National CABIN Science Forum 2014 Agenda and Abstracts

December 2-3, 2014 Guelph, Ontario

Canada

Aussi disponible en français

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Preface

The Canadian Aquatic Biomonitoring Network (CABIN) is an aquatic bio-monitoring program for assessing the health of fresh water ecosystems in Canada. CABIN is based on the network of networks approach that promotes inter-agency collaboration and data-sharing to achieve consistent and comparable reporting on fresh water quality and aquatic ecosystem conditions in Canada. The program is maintained by Environment Canada (EC) to support the collection, assessment, reporting and distribution of biological monitoring information. CABIN allows partners to take their observations and make a formalized scientific assessment using nationally comparable standards.

With the aim of engaging CABIN stakeholders from all organizations across the country, Environment Canada's CABIN team and the University of Guelph's Biodiversity Institute partnered to host the third biannual CABIN Science Forum in Guelph, Ontario on December 2nd to 3rd, 2014. The first CABIN Science Forum took place in Vancouver, BC in 2010 and the second CABIN Science Forum took place in Fredericton, NB in 2012. The objectives of the Science Forum were to:

- To provide an opportunity for network users to learn about different applications of CABIN in a variety of sectors, successes and challenges, scientific advancements and the future directions of the program.
- To provide a forum for users to interact and collaborate with other members of the network.
- To provide an opportunity for information exchange and collaboration among CABIN users and the Environment Canada CABIN team to address user needs.

Twenty two platform presentations were given at the forum in the following sessions: CABIN activities in Ontario, Genomics and its application to Biomonitoring, What to do when a site "fails", Geographical scale of models, Environmental descriptor variables and other volunteered presentations.

The forum included a plenary presentation and a lively discussion period on the potential application of next generation genomics technologies (BIO-DNA barcoding and bio-informatics tools) to CABIN including examples of the integration of these tools in other jurisdictions. It also included a tour the DNA barcoding facilities of the University of Guelph's Biodiversity Institute and Centre for Biodiversity Genomics. A total of 115 people participated in the forum; 63 in-person, and 52 remotely via web-Ex.

Agenda

DAY 1 – Tuesday December 2

08:30 Registration & sign up for the University of Guelph's Biodiversity Institute of Ontario (BIO) and Centre for Biodiversity Genomics (CBG) tour (2 options)

09:00 Welcome & CABIN updates

Theme 1. CABIN Activities in Ontario *(Facilitator: Lee Grapentine)*

9:10 J. Bailey (Laurentian U.): Collection of Reference Stream Site Data in the Far North of Ontario: Preparing for Development in the Ring of Fire

9:30 L. Grapentine (EC): Bioassessment of Great Lakes Nearshore Sediment with Changing Reference Conditions

9:50 A. Yates (UWO): Long-Term Variation of Riverine Biological Communities and its Integration in Current Ecological Assessment Systems

10:10 T. Laing (RMC): CABIN biomonitoring at 4th Canadian Division Training Centre, Meaford, Ontario

10:30 break (30 min)

11:00 Plenary Address: Genomics, Biodiversity, Environment M. Hajibabaei (Biodiversity Inst.) *(Introduction by Joel Gibson)*

11:50 lunch (1 hr 20 min)

Theme 2. Genomics and its application in Biomonitoring *(Facilitator: Joel Gibson)*

13:10 Xiaowei Zhang- Environmental Genomics Reveal Environmental Threshold of Ammonia for the Protection of Zooplankton in Freshwater Ecosystem

13:30 E. Stein (SCCWRP): Application of eDNA and Metabarcoding to Routine Stream and Wetland Biomonitoring Programs in California.

13:50 E. Pilgrim (US EPA): Expanding Bioassessment into Understudied or Novel Communities through DNA Metabarcoding.

14:10 J. Gibson (Biodiv. Inst. Ont.): Assessing Boreal Aquatic Ecosystems using DNA Metasystematics and Next-generation Sequencing.

14:30 break (30 min)

15:00 Group discussion of genomics and CABIN *(Facilitator: Donald Baird)*

16:15 Tour 1 Bio and CBG tour (1 hr) and meeting at local

17:30 Informal social and get-together at Fionn MacCool's

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DAY 2 – Wednesday December 3

08:30 Tour 2 BIO and CBG tour (1 hr)

Theme 3. What to do next when a site "fails" *(Facilitator: Jan Ciborowski)*

9:40   J. Ciborowski (U. Windsor): What to do When a Site "Fails"- Exploring the Unknown using the Reference-Degraded Continuum.

10:00   D. Baird (Env. Canada) Diagnostic Biomonitoring: Separating the Human Factor.

10:20   M. Bowman (Forensecology): Communicating the Findings of Long-term Monitoring of Canadian Rocky Mountain Rivers to National Park Managers

10:40   break (30 min)

Theme 4.   Geographical scale of models *(Facilitator: Stephanie Strachan)*

11:10   N. Novodvorsky (Laurentian U.): Expansion of the Application of Benthic Invertebrate RCA Bioassessment Reference Sites: How Far Can We Go?

11:30   D. Armanini (Prothea): A RIVPACS-based Biomonitoring Model Incorporating Taxon Relative Abundance to Improve Diagnostic Performance

11:50   C. Curry, D. Baird (UNB): Variation in riverine insect biodiversity along the river continuum in Canada

12:10   lunch (1 hr 20 min)

Theme 5. Environmental descriptor variables *(Facilitator: Robert Bailey)*

13:30   R. Bailey (Cape Breton U.): Running After we Walk: Leveraging Landscape-Scale Information and GIS Tools to do Better Bioassessments.

13:50   T. Reynoldson (GHOST): Site scale versus Landscape Scale Predictors: the Implications of Moving out from a Bug's Eye View! "

14:10   M. White (Minnow Environmental) – Reference Condition Approach (RCA) Models, Spatial Scale, and Environmental Variables: so Many Choices

14:30   break (30 min)

Theme 6.   Other volunteered talks *(Facilitator: Tana McDaniel)*

15:00   R. Mallinson and H. Leschied, (Living Lakes): A Citizen Science Approach to CABIN: Case Studies in the Columbia and Athabasca.

15:20   N. Glozier (Env. Canada): Bioassessment of Tributaries of the Athabasca River in the Oil Sands Minable Area: Summary of the Implementation of the Joint Oil Sands Monitoring Program from 2012-2014

15:40   M. Gray (Canada Rivers Institute): An overview of CABIN Online and Field Training Past, Present, and What's in the Future?

16:00   J. Snider (WWF-Canada): The Role of CABIN in WWF's Canada-wide Assessment of Freshwater Ecosystem Health

16:20   Wrap-up and final remarks

16:30   Forum adjourned

Presentations and Discussions:

Welcome and CABIN updates

Nancy Glozier, Environment Canada and Joel Gibson, Biodiversity Institute, University of Guelph

The CABIN program started in the 1990s with a research monitoring program and was implemented nationally in 2006. CABIN has grown to include almost 1,000 users from diverse organizations. CABIN is an important component of Environment Canada's national water quality monitoring program to assess ecosystem health. CABIN's strength is its data sharing and collaboration principles among a diverse range of partners, such as consultants, NGOs, first nations, universities and other government departments. The partnership of Environment Canada with the Biodiversity Institute to host the Science Forum provides the opportunity for the exchange of information of genetic tools in bio-monitoring and boost collaborations for implementation within CABIN.

Theme 1. CABIN Activities in Ontario

Collection of reference stream site data in the far north of Ontario: Preparing for development in the Ring of Fire.

John L. Bailey (jbailey@laurentian.ca), Ontario Ministry of Environment and Climate Change, Cooperative Freshwater Ecology Unit, Laurentian University, Aaron Todd, Ontario Ministry of Environment and Climate Change

The Ring of Fire in the Far North of Ontario is considered be one of the most promising mineral development opportunities in Ontario in almost a century. Covering an area of about 5,000 km², recent estimates suggest that the Ring of Fire holds significant potential production of nickel, copper and platinum as well as potential for world-class multi-generational production of chromite. In advance of development in this region, the Environmental Monitoring and Reporting Branch of the Ontario Ministry of Environment and Climate Change embarked on a programme to collect baseline environmental data that can be used for future detection and assessment of the effects of development. A key element of this data collection programme is establishing a network of stream reference sites sampled using the CABIN field and laboratory protocols. Many of these sites have or will also be sampled for a comprehensive suite of water chemistry indicators under the Ontario Provincial Water Quality Monitoring Network. We will provide an overview of Far North stream sampling efforts in 2013 and 2014, including preliminary results, First Nation and other collaborations and plans for development of CABIN models to provide for online site evaluations. Guiding principles for the design of the monitoring programme will be outlined and logistical considerations of working in a remote undeveloped region will be discussed. We will also outline our sampling plans for 2015 and beyond, with details of a planned study to evaluate seasonal variability in stream water chemistry and benthic invertebrate community composition.

Bioassessment of Great Lakes Nearshore Sediment with Changing Reference Conditions

Lee Grapentine (Lee.Grapentine@ec.gc.ca) and Danielle Milani, Water Science and Technology Directorate, Environment Canada, Burlington

Since the early 1990s, benthic macroinvertebrate communities have been periodically sampled from sediments in over 160 undisturbed sites in nearshore areas of the Great Lakes. The data obtained are used to describe reference conditions for impact assessments of benthic communities in sites with

contaminated sediment. Through the years, reference sites in the Great Lakes have been affected by invasive species, climate change, and other regional stressors, potentially resulting in unstable or moving benchmarks for bioassessments of test sites. The simplest approach for accommodating varying reference conditions in environmental assessments is to exclude older data determined to be nonrepresentative of current conditions. Alternatively, a statistical adjustment for effects of time can be made by including it as a predictor in faunal-habitat predictive models. A third approach is to apply a temporally-replicated sampling design that allows examination of the time trajectories of conditions in test and reference sites. Results of the application of these procedures for test site assessments will be shown and compared and their implications for the design of the Great Lakes benthic monitoring program will be discussed.

Long-term variation of riverine biological communities and its integration in current ecological assessment systems.

Adam Yates[1] (adam.yates@uwo.ca), Almudena Idígoras Chaumel[1&2], Wendy A Monk[3&4], David Armanini[1&2] [1]Western University & Canadian Rivers Institute, [2]Prothea Srl, Milan, Ital, [3] Canadian Rivers Institute University of New Brunswick, [4]Environment Canada @ Canadian Rivers Institute

An important property of a biomonitoring tool is the ability to tease apart natural sources of variability from the potential effects of anthropogenic activities. In river biomonitoring, extensive research has been addressed to achieve this goal focusing mainly on spatial and seasonal properties, whereas temporal variability has not been yet fully explored. Current assessment systems, in use in Canada and abroad, use the assumption that community composition is stable through time and that community variation is driven predominantly by changes in anthropic condition. This assumption remains largely untested in freshwater biomonitoring, probably due to the lack of long term community data. Studies aimed at quantifying the magnitude and sources of biological variability are necessary for the refinement of ecological assessment systems. Quantifying the magnitude and sources of temporal variability in biological data is a critical step in the validation of ecological assessment systems. Long term biological datasets collected in southern Ontario using the Canadian Aquatic Biomonitoring Network (CABIN) protocol were matched with relevant environmental variables, including water quality, hydrological and land use data. Several biological community descriptors were employed to quantify biological variation through time, including measures of community stability and persistence. High values of annual turnover were observed in the community, although no significant temporal trends were observed. Biological metrics currently used for ecological assessment such as Taxa richness, Berger–Parker dominance index, the Canadian Ecological Flow Index, the Hilsenhoff Family Biotic Index and % of EPT families showed more limited ranges of inter-annual variation. The implications of the results will be discussed in light of current ecological assessment in use in Canada and approaches to integrate such results will be suggested.

CABIN biomonitoring at 4th Canadian Division Training Centre, Meaford, Ontario

Tamsin Laing (Tamsin.laing@rmc.ca), Royal Military College of Canada, Ted Keunecke, 4th Canadian Division Training Centre, Meaford, Ontario, Viviane Paquin, Royal Military College of Canada

The 4th Canadian Division Training Centre (4 Cdn Div TC) located near Meaford, Ontario is a Canadian Forces training facility on the south shore of Georgian Bay (Lake Huron) that has been operated as a tank range and artillery and small arms training facility for over 70 years. The property contains numerous watercourses, wetlands, grasslands and mixed forests. The most prominent watercourses are Sucker Creek, which drains the western and central portions of the property, and Mountain Lake, which forms the

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northern boundary of the Restricted Impact Area (RIA). A biomonitoring program for 4 Cdn Div TC was initiated in 2011 using the CABIN protocols to assess the water and sediment quality and the health of the benthic community. The goals of the 4 Cdn Div TC benthic invertebrate monitoring program are: (1) to assess the condition of the aquatic ecosystem on the 4 Cdn Div TC property; and (2) to establish a baseline that would allow the early detection of changes to the aquatic environment related to range activities. This presentation will discuss the design of the program and a summary of overall results to date. Ongoing challenges for data interpretation, such as the need for more regional CABIN reference sites, will also be discussed.

Discussion on Temporal Variability

Comment: In regards to the robustness of CABIN models to temporal variation pointed out that the original BEAST models were developed using long term datasets and there is confidence that temporal variability stays within the bounds of reference conditions. Should show how reference sites vary spatially within the bounds of reference conditions.

Comment: In regards to fact that when temporal variation is taken into account reference group structure is often unstable, i.e. sites switch groups. Perhaps it doesn't matter which group the reference site is assigned to as long as the model predicts correctly.

Comment: The Atlantic model shows very little discernable types in groups but this doesn't matter as long as the model can discern impacts. Canada has high insect biodiversity. There are patterns of beta diversity that suggest meta-community structure (everything everywhere) so there is high potential for recolonization and rapid turnover.

Theme 2. Genomics and its Application to Biomonitoring:

Biomonitoring 2.0: A high-throughput genomics approach for comprehensive biological assessment of environmental change.

Shadi Shokralla, Mehrdad Hajibabaei (mhajibab@uoguelph.ca). Biodiversity Institute of Ontario & Department of Integrative Biology, University of Guelph

Sustainable development of the Canadian economy requires wise, responsible stewardship of our environmental and natural resources. An important tool for this is biomonitoring, which provides an "early warning system" for environmental degradation by using the differential sensitivity of certain groups of organisms (bioindicators) to environmental stressors. Canada is recognized as a world leader in biomonitoring, however, conventional biomonitoring approaches are personnel-intensive as they involve sampling organisms and identifying them from their physical appearance. Given the difficulties in accurate identification of bioindicator organisms, such as the larvae of aquatic insects, biomonitoring is performed with a limited frequency and intensity and has become a major bottleneck in environmental assessment programs. We have developed Biomonitoring 2.0, which uses DNA sequence information for identifying all organisms in an environment. Our approach can circumvent the identification bottleneck through bulk sampling and directly identifying organisms from mixtures. We obtain species specific DNA fragments (DNA barcodes) from any environmental sample (soil, water, sediment, air) using cutting-edge, high throughput next generation sequencing technologies rapidly and cost effectively. By targeting multiple habitats in an environmental setting, we can provide a comprehensive (all taxonomic groups from mammals to microbes) and high resolution (species level) view of environmental change. Hence, the

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Biomonitoring 2.0 approach can simultaneously lower biological sampling costs while dramatically increasing the knowledge gained from those samples.

Biomonitoring 2.0 in Practice:

We have successfully tested Biomonitoring 2.0 in a number of proof-of-concept studies. Since 2011, we have been conducting the first large-scale pilot project for this approach at Wood Buffalo National Park (WBNP), a globally unique region spanning Alberta and the Northwest Territories that is downstream from the Alberta oilsands. This project gained first ranking in a national Genome Canada Large Scale Applied Genomics competition, and involves seven research groups at five universities as well as researchers and officers of Environment Canada and Parks Canada. Our project has now been integrated in the recently announced Integrated Monitoring Plan for the Oil Sands.

Future of Biomonitoring:

In addition to continuing our biomonitoring program in WBNP and the oil sand, we have highlighted a number of national Priority Biomonitoring Programs where are approaches can address various environmentally and economically important issues. We are embarking on international collaborations to promote the dissemination and adoption of the methodologies that we have pioneered, and to link ongoing projects currently underway in Canada, the USA, the UK, France and Australia. Our expanding network includes academia, industry, government and NGOs. Biomonitoring 2.0 is poised to play a significant role in informing crucial decisions on management and conservation in Canada and the world.

Environmental Genomics Reveal Environmental Threshold of Ammonia for the Protection of Zooplankton in Freshwater Ecosystem

Xiaowei Zhang (zhangxw@nju.edu.cn), Jianghua Yang, Yuwei Xie, Nanjing University

Environmental quality criteria (EQC) are the maximum concentration of pollutants allowed for the protection of the living organisms in the environment. Although the objective of EQC is to protect the ecological community in the field, historically, the development of EQC heavily relies on the acute and chronic toxicity values of single-species bioassays conducted in laboratory. Here we present a derivation of EQC of ammonia in freshwater lake by integrating environmental genomic technology and field monitoring data.

The PCR-based analysis of homologous genes has become one of the most powerful approaches for species detection and identification. Particularly with the recent availability of Next Generation Sequencing (NGS) platforms, it is now possible to identify species composition from a broad range of environmental samples. Here, we demonstrated that most of the zooplankton could be detected based on DNA obtained directly from small water samples of lakes. Furthermore, through operational taxonomic unit (OTU) analysis, we found that some OTUs are sensitive to specific environmental factors (e. g. ammonia). A OTUs based-species sensitivity distribution model was developed to derive the site-specific environmental threshold of chemicals and provide a reference for EQC derivation.

Application of eDNA and Metabarcoding to Routine Stream and Wetland Biomonitoring Programs in California

Eric D. Stein (erics@sccwrp.org), Raphael Mazor, Bryan White, Southern California Coastal Water Research Project, Costa Mesa California

Biological monitoring and assessment is routinely used to help answer questions about stream and wetland health or presence of species of interest, such as invasive or sensitive species. Molecular methods, such as traditional DNA barcoding, have been explored as tools to improve resolution and efficiency of biomonitoring programs. Despite the advantages of these tools, they require intensive sample processing (e.g., sorting individual organisms) and can only detect targeted species. Extracting DNA from environmental samples (eDNA), combined with next generation sequencing offers promise by allowing for relatively rapid detection of species presence without the need to sort individual specimens. However, interpretation of eDNA data depends on understanding issues such spatial fidelity, temporal persistence, and bias among species (i.e. relative probably of detecting one species vs. another). We have begun to evaluate some of these factors by testing applications of eDNA to biomonitoring programs in California wadeable streams. Here, we present preliminary results testing the use of eDNA to 1) detect the presence of an invasive mussel, the New Zealand Mud Snail, 2) determine how far downstream a eDNA signal may travel, 3) compare assemblage structure based on eDNA to traditional morphology-based analysis of benthic macroinvertebrate samples, and 4) evaluate the ability of eDNA to detect species typically excluded from stream bioassessments. Our results suggest that eDNA and metabarcoding hold promise for application to routine biomonitoring, but several interpretation and methodological issues remain to be resolved.

Expanding bioassessment into understudied or novel communities through DNA metabarcoding
Erik M. Pilgrim (pilgrim.erik@epa.gov) Sara Okum, John Martinson, US EPA

Aquatic biota exhibit varied responses to changes in environmental health, and are influenced by such characteristics as body size, life span, life history, mobility, dispersal, and evolutionary history. Some groups respond more quickly to environmental stressors than others, and these differences can be key in assessing environmental condition. More expansive investigation of biotic communities is now possible through DNA metabarcoding, particularly into groups of organisms that often have been understudied or avoided as bioindicators. In this presentation, we will discuss preliminary exploration of metabarcoding as a means for understanding biodiversity for groups that have largely untapped potential for biological monitoring, including periphyton, meiofauna, and larval fishes. We will also outline strengths, pitfalls, and challenges, and necessary future research efforts to expand bioassessment beyond macroinvertebrates and fishes.

Assessing boreal aquatic ecosystems using DNA metasystematics and next-generation sequencing

Joel Gibson[1] (jfgibson@uoguelph.ca), S. Shokralla[1], C. Curry[2], T.M. Porter[3], S. Connor[2], D. J. Baird[2], M. Hajibabaei[1] [1]Biodiversity Institute of Ontario, University of Guelph [2]Environment Canada, Canadian Rivers Institute, University of New Brunswick [3]McMaster University

Conventional biodiversity research via individual identification is costly and slow. To draw conclusions about changes in communities in response to natural and anthropogenic effects, biodiversity analysis needs to become more rapid, comprehensive, and cost-effective. High-throughput next-generation sequencing (NGS) technology (e.g. Illumina MiSeq) allows the biodiversity of a given locale at a given time to be determined rapidly, accurately, and at a much lower cost per sample. We will present research

that employs NGS and a metasystematic approach to better assess the biodiversity contained within mixed environmental samples. Samples include soil cores, water samples, benthic samples, and terrestrial Malaise trap samples. Each NGS sequencing run generates over a million DNA sequences from the organisms contained in each sample. Multiple target gene regions have been chosen for each kingdom of life, from bacteria, to plants, to fungi, to invertebrates, to vertebrates. By facilitating greater biodiversity recovery in a shorter amount of time, DNA-based massively-parallel sequencing approaches will greatly multiply the force of human impact on assessing, and improving, the status of pristine and impacted ecosystems.

Group Discussion on Genomics and CABIN

Q: Can any of these sequencing methods give information on relative abundance of taxonomic units?
A: It depends on the marker and method of generating sequence. Current methods use PCR amplification, which can introduce bias in sequencing results. Other molecular factors such as gene copy number may also introduce bias. People working with microbes have a different definition of 'abundance'. Nobody talks about number of bacterial cells. We are now working with number of sequence copies rather than number of individuals.

Q: The benefits of DNA barcoding have been discussed for a while. How long will it be before we can send a tube to someone and get a taxonomic list back?
A: Results of a sample can be generated in a couple of days or a week. This depends, however, on the degree of pre-processing necessary and the depth of the sequencing work being done. Samples can be batched together, but multiple genetic markers or multiple different types of samples will slow down the process. Also, novel sample types or new genetic markers will require some R&D time.

Q: Can I send samples from 50 sites and get the answers back soon?
A: Yes; we process at least 24 samples in one run, which is a week; cost depends on coverage and markers needed and depends on the estimated diversity of the community you want sequenced. With the existing work going now, one of the issues has been related to sterile sampling and handling techniques to avoid contamination. Another issue is developing a suitable public database for associating sequences with taxa; that's an ongoing process and in some areas we have good coverage. Soon we can do more complete direct comparisons. We are getting so much more information than originally anticipated working with wetland samples, which are exceedingly rich (>20,000 individuals per sample). Right now, the only limitation is the number of species that we have in the public libraries. We know the phylogenetic identity or bar code sequence, but can't put names to it because don't have the morphological species in the library. Species will eventually be easier to work with than genus.

Q: We will need a method of archiving samples for barcoding analysis in the future when things become standardized. Can you give us guidance on how to store samples for the future at which time molecular methods become standardized enough to be informative? It is important to archive some of the current samples in a time of incredible environmental change.
A: Store samples in 95% ethanol and store in -20°C freezer. We are moving forward on archiving for sequencing for the future. If you want to add a sequence of an extinct museum specimen, can do this now with the combination of techniques. Once a sample's DNA has been extracted, it can be stored in the freezer and can go back to it years later; as our expertise and knowledge builds will be able to come back to it later.
Comment: Related to cryptic biodiversity, keep in mind that biodiversity doesn't necessarily translate to

community structure, function and integrity. If we're trying to assess community integrity, we recognize that biodiversity is only part of it.

Q: In terms of compatibility with sampling as it occurs now, do you envision that we will need to clean DNA from all of our nets, waders, etc., at each site?
A: Cross contamination remains a significant problem. We have not done any detailed studies yet, but we are planning to do some. The question is whether small amounts of material from one site can contaminate other sites, which is one of many concerns of field sampling. In the US, we always treat nets and boots with mild bleach solutions. The bigger problem of contamination is in the lab. Thus, chain of custody becomes important. It is even more critical than in the field. We want minimal deviation from standard protocols as possible.

Q: In my simple world, I would take kick net out to the river, send the samples to someone and get a list of taxa back. This new method would give the same thing, but without abundance. If we were going to do a comparison, the best way to do it would be to take a series of samples for which we currently have a model, build a new set of data and see how the model works. Is it better or different?
A: The question of abundance is a dominant one. There are many answers to the question and we can build models without abundance. Although RIVPACs are used in many places but there have been some problems with its use in Canada because of taxonomic paucity. A switch like this would have to be done with caution.

Comment: I wonder about the transition of methods. For example, in the Yukon there are a few hundred reference sites and we have 100 in northern ON, OMOE has several hundred. The major cost is in sampling and hundreds of thousands of dollars have been spent to collect the samples.
Comment: After the biomonitoring step, the next question is 'why are we having a problem?' Is there more information to be gained from molecular assessment? Can we look at some of the causal questions and supplement what we're doing now with new diagnostic methods?
Comment: In southern Ontario in the last few years, Green Drake mayflies have been disappearing. CABIN methods are both community-level and genus-level data and have been criticized for a lack of sensitivity. Green Drake could disappear from streams and wouldn't be detected by CABIN. Could we have a short list of key taxa of special concern? Could we run a scan for the short list of taxa? The list might shift regionally. If part of the task is to provide early warning, maybe we haven't been quite fitting that need.
Comment: We're talking about using current sampling regime for genomic analysis but we should also ask how a sampling design should be developed specifically for genomic analysis. If we continue to identify taxa that we can't put names on, we may end up developing new diagnoses that don't even need named species. Because DNA samples have more taxa than can be identified morphologically, those samples will never be identical to CABIN type samples. This fact troubles a lot of people when DNA samples turn up things that they know aren't supposed to be there but this is related to interpretation of the data.
Comment: Maybe the initial pursuit of DNA is where CABIN is limited. Currently we are restricted to wadeable streams. DNA sampling may be a way to approach large rivers or lakes and wetlands for which we have no protocol. It seems that maybe the first direction to follow is where we have systems that we can't sample adequately by other means.
Comment: Certainly wetlands are an example. We are paralleling the Peace/Athabasca Delta oil sands sampling by traditional and DNA sampling. There is a very diverse interface between terrestrial and aquatic habitats; some organisms are part of the terrestrial system but are feeding on the aquatic food web.
Comment: A problem might be that we're trying to shoe horn genomic information into our preconception

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of CABIN as a community-level assessment method. Maybe we should refocus on what we expect; just as we as stream people discard terrestrial incidentals, we should do the same thing with the genomic information.

Q: What about things that persist in the environment long after the living material is gone (e.g. Didymo in mountain streams; palaeo carcasses in the sediments).
A: We have heard about this before -"zombie" DNA. This is present, but the fraction comprised is very small, and this could be accommodated in the sampling design. When people detect these, they're looking for very small DNA fragments that may persist in the environment. We can design a study to analyse larger DNA fragments which can get degraded after a couple of days in the environment, This can and essentially eliminate the effect of zombie DNA. We can also target the sampling and use appropriate ground-truthing.

Comment: Donald Baird is workin g to build a taxonomic list of major genera in the CABIN database as well as other things expected to be found but not in the CABIN database. We are looking at what proportion of the species that we have a good sample for and what proportion we could identify are being missed because their sequence isn't in the library. For example, we are often missing key chironomids because we don't have library data not just because of the difficulty of morphological identification but also because the specimens are destroyed before the barcoding analysis. Over the next 2-3 years a new guidance manual for how to collect materials for DNA analysis within CABIN will be developed. That is going to be a long-term resource for everyone which may also have international implications too.
Comment: Think about the additional questions that we could ask with a DNA sample that can't be addressed with traditional identification (e.g. diversity of nematodes in the samples, etc). The molecular information can add lots of interesting information whereas being stuck at the family level has limited value. DNA information can also help inform us about food web structure and associations among species as well as contaminant dynamics. It is important for taxonomists to work in parallel with DNA sequencing; without taxonomists to confirm or associate organisms, the sequences are meaningless.

Theme 3. What to do next when a site "fails"

What to do when a site "fails" - Exploring the unknown using the Reference-Degraded Continuum.

Jan J.H. Ciborowski[1] (cibor@uwindsor.ca), Lucinda B. Johnson[2], Katya E. Kovalenko[1,2], Valerie Brady[2], Terry Brown[2], Nick Danz[3], George Host[2], Robert Howe[3], Gerald Niemi[2], Euan Reavey[2]
[1]Department of Biological Sciences, University of Windsor, [2]University of Minnesota Duluth, [3]University of Wisconsin

Environmental assessment typical entails comparing a biological characteristics at a test site to those of sites in the reference condition (the RCA), whose limits are determined empirically by sampling many reference sites. The reference condition is defined by physicochemical characteristics of 'best available' sites and associated biota. Test sites are then classified as 'equivalent to reference' (biota are not significantly different than a reference) or 'nonreference'. Applying the RCA is difficult when most of the study region is subject to varying degrees of disturbance. However, even when the Reference Condition is well defined, the relative status of 'failing' test sites (designated 'nonreference') is undefined because classification is binary.

The complementary 'degraded condition' is operationally defined as the set of sites whose

physicochemical characteristics are deemed unacceptable by consensus (the 'worst sites in the system'). Consequently, any test site can be ordinated along a reference-degraded continuum (anthropogenic disturbance gradient), and its relative quality (and associated biota) summarized by its position along the continuum.

We have analysed changes in assemblages of Great Lakes biota across reference-degraded continua to derive taxon-specific bioindicators (various assemblages at Great Lakes coastal margins; zoobenthos in the Lake Huron-Lake Erie Corridor). Change points are common manifestations of responses to anthropogenic disturbance, permitting one to estimate boundaries of the reference and degraded conditions, respectively, as points on the RDC. These boundaries can serve as protection/restoration criteria by which to set guidelines on permissible levels of stress. Alternatively, prediction limits placed on the Biological Response vs. Stress Score relationship curve can be used to derive quantitative measures for determining the relative likelihood that a failing site is truly degraded rather than being 'significantly nonreference.'

Diagnostic biomonitoring: separating the human factor.

[1]Donald J Baird (djbaird@unb.ca), [2,3]David G Armanini, [3]Wendy A Monk. [1]Environment Canada @ Canadian Rivers Institute, University of New Brunswick [2]Prothea srl, Milan, Italy. [3]Canadian Rivers Institute, University of New Brunswick

The CABIN biomonitoring data set provides a unique opportunity to explore patterns of macroinvertebrate taxon occurrence at national scale in relation to environmental drivers. Specifically, this can support the development of stressor-specific diagnostic indices (e.g. the Canadian Ecological Flows Index). Such indices expand CABIN tools from general 'screening level assessments', by addressing specific questions regarding causes of ecosystem impairment. Here I will briefly discuss some of the challenges we face in developing and implementing such tools, and how we may overcome these by applying emerging techniques in ecology and ecogenomics.

Communicating the Findings of Long-term Monitoring of Canadian Rocky Mountain Rivers to National Park Managers

Michelle Bowman (michelle.f.bowman@gmail.com), Forensecology

Studies of the effects of low-level eutrophication on oligotrophic mountain rivers were the basis for mitigation measures and a long-term monitoring program. The metrics used in the monitoring program include riverine nutrient chemistry, algal nutrient content and algal & benthic macroinvertebrate community composition. To convey the results of monitoring to park managers, riverine sites are classified as in reference condition, potentially impaired or impaired as well as improving, stable or deteriorating for each metric and overall. Both upstream-downstream and regional (CABIN) evaluations are used to assess the ecological integrity of the rivers over time.

Theme 4. Geographical scale of models

Expansion of the Applicationof Benthic Invertebrate RCA Bioassessment Reference Sites: How Far Can We Go?

Nicole-Marie Novodvorsky (nnovodvorsky@laurentian.ca), Dept. of Biology, Laurentian University, John L. Bailey, Ontario Ministry of the Environment, Trefor B. Reynoldson, GHOST Environmental Consulting, Nova Scotia.

Benthic invertebrate RCA bioassessments generally rely on comparisons of exposed test sites to relatively unexposed reference sites within the same basin or geographic region. In remote areas, collecting reference site data can be time-consuming and costly and if such data can be applied outside their geographic scope, it would provide major cost-savings. In this study, we examined invertebrate and habitat data from three areas in Canada: the Attawapiskat River basin in northern Ontario, the Fraser River basin in British Columbia and the Yukon River basin. All sites were sampled and benthos samples processed following the standardized CABIN field and laboratory protocols. We measured concordance of benthic community structures among the three basins and the habitat predictors that determine them. RCA bioassessments were developed based on reference sites from the individual basins and on pooled data from the three, and applied these to a common set of simulated impact ("simpacted") sites. The effectiveness of assessments using only local basin reference sites was compared to those that included sites from other watersheds. Similar benthic communities were found among basins and minor geographic clustering of groups were found in the pooled model. The results of this study show us that the pooled model has comparable accuracy to the individual basin models but lacks the precision that models for individual basins possess. Our results suggest that reference sites sampled in one watershed can be "exported" for effective bioassessment in other adjacent or more distant watersheds however users need to be aware of the chance of committing type I and II errors. We recommend developing models that target a single stressor of concern to increase the pool of available candidate predictors; such a model may possess more robustness and precision.

Atlantic Canada reference condition approach: performance of a relative abundance rivpacs-based biomonitoring model.

David G. Armanini [1&2] (d.armanini@protheagroup.com), Almudena Idígoras Chaumel[1&2], Wendy A. Monk[2], Alain Armellin[3], Vincent Mercier[4], Lesley Carter, Donald J. Baird[2] [1]Prothea srl, Milan, Italy [2]Environment Canada @ Canadian Rivers Institute, Department of Biology [3]Environment Canada – Québec Region, Water Sciences and Technology Branch [4]Environment Canada - Atlantic Water Quality Monitoring and Surveillance

Reference condition approach (RCA) biomonitoring models have been developed to support bioassessment for river sites. However, traditional RCA models are often based on simple presence/absence-based taxonomic information or limited relative abundance data which can constrain the model's capacity to diagnose response to environmental stressors. While a number of diagnostic tools and assessment models have been developed to support the interpretation of biological response to environmental stressors in river ecosystems, most require relative abundance data. A RIVPACS-based RCA model that employs taxon relative abundance data to characterise observed and expected communities, thus permitting explicit incorporation of diagnostic metrics, is currently in use for Atlantic Canada. The model relies heavily on the CABIN biomonitoring data, standards and approaches. The model was developed for Atlantic Canada and it uses biological monitoring data collected from wadeable

streams paired with freely-available, nationally-consistent geospatial data layers with minimal anthropogenic influence. The performance of the model in a range of validation and test dataset is here presented and discussion on potential improvement of the approach are also discussed. Particular focus is given to areas of interest for the development of stressor specific biological metrics to further improve the diagnostic power of the approach.

Variation in riverine insect biodiversity along the river continuum in Canada.

Colin Curry (colin.curry@unb.ca), Donald Baird Environment Canada @ Canadian Rivers Institute, Wendy Monk, University of New Brunswick

Aquatic biodiversity is widely believed to be in decline, but few data exist to document these trends. The Canadian Aquatic Biomonitoring Network has accumulated what is arguably the largest set of consistently observed freshwater biodiversity data in Canada, and possibly in North America and globally. The efforts of CABIN partners have generated a versatile resource for observing national scale biodiversity patterns, particularly for aquatic insects that account for the majority of freshwater invertebrate taxa. Here we present the first analysis of local and regional patterns of aquatic insect biodiversity in Canada using the CABIN dataset, and explore how these patterns are being shaped by environmental change. Our analyses focus on samples with high resolution taxonomic information, and we use information from data-rich regions (i.e. the Pacific Coastal Drainage) to investigate relationships governing freshwater biodiversity in greater detail. In addition to relating patterns of biodiversity to broad geographic and environmental gradients, we also document gaps in our understanding of Canada's freshwater biodiversity and suggest ways to address these problems. Focused studies that take into account the hierarchical nature of stream networks are necessary to better understand the scale of variation in freshwater insect assemblages and the forces that structure them. In turn, this will aid in identifying the relevant scales for sampling in biomonitoring programs and potentially inform biodiversity assessments in uncharted regions. Utilizing biomonitoring data to conduct larger scale biodiversity assessments provides added value to the Canadian Aquatic Biomonitoring Network and should foster commitment from government and industry to support CABIN in the future.

Theme 5. Environmental descriptor variables

Running After We Walk: Leveraging Landscape-Scale Information and GIS Tools to do Better Bioassessments

Robert C. Bailey (Robert_Bailey@cbu.ca) Department of Biology, Cape Breton University

Although CABIN and other bioassessment programs have used landscape-scale observations and Geographic Information System (GIS) tools for more than a decade, the full potential of a landscape-scale perspective in bioassessment is as yet unrealized. "GIS variables" have crept into predictive models, but landscape-scale descriptors are often looked at with suspicion. How can we say anything about climate in the area of the site based on records from a weather station 100km away? There is also a wealth of GIS geodatabase, analytical and cartographic tools available that could significantly improve the data management, analysis, and reporting of bioassessments, but these have just not found their way into most bioassessment programs. I will briefly review the general data model of RCA bioassessment, and contrast the pros and cons of site- (e.g. current velocity) and landscape-scale (e.g. % granitic bedrock geology in catchment area) observations, including the collection, aggregation, management, analysis, and quality assurance of these different types of data. I will argue, provocatively, that even if site-scale

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environmental features better explain variation in biota among reference sites, the relationships between biota and the landscape-scale environment are much more useful in bioassessment.

Site scale versus Landscape scale predictors: the implications of moving out from a bug's eye view!

Trefor B Reynoldson (trefor.reynoldson@gmail.com) GHOST Environmental, Nova Scotia.

The basis of RCA predictive modelling is the establishment of a relationship between the pattern and structure of the taxonomic composition of the invertebrate fauna and associated measures describing the habitat in which the organisms are found. In both the UK and the early Canadian models for the Great Lakes and Fraser River the predictor variables used were largely site scale focussing on attributes of discharge, substrate and location. The rationale for selecting these variables was based on an understanding of the ecology of the benthic invertebrate community. At the time of the initial development of these models landscape scale GIS data was largely unavailable. In recent years, in Canada at least, there has been a shift toward far less emphasis on locally acquired habitat data and a reliance on landscape scale data. While there are many attractions to the use of this data, it is readily available, it is less likely to be modified by site specific disturbances, there are a number of issues that need to be examined. For example, at what distance from the stream is it appropriate to use a catchment characteristic? In small catchments there is an intimate relationship between the drainage and the stream, but in large rivers this is not so clear. Temperature and climate data used are averaged over various periods, what is most appropriate? With time merged data, annual variability cannot be discriminated. It is argued that a discussion and agreement on what GIS variables and what measures of those variables should be used is an important requirement for CABIN models.

Reference Condition Approach (RCA) models, spatial scale, and environmental variables: so many choices.

Mike White (mwhite@minnow.ca), P. Orr, C. Russel, Minnow Environmental

The concept of defining a reference condition for benthic macroinvertebrates was developed concurrently in several countries during the late 80's and early 90's. In Canada, the term Reference Condition Approach (RCA) has most often been used to describe the selection and predictive modeling procedures associated with a large set of randomly selected reference stations from a broad range of natural aquatic environmental gradients over a large geographic area. A community sampled in a potentially disturbed area is then assessed against the group of reference communities to which it is predicted to belong based on the environmental variables selected in model development. The regional models employed by the Canadian Aquatic Biomonitoring Network (CABIN) are of this nature and primarily use the BEnthic Assessment of SedimenT (BEAST) methodology to define multiple groups of reference stations. However, RCA experimental designs are not limited to broad scale investigations, or any one particular modeling methodology. We present three case studies that highlight RCA applied at three geographic scales and assessed using two different modeling procedures; BEAST and ANNA (Assessment by Nearest Neighbour Analysis). Specific attention will focus on the utility and selection of environmental variables during model development.

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Theme 6. Other volunteered talks

A Citizen-Science Approach to CABIN: Case Studies in the Columbia and Athabasca

Heather Leschied, (heather@wildsight.ca) Programs Director, Living Lakes Canada,Raegan Mallinson, (raegan@wildsight.ca) Program Coordinator, Living Lakes Canada

Protecting and conserving Canada's lakes, rivers and wetlands are a top priority for community based water stewardship groups. These groups face many challenges developing and implementing monitoring plans that are appropriate for addressing concerns in their watersheds. Living Lakes Canada provides stewardship groups with the tools and training needed to conduct their own monitoring. With increasing industrialization, urbanization and climate change pressures on the both landscapes and infrastructure, events such as spills or sedimentation are occurring more frequently, and communities want to be engaged in solutions.

Using the CABIN protocol, Living Lakes Canada supports and trains groups, develops sampling plans, assists with data interpretation and implementing steps for appropriate action. Benefits for water stewardship groups include access to the online database and the initial analysis and report generating tools. CABIN also helps groups stay organized and focused, which leads to meaningful and credible water quality monitoring results.

This session will focus on three case studies: the Flathead River, BC; Windermere Creek, a tributary of the Columbia River, BC; and, the Upper Athabasca, AB. These case studies have a variety of applications using citizen science; from supporting parks and protected area efforts to rapid response for impact events.

Bioassessment of Tributaries of the Athabasca River in the Oil Sands Minable Area – Summary of the Implementation of the Joint Oil Sands Monitoring Program from 2012-2014.

Nancy E. Glozier (Nancy.Glozier@ec.gc.ca) Joseph M. Culp, Bob Brua and Fred Wrona Water Science and Technology Directorate, Environment Canada, Saskatoon SK, Fredricton, NB and Victoria BC.

As per the Joint Canada-Alberta Implementation Plan for Oil Sands Monitoring: Aquatic bioassessment of the Athabasca River tributaries is being conducted through integrated analysis of historical biological and physio-chemical information, GIS data and contemporary field sampling. To date, sampling has been completed at just over 80 sites based on study designs as described in the Phase 2 "Integrated Monitoring Plan for the Oil Sands (2011). The sampling included an initial reconnaissance year (2011/12) during which sites were selected and methods tested. Following the reconnaissance year, benthic monitoring was implemented each fall for a 3-year period (2012/13 to 2014/15) with standard CABIN sampling methods as well as additional measures such as Periphyton biomass. There are multiple sites on the major tributaries (Steepbank, Firebag, Jackpine/Muskeg, Ells/Joslyn, MacKay, and Dover rivers) as well as sites in the Birch River and Lake Claire basin. Sites include two types of reference categories; 1) outside (n=15) and 2) inside with little development (n=25), the Oil Sands formations; as well 3) test sites were sampled within the OS formations (n=30) with a gradient of exposure to land disturbance. Finally, many sites of these sites are considered as a BACI (Before, After, Control, Impact) design where activity is expected in future years. Next steps for the assessment include performing statistical multivariate and gradient assessments; completing a comparison of historical and contemporary benthic macroinvertebrate data for available tributary sites; comparing benthic data collected with 400um and 250um kick net samplers as well as with the Neill cylinder samplers 250 um. Finally, the usefulness of

community metabolism, ecological traits assessments, and food web structure as emerging tools will be assessed.

An overview of CABIN online and field training past, present, and what's in the future?

Michelle Gray (m.gray@unb.ca) Canada Rivers Institute, University of New Brunswick

The online training component of the Canadian Aquatic Biomonitoring Network (CABIN) went "live" in 2008 and we have had more than one thousand participants enroll in one of the four (4) training levels: 1) Data Entry technicians, 2) Data Analysts, 3) Field Technicians, and 4) Project Managers. Participants have come from all regions of Canada, Newfoundland to British Columbia and north to Inuvik, and from watershed and college to consultants and government agencies. With the support of a 5-year Grants and Contribution from Environment Canada to the Canadian Rivers Institute, the training modules will be expanded to offer more specialized topics. The new training modules will support the mandate of the CABIN program to collect nationally consistent, credible, and comparable data to assess Canada's freshwater aquatic ecosystems and continue to support and build the National CABIN database. Topics to be development include: 1) Atlantic Reference Model background content and training, 2) Using geospatial data to improve regional models across Canada, 3) CABIN wetland protocol background and training, and 4) Methodologies for DNA sampling in environmental and aquatic biomonitoring.

The role of CABIN in WWF's Canada-wide assessment of freshwater ecosystem health.

James Snider (jsnider@wwfcanada.org), World Wildlife Fund, Anna Labetski, University College London, Sophie Taddeo, University of California at Berkeley.

WWF-Canada has worked since 2011 to develop a framework for evaluating and reporting on freshwater ecosystem health across Canada. Through review of international best practice and expert consultation, we have created an approach for reporting on the condition of freshwater ecosystems across the country using a consistent methodology and building upon existing monitoring data. As of June 2014, WWF has completed Freshwater Health Assessments (FHAs) for 17 watersheds, representing 25% of Canada's watershed area. CABIN monitoring has been one of the primary data sources used in the completed assessments, including through analysis of benthic invertebrate communities and water quality parameters. This presentation will provide an overview of the methodology used in the FHAs, results of the assessments completed to date, and examples of how CABIN monitoring have been applied in our work. Further, the presentation will include discussion of additional FHAs we are completing for publication in 2015, a description of a new stressor-based analysis that we are developing, as well as an overview of a funding program that we have implemented to support local freshwater monitoring and conservation projects. Combined, the Freshwater Health Assessments, the new stressor-based analysis, and our local water fund are part of a concerted effort towards improving condition of freshwater ecosystems across Canada.

Summary of CABIN recommendations and suggestions from participants

1. **Modify the CABIN website to provide geospatial information:** Recommend that the CABIN website be upgraded to automatically generate relevant geospatial information when users input their location information. This information could then be utilized to derive environmental descriptor variables for model building and analysis. This would ensure that GIS derived environmental descriptor variables for sites are consistent, particularly important when they are being compared to reference models.

2. **Provide and finalize more alternate CABIN protocols for different habitats:** Development of CABIN protocols for other aquatic habitats. In particular for the wetland protocol information on how it works, its current status and how it may differ based on regions, i.e. pacific vs prairies. There is a particular desire to have the wetland protocol finalized so that partners may start employing it.

3. **Model Guidelines**: Provide a model building guideline for consistency in research that is relevant to CABIN. Provide guidance on how a model can be assessed for sensitivity to detect a statistical difference from test sites.

4. **Overview of uses of CABIN program:** Provide a general overview of what the CABIN approach is really good at, what it does not do well at, common pitfalls and avoidance thereof might be useful, especially for those relatively new to the program or considering expansion of a program.

Science Forum Feedback

Overall interest and satisfaction

- Most people in attendance were on the CABIN distribution list but more than 1/3 were not CABIN users and participated as a result of seeing the website or talking with colleagues.

- Half of the people in attendance were participated to stay current with the state of the program and science; another 1/3 was interested in networking with other CABIN users and learning about new science.

- Everyone who provided feedback indicated that the forum was informative and relevant to their interests and of the appropriate quality and quantity.

- One third of the participants were most interested in the genomics session followed by the volunteered contributed papers by other CABIN users.

- Most people indicated that they would like to see more time for discussion which is a recommendation for the next science forum.

- Overall the webinar option was a success without technical difficulties. There are opportunities to improve the experience for all users which will be taken into consideration for the next science forum.

Improvements

- Provide more interactive discussion sessions about ways to improve the CABIN program where users can directly query members of the CABIN team. Include focused discussion sessions with break out groups to further delve into specific topics.

- Structure the forum as plenary talks in addition to directed discussion sessions instead of having short invited or volunteer talks.

- Increase the number of talks on monitoring programs by CABIN users and make sure these are placed early on in the forum.

- Make sure there are also presentations suitable for newer users of CABIN and those looking to determine if CABIN might be a good addition to their program, for example those from the NGO community.

- Make sure future locations are closer to an airport to reduce travel costs. Make sure the location is relevant to the program, ie, having the location near the Biodiversity Institute when the theme is genomics related.

- Provide more time for discussion and commentary. Suggest increasing conference to three days to include workshops and more interactive discussions.

Remote participation

- Increase the accessibility for those from other time zones by recording sessions and allowing registered participants to sign up to view at their convenience.

- Improve the sound quality by encouraging listeners to mute their lines. Also encourage people asking questions to use the microphone or have the presenter repeat the question.

- More encouragement of chat based questions from webinar audience.

- Use the mouse instead of the laser pointer so people on-line can see where you are pointing.

- Provide audio over the webinar as well as by teleconference.

Future sessions

- How to incorporate climate change adaptations into new models.

- How we can collect better environmental variables to use in models.

- How to better define stressor gradients.

- Ways to improve the power of reference condition approach models.

- Explore alternative model building techniques such as maximum likelihood and Bayesian methods more suitable for observational data.

- Reference models to look at effects of disturbance related to forest fires or mountain pine beetle.

- More emphasis on the relationship between CABIN and environmental assessments especially how within site variability affects the ability to define a reference condition for a particular area.

- How to include traditional ecological knowledge into CABIN.

- Approaches to implementing CABIN in environments where it is difficult to identify non-impacted sites or reference conditions. How to select least disturbed sites and how to evaluation whether selected sites are appropriate.

- If a test sites fails is it impacted? Specific examples on how to demonstrate this using supporting biotic endpoints, richness diversity etc.

- Recent developments in taxa based environmental indicators such as metal tolerance index, sediment tolerance index. The BMI is useful for stressor identification in addition to general impairment status, which greatly improves the value of BMI to mangers who are struggling.

- Traits based analysis and changes in community structure from a functionality point of view.

- Periodic updates on Biomonitoring 2.0 so that the user community can see the most recent developments and how they might be deployed.

Workshops

- An introduction to R

- Maximum likelihood methods for ecologists

- Hosting an SFS certification session

- Periphyton taxonomy

Summary of Participants

A total of 115 people participated in the CABIN Science forum; 63 in person and 52 live over the internet via web-Ex. Participants included those from government, private industry, First Nations, the non-governmental community, universities and private individuals. The pie chart below shows the breakdown of those attending by user group.
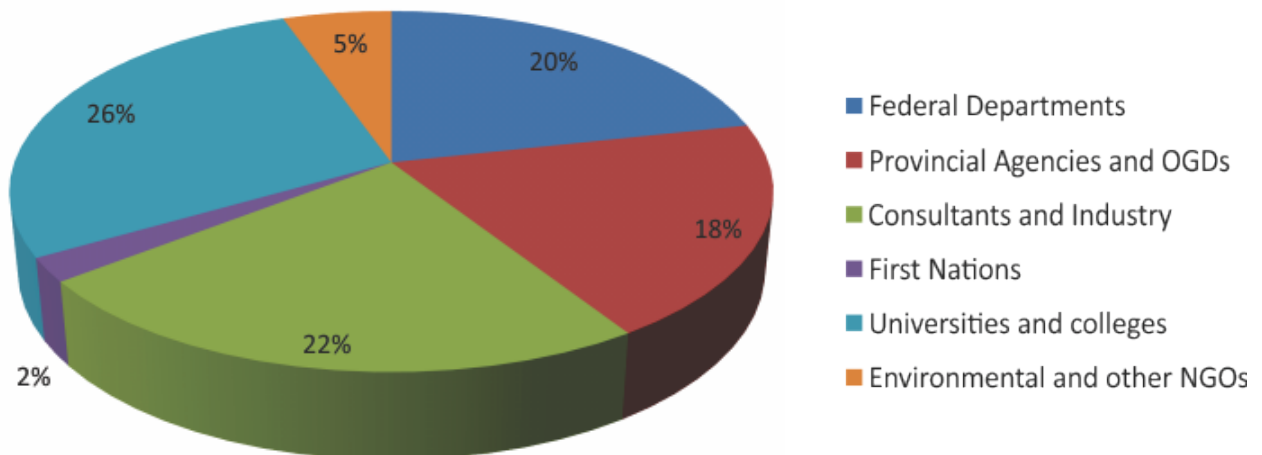
List of Participating Organizations

Provincial agencies and OGDs
Government of Yukon
BC Ministry of Environment
Alberta Agriculture and Rural Development
Ontario Ministry of Environment & Climate Change
District Municipality of Muskoka
Grand River Conservation Authority
Essex Region Conservation Authority
PEI Department of Environment
New Brunswick Dept of Environment & Local Gov
Dept of Environment, Newfoundland
Southern Californian Coastal Water Research

Consultants and Industry
CRA-Québec
Cordillera Consulting
EcoAnalysts, Inc.
Ento Consulting
Forensecology
GHOST Environmental
Golder Associates
Hemmera
Integrated Ecological Research
Kerr Wood Leidal Associates
Living Streams Environmental
Mining Morality Canada
Minnow Environmental
North/South Consultants Inc.
Prothea Srl
SNC Lavalin
Stantec
Streamline Consulting
Triton Environmental Consultants Ltd.
WorleyParsons
Yeti Environmental Research
Research & Development Corporation

Federal Departments
Environment Canada
Parks Canada
National Defense
US EPA
US National Park Service

First Nations
Ta'an Kwach'an Council
Gespe'gewaq Mi'gmaq Resource Council (QC)

Environmental and other NGOs
Hope Mountain Centre
Living Lakes Canada
Northeast Avalon ACAP
WWF-Canada

Universities and Colleges
Brock University
Canadian Rivers Institute
Environmental Sciences Group
Laurentian University
Nanjing University
Okanagan College
Ontario Genomics Institute
Pace University
Royal Military College
University of Western Ontario
University of Cape Breton
University of Guelph
University of Laurentian
University of Waterloo
University of Western Ontario
University of Windsor
University of Wisconsin-Parkside

APPENDIX: Presenter Biographies

David G. Armanini (d.armanini@protheagroup.com), **Almudena Idígoras Chaumel**
David Armanini holds a Ph.D in Environmental Science from the University of Milan (Italy). He founded Prothea, an environmental consultancy, in 2008 and he has been a Science Director at the Canadian Rivers Institute since 2011. He has advised several governments and public bodies in the implementation of science-based policy in the field of freshwater ecology. He has led the development of the Canadian Ecological Flow Index and of the Atlantic Canada Reference Condition Model, a RIVPACS-based bioassessment method.

John L. Bailey (jbailey@laurentian.ca), **Ontario Ministry of Environment and Climate Change**
John Bailey received his B.Sc. in Zoology from the University of Guelph and his Ph.D. in Biology from the Western University. He is currently the Ontario Ministry of Environment and Climate Change Research Scientist and Adjunct Professor with the Cooperative Freshwater Ecology Unit at Laurentian University. He oversees the Sudbury lake recovery monitoring programme and the Freshwater Invertebrate Reference Network for Northern Ontario (FIRNNO) and is also involved in freshwater ecotoxicology and metabolomics research related to the effects of multiple stressors. Prior to moving to Sudbury in 2011, Bailey spent 30 years in the Yukon, Northwest Territories and Nunavut, specializing in aquatic biomonitoring programme design, implementation, data analysis, GIS and training, as well as environmental assessment, policy, legislation and management and Aboriginal land claim negotiations and implementation. John began his career in renewable resource management and research with the Ontario Ministry of Natural Resources in the mid-1970s.

Robert C. Bailey (Robert_Bailey@cbu.ca**) Department of Biology, Cape Breton University**
A BSc and MSc graduate of the University of Guelph, Dr. Bailey did his doctoral studies at The University of Western Ontario, and became a faculty member at Western in 1986, where he eventually led development and operation of campus-wide, interdisciplinary research and education programs in Environment and Sustainability. Dr. Bailey's research activities have centred on bioassessment of freshwater ecosystems, from Yukon streams affected by placer gold mining to Alberta wetlands exposed to agricultural, urban, and energy industrial activity, to stream agroecosystems in southwestern Ontario exposed to intense and varied agricultural activities. In 2009, Dr. Bailey started an appointment at Cape Breton University in Sydney, Nova Scotia, where his research focus is bioassessment and he teaches statistics for biological researchers.

Donald J. Baird (djbaird@unb.ca**), Environment Canada @ Canadian Rivers Institute, University of New Brunswick**
Dr. Donald Baird is an Environment Canada research scientist, and is also a Visiting Research Professor and Science Director at the Canadian Rivers Institute at the UNiversity of New Brunswick in Fredericton.

He leads a research group focusing on the measurement of aquatic biodiversity, diagnostic bioassessment, ecological flow needs for rivers and wetlands and ecological risk assessment. He is alo exploring the application of ecogenomics approaches in ecosystem assessment, including CABIN.

Michelle Bowman (michelle.f.bowman@gmail.com**), Forensecology**

Michelle Bowman is an aquatic ecologist. She recently founded Forensecology to meet the growing demand for scientific support of academia, government and non-governmental agencies. Her research includes the study of aquatic communities & ecosystems, bioassessment, eutrophication, invasive species, multiple stressors and multivariate analyses.

Jan J.H. Ciborowski (cibor@uwindsor.ca), **Department of Biological Sciences, University of Windsor**
Jan Ciborowski is an aquatic ecologist in the Department of Biological Sciences at the University of Windsor. He works on a number of collaborative projects to assess ecological conditions in western Lake Erie, Great Lakes coastal wetlands, and wetlands in the oil sands reclamation landscape of northeastern Alberta. He is particularly interested in developing diagnostic indicators of stress-response relationships that can be used to assess the biological condition of disturbed landscapes.

Colin Curry (colin.curry@unb.ca**), Environment Canada @ Canadian Rivers Institute, University of New Brunswick**
Dr. Colin Curry studied ecology at the University of Calgary and received his PhD. from the University of New Brunswick in 2013. He is currently a Visiting Fellow with Environment Canada in Dr. Donald Baird's lab, where he is involved with the development of the wetlands monitoring program for the Peace-Athabasca Delta and the application of genomic tools in freshwater biodiversity assessment under the Biomonitoring 2.0 project.

J. Gibson (jfgibson@uoguelph.ca**), Biodiversity Institute of Ontario, University of Guelph**

Joel Gibson completed his graduate work in insect systematics at Iowa State University, Carleton University, and the Canadian National Collection of Insects, Arachnids, and Nematodes. He is now the Project Manager of the Biomonitoring 2.0 project and an NSERC Postdoctoral Research Fellow at the Biodiversity Institute of Ontario, University of Guelph. He is also President Elect of the Entomological Society of Ontario. His current research focusses on using next-generation sequencing to explore biodiversity patterns in aquatic and terrestrial systems.

Nancy E. Glozier (Nancy.Glozier@ec.gc.ca**) Water Science and Technology Directorate, Environment Canada**

Nancy graduated from the University of Calgary with a B.Sc. in Zoology and a M. Sc. degree in Aquatic Ecology in 1989. She has worked on aquatic related projects for over 30 years and started her career as a summer student with the Ontario Ministry doing fish inventories in Southern Ontario. She has been with Environment Canada in Saskatoon for 24 years and has worked on benthic invertebrate and water quality assessments and has been a long standing member of the EEM and CABIN Science Committees. Currently she is Acting WQ Manager for the Athabasca Arctic Watershed and leads a subcomponent of Joint Oil Sands Monitoring Program.

Lee Grapentine (Lee.Grapentine@ec.gc.ca**) Water Science and Technology Directorate, Environment Canada**

Lee Grapentine is a research scientist with the Water Science and Technology Directorate of Environment Canada, in Burlington, Ontario. Originally from Winnipeg, he received his B.Sc. and M.Sc. at the University of Manitoba, and his Ph.D. at the University of Western Ontario. After working for several years at an environmental consulting company in Vancouver, he moved to the Canada Centre for Inland Waters in 1999.
Lee's general area of research is on developing and evaluating methods for assessing disturbances to freshwater benthic environments. His recent work includes studies of effects on benthic invertebrates of contaminants from metal mining activities, nearshore Great Lakes sediments, and groundwater discharges.

Michelle Gray (m.gray@unb.ca**) Canada Rivers Institute, University of New Brunswick**

Michelle Gray has been running the the training and professional development for the Canadian Rivers Institute since 2006 and has been involved since the inception of the online CABIN training program in 2008. Her research background is investigating environmental impacts using stream biota, her PhD looked at impacts of potato production and now she will be developing a freshwater monitoring program for the shale gas industry under development in New Brunswick.

Mehrdad Hajibabaei (mhajibab@uoguelph.ca) **Biodiversity Institute of Ontario, University of Guelph**

Mehrdad Hajibabaei is an expert in molecular biodiversity and evolutionary biology, bioinformatics, and genomic technologies. He obtained his PhD from the University of Ottawa focusing on building a DNA-based framework for studying evolutionary relationships among seed plants. He then pursued a postdoctoral fellowship at the University of Guelph where he contributed to high-throughput analysis of DNA sequence data for species identification. As an Associate Professor at Biodiversity Institute of

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Ontario and Department of Integrative Biology of the University of Guelph, he has continued his work on the use of genomics information in biodiversity analysis. By specializing on the development and application of cutting-edge technologies, he has helped lead the development of rapid and accurate analysis of biological diversity from genes to ecosystems. He has played a leadership role in establishing large-scale research projects and networks, such as the Canadian Barcode of Life Network and the International Barcode of Life (iBOL). He currently leads Biomonitoring 2.0 (www.biomonitoring2.org), a large-scale applied genomics project that employs NGS technologies, as well as sophisticated bioinformatics tools, for the comprehensive assessment of biological diversity in environmental samples from Canada's largest national park, Wood Buffalo National Park.

Tamsin Laing (Tamsin.laing@rmc.ca**), Royal Military College of Canada**
Tamsin Laing holds a Ph.D. in aquatic biology from Queen's University and is currently the scientific advisor and project leader for aquatic contaminated site programs at ESG. Over the past 10 years, she has worked on a variety of projects including the assessment and management/remediation of contaminated sediments, ecological risk assessment, and long-term monitoring. Recent projects include designing aquatic assessment and monitoring programs, as well as developing scientific guidance for federal aquatic contaminated sites.

Heather Leschied, **(**heather@wildsight.ca**) Programs Director, Living Lakes Canada**

As Programs Director with Living Lakes Canada, Heather has been involved in community based water stewardship and citizen science initiatives in the Columbia, Mackenzie, and Winnipeg Basins. She works with individuals and groups to increase capacity and knowledge to better protect our watersheds. Her work has won awards by foundations and industry, and has been recognized by the federal government as a best-practices example in community based monitoring.

Raegan Mallinson, (raegan@wildsight.ca**) Program Coordinator, Living Lakes Canada**
Raegan received her undergraduate degree from the University of Calgary in the Environmental Science Program, Biology Concentration. Raegan is enjoying her time in the Kootenay's of British Columbia, living in Nelson. As Living Lakes Canada's Water Stewardship Coordinator, she works with citizen- based water stewardship groups to protect Canada's watersheds.

Nicole-Marie Novodvorsky (nnovodvorsky@laurentian.ca**), Dept. of Biology, Laurentian University,**
Nicole Novodvorsky completed her BSc in Environmental Sciences at the University of Guelph in 2010, where she developed an interest in aquatic ecosystems, specifically in the use of benthic invertebrates as ecological indicators. In 2012, she was involved with an interesting research project with Trent University assessing the effects of nanosilver on aquatic ecosystems at the Experimental Lakes Area. This

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experience piqued her interest in academia/research and inspired her to pursue my Masters in Biology at Laurentian University in Sudbury, where she is currently conducting her research. she expects to defend in January 2015.

Erik M. Pilgrim (pilgrim.erik@epa.gov**) Sara Okum, John Martinson, US EPA**
Erik Pilgrim has been a research biologist with the U.S. EPA in Cincinnati since 2009. He is principal investigator in the EPA's research efforts in applying high-throughput DNA sequencing both to aquatic bioassessment and to invasive species detection and monitoring in the Great Lakes. The overarching goal of his research is to produce molecular genetic applications for measuring aquatic biodiversity that are useful and reliable for end users and decision makers.

Trefor B. Reynoldson (trefor.reynoldson@gmail.com**) GHOST Environmental, Nova Scotia.**
Dr Trefor Reynoldson received his Ph.D. from the University of Lancaster, UK in 1983 and his M.Sc. in aquatic ecology from the University of Calgary in 1974. He was a Research Scientist at the National Water Research Institute (Environment Canada) from 1987 until his retirement in 2004. Prior to that he worked for 10 years with Alberta Environment, and for three years with the International Joint Commission. He is now a senior scientist at GHOST Environmental Consulting, Canada, an adjunct professor at Acadia University in Nova Scotia, and has just completed a one year Professorial Fellowship at the Institute for Applied Ecology, University of Canberra. His research has been directed at developing improved techniques for using benthic invertebrate assemblages in diagnostic environmental assessment and formalising the Reference Condition Approach as the basis of a national biomonitoring network for Canada. He has over 150 publications and reports, with more than 90 in the primary literature. Dr Reynoldson's expertise lies in the application of multivariate statistical methods to analysis of invertebrate community structure data, and to linking effects at the community level to both organism and smaller biological scales. He has also worked in developing numeric biological criteria for both invertebrate communities and for laboratory tests with invertebrate species.

James Snider (jsnider@wwfcanada.org**), World Wildlife Fund**
James Snider is Conservation Science Specialist on WWF-Canada's Science, Research and Innovation team. He has a B.Sc. in Biodiversity and Conservation from McGill University with a specialization in landscape ecology, and a graduate degree from Concordia University in environmental impact assessment. James has been providing spatial analysis and conservation science expertise for WWF since 2007. In his 7 years working with the World Wildlife Fund, James has focused on building quantitative analyses through collaborative partnerships with academia, industry and government institutions. He is interested in creating rigorous, science-based analysis of environmental issues in Canada and around the world.

Eric D. Stein (erics@sccwrp.org**), Southern California Coastal Water Research Project, Costa Mesa California**
Dr. Eric Stein is currently a principal scientist at the Southern California Coastal Water Research Project (SCCWRP), where he is head of the Biology Department. Dr. Stein oversees a variety of projects related to in-stream and coastal water quality, bioassessment, hydromodification, watershed modeling, and assessment of wetlands and other aquatic resources.   His research focuses on effects of human activities on the condition of aquatic ecosystems, and on developing tools to better assess and manage those effects. Dr. Stein has authored over 100 journal articles and technical reports and participates on numerous technical workgroups and committees related to water quality and wetland assessment and management.

Mike White (mwhite@minnow.ca**), P. Orr, C. Russel, Minnow Environmental**
The majority of Mike's research has focused on the response of benthic macroinvertebrate community structure to disturbance (M.Sc. - forestry, Ph.D. - water level, Post-doc - mining). Mike was first introduced to CABIN in 2001 while working for Environment Canada in the Reynoldson/Grapentine lab located at the Canada Centre for Inland Waters (CCIW). In his current position, at Minnow Environmental, Mike provides expertise concerning experimental design and statistical assessment of aquatic communities. Mike lives in Guelph, Ontario with his partner Heather, their sons Alden and Clark, along with their occasionally obedient dog Murray.

Adam Yates (adam.yates@uwo.ca**), Western University & Canadian Rivers Institute**
Adam is an assistant professor in the Department of Geography at Western University and Science Director with the Canadian Rivers Institute. His research integrates landscape and aquatic sciences to develop and apply environmental assessment approaches with the goal of detailing the effects of landscape patterns on aquatic ecosystem conditions.