

University of Alberta

A multifaceted appraisal of a large-scale, multi-taxon biodiversity
monitoring initiative

by

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For Alberta's boreal biodiversity



Eriophorum growing on a cut line through a *Picea mariana* stand,
Anzac, Alberta

ABSTRACT

Conservationists have long debated how best to measure and conserve biodiversity. While many scientists called for long-term, large-scale ecological monitoring in the 1990's, the concurrent increased appreciation of statistical power and detectability-related sampling error meant that many programs endeavoring to be more inclusive were contentious. The Alberta Biodiversity Monitoring Institute (ABMI) provided a unique opportunity to assess a large-scale, long-term, systematic biodiversity monitoring program, employing largely undergraduate field technicians. Given these design attributes, I examined the sampling error and data quality in select components of ABMI, largely within the boreal forest ecozone of Alberta. Components examined included the collection of bryophyte field samples, identification of lichen samples in the laboratory, and the resultant statistical power and ecological value of these data for assessing changes in multiple taxa. In the first comprehensive assessment of detectability in bryophytes, I showed that while detection error was high for individual bryophyte species, multivariate community composition was highly repeatable between surveys of the same site by different technicians. With quality control and a week of training, technicians accurately detected and identified common lichen species in the laboratory, mitigating some of the field detection error. Preliminary data suggest that ABMI will have high statistical power to detect -3% annual declines in the occurrence of individual species at the scale of natural regions and provincially within 20 years, but smaller-scale assessments will require longer

time frames or metrics more robust to detection error such as community composition.

To assess the value of monitoring multiple assemblages, I examined the congruence and sensitivity to natural and anthropogenic gradients of soil oribatid mites, breeding birds, bryophytes, and vascular plants. I demonstrated that mites and vascular plants were the most sensitive and complementary set of assemblages, but if funding limited field surveys to one taxon, vascular plants provided the greatest sensitivity to multiple gradients. ABMI provides great ecological value and has been adopted by provincial and federal monitoring agencies, but it remains unclear whether better data will result in better biodiversity conservation given the current economic climate.

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SYMBOLS

- α : Alpha diversity; Type I statistical error (probability of rejecting a true null hypothesis)
- β : Beta diversity; Type II statistical error or statistical power (probability of failing to detect a real effect); Statistical model coefficient
- γ : Gamma diversity

ABBREVIATIONS

- ABMI: Alberta Biodiversity Monitoring Institute
- AFBMP: Alberta Forestry Biodiversity Monitoring Program
- DWM: downed woody material
- Floristic TL: microhabitat directed time-limited survey
- Floristic TU: microhabitat directed time-unlimited survey

MM: Medium nutrient mesic ecosite
NFI: National Forest Inventory
NM: Nutrient moisture ecological site conditions a.k.a. ecosite
PD: Nutrient-poor hydric ecosite
PU: parataxonomic unit
PX: Nutrient-poor xeric ecosite
RAP: rapid assessment protocol
RG: Nutrient-rich hydric ecosite
SAC: species area curve
Systematic TL: systematic transect-based time-limited survey
TL: time-limited
TU: time-unlimited

GLOSSARY

This glossary is provided to define specialized terminology and terminology used uniquely in this dissertation. Terms without a chapter reference are used throughout the dissertation.

Assemblage: a group of phylogenetically related species

Community composition sensitivity (Chapter 6): a metric of the responsiveness of an assemblage's multivariate community composition to different gradients. This was estimated as the degree of correlation between ordinations of assemblage community composition, environmental gradients, and anthropogenic gradients.

Completeness (Chapter 6): proportion of the expected or predicted species in an assemblage recorded in a survey or set of samples

Concordance (Chapter 6): correlation of a community metric such as community composition or species richness of two assemblages

Detectability: probability of recording a species or individual when present

Detection error: bias in capture of individuals during a survey

Diversity sensitivity (Chapter 6): a metric of the responsiveness of an assemblage to anthropogenic disturbance. This was estimated as the change in species richness and in species turnover of an assemblage between disturbed and undisturbed sites.

Ecosite (Chapter 6): ecological nutrient and moisture classification, considered to be the result of long-term, relatively permanent geological and climatic site conditions

Efficiency (Chapter 3): a metric of survey quality, as measured by the ratio of the number of samples collected to the number of species recorded. A maximally efficient survey would record or collect one specimen per species.

Floristic habitat sampling (Chapter 3): a method of surveying a stand or relevé that focuses on sampling the diversity of meso- and microhabitats present in the stand rather than on systematic or randomly placed plots. The goal of floristic habitat sampling typically is to construct a very complete species list, sometimes with species cover estimates.

Inclusiveness (Chapter 3): a metric of survey quality, as measured by the proportion of species known to be present in a site recorded in a given survey

Indicator species (Chapter 2,6): Statistical definition - a species that occurs more commonly and is more abundant in a given habitat than expected by chance. Ecological definition – a species that offers a signal of biological condition, including changes in occurrence or abundance of other species.

Mesohabitat (Chapter 3): a feature present in a dominant stand or relevé such as a cliff, stream, or forest type that hosts characteristic bryophyte and lichen assemblages

Microhabitat: features of a mesohabitat (e.g., individual rocks, parts of trees (e.g., base, roots, or branches), or soils) that are affected by local factors such as microclimate and nutrient availability and often host characteristic bryophyte and lichen assemblages

Parataxonomist (profession: **parataxonomy**, Chapter 4): an individual not traditionally trained in taxonomy who plays a supporting role in biodiversity surveys, both in the field and the laboratory. A parataxonomist may collect samples, prepare samples for identification by experts, and/or identify samples.

Prevalence (Chapter 5): the proportion of samples or sites a species is recorded at

Relevé (Chapter 3): an area judged to be uniform in floristic composition, geology, and geography. Species surveys typically are conducted throughout the relevé until the surveyor judges the search exhaustive, i.e., additional searching does not result in recording additional species.

Repeatability (Chapter 3): a metric of survey quality, as measured by the correlation between community composition of two separate surveys conducted at the same site. Repeatability was also estimated as the correlation between species detectability estimates from different field technicians conducting surveys at the same sites.

Representativeness (Chapter 3): a metric of survey quality, as measured by the correlation between the best estimate of community composition and community composition of a less-complete survey of the same site

Species richness sensitivity (Chapter 6): a metric of the responsiveness of an assemblage to anthropogenic gradients. This is estimated as the rarefied percent change in species richness between a pool of intact sites and a pool of disturbed sites.

Voucher: a specimen designated as a representative example of a species from a given location, typically deposited in a herbarium

Thallus (plural: **thalli**, Chapter 4): the body of a macrolichen, which may be composed of more than one genotype or individual strain of the species

CHAPTER ONE

Introduction

Biodiversity management and monitoring

Biodiversity is commonly defined as the variability within species, between species, and of communities (see review in Magurran 2004). It is estimated that human-caused environmental changes have triggered the earth's current and sixth major extinction event (Chapin et al. 2000). Monitoring and quantifying biodiversity is the first step in managing this decline. In 1992, 164 government leaders signed the United Nations Convention on Biological Diversity (The Convention on Biological Diversity 2006), and agreed to maintain biodiversity and develop it in a sustainable manner (Subsidiary Body on Scientific Technical and Technological Advice 2003). Since that time, monitoring is recognized as a high priority by society, government, and scientists (Lubchenco et al. 1991, Minister of Supply and Services Canada 1995, Canadian Standards Association 2002, McDonald and Lane 2004, Dudley et al. 2005, Lovett et al. 2007).

Managing landscapes for biodiversity maintenance is challenging due to the inability to accurately measure biodiversity, even at the scale of species (Purvis and Hector 2000, Higgins et al. 2004). Biodiversity indicators or surrogates range from species at risk ("state" indicators) to types of stressors ("pressure" indicators, Organisation for Economic Co-operation and Development 2003), and there is an extensive literature on their selection (e.g., Soberon et al. 2000, Carignan and Villard 2002, Hannon and McCallum 2003, Dudley et al. 2005, Favreau et al. 2006, Pearman et al. 2006, Wray and Bailey 2006, Rodrigues and Brooks 2007). A common strategy is to monitor structural features, under the assumption that maintaining the full complement of natural landscape and stand-level composition and structure will preserve biodiversity and ecosystem functionality (Noss 1987, 1990). To ensure that such an approach is effective however, requires monitoring a subset of biodiversity (Franklin 1993, Karr and Chu 1999, Hunter 2005).

Monitoring programs can be classified along a spectrum; at one end are programs that tend to focus on relatively few indicators (narrow in breadth but depth of detail for the chosen components), and at the other end are programs that are more comprehensive and broadly-based (wide in breadth but relatively shallow in detail for any given component). The former is called stress-oriented monitoring; particular indicator species or assemblages are monitored because of their known response to particular environmental stressors (Thornton et al. 1994, Noon et al. 1999). Stress-oriented monitoring is well-suited for single-stressor systems where impacts are expected to be acute. Stress-oriented monitoring tends to involve management experiments such as before-after control-impact studies. The Ecosystem Management Emulating Natural Disturbance Project (EMEND, Spence and Volney 1999) is an Albertan example of such a project. EMEND is designed to compare the effects of various fire and harvesting treatments on a wide variety of mixedwood boreal forest assemblages over one forestry rotation (80-100 years). This approach is fruitful scientifically, but in landscapes where impacts are evolving and accumulating rapidly, its long-term applicability may be limited.

In contrast, broad-based monitoring programs are passive in design (but active in inquiry); numerous variables are measured, some of which may not have established cause/effect relationships with environmental stressors (Thornton et al. 1994, Noon et al. 1999, Manley et al. 2004, Magnusson et al. 2008). Rather than conduct management experiments, these programs use the diversity of impacts already present on the landscape to investigate biodiversity change. Broad-based monitoring is well suited for programs designed to operate over long time scales and large geographic areas that are experiencing diverse, cumulative anthropogenic impacts. Despite recent criticism, a few jurisdictions around the world are implementing broad-based monitoring (reviewed in Chapter Two). Alberta, Canada is one such jurisdiction, permitting me the rare opportunity to assess the utility of this approach.

The Alberta Biodiversity Monitoring Institute

In the 1990's, the Alberta Forest Biodiversity Monitoring Program (AFBMP) was formed in response to the rapid increase in anthropogenic activity in the forested or 'green' zone of the province of Alberta (Farr et al. 1999). While policy required industry to document and mitigate their impact on biodiversity, resultant research and monitoring was narrow in scope and biased towards game or harvested flora and fauna (Lee and Hanus 1998). This made it impossible to assess the success of sustainable development and biodiversity conservation policies for most taxa. Farr et al. (1999) outlined the key principles underlying this initiative, including standardized methods, integrated monitoring across space, diversity of aquatic and terrestrial elements, and transparency. They assumed that biodiversity was valued by Albertans and that natural resource management decisions were changing biodiversity, sometimes at larger spatial and longer temporal scales than addressed through traditional science. The key design attributes are (www.abmi.ca, Stadt et al. 2006):

- Adoption of the National Forest Inventory (NFI, Gillis et al. 2005) 20 x 20 km grid as the sole stratum for terrestrial surveys, resulting in a grid of 1656 sites evenly spaced across Alberta (**Figure 1.1**);
- No stratification across space, but stratification at each grid point, with a terrestrial and a wetland site established within a set radius of the NFI grid point;
- Inclusion of both terrestrial and wetland monitoring across the entire province;
- Inclusion of multiple assemblages (*sensu* Fauth et al. 1996) assessed via rapid assessment protocols designed to record occurrence and/or measure relative abundance (**Figure 1.2**);
- Establishment of permanent sites, with surveys of approximately 320 terrestrial and 320 wetland sites every five years;
- Construction of species response relationships (dose-response curves, *sensu* Karr 1987) using the current distribution of impacted and natural or physically-intact sites, with supplementary data collection where information is sparse;

- Assessment of biodiversity at different scales using Biodiversity Intactness indices (Scholes and Biggs 2005, Nielsen et al. 2007) that summarize the predominant pattern in individual species dose-response curves.

