Stream Health Workgroup Technical Advisory Group Call Notes

1/15/16; 10 am – 12 pm

Participants:

Claire Buchanan, ICPRB

Zack Smith, ICPRB

Andrea Nagel, ICPRB

Kyle Runion, CRC

Dan Boward, MDNR

AJ Smith, NYDEC

Ginny Rogers, Versar

Greg Pond, EPA

Jim Cummins, ICPRB

Kelly Maloney, USGS

Mark Secrist, USFWS

Michael Bilger, Susquehanna U

Peter Tango, USGS

Elisha Rubin, DOEE

Brianna Hutchison, SRBRC

Mike Whitman, WV DEP

Jeff Bailey, WV DEP

Chris Victoria, AAC DPW

Gary Walters, PA DEP

Mike Selckmann, ICPRB

Mark Melino

Background

* The 2014 Chesapeake Agreement had a Stream Health Outcome to improve stream health and function above 10% of the 2008 baseline, but no final metric for improvement or baseline. The 2015 Management Strategy selected the Chessie BIBI as a potential metric. The Chessie BIBI is not intended for regulatory purposes, but rather regional planning purposes and to meet Bay Program needs. It provides a means for comparing streams across state boundaries as an evolving database.
* Objectives of this project: 1) update the CBP database with non-tidal stream data, 2) refine the Chessie BIBI index, and 3) support the SHWG in its development of the 2008 baseline of stream miles.
* The role of the TAG is to review approaches for refining index, provide feedback on key technical details, and participate in development of 2008 baseline later this year.

Today we’ll give an overview of the updated non-tidal stream biological database, review and discuss the proposed approach for refining the index, and describe the BIBI 2 R-package

Update

* We are missing data from several Washington County areas. Non-traditional partner data may be incorporated (organized by Leah Miller at IWLA).
* Source data are in different database formats and database management varies, which causes issues. Water Quality has a tool for data providers to upload various data for CBP review and archive; this is a system we could emulate.

Proposed approach for refining the Chessie BIBI index

* We are trying to develop a BIBI package using r functions to conduct analysis.
* Data preparation
  + Master Taxa List
    - Integrated Taxonomic Identification System, [www.itis.gov](http://www.itis.gov), available on the CBP website, today’s event page
    - Enables the data counts to be transformed from a long data format to a wide data format
      * *Bilge*r: When was the last time last taxa list was reviewed & who reviewed it?
        + Smith: Just created within the past month, contains all of the taxa we are currently finding in the data. We are looking for volunteers for review. Spelling errors, invalid taxa, question marks, etc. were corrected or rolled up to the next taxa level.
  + Taxa attributes table
    - To include family and genus level functional feeding groups, habits, and tolerance values.
      * TVs vary from the agency reporting. Mean TVs within a bioregion will be used for the final representation of the TV for that bioregion.
        + *Bilger*: Prefer not to use tenths of a TV. Time to update these TVs.
        + *Pond*: Averaging is ok, but we certainly need to pay attention to taxa by taxa issues across bioregions.
        + Smith: Volunteers to update the taxa attribute table? Possibility of incorporating other attributes such as temperature sensitivity, gills, surface breathing, etc. (USGS attributes). Draft of the table will come in the next month. Please send in TV tables you may have as this info for review would be helpful.

*Boward, AJ Smith, Bilger*: Volunteer to help

* + - * + Comment: WV DEP is currently updating TV; what you have from us will soon be out of date.
  + Index refinement
    - Subsetting data to only include wadeable streams (order 1-4) with a similar sampling method (mostly kick net), and site must have all necessary environmental variables (rapid habitat assessment, specific conductivity, pH, DO; will look at some watershed parameters).
    - Seven different bioregions defined by EPA Region 3.
    - Not all agencies identify taxa to the genus level; this data will be excluded. Only stations with 80% genus level identification will be used
    - *Boward*: It is important to pay close attention to every dataset’s rules and how variable they may be. For example, our lab doesn’t take worms, some labs don’t include mites.
      * Smith: Could roll these up to the next level taxa or drop entirely. Could compare datasets/analysis and determine how much of an effect this will make.
  + Rarefaction
    - Standard sampling count differs between agencies and richness is positively correlated with sampling count, so a rarefaction function is required.
    - Samples within the range of 100 will not be brought down, as long as they are in the normal range returned (~115). This takes into account rounding.
    - The rare taxa are excluded are eliminated because of their low probability of being selected.
      * Threshold of excluded taxa is given by rarefy function. Example given is 5.2, how should we round? Up/down?
      * Hate to lose rare taxa, but this will only be used in a few metrics: richness, diversity… The rare taxa will be present in other metrics.
* Site Classification
  + Categorized into reference, mixed or degraded
    - Based on environmental variables, rapid habitat assessment, water quality variables, watershed variables, etc.
    - Comparable at the HUC-12 level? Topic for next call.
* Metric Selection and Scoring
  + Using discrimination efficiency and metric redundancy to score based on an optimal discrimination threshold.
  + Discrimination efficiency (DE)
    - Used to characterize how well a metric can discriminate between site classifications of reference and degraded conditions.
    - The DE statistic is the frequency of correctly classified reference and degraded sites for a given metric value. High DE’s indicate good separation (equation and more detailed explanation available on CBP event webpage).
  + Metric redundancy
    - Pearson correlation is used to assess metric redundancy within each metric type.
      * Is a correlation coefficient of -0.7 ≤ r ≤ 0.7 acceptable?
        + *Pond*: That’s great, adds up to about 50% variation of each metric. Two schools of thought with redundancy: use only reference sites as stressors are correlated and can effect each other, or can use all (included degraded sites) which includes more information.

*Buchanan*: Considering trying to develop metrics that indicate different kinds of degradation. Redundancy can be very helpful when trying to tell different kinds of degradation.

* + - *Boward*: Redundancy among the metrics may eliminate certain measures that we want in.
      * *Rogers*: Based on best judgement… in some cases, categories sounded redundant, but both may be necessary in the model.
* Metric Scoring
  + Using bin process similar to 2011 BIBI where bin 1 is degraded, bin 2 is mixed (optimal discrimination threshold to reference median), and bin 3 is reference. Bin 2 to 3 cut-off could be moved around by metric, but 50% generally returns the best results.
    - Bins are set as they are to try to make the index equally sensitive to reference and degraded.
    - Bin 1 receives a score of 0. Bin 3, 100. Equation used for bin 2 (available on event webpage).
* Taking the IBI one step further
  + Determining the stressor that is driving degradation, two different R packages are available. *Pond*: Observed over expected models can help uncover uncertainty in an IBI score.
    - IndiSpecies
    - Titan2
  + *Victoria*: Depending on what stressors you measure, you might have different IBI’s for different types of watersheds? Metrics may respond differently in urban vs ag watersheds

Summary:

* Joining the count data to the master taxa list and the taxa attributes table
* Subsetting the data
  + Wadeable streams, kick net samples, and all environmental parameters
* Dividing the data into bioregions
* Selecting the metrics and scoring the metrics specific to each bioregion
* Merging the station scores for each bioregion into one final output

BIBI 2 R Package:

* Easily shared, functions run quickly, user manual built in, can be used to assess data unrelated to the Chessie BIBI
* Live demonstration
  + Open R, import BIBI package, open BIBI help page to review all functions
  + The package is still under construction. Email Smith if you would like to give the package a test run.
  + Should use R-studio rather than just R so you can save scripts.

Discussion

* *Pond*: Does metric testing have a relationship with catchment area? Sites are 1st-4th, expect some variation across reference sites even within bioregions. Will we need a catchment adjustment?
  + *Buchanan*: Yes, in a nutshell. The 2011 BIBI priority selected reference sites, looking for significant differences in attributes to catchment. Ecoregion was typically the strongest separator of data, with elevation and latitude also being significant factors… that analysis will be done again.
* *Maloney*: What season of sampling are you using?
  + *Buchanan*: Mostly collected during the summer, but the tool may be open to all times of the year. We will examine differences in data through seasons.
* In the help guide, we will have to specify that the data is collected using the same sampling methodology.

Please provide comments, suggestions, feedback, or thoughts to Zach Smith at [zsmith@icprb.org](mailto:zsmith@icprb.org). Our next call will be in about a month. Materials to be posted on the meeting site.