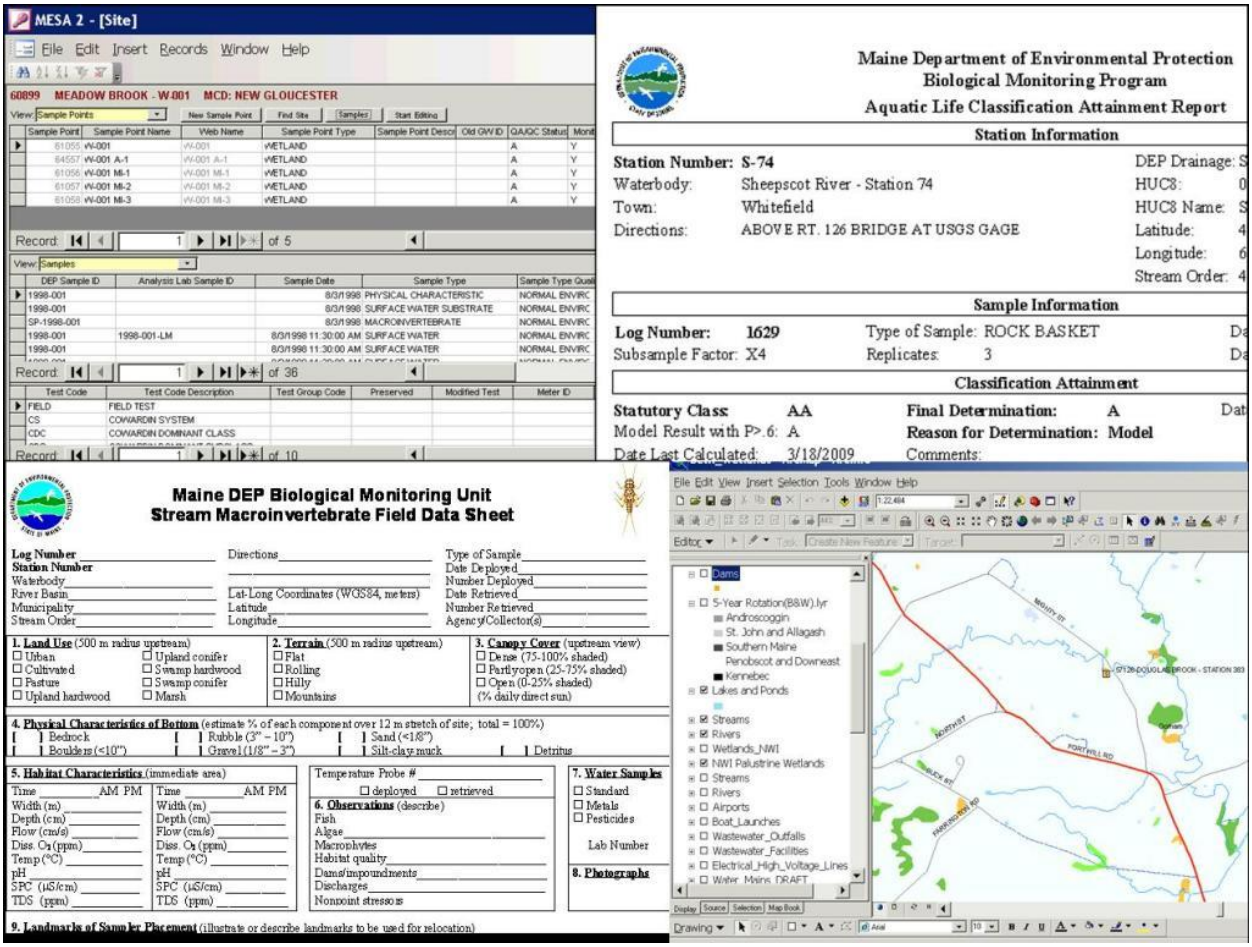
Protocols for Managing Biomonitoring Data



Beth Connors
Maine Department of Environmental Protection
312 Canco Road, Portland, ME, 04103
beth.connors@maine.gov

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Bureau of Land and Water Quality
Division of Environmental Assessment
Biomonitoring Program

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TABLE OF CONTENTS

1. **Applicability.** This standard operating procedure (SOP) applies to the entry and management of data related to the sampling and assessment of river, stream and wetland macroinvertebrate and algal communities. These data come from aquatic macroinvertebrate and algal monitoring activities carried out by the Maine Department of Environmental Protection (MDEP), outside agencies or contractors. This SOP does not cover data collection; sampling methods are described in the appropriate SOP, see 5. A. (1), below. Rather, it focuses on how the samples are tracked and managed from when they are collected to when they are entered into the MDEP's database and analyzed. This SOP applies to all data collected by the MDEP or outside agencies during aquatic macroinvertebrate and algal sampling, including habitat data (e.g., substrate composition), physical/chemical water quality parameters, including field measurements and laboratory analyses (e.g., temperature, dissolved oxygen, nutrient concentrations), and biological data (e.g., taxa counts).

2. **Purpose.** The purpose of this SOP is to describe and standardize the way data are entered and managed. The process outlined in this document is applied to all Biomonitoring Program data, including data received from outside sources, but it is not always a linear process and some steps may be done in a different order depending on the needs of the program.

3. **Definitions**
   A. **Aquatic Macroinvertebrate** – aquatic animals without backbones that can be seen with the naked eye. Generally, this includes animals that are retained by a 600 micron mesh.

   B. **EGAD** – Environmental and Geographic Analysis Database used to electronically store Department sampling data.

   C. **EDD** – Electronic Data Deliverable, a standard Excel file that EGAD users use to load data into the database. A 'pre-EDD' is an Excel file designed to mimic a field or taxonomy sheet already in use by the Biomonitoring program; a pre-EDD must be converted to an EDD using a specific script before data can be loaded into EGAD.