Adopting the NFI grid permitted Alberta to simultaneously fulfill forestry-related NFI monitoring obligations while providing an acceptable sample size at scales such as watersheds and natural regions. The provincial government requested the AFBMP be expanded to the entire province, thus in 2004 the AFBMP became the Alberta Biodiversity Monitoring Program. In 2007 it received its final moniker, the Alberta Biodiversity Monitoring Institute, when it was incorporated as a not-for-profit organization. At present, ABMI is not at full capacity, but is scheduled to survey approximately 190 terrestrial and 175 wetland sites across the province in 2012. In collaboration with the Alberta Conservation Association, the ABMI also is implementing river and lake monitoring. Alberta is one of a only a few jurisdictions that have made similar choices, and as such, represents an opportunity to assess whether this approach can improve land management more than the status quo of small-scale cumulative impact assessments and research.

Alberta's boreal forest

The toughest test of ABMI's ability to improve land management likely will be in Alberta's boreal forest. The boreal natural region is approximately 381,000 km² and covers 58% of Alberta (Natural Regions Committee 2006). The extent of physical anthropogenic disturbance is estimated at 17.6%, with agriculture (11.7%), forestry (2.5%), and oil and gas (2.3% heavy industry, cut lines, pipelines and power lines) as the dominant disturbances (Hird et al. 2009, Alberta Biodiversity Monitoring Institute 2011). Despite the low areal coverage of disturbance, recent oil and gas activity impact most of the boreal forest. Even fourteen years ago only 13% of the boreal forest natural region was considered core, unfragmented habitat (Alberta Environmental Protection 1998). Approximately 78% of Alberta's forested lands are in forestry management units under either forest management area tenures to forestry companies (66%) or under

the management of the provincial government (12%, Alberta Sustainable Resource Development 2010).

While species richness is lower than in tropical forests, diversity within the boreal is promoted by heterogeneity due to natural disturbances such as fire (e.g., Bergeron et al. 2002) and defoliating insect outbreaks (e.g., Timoney 2003, Jasinski and Payette 2005). Another key feature of Alberta's boreal is the prevalence of wetlands such as bogs and fens. Approximately 30% of Alberta's boreal is estimated to be wetland. The boreal is a relatively young ecozone due to extensive glaciation as recently as 6,000-9,000 years ago (Chapin and Danell 2001). As a result of the short time since glaciation and short and/or variable succession cycles, the boreal is home to many generalist species (Chapin and Danell 2001).

What does ABMI monitor in the boreal?

The term assemblage refers to a group of phylogenetically related species, after Fauth et al. (1996). Terrestrial assemblages currently monitored by ABMI include vascular plants, bryophytes, macrolichens, soil oribatid mites, breeding birds, winter active mammals, and incidental species, including non-passerine birds, amphibians, reptiles and mammals. Additional information on the subset of assemblages discussed in this thesis is provided in the following chapters: bryophytes - Chapter Three, Five, and Six, macrolichens – Chapter Four, vascular plants – Chapter Five and Six, breeding birds – Chapter Five and Six, and soil oribatid mites – Chapter Six. An overview of the taxonomy of these assemblages is provided in **Appendix 6.1**.

ABMI uses a standardized suite of presence/absence (or detection/non-detection) and relative abundance surveys, similar to those used in community ecology research. These methods are best described as indices of habitat quality, population size and distribution. Indices such as these share a fundamental set of biological assumptions.

Detection/non-detection and relative abundance surveys: what are the assumptions?

Indices of occurrence or abundance, as well as statistical indices of habitat quality and anthropogenic dose-response relationships share a key assumption: presence at a site (particularly an apparently intact or undisturbed site) is indicative of conditions favourable to survival and reproduction (e.g., Cassini 2011, Skagen and Adams 2011). Pulliam and Caraco (1984) called this the ‘habitat matching rule’, but the concept has a long and storied history in different fields of research (reviewed by Cassini 2011). If relatively high density or abundance is deemed a signal of good habitat, there is the additional assumption that individuals of each species are distributed according to the ideal free distribution (Fretwell 1972), where individuals consistently are at greater density in favourable habitat. This assumption could be violated in the following circumstances:

1. evolutionary traps,
2. individual use of habitat does not reflect habitat quality, but rather intraspecific social cues,
3. presence reflects historical rather than current habitat quality (extinction debt),
4. individuals detected do not contribute to population persistence (sinks due to large population and ideal despotic or ideal pre-emptive distributions), or
5. methods create a systematic bias in the detection of presences and misleading correlational structure.

The first four are ecologically-driven, while the latter is driven by interactions between methods and autecology.

Ecological phenomena that degrade index utility

While not the focus of this dissertation, here I briefly outline these phenomena and estimated probability of occurrence, as well as ABMI’s ability to detect them.

Evolutionary traps

Ecological and evolutionary traps (preferentially occupied habitats that result in net negative population growth or 'attractive sinks', (Dwernychuck and Boag 1972, Delibes et al. 2001, Schlaepfer et al. 2002), as well as undervalued resources (habitats that support net positive population growth but are avoided, see the review and glossary in Gilroy and Sutherland 2007) decouple the correlation between presence and habitat quality.

Habitat selection via social cues

Social cues may sometimes influence habitat choice more than the quality of the habitat itself, particularly when breeding close to conspecifics confers fitness advantages (reviewed in Skagen and Adams 2011). This phenomenon is documented in birds, and its effect will be strongest in species that actively choose habitat.

Extinction debt

I interpret extinction debt as manifesting proximately and ultimately. Proximately, a habitat that initially resulted in high fitness may be altered during an individual's life span such that future fitness is not conducive to net population growth. Species most susceptible to extinction debt include non-motile species with relatively long-lived thalli. Proximate extinction debt is highest immediately post-disturbance and the 'repayment' schedule (time between disturbance and loss of the last individual in the disturbed area) is species- and disturbance-specific. While not theoretically framed as such, there are ample studies examining proximate extinction debt via short-term impacts of disturbance. Ultimate extinction debt occurs when anthropogenic disturbance fragments and isolates a species habitat, changing population and community structure via metapopulation dynamics such that the probability of extinction is elevated (e.g., Berglund and Jonsson 2005, Helm et al. 2006). This is Tillman et al.'s (1994) version of extinction debt, first conceptualized by MacArthur and Wilson (1967). Extinction debt violates the habitat matching rule by artificially expanding our estimation of species' niches in the short-term, and degrading the accuracy of predicted species' persistence over the long-term.

Detecting the above ecological phenomenon: what can ABMI do?

ABMI will not collect the data required to establish evolutionary traps or habitat choice based on social cues (which includes habitat preference, understanding of cues used in habitat selection, effect of habitat versus other factors in determining fecundity, lifetime fitness in different quality habitats, (e.g., Skagen and Adams 2011), but then, few studies do (Schlaepfer et al. 2002, Battin 2004, Robertson and Hutto 2006). There is little consensus on how prevalent traps are, and confounding this, the impact of evolutionary traps on species persistence depends on population size, and thus will vary geographically and temporally. However, a rapid rate of landscape alteration is thought to increase the probability of evolutionary entrapment (Schlaepfer et al. 2002, Kristan 2003, Battin 2004, Fletcher et al. 2012), so this assumption should be revisited whenever additional research permits.

ABMI is well-suited for investigating extinction debt, a phenomenon that is certain to occur. ABMI's long time horizons and large geographic scale provide inference beyond the typical remnant [habitat]-matrix [non-habitat] metapopulation dichotomy (Ewers and Didham 2006, Kupfer et al. 2006). ABMI can provide data for estimates of status and trends in regions impacted by different suites of anthropogenic disturbances, something that will prove useful in discriminating stochastic events from climate change or anthropogenic disturbance. Currently, the multiple lines of support for the habitat matching rule suggest a sound foundation in ecological and evolutionary principles (Cassini 2011). Until research suggests otherwise, it makes a valid null hypothesis (Cassini 2011). However, before ABMI data can be used to investigate ecological phenomena, managers and scientists alike need to understand the statistical population assessed by ABMI methodologies, along with the degree of sample error and bias.

Detection biases that degrade index accuracy

Detectability (the probability of detecting a species that is present) is almost always less than perfect, and sources of detection bias can be divided into

availability and perceptibility (Marsh and Sinclair 1989, Johnson 2008), although many factors affect both (**Table 1.1**). Availability is driven by the biology of the species (e.g., motility, phenology, geographic range), while perceptibility, defined as the probability of an individual being recorded given it was available, is driven more by methodology (Marsh and Sinclair 1989). Understanding detection biases are critical because it allows us to delimit the statistical population the results apply to as well as the appropriate level of inference.

Detection probabilities of less than one will not bias data interpretation if a) the real population size at a given survey point is independent of the probability of detection, b) the variation in detection probability is low, c) the subset of the population detected is ecologically similar, or d) detectability is constant across the gradient/factors under investigation (Lynch and Johnson 1974, Marsh and Sinclair 1989, Wolf et al. 1995, MacKenzie et al. 2002, Royle et al. 2005, Johnson 2008, Kéry and Schmidt 2008). Unfortunately, most survey methods and ecological situations do not fulfill these criteria.

Dealing with unequal detection: what can ABMI do?

Different fields of ecology have different traditions and methods that may or may not explicitly account for detectability of individual species. Methods are most established in vertebrate ecology, and least established in fields such as botany, bryology, and lichenology, and this dichotomy is evident in the ABMI's methods. ABMI survey design is equipped to deal with detectability for songbirds using repeat survey modelling (see www.abmi.ca for more detailed field methods), an assemblage for whom detection has been studied extensively (reviewed in Johnson 2008, Skagen and Adams 2011). It is not designed to deal with species-specific detectability of the other four assemblages in **Table 1.1.**, and the literature in this area is sparse (e.g., Lynch and Johnson 1974, Chen et al. 2009). In many taxa, the traditional method of ensuring comparable samples is with species area curves (SACs) and rarefaction (e.g., Colwell and Coddington 1994, Gotelli and Colwell 2001). The difficulty for a program like the ABMI is that sampling is not exhaustive enough at every site for a SAC asymptote to be

reached, and it is probable that even if an asymptote were reached, the identity of the species contributing to asymptotes for different technicians would vary.

Programs such as the ABMI that adopt non-traditional rapid assessment methods, largely employed by novice technicians, can find themselves outside of the prevailing paradigm, and subject to justifiable scrutiny or even outright, often-unjustified dismissal. Given ABMI's recent inception, research focused on methods that examine the sources and effect size of sampling error in its non-traditional survey techniques is a valuable contribution, and as a result, was a major focus of this dissertation.

