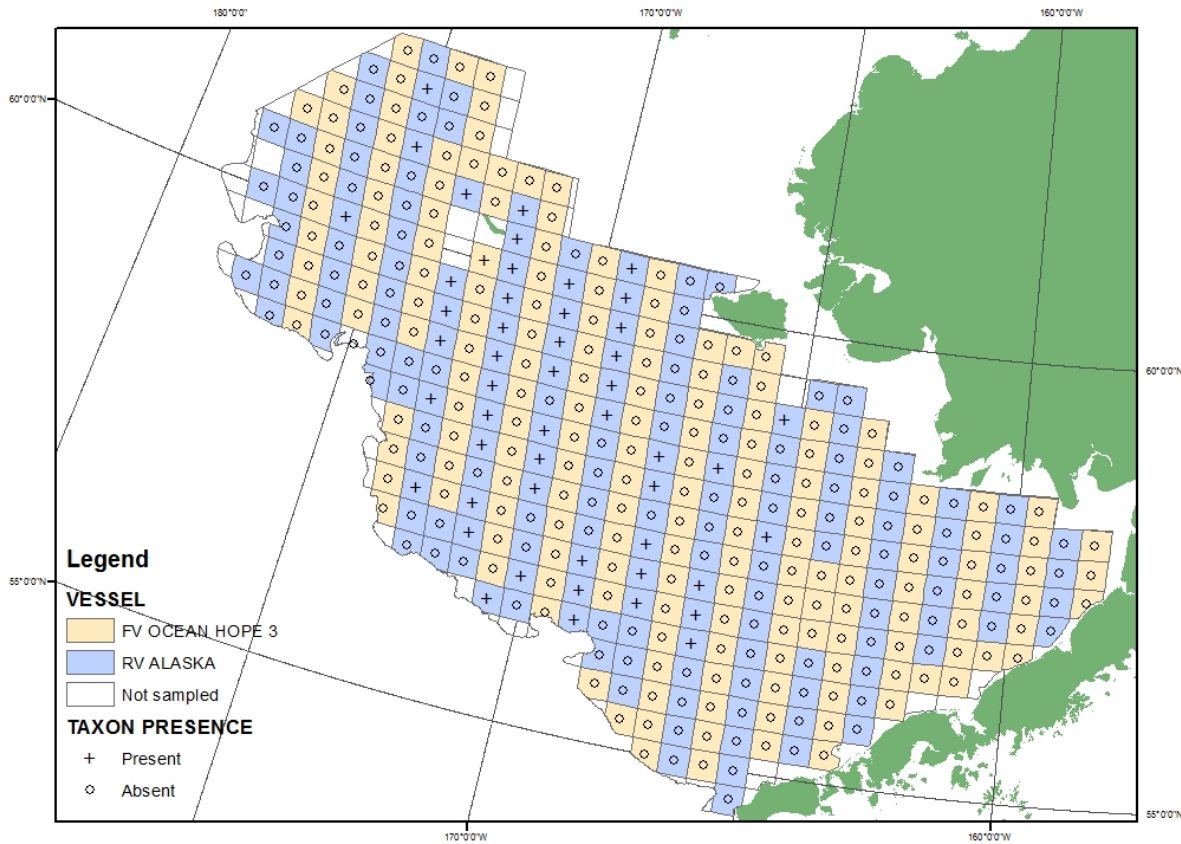


Figure 5. -- Presence or absence of catch classified only to the genus as *Buccinum* species unidentified, at center-of-square stations in the eastern Bering Sea groundfish and invertebrate bottom trawl survey, 1990. Color indicates sampling vessel. Blank squares were not sampled.

Figure 5 shows the distribution of the classification of catch as “*Buccinum* sp.” (present or absent) at 1990 survey square-center stations. Of 93 station pairs having a common boundary but sampled by different vessels, and wherein one or both stations reported the classification present, 92 showed *Ocean Hope 3* = “0”, *Alaska* = “+”. The reverse of such a pair, *Ocean Hope 3* = “+” and *Alaska* = “0”, did not occur. The remaining pair showed present (+) for both vessels.

Examining Figures 4 and 5, the vessel effect is only evident in the central part of the survey. The eastern part shows no classification of either type, probably due to absence of the genus there. The far western part shows both vessels classifying *Buccinum* to the species,

apparently due to changes in personnel on field parties and or changes in the individual species representing the genus in that area.

### **RACE Countermeasures**

Resource Assessment and Conservation Engineering taxonomists have observed problems and anomalies in the taxonomic data from the annual groundfish and invertebrate surveys conducted by the Division. These are, namely, the difficulty of species identification under field conditions, the difference in taxonomic knowledge and identification skills brought to the surveys historically over the entire time series of 1982 to 2015, as well as such differences existing between personnel aboard the various survey vessels for various survey legs in a region during a given year. The taxonomists have responded by examining the data, and based thereon and on their own experiences interacting with RACE personnel on the surveys have reported a list of confidence ratings to be applied by data users, in accepting the identification of marine faunal taxa as reported in the annual EBS surveys, from 1982 to 2008 (Stevenson and Hoff 2009). The report lists each taxon, and assigns a confidence index to each for each survey year in which it was reported. The rating index and rate definitions as related in the publication are as follows:

1. High confidence and consistency. Taxonomy is stable and reliable at this level, and field identification characteristics are well known and reliable.
2. Moderate confidence. Taxonomy may be questionable at this level, or field identification characteristics may be variable and difficult to assess consistently.
3. Low confidence. Taxonomy is incompletely known, or reliable field identification characteristics are unknown, or the occurrence of this taxon in the Bering Sea is doubtful and survey records have not been verified.

For example, for the taxa compared in the previous examples of inconsistent resolution in classification on the 1983 and 1990 surveys, confidence in the identifications is rated as follows:

1) Asteroidea unidentified, confidence high; 2) Individual Asteroidea subtaxa (identified genera

or species), confidence ranging between high, moderate, or low; 3) *Buccinum* sp., confidence high; 4) Individual identified *Buccinum* species, confidence low.

While providing a method of adjusting for variation in such elements as taxonomic knowledge and identification skills brought to the field, saliency of unique taxon characteristics, and stability of pertinent systematics, this method is based on a subjective assessment of each taxon as reported. In addition, it does not mitigate the possibility that a given reported taxon for which identification confidence is high, is also present among catch identified only at a higher taxonomic level. Thus, one cannot unambiguously assume that the higher-level taxon as reported does not contain that given subtaxon, present but not reported per se (e.g., some catch recorded as Asteroidea may include *Lethasterias nanimensis*, while in other cases *L. nanimensis* may be listed separately). Such an inconsistency in resolution of taxon identification is in fact possible, given historical differences among RACE personnel not only in knowledge and identification skill but also differences in satisfaction with identification above the species level. Lastly, the rating system does not specify a way to compare data for a taxon across a set of years during which the identification confidence level changes. A way of mitigating these problems with a systematic and objective method is therefore desirable. For invertebrate taxa in the EBS shelf annual surveys, the following method is presented.

## **THE LAIT METHOD**

An objective system was developed to address inconsistencies in the resolution of taxonomic classification of benthic invertebrates caught during annual RACE bottom trawl surveys in the EBS since 1982. The system consists of two SQL\*Plus<sup>®</sup> queries, run sequentially, accessing survey data in an ODBC database, and regrouping catch data (numbers and weights) unambiguously by taxon based on a relatable table of hierarchical relationships among reported taxa and a subset of the original catch data, chosen for analysis, corresponding to user-selected survey years. In each case, running the queries groups data according to the lowest accountable inclusive taxon (LAIT). For any given taxon reported in a chosen set of catch data the LAIT is determined as that taxon also reported therein, which by definition includes the given taxon and which itself is not defined as a subtaxon of another reported taxon. The LAIT of the given taxon



could thus be the same or a different taxon. Regardless, when the weights and numbers reported for the LAIT and for any of its reported sub-taxa are combined as being its total weight and number, the result necessarily includes 100% of the individuals of the given taxon possible in the reported catch. For example, if a dataset chosen for analysis by the system includes catch reported as *Buccinum scalariforme*, the system recognizes that taxon's place in the appropriate hierarchy, then searches the catch reported for each survey year included in the dataset, for any taxon defined as including *B. scalariforme* (e.g., *Buccinum* sp. or gastropod unidentified). If it finds any such classification(s), it accepts the highest-level one as the LAIT of *B. scalariforme*. If there is no other taxon inclusive of *B. scalariforme*, the LAIT in such case is *B. scalariforme*. Together, all LAITs for a data set unambiguously account for the invertebrate catch in the selected hauls, albeit with some possible loss of taxonomic resolution. *Nevertheless, using LAITs in invertebrate classification avoids the incorrect quantification of the catch of lower taxa, possible should records of the latter be used as if representing the only catch thereof, to the unknowing exclusion of individuals that have been present in catch reported only at higher, more inclusive taxonomic levels.*