4. **Responsibilities** Specific duties are assigned to individuals as outlined in Appendix 12.
   A. **Leon Tsomides** – Leader of the Biomonitoring Program and the Rivers and Streams Subsection.
      (1) Supervises laboratory and field services related to the collection of stream macroinvertebrates.
      (2) Supervises data management and analysis related to stream macroinvertebrates.
      (3) Manages contract for taxonomic identification of aquatic macroinvertebrate samples.
      (4) Manages contract for laboratory services (i.e., picking).

   B. **Jeanne DiFranco** – Wetlands Subsection Leader.
      (1) Supervises field services related to collection of wetland macroinvertebrates and algae.
      (2) Supervises data management and analysis related to wetland macroinvertebrates and algae.
      (3) Manages Biomonitoring GIS data layers and wetland GIS projects.

C. **Tom Danielson** – River and Stream Algae Subsection Leader.
(1) Supervises field services related to collection of river and steam algae.
(2) Manages contract for taxonomic identification of algal samples.
(3) Manages the Biomonitoring GIS data layers and river and stream GIS projects.

D. **Beth Connors** – responsible for maintaining the official approved QAPP and SOP coordination.

E. **Susanne Meidel** – the contact for database questions.

5. Guidelines and Procedures

A. **Sample Collection and Processing.** See Appendix 1 for an overview of the sample processing steps
(1) Field Sampling
(a) Sites are selected as described in the Biomonitoring Program Quality Assurance Project Plan, section B1 Sampling Process Design (Experimental Design).
(b) River and stream macroinvertebrate samples are collected as described in *Methods for Biological Sampling and Analysis of Maine's Rivers and Streams* (Davies and Tsomides 2002).
(c) Wetland macroinvertebrate samples are collected as described in *Protocols for Sampling Aquatic Macroinvertebrates in Freshwater Wetlands* (DiFranco 2014)).
(d) Algal samples are collected as described in *Protocols for Sampling Algae in Wadeable Rivers, Streams, and Freshwater Wetlands* (Danielson 2014a).
(e) Water grab samples are collected and process as described in *Protocols for Collecting Water Grab Samples in Rivers, Streams, and Freshwater Wetland* (Danielson 2014b).
(f) Instantaneous levels of dissolved oxygen, specific conductance and temperature are collected as described in *Protocols for Using the Hanna Dissolved Oxygen and Specific Conductance/pH Meters in Rivers, Streams, and Freshwater Wetlands* (Danielson 2014c).
(g) At all wetland monitoring locations, the Wetland Human Disturbance Assessment form is completed, as described in *Protocols for Completing the Biological Monitoring Wetland Human Disturbance Assessment* (Connors and DiFranco 2014).
(h) A GPS point is recorded at every new site, see Appendix 12. The waypoint name, Latitude and Longitude coordinates, and accuracy are written on the appropriate field sheet(s).
(i) At all sites and during each site visit, photos are taken and photo numbers and a brief description of the photo (e.g. up, down, substrate) are written on the appropriate field sheet.
1. For river and stream sites take an upstream photo, a downstream photo, a representative photo of the substrate (algal sites only) and photos of any other site characteristics of interest.

2. For wetland sites take 2 or 3 representative photos and photos of any other site characteristics of interest.

(j) Deploy and retrieve continuous water temperature data loggers as described in *Protocols for Measuring Continuous Water Temperature Using an Onset Data Logger* (Connors 2014).

(2) Storing/sorting/logging in biological samples

(a) Macroinvertebrate samples

1. Place cases of canning jars containing macroinvertebrate samples in the field support area in the Ray Building basement.
2. Make sure that all jars are labeled according to the appropriate SOP (see 5. A. (1), directly above).
3. Make sure that each jar does not need to be split into two jars, check with section leader if unsure. Refresh the ethanol, if necessary
4. Label cases with macroinvertebrate samples with the following information:
   i. An indication that samples are preserved with ethanol.
   ii. Waterbody names
   iii. Sample IDs (see 5. A (3), directly below)
   iv. Collection dates
   v. Numbers of jars per sample ID
5. Pick macroinvertebrate samples according to Davies and Tsomides 2002. Staff sorting macroinvertebrate samples will track their time at the end of each workday, noting percentage of each Sample IDs sorted and the time spent on each.
6. Checkpick 10% of macroinvertebrate samples according to Davies and Tsomides 2002.
7. Track picking progress and samples check picked in appropriate sample tracking file (see 5. A (4), below).

(b) Algal samples

1. Place nalgene bottles containing algal samples in the Biomonitoring area in the DEA barn or in the SMRO garage.
2. Make sure that all bottles are labeled according to the SOP (see 5. A. (1) (d), above). Ensure that the label indicates if and with what the sample is preserved.

(3) Assign sample IDs

(a) Enter new river and stream macroinvertebrate samples into the Log Book and assign next consecutive log number. Write this sample ID number on the field sheet, the sample jar, and the case label.

(b) Assign a sample ID to wetland macroinvertebrate samples based on sample collection method (DN= dipnet measured sweep method), year collected and the numeric part of the site number (assigned in 5. B (2), below), e.g. DN-2008-175. Use this sample ID in step 5. A. (4) (b) directly below, while filling in the sample tracking file.

(c) Assign a sample ID to algal samples as follows

1. The first three characters are "SA-"(Stream Algae) or "WA-"(Wetland Algae).
2. The next section is the station number, such as 447, followed by a "-". Station (site) numbers are assigned in 5. B (2), below).
3. The next section is the sample year, such as 2010.
4. After the year, put in the code for the sample method. (r = rocks, c = petri dish cores, y = phytoplankton, e = epiphytes, s = slides, l = logs). A'd' following the collection method abbreviation indicates that the sample is a duplicate.
5. Add a space, and then the bottle number in parentheses, such as " (980)" for bottle #980.
   i. Bottle numbers are assigned in preparation for shipping the samples to the taxonomist for identification (see 5. A. (5) (b), below).
6. For example, a phytoplankton sample collected at wetland site W-175 in 2008 stored in bottle number 786 would have 'WA-175-2008y (786)' as the sample ID.