Dissertation objectives and organization

The overarching goal of my dissertation was to assess the ability of select components of broad-based, multi-taxon biodiversity monitoring to inform land management. I focused on a subset of terrestrial protocols and their application in the boreal forest. My dissertation chapters are organized according to the flow of data generation and utilization. I began by examining the philosophy underlying the decisions that determined the scale, design, measured parameters, and intensity of effort of the ABMI (Chapter Two). I then explored the repercussions of those philosophies, namely the reliance on time-limited rapid assessment protocols employed by non-expert technicians. I experimentally examined how survey attributes such as temporal length, method of survey, and plot size affected the ability of technicians to capture species diversity, generate repeatable samples, and detect bryophyte species consistently (Chapter Three). As detectability of individual species was variable between field technicians, I assessed the ability of novices to identify cryptogams (macrolichens in this instance) in the laboratory (Chapter Four). I hypothesized that high accuracy and low overlooking rates in the laboratory would counteract some of the sampling error from field protocols. In Chapter Five, I collaborated with Dr. Scott Nielsen, Dr. Erin Bayne, and Dr. Jim Schieck to forecast the statistical power of the ABMI, given the level of detection error in the data. The ABMI has not completed a full rotation and data are sparse in parts of the anthropogenic gradient used in dose-response

relationships, precluding a robust examination of this aspect of ABMI at this time. However, based on the apparent robustness of community ordination to high species detection error, I used ABMI data to conduct a preliminary examination of the complementarity and sensitivity of assemblages to natural gradients such as climate and nutrient-moisture gradients as well as anthropogenic disturbance gradients. I conclude by briefly discussing the role of the ABMI in informing biodiversity conservation (Chapter Seven).

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Table 1. 1 Factors affecting detection of flora and fauna discussed in this dissertation

Taxa	Factors affecting availability only	Factors affecting perceptibility only	Factors affecting both
Birds (time limited audio recordings, Chapter Five & Six)	<ul style="list-style-type: none"> • Geographic range • Rate, frequency and amplitude of emission of audible cues • Biology such as reproductive status, age 	<ul style="list-style-type: none"> • Hearing range, skill level (observer) • Sensitivity, range, and direction (microphone and recording equipment) • Distance of bird to observer/recorder 	<ul style="list-style-type: none"> • Weather • Seasonal and diurnal survey timing • Habitat • Abundance
Soil-dwelling oribatid mites (Soil cores and extraction of live mites with heat/light, Chapter Six)	<ul style="list-style-type: none"> • Geographic range • Habitat 	<ul style="list-style-type: none"> • Collection method • Extraction technique • Observer visual perception • Observer skill level • Width, length 	<ul style="list-style-type: none"> • Behaviour • Abundance
Macrolichens & Bryophytes (Time-limited surveys, Chapter Three to Six)	<ul style="list-style-type: none"> • Geographic range • Thallus/colony size • Thallus/colony contrast with substrate • Substrate type & specificity 	<ul style="list-style-type: none"> • Collector visual perception • Collector skill level • Survey area & search duration • Diversity of assemblage 	<ul style="list-style-type: none"> • Weather • Seasonal and diurnal survey timing • Habitat • Cover
Vascular plants (Time-limited surveys, Chapter Five & Six)	<ul style="list-style-type: none"> • Geographic range • Size • Phenology 	<ul style="list-style-type: none"> • Collector visual perception • Collector skill level • Survey area & search duration • Diversity of assemblage 	<ul style="list-style-type: none"> • Weather • Seasonal and diurnal survey timing • Habitat • Cover

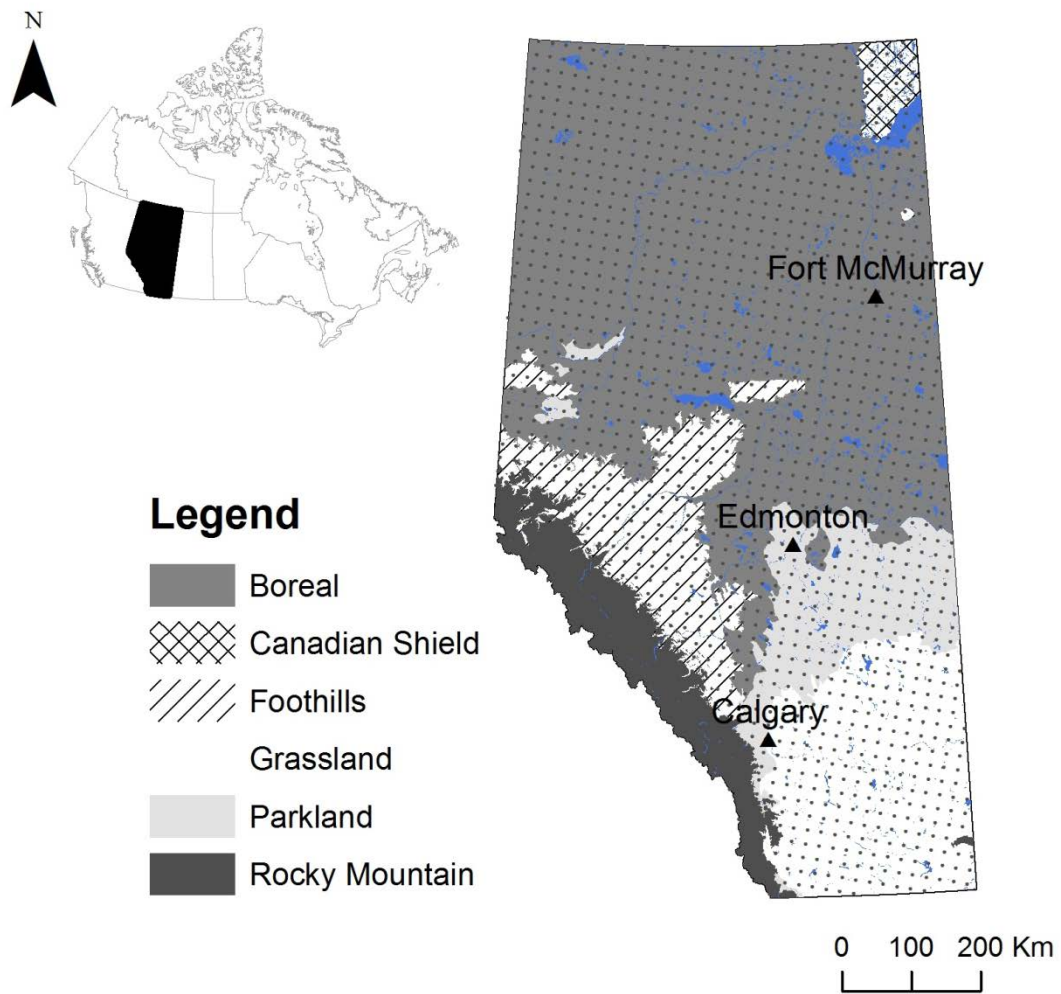


Figure 1. 1 Natural regions of Alberta (Natural Regions Committee 2006), overlain with the National Forestry Inventory grid of 1,656 points that the ABMI is based on.

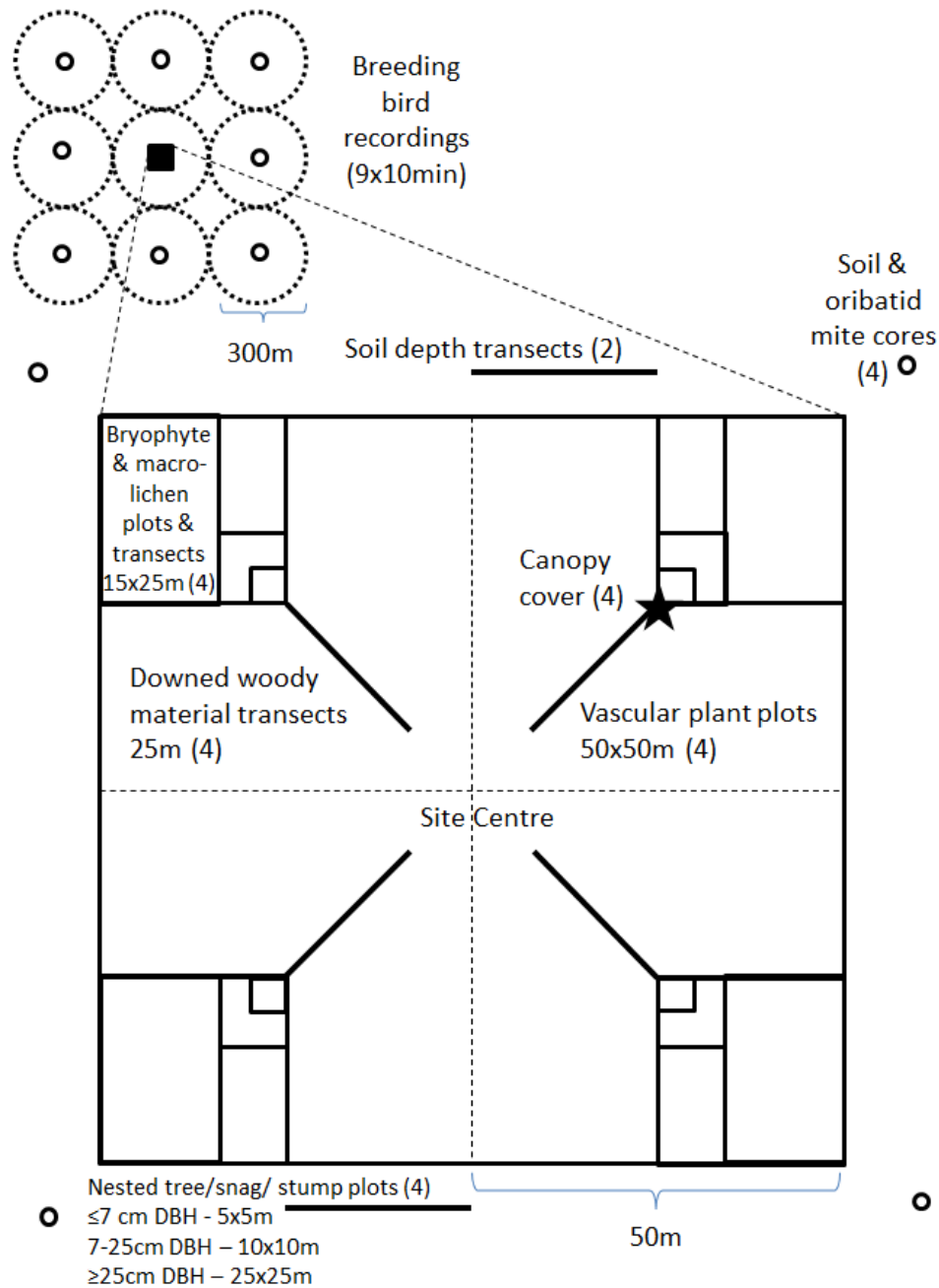


Figure 1. 2 Overview of key terrestrial protocols employed by the Alberta Biodiversity Monitoring Institute (from 2009 onwards - more detailed information is located at www.abmi.ca and throughout this dissertation). Figure modified from Alberta Biodiversity Monitoring Institute (2010).

CHAPTER TWO

Can we better our biodiversity monitoring by breaking the rules?

Two versions of the contents of this chapter are published:

Boutin, S., D. L. Haughland, J. Schieck, J. Herbers, and E. Bayne. 2009. A new approach to forest biodiversity monitoring in Canada. *Forest Ecology and Management* **258S**:S168-175.

Haughland, D. L., J. M. Hero, J. Schieck, J. G. Castley, S. Boutin, P. Sólomos, B. E. Lawson, G. Holloway, and W. E. Magnusson. 2010. Planning forwards: biodiversity research and monitoring systems for better management. *Trends in Ecology & Evolution* **25**:199-200.

Summary

Most countries have committed to reducing the rate of biodiversity loss and accepted that monitoring is necessary to assess their progress. Establishing biodiversity monitoring is difficult however, in part because of debate around how to design monitoring programs for multiple species affected by multiple stressors across multiple scales. The most common solution is to amalgamate data from existing monitoring programs and to label species from those programs as indicators or surrogates of biodiversity. I argue that programs designed specifically to monitor biodiversity, although sometimes criticized as inefficient and ineffective, are a better solution, and that following traditional rules of monitoring design in the special case of biodiversity monitoring can be counter-productive. The benefits of biodiversity monitoring as described are calculable and exceed by that realized by the current indicator species approach. Finally, I show how the benefits of effective biodiversity monitoring need not come at the expense of conservation and research as is often perceived.