### **Query System Structure**

The first, preliminary query (Invert\_Taxa\_Sig\_EBS\_82\_Present.sql) of the LAIT classification system addresses a concern regarding data entered for analysis in the second. It is possible that ambiguity in a given set of catch data from the EBS surveys due to the occurrence of a given taxon in addition to one or more of its subtaxa would be of minor proportion. This could happen if the less specific identification to the higher level were isolated, occurring in only one or a few hauls. In order to avoid disproportionate loss of specificity if catch of all its subtaxa in the database were to be consolidated under such an “outlier” taxon, the first query screens the EBS shelf survey invertebrate catch data from 1982 to 2015 for such instances. It allows the user to choose a minimum required of the weight proportion constituted by an upper-level taxon, relative to that of itself plus any of its reported subtaxa combined, in order for said upper-level taxon to be eligible for consolidation therein of such subtaxa, and thus the LAIT of the latter. This proportion is termed the “relative presence” of a taxon, and those meeting the criterion (e.g., relative presence  $\geq 0.1$ ) are said to be “significantly present” in the data and are therefore

potential LAITs. For example, in the 1992 survey a total of 2,465.6 kg of catch were classified as unidentified Asteroidea, while 33,532.1 kg were variously classified as species or genera within that class. The proportion of the total 1992 catch of Asteroidea (35,997.7 kg) constituted by the catch classified only to the class was thus 0.069. If a relative presence of  $\geq 0.05$  was specified as the criterion for significant presence during running of `Invert_Taxa_Sig_EBS_82_Present.sql`, then for 1992 catch classified as unidentified Asteroidea would be labeled significant.

The script for this query is in Appendix A. When copied into a \*.sql file by a user having ODBC access to the RACE EBS survey database, running it creates or replaces the table “`INVERT_TAXA_EBS_82_2015`” (ITEBS2015), containing the entire recorded RACE EBS bottom trawl survey catch of invertebrates, from all standard station hauls successfully completed on the EBS shelf from 1982 to 2015, extracted from the table `RACEBASE.CATCH` (RC). The new table lists catch according to taxon code, taxon rank, scientific name, common name, survey year, total aggregate weight for the year, and number of hauls where occurring. The query also calculates the relative presence for each reported taxon in each year, and subsequently labels each taxon record in the table field “`Sig_Pres`”, as showing significant presence (“Y”) in that year or not (“N”), based on the user's choice of a significant presence criterion for the query, when prompted. The pertinent hierarchical taxonomic relationships used in this analysis are determined by joining to the AFSC ODBC systematics hierarchy table `SMITHK.INVERT_CODE_HIERARCH_2015` (SKIH). This hierarchy lists the catch code for each invertebrate taxon reported in RACE bottom trawl surveys, from a lowest-level rank of species up to the rank phylum, and for each such taxon, any catch codes and rank assigned to higher-level taxa that include it (Thus, there are no inclusive-taxon codes associated with those for taxa of the highest-level rank, phylum). As a matter of course, when the first script is run any subtaxa of a higher-level taxon which has thereby been assigned “Y” in its `Sig_Pres` field for a given year, are also automatically assigned that value in their own field for the same year, even if their weight relative to that of any of their own subtaxa also reported in the year is insignificant. This is because, if the year in question is included in the dataset chosen (in the second script) for LAIT analysis, then for that dataset *each* subtaxon of said significant taxon should be included in the input for the second query, for incorporation into the higher-level taxon sure to be designated the LAIT, with none of those subtaxa eliminated as insignificant. All records for taxa at species

level are assigned a “Y” in the Sig\_Pres field, as there are no lower-level taxa whose presence in the final system output could be affected by consolidation within a species.

After all values of “Y” have been assigned in the Sig\_Pres field wherever justified by the operator’s chosen criterion, any records still with a null value in the field are updated to “N”, as not meeting that criterion for inclusion in LAIT catch calculations.

The classifications unsorted catch, unsorted SHAB (shells, hermit-crabs, and assorted bycatch), invertebrate unidentified, and worm unidentified, when reported, occur in the catch data of table RC and could conceivably include invertebrates. However, they are considered too undefined to be useful, are usually of minor relative presence, and are never included in the determination of LAITs and catch amounts thereof.

The second script, INVERT\_LAIT\_CATCH\_EBS82\_PRESENT.sql, is given in Appendix B and joins tables ITEBS2015, RC, and SKIH on certain fields pertaining to taxon code. Running it ultimately assigns LAITs to the taxa of invertebrate catch reported in RC from standard hauls of the EBS survey for each of a subset of the years from 1982 through 2015, chosen as the dataset of interest by the operator when prompted. Upon a second prompt the user chooses to include, in the determination of LAITs and the catch weights thereof, “all data” or only those records which have been assigned a “Y” (indicating significant relative presence) in the table field ITEBS2015.SIG\_PRES. Choosing “all data” eliminates any consideration of a minimum relative presence criterion for significance (*i.e.*, the criterion is “> 0”), including instead among the input of the second query any taxon inclusive of another in the data subset, regardless of how infrequent the occurrence of the higher-level taxon.

Alternatively, choosing “significant presence picks only” (records having Sig\_Pres = “Y” in table ITEBS2015) restricts input for LAIT calculation to taxa which have been marked significantly present by the first script, in one or more years of the subset.

The system then calculates LAIT for each given input taxon in the catch of the subset of years by searching the set of records in ITEBS2015 corresponding to those years, for any also-reported taxon designated as input and inclusive of the given taxon according to table SKIH. Of any such taxa found, the highest one in the taxonomic hierarchy is taken as the LAIT. In the absence of any inclusive higher-level taxon, the LAIT is the given taxon itself. Then by substituting for each input taxon, the query creates a new table re-assigning the weight and

numbers for each to its LAIT. The reclassified catch is listed by LAIT code, region (EBS), cruise, vessel, hauljoin (unique identifier of particular haul by a vessel in the time series), date, position, survey (EBS shelf), weight (always specified), and number of individuals (if counted). The operator names the new LAIT catch output table when prompted.

Because multiple taxa originally reported in a single haul could be assigned the same LAIT, in each such case the catch amounts are summed and the data consolidated to a single record. However, wherever individuals are counted for one taxon within a haul but not for another having the same LAIT, no count of individuals of the LAIT is given for that haul.

After catch weights and numbers have thus been re-assigned to LAITs, if the operator has chosen to calculate LAITs using only data for each taxon classified as significantly present in at least one of the years studied, then catch records for any upper-level (higher than species) taxa consistently rated insignificant every year of the dataset are listed in a separate table, named by the operator upon a prompt from the script. Thus, all catch amounts originally reported are accounted for in the total output.

If the operator, having once run the analysis system using a particular significance criterion, wishes to rerun it choosing “all data” or a different set of survey years, he or she may do so by merely re-running the second query without re-running the first.

The scripts of the two queries, included in this paper respectively as Appendix A and Appendix B, can be copied and run in that sequence by readers having ODBC access to the AFSC/RACE survey databases, subdirectories RACEBASE and SMITHK, using SQL\*Plus® or SQL Developer®. Readers can also observe the mechanics of the queries in the scripts, as a guide to building a system of similar capabilities using other databases.