(4) Track and prioritize samples

(a) River and stream macroinvertebrate samples

1. Open file 'Sample Tracking.xls' on 'Augusta H\…\Biomonitoring\Sample tracking\' and either select the applicable year's worksheet or if necessary create a new worksheet for the sample year. Enter relevant site and/or sample data.
2. Prioritize samples for picking in the worksheet by indicating the samples collected for the Surface Water Ambient Toxics (SWAT) program with bold font and post printed spreadsheet in the picking lab. Organize cases of jars accordingly.
3. Periodically update 'Sample Tracking.xls' with picking information from lab printout.

(b) Wetland macroinvertebrate samples

1. Open file 'WetlandSampleTracking.xls' on 'Augusta H\…\Biomonitoring\Sample tracking\wetland sample tracking' and either select the applicable year's worksheet or if necessary create a new worksheet for the sample year. For each site sampled in a year, enter the sample ID, site number, waterbody name, town, method (DN), number of replicates (usually 3) and the total number of jars.
2. Prioritize samples for picking in the worksheet with bold font, as necessary, and post printed spreadsheet in the picking lab. Organize cases of jars accordingly.
3. Periodically update 'WetlandSampleTracking.xls' with picking information from lab printout.

(c) Algal samples (river/stream and wetland samples)

1. Open file 'ALGAL SAMPLE TRACKING.xls' on 'Augusta H\…\Biomonitoring\Sample tracking\ALGAE' and either select the applicable year's worksheet or if necessary create a new worksheet for the sample year. Enter the sample ID, station number, waterbody name, town, location, the type of algal sample collected (rock scraping, petri core, epiphytes, phytoplankton, etc.), and any applicable notes about the sample.

(5) Prepare biological samples for identification

(a) Macroinvertebrate samples

1. Organize and label macroinvertebrate vials according to Davies and Tsomides 2002.
2. Pack samples and ship to taxonomist
   i. Tape the lid of each vial down with clear tape.
   ii. Place all replicates comprising a sample in one (or as many as necessary) bubble bag and tape bag closed.
   iii. Stick masking tape on bag and note the log number/sample ID of all vials inside bag.
   iv. Place whole set of labeled bubble bags in a sturdy cardboard box with lots of styrofoam beads, add a packing list with custody information and seal box very securely with tape on all sides.
      - Each taxonomists has a folder with past chain of custody forms (Augusta H:\ …Biomonitoring\SAMPLE TRACKING). Create a new file for each shipment, using the most recent file as a template for the new chain of custody.
   v. Ship First Class by UPS (Ray building front desk staff will send out) or deliver samples to taxonomists in person.
3. Record date sent and taxonomist's name in appropriate Log Book and/or sample tracking file.

(b) Algal samples

1. Create a new worksheet in the Algal_chain_of_custody.xls file (Augusta H:\…Biomonitoring\SAMPLE TRACKING\ALGAE) and assign bottle numbers to all algal samples and duplicate samples. Write bottle numbers on appropriate field sheet(s).
   i. Determine the last bottle number assigned to the previous year's samples and start the current year's samples by assigning the next consecutive bottle number.
   ii. If a sample is in more than one bottle it will only be assigned one bottle number and the bottles should be labeled, Bottle number XXX, '1 of 2', '2 of 2', etc.
   iii. Starting in 2013, the wetland phytoplankton sample is collected in two bottles, one 1 liter bottle for diatoms and one 500ml bottle for soft algae. Assign the sample numeric bottle number to both bottles, adding a '-d' to the diatom sample and a '-s' to the soft algae sample, i.e. 1262-d and 1262-s.
   iv. Enter the EGAD_SEQ as the EGAD site sequence number assigned when the site is established in MESA2, see 5. B. (3) (a) below.
   v. The Sample Point ID is the station number followed by " A-1" for most samples. For a paired sample, such as a shady site, the sample point is " A-2".
      - Note that the wetland Sample Point ID includes the "W-".
   vi. Enter the DEP_Sample_ID as assigned above in 5. A. (3) (c), such as SA-447-2010r (980).
   vii. Acquire necessary sample and site information (date, waterbody name, station number, method, etc.) from EGAD and/or field sheets, and then ask the Land and Water Quality Bureau EGAD Project Manager to populate the remaining information like the Town, County, Elevation, Lat, Long, etc.

viii. Enter the Field Volume as noted on the applicable field sheet. The volume of phytoplankton samples are assumed to correspond to the volume of the container that the sample was collected in, e.g. a sample in a 1L bottle is assumed to have a volume of 1000 mL.

ix. Enter the surface areas based on the sample type and number of replicates (e.g., 18 rocks, 3 petri dish cores) (Danielson 2014a), or the calculated surface area, see 5. B. (6), below.

x. For stream samples, the Lab Sample ID must be 8 characters or less, such as "10She3Rd", which is used for statistical packages.

- The first two characters are the last two digits of the year.
- The next 4-5 characters are a short code for the site. The code for Sheepscot River (Station 74) is "She3" because it is the third station downstream on the Sheepscot. Check MESA2 or old chain of custody worksheet to find codes for sites that have been previously sampled.
- Next is an uppercase letter denoting the sample method (R= rocks, C = petri dish cores, Y = phytoplankton, E = epiphytes, S = slides, L = logs).
- If needed, the last character is for denoting something special about the sample, for example "d" denotes a duplicate sample, "b" denotes a nearby secondary sample location or a sample collected later in the year, and "c" denotes a closed canopy site.

xi. For wetland samples, the Lab Sample ID must be 8 characters or less, such as "175-08e", which is used for statistical packages.

