

A Credible Water Quality Assessment Using Citizen-Collected Macroinvertebrate Data



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Which evaluates the relative biological health of the State's river and streams

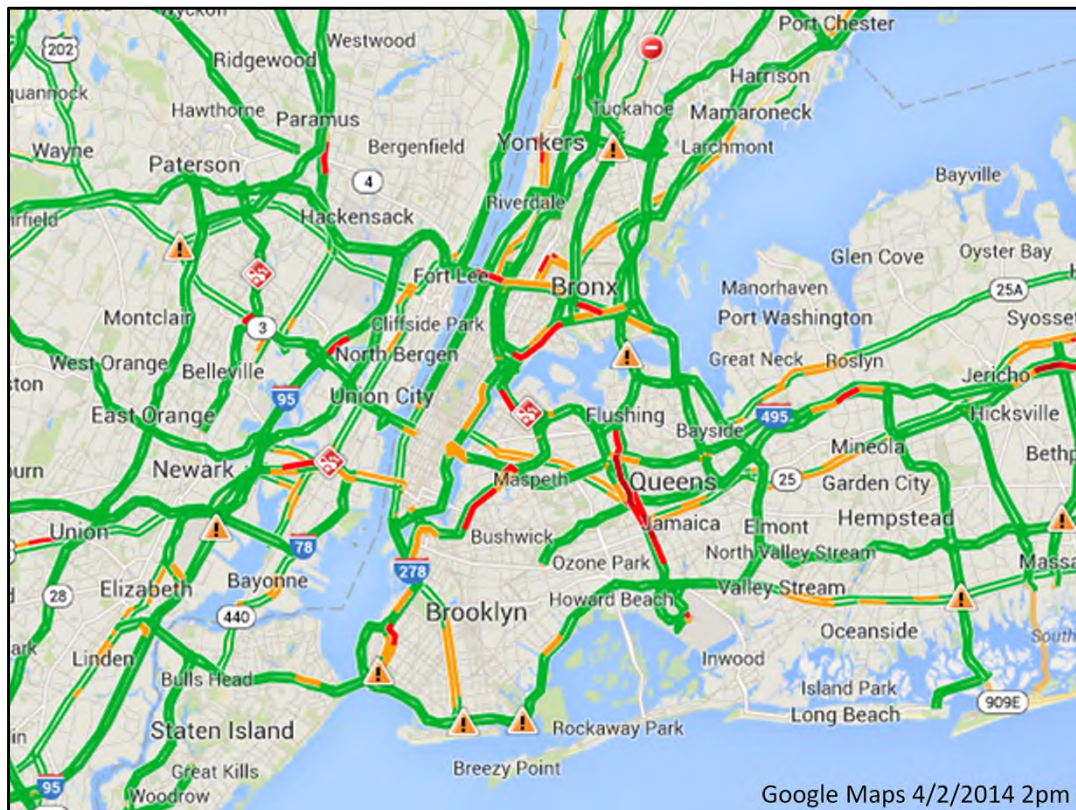


Defining Credible

Human Error in Macroinvertebrate Sampling

How we developed the WAVE Method

Summary of today's presentation



The meaning of “credible” is best described by the following analogy:

If a colleague tells me about a traffic problem, I will change my drive to avoid this traffic because I trust this source. When data comes from a larger and more diverse population, however, it becomes more and more difficult to trust all the sources. The Google solution is to harvest speed and location information from all our smart phones. This way, the sources of human error are removed and the data are credible no matter the source.

How does this apply to water quality monitoring:

With a small population of data collectors, it is completely reasonable to develop relationships and trust the data credibility.

A statewide citizen science project, however, includes hundreds of data collectors. At this level, it becomes more difficult to develop this relationship of trust. For this reason, we wanted to develop a method that would remove sources of human error so the data are credible no matter the source.

Reference describing how traffic data are collected by Google:

<http://googleblog.blogspot.com/2009/08/bright-side-of-sitting-in-traffic.html>

Sources of Human Error in Macroinvertebrate Sampling

Summary of today's presentation



Sources of Human Error – Collecting a Representative Sample:

The goal of this step is to collect a representative sample of macroinvertebrates living in the stream.

In NY State, the standard method is to kick a 5m transect of a riffle habitat, 3" deep, in 5 minutes.

Habitat selection, level of effort, and technique are all potential sources of human error.