### **Hierarchy Employed**

The taxonomic hierarchy employed in table SKIH for the query system generally follows that recognized by RACE for naming and classifying marine invertebrate fauna from all surveys the division has conducted, including in the Gulf of Alaska, Aleutian Islands, Bering Sea Slope, and West Coast regions as well as in the EBS shelf region. The hierarchy, descending from kingdom (Animalia) to each taxon assigned a code for reporting it in the surveys, is outlined in the table RACEBASE.SPECIES\_CLASSIFICATION. For invertebrates, SKIH shows a total of

14 taxonomic ranks represented among the coded taxa themselves, namely phylum, subphylum, class, subclass, infraclass, superorder, order, suborder, infraorder, superfamily, family, subfamily, genus, and species. I have added one “rank” classification to these in SKIH, “non-monophyletic group” (NMG), because some of the coded taxon names appear to apply to polyphyletic or paraphyletic groups of organisms, especially as the names were likely applied in the field (e.g., “snail unidentified” was a common name used on surveys in association with “Gastropoda”, but likely was applied to a paraphyletic portion of Gastropoda rather than the entire class). However, it was usually apparent what taxa each of these reported NMG classifications would include, and how to use them in the LAIT determinations accordingly. The problem of NMG classifications will likely decline as the quality of field classifications improves with time.

## **RESULTS AND EXAMPLES**

### **Reported Taxa**

The individual invertebrate taxa reported for the EBS shelf between 1982 and the present included the following: 12 phyla, 14 classes, 2 subclasses, 1 infraclass, 4 superorders, 11 orders, 13 NMGs, 1 suborder, 29 families, 138 genera, and 397 species. From the EBS, no taxa were reported at the levels subphylum, infraorder, superfamily, or subfamily. Thus not all the ranks given to taxa in the table SKIH were included, as that table is designed to accommodate all invertebrate taxa assigned codes by RACE for reporting catch in any of its survey regions, listed previously. This allows for the table to be used in future, in designing a similar query system to include regions other than the EBS. The total number of invertebrate taxa historically reported in the EBS surveys was 622, not including the classifications unsorted catch, unsorted SHAB, invertebrate unidentified, and worm unidentified.

### **Results of Query Trials**

To illustrate results obtained by using the query, the LAIT system was run separately for three datasets covering the survey years 1982-2015: 1) Data from 1982-1998 (the first half of the overall period); 2) the full dataset covering the entire period; and 3) 1999-2015 (the latter half of

the period). Overlapping the datasets in this way allowed for certain comparisons. Table 1 presents the number of taxa of each rank, originally reported in each dataset before any consolidation by LAIT (column “No Consolidation”). In addition, it shows the number of taxa by rank in the output of three different LAIT analyses of each dataset, at respective criteria of  $\geq 0.1$ ,  $\geq 0.05$ , or no limit ( $> 0$ ) required of the weight of a reported taxon relative to the total weight of itself plus any reported subtaxa (significant presence), in order for the taxon to be listed as an LAIT incorporating itself and subtaxa. For a given running of the system to establish LAITs for a dataset, this criterion is chosen at the appropriate prompt in the first script.

Table 1. --Number of taxa at each level represented in the original RACEBASE.CATCH EBS data and in LAIT reclassifications thereof, using each of three significant presence criteria ( $\geq 0.1$ ,  $\geq 0.05$ , and  $> 0$ ) required of a reported taxon before consolidation within it of the catch of subtaxa. Three table sections each pertain to a given dataset selected from the survey years 1982 through 2015. Background color designates the cells for each dataset.

Dataset	1982-1998				All Years				1999-2015			
	No consolidation	$\geq 0.1$	$\geq 0.05$	$> 0$	No consolidation	$\geq 0.1$	$\geq 0.05$	$> 0$	No consolidation	$\geq 0.1$	$\geq 0.05$	$> 0$
Phylum	10	10	10	10	12	12	12	12	11	11	11	11
Class	12	9	9	11	14	10	10	12	14	6	8	12
Subclass	2	2	2	2	2	1	1	1	2	1	1	1
Infraclass	1	1	1	1	1	1	1	1	1	0	0	1
Superorder	3	2	2	1	4	3	3	2	4	4	4	2
Order	8	8	8	5	11	10	10	7	10	9	9	7
NMG	12	5	7	7	13	4	6	6	13	5	5	6
Suborder	1	0	0	0	1	0	0	0	1	0	0	0
Family	17	6	1	0	29	8	1	0	26	8	3	0
Genus	74	15	4	0	138	29	7	2	131	62	22	2
Species	253	31	14	2	397	26	18	2	351	70	43	1
Total	393	89	58	39	622	104	69	45	564	176	106	43

Comparing the results presented in Table 1 by taxon rank provides insights into the taxonomic resolution achieved in identification of invertebrate taxa, occurring historically in the EBS surveys. For a given dataset, when the number of taxa of a given rank (row) differs at a given significant presence criterion (column) from the number in the raw data column (No Consolidation), it is due to one of two causes. One or more taxa were each either 1) eliminated by analysis at that significance criterion, by consolidation within a higher-level taxon (LAIT), itself judged as significantly present at that criterion, or 2) eliminated from the system output as not being a LAIT, due to constituting too small a fraction of the total weight of itself plus any subtaxa present, to meet the significance criterion when that is specified as  $\geq 0.1$  or  $\geq 0.05$ . For the significance criterion  $> 0$ , elimination of a taxon can only occur due to consolidation in a higher-level inclusive one, as all taxa in the raw data are considered significant.

In addition, for a given taxon at a given rank occurring in the raw data for both subsets, and while employing a particular significance criterion, elimination of the taxon from one subset but not the other will take one of the following forms: 1) One taxon less in one of the subsets and in the total dataset, due to the given taxon being consolidated within a significant higher taxon in said subset and therefore also in the entire dataset, but remaining present and unconsolidated in the other subset analyzed alone; or 2) For analysis using a criterion of either  $\geq 0.1$  or  $\geq 0.05$ , one taxon remaining in one of the subsets and therefor necessarily in the total dataset, but eliminated from the other subset as being judged insignificant in only that subset.

The following is a brief outline of the results in Table 1 according to taxon rank. In some cases where results for the inclusive dataset can be inferred from the results for the two subsets, only the latter are given.

### **Phylum**

Since this is the highest-level rank in the reported EBS invertebrate catch considered in this analysis, none of the phyla originally reported as such would be absent from any query output due to being consolidated with a parent taxon. However, phyla could theoretically be eliminated during analysis due to not meeting a particular significance



criterion. This did not occur for any of the three datasets, as there were no deviations from the number in the raw data (“No Consolidation”) column.

Of the 10 phyla originally reported as such in years 1982-1998 (older dataset), 9 also occurred in 1999-2015 (recent dataset). Two additional phyla of the total 11 in the recent dataset were in turn not included in the older dataset.

### **Class**

Twelve taxa of rank class were reported in the older dataset. All these plus an additional two classes totaled 14 in the recent dataset.

In the older dataset, three classes were eliminated, being either too insignificant for consolidation of their subtaxa therein or consolidated within a significant parent phylum, at each significance criterion  $\geq 0.1$  and  $\geq 0.05$ . One was eliminated by consolidation when the criterion was  $> 0$ . In the recent dataset, 8 classes at criterion  $\geq 0.1$  and 6 classes at criterion  $\geq 0.05$  were either insignificant for consolidation of their subtaxa therein and so eliminated, or were themselves consolidated upward in level. In addition, two classes at criterion  $\geq 0.1$  were consolidated upward.

### **Subclass**

Both datasets reported the same two subclasses. However, neither taxon was ever eliminated in analysis of the older dataset by itself, at any of the three significance criteria. By contrast, analysis of the recent dataset resulted in the consolidation upward of one subclass, regardless of the significance criteria used. Because this elimination occurred in the recent dataset and also in analysis of the entire data, but not in the older dataset, it could not have been due to not meeting a significance criterion in only the recent dataset. If such were the case, the elimination would not have occurred for the entire dataset.

### **Infraclass**

Both datasets reported the same single infraclass, which was not eliminated from the older dataset by analysis at any of the three significance criteria. However, analysis of the

recent dataset resulted in the elimination of the infraclass at the significance criteria  $\geq 0.05$  and  $\geq 0.1$ , as not meeting those respective requirements.

### **Superorder**

The older dataset contained three superorders, all of which occurred in the recent dataset, which also had a fourth superorder. It is likely that at the significance criterion  $> 0$ , two of these superorders were eliminated from both the older and recent datasets due to consolidation upward. In contrast, at each criterion  $\geq 0.05$  and  $\geq 0.1$  one superorder was consolidated upward in the older data subset but not in the recent one.