- The first three characters are the numeric part of the site number.
- The next three characters are the last two digits of the year preceded by "-".
- Next is a letter denoting the sample method (y = phytoplankton, e = epiphytes).
- If needed, the last character is for denoting something special about the sample, for example "d" denotes a duplicate sample.

xii. For stream samples, the Sample_ID field is for linking to water samples. It is the same as the DEP_SAMPLE_ID, but does not include the information from the last two bullets. For example, the Sample_ID for SA-447-2010r (980) is simply SA-447-2010. For wetland phytoplankton samples, the Sample_ID is the same as the DEP_SAMPLE_ID but also includes the '-d' or '-s' assigned to the bottle number. For the wetland epiphyte samples it is the same as the DEP_SAMPLE_ID

xiii. The Analysis_Lab is an abbreviation indicating where the samples are being sent for identification, currently "ANS" for the Academy of Natural Sciences.

xiv. Some fields in the file are fixed.

- Sample_Type = AL
- Sample_Type_Qualifier = N for normal samples or D for duplicates
- RESULT_TYPE = PM
- SAMPLE_LOCATION = U
- TREATMENT STATUS = NA

- SAMPLED BY = BIOMONITORING UNIT

xv. The SAMPLE_COLLECTION_METHOD is dependent on the sample type (rock scrapings = RSP1, log scrapings = LSP1, petri dish core = PDC, phytoplankton = GS, epiphyte sample = EPI, slides = PPM). If a sample includes both log and rock scrapings, then use the code for predominant method.

2. Write the assigned bottle number on each bottle and double check site and sample information and preservation status on each bottle label.
3. Pack samples securely in as many boxes as necessary and note box number on chain of custody form for each bottle.
4. Ship overnight or two-day ground (Ray building front desk staff will send out).
5. Email chain of custody form and sample list to taxonomist.
6. Record date shipped and taxonomist name in appropriate sample tracking file (see 5. A. (4) (c), above).

B. **Preparing Data for Entry**

(1) Review all applicable field data sheets for accuracy and completeness.

(2) Assign new station (site) numbers as necessary (see Appendix 2). Record station number on field data sheet(s), in Log Book (for river and stream macroinvertebrate samples), and in all applicable Sample Tracking file(s) (see 5. A (4), above).

(3) Adding new site (station) to EGAD

(a) Creating site in MESA2: Follow the instructions in Appendix 2 to create the site in EGAD. Write the EGAD site sequence number on the field data sheet.

(b) Establishing spatial location in ArcMap. Note: spatial information can be assigned to the site and to the sample point(s), but at this time Biomonitoring assigns spatial information to the site only.

1. Using the ArcMap Add Site point tool

i. Open a map document in Arc 10 and use the Add Site Point tool in ArcToolbox>DEP_Custom_Toolbox>Add_Data>EGAD Site Points

ii. This tool adds a point in the center of the current view, so make sure to center the map window on the desired location for the new point before running tool.

- If using the GPS Waypoints as a guide (see 2. directly below), you can ensure the point is in the center of the map window by double clicking on the point with the "Zoom In" tool (the magnifying glass with the plus sign).
- If point is added to the wrong location, contact the DEP GIS Coordinator to delete or move it.

iii. The EGAD_SEQ number is the Site sequence number assigned in (a) directly above.

iv. Select accuracy according to the waypoint accuracy recorded on the field data sheet.

v. Enter the site number (i.e. W-238, S-1003) in the Notes field.

2. It is useful to download the GPS WayPoints to use as a guide during this process. Follow the instructions in Appendix 13 to download the current year's waypoints to a shapefile.

(4) Transfer photos from the camera(s) to the appropriate location on the Augusta H drive
   1. River and stream sites: create a folder for each site (include waterbody name and station number in folder name) and store photos here: Augusta H:\...\Biomonitoring\IMAGES\Stream Stations\YEAR. Use the following format to name each photo: EllisRiver_s101(down)_8-2008.jpg, where 'EllisRiver' is the waterbody name, 's101' is the site number, 'down' is the direction along the stream the photo is showing, and '-8-2008' is the month and the year the photo was taken.
   2. Wetland sites: create a folder for the year and save photos here: Augusta H:\...\Biomonitoring\WETLAND FILES\Wetland photos\Wetland Sites.
      i. Use the following format to name each photo: w194_08painepond1.jpg, where 'w194' is the site number, '08' is the last two digits of the year sampled and 'painepond' is the waterbody name. Add a number to the end of the file name (1, 2, etc.) or any applicable descriptor (w194_painepond_waterscorpion.jpg).
      ii. Save photos of specific content (plants, animals, procedures) in the applicable folder within Wetland Photos instead of the Wetland Sites folder.

(5) Continuous water temperature data loggers
   1. Download data from continuous water temperature data loggers and process as described in *Protocols for Measuring Continuous Water Temperature Using an Onset Data Logger* (Connors 2014).

(6) Calculate the surface areas of the plant stems used to collect the epiphytic algal samples.
   1. Use a previous years' "Epiphytic Algae Surface Area_YEAR.xls" (Augusta H:\…\Biomonitoring\WETLAND FILES\Wetland Assessment\Wetland algae) to create a new file for the current year. Create a new worksheet for each site. Name each worksheet with the site number. Enter the waterbody name, site number, and sample volume. Enter the type of plant and the dimensions of each plant collected. Complete a summary worksheet for the year.
   2. For each wetland sites, write the total surface area on the "MEDEP Wetland Bioassessment Field Data Form".

(7) At the discression of the Wetland subsection leader, complete a "DEP Biomonitoring Program Freshwater Wetland Characterization Form" for the new wetland sites, using Appendix 3 for guidance.
   (a) For sites that have a River or Stream *Waterbody Type*, add a "River/Stream" Site Type in the 'Site Type' view in MESA2, as described in Appendix 2 (see W-001 in MESA2 as an example).