Sources of Human Error – Chain of Custody:

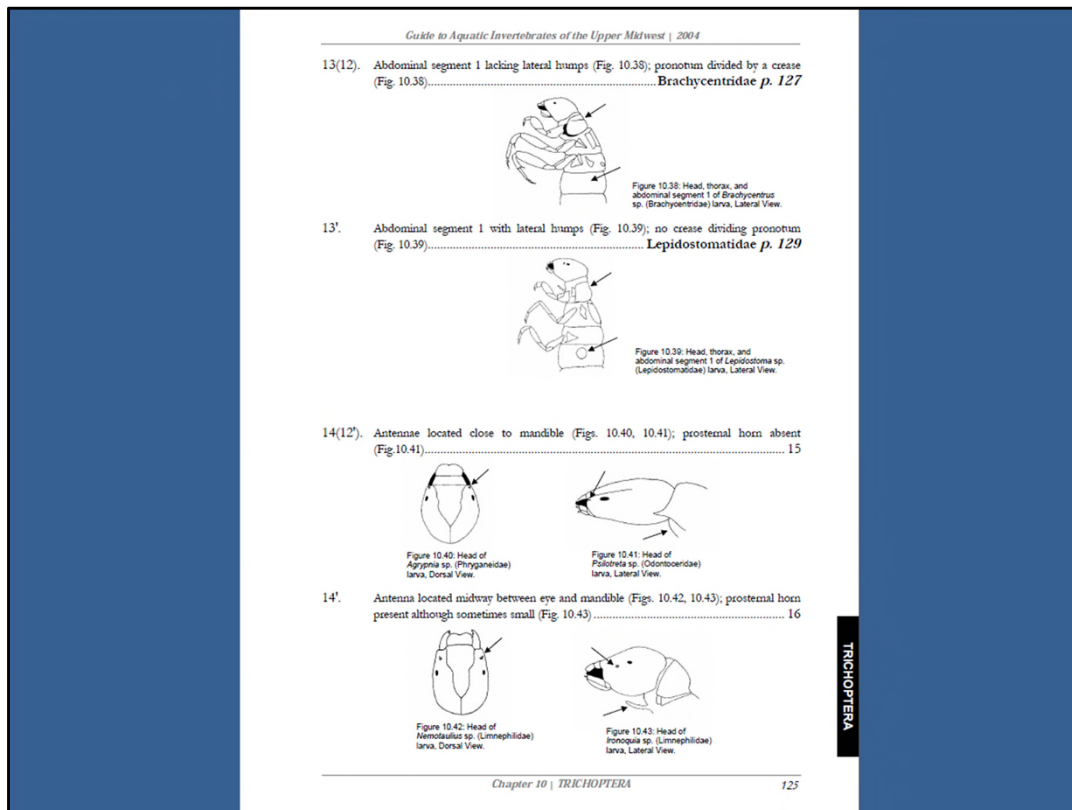
The next step is to preserve, label, and transport the sample to the laboratory. All of these steps are potentially vulnerable to human error.



Sources of Human Error – Picking a Macroinvertebrate SubSample:

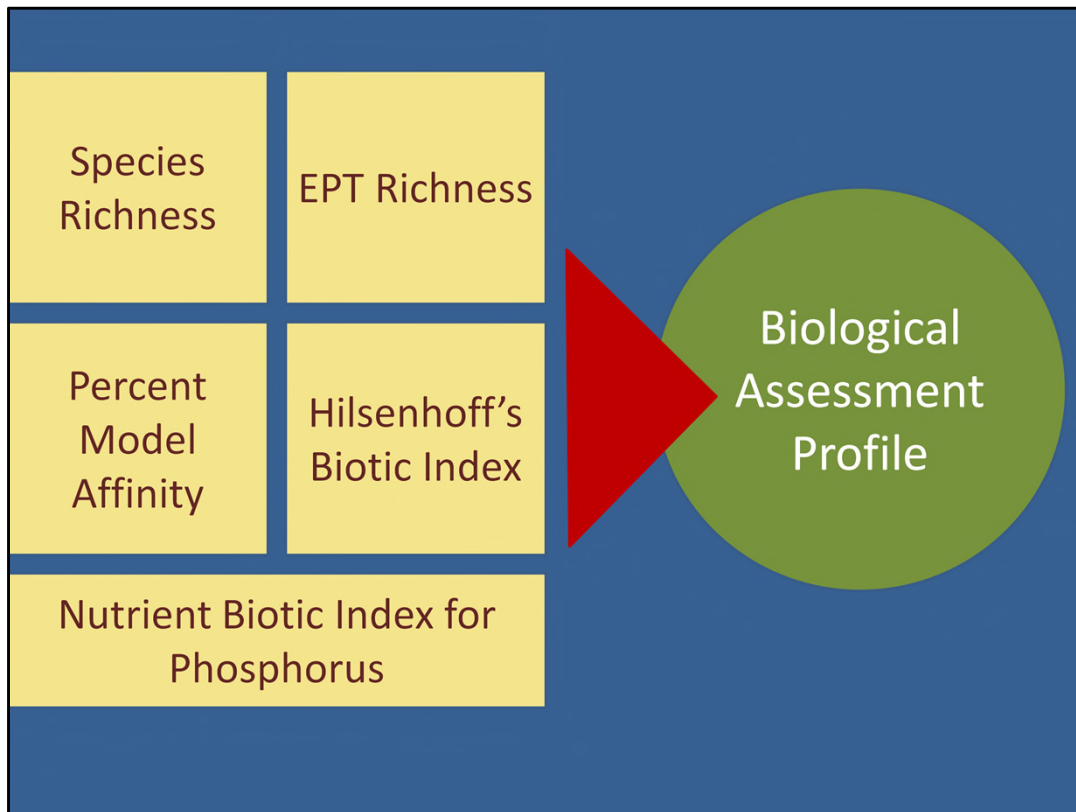
The goal of this step is to pick a representative subsample of macroinvertebrates from the sample debris.