### **Order**

With the exception of trial results for the rank suborder, results at the ranks of Order and below display more complex variation according to data subset and significance criterion, with multiple explanations possible by inference from the table data. Therefore, characterizations herein of results for these ranks are limited to those indicated as unambiguous. The older dataset contained 8 orders, 7 of which also occurred in the recent dataset. The recent dataset also contained 3 additional orders which did not occur in the older one.

### **Non-monophyletic groups (NMG)**

The taxa referred to as non-monophyletic in this reclassification system numbered 12 in the older dataset. All these plus one additional such group occurred in the recent dataset.

### **Suborder**

Both the older and the recent datasets contained the same single suborder, which was eliminated from each dataset at all three of the trial significance criteria. At the criterion  $> 0$ , this was due to consolidation upward. At each criterion  $\geq 0.05$  or  $\geq 0.1$  it could have been for the same reason or due to too low a relative presence to meet the criterion.

## **Family**

Families reported in the older dataset numbered 17, of which 14 also occurred in the recent dataset. An additional 12 families occurred only in the recent dataset.

## **Genus**

Genera reported in the older dataset numbered 74, of which 67 also occurred in the recent dataset. An additional 64 genera occurred only in the recent dataset.

## **Species**

Species reported in the older dataset numbered 253, of which 207 also occurred in the recent dataset. An additional 144 species occurred only in the recent dataset.

## **Total Taxa of Output**

Examination of the total taxa reported for each dataset, including the complete dataset 1982 to 2015, along with the total taxa obtained given each significance criterion provides an idea of the magnitude of taxonomic diversity available when using the classification system for RACE EBS shelf survey invertebrate data. In the raw data, 393 total taxa occurred in the older dataset, of which 335 also occurred in the recent dataset. With an additional 229 taxa in the recent dataset, the total of invertebrate taxa reported during the entire 34-year period was 622. Analyzing the datasets using the LAIT system of course reduces the number of taxa below these figures, in the output, depending on the significance criterion specified. However, taking an arbitrary 90 as the minimum number of taxa desired in the result and specifying significance criteria to three decimal places, LAIT analysis yields the following:

Older dataset (1982-1998):  $\geq 0.116$  results in 93 taxa;

All Years (1982 – 2015):  $\geq 0.095$  results in 104 taxa; and

Recent dataset (1999-2015):  $\geq 0.002$  results in 91 taxa.

## DISCUSSION

### Pertinent Observations

The LAIT-analyzed data in Table 1 display three noticeable patterns. First, at the ranks of superorder and below, taxon numbers in each dataset for a given rank often decrease from those for the raw data (column: No Consolidation) as the significant presence criterion allowing consolidation decreases, with attendant increasing chance of a taxon of that rank being consolidated within a higher-level LAIT. This tendency becomes more pronounced as the taxonomic level decreases and there are more chances for incorporation into a higher-level taxon.

Secondly, at a given rank the numbers of taxa in the raw data or for a given significant presence criterion tend to be greatest in the overall dataset, compared with the corresponding factors for the years 1982 through 1998 or 1999 through 2014, respectively. This is reasonable, given that the complete dataset includes all catch from each of the two data subsets, while either of the latter could lack certain taxa which were however listed for the other subset and therefore also for the whole. Exceptions to this pattern occur when a given taxon is consolidated within an including taxon significant at a particular criterion in one data subset but not the other. In this case the elimination of the given taxon of lower rank, by consolidation with the including taxon, necessarily also occurs for the entire dataset, as well. This leaves the given taxon, per se, in only one of the data subsets.

The third pattern emerging is that, for the original data and also for LAIT analysis using any one of the three significance criteria ( $\geq 0.1$ ,  $\geq 0.05$ ,  $> 0$ ), outputs for the recent subset generally contain more taxa at a given rank than does the equivalent analysis of the earlier subset. It is unlikely that this phenomenon is due to a major increase in the overall taxonomic diversity of the invertebrate benthos in the region, caused by an influx of previously absent taxa. A detailed study of the EBS epibenthic communities as indicated by survey results from 1982 to 2002 found general consistency over that period in geographic location and membership for each of two major taxonomic domains evident from the data: inshore (depth  $\leq 50$  m) and offshore (depth  $> 50$  m,  $\leq 200$  m) communities (Yeung and McConnaughey 2006). Instead, Table 1 supports the hypothesis of gradually increasing familiarity with the EBS benthic invertebrate taxonomy, among RACE survey personnel, with a resulting decline in generality and increase in specificity of identifications.

The query system allows the user to adjust the scripts to provide desired minimization of ambiguity in taxonomic identification, balanced against achieving desired resolution and number of classifications (taxa) in that variable. For this purpose, the user is able to choose the minimum relative presence constituting significance (significance criterion) for a taxon in the data analyzed and thereby requiring that said taxon be considered a LAIT for consolidating any of its subtaxa present.

The inability to quantify catch restricted to a given species over a chosen period in the survey time series due to consolidation in a LAIT need not diminish the usefulness of the analyzed data. It is not always necessary or even desirable to classify sample fauna to the lowest possible taxonomic level for purposes of data analysis. Several studies comparing abundance with variables of environmental stress found no drop in correlations observed at the level of family or even phylum compared to those seen at the level of species (Ferraro and Cole 1995; Olsgard et al. 1997; Olsgard et al. 1998). This was especially so for an anthropogenic perturbation of considerable range. Only where completely “natural” variations were being observed did classification to species sometimes reveal additional significant associations. Indeed, where the purpose is other than examining this sort of correlation or simply observing phylogenetic diversity, resolution to the species level may only add “noise” variance (Warwick 1988; Warwick 1993). Such considerations may be included in decisions on how to use the LAIT taxonomic classification system outlined in this paper.

### **Limitation: Incorrect Identification**

Although capable of mitigating ambiguity in data resulting from inconsistent resolution in taxonomic identification, the LAIT system cannot mitigate incorrect specificity; that is, the classification of an organism in an incorrect taxon. It is possible that such mistakes occur when field personnel desire to get the best data by identifying individuals to the lowest-level taxon possible, and thus make an identification without being certain of the presence of the necessary characteristics. It is thus prudent to limit identification to the lowest-level taxon of which the observer can be certain, if the specimen cannot be retained for examination in a laboratory setting. LAIT system users are directed to the identification confidence rating table for EBS invertebrates by Stevenson and Hoff (2009), for consideration of taxa classified as LAIT in a

dataset analysis. Where a dataset spans years having different ratings for a given LAIT, choosing the lowest such rating would acknowledge ambiguity remaining in the analysis results.

### **Maintenance of the LAIT System**

Any future changes in recognized taxonomy affecting classification of invertebrates in the table RC must also be made in the table SKIH, which is essential to the query system but is hardcoded. Thus this pivotal table must be regularly checked against the RACE taxonomy for invertebrates in the survey catch, as represented in such sources as the RACE ODBC table RACEBACE.SPECIES\_CLASSIFICATION.

For visual reference, records in the tables SKIH and ITEBS2015 can be ordered by ascending taxon code, which process generally groups taxa with appropriate encompassing higher taxa in order of decreasing level. For example, polychaetes identified only to the family Polynoidae are followed by polynoids identified as of the genus *Eunoe*. Table SKIH carries copying/reading permission.

## CONCLUSIONS

The taxonomic framework upon which marine invertebrate classification is based is in a continuous state of development. The phylogenies of these fauna are not universally agreed upon, by even the most informed sources (Ruppert et al. 2004). New information is continuously being incorporated and systems revised. For example, the former class Turbellaria, placed by taxonomists within the phylum Platyhelminthes, has now been deemed invalid by both I.T.I.S and WoRMS, as having been polyphyletic (it included both protostome and deuterostome subtaxa). Nevertheless, taxonomy remains an important characterization of genotypic and phenotypic diversity: many of the lower-level taxa remain recognized and identifiable despite changes to accepted phylogenies involving higher taxa (Cairns et al. 2002, McLaughlin et al. 2005, Ruppert et al. 2004, Turgeon et al. 1998).

### **The LAIT Classification System**

Inconsistency of taxonomic resolution in field classification of marine organisms during surveys can introduce ambiguity, and even misinterpretation of data if catch correctly reported for a lower taxon were then mistakenly taken to represent the entire catch thereof, to the exclusion of individuals identified to one or more higher-level, more inclusive taxa. The LAIT SQL\*Plus<sup>®</sup> query system is an objective method for resolving such inconsistency. The concept is developed here using benthic invertebrate catches from 34 years of annual bottom-trawl surveys in the EBS.

Consolidation under LAITS in the manner of this system may lose some taxonomic detail when weights and numbers reported for lower taxa are combined with those originally reported only for higher-level, inclusive ranks, but this need not negate the usefulness of the data. The use of LAITs allows more confident comparison of data where classification may have varied among years, vessels, cruises, hauls, etc.





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## APPENDIX A

### Invert\_Taxa\_Sig\_EBS\_82\_Present.sql

accept xcriteria prompt 'Specify sig. rel. wgt. (minimum) for designating an LAIT encompassing other taxa (e.g., ">=0.1"):'

```
drop table EBS_STANDARD_HAULS_82_PRESENT;
drop view EBS_STANDARD_HAULS_82_PRESENT;
create table EBS_STANDARD_HAULS_82_PRESENT as
SELECT to_number(to_char(hl.start_time,'yyyy')) year,hl.*
FROM RACEBASE.HAUL hl
JOIN RACE_DATA.V_CRUISES cr
ON (cr.CRUISEJOIN = hl.CRUISEJOIN)
WHERE hl.PERFORMANCE >= 0
AND hl.HAUL_TYPE = 3
AND hl.STATIONID IS NOT NULL
AND hl.STRATUM IN (10,20,31,32,41,42,43,50,61,62,82,90)
AND cr.SURVEY_DEFINITION_ID = 98;
```

```
DROP TABLE INVERT_TAXA_EBS_82_PRESENT;
CREATE TABLE INVERT_TAXA_EBS_82_PRESENT AS
SELECT DISTINCT hi.TAXON_CODE, hi.TAXON_LEVEL, hi.SCI_NAME,
hi.COMM_NAME, st.YEAR SURVEY_YEAR, SUM(ca.WEIGHT) KG_WGT,
SUM(ca.NUMBER_FISH) NUMBER_INDIV, COUNT(st.HAULJOIN) NUMBER_HAULS
FROM SMITHK.INVERT_CODE_HIERARCH_2014 hi,
EBS_STANDARD_HAULS_82_PRESENT st, RACEBASE.CATCH ca WHERE st.REGION =
ca.REGION AND st.CRUISEJOIN = ca.CRUISEJOIN AND st.HAULJOIN = ca.HAULJOIN
AND hi.TAXON_CODE = ca.SPECIES_CODE AND st.CRUISE >=198200 AND st.REGION
='BS'
GROUP BY TAXON_CODE, TAXON_LEVEL, SCI_NAME, COMM_NAME, YEAR;
ALTER TABLE INVERT_TAXA_EBS_82_PRESENT
ADD SIG_PRES VARCHAR2(2 BYTE)NULL;
```

```
DROP TABLE Phyl_Wgt_Pres;
CREATE TABLE Phyl_Wgt_Pres AS SELECT distinct tp.taxon_code, tp.taxon_level,
tp.survey_year, tp.kg_wgt, (tp.kg_wgt)/(Sum(t.kg_wgt)) phyl_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tp, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tp.taxon_code = h.phylcode AND
h.taxon_code = t.taxon_code AND tp.survey_year = t.survey_year AND tp.taxon_level = 'P'
GROUP BY tp.taxon_code, tp.taxon_level, tp.survey_year, tp.kg_wgt;
```

```
UPDATE INVERT_TAXA_EBS_82_PRESENT
```

```

SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT phyl_rel_wgt FROM Phyl_Wgt_Pres ph,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE ph.taxon_code = h.phylcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND ph.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND ph.phyl_rel_wgt &xcriteria);

```

```

DROP TABLE subPhyl_Wgt_Pres;
CREATE TABLE subPhyl_Wgt_Pres AS SELECT distinct tsbp.taxon_code, tsbp.taxon_level,
tsbp.survey_year, tsbp.kg_wgt, (tsbp.kg_wgt)/(Sum(t.kg_wgt)) subphyl_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tsbp,
smithk.INVERT_CODE_HIERARCH_2014 h, INVERT_TAXA_EBS_82_PRESENT t
WHERE tsbp.taxon_code = h.subphylcode AND h.taxon_code = t.taxon_code AND
tsbp.survey_year = t.survey_year AND tsbp.taxon_level = 'subP'
GROUP BY tsbp.taxon_code, tsbp.taxon_level, tsbp.survey_year, tsbp.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT subphyl_rel_wgt FROM subPhyl_Wgt_Pres sbp,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE sbp.taxon_code = h.subphylcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND sbp.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND sbp.subphyl_rel_wgt &xcriteria);

```

```

DROP TABLE Class_Wgt_Pres;
CREATE TABLE Class_Wgt_Pres AS SELECT distinct tc.taxon_code, tc.taxon_level,
tc.survey_year, tc.kg_wgt, (tc.kg_wgt)/(Sum(t.kg_wgt)) class_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tc, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tc.taxon_code = h.classcode AND
h.taxon_code = t.taxon_code AND tc.survey_year = t.survey_year AND tc.taxon_level = 'C'
GROUP BY tc.taxon_code, tc.taxon_level, tc.survey_year, tc.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT class_rel_wgt FROM Class_Wgt_Pres c,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE c.taxon_code = h.classcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND c.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND c.class_rel_wgt &xcriteria);

```

```

DROP TABLE subClass_Wgt_Pres;
CREATE TABLE subClass_Wgt_Pres AS SELECT distinct tsc.taxon_code, tsc.taxon_level,
tsc.survey_year, tsc.kg_wgt, (tsc.kg_wgt)/(Sum(t.kg_wgt)) subclass_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tsc, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tsc.taxon_code = h.subclasscode AND
h.taxon_code = t.taxon_code AND tsc.survey_year = t.survey_year AND tsc.taxon_level =
'subC'
GROUP BY tsc.taxon_code, tsc.taxon_level, tsc.survey_year, tsc.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT subclass_rel_wgt FROM subClass_Wgt_Pres sbc,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE sbc.taxon_code = h.subclasscode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND sbc.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND sbc.subclass_rel_wgt &xcriteria);

```

```

DROP TABLE infraClass_Wgt_Pres;
CREATE TABLE infraClass_Wgt_Pres AS SELECT distinct tic.taxon_code, tic.taxon_level,
tic.survey_year, tic.kg_wgt, (tic.kg_wgt)/(Sum(t.kg_wgt)) infraclass_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tic, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tic.taxon_code = h.infraclasscode AND
h.taxon_code = t.taxon_code AND tic.survey_year = t.survey_year AND tic.taxon_level = 'infC'
GROUP BY tic.taxon_code, tic.taxon_level, tic.survey_year, tic.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT infraclass_rel_wgt FROM infraClass_Wgt_Pres ic,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE ic.taxon_code = h.infraclasscode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND ic.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND ic.infraclass_rel_wgt &xcriteria);

```

```

DROP TABLE superOrder_Wgt_Pres;
CREATE TABLE superOrder_Wgt_Pres AS SELECT distinct tspo.taxon_code,
tspo.taxon_level, tspo.survey_year, tspo.kg_wgt, (tspo.kg_wgt)/(Sum(t.kg_wgt))
superorder_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tspo,
smithk.INVERT_CODE_HIERARCH_2014 h, INVERT_TAXA_EBS_82_PRESENT t
WHERE tspo.taxon_code = h.superordcode AND h.taxon_code = t.taxon_code AND
tspo.survey_year = t.survey_year AND tspo.taxon_level = 'supO'
GROUP BY tspo.taxon_code, tspo.taxon_level, tspo.survey_year, tspo.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT superorder_rel_wgt FROM superOrder_Wgt_Pres spo,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE spo.taxon_code = h.superordcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND spo.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND spo.superorder_rel_wgt &xcriteria);

```

```

DROP TABLE Order_Wgt_Pres;
CREATE TABLE Order_Wgt_Pres AS SELECT distinct tord.taxon_code, tord.taxon_level,
tord.survey_year, tord.kg_wgt, (tord.kg_wgt)/(Sum(t.kg_wgt)) order_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tord,
smithk.INVERT_CODE_HIERARCH_2014 h, INVERT_TAXA_EBS_82_PRESENT t