C. **Entering and QAing Data**

(1) Field data

(a) Create Field Data pre-EDDs

1. For all data types, make sure to obtain the most recent copy of the respective pre-EDD from Susanne Meidel or Beth Connors before starting. Also make sure that it still meets all program needs; this should be done before field season if possible.
2. Field data collected with river and stream macroinvertebrate samples
   i. Create a new folder for the current year's pre-EDDs here: Augusta H:\...\Biomonitoring\STREAM DATA\Field EDDs. Create a field data pre-EDD for each site. Open the file "Pre-EDD_Stream_MI_Field.xls" and save it as a new file with log number–site name-station number as the file name (e.g. "2041 Crooked Brook S510.xls").
   ii. See Read Me sheet in the pre-EDD for detailed instructions on how to complete the pre-EDD and use "Pre-EDD_Stream_MI_Field_sample.xls" (obtained from Susanne Meidel) as a guide while filling in the pre-EDD.
3. Field data collected with river and stream algal samples
   i. Create a new folder for the current year's pre-EDDs here: Augusta H:\...\Biomonitoring\STREAM DATA\Field EDDs. Create a field data pre-EDD for each site visit. Open the file "Pre-EDD_Algae_Field.xls" and save it as a new file using this format: SA-357-2008.xls, where SA= stream algae, 357= the site number and 2008= the year sampled.
   ii. See Read Me sheet in the pre-EDD for detailed instructions on how to complete the pre-EDD and use "Pre-EDD_Algae_Field_sample.xls" (obtained from Susanne Meidel) as a guide while filling in the pre-EDD.
4. Field data collected with wetland macroinvertebrate and algal samples
   i. Create a new folder for the current year's field data pre-EDDs here: Augusta H:\L&W\WATERSHED\Monitoring and Assessment\Waterbody Type\Wetlands\DATA\field data. Create a pre-EDD for each site visit. Open "Pre-EDD_Wetland_MI_field.xls" and save as a new file with the site number at the end (e.g. "EDD_Wetland_MI_field_w156.xls").
   ii. See Read Me sheet in the pre-EDD for detailed instructions on how to complete the pre-EDD and use "Pre-EDD_Wetland_MI_Field_sample.xls" (Augusta H: L&W\WATERSHED\Monitoring and Assessment\Waterbody Type\Wetlands\DATA\field data) as a guide while filling in the EDD.

(b) QAing Field Data before loading into EGAD

1. Staff other than the one who created the pre-EDDs will check the information entered into the pre-EDD against the field sheet(s) to make sure it was entered correctly. If an error is found, correct it in the pre-EDD before loading to EGAD.
2. Initial field sheet(s) and note date QA'd.
3. Update applicable Sample Tracking files, see 5. A (4), above.
4. Fill in appropriate fields in the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-Instructions\BIOMON TRACKING LISTS\).
5. File all field sheet(s) in the appropriate location(s).

(c) Loading Field Data into EGAD

1. Follow Appendix 4 to load the field data pre-EDDs into EGAD.
2. Initial field sheet and note date loaded.
3. For the river and stream macroinvertebrate and algal field data pre-EDDs, add "DONE" to the file name after the EDD has been loaded.
4. After the field info has been checked and the data loaded, change the 'QA/QC Status' of the applicable sample IDs in the MESA2 "Sample Points" and "Samples" view to 'A' (Accepted). You must click on the "Start Editing" button in order to change the status. These changes should be made in both the "Samples" and "Sample Points" views as well as the "Site Info" view.

(d) Additional QAing of Field Data after loading into EGAD

1. To check river and stream algal field data in MESA2, check all new data for the first four sites loaded into EGAD. If no errors were found for the first four sites, field data from the remaining sites can be spot-checked: 2-3 viewing bucket transects, one canopy cover with real numbers (not just zeroes), and 3-4 of the high gradient survey. All other sections should be checked 100%.
2. Add any applicable information to the Sample Point Descriptor. For example, Sun/Shade for the A-1, A-2 sample points or above road/below road for the macroinvertebrate sample points.

(2) Water Chemistry Data

(a) Create pre-EDD

1. Follow Appendix 5 to download and edit data from HETL's (Health and Environmental Testing Laboratory) StarLIMS system.

(b) Loading Water Chemistry Data into EGAD

1. Follow Appendix 4 to load the water chemistry data EDDs into EGAD.

(c) QAing Water Chemistry Data

1. In MESA2 verify the presence of the water chemistry sample IDs and change their 'QA/QC Status' to 'A' (Accepted). Use start editing button as mentioned in (1) (c) 5 above.
2. Fill in appropriate fields in the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-instructions\BIOMON TRACKING LISTS\).

(3) Macroinvertebrate Data

(a) Create macroinvertebrate EDDs for loading into EGAD

1. Open the file sent from the taxonomist and save file in appropriate location, listed below, with the Sample ID or the log number(s)-Orig as the file name (e.g. DN_2004_076.xls or 1728-Orig.xls). We will keep this file as a record of the unaltered file sent by the taxonomist.
   i. Save river and stream sheets here: Augusta H:\…Biomonitoring\ELECTRONIC BUG IDs\Stream Samples\Year
   ii. Save wetland sheets here: Augusta H:\…Biomonitoring\ELECTRONIC BUG IDs\Wetland samples\Year\raw_data