This is also a source of error. Inexperienced pickers can disproportionately pick larger organisms.



Sources of Human Error – Macroinvertebrate Identification:

The goal of this step is to identify all the macroinvertebrates in the subsample. Error is introduced especially when people doing the identification are less experienced or don't have the appropriate equipment.



Sources of Human Error – Water Quality Assessment Calculation:
Human error can result in calculation errors.

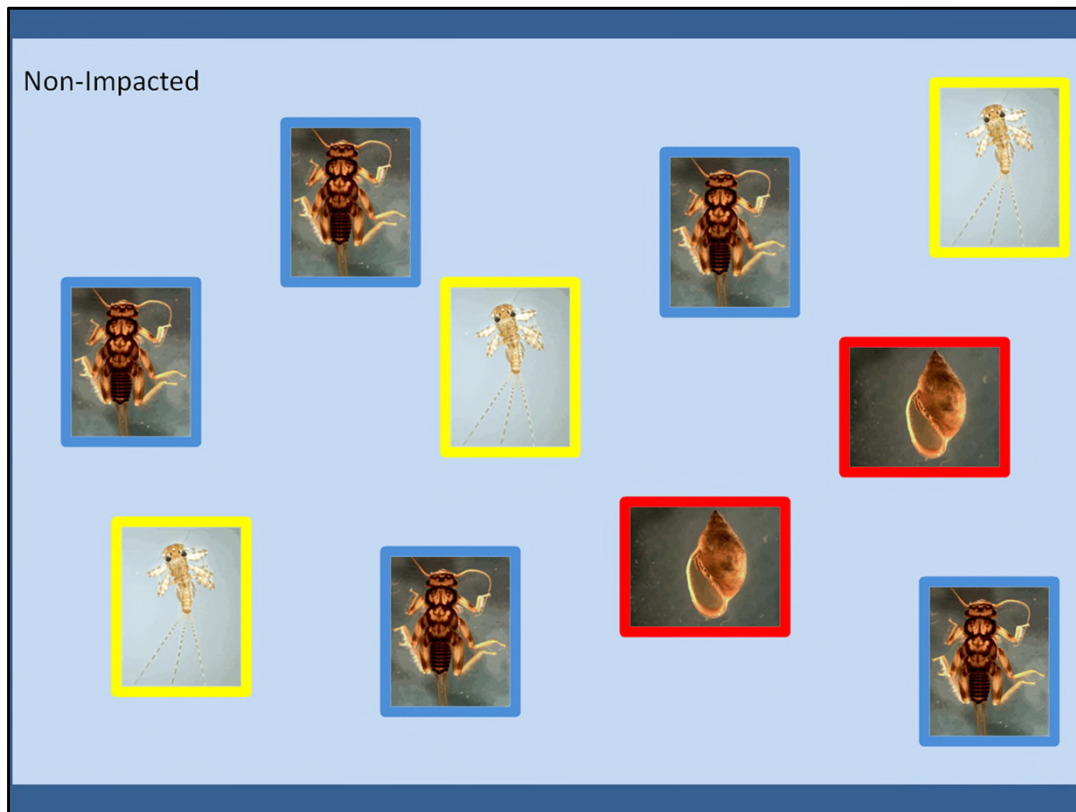
Sources of Human Error in Macroinvertebrate Sampling

- ~~1. Collecting a representative sample~~
2. Chain of Custody
- ~~3. Picking a representative subsample~~
- ~~4. Macroinvertebrate Identification~~
- ~~5. Calculating Water Quality Assessment~~