To understand the tone of this chapter requires a brief history. We were originally motivated to write a discussion piece as an alternate viewpoint to that of Nichols and Williams (2006). In collaboration with Stan Boutin, Jim Schieck, C. Lisa Mahon, and Erin Bayne I took the lead on an aggressive discussion piece (the basis of this chapter), which discussed the logic of the design decisions made by a

larger group of scientists involved in the Alberta Biodiversity Monitoring Institute. I sent proposals to three journals before it was accepted by *Frontiers in Ecology and the Environment*, where the manuscript was then soundly rejected. During this process, we became aware of Lindenmayer and Likens forthcoming article (2009), which by being critical of the ABMI, gave us the leverage to publish a rebuttal (Haughland et al. 2010). The rebuttal was developed in collaboration with Bill Magnusson from Brazil, Jean-Marc Hero, Guy Castley, and Ben Lawson from Australia, and much of it was developed in person during the 10th International Congress of Ecology in Brisbane, Australia in 2009 (Haughland et al. 2010). This chapter is based on the original discussion piece. However, I revised it to include recent literature as well as the comments of the anonymous *Frontiers* referees. I use the singular in this chapter because my revisions include personal opinions with which my original coauthors may not agree.

Introduction

Increased debate about effective ecological monitoring is the natural result of a swinging pendulum of scientific debate put in motion in the 1990s. As the importance of scale in ecology was appreciated, and the reach of anthropogenic activity increased, scientists prioritized long-term large-scale monitoring to inform management and ecological theory (e.g., Lubchenco et al. 1991, Bawa and Menon 1997). Globally, a burst of monitoring was initiated in terrestrial and aquatic systems (many are reviewed in Busch and Trexler 2003, Lindenmayer and Likens 2010). Because these programs are conspicuous in their scale and expense, their design is a topic of sometimes rancorous debate. In an effort to curb monitoring for monitoring's sake, various proponents argued for a set of rules or criteria to guide new ecological monitoring initiatives and to judge existing monitoring as 'problematic' or 'effective', or even 'ugly' (sensu Lindenmayer and Likens 2010, e.g., Lindenmayer et al. 2006, Ferraz et al. 2008, Lindenmayer and Likens 2009, Nichols, 2006). I think these rules push back the pendulum too far and are harmful to some ecological monitoring programs,

especially a specialized subset designed to deal with biodiversity at large temporal and spatial scales. Here I outline an alternate biodiversity monitoring paradigm that doesn't follow some of the aforementioned rules of monitoring. The Alberta Biodiversity Monitoring Institute is just one of a growing body of organizations prepared to do the experiment and test these ideas, and below, I'll explain why.

Current approaches aren't working

It's globally acknowledged that biodiversity monitoring is necessary (The Convention on Biological Diversity 2006). However, despite the success in other areas of environmental monitoring (e.g., Lovett et al. 2007) monitoring programs struggle to measure or monitor biodiversity well. A principle problem is the multidimensionality of the term biodiversity, which makes it difficult to choose which aspects to measure, and is compounded by the variability and imprecision in even basic metrics like species richness. In addition, biodiversity monitoring that informs land management often occurs through Environmental Impact Assessments (EIAs) or Environmental Protection and Enhancement Act (EPEA) requirements, which are localized, of short duration, and tend to be biased towards taxa such as songbirds or mammals (Chapter Six) The following is meant to illustrate these issues by highlighting the deficits faced by land managers (in this case the fictional 'Jo' , short for either Josephine or Joseph) as they try to incorporate biodiversity into land use planning.

There are no regional data to help Jo understand what diversity can be expected to occur naturally in the region Jo works in, or how Jo's region compares to similar areas. No trend data exist for Jo to examine to determine how either species or landscape attributes such as occurrence, abundance or distribution are responding to higher levels of human activity. At the scale of individual proposed projects, Jo can ask for biodiversity assessment as part of the larger EIA. But this provides two years of pre- and post-impact data at a very small scale; each proponent often uses a different contractor, and each contractor considers the data they collect proprietary. In addition, the impact of any one proponent is relatively small; it is often the combined impact of many proponents (i.e., cumulative impacts) that is problematic. Unfortunately the overall result is

consistent; Jo has no scientifically credible data on biodiversity change that will help Jo set thresholds for disturbance or fragmentation levels deemed acceptable or prioritize areas for conservation. This puts land managers in a reactive mode and susceptible to shifting baselines (e.g., Pauly 1995, Sáenz-Arroyo et al. 2005).

Jo can use scientific studies to understand potential management impacts, but Jo is grappling with combinations of impacts that are novel and/or not understood. Most scientific studies are short-term and deal with well-defined impacts on a limited number of species at a small scale. Species-at-risk and harvested species provide better legal mechanisms for Jo to protect habitat or alter management plans, but species-specific management actions/interventions may not provide protection for other species. Global indicators of biodiversity such as the Living Planet Index (Loh et al. 2005) or the Red List Index (Butchart et al. 2004) tell Jo that indeed biodiversity is declining, but they are useless at telling Jo where a proposed development is best situated, or how each approved project impacts the biodiversity in the region. Jo, and the provincial government that employs Jo, are responsible for every land-use decision in an area roughly the size of France. I suspect Alberta is not unique – Jo and others like Jo are making the decisions that directly impact biodiversity around the world.

The alternative

I predict that successful biodiversity management can benefit from monitoring with the following features:

- long time frames,
- large geographic scale,
- measurement of multiple attributes, including multiple taxa with varying life history traits and ecological roles, coarse filter landscape metrics and fine filter habitat features,
- systematic design,
- consistent application of simple methods over space and time
- habitat and human land-use information, and
- statistical power at the scale of powerful management.

The hypothesis is that biodiversity monitoring with these characteristics will provide timely, transparent data that allow managers to quantify the trade-offs of different management decisions. It also breaks some important rules recently published by authors advising us about effective monitoring. In particular, our list of desired features does not include:

- the indicator species approach - we stress monitoring a breadth of species instead of using a small number of species at risk or managed species,
- design driven by a narrow set of system models and quantitative *a priori* hypotheses, or imposed Before-After Control-Impact management experiments – we stress an adaptable monitoring system that optimizes the potential to examine multiple hypotheses simultaneously,
- a sampling design optimized for strata of interest - we stress a systematic design to facilitate use of information across multiple overlapping natural and management regions whose boundaries change over time.

Long time frames

Natural stochasticity and the continuous nature of land management means current data are needed continually. Long time frames provide a robust initial sample (that includes year-to-year variation) to determine starting conditions, the ability to detect slow incremental change, and the ability to place the change in context of historical conditions (Powell and Steele 1995). Temporal trend data are invaluable in understanding population dynamics (e.g., Krebs 1991, Ims et al. 2008). This is valuable when managers are operating under the emulation of natural disturbances paradigm (Hunter 1993).

Large geographic scale

While the ecological benefits of monitoring across large geographic scales are recognized (e.g., inclusive of multiple populations of species, communities or biogeographic regions, furthers understanding of natural stochasticity, Holling

and Meffe 1996, Schwartz 1999), the importance of scale in biodiversity management often is not appreciated. Most biodiversity management occurs not at the global level, nor at the level of individual projects, but at some intermediate scale determined by a country's political divisions and allocation of responsibility. For example, in Canada, the most powerful land managers are the provinces and territories because the Canadian Constitution places the management of natural resources on public or crown land (including forestry, oil, and gas) under their jurisdiction. Currently 93% of forested land in Canada is publicly owned and 71% is under the purview of the provinces and territories (Canadian Council of Forest Ministers 2012). Thus, in Alberta industry leases land or rights to certain resources from the province. While industry determines where and how resource extraction occurs within the lease, the province is responsible for approving the level of resource extraction, often requiring both a minimum and maximum level of extraction for the lease to be maintained. Multiple industries can lease the same area, so overlapping extraction by industries such as oil and gas, forestry, and agriculture is common. In addition, multiple companies may extract different components of a same resource in the same area; nine additional forest companies operate within ALPac Forest Products forestry management area as an example (area=65,520 km², Ministry of Sustainable Resource Development 2012).

Large-scale monitoring encompasses multiple management areas, providing both intra-region and inter-regional comparative information to the province to help determine whether large-scale processes such as climate change are driving change (e.g., intra-regional biodiversity change is similar) or whether specific operations are more influential (intra-regional biodiversity shifts are dissimilar). Large-scale monitoring is adaptable as land-management regimes and stressors evolve in response to changing economic drivers.

Inclusive of multiple taxa with varying life history traits and ecological roles

A major question in biodiversity monitoring is what to measure. While Noss's (1990) hierarchy provides some guidance, it is only slightly less overwhelming in scope than biodiversity itself. Given the limitations faced by even the most ambitious well-funded biodiversity initiative, any attributes chosen

are *de facto* indicators or surrogates, so the real question is how to choose those indicators and how much each additional attribute adds to the understanding of the status of biodiversity. Established criteria for indicator selection (**Table 2.1**) require extensive autecological knowledge. Subsequently, many indicators are single species or single taxa that represent a biased subset of biodiversity. These indicators can be problematic when their surrogacy and sensitivity are untested (Lindenmayer et al. 2000); even when they are, indicator utility in even adjacent regions can be contradictory (e.g., Sergio et al. 2006, Roth and Weber 2008). Especially problematic for long-term biodiversity monitoring is single-species management remedies that further decouple the indicator from the broader biodiversity it is purported to represent. Solving a series of single-species issues via applied research keeps conservation anchored firmly in reactive, crisis conservation mode (**Figure 2.1**) whereby we learn how to manage the stressor for that species, but do not necessarily learn how ecosystems change with human intervention or cumulative impacts.

While a ‘complete picture’ of biodiversity change may not be feasible, there is an intermediate solution that may gather enough ‘pixels’ to interpret the underlying image: including taxa from across gradients of trophic levels, life histories and ecological roles. Manley et al. (2004) describe this “bet-hedging” strategy as a middle ground between the impossible (measuring all aspects of biodiversity) and the ineffective (the traditional indicator approach). The ABMI is hedging its bets and spreading its resources across multiple coarse-, meso-, and fine-filter attributes (Noss 1987, Schulte 2006, Stadt et al. 2006). Landscape vegetation distribution and composition are monitored through remote sensing as coarse filter correlates of ecosystem integrity (Franklin 1993, Attiwill 1994, Lindenmayer and Franklin 1997). Because landscape metrics are not sufficient to document changes in local habitat structure (Lindenmayer et al. 2000, Hunter 2005), meso-filter attributes are monitored, including downed woody material, soil depth and composition, and density, size and species composition of trees, snags and stumps at terrestrial sites, and depth, area, and vegetation characteristics at wetlands site. As species may not be tightly linked to particular landscape or

habitat characteristics, some fine-filter monitoring ensures that biota are responding as predicted from changes in coarse- and meso-filter attributes (Franklin 1993, Hunter 2005). The ABMI currently monitors approximately 2,000 species from the following taxa: macrolichens and calicioid/dwarf fruticose/pin lichens (*sensu* Goward 1999), mosses and liverworts, vascular plants, soil mites, songbirds, winter-active mammals, benthic macroinvertebrates, and fish (**Figure 2.2**).

Taxa were selected for a diversity of reasons, including high species diversity, and the ability of some species to act as classic indicators (fulfilling many criteria in **Table 2.1**), including engaging to the public, and responding to human disturbances. Species that may not respond to current stressors were also included because a) future stressors may not be predictable, and b) it is just as important to know which taxa are resilient as to know which taxa are sensitive to anthropogenic activity.

The suite of attributes described above largely reflect composition and structure (Franklin et al. 1981), however function may be assessed indirectly from the relative amounts of these indicators (Karr 1981, Bonada et al. 2006). The only controversial component of these attributes is the breadth of taxa included. The combination of long time frames and large geographic scale, a lack of understanding of natural systems, continued extinctions and extirpations, and our inability to directly measure many ecosystems services humans provoked ABMI to include multiple taxa with varying life history traits and ecological roles. However, as a consequence of being broad, the ABMI is also shallow in information for any one species, largely focusing on occurrence and/or relative abundance as measured by taxon-specific protocols at each permanent site (see www.abmi.ca for more information). Many specialists are skeptical of data generated by rapid assessment protocols (Abate 1992) and largely undergraduate field technicians. ABMI would be well served by becoming more transparent about the experience level of the technicians, the training they receive, data quality control, and the repeatability or relative amount of sampling error that can be expected. The former two are easily supplied, but the latter two will require

investigation of parameters such as species detectability across different vegetation types and anthropogenic disturbances (see Chapter Two for one such study on bryophytes).

Systematic design, with consistent, simple methods

There is no one right stratification scheme when multiple stakeholders and long time frames are involved (e.g., anthropogenic biomes (Ellis and Ramankutty 2008), natural regions (Natural Regions Committee 2006), or forest management areas (Ministry of Sustainable Resource Development 2012)). Consequently, a simple design such as a systematic sampling regime is logistically attractive. This also allows multiple management organizations that have different, overlapping regional boundaries to use the data, accommodates shifts in boundaries over time, and is powerful for detecting large-scale events such as climate change. In addition, starting in 2007 supplementary sites have been carefully chosen and surveyed using standardized ABMI protocols to address more specific questions requiring additional data. Large-scale long-term programs also benefit from simple methods, particularly because of the many observers involved. These methods can be used to measure trends in occurrence, relative abundance or composite metrics such as indices of biological intactness (IBIs) (Karr and Chu 1999). Lindenmayer and Likens (2010) characterize this design as “statistically unusual” for a monitoring program; it may be unusual because it is more challenging logistically, but it is second only to random sampling for ensuring unbiased data while also providing representation across the entire region of interest (Krebs 1999, McDonald et al. 2001). While systematic designs are not the most statistically powerful design initially, the ABMI’s systematic grid will not become less powerful as management priorities and landscapes change, a certainty given the rate of development in Alberta (Edwards 1998).

Inclusive of landscape and anthropogenic land-use information

Often impacts within a region are the result of decisions by multiple land managers, each with competing objectives. This leads to 'silo management' (B. Stelfox, personal communication), a variant of the classic tragedy of the commons, where each manager plans to extract maximum resources for

themselves from the same area without taking into account competing interests. For example, in the time it takes to investigate how changes in forestry practices affect a species, the system may be altered by agriculture and non-renewable resource extraction. Shifting economies translate into shifting demands for natural resources. In the province of Alberta Canada, land uses such as agriculture initiated in the 19th century continue to expand, while additional land uses such as forestry and energy extraction accelerate (**Figure 2.3a**), often in the same management areas (e.g., Peace River District). Booming economies bring booming populations (**Figure 2.3b**), even in northern regions where population density historically was low. These shifts sometimes cause unpredictable cumulative impacts: seismic lines cut in the forest, once thought to be a minor impact, are now considered a major driver of change in boreal predator-prey communities (McKenzie et al. 2012). Stressor-specific applied research and monitoring alone provide limited system knowledge. To aid in understanding which activities are associated with the highest loss, biodiversity programs should collect correlative information on human activities as part of their landscape-level data collection.

Statistically powerful at the scale of powerful management

Conversion of intact habitat (estimated as the largest threat to biodiversity, (e.g., Venter et al. 2006) often is dictated by intermediate-level agencies such as the provincial governments in Canada. Biodiversity monitoring programs that can deliver statistically powerful results at the operational scale of the most politically-powerful land management agency increase their odds of informing management. Focusing planning, management and monitoring at smaller scales to evaluate individual developments overlooks cumulative impacts. Focusing at very large scales (i.e., globally) does not help land managers determine how their decisions impact their jurisdiction. It's undeniably useful if a core set of monitoring variables can be standardized across jurisdictions to allow scaling up of results and comparisons nationally and globally (e.g., Pereira and Cooper 2006) - but that should not be the primary goal.

How to fund biodiversity monitoring and why it need not come at the cost of research

Justifiably, conservationists tend to exhibit a scarcity mentality, fostered by the competition for limited, fluctuating funds. This leads to the false perception that large-scale, expensive monitoring programs (as compared to most research programs) will monopolize resources. An alternative method of securing what is arguably the keystone component of biodiversity monitoring - long-term funding - that actually enhances opportunities for research is detailed below.

Long-term, stable funding for biodiversity

While some advise monitoring be supported through research funds (Pereira and Cooper 2006) or through government agencies (Lovett et al. 2007), we suggest that core funding for biodiversity monitoring should be generated from the activities that provide the most impetus for monitoring - resource development. Industry spends money on environmental impact assessments and assessments for ongoing impacts, mitigation and remediation. However, there often is disconnect between the scale of operation of an individual proponent and the scale of the biodiversity issues an individual proponent is asked to assess, monitor and mitigate. In addition to being ecologically impotent, these small-scale results rarely are published, often become the property of the individual contractor hired by the proponent, and are difficult to amalgamate across studies due to incompatible design and survey methodologies (Chapter Six). By requiring proponents to allocate part of their environmental impact and enhancement-related funds towards independent, arms-length, large-scale programs, more efficient use is made of these funds. If funding was contributed to an endowment fund, constructed with original investment by all stakeholders including government, there could be sufficient funding for the program to conduct annual operations from the interest generated.

Some critics consider these ideas naïve, but our experience working with multiple industries in Alberta suggest that ABMI's industrial partners are (perhaps surprisingly to some) eager to use their monitoring funds effectively, and not-so-surprisingly, eager to benefit from the efficiencies gained in supporting a

centralized monitoring agency (Chapter 6). Government and industry realize that effective monitoring (regardless of the results) increases their social capital, a critical component of successful businesses in an era where the mineable oil sands are a topic of global debate and forest certification is becoming the norm. They will lose this acquired social capital if industry continues practises shown to be unduly detrimental or government continues to approve projects in highly impacted regions without making conservation trade-offs elsewhere.

An integrated program can be cost-neutral if funding spent on the existing small, disconnected programs that are organization-specific and issue-specific are redirected. For example, the immediate, measurable savings provided by the Alberta Biodiversity Monitoring Institute for government, forestry, and oil and gas companies were estimated at \$7.7 million per year or 79% of the projected total cost of the program (Alberta Biodiversity Monitoring Program 2006). Most savings were realized by forestry through reduction of redundant monitoring and lengthened inventory intervals. While the projected total program cost (approximately \$10 million annually) is high relative to the average ecological research project, environmental monitoring in the oil sands region of northeastern Alberta alone recently was allotted \$50 million (Government of Alberta 2012).

Ecological and economical spin-offs of biodiversity monitoring

Long-term biodiversity monitoring is an incredible resource for taxonomists, both in terms of research material and employment. Biodiversity data are a valuable research resource that seed research and improve study design for many species (e.g., answering “Where and in what abundance do I find my species of interest?”). Few jurisdictions have these data, and this is reflected in fundamental metrics such as species distribution maps and conservation rankings. For example, ABMI has documented many lichen species formerly considered either rare or restricted to Alberta’s mountain regions throughout the boreal forest (e.g., *Cetraria ericetorum*).

The need for taxonomy creates apprenticeship opportunities for future taxonomists, ensuring that specialized knowledge is passed on. For example, as of February 2012 the Royal Alberta Museum employs four taxonomists

(lichenologist, botanist, mite specialist, and aquatic invertebrate specialist), and multiple contractors specialized in either bryology or songbirds specifically for the ABMI. In addition, three full-time technicians currently are employed and undergoing taxonomic training. Finally, last summer alone the ABMI employed an additional 44 technicians who received a month or more of intensive training and practise in the identification of a taxon of their choosing. The number of technicians employed continues to grow as the program expands.

Economically, much of ABMI's funds are returned to communities through local expenditures. The greatest cost is field data collection, which involves technicians working in every region of the province, using various resources and contractors such as helicopter pilots, grocery stores, camping facilities, and gas stations.

Criticisms

Programs with traits deemed desirable by ABMI have been criticized or discontinued because they were perceived as poorly designed and inefficient (National Research Council 1995, Nichols and Williams 2006, Lindenmayer and Likens 2010). I think this criticism is often misdirected, and the ABMI's discussions with Lindenmayer and Likens about their critiques suggested that the original criticisms were not well researched, many judgements were subjective, and others based on overly rigid criteria. Certainly the ABMI can work to prevent future misunderstandings by placing more impetus on publication, but that has proven difficult given the prevailing monitoring paradigm. I believe we also have been guilty of being overly prescriptive and aggressive in our messaging within the scientific community. Pride in the project is laudable, but proclaiming yourself a world-class institute can raise eyebrows rather than support (e.g., Lindenmayer and Likens 2010). Biodiversity monitoring as described here is neither a cure-all nor will it work in every ecological/economic climate. Here I address the most commonly cited criticisms faced by ABMI both locally and globally.

Criticism 1: Bad for rare species

This is often true and should be communicated to stakeholders to avoid false expectations. Many species will be detected sporadically, making inference at the species level difficult. Acute, small-scale impacts will likely not be measured well. However, species-at-risk and acute, localized stressors are dealt with more effectively within existing management approaches such as environmental impact assessments, environmental protection and enhancement monitoring, and species-at-risk legislation. Many rare species can only be well-addressed through focused monitoring and research, and even then, gathering statistically-powerful data is difficult (Thompson 2004). In comparison, most common species have no mechanisms to conserve them. The importance of common species in ecosystem structure and function is increasingly recognized (Gaston and Fuller 2008). Biodiversity monitoring as described here can redress this.

ABMI-style programs do provide some information to further rare species management. Improved and unbiased information on species abundance and distribution means that funds for conservation can be allocated towards those truly rare species, rather than to species that are rare because of deficient information. For example, lichens formerly ranked as rare have been reassessed as secure based on ABMI information (e.g., *Ramalina dilacerata* [Figure 1.2], Alberta Conservation Information Management System 2011). To date over 2,000 occurrences of S1 to S3 species have been detected by ABMI and provided to the provincial species and ecosystems information management system.

Criticism 2: Lack of statistical power

For the relatively common species these programs best serve, biodiversity monitoring can be powerful enough to detect declines of 3% or more a year (Chapter Four, Manley et al. 2005, Nielsen et al. 2009). When power is low for individual species, amalgamating species into guilds or other composite indices or multivariate metrics can provide a more powerful measure of community change (McCune et al. 1997, Maxwell and Jennings 2005). There are multiple ways to address this concern, including quantifying the magnitude of natural and observer

variability through model covariates and/or methods-specific research, interspersing observer error across the stand and disturbance gradients, and being transparent about statistical power (Chapter Two, Three and Four).

Criticism 3: Not mechanistic or model-based

For species at risk or managed species, monitoring reproductive rates and causes of mortality are undeniably important. Sectors of society such as hunters contribute funding towards in-depth programs for species they have an interest in maintaining. It is also undeniable that very few species will ever be studied to that depth. There are practical trade-offs between the level of inference that can be derived for a given species and the number of species that are monitored. By monitoring the presence, abundance, and range of many species, biodiversity monitoring can alleviate the risk we take when we ignore the status of species that society does not perceive as being of concern. In addition, habitat conversion and loss are still thought to be the biggest drivers of biodiversity change.

Consequently, correlative measures of human activity may be sufficient to highlight activities with a disproportionate impact on biodiversity in general.

Criticism 4: No explicit quantitative a priori hypotheses or models

Many authors have written about the importance of quantitative hypotheses (Legg and Nagy 2006, Nichols and Williams 2006), and we don't disagree, if the questions can be addressed within the existing monitoring framework. Designing large-scale, long-term biodiversity monitoring around species- or taxon- specific research questions is more likely to limit long-term utility than enhance it. Biodiversity monitoring as described here provides exciting opportunities to address more specific hypotheses economically, particularly when the baseline monitoring data are combined with supplementary data collection. An example of this is the current partnership between AIPac Forest Products and ABMI to compare biodiversity at sites subject to forest fire or logging 15 years post-disturbance. Biodiversity monitoring can provide comparisons of ecosystem state along a gradient of multiple stressors across geographic regions. With the low-levels of ecological research funding relative to many other disciplines (Natural Sciences and Engineering Research Council of

Canada 2004), biodiversity monitoring may facilitate faster learning than a multitude of applied research programs. In essence, the ABMI is a 'biodiversity atlas', one of the few that is systematic and unencumbered by varying data collection methods and poor representation of difficult-to-access regions.

My experience with ABMI leads me to hypothesize ABMI's susceptibility to this criticism is due to a lack of communication through peer-reviewed journals as well as a false dichotomy between different research styles. Mensurative studies often are perceived as passive and epidemiological, while manipulative studies are viewed as active and predictive, but there is no reason why ABMI can't be active and predictive within its current framework. In fact, the ABMI is progressing towards predictive mapping of future conditions as explicit hypotheses of the future state of biodiversity (E. Bayne, personal communication). One of the foundational models the ABMI has adopted, the dose-response framework (Karr 1987, Nielsen et al. 2007), is a natural fit for forecasting future conditions which can be tested against data from future monitoring cycles. Using data collected systematically throughout Alberta, the natural variation in species' occurrences and abundances are measured, and the response of those metrics to increasing 'doses' of anthropogenic disturbance are estimated as departures from the natural or intact condition. One area where ABMI can improve is modelling natural variation such as the effects of stand composition and age on species' ranges of natural variability. This will enable better separation of sampling error, natural variability, and change due to land use practises.

Finally, ABMI's choice of attributes evolved from a series of extensive original reviews by experts, where both the choice of attributes and methods to measure those attributes was justified with regards to different type of anthropogenic activity. These reports are available online in the Technical Reports and Science Development section <http://www.abmi.ca/abmi/reports/reports.jsp?categoryId=183>). I think it behooves ABMI to do the experiment and test whether formalizing these models improves existing monitoring. Models can be objectively formalized in collaboration with additional experts. We can then examine how the ABMI's current suite of

measured attributes correspond to those suggested by the original implicit models and the updated more explicit models, implementing any changes that would result in large improvements in interpretability of the data.

Criticism 5: Impractical and wasteful

Given the numerous environmental and management issues currently faced, some find the idea of planning for common species and cumulative impacts economically wasteful. However, biological systems are so poorly understood that defining ‘crucial’ based on the biased subset of variables we understand relatively well (e.g., vertebrates, trees) may well be detrimental. Biodiversity monitoring as described herein can lessen this knowledge gap.

Some conservationists fear that biodiversity monitoring programs can “become a form of political and intellectual displacement behaviour, or worse, a deliberate delaying tactic” (Nichols and Williams 2006). I argue the opposite. A well-designed program can prevent delays and counter-act politically-driven mismanagement via three key tactics. First, systematic monitoring can provide data on system state within the first monitoring cycle by allowing researcher to substitute space for time and make comparisons across natural or existing management treatments. Used in this sense, with *a priori* hypotheses driving very specific comparisons within the larger dataset, data from biodiversity monitoring can be used prospectively. Second, when stakeholders such as academia, government, industry, and environmental not-for-profit groups partner in the design and implementation of the program, biodiversity monitoring provides a common resource for decision-makers. This circumvents delays incurred trying to synthesize data from disparate monitoring or research programs (Parr et al. 2002) or achieve stakeholder consensus. Third, biodiversity monitoring enables managers to put the potential impacts of projects in perspective. For example, if an industrial development is predicted to reduce a species by 20%, managers can examine the regional implications of that reduction using monitoring data to inform their decision. This is a fundamental advantage over normative research where generalizability is often questionable due to small-scale geographic and stochastic effects.

Conclusions

To effectively manage biodiversity, the priority needn't be global assessments or species level assessment, but rather assessments of biodiversity at the scale of powerful management. While there is debate about the fiscal responsibility and utility of biodiversity monitoring programs, current monitoring practises are not providing good measures of the changing status of most of biodiversity. Biodiversity programs as described here provide valuable measures of status and trends due to landscape alteration, climate-change, wide-spread chronic pollution, and management policy. These broad monitoring programs allow all stakeholders to assess changes to ecological health. Other jurisdictions that have arrived at similar solutions include Biodiversity Monitoring in Switzerland (Hintermann et al. 2002, Weber et al. 2004), the National Inventory of Landscapes (NILS) in Sweden (Ståhl et al. 2011), Program for Planned Biodiversity and Ecosystem Research in Brazil (Magnusson et al. 2008) and Australia (Hero et al. 2010)

Many of these programs are less than a decade old. They are vulnerable to criticism and quick judgement, hence the necessity of communicating the logic underlying the design. However, it will soon be time to stop debating and start delivering. The ABMI has been operational for five years, and its future depends on its ability to fully deliver on its potential. The very breadth and diversity of ABMI is part of the reason why ABMI is sometimes perceived as less productive than desired, as the relatively small number of researchers involved are addressing a string of high priority issues rather than publishing their solutions. Operating counter to the prevailing monitoring paradigm also makes publishing challenging. Recruitment of additional graduate students to address very specific questions would help address these limitations. In conclusion, while biodiversity monitoring as described here has many commonalities with traditional research involving explicit hypotheses, and adaptive monitoring as described by Nichols and Williams (2006) and Lindenmayer and Likens (2009, 2010), it also has unique attributes that act as strengths rather than deficiencies (**Table 2.2**). I hope enough of these experiments persist so that researchers a decade from now can

evaluate their success against the ultimate criterion, reducing the rate of biodiversity loss.

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Table 2. 1 Criteria for the selection and evaluation of indicators for biodiversity monitoring.

Criterion	Description	Details and Methods to Evaluate Criterion
Scientific soundness	<ul style="list-style-type: none"> • Proven indicator of certain condition or surrogate of larger component of biodiversity (Landres et al. 1988, Andreasen et al. 2001, Subsidiary Body on Scientific Technical and Technological Advice 2003) 	<ul style="list-style-type: none"> • Based on natural history & knowledge of systems in the field (Karr and Chu 1999) • Biota are taxonomically well known and stable (Pearson 1994) • Has existing scientific studies validating relationship between indicator and attribute of interest (provide measure of statistical confidence and amount of variation explained if possible)
Feasible	<ul style="list-style-type: none"> • Cost-effective (Andreasen et al. 2001) • Should be relatively easy to identify and detect 	<ul style="list-style-type: none"> • Measurable with sufficient accuracy at an affordable price (Subsidiary Body on Scientific Technical and Technological Advice 2003, Biggs et al. 2006) • Preferably can calculate values for at least 90% of sites (Astin 2006) • Has a relatively small range of natural variation (e.g., coefficient of variation at reference sites less than 0.5; Astin 2006) • Should consider the spatial variation and detectability of indicator (Yoccoz et al. 2001)
Diagnostic ability	<ul style="list-style-type: none"> • DA = 100 (a/b) • Where the metric is expected to increase with impairment, a = # stressed sites with metric values > 75th percentile of reference distribution; where metric expected to decrease with impairment, a=# stresses sites where metric <25th percentile of reference distribution; b = total # stressed sites 	<ul style="list-style-type: none"> • Responds to a given stressor in a highly predictable way (Jameson et al. 2001, Houde et al. 2005) • Early indicator of change (in relation to the response of the ecological system at large) to enable risk management • Predicts changes that can be averted by management actions (Houde et al. 2005) • Focuses attention on the decisions/actions that the program might influence rather than on the indicator (Watson and Novelty 2004)
Amenable to aggregation	<ul style="list-style-type: none"> • Should be able to indicate change at a temporal and spatial scale that matches adaptive management goals and policy (Subsidiary Body on Scientific Technical and Technological Advice 2003, Biggs et al. 2006) 	<ul style="list-style-type: none"> • Applicable across entire range of monitoring program (Andreasen et al. 2001) • Metrics behave similarly in different regions (Astin 2006)
Amenable to communication	<ul style="list-style-type: none"> • Relatively simple and easy to understand (Subsidiary Body on Scientific Technical and Technological Advice 2003, Biggs et al. 2006) 	<ul style="list-style-type: none"> • Best indices combine straight-forward sampling designs and statistical analyses • Aids in communicating ecological changes and subsequent consequences to citizens, policymakers, and political leaders (Holling and Meffe 1996, Holling 1998)

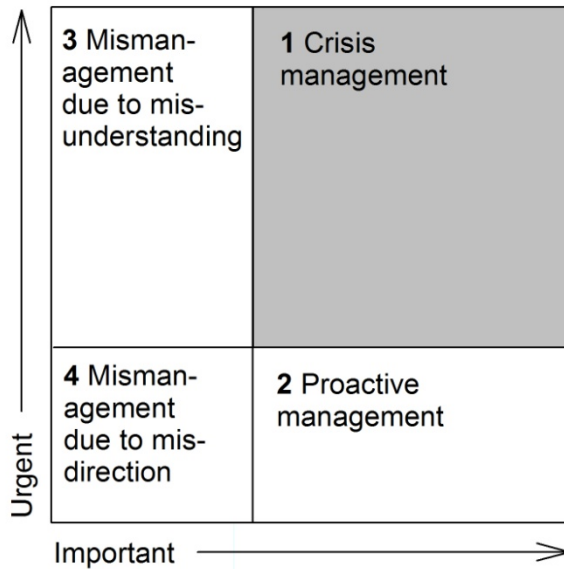
Table 2. 2 Comparison of the characteristics of successful long-term biodiversity research and monitoring systems and traditional research and monitoring studies¹.

Characteristic	Value
Monitoring for All Types of Research	
Focus on a well defined question	Monitoring targeted toward evaluating status and trends of parameters that are affected by, and responsive to, the defined mensurative or manipulative study ensures monitoring is effective and efficient.
Use a rigorous statistical design	Study design, sample methods, and sample size appropriate to identify relationships with the degree of precision appropriate for the research question ensures monitoring is statistically powerful.
Additional Benefits of Monitoring for Applied Research/Management	
Address questions that are important to managers	Applied research that provides information that facilitates making decisions between potential management actions ensures monitoring results are useful to managers.
Conduct outreach and education	Results that are communicated in forums where managers participate, and in a format that is understandable by non-scientific audiences ensures that information is relevant to and useable by managers.
Provide data freely to managers and other stakeholders in a timely manner	Making data available quickly to managers and stakeholders attracts other researchers and makes the program transparent so that there is no danger of monitoring for monitoring's sake. A common resource is created for all stakeholders to work from, permitting more rapid, educated decision making.
Additional Benefits of Long Term Biodiversity Research & Monitoring Systems	
Use simple, standardised survey methods	Comparisons are easily made between data collected at different sites, regions and even countries. Participants of varying skill levels and experience can be trained to ensure quality data collection.
Use a modular design for data collection	The intensity of study can be increased in specific areas and for specific questions by increasing the number of modules (integrated sampling units), while maintaining comparability among all sites. Supplementary surveys by stakeholders interested in increasing sample size are easily incorporated in the network.
Integrate information on many taxa	Biodiversity-related questions are best addressed with a combination of fine-filter measures of multiple taxa, as well as coarse-filter

Survey throughout a broad area	<p>measures of habitat and landscape rather than a few indicator species. By including many taxa the resulting information will be valuable to many different stakeholders.</p> <p>Large geographic scale is important for biodiversity monitoring to ensure that large-scale ecosystem processes are assessed. By sub-selecting sites from the broad area, local data can be used by managers and researchers for focused analyses or as the nucleus from which additional research is built.</p>
Systematic data collection in perpetuity	<p>Long-term data collection is required for biodiversity monitoring to ensure that trends can be identified even when there is extensive background variability in the ecosystems.</p>
Integrate data collection with existing programs	<p>Where possible, biodiversity monitoring should build on pre-existing well-designed monitoring initiatives to facilitate calibration and reduce program development costs.</p>
Ensure data collection is cost-effective	<p>Long-term continuity is critical for biodiversity monitoring. This can only be achieved by operating within the funding constraints of stakeholders. However, costs for biodiversity monitoring can be reasonably high and still be acceptable because the resulting information will be used to address both specific targeted questions as well questions about status and trend for a diversity of taxa. If government, industry and research funding is combined, costs for each stakeholder will be relatively low.</p>

¹This table was prepared in cooperation with Jean-Marc Hero, Jim Schieck, J. Guy Castley, Stan Boutin, Péter Sóllymos, Ben E. Lawson, Gillian Holloway and William E. Magnusson as supplementary material for Haughland et al. (2010)

A. Current allocation of effort



Examples of Activities

Quadrant 1 - Reactive

- Species-at-risk management including captive breeding and reintroduction
- Overharvested species management
- Habitat destruction mitigation
- Management of biological invasions
- Pollution mitigation

Quadrant 2 - Proactive

- Baseline monitoring
- Human stressor monitoring
- Prioritization exercises
- Matrix management
- Reserve design
- Preventing biological invasions
- Predictive pollution monitoring

Quadrant 3 - Undesirable

- Any Quadrant 1 activity where effort is misdirected due to lack of knowledge or incorrect information

Quadrant 4 - Unethical

- Any activity where effort is misdirected due to politically-motivated delay tactics

B. Proactive allocation of effort

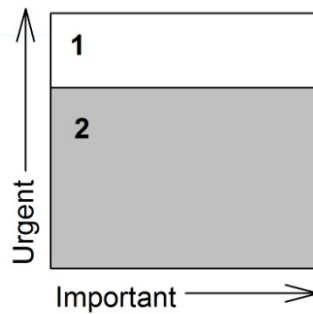


Figure 2. 1 Putting first things first (Adapted from Covey 1989). Four-quadrant activity-management paradigm for conservation and management of the environment. Conservation is perceived as a crisis-oriented discipline (Soulé 1985), where most effort is allocated to urgent, important activities (Quadrant 1). However, conservation could benefit from following the four-quadrant activity-management paradigm (Covey 1989). The number of ‘fires’ to put out will only increase unless conservationists can allocate more effort to important activities before they become urgent. By reallocate our effort towards Quadrant 2 activities, we can potentially circumvent future crises.

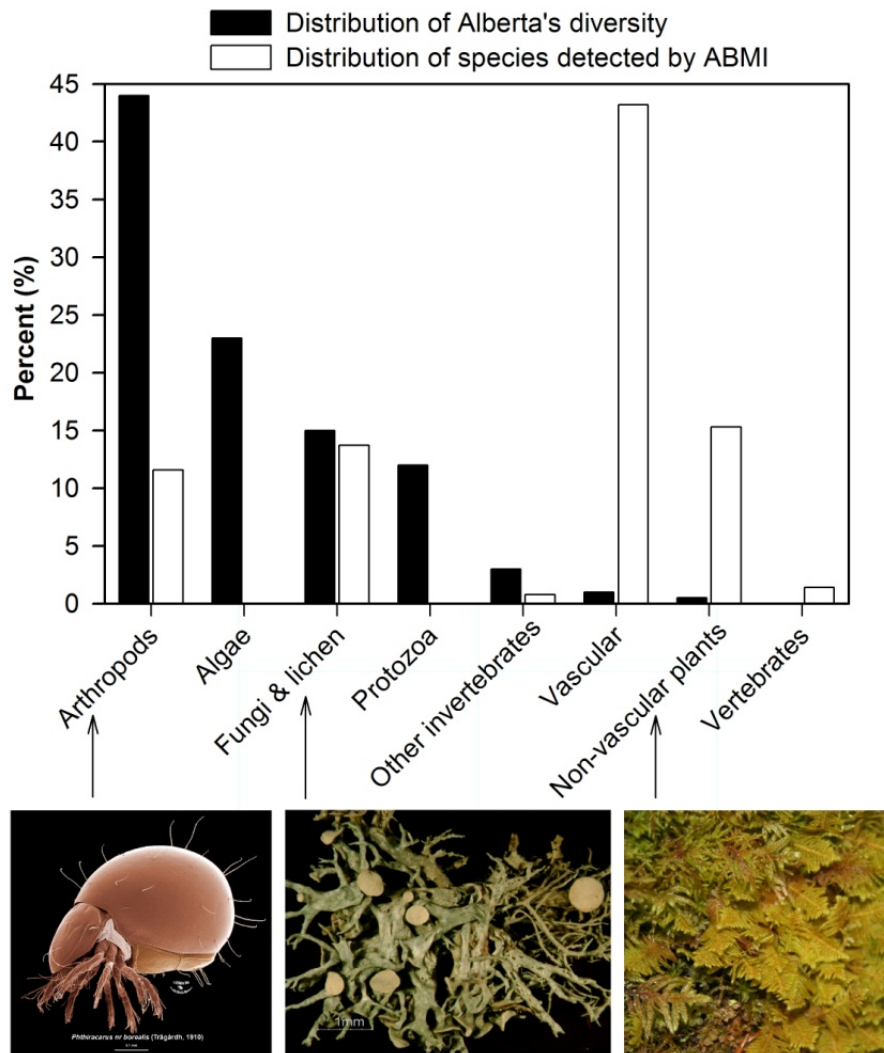


Figure 2. 2 The distribution of Alberta, Canada's estimated 80,000 species, in comparison with the distribution of the 1,400 species currently detected by ABMI (Alberta Biodiversity Monitoring Institute 2012). Some of the less charismatic species included in the program are pictured. Soil mite *Phthiracarus nr borealis* © David Walter and the Royal Alberta Museum, Punctured cartilage lichen, *Ramalina dilacerata*, and Knight's Plume moss *Ptilium crista-castrensis*, D.L. Haughland.

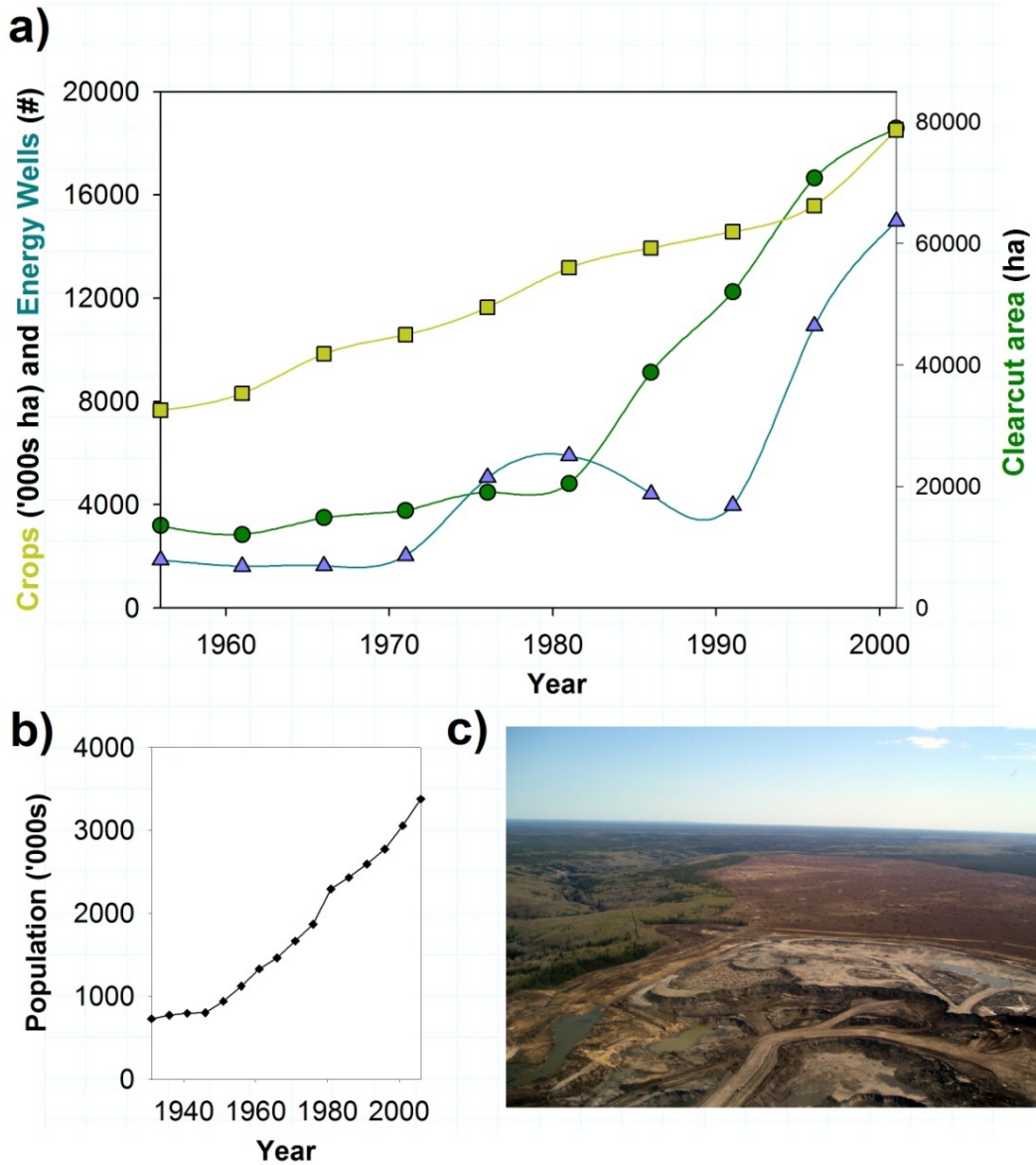


Figure 2. 3 Examples of cumulative impacts in Alberta, Canada. a) Land altered annually via new clearcuts [circles], crop production [squares] and oil and gas well creation [triangles] from 1956 to 2001. b) Population from 1931 to 2006. (Data: Forum Consulting Ltd. , National Forestry Database) c) Aerial view of an oil sands mine transitioning to boreal forest.

CHAPTER THREE

Floristic rapid assessment protocols for bryophytes, and their application in landscape-scale biodiversity research and monitoring

Introduction

Rapid assessment protocols (RAPs) have been implemented and scrutinized in some fields of biology such as ornithology and invertebrate biology (e.g., Jones and Eggleton 2000, Ward and Larivière 2004, Gillies et al. 2009), but the utility of RAPs for bryophyte surveys has not been examined. This gap means that few studies provide detectability estimates, examine the effect of using novice collectors (including undergraduate and some graduate students), or compare the economic costs of different survey methods for cryptogamic taxa. Understanding the relative impact of different sources of sampling error has immediate utility for research and monitoring, particularly biodiversity-related studies interested in multiple species. Cryptogamic flora such as bryophytes are valuable indicators of natural gradients (e.g., Gignac 1992, Økland et al. 2004), pollution (e.g., Zechmeister et al. 2007), habitat alteration (e.g., Hylander et al. 2002, Lõhmus et al. 2006), and edge effects (e.g., Baldwin and Bradfield 2005, Gignac and Dale 2005, Hylander 2005), and can dominate the understory in many boreal forest stands (Laroi and Stringer 1976). These traits make them attractive for studies examining anthropogenic impacts on the environment; however, it is unclear how variation in assessment methods affects quality and interpretation of bryophyte data, particularly when employed by novices.

Existing research has shown that both novices and experts impose sampling error on plots of any size. For example, Archaux et al. (2009) found that experienced botanists missed 20% of the understory vascular and non-vascular plant species in a 100 m² plot on average, and McCune et al. (1997) revealed that experts routinely missed half of the epiphytic macrolichen species in a 0.378 ha plot. In the latter study, novices generally collected even fewer species, detecting 38-95% of the species detected by experts. High rates of non-detection are not

limited to large plots; Vittoz and Guisan (2007) report that only 45-63% of vascular plants had perfect detection by experienced botanists in a multiple observer study, regardless of whether the plot was 0.4 m² or 40 m².

Much of existing monitoring for cryptogamic taxa, as well as the research on sources of error and sample design, has focused on traditional plot sampling (i.e., 0.01 m² to 1 m², as reviewed in Doubt and Belland 2000, see also Jiang et al. 2011). Small systematic or random plots contain few species because species distributions are patchy and rely on the presence and quality of specific microhabitats (McCune and Lesica 1992, Belland and Vitt 1995, Vitt et al. 1995, Vitt and Belland 1997, Vitt et al. 2003, Newmaster et al. 2005, Cole et al. 2008). Microhabitats such as rocks, trees, and soils are affected by local factors such as microclimate and nutrient availability and play host to characteristic cryptogam assemblages (Crites and Dale 1998, Mills and Macdonald 2004). The alternative to small plots is floristic sampling (see Newmaster 2000 for overview) or relevés (Braun-Blanquet 1951). Floristic sampling traditionally is bounded only by the extent of the stand being surveyed. Due to the relatively large survey area, diverse microhabitats are included and can be targeted by an experienced observer able to differentiate species in the field. Newmaster (2000) presented a refined version of this method called 'floristic habitat sampling' in which both common (e.g., forest) and relatively rare mesohabitats (e.g., streams and cliffs) within the dominant stand are sought out and all microhabitats present in each mesohabitat are sampled. If the research or monitoring goal is to include the greatest diversity of species, a floristic approach is valuable.

Research objectives

Our objective was to investigate the effect of observer error, time constraints, and search methodology on the effectiveness of different floristic rapid assessment protocols for bryophytes. Effectiveness for a given survey was estimated as a) the ability of novice practitioners to record a high proportion of the known bryophyte species at a site, and b) the repeatability of surveys by different practitioners. We also assessed the number of duplicate collections for each survey method, as these elevate costs for taxa that are collected in the field

and processing and identified in the laboratory. In addition, we examined how collections by novice technicians compared to published species lists for similar boreal forest stand types.

The economic and logistic constraints bounding the survey parameters were adopted from a province-wide biodiversity monitoring initiative, the Alberta Biodiversity Monitoring Institute (ABMI, www.abmi.ca). The ABMI is a multi-taxon province-wide program that is designed around a systematic grid of 1,656 permanent sites, which will ultimately each be surveyed every five years. The ABMI includes bryophytes and macrolichens in its terrestrial protocols, allocating 2.5 hours per assemblage. There are not enough experienced bryologists to conduct the field work, thus field technicians are mostly students late in an undergraduate degree or recent MSc and PhD graduates with limited experience in bryology. Within these constraints, we evaluated the costs and benefits of modifying the following parameters: plot size, intensity of effort (time spent per unit area searched), amount of information recorded for each sample taken in the field, and search pattern followed during the survey.

Methods

Experimental field study

In the summer of 2006, we conducted field work southeast of Lesser Slave Lake, Alberta (55°27'N, 115°26'W, **Figure 3.1**) to explore the impact of different surveys. We used a factorial repeated-measures complete block design to examine how different surveys performed in different boreal forest stands. Six 1 ha forested sites reflecting different boreal forest nutrient and moisture conditions were surveyed by two different collection teams (**Figure 3.1**). The sites included two dry low-nutrient jack pine stands (dominated by mature *Pinus banksiana*), two mesic moderately nutrient-rich mature mixedwood (dominated by mature *Populus tremuloides*, *Populus balsamifera*, and *Picea glauca*), and two treed bogs (dominated by *Picea mariana*).

Using remote sensing imagery and *in situ* field assessment we positioned our sites within stands to be either 'homogeneous' or 'heterogeneous'.

Homogeneous stands had similar dominant tree species, understory vegetation, and nutrient-moisture conditions throughout the 1 ha. Heterogeneous sites included secondary nutrient-moisture conditions with concomitant differences in understory vegetation and canopy composition. Heterogeneous sites were meant to mimic the increased microhabitat diversity encountered with randomly or systematically-placed sites. Both the heterogeneous lowland and pine stand were approximately 30% secondary stand types, including nutrient-rich hygric treed fen, anthropogenic cutlines, and dry black spruce forest with feather moss understory. The mixedwood contained 15% nutrient-poor hygric bog. More site information is available from the senior author.

Each 1 ha site was flagged into four quadrants of 50x50 m, and each quadrant was flagged into 4 subquadrants of 25x25 m (**Figure 3.1**). In each quadrant of each site we conducted three different survey types. The first survey type was a 20–25 minute time-limited floristic habitat search (hereafter referred to as **floristic TL**), and provided the most in-depth collection information. Collectors moved freely within the plot, directly seeking what they perceived to be the most species-rich example of each *a priori* named microhabitat from **Table 3.1**. If time allowed, multiple examples of each microhabitat were visited. Each microhabitat sample was bagged separately and the location (subquadrant) and a brief description of the microhabitat, including light exposure, approximate log decay stage, or approximate diameter at 1.3 m height (DBH) for standing trees was included.

The second survey type was a 20-25 minute time-limited systematic search, and provided little specimen-level information (hereafter referred to as **systematic TL**). The collector walked a standard 'U' shaped transect (**Figure 3.1**), but was allowed to meander up to 10m to either side to seek out speciose examples of microhabitats. A single bag was used to collect samples from each microhabitat type; as examples of each microhabitat were encountered new morphotypes were collected and added to the prepared bag. Because the collections were composite samples, supplementary data were not recorded, fewer collection bags were created and field-processing time was minimized.

Finally, a time-unlimited systematic search of microhabitats was conducted with the intent of recording all species present in each quadrant (hereafter referred to as **floristic TU**). Using the inside perimeter of each subquadrant for guidance, the collector systematically surveyed each subquadrant and collected examples of each unique morphotype in each microhabitat in separate bags. These surveys took four to six hours per ha. Subquadrant and some microhabitat data were recorded for each collection bag.

In late July and early August, the first team conducted the three survey types at each of the 24 quadrants (i.e., 6 sites x 4 quadrants each). Teams were composed of a bryophyte collector and a lichen collector. Prior to surveying each site, the team spent 20-25 minutes searching for and recording what microhabitats were present. To control for the effect of familiarity with the site, the first team alternated the order they conducted the floristic TL and systematic TL surveys; the floristic TU survey was always conducted last. In August the second team repeated the first two survey types in the opposite order as the first team. To emulate the predominant experience level of technicians hired by ABMI, bryophyte collectors were novices with regards to bryophytes, but had a minimum of four years of field experience in northern forests. Training was limited to PU recognition, diversity within common genera such as *Sphagnum*, microhabitats and their variability, and the protocols themselves. Bryophyte experience was limited to that gained conducting similar surveys prior to this study, formal education in university courses (all collectors held a minimum of a Bachelor degree in biology), and self-study. Team One had more field experience collecting their respective taxa than Team Two, but neither team had extensive experience identifying bryophytes in the field or laboratory.

Identification

Specimens were not identified in the field; the technicians collected examples of each parataxonomic unit (PU) that appeared unique or inhabited a unique aspect of the microhabitat. Contents of collection bags were sorted using dissecting and compound microscopy by a technician with four field seasons of experience identifying common bryophytes in the laboratory. The technician

recorded the presence of common species and packeted all unidentified specimens for expert identification, as well as a voucher of each common species from each site for verification. Eleanor Edye conducted the expert identification. She used the Cryptogamic Herbarium at the University of Alberta for verification where necessary, as well as microscopy and staining (for Sphagnaceae). Taxonomy for the mosses follows the Bryophyte Flora of North America . Liverwort taxonomy follows (Crandall-Stotler et al. 2009) and TROPICOS (Missouri Botanical Gardens 2012).

Statistical analyses

Because we didn't estimate cover we focus on species occurrence at each site. We didn't use the number of occurrences as a measure of abundance to avoid confusing detectability and abundance metrics.

Ability of novice technicians to detect a diversity of bryophytes

We tabulated the number of times each species was detected (=collected) in each quadrant and site (total possible detections = 5). While we can't eliminate the possibility that species were eliminated from a quadrant during the first set of surveys, we suspect this was a rare occurrence given the large plot size. McCune et al. (1997) did similar repeated measures surveys for lichens and found no evidence that overall diversity was diminished even after 7 surveys of the same plot.

We compiled species lists from published research employing TU surveys and summarized the species shared between the collections of our novices and those documented by experts in ecologically similar boreal stands in Canada. In addition, we compared the proportion of those lists composed of liverworts. Liverworts were of particular interest because they are known to be sensitive indicators of altered habitat conditions (Newmaster et al. 2003, Baldwin and Bradfield 2007, Caners et al. 2010), yet they may be overlooked by novices because many are small and cryptic.

The influence of plot size on microhabitat diversity

For each of the 16 25x25m subquadrants per site we tabulated occupied microhabitats and created sample-based rarefaction curves, treating microhabitat types as unique 'species'. We focused on occupied microhabitats as this more accurately reflects the plot size required to capture a diversity of bryophytes.

Completeness of community sample

We used the 1 ha sites to delimit the bryophyte assemblages, and we examined the ability of each survey to accurately and repeatedly represent that assemblage. Our measure of the true bryophyte assemblage consisted of the combined results of all surveys at a site, hereafter referred to as total diversity. For each of the four quadrants, this amounted to a floristic TU survey, two floristic TL, and two systematic TL surveys, for a total of 20 surveys per site or roughly 12 hours of sampling over two to three field days. This approach overestimates the completeness of our samples by an unknown factor that depends on the number of species present in the site but missed from the total (McCune and Lesica 1992, Cao et al. 2002). To examine the completeness of this representation, we constructed occurrence-based species accumulation curves for each site (Colwell and Coddington 1994, Gotelli and Colwell 2001) in the program EstimateS (Colwell 2009), using collection bags as the sample unit and the Mao Tau exact expected richness function (Colwell et al. 2004).

Optimizing survey design

We examined different plot sizes, survey types and survey intensities to quantify their ability to fulfill the following criterion: representative, inclusive, repeatable, and efficient. To examine the effect of increased effort or intensity, we pooled samples either by survey type or by team for each quadrant to emulate the effect of either increasing the time spent per unit area or doing repeated surveys for detectability modelling.

Criterion One: Surveys should be