2. Then save the file as another new file - this will be the file to be edited for loading and subsequently loaded.
   i. For river and streams, save here: Augusta H:\...\Biomonitoring\ DATABASE MGT with the log number as the new file name (e.g. 1728.xls).
   ii. For wetlands, save here: Augusta H:\…Biomonitoring\ELECTRONIC BUG IDs\Wetland Samples\Year\edds and add "EDD_" preceding the Sample ID (e.g. EDD_DN_2004_076).
3. Use the most recent Macroinvertebrate pre-EDD template (obtain from Susanne Meidel) to determine if all required information is included.
4. Enter any site information that is missing from the top (station #, town, etc.), add the 'Time of Collection' (either as military time or with AM or PM) and the Depths for each replicate from the applicable field sheet; if no depth is available, delete the 'CM' in the unit field. Make sure depths are only recorded for each available replicate (i.e. if one bag was lost during sampling, there will only be taxonomy data for two replicates. There should not be a depth measurement for "Rep 3").
5. Alphabetize entries by "Taxon name." If two entries are found for the exact same taxon/stage, contact the taxonomist to resolve the duplicate issue.
6. Delete any zeros reported as taxon counts in Rep 1, Rep 2 or Rep 3 columns.
   i. Use the Find/Replace tool to globally replace all the zeros with nothing, make sure to select 'match entire cell content' in the Options window.
7. The taxonomists may include additional info in the Comment column on certain macroinvertebrates. If there are for example two *Tanytarsus* records with Comments saying 'sp. 06b' and 'sp. 06d', manually add up the counts for each replicate in the Excel file, delete the second record and write in the comments field for the remaining record the counts for each species. Similar editing typically has to be done for Chironomidae.
8. The taxonomists may include a taxon that we do not include in the database (i.e. cladocera, copepoda, Chironomidae tribes), and these should be deleted from the pre-EDD file.
9. ALWAYS check with Biomonitoring Program staff to verify edits are appropriate.
10. Delete extra empty rows, adjust Header/Footer, if necessary, and print.
11. Any taxa without ME Taxonomic codes may need to be added to the MDEP Taxa list. Check the most current MDEP Taxa list and see if the taxon is listed - sometimes the taxa have codes, but the taxonomists does not include them or the taxon is misspelled in the datasheet. Make a note on the print-out that these taxa have not been entered. Have biomonitoring staff (Leon Tsomides or Tom Danielson) assign a code to the new taxon, if appropriate, as described in Appendix 6.

(b) QAing Macroinvertebrate data

1. Before the macroinvertebrate data EDDs are loaded into EGAD, the data needs to be checked for accuracy by staff other than the one who edited the data.

2. Check all steps where Biomonitoring staff altered the original file sent from the taxonomists, including the Station number, the sample log number, the town name, the date, the time and the depth units and values.
3. Double check that questionable taxa have been correctly adjusted in the pre-EDD (taxa deleted, records combined, codes entered for new taxa, tribes entered as Chironomidae, etc.), by looking for duplicate records, taxa without codes, etc.
4. Initial data sheets and note date QA'd.
5. Fill in appropriate fields in the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-Instructions\BIOMON TRACKING LISTS\).

(c) Loading Macroinvertebrate data into EGAD

1. Follow Appendix 4 to load the macroinvertebrate data pre-EDDs into EGAD.
2. After each EDD is loaded into EGAD, write your initials, "Loaded into EGAD" and the date loaded on the macroinvertebrate sheet.
3. While in editing mode, change the Sample QA/QC status for all three sample points (MI-1, MI-2, and MI-3) to "A". Note: for new sites, the Sample Point QA/QC status may need to be changed to "A" prior to changing the status on the Sample records.
4. Open the appropriate sample tracking file, see 5.A. (4) above for file path, and enter the date when the IDs were received in column "IDENTIFICATION/Date Back" and the original file name (name assigned in step 5 C. (3) (a) 1., above) in column "IDENTIFICATION/ E-copy name". Add the date loaded into EGAD in column "DATES DATA ENTERED/Bugs". Add the date QA'd in the column "DATES DATA ENTERED/Bugs QA'd".
5. File data sheet in the appropriate location.

(4) Algal Data

(a) Preparing and QAing data

1. Sample data are sent from the taxonomist in batches with multiple samples in one MS Excel sheet (Tom Danielson does the following steps).
2. Create a folder for the year the samples were collected in Augusta H:\...\Biomonitoring\ELECTRONIC ALGAL IDs
   i. Save a copy of the file sent from the taxonomist in the folder you just created and include '-ORIGINAL' at the end of the file name
   ii. Save another copy of the file sent from the taxonomist in the folder you just created and include '-EDITED' at the end of the file name. This will be the file used for editing data in preparation of loading.
3. Open the 'ALGAL SAMPLE TRACKING.xlsx' workbook and enter the date the data was received from the taxonomists in the 'Bottles/Data Back' field (Augusta H:\...\Biomonitoring\SAMPLE TRACKING\ALGAE).
4. Filter the '-EDITED' file, created in step (4) (a) 2, directly above, by CAS_NO to find the list of potentially new taxa (those with no CAS number supplied). Determine which taxa need to be added or modified in EGAD.
5. Assign a code to the new taxon as described in Appendix 7.
6. Run a query to determine that all taxa are already in EGAD

(b) Creating separate EDDs for each sample bottle

1. Open the '-EDITED' file in MS Excel. In the 'Master' worksheet, put the cursor in cell A1, and click the 'Filter' icon in the 'Data' tab.
2. Click on the downward pointing triangle icon in the lower-right corner of cell A1, deselect all bottle numbers, and select the bottle number you want to copy the data for.
3. Select all the contents in the worksheet, determine how many records (rows) there are in the filtered worksheet, and copy the contents.
4. Create a new workbook.
5. Click in cell A1 and paste the content from the previous worksheet
6. Save the new workbook with the bottle number, such as *1170.xlsx*, in the same folder as the '-EDITED' file.
7. QA check to make sure the new worksheet, such as *1170.xlsx*, has the same number of records as the filtered '-EDITED' worksheet.
8. Record the file name and date in the 'ALGAL SAMPLE TRACKING.xls' workbook (See 4.(a) 3 directly above)

(c) Loading algal data into EGAD

1. Follow Appendix 4 to load the algal EDDs into EGAD.
2. Record the date loaded into EGAD in column "DATA ENTERED?/Algal Data" in the 'ALGAL SAMPLE TRACKING.xls' workbook (See 4.(a) 3 directly above).

