# Biological Reconnaissance Field Method

The Biological Reconnaissance (BioRecon) sampling procedure requires specific training and a demonstration of competency due to the expert judgment exercised during field sampling. Individuals conducting these procedures must train with DEP staff (via Stream Condition Index [SCI] training workshops and/or participating in field sampling), complete the training requirements outlined in BRN 1200 and pass initial and continuing proficiency demonstrations per BRN 1300. All BioRecon sampling and analysis shall be conducted according to the requirements of this BioRecon method and the SCI Primer (Sampling and Use of the Stream Condition Index [SCI] for Assessing Flowing Waters: A Primer [DEP-SAS-001/11]). The SCI Primer provides comprehensive guidance on use of the BioRecon and other biological measures in the context of specific study objectives. The use of this BioRecon method must adhere to the assessment principles discussed in the SCI Primer.

## Biological Reconnaissance (BioRecon) Sampling Method

See also the following sections:

###### FT 3100 Aquatic Habitat Characterization

###### FT 3001 Physical/Chemical Characterization

###### FT 1000 General Field Testing and Measurement

###### SCI 1000 Stream Condition Index Methods

##### Introduction

##### This method was designed to be primarily a screening tool to determine the macroinvertebrate community health of flowing freshwater streams and rivers.

##### Equipment and Supplies

###### Completed Physical/Chemical Characterization Field Sheet (FD 9000-3) or other datasheet to capture documentation required in FD 5311

###### Completed Stream/River Habitat Sketch Sheet (FD 9000-4) or other datasheet to capture documentation required in FD 5312

###### Completed Stream/River Habitat Assessment Field Sheet (FD 9000-5)

###### BioRecon Field Sheet (FD 9000-1) or other datasheet to capture documentation required in BRN 1110

###### Forceps

###### Transfer pipettes

###### White picking pans

###### 10X hand lens or other means of magnification

###### Jars filled with alcohol (80% ethanol)

###### D-frame dip net with No. 30 mesh (approximately 600 µm) and handle marked in 0.1-m increments

###### Meters (DO, pH, Conductivity)

###### Wide-mouth jug

###### Cooler with ice

##### Methods

##### The SCI Primer must be read and followed prior to carrying out this SOP. Ensure that the site and conditions are appropriate for the study objectives (see SCI Primer). Visually examine the area or reach to be sampled. Either walk or boat throughout the aquatic system, paying close attention to its physical and habitat characteristics. Be very careful when walking through the system not to disturb aquatic habitats. Such disturbances could lead to inaccurate BioRecon and/or habitat assessment results. The length of a discrete BioRecon station consists of a 100-m stretch of stream, and the width is from bank to bank. Do not sample if site conditions (habitat, hydrology, etc.) are not consistent with study objectives, as described in the SCI Primer.

##### You must be familiar with the rainfall, stage height patterns, and stream flows in the area to be sampled. If you do not know how the water has fluctuated in the stream, do not sample. You must ensure that antecedent hydrologic conditions were sufficient to support the expected stream macroinvertebrate community appropriate for that site, and to avoid BioRecon failures which are due to natural water level fluctuations.

##### Do not conduct BioRecon sampling if the velocity is less than 0.05 m/sec (unless study objectives dictate otherwise, see SCI Primer). If the stream has had low flow (low water level and velocity, but not completely dry) with insufficient habitat or velocity for sampling, do not perform the BioRecon until sufficient habitat has been wetted and the stream has maintained a minimum of 0.05 m/sec velocity for at least 28 days (unless study objectives dictate otherwise, see SCI Primer).

##### If information indicates that the stream has been completely dry (i.e., with no refugia for the aquatic organisms), wait a minimum of six months (180 days) after dry conditions have abated to allow for biological recolonization from the desiccation event. However, if site specific information indicates that a particular stream invertebrate community recovers more quickly than six months, then that site may be sampled prior to 6 months, but not sooner than 3 months after desiccation event. Ensure that the stream has maintained a minimum of 0.05 m/sec velocity for 28 days before performing the BioRecon (unless study objectives dictate otherwise, see SCI Primer).

##### If the water level is >0.5 meters above recent levels, preventing access to substrates that are inhabited by invertebrates, delay sampling until those substrates are accessible or wait 28 days for the invertebrates to colonize the newly inundated substrates. If you are not confident that the reachable substrates have been inundated for greater than 28 days, do not sample. If water levels have risen, but are < 0.5 meter above the previous level, sample only the ‘deep” habitats where organisms are expected. If the normal stream channel is not accessible (water in floodplain), postpone sampling until the normal stream channel and habitats may be accessed.

##### Complete the Physical/Chemical Characterization per FT 3001 and Stream/River Habitat Assessment per FT 3100. The percent coverage of substrate type refers to how much of each habitat type is actually present and in the water (able to be sampled) at the sampling site.

##### Determine the “best” or “most productive” habitats, which, when sampled, will provide an accurate estimate of the site’s maximum biological diversity. Generally, the most productive habitat types are as follows: leaf packs, roots, snags, aquatic vegetation, and rocky outcrops. All of these are considered “productive” habitats. In the rare instance where all five productive habitats are present and of sufficient quality, you should do a single sweep in leaf packs, roots, and snags and a half sweep each in aquatic vegetation and rock to maximize taxa richness. Sand and silt are considered “minor” habitats and are not sampled for the BioRecon. For sampling purposes, select habitats receiving good water velocity (>0.2 m/sec) over those in more sluggish areas. If there is less than 0.05 m/sec velocity flowing over the substrates, do not sample the site (unless study objectives dictate otherwise, see SCI Primer). If fewer than four productive habitats are available, select a particularly productive habitat (based on taxa obtained in earlier sweeps or site-specific knowledge) sampled in the earlier sweeps to complete four sweeps. See the SCI Primer for additional description of the methodology for determining productive habitats.

##### Perform four separate 0.5-meter sweeps with the D-frame dip net in the “most productive” habitats as determined by the above procedures. If field sorting (see 3.5.1), sort and remove all organisms **between** each sweep. If laboratory sorting (see 3.5.2) or if conditions pose a hazard (e.g., severe weather), the material from all four sweeps may be stored in jugs, placed on ice, and sorted at the laboratorywithin a 24-hour period. Three passes over the same 0.5-meter area are required to capture all organisms. This sampling effort in a discrete 0.5-meter area is considered to be one sweep. Dislodge organisms from the substrate into the net by using your hands or a brush to dislodge them from the substrate and by creating a flow of water into the net. Make sure the dislodged material and organism mixture is completely collected by the net. Where a continuous 0.5 m sweep is not available, take two 0.25 m sweeps or three 0.17 m sweeps of the same habitat type to obtain a full 0.5 m sweep. Due to the potential spatial heterogeneity in the distribution of the organisms, selecting two separate 0.25 m sweeps (or three 0.17 m sweeps) of a given productive habitat is the preferred technique to comprise the 0.5 m “sweep.” If you are sampling from a boat, you can get out of the boat and wade in shallow shore areas to obtain the sweeps. You can also approach a habitat with the boat from downstream, agitate and sweep the reachable portion of the habitat (typically by leaning from the bow of the boat), to capture organisms. See SCI 1100 section 2.6 and the SCI Primer for further discussion on proper sweeping techniques.

##### There are two sorting options for the BioRecon: field and laboratory sorting. Due to the difficulty and time-consuming nature of field sorting, this method may not be advisable under certain conditions.. For both options, refer to Table BRN1100-1 to determine the number of individual specimens in each target taxonomic group to target for laboratory identification. Do not retain more than the specified number of individuals. For both options, perform a quality control (QC) check as outlined in 3.5.3.

##### Field Picking BioRecon Method: Accurate field sorting is challenging and time-consuming especially at highly productive sites. The organisms encountered are often extremely small and cryptically colored, which makes them difficult to see and accurately identify. Low ambient light levels, uncomfortably hot or cold temperatures, and rain splattering in sorting trays pose additional challenges. To ensure accurate sorting, find a comfortable, dry location, with ample ambient light. Examining habitats separately helps the investigator learn which taxa are found in which habitat type and aids in future BioRecon sampling and in identifying which habitat(s) to target for the remaining sweeps (if three or fewer productive habitats are available). If the decision has been made to field sort, perform the following steps. After each habitat sweep, return to a comfortable spot on the bank with the dip net containing the sampled material. A sunny location aids in the ability to see the organisms. Place small aliquots of the detritus plus organism matrix in a picking pan diluted with a small amount of site water. Make sure the density of detritus is low, so organisms are easily seen and captured. Scan the entire pan for organisms. When an organism is found, remove it with forceps or a pipette, examine it with the hand lens, determine its identity to the lowest possible taxonomic level in the field (usually family or genus), and record its presence. In a jar filled with alcohol, **save the target number of specimens as indicated in Table BRN 1100-1** for laboratory verification. Repeat these procedures until **all** the material in the net has been examined. Repeat sorting method until material from four sweeps has been processed. Organisms from all habitat types, up to the target number of specimens, may be combined in the jar for laboratory verification. Record all data on FD 9000-1.

##### Laboratory Picking BioRecon Method: If conditions are hazardous or otherwise not conducive to field sorting, this option may be used. To employ this option, sorting must be done within 24 hours on iced samples (do not preserve with alcohol or formalin). Transfer the material from the net to a wide-mouth jug, performing a cursory examination of the diversity of organisms collected in that given habitat. Repeat until material from four sweeps (see section 3.4) has been collected and placed into a wide-mouth jug. Store on ice and sort within 24 hours. After returning to the laboratory, sort the material with a hand-lens or magnifying glass, and save up to, but do not exceed, the target number of specimens as indicated in Table BRN 1000-1 for identification.

##### Perform a QC check on all samples sorted in the field or laboratory. Have a second taxonomist randomly select a minimum of 10% of the sorted aliquots and perform a QC check by examining the aliquot and retrieving and counting any new taxa found. The sorting and QC check can be performed simultaneously by the sampling team. The aliquot can be discarded after the team reaches a consensus that no new taxa are present.

##### If fewer than 100 individuals in the four D-frame dip net sweeps are collected, this suggests that conditions are inhospitable to invertebrates. This could be due to recent desiccation, habitat limitation, toxicity, and/or other factors. If you encounter fewer than 100 individuals, perform a follow-up Stream Condition Index sampling during conditions appropriate for the study objective (see SCI 1100) to further evaluate the stream.

##### See BRN 2100 for laboratory verification of organism identification, BioRecon score determination, and BioRecon score evaluation.

### Required Documentation for Biological Reconnaissance (BioRecon) Sampling

Record the following information or use the BioRecon Field Sheet (Form FD 9000-1).

###### STORET station number

###### Location, including latitude and longitude

###### Watershed or basin name

###### Identification to appropriate taxonomic levels of the target number of individuals as outlined in Table BRN 1100-1 for all four dipnet sweeps

###### Total taxa tallies

###### Abundance code for each taxon

R – Rare (1-3 individuals)

C – Common (4-10 individuals)

A – Abundant (11-100 individuals)

D – Dominant (> 100 individuals)

###### Taxa richness, Ephemeroptera taxa, Trichoptera taxa, Long-lived taxa, Clinger taxa, and Sensitive taxa

###### Name(s) of analysts collecting and sorting samples

###### Habitat types (substrates) sampled and number of sweeps from each

###### Name(s) of analyst(s) performing quality control

###### Signatures

###### Collection date and time

**Table BRN 1100-1:**

**TARGET NUMBER OF SPECIMENS RETAINED FOR BIORECON**

**IDENTIFICATION**

| **Taxon** | **Target # to Pick** |
| --- | --- |
| **Acarina** | 5 |
| **Amphipoda** | 15 |
| **Collembola** | 5 |
| **Decapoda** | 5 |
| **Gastropoda** | 15 |
| **Hirudinea** | 5 |
| **Hemiptera (any)** | 5 |
| **Isopoda** | 5 |
| **Lepidoptera** | 5 |
| **Megaloptera (any)** | 5 |
| **Neuroptera** | 5 |
| **Odonata** | 15 |
| **Oligochaeta** | 5 |
| **Pelecypoda** | 5 |
|  |  |
|  |  |
|  |  |
| Baetidae1 | 15 |
| Baetiscidae1 | 15 |
| Behningiidae1 | 5 |
| Caenidae1 | 15 |
| Ephemeridae1 | 15 |
| Ephemerellidae1 | 15 |
| Heptageniidae1 | 15 |
| Isonychiidae1 | 5 |
| Leptohyphidae1 | 15 |
| Leptophlebiidae1 | 15 |
| Metretopodidae1 | 5 |
| Neoephemeridae1 | 15 |
| Oligoneuriidae1 | 5 |
| Polymitarycidae1 | 5 |
| Pseudironiidae1 | 5 |
|  |  |
| Beraeidae2 | 5 |
| Brachycentridae2 | 5 |
| Calamoceratidae2 | 5 |
| Dipseudopsidae2 | 5 |
| Glossomatidae2 | 5 |
| Helicopsychidae2 | 5 |
| Hydropsychidae2 | 15 |
| Hydroptilidae2 | 15 |
| Lepidostomatidae2 | 15 |
| Leptoceridae2 | 15 |
| Limnephilidae2 | 5 |
| Molannidae2 | 5 |
| Odontoceridae2 | 5 |
| Philopotamidae2 | 5 |
| Phryganeidae2 | 5 |
| Polycentropodidae2 | 15 |
| Psychomyiidae2 | 5 |
| Rhyacophilidae2 | 5 |
| Sericostomatidae2 | 5 |
| Uenoidae2 | 5 |
| Capniidae3 | 15 |
| Chloroperlidae3 | 15 |
| Leuctridae3 | 5 |
| Nemouridae3 | 5 |
| Peltoperlidae3 | 5 |
| Perlidae3 | 15 |
| Perlodidae3 | 15 |
| Pteroncyidae3 | 5 |
| Taeniopterygidae3 | 5 |
|  |  |
|  |  |
|  |  |
| **Diptera (of any other kind)** | 5 |
| Ceratopogonidae4 | 5 |
| Chaoboridae4 | 5 |
| Empididae4 | 5 |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
| Chrysomelidae5 | 5 |
| Dryopidae5 | 5 |
| Dytiscidae5 | 15 |
| Elmidae5 | 15 |
| Gyrinidae5 | 5 |
| Haliplidae5 | 5 |
| Hydraenidae5 | 5 |
| Hydrophilidae5 | 15 |
| Noteridae5 | 5 |
| Psephenidae5 | 5 |
| Ptilodactylidae5 | 5 |
| Sciritdae5 | 5 |

##### 1**Ephemeroptera order**

##### **2Trichoptera order**

##### **3Plecoptera order**

##### **4Diptera order**

##### **5Coleoptera order**

## Training for BioRecon Sampling

##### Training for BioRecon Sampling: Personnel anticipating performing BioRecon sampling according to BRN 1100 shall complete the training specified in the SCI 1100 Training Checklist included in Form FD 9000-35.

##### Qualifications for BioRecon Sampling: Personnel submitting data to DEP from macroinvertebrate sampling according to BRN 1100, Biological Reconnaissance (BioRecon) Method for the purpose of determining biological indices as calculated per BRN 2100, BioRecon Determination shall successfully complete an audit evaluation administered by DEP according to BRN 1300, Proficiency Criteria for BioRecon Sampling.

## Proficiency Criteria for BioRecon Sampling

##### Scope and Applicability

This auditing protocol is applicable to the BioRecon sampling procedures described in BRN 1100 and the SCI Primer.

##### Personnel must complete the training topics in BRN 1200 and be familiar with FT 3000 prior to requesting an audit.

##### Personnel wishing to submit data to DEP associated with the procedures in BRN 1100, Biological Reconnaissance (BioRecon) Method for the purpose of determining biological indices as calculated per BRN 2100, BioRecon Determination shall be audited by DEP according to the auditing protocol described in section 2 below and produce a satisfactory evaluation and score according to the audit and scoring criteria listed below in sections 3 & 4 prior to collecting samples.

##### After the initial demonstration of proficiency, personnel performing the procedures in BRN 1100, Biological Reconnaissance (BioRecon) Method for the purpose of determining a BioRecon score as calculated per BRN 2100, BioRecon Determination, shall undergo a refresher audit every five years (see section 5, below).

##### First-Time Auditing Protocol for BioRecon Sampling

##### First-time audit candidates must pass a test of stream and river macroinvertebrate sampling concepts before undergoing the field audit.

##### General Field Auditing Protocols

##### Audits are conducted in an appropriate field setting selected by DEP.

##### Audit candidates are required to provide proper equipment in good working order necessary to conduct sampling.

##### Audit candidates will be asked a series of questions designed to evaluate their conceptual knowledge of appropriate sampling methods.

##### Audit candidates are expected to demonstrate satisfactory skill in performing the procedures detailed in the BioRecon and SCI sampling SOPs.

##### First-Time Auditing Evaluation Criteria for BioRecon Sampling

Personnel must demonstrate a satisfactory working knowledge of and demonstrate the ability to perform the following:

##### Identify the best available habitats in a 100-meter stream reach (snags, leaf packs, roots, aquatic plants, limestone).

##### Identification of best available habitat must include the following:

##### Length of inundation considered

##### Siltation and sedimentation effects considered

##### Condition of leaf packs

##### Flow considerations taken into account

##### Discuss and recognize circumstances where SCI or BioRecon sampling should be postponed, (e.g., in the event of recent increase in water level or prolonged dry period).

##### Know correct number of dip net sweeps for BioRecon (4).

##### Properly apportion dip net sweeps to available habitats.

##### Efficiently capture invertebrates during dip net sweeps while properly agitating substrates with at least 3 passes of the dip net along a 0.5-meter sample sweep length (sweep length sampled is 0.5 meters, plus or minus 0.1 m, without consistently high or low bias).

##### Sample only productive portions of habitats while not diluting sample with unproductive detritus.

##### Properly transfer sampled material to sorting pan or sample container without sample loss.

##### BioRecon Sorting

##### Dispense proper density of detritus into pick pan for sorting efficiency.

##### Methodically search for organisms in pick pan.

##### Correctly identify organisms to taxonomic level practical in the field.

##### Efficiently capture organisms using forceps and pipettes.

##### Accurately record and achieve the target number of organisms for each taxonomic group, as specified in BRN 1100.

##### Process entire dip net contents.

##### Attain >95% picking efficiency (1 point; between 90% and 95% efficiency, 0.5 point; < 90%, no points, non-attainment).

##### Once the target number of organisms has been achieved for a given taxonomic group per BRN 1100, additional organisms left in the detrital matrix will not count against the overall sorting efficiency.

##### First-Time Audit Evaluation Scoring for BioRecon Sampling

To pass the test in section 2.1 above, the audit candidate must attain a score of 90% correct answers. For mastery of each component in section 3 above, 1 point is awarded. Only 0.5 point is awarded if the applicable component is evaluated as partially correct. To pass, only 0.5 point can be missed.

##### Refresher Auditing Protocol for BioRecon Sampling

##### Refresher audit candidates must pass a test of stream and river macroinvertebrate sampling concepts with a minimum score of 90% correct answers. The test shall be completed by each individual wishing to conduct BioRecon sampling and submit BioRecon results to the Department, without assistance from others.

##### Field refresher audit consistency demonstration procedures for BioRecon are as described in Section 3 above.

##### Refresher audit evaluation shall be as described in Section 4 above.

# Biological Reconnaissance Laboratory Procedures and Index Determination

See also the following sections:

###### FA 1000 Administrative Procedures

###### FC 1000 Cleaning/Decontamination Procedures

###### FD 1000 Documentation Procedures

###### FM 1000 Field Planning and Mobilization

###### FQ 1000 Field Quality Control Requirements

###### FS 1000 General Sampling Procedures

###### FS 7000 Biological Community Sampling

###### FT 1000 General Field Testing and Measurement

###### FT 3000 Aquatic Habitat Characterization

SCI 2200 Laboratory Quality Control for Macroinvertebrate Taxonomic Identification

## BioRecon Determination

##### Definition: Biological Reconnaissance (BioRecon) is a rapid community based biological assessment of stream health using benthic macroinvertebrates sampled via four sweeps of a D-frame dipnet, with organisms identified to the lowest practical taxonomic level in SCI 2230 (except for Oligochaeta, Chironomidae, and Acarina which are identified to higher taxonomic levels).

##### Sampling

##### Perform physical/chemical characterization and habitat mapping according to FT 3001.

##### Perform a Habitat Assessment according to FT 3100.

##### Conduct Biological Reconnaissance (BioRecon) sampling according to BRN 1100.

##### Sort the organisms in the field or lab according to BRN 1100.

##### Laboratory Analyses

##### Laboratory Verification of Field Identifications (modified from *Standard Methods for the Examination of Water and Wastewater,* Section 10500 C, Biological Examination, Benthic Macroinvertebrates, Sample Processing and Analysis*;* reference provided for informational purposes only)

##### Equipment and Supplies

###### Dissecting microscope

###### Identification references

###### Forceps

###### Petri dishes (100 x 15 mm or 60 x 15 mm) or other appropriate containers

###### Laboratory counter (optional)

###### Macroinvertebrate Bench Sheet (may vary from lab to lab)

###### Pen

##### Methods

##### First, empty the contents of the vial into an appropriate container (100-mm diameter petri dish).

##### You may choose to separate the organisms into like groups. To do this, place the groups into smaller (60-mm diameter) individual petri dishes or group the animals within the larger dish.

##### Use the dissecting microscope to identify the organisms to the lowest practical taxonomic level (as defined in SCI 2230), with the following exception. For the BioRecon procedure, do not identify Oligochaeta, Chironomidae, and Acarina below class, family, and order, respectively. Do not include any terrestrial organisms or pieces of worms or other organisms without heads. Use the most appropriate identification reference for each group. It will take some time until sufficient experience with identification procedures and references is gained. In addition to the identification manuals, maintain a reference collection that can be used to compare specimens and facilitate identification. After using a dichotomous key to arrive at the name of an unknown organism, check the organism’s geographic range, habitat preferences, and morphological diagnosis to confirm that the identification is correct. Do not identify an organism by simply flipping through some pictures and assigning a name based on a superficial resemblance.

##### Enumerate organisms concurrently with identification and then place them back into the ethanol filled, labeled vial with the forceps. Remove the animals as you count them in order to avoid counting them twice. If a large number of one or a few taxa are present, use a laboratory counter to keep a running total to facilitate the enumeration process. You may temporarily label counters to avoid mistakes. If you do not use a counter, tally the number of each taxon on your bench sheet.

##### If an organism is encountered in your laboratory for the first time, remove it and place it in an individual, labeled vial for inclusion in the reference collection. Make a note of this on the bench sheet, so that it can be located in the future, if necessary.

##### Record the individual taxon names and their numbers on the bench sheet.

##### Follow Taxonomic Quality Assurance procedures in SCI 2220.

##### Data Reduction

##### For DEP staff only, enter all data into SBIO (the Florida Statewide Biological Database).

##### Follow the counting and collapsing procedures listed below. Keep a record of the original taxa list and the resulting collapsed list.

##### When combining biological data (taxa and counts), the number of taxa may become artificially inflated by the incorporation of the same taxon under different names and by counting high-level identifications (family or genus). An erroneously high taxa count creates additional anomalies among metrics involving these counts, such as the number of Ephemeroptera and Trichoptera taxa.

##### Prepare a list of all the taxa in the sample identified to the lowest practical taxonomic level per SCI 2230.

##### Collapse taxa further according to the following:

##### Starting at the bottom of the phylogenetic tree (usually species), determine if any entries have a "parent" entry (e.g., a genus level entry and entries for species within that genus). Remove the higher-level entry and add its number of individuals to the lower level entries proportional to their counts, i.e., the genus level identification will be removed and its number of individuals will be added proportionally to the species on the list within that genus.

##### Make sure that the sum of the counts is the same as it was before the collapsing step. It may be necessary to adjust the counts with the lowest number of individuals. For example, suppose there is a genus level entry with a count of 1 and entries for 3 species within that genus each with a count of 1. Only one of the species entries can have 1 added to it, otherwise, the number of individuals will become inflated. The first entry in the list is the one to have the 1 added to it.

##### Move one step up the phylogenetic tree and see if there are any family entries with genus and/or species under it. If there are remove the family entry and add its number of individuals proportionally to the entries below it phylogenetically. Continue up the phylogenetic tree until there are no more high level entries to be evaluated and proportioned.

##### As an example, see the following species list:

*Stenacron* sp. (2)

*Stenonema* sp. (4)

*Oecetis inconspicua* (21)

*Oecetis avara* (1)

*Oecetis* sp. (20)

*Hyalella azteca* (20)

*Planorbella* sp. (1)

7 taxa and 69 individuals

Upward collapsing will apportion the individuals from *Oecetis* sp. to the two identified species of that genus, resulting in:

*Stenacron sp. (2)*

*Stenonema* sp. (4)

*Oecetis inconspicua* (40)

*Oecetis avara* (2)

*Hyalella azteca* (20)

*Planorbella* sp. (1)

5 taxa and 69 individuals

Note that if *“Oecetis* sp.” had represented a distinct species level entity with no available or known name, it would have properly been entered as *“Oecetis* sp. C Floyd” or a similar name, and would then not have been combined. Collapsing will also take place at other taxonomic levels: family level identifications will combine with generic level identifications, species will combine with subspecies, etc.

##### Index Calculation

##### Perform the following calculations based on collapsed data as outlined in Section 4.2.

##### Calculate and record the number of long-lived taxa score according to Table BRN 2000-1 (based on Fore, 2007 with minor modifications). Use the taxonomic order, family, and genus (or species) name of each taxon to calculate long-lived taxa richness. Taxonomic synonyms present in the current Florida data base are also shown as additional information. Long-lived taxa require more than one year to complete their life cycles.

##### Table BRN 2000-1. Long-lived taxa for BioRecon index calculation.

| **Order** | **Family** | **Genus** | **Species (Long-lived)** | **Synonyms** |
| --- | --- | --- | --- | --- |
| Decapoda | All familes | All genera | All species |  |
| Basommatophora | Lymnaeidae | *Fossaria* | All species |  |
| Mesogastropoda | Ampulariidae | *Pomacea* | All species |  |
| Veneroida | Corbiculiidae | *Corbicula* | All species |  |
| Unionoida | Unionidae | All genera | All species |  |
| Odonata | Aeshnidae | *Basiaeschna* | *Basiaeschna janata* |  |
| Odonata | Aeshnidae | *Boyeria* | All species |  |
| Odonata | Cordulegastridae | *-* | All species |  |
| Odonata | Gomphidae | *Gomphus* | All species | *Gomphurus* |
| Odonata | Gomphidae | *Hagenius* | All species |  |
| Odonata | Gomphidae | *Progomphus* | All species |  |
| Odonata | Micromiidae | *Macromia* | All species |  |
| Odonata | Corduliidae | *Somatochlora* | All species |  |
| Odonata | Corduliidae | *Tetragoneuria* | All species | *Epitheca* |
| Odonata | Petaluridae | *Tachopteryx* | *Tachopteryx thoreyi* |  |
| Plecoptera | Pteronarcidae | *Pteronarcys* | All species | *Allonarcys* |
| Plecoptera | Leuctridae | *All genera* | All species |  |
| Plecoptera | Peltoperlidae | *Tallaperla* | *Tallaperla cornelia* |  |
| Plecoptera | Perlidae | *Acroneuria* | All species |  |
| Plecoptera | Perlidae | *Agnetina* | *Agnetina annulipes* |  |
| Plecoptera | Perlidae | *Eccoptura* | *Eccoptura xanthenes* | *Acroneuria xanthenes* |
| Plecoptera | Perlidae | *Neoperla* | All species |  |
| Plecoptera | Perlidae | *Paragnetina* | All species | *Banksiana,*  *Banksiella* |
| Plecoptera | Perlodidae | *Clioperla* | *Clioperla clio* | *Isoperla clio* |
| Plecoptera | Perlodidae | *Perlinella* | *Perlinella drymo* | *Atoperla ephyre* |
| Plecoptera | Perlodidae | *Perlinella* | *Perlinella ephyre/zwick*i |  |
| Plecoptera | Perlodidae | *Isoperla* | *Isoperla orata* |  |
| Megaloptera | Corydalidae | All genera | All species |  |
| Trichoptera | Brachycentridae | *Brachycentrus* | *Brachycentrus americanus* | *Oligoplectrum amercanum* |
| Trichoptera | Brachycentridae | *Micrasema* | All species |  |
| Trichoptera | Calamoceratidae | *Heteroplectron* | *Heteroplectron americanum* |  |
| Trichoptera | Hydropsychidae | *Diplectrona* | *Diplectrona modesta* |  |
| Trichoptera | Hydropsychidae | *Macrostemum* | *Macrostemum carolina* | *Macronema carolina,*  *Macronemum carolina* |
| Trichoptera | Lepidostomidae | *Lepidostoma* | All species | *Alepomyia,*  *Alepomyiodes,*  *Arcadopsyche,*  *Atomyia,*  *Jenortha,*  *Mormomyia,*  *Neuropsyche,*  *Nosopus,*  *Notiopsyche,*  *Olemira,*  *Oligopsyche,*  *Phanopsyche,*  *Pristosilo,* |
| Trichoptera | Leptoceridae | *Ceraclea* | All species | *Athripsodes* |
| Trichoptera | Limnephilidae | *Ironoquia* | *Ironoquia punctatissisma* |  |
| Trichoptera | Limnephilidae | *Pycnopsyche* | All species |  |
| Trichoptera | Molannidae | *Molanna* | All species |  |
| Trichoptera | Phryganeidae | *Banksiola* | *Banksiola concatenata* | *Neuronia concatenata* |
| Trichoptera | Phryganeidae | *Ptilostomis* | *Ptilostomis postica* | *Neuronia postica* |
| Trichoptera | Phryganeidae | *Agrypnia* | *Agrypnia vestita* |  |
| Trichoptera | Psychomyiidae | *Lype* | *Lype diversa* |  |
| Trichoptera | Rhyacophilidae | *Rhyacophila* | All species |  |
| Trichoptera | Uenoidae | *Neophylax* | All species |  |

##### Calculate and record the number of sensitive taxa score according to Table BRN 2000-2 (based on Fore, 2007 with minor modifications). These taxa are identified as sensitive to human disturbance. Synonyms in the current Florida database are also included as additional information.

##### Table BRN 2000-2. Sensitive macroinvertebrate taxa for BioRecon index calculation.

| **Order** | **Family** | **Genus** | **Taxon (sensitive)** | **Synonyms** |
| --- | --- | --- | --- | --- |
| Acariformes | Lebertiidae | *Lebertia* | All species |  |
| Amphipoda | Crangonyctidae | *Crangonyx* | *Crangonyx* |  |
| Coleoptera | Elmidae | *Ancyronyx* | *Ancyronyx variegatus* |  |
| Coleoptera | Elmidae | *Gonielmis* | All species |  |
| Coleoptera | Elmidae | *Macronychus* | All species |  |
| Diptera | Chironomidae | *Microtendipes* | All species |  |
| Diptera | Chironomidae | *Parametriocnemus* | All species |  |
| Diptera | Chironomidae | *Polypedilum* | *Polypedilum aviceps* |  |
| Diptera | Chironomidae | *Rheocricotopus* | All species |  |
| Diptera | Chironomidae | *Stempellinella* | All species |  |
| Diptera | Chironomidae | *Tanytarsus* | *Tanytarsus sp. d epler* |  |
| Diptera | Chironomidae | *Tanytarsus* | *Tanytarsus sp. m epler* |  |
| Diptera | Chironomidae | *Tribelos* | *Tribelos jucundum* |  |
| Diptera | Empididae | *Hemerodromia* | *Hemerodromia* |  |
| Diptera | Simuliidae | *All genera* | All species |  |
| Ephemeroptera | Baetidae | *Acerpenna* | *Acerpenna pygmaea* | *Baetis pygmaeus* |
| Ephemeroptera | Ephemerellidae | *All genera* | All species |  |
| Ephemeroptera | Heptageniidae | *All genera* | All species |  |
| Ephemeroptera | Leptophlebiidae | *All genera* | All species |  |
| Ephemeroptera | Leptohyphidae | *All genera* | All species |  |
| Isopoda | Asellidae | *Caecidotea* | *Caecidotea* | *Asellus* |
| Odonata | Libellulidae | *Macromia* | All species |  |
| Plecoptera | All families | *All genera* | All species |  |
| Trichoptera | Hydropsychidae | *Hydropsyche* | All species |  |
| Trichoptera | Leptoceridae | *Triaenodes* | All species |  |
| Trichoptera | Philopotamidae | *Chimarra* | *Chimarra* |  |
| Trichoptera | Psychomyiidae | *Lype* | *Lype diversa* |  |

##### Tally the number of total taxa (taxa richness), Ephemeroptera taxa, and Trichoptera taxa.

##### Refer to the FDEP Statewide Biological Database webpage (<https://floridadep.gov/dear/florida-dep-laboratory/content/statewide-biological-database> for the list of macroinvertebrates categorized as clinger and filter feeder (categorization for insects taken from Merritt *et al*., An Introduction to the Aquatic Insects of North America). For clinger taxa, include only those taxa whose sole habit is listed as “clinger”.

##### Determine region according to Figure BRN 2100-1. Regional metric expectations are listed in Table BRN 2100-1.

##### Use Table BRN 2100-2 to calculate metrics based on values obtained in 5.1-5.4. Check that none of the metric scores are >1 or <0. If so, change the scores to 0 or 1 as appropriate.

##### Sum the metric scores; check that the sum is between 0 and 6.

##### Divide the sum of scores by 0.6. This is a correction factor to change the BioRecon range from 0–6 to 0–10. Refer to Table BRN 2100-3 for categorical descriptions of scores.

##### References

##### Merritt, R.W., Cummins, K.W., and M.B. Berg, An Introduction to the Aquatic Insects of North America, Fourth Edition, 2008 (reference provided for informational purposes only).

##### Fore, L., R.B. Frydenborg, D. Miller, T. Frick, D. Whiting, J. Espy, and L. Wolfe. Development and Testing of Biomonitoring Tools for Macroinvertebrates in Florida Streams. Florida Department of Environmental Protection, 2007. (reference provided for informational purposes only)

##### American Public Health Association, American Water Works Association, Water Pollution Control Federation, SM10500C, Standard Methods for the Examination of Water and Wastewater, 20th Edition, 1999. (reference provided for informational purposes only)

### Required Documentation for Laboratory Procedures For BioRecon Determination

###### Sample receipt or log-in record

###### Site, sample identification number, STORET station number, sample type, replicate number and date collected

###### Total number of taxa

###### Name of any organism encountered in the laboratory for the first time

###### Individual taxon names

###### Numbers of each taxon counted

###### Total number of individuals counted

###### Data entry into the Florida Statewide Biological Database (DEP staff only)

###### Method and notes for counting and collapsing taxonomic data

###### Collapsed taxa list

###### Index calculations per BRN 2100, section 5:

###### Long-lived taxa score

* + Sensitive taxa score
  + Taxa richness (total taxa)
  + Number of Ephemeroptera taxa
  + Number of Trichoptera taxa
  + Number of clinger taxa

###### BioRecon index metrics and evaluation as scored per Tables BRN 2100-2 and BRN 2100-3

**Appendix BRN 2100**

**Tables, Figures and Forms**

Table BRN 2100-1

Table BRN 2100-2

Table BRN 2100-3

Figure BRN 2100-1

**Table BRN 2100-1**

**BioRecon metric name and range of metric values used to assign a score of 0 to 1 by region.** Metric values higher or lower than the listed range were assigned a score of 0 or 1 as appropriate. Bold values indicate scoring ranges that differ from the same SCI metric.

| **BioRecon metric** | **Northeast** | **Panhandle** | **Peninsula** |
| --- | --- | --- | --- |
| Total number of taxa | **14–37** | 16–49 | **11–36** |
| Number of Ephemeroptera taxa | 0–3.5 | **0–12** | 0–5 |
| Number of Trichoptera taxa | 0–6.5 | 0–7 | 0–7 |
| Number of Long-lived taxa | **0–6** | **0–10** | **0–7** |
| Number of Clinger taxa | **0–7** | 0–15.5 | 0–8 |
| Number of Sensitive taxa | 0–11 | 0–19 | 0–9 |

**Table BRN 2100-2**

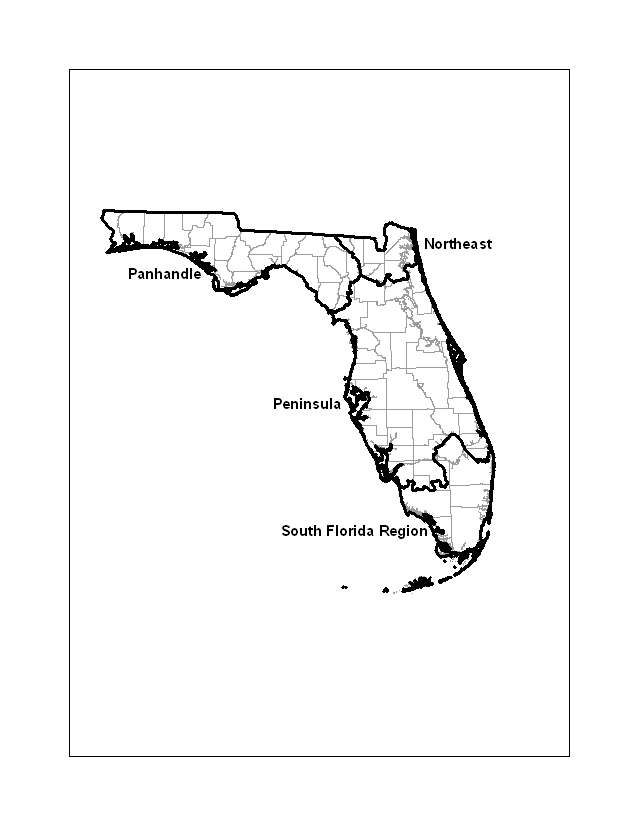
**BioRecon metric scoring formula for converting metric values to a metric score ranging from 0 to 1.** In each equation, ‘X’ stands for the raw metric value. For calculated values >1, score equals 1; for calculated values <0, score equals 0.

| **BioRecon metric** | **Northeast** | **Panhandle** | **Peninsula** |
| --- | --- | --- | --- |
| Total number of taxa | (X–14)/23 | (X–16)/33 | (X–11)/25 |
| Number of Ephemeroptera taxa | X /3.5 | X /12 | X /5 |
| Number of Trichoptera taxa | X /6.5 | X /7 | X /7 |
| Number of Long–lived taxa | X /6 | X /10 | X /7 |
| Number of Clinger taxa | X /7 | X /15.5 | X /8 |
| Number of Sensitive taxa | X /11 | X /19 | X /9 |

**Table BRN 2100-3**

**Categorical descriptions and range of index values for the BioRecon Index.** Square brackets indicate a value is included in the range; round brackets indicate a value is not included.

| **BioRecon (for 1 sample)** | **Index range** |
| --- | --- |
| Category 1 | [7–10] |
| Category 2 | [4–7) |
| Category 3 | [0–4) |

****

**Figure BRN 2100-1.**

**Map of BioRecon Regions (black lines) and Florida counties (gray lines).** Note that the BioRecon has not been calibrated for the South Florida Region.