```

```
WHERE tord.taxon_code = h.ordcode AND h.taxon_code = t.taxon_code AND tord.survey_year
= t.survey_year AND tord.taxon_level = 'O'
GROUP BY tord.taxon_code, tord.taxon_level, tord.survey_year, tord.kg_wgt;
```

```
UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT order_rel_wgt FROM Order_Wgt_Pres o,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE o.taxon_code = h.ordcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND o.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND o.order_rel_wgt &xcriteria);
```

```
DROP TABLE NMG_Wgt_Pres;
CREATE TABLE NMG_Wgt_Pres AS SELECT distinct tnmg.taxon_code, tnmg.taxon_level,
tnmg.survey_year, tnmg.kg_wgt, (tnmg.kg_wgt)/(Sum(t.kg_wgt)) nmg_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tnmg,
smithk.INVERT_CODE_HIERARCH_2014 h, INVERT_TAXA_EBS_82_PRESENT t
WHERE tnmg.taxon_code = h.nmgcode AND h.taxon_code = t.taxon_code AND
tnmg.survey_year = t.survey_year AND tnmg.taxon_level = 'NMG'
GROUP BY tnmg.taxon_code, tnmg.taxon_level, tnmg.survey_year, tnmg.kg_wgt;
```

```
UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT nmg_rel_wgt FROM NMG_Wgt_Pres nmg,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE nmg.taxon_code = h.nmgcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND nmg.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND nmg.nmg_rel_wgt &xcriteria);
```

```
DROP TABLE subOrder_Wgt_Pres;
CREATE TABLE subOrder_Wgt_Pres AS SELECT distinct tsbo.taxon_code, tsbo.taxon_level,
tsbo.survey_year, tsbo.kg_wgt, (tsbo.kg_wgt)/(Sum(t.kg_wgt)) suborder_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tsbo,
smithk.INVERT_CODE_HIERARCH_2014 h, INVERT_TAXA_EBS_82_PRESENT t
WHERE tsbo.taxon_code = h.subordcode AND h.taxon_code = t.taxon_code AND
tsbo.survey_year = t.survey_year AND tsbo.taxon_level = 'subO'
GROUP BY tsbo.taxon_code, tsbo.taxon_level, tsbo.survey_year, tsbo.kg_wgt;
```

```
UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT suborder_rel_wgt FROM subOrder_Wgt_Pres sbo,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE sbo.taxon_code = h.subordcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND sbo.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND sbo.suborder_rel_wgt &xcriteria);
```

```
DROP TABLE infraOrder_Wgt_Pres;
```

```

CREATE TABLE infraOrder_Wgt_Pres AS SELECT distinct tino.taxon_code, tino.taxon_level,
tino.survey_year, tino.kg_wgt, (tino.kg_wgt)/(Sum(t.kg_wgt)) infraorder_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tino, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tino.taxon_code = h.infraordcode AND
h.taxon_code = t.taxon_code AND tino.survey_year = t.survey_year AND tino.taxon_level =
'infO'
GROUP BY tino.taxon_code, tino.taxon_level, tino.survey_year, tino.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT infraorder_rel_wgt FROM infraOrder_Wgt_Pres ino,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE ino.taxon_code = h.infraordcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND ino.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND ino.infraorder_rel_wgt &xcriteria);

```

```

DROP TABLE superFam_Wgt_Pres;
CREATE TABLE superFam_Wgt_Pres AS SELECT distinct tspf.taxon_code, tspf.taxon_level,
tspf.survey_year, tspf.kg_wgt, (tspf.kg_wgt)/(Sum(t.kg_wgt)) superfam_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tspf, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tspf.taxon_code = h.superfamcode AND
h.taxon_code = t.taxon_code AND tspf.survey_year = t.survey_year AND tspf.taxon_level =
'supF'
GROUP BY tspf.taxon_code, tspf.taxon_level, tspf.survey_year, tspf.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT superfam_rel_wgt FROM superFam_Wgt_Pres spf,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE spf.taxon_code = h.superfamcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND spf.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND spf.superfam_rel_wgt &xcriteria);

```

```

DROP TABLE Family_Wgt_Pres;
CREATE TABLE Family_Wgt_Pres AS SELECT distinct tf.taxon_code, tf.taxon_level,
tf.survey_year, tf.kg_wgt, (tf.kg_wgt)/(Sum(t.kg_wgt)) family_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tf, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tf.taxon_code = h.famcode AND
h.taxon_code = t.taxon_code AND tf.survey_year = t.survey_year AND tf.taxon_level = 'F'
GROUP BY tf.taxon_code, tf.taxon_level, tf.survey_year, tf.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT family_rel_wgt FROM Family_Wgt_Pres f,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE f.taxon_code = h.famcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND f.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND f.family_rel_wgt &xcriteria);

```

```

DROP TABLE subFam_Wgt_Pres;
CREATE TABLE subFam_Wgt_Pres AS SELECT distinct tsbf.taxon_code, tsbf.taxon_level,
tsbf.survey_year, tsbf.kg_wgt, (tsbf.kg_wgt)/(Sum(t.kg_wgt)) subfam_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tsbf, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tsbf.taxon_code = h.subfamcode AND
h.taxon_code = t.taxon_code AND tsbf.survey_year = t.survey_year AND tsbf.taxon_level =
'subF'
GROUP BY tsbf.taxon_code, tsbf.taxon_level, tsbf.survey_year, tsbf.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT subfam_rel_wgt FROM subFam_Wgt_Pres sbf,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE sbf.taxon_code = h.subfamcode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND sbf.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND sbf.subfam_rel_wgt &xcriteria);

```

```

DROP TABLE Genus_Wgt_Pres;
CREATE TABLE Genus_Wgt_Pres AS SELECT distinct tg.taxon_code, tg.taxon_level,
tg.survey_year, tg.kg_wgt, (tg.kg_wgt)/(Sum(t.kg_wgt)) genus_rel_wgt
FROM INVERT_TAXA_EBS_82_PRESENT tg, smithk.INVERT_CODE_HIERARCH_2014
h, INVERT_TAXA_EBS_82_PRESENT t WHERE tg.taxon_code = h.gencode AND
h.taxon_code = t.taxon_code AND tg.survey_year = t.survey_year AND tg.taxon_level = 'G'
GROUP BY tg.taxon_code, tg.taxon_level, tg.survey_year, tg.kg_wgt;

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET INVERT_TAXA_EBS_82_PRESENT.sig_pres = 'Y'
WHERE EXISTS (SELECT genus_rel_wgt FROM Genus_Wgt_Pres g,
smithk.INVERT_CODE_HIERARCH_2014 h WHERE g.taxon_code = h.gencode AND
h.taxon_code = INVERT_TAXA_EBS_82_PRESENT.taxon_code AND g.survey_year =
INVERT_TAXA_EBS_82_PRESENT.survey_year AND g.genus_rel_wgt &xcriteria);

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET sig_pres = 'Y'
WHERE taxon_level = 'Spec';

```

```

UPDATE INVERT_TAXA_EBS_82_PRESENT
SET sig_pres = 'N'
WHERE sig_pres IS NULL;

```



## APPENDIX B

### INVERT\_LAIT\_CATCH\_EBS82\_PRESENT.sql

set heading on

```
/* THIS QUERY RETURNS EBS 1982-PRESENT RACEBASE.CATCH DATA FOR  
INVERTEBRATE TAXA, RECLASSIFIED ACCORDING TO LOWEST ACCOUNTABLE  
INCLUSIVE TAXON (LAIT). THE LAIT OF A GIVEN REPORTED TAXON IS THAT  
LOWEST REPORTED TAXON, DEFINED AS INCLUDING ANY OF ITS SUB-TAXA  
ALSO REPORTED, WHICH ACCOUNTS FOR CATCH INCLUDING IN PRINCIPAL ALL  
INDIVIDUALS OF THE TAXON OF INTEREST AMONG REPORTED CATCH. THUS,  
THE LAIT COULD BE THE TAXON OF INTEREST OR A HIGHER TAXON.
```

THE QUERY ACCOMODATES ONLY TAXA RECORDED FOR STANDARD HAULS, i.e. THOSE WITH PERFORMANCE  $\geq 0$  AND TYPE 3 IN THE TABLE RACEBASE.HAUL, EXECUTED FROM 1982 THROUGH PRESENT, AND APPEARING IN THE TABLE RACEBASE.CATCH FOR REGION BS, STANDARD SHELF CRUISJOINS. HAULS QUALIFYING IN THIS WAY ARE IDENTIFIED IN THE QUERY BY JOINING TO THE TABLE EBS\_STANDARD\_HAULS\_82\_PRESENT (CREATED PREVIOUSLY BY RUNNING THE SEPARATE QUERY OF THIS SYSTEM, INVERT\_TAXA\_SIG\_EBS\_82\_PRESENT.sql). WHEN PROMPTED, THE OPERATOR CHOOSES THE YEARS OF EBS SURVEY CATCH DATA TO BE RECLASSIFIED. THE TAXONOMIC HIERARCHY USED HEREIN IS SPECIFIED IN THE SUPPORTING TABLE SMITHK.INVERT\_CODE\_HIERARCH\_2014, AND FOLLOWS THAT USED BY RACE DIVISION FOR INVERTEBRATE SPECIES AS OF SUMMER, 2015. HOWEVER, THE HIERARCHY IS HARD-CODED, SO ANY SUBSEQUENT TAXONOMIC CHANGES BY THE DIVISION MUST BE INTEGRATED INTO THE TABLE.

THE PREVIOUS QUERY IN THE LAIT SYSTEM, INVERT\_TAXA\_SIG\_EBS\_82\_PRESENT.sql, CREATES THE TABLE INVERT\_TAXA\_EBS\_82\_PRESENT, IDENTIFYING CATCH OF EACH UPPER TAXA CLASSIFIED AS INCLUSIVE OF OTHER TAXA ALSO REPORTED, AND ADDITIONALLY DEEMED A SIGNIFICANT FRACTION OF THE TOTAL CATCH FOR THE CLADE IT DEFINES. THE OPERATOR CHOOSES THE CRITERIA FOR SIGNIFICANCE (e.g.,  $\geq 0.1$ ). SUBSEQUENTLY, IN THIS QUERY HE/SHE CAN THEN OPT FOR INCLUDING ALL UPPER TAXA OR ONLY THOSE THUS DEEMED SIGNIFICANT, WHEN DESIGNATING LAIT'S. AFTER RECLASSIFICATION, ALL CATCH DATA FOR RECLASSIFIED TAXA IN THE CHOSEN YEARS IS PRESENTED AS LAIT'S BY HAUL IN AN OPERATOR-NAMED TABLE. CATCH REPORTED FOR ANY UPPER TAXON HAVING ALSO-REPORTED SUB-TAXA BUT NOT IN ITSELF SIGNIFICANT ENOUGH TO BE DEEMED AN LAIT IS LISTED IN A SEPARATE TABLE, ALSO NAMED BY THE OPERATOR.\*/

prompt 'MEMO: DO NOT USE QUOTE MARKS IN RESPONDING TO QUERY AND USE 4 DIGIT YEARS. SELECTING ONLY SIGNIF PRESENCE PICKS WHEN PROMPTED MAY INCREASE TAXONOMIC RESOLUTION OF OUTPUT BUT LOSE A SMALL AMOUNT OF DATA, SO YOU MAY WISH TO FIRST RUN THE QUERY SELECTING ALL DATA AND EXAMINE OUTPUT TAXA LISTED IN THE INCIDENTALLY CREATED TABLE LAIT\_CHECK, for sufficiency of resolution.'

accept xyear prompt 'Specify year(s) in sqlplus syntax (e.g., "= 1985", "in (1985, 1986)": '

accept xsig\_pres prompt 'select ("1") all data or ("2") signif. presence picks only: '

accept xhaultab prompt 'Enter haul table name for selected years: '

accept xcatchout prompt 'Enter grouped-catch table name for selected years: '

accept xinsigcatch prompt 'Enter insignif ungrouped-catch table name for selected years: '

/\* THIS SECTION GETS THE CODE AND TAXON LEVEL FOR EACH INVERTEBRATE TAXON CAUGHT WITHIN THE YEAR(S) SPECIFIED AT PROMPT "SPECIFY YEAR(S)". TAXON LEVELS AS CODED IN TABLES SMITHK.INVERT\_CODE\_HIERARCH\_2014 AND INVERT\_TAXA\_EBS\_82\_PRESENT ARE SPECIES = Spec, GENUS = G, SUBFAMILY = subF, FAMILY = F, SUPERFAMILY = supF, INFRAORDER = infO, SUBORDER = subO, NON-MONOPHYLETIC GROUP = NMG, ORDER = O, SUPERORDER = supO, INFRACLASS = infC, SUBCLASS = subC, CLASS = C, SUBPHYLUM = subP, PHYLUM = P. FOR UNSORTED CATCH REPORTED SUCH AS "INVERTEBRATE UNIDENTIFIED" OR "UNSORTED SHAB", THE TAXON\_LEVEL ENTERED IS "NA" AND THE CATCH DATA ARE NOT INCLUDED IN THE OUTPUT. FOR THE PURPOSE OF DETERMINING LAIT'S, TYPING "1" AT THE PROMPT "SELECT (1) ALL DATA OR (2) SIGNIF. PRESENCE PICKS ONLY" INPUTS TAXON CATCH DATA FOR ALL OTHER TAXON\_LEVEL DESIGNATIONS. TYPING "2" INPUTS ALL SPECIES-LEVEL DATA BUT RESTRICTS ANY INPUT DATA FOR A GENUS-OR-HIGHER TAXON TO THAT OF ANY YEAR(S) INCLUDED WHERE THE CATCH WAS JUDGED SIGNIFICANT. THIS EXCLUDES YEARS WHEN THE AMOUNT WAS JUDGED SMALL ENOUGH TO BE DISREGARDED IN ESSENTIALLY UNAMBIGUOUS USE OF DATA FOR LOWER, ENCOMPASSED TAXA.

QUERY OUTPUT IS THE VIEW INVERT\_YEAR\_SUBSET. \*/

set verify on

drop view presence;

create view presence as

select decode (&xsig\_pres,2,'= "Y"',1,'in ("Y","N")') yesno from dual;

drop view invert\_year\_subset;

spool test2.sql

select 'create view invert\_year\_subset as ', 'select distinct taxon\_code, taxon\_level  
from INVERT\_TAXA\_EBS\_82\_PRESENT ', 'where sig\_pres '||yesno||' and survey\_year &xyear;'  
from presence;

spool off  
start test2.sql

```
/* THIS SECTION CALCULATES THE LAIT FOR EACH TAXON REPORTED WITHIN  
THE YEARS SPECIFIED IN INVERT_YEAR_SUBSET. QUERY OUTPUT IS TABLE  
INVERT_YEARSET_LAIT. */
```

```
drop table invert_yearset_lait;
```

```
create table invert_yearset_lait as select s.taxon_code, s.taxon_level, sci_name, comm_name,  
sp.taxon_code lait_code, sp.taxon_level lait_level from invert_year_subset s, invert_year_subset  
sp, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND  
h.phylcode = sp.taxon_code  
union select s.taxon_code, s.taxon_level, sci_name, comm_name, sspb.taxon_code lait_code,  
ssbp.taxon_level lait_level from invert_year_subset s, invert_year_subset sspb,  
smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND  
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM  
invert_year_subset))) AND h.subphylcode = sspb.taxon_code  
union select s.taxon_code, s.taxon_level, sci_name, comm_name, sc.taxon_code lait_code,  
sc.taxon_level lait_level from invert_year_subset s, invert_year_subset sc,  
smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND  
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM  
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT  
taxon_code FROM invert_year_subset))) AND h.classcode = sc.taxon_code  
union select s.taxon_code, s.taxon_level, sci_name, comm_name, ssrc.taxon_code lait_code,  
ssbc.taxon_level lait_level from invert_year_subset s, invert_year_subset ssrc,  
smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND  
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM  
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT  
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT  
IN (SELECT taxon_code FROM invert_year_subset))) AND h.subclasscode = ssrc.taxon_code  
union select s.taxon_code, s.taxon_level, sci_name, comm_name, sinc.taxon_code lait_code,  
sinc.taxon_level lait_level from invert_year_subset s, invert_year_subset sinc,  
smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND  
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM  
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT  
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT  
IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode IS NULL) OR  
(h.subclasscode NOT IN (SELECT taxon_code from invert_year_subset)))AND h.infraclasscode  
= sinc.taxon_code  
union select s.taxon_code, s.taxon_level, sci_name, comm_name,  
sspo.taxon_code lait_code, sspo.taxon_level lait_level from invert_year_subset s,  
invert_year_subset sspo, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =  
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
```

```

FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND h.superordcode = sspo.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
so.taxon_code lait_code, so.taxon_level lait_level from invert_year_subset s, invert_year_subset
so, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT
IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode IS NULL) OR
(h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND h.ordcode = so.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
snmg.taxon_code lait_code, snmg.taxon_level lait_level from invert_year_subset s,
invert_year_subset snmg, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND h.nmgcode = snmg.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
ssbo.taxon_code lait_code, ssbo.taxon_level lait_level from invert_year_subset s,
invert_year_subset ssbo, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND h.subordcode =
ssbo.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,

```

```

sino.taxon_code lait_code, sino.taxon_level lait_level from invert_year_subset s,
invert_year_subset sino, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
h.infraordcode = sino.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
sspf.taxon_code lait_code, sspf.taxon_level lait_level from invert_year_subset s,
invert_year_subset sspf, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraordcode is NULL) OR (h.infraordcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND h.superfamcode = sspf.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
sf.taxon_code lait_code, sf.taxon_level lait_level from invert_year_subset s, invert_year_subset
sf, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT
IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode IS NULL) OR
(h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraordcode IS NULL) OR (h.infraordcode NOT IN (SELECT taxon_code FROM

```

```

invert_year_subset))) AND ((h.superfamcode IS NULL) OR (h.superfamcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND h.famcode = sf.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
ssbf.taxon_code lait_code, ssbf.taxon_level lait_level from invert_year_subset s,
invert_year_subset ssbf, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code =
s.taxon_code AND ((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code
FROM invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR
(h.classcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode
IS NULL) OR (h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset)))
AND ((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraordcode IS NULL) OR (h.infraordcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superfamcode IS NULL) OR (h.superfamcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.famcode IS NULL) OR
(h.famcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND h.subfamcode =
ssbf.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
sg.taxon_code lait_code, sg.taxon_level lait_level from invert_year_subset s, invert_year_subset
sg, smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT
IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode IS NULL) OR
(h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraordcode IS NULL) OR (h.infraordcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superfamcode IS NULL) OR (h.superfamcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.famcode IS NULL) OR
(h.famcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subfamcode
IS NULL) OR (h.subfamcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
h.gencode = sg.taxon_code
union select s.taxon_code, s.taxon_level, sci_name, comm_name,
h.speccode lait_code, h.taxon_level lait_level from invert_year_subset s,
smithk.INVERT_CODE_HIERARCH_2014 h where h.taxon_code = s.taxon_code AND
((h.phylcode IS NULL) OR (h.phylcode NOT IN (SELECT taxon_code FROM

```

```
invert_year_subset))) AND ((h.subphylcode IS NULL) OR (h.subphylcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.classcode IS NULL) OR (h.classcode NOT
IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subclasscode IS NULL) OR
(h.subclasscode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraclasscode IS NULL) OR (h.infraclasscode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superordcode IS NULL) OR (h.superordcode NOT IN (SELECT
taxon_code FROM invert_year_subset))) AND ((h.ordcode IS NULL) OR (h.ordcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.nmgcode IS NULL) OR
(h.nmgcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subordcode
IS NULL) OR (h.subordcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.infraordcode IS NULL) OR (h.infraordcode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND ((h.superfamcode IS NULL) OR (h.superfamcode NOT IN
(SELECT taxon_code FROM invert_year_subset))) AND ((h.famcode IS NULL) OR
(h.famcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND ((h.subfamcode
IS NULL) OR (h.subfamcode NOT IN (SELECT taxon_code FROM invert_year_subset))) AND
((h.gencode IS NULL) OR (h.gencode NOT IN (SELECT taxon_code FROM
invert_year_subset))) AND (h.speccode IN (SELECT taxon_code FROM invert_year_subset))
ORDER BY taxon_code;
```

```
/* THIS SECTION CREATES A HAUL DATA TABLE AND CATCH DATA TABLE FOR
THE CHOSEN YEARS */
```

```
drop table &xhaultab;
create table &xhaultab as
select * from EBS_STANDARD_HAULS_82_PRESENT where year &xyear;
```

```
set heading off
```

```
drop table tempcatch;
create table tempcatch as
select c.* from racebase.catch c,&xhaultab h where c.region='BS' and c.hauljoin=h.hauljoin and
species_code>=40000;
```

```
/* THIS SECTION CREATES A TABLE ASSIGNING THE RESPECTIVE NEW, LAIT
CODES TO THE TAXA IN THE CATCH DATA SET. IT ALSO CREATES A TABLE
CONTAINING THE CATCH DATA FOR UPPER-LEVEL TAXA WHICH HAVE BEEN
EXCLUDED FROM LAIT CALCULATION AS OF INSIGNIFICANT AMOUNT. THUS ALL
CATCH AMOUNTS ARE ULTIMATELY ACCOUNTED FOR IN THE TOTAL OUTPUT*/
```

```
drop table newcatch;
create table newcatch as
select species_code, sci_name, comm_name, cruisejoin, hauljoin, region, vessel, cruise, haul,
lait_code, weight, number_fish number_indiv
```

```
from tempcatch, invert_yearset_lait
where species_code = taxon_code;
```

```
drop table &xinsigcatch;
create table &xinsigcatch as
select t.species_code, h.sci_name, h.comm_name, cruisejoin, hauljoin, region, vessel, cruise,
haul,
weight, number_fish number_indiv
from tempcatch t, invert_yearset_lait i, smithk.INVERT_CODE_HIERARCH_2014 h
where t.species_code = h.taxon_code and h.taxon_code = i.taxon_code (+) and i.taxon_code IS
NULL;
```

```
/* THIS SECTION CREATES A TABLE SHOWING THE DISTINCT TAXA ULTIMATELY
LISTED AS LAIT'S IN THE FINAL OUTPUT, FOR EASY OBSERVANCE. LAIT'S ARE
LISTED THEREIN BY TAXON CODE, TAXON NAME, COMMON NAME, AND
TAXONOMIC LEVEL.*/
```

```
drop table lait_check;
create table lait_check as
select distinct lait_code, lait_level, species_name lait_name, common_name from
invert_yearset_lait i, race_data.race_species_codes r
where i.lait_code = r.species_code
order by lait_code;
```

```
/* THIS SECTION SUMS WITHIN EACH HAUL IN THE DATA-SET THE WEIGHTS AND
NUMBERS OF INDIVIDUALS FOR TAXA RE-CLASSIFIED UNDER EACH
APPROPRIATE LAIT. NOTE THAT WHILE WEIGHTS HAVE BEEN REPORTED FOR
ALL TAXA, ORIGINAL NUMBER RECORDS FOR TAXA CONTRIBUTING TO A
SINGLE LAIT IN A HAUL COULD BE BOTH NULL AND NOT-NULL. THEREFORE
WHEREVER THIS OCCURS THE RESULTING TOTAL NUMBER OF INDIVIDUALS FOR
THE LAIT IS UPDATED TO NULL, TO AVOID UNDER-REPRESENTATION OF
NUMBERS */
```

```
drop view nocount_haul_lait;
create view nocount_haul_lait as
select distinct hauljoin, lait_code
from newcatch
where number_indiv IS NULL;
```

```
drop table &xcatchout;
create table &xcatchout as
select cruisejoin,hauljoin,region,vessel,cruise,haul,
lait_code,sum(weight) weight, sum(number_indiv) number_indiv
from newcatch
```



```
group by cruisejoin,hauljoin,region,vessel,cruise,haul,  
lait_code;
```

```
update &xcatchout  
set number_indiv = NULL  
where (hauljoin, lait_code) IN (select hauljoin, lait_code from nocount_haul_lait);
```

```
set heading on
```

```
prompt 'OUTPUT HAUL TABLE IS NAMED &XHaulTab. OUTPUT GROUPED CATCH  
TABLE IS NAMED &XCatchout. REMEMBER THAT NUMBERS FOR AN LAIT IN A  
HAUL ARE GIVEN ONLY WHEN NUMBER-RECORDS FOR EACH CONTRIBUTING  
TAXON WERE NOT NULL'
```



## RECENT TECHNICAL MEMORANDUMS

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