(d) QAing algal data in MESA2

1. Open the algal counts for the bottle in EGAD MESA 2
2. For a random subset of the batch of data loaded, complete an intense QA check of the algal Counts by comparing the counts in MESA2 to the Excel worksheet for the bottle, such as *1170.xlsx*.
3. Once the in-depth QA check is complete, QA the remaining bottles entered by verifying the presence of the Counts in MESA2, but checking every Count record is not necessary.
4. Record the date loaded into the DATA ENTERED?/ Algal Data QA column in the 'ALGAL SAMPLE TRACKING.xls' workbook (See 4.(a) 3 directly above).
5. While in editing mode, change the Sample QA/QC status for the sample point (e.g., A-1, A-2) to "A". Note: for new sites, the Sample point QA/QC status may need to be changed to "A" prior to changing the status on the Sample records.

(5) Prepare and upload data from continuous water temperature data loggers to EGAD as described in *Protocols for Measuring Continuous Water Temperature Using an Onset Data Logger* (Connors 2014b).

D. **Data Analysis**

(1) Follow Appendix 8 to run applicable algorithms.
(2) Qualified Biomonitoring staff will make the final attainment decision based on model outcome and/or Best Professional Judgment as described in Davies and Tsomides 2002.

(3) Follow Appendix 8 to enter final determinations.
(4) River and Stream Macroinvertebrate
  (a) Follow Appendix 8 to generate and save all applicable reports as pdf files. Save them here: Augusta H:\...\Biomonitoring\ELECTRONIC KEY REPORTS
  (b) Print and file report in binder 'Log # ###-###: Key Reports' in biomonitoring office area.
  (c) Update applicable Sample Tracking file, see 5.A. (4) above, and the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-Instructions\BIOMON TRACKING LISTS\) with the dates the above steps were completed.
(5) Wetland Macroinvertebrate
  (a) Follow Appendix 8 to generate and save all applicable reports as pdf files. Save them here: Augusta H:\...\Biomonitoring\ELECTRONIC KEY REPORTS\wetland reports.
  (b) Update applicable Sample Tracking file, see 5.A. (4) above, and the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-Instructions\BIOMON TRACKING LISTS\) with the dates the above steps were completed.
(6) River and Stream Algae
  (a) Follow Appendix 8 to generate and save all applicable reports as pdf files.
  (b) Update applicable Sample Tracking file, see 5.A. (4) above, with the dates the above steps were completed.

E. **Data Extraction and Reporting (need to add)**
(1) General data extractions to update Biomonitoring databases (water chemistry, algae, macroinvertebrate)
(2) Data extractions for transfer to statistical packages (SYSTAT, PCORD, R)
(3) Data extraction for reporting in the SWAT Report
  (a) "Instructions for compiling the annual SWAT report.doc"

F. **Watershed Delineation and Landuse Calculations**
(1) Watershed delineations are not an exact science and the final product will involve best professional judgment. Consult with Biomonitoring staff to determine which method to follow to delineate watersheds for desired purpose.

(2) Appendix 9 describes how to delineate watersheds for sampling stations and how to use the custom Biomonitoring ArcMap tool to calculate the landcover classes with in the watershed. This is the tool that links the land use data to EGAD.

(3) Appendix 10 describes how to calculate the landcover within a polygon, which could be a watershed or a buffer(s) surrounding a sampling station, stream, etc.

G. **Editing Biomonitoring Site Point locations**
(1) Find and select the site points that need to be moved in the *EGAD_site_locations* GIS layer

(2) Copy them into a new shapefile and make edits in this shapefile
(3) Send the edited shapefile to John Lynam who will copy changes into the *EGAD_site_locations* layer.

H. **Documents for Biomonitoring Google Earth Project**

(1) Site Photos

(a) Review all site photos available and select the best representative photo for each site from all photos taken. In general, for river and stream site photos use the August "up" and "down" photos. If the site doesn't have August photos (it's an Algae only site or if the August photos are not very good) use the June/July "up" and "down" photos.

1. Wetland site photos are found here: Augusta H:\...\Biomonitoring\WETLAND FILES\Wetland photos\Wetland Sites.
2. Stream macroinvertebrate and algae site photos are found here: Augusta H:\...\IMAGES\Stream Stations\YEAR, within this folder there are folders for each site sampled.

(b) The photo should open in Microsoft Office Picture Manager by default when opened though Windows Explorer. Compress the photo for 'Web pages' using 'Compress Pictures' on the 'Edit Pictures' menu.

(c) Save the compressed photos here: Augusta H:\...\Biomonitoring\Images\Web photos\Temp folder following this naming convention:

1. For wetland site photos: w171_2008.jpg
2. For river and stream site photos (macroinvertebrate sites, algae sites, and both macroinvertebrate and algae sites are all treated the same): s076(up)_8_2003.jpg, s076(dwn)_8_2003.jpg. NOTE: the site number must have 3 digits, so add zero(s) preceding the site number as necessary.
3. **Note**: When Picture Manager is closed, you may get a message about unsaved edits, do not save these edits – this is save the original photo at the smaller size.

(d) When a group of photos have been resized and are ready to be linked to the appropriate site in MESA2, move the resized photos into the following folder before linking them: Augusta H:\...\Biomonitoring\Images\Web photos\.

1. Note: the "temp folder" is for resized photos that have <u>not</u> been linked in MESA2.
2. It may be useful to take and print a screenshot of the Temp folder contents prior to moving the files into the Web photos folder in order to keep track of what needs to be linked. Do this by having the desired view showing on the monitor, press and hold "Crtl" and "Print Screen" at the same time, open a new Word document and paste the image.

(e) Follow instructions in Appendix 8 to link the photos to the <u>site</u> in MESA2.
(f) For river and stream sites, update the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-QAPP\BIOMON TRACKING LISTS\).
(g) For wetland sites, update this file, Augusta H:\...\Biomonitoring\SOP-QAPP\BIOMON TRACKING LISTS\Tracking_site_photos_for_GE.xls.