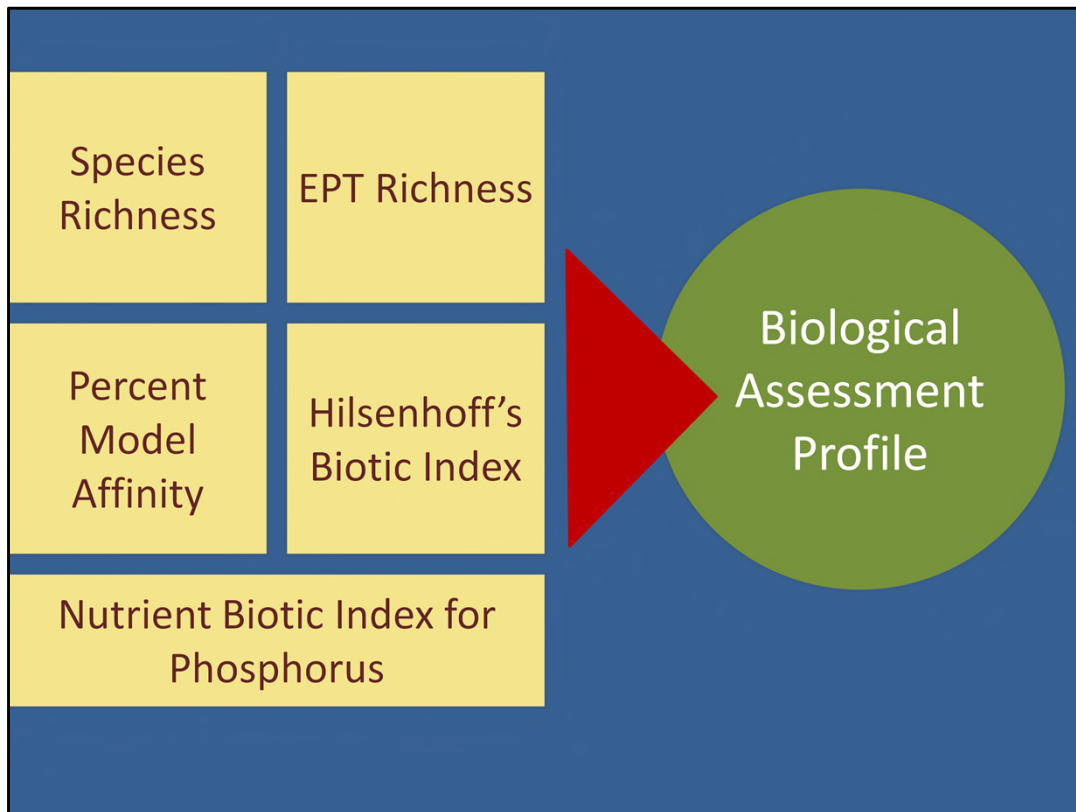
The crossed out errors are those that are removed by the WAVE method.

There are many citizen science macroinvertebrate monitoring programs that remove errors 3-5. They simply require these be performed by staff or other professional.

This method (and the CT method this is based on) are unique in that they remove human error associated with collecting the sample. This is done by using a presence only metric.



Simulation of a simplified macroinvertebrate population responding to an environmental stressor





Traditional macroinvertebrate metrics look for the presence as well as the absence of indicator organisms.

These metrics, however, are vulnerable to sampling error – indicator organisms could be absent because they were not in the stream or they could be absent because of poor sampling technique.

The solution this method offers is to look for **ONLY** the presence of indicator species. This removes human error concerns involved with sampling


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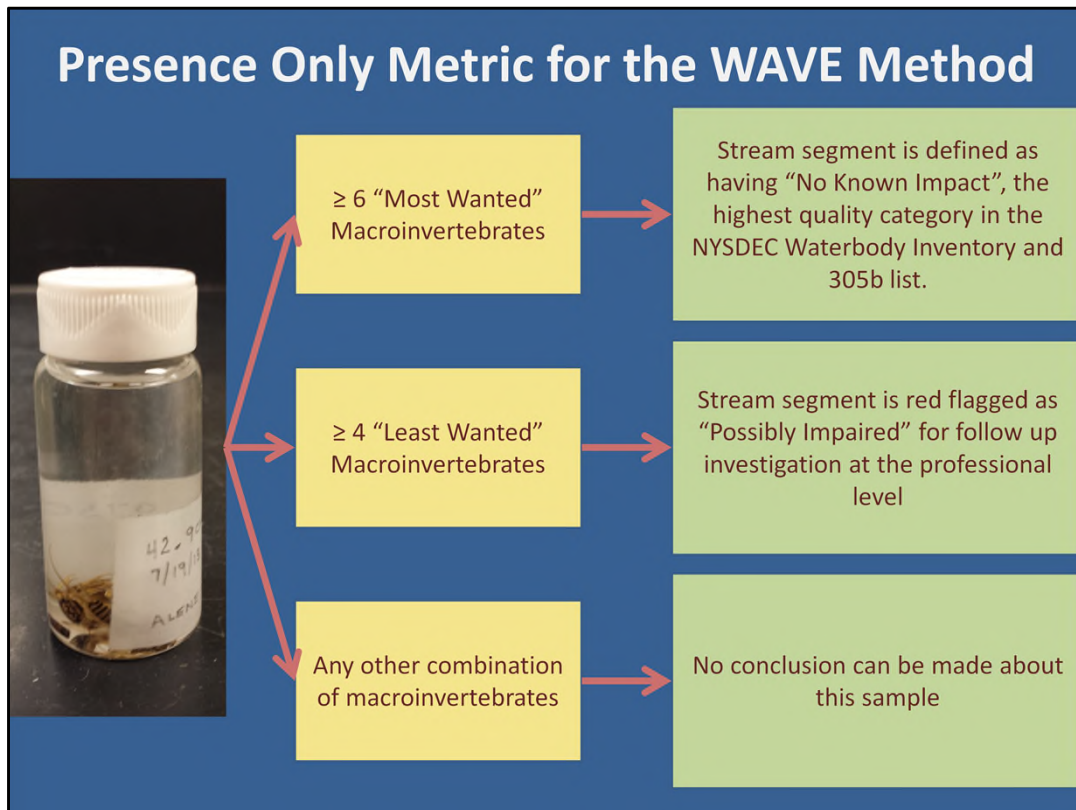
River Bioassessment by Volunteers (RBV) Program
CT DEEP Tier 2 Volunteer Water Quality Monitoring Network

About the Program:
RBV is a citizen-based water quality-monitoring program developed by the Connecticut Department of Energy and Environmental Protection's (DEEP) ambient monitoring program. The RBV program is a standardized screening method that keeps the equipment, expertise, and time commitment to a minimum while simultaneously identifying sections of streams with pollution sensitive organisms. In some instances, more formal DEEP methods may be required to provide a definitive water quality assessment.
The entire RBV process is completed at the stream and usually takes 2-3 hours. The final product is a completed RBV data sheet and a voucher collection (one of each type of organism observed). RBV training is available free of charge for groups of 6 or more adults.
For additional information, please contact Meghan Ruta, Volunteer Monitoring Coordinator, at (860) 424-3061 or meghan.ruta@ct.gov

Interested in Volunteering?
Individuals can contact the Volunteer Monitoring Coordinator to be put in touch with a participating local RBV group in your area. Groups interested in establishing a new local RBV program in Connecticut should contact the Volunteer Monitoring Coordinator to determine whether RBV is right for your watershed.

Program Materials:
[2013 Summary of Volunteer Monitoring](#) (PDF)
[2012 Summary of Volunteer Monitoring](#) (PDF)
[2011 Summary of Volunteer Monitoring](#) (PDF)
[2010 Summary of Volunteer Monitoring](#) (PDF)

CT's RBV program uses a presence only metric which was the inspiration for our project



The presence only metric for the WAVE Project

Indicators for High Quality Streams

Sørensen similarity index analysis:

Families more abundant in High Quality Streams

- Those that contribute >2% to Impaired similarity
- Those that contribute 0 to High Quality similarity

Athericidae	Isonychiidae	Potamanthidae
Brachycentridae	Lepidostomatidae	Psephenidae
Caenidae	Leptohyphidae	Pteronarcidae
Chloroperlidae	Leptophlebiidae	Rhyacophilidae
Corydalidae	Leuctridae	Uenoidae
Ephemerellidae	Odontoceridae	
Ephemeridae	Peltoperlidae	
Glossosomatidae	Perlidae	
Gomphidae	Perlodidae	
Helicopsychidae	Philopotamidae	
Heptageniidae	Polycentropodidae	
Hydroptilidae	Polymitarcyidae	

How we developed NY's presence only metric: The NYS database has >2000 macroinvertebrate samples from NY streams. We randomly split this into two batches.

With the first batch, we performed a Sørensen similarity index analysis. We pulled out those families which were more abundant in High Quality Stream samples (with a BAP >7.5). We then removed those families that contributed more than 2% to the similarity of samples collected from Impaired streams (with a BAP <5) as well as those that contributed nothing to the similarity of the samples from high quality streams.

We then used the second batch to test the error associated with this method.

Indicators for Impaired Streams

Sørensen similarity index analysis:

Families more abundant in Impaired Streams

- Those that contribute >2% to High Qual similarity
- Those that contribute 0 to Impaired similarity

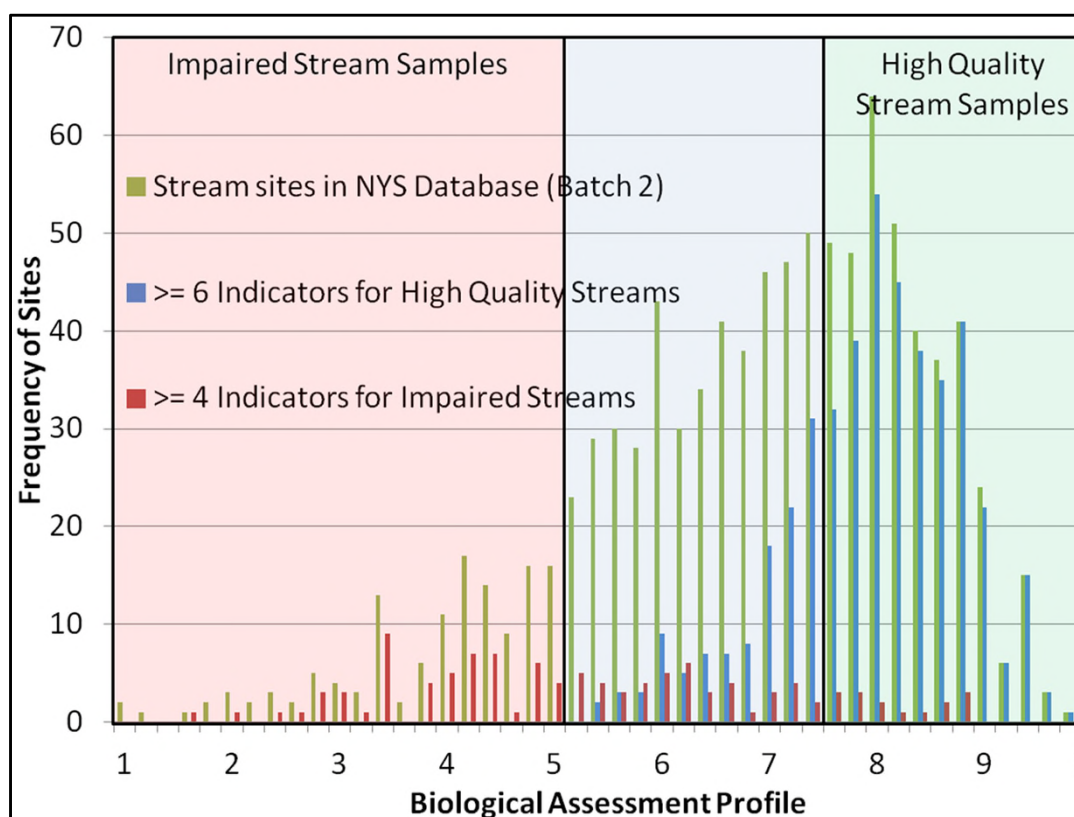
Amphipoda
Asellidae
Calopterygidae
Chironomus
Coenagrionidae
Cordulegastridae
Corixidae
Haliplidae
Hirudinea
Lymnaeidae
Pelecypoda

Physidae
Sialidae
Simuliidae
Tabanidae
Turbellaria

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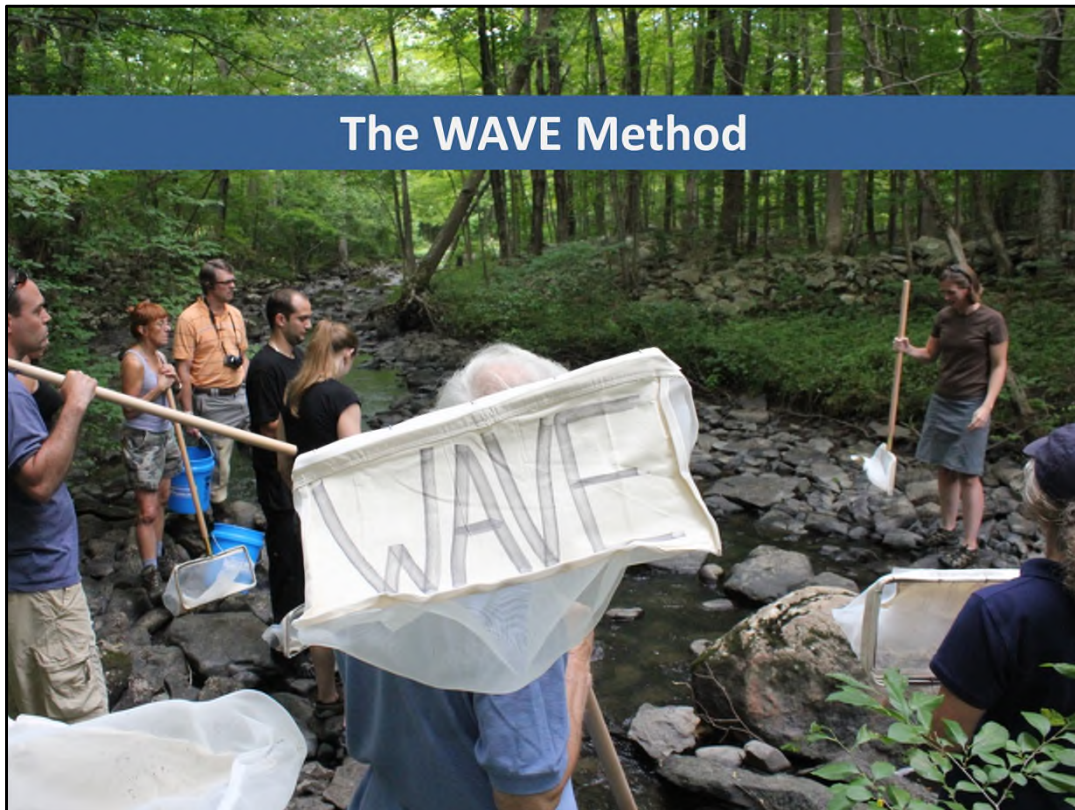
With the first batch, we performed a Sørensen similarity index analysis. We pulled out those families which were more abundant in Impaired Stream samples (with a BAP ≤ 5). We then removed those families that contributed more than 2% to the similarity of samples collected from High Quality streams (with a BAP > 7.5) as well as those that contributed nothing to the similarity of the samples from Impaired streams.

We then used the second batch to test the error associated with this method.



We identified all the samples in the NYS database which had ≥ 4 , ≥ 5 , ≥ 6 , and ≥ 7 indicators for High Quality Streams. For the high quality stream assessment, we consider any false positive in the impaired category to be unacceptable. We found that using ≥ 6 indicators captured the most high quality stream sites while maintaining no false positives among impaired sites.

Similarly, we identified all the samples in the NYS database which had ≥ 3 , ≥ 4 , and ≥ 5 indicators for Impaired Streams. Through this process, not surprisingly, we learned it was not possible to remove all false positives among high quality sites. For this reason, we settled on a metric, ≥ 4 indicators, that had the smallest false positive rate while capturing a reasonable number of impaired stream sites.



As a review, here is a summary of the WAVE method



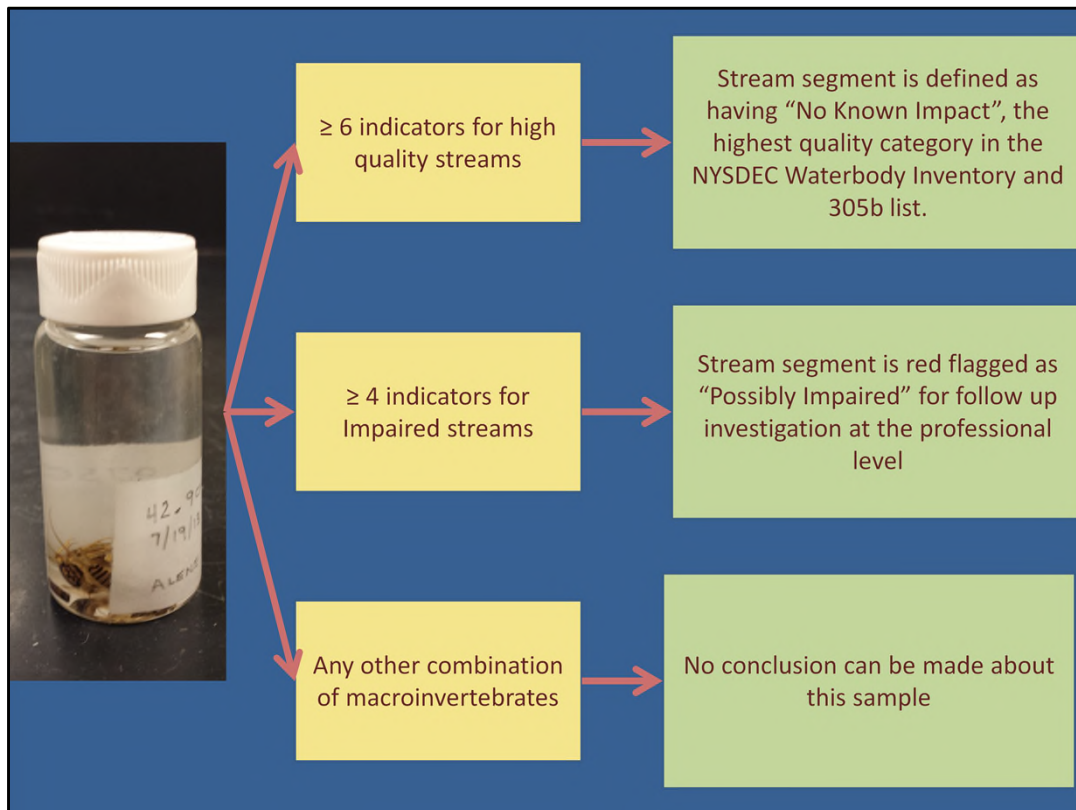
WAVE participants collect a 5 minute traveling kick sample



Streamside or inside at the kitchen table, WAVers pick out all the different types of organisms they find.
NOTE – they simply need to find the different types, they don't need to identify them.



WAVErs create a voucher collection with one or two examples of each macroinvertebrate type that they find and send this to the WAVE Coordinator

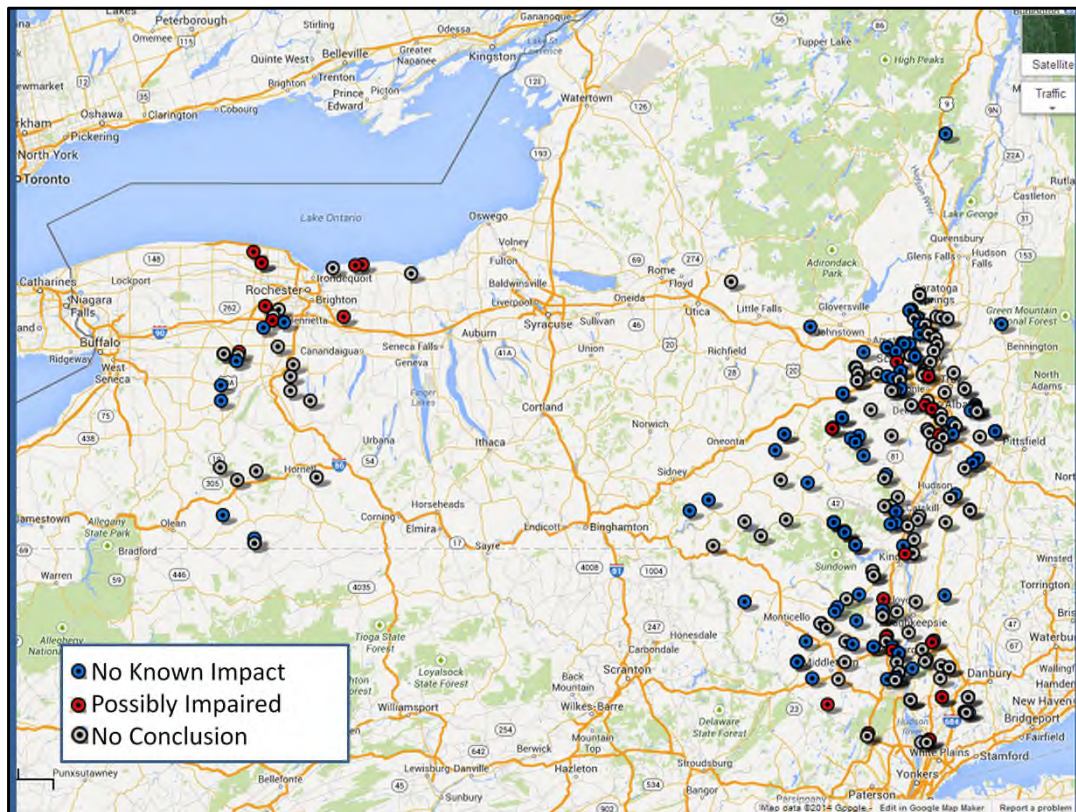


WAVE Coordinator identifies all the macroinvertebrates in the voucher collection to the level of family and applies the WAVE metric to produce a water quality assessment.

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In review, the WAVE method has removed 4 out of 5 major sources of human error.



Approximately 50% of the samples collected provide a No Known Impact or Possibly Impaired assessment. The other half of the samples do not have enough indicator organisms to make a conclusion.

The CT RBV program uses fewer indicator species so 25% of their samples provide a water quality assessment.

Advantages	Disadvantages
1. Removes all sources of human error except chain of custody = credible data from any source	1. Only provides information for ~50% of the samples collected
2. Easily scaled up: train the trainer fast sample processing	2. Possibly impaired sites can only serve as a red flag

Thank you



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This year WAVE is being piloted in the HR Watershed.