(2) Data Reports

(a) Create report as a pdf file (see 5. D., above). Save river and stream reports here: Augusta H:\...\Biomonitoring\ELECTRONIC KEY REPORTS and wetland reports here: Augusta H:\...\Biomonitoring\ELECTRONIC KEY REPORTS\wetland reports.
(b) Follow instructions in Appendix 8 to link report to the sample in MESA2.
(c) For river and stream sites, update the 'Tracking data QA.xls file (Augusta H:\...\Biomonitoring\SOP-QAPP\BIOMON TRACKING LISTS\).
(d) For wetland sites, update the 'WetlandSampleTracking.xls' file (Augusta H\…\Biomonitoring\Sample tracking\wetland sample tracking\).

I. Managing Data from Outside Sources

(1) Outside data are only accepted for use by the Biomonitoring Program if they were collected by a qualified biologist using standard biomonitoring methods as specified in the Biomonitoring QAPP. Alternative methods can be used if prior approval is given by Biomonitoring staff. Sample taxonomy for macroinvertebrates must be performed or supervised by a professional freshwater macroinvertebrate taxonomist who has the qualifications specified in the Biomonitoring QAPP. Sample taxonomy for algae must be performed or supervised by a professional freshwater algal taxonomist with a closely related advanced degree with specialized training or experience in the taxonomy of northeastern freshwater algae.

(2) Field and taxonomic data must be submitted to Biomonitoring staff using standard Biomonitoring pre-EDDs. Prior to submitting data, Biomonitoring staff should be contacted to obtain the most current pre-EDDs. To enable QA of field data, hard copies of field sheets must also be submitted via fax or mail.

(3) On receipt of electronic field pre-EDDs, Biomonitoring staff will QA the data against the hardcopies, and examine the data for completeness and accuracy (as far as possible). If there are questions, contact the person who submitted the data.

(4) When all required data are in hand, assign a log number to the sample as explained in 5. A. (3) (a), above; also enter sample information in appropriate "Sample Tracking" file (Augusta H:\...\Biomonitoring\Sample tracking). Write log number(s) on field sheet and enter into applicable files. If the data were collected at a new site, assign a new station number as explained in 5. B. (2), above.

(5) Stream macroinvertebrate data
(a) Save the field pre-EDD here: Augusta H:\...\Biomonitoring\STREAM DATA\Field EDDs with the name of the data originator preceding the assigned log number followed by 'field–Orig' (e.g. originator-1728field–Orig). Save the macroinvertebrate taxonomic pre-EDD here: Augusta H:\…\Biomonitoring\ELECTRONIC BUG IDs\Stream Samples\Year\ with "taxonomist-log number(s)-Orig" as the file name (e.g. Taxonomist-1728-Orig.xls) and add pertinent site information or site number as necessary.

(b) Save both files with just the log number (and '-field' for field data) here: Augusta H:\…\Biomonitoring\DATABASE MGT\ and make any necessary edits (see 5. C. (3) above for instructions on typical edits); use these files for loading to EGAD.
(c) Load and QA the data as explained above in sections 5. B. and C. After loading, move the loaded files to the location where the originals were saved [see (a) immediately above].
(d) Analyze data as described in 5. D. (1) and send completed reports to data originator.

(6) Stream algal data
(a) Save all pre-EDDS in appropriate file locations, as described above in 5.C. (1) (a) 3. Add originator's name to file name. Prepare, load, QA and analyze the data as described in 5. B. C. and D.

(7) Wetland data
(a) Save all pre-EDDS in appropriate file locations, as described above in 5.C. (1) (a) 4. Add originator's name to file name. Prepare, load, QA and analyze the data as described in 5. B. C. and D.

6. References

Connors, B., 2014. *Protocols for Measuring Continuous Water Temperature Using an Onset Data Logger* DEPLW-700A-2014. Maine Department of Environmental Protection, Augusta, ME.

Connors, B., 2014b. *Protocols for Decontaminating Biomonitoring Sampling Equipment.* Maine Department of Environmental Protection, Augusta, ME. DEPLW0919A-2014.

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Danielson, T. J., 2014a. *Protocols for Sampling Algae in Wadeable Rivers, Streams, and Freshwater Wetlands.* Maine Department of Environmental Protection, Augusta, ME. DEPLW-0634B-2014.

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Davies, S.P., and L. Tsomides, 2002. *Methods for Biological Sampling and Analysis of Maine's Rivers and Streams.* Maine Department of Environmental Protection. Augusta, ME. DEP LW0387-B2002.

DiFranco, J. L., 2014. *Protocols for Sampling Aquatic Macroinvertebrates in Freshwater Wetlands.* Maine Department of Environmental Protection, Portland, ME. DEPLW0640A-2014.

7. **Appendices**

Appendix 1 – Overview of how biological samples are handled

Appendix 2 – Instructions for How to add New Sites (Monitoring Stations) to EGAD Using MESA2

Appendix 3 – How to assign landscape level classification to wetland biomonitoring sites

Appendix 4 – Procedures for Using the EGAD Uploader Module

Appendix 5 – How to download and edit data from HETL's StarLIMS to go into EGAD

Appendix 6 –How to Assign New Codes to Macroinvertebrate Taxa from River, Stream and Wetland Samples

Appendix 7 –How to Assign New Codes to Algal Taxa from River, Stream and Wetland Samples

Appendix 8 – Instructions for Using EGAD, Maine DEP's Environmental and Geographic Analysis Database

Appendix 9 – DRAFT Delineating Watersheds for Biomonitoring Sampling Stations

Appendix 10 – Biomonitoring MELCD Tool Summary

Appendix 11 –Biological Monitoring Data Management SOP Duties

Appendix 12 – How to Use the Garmin GPSmap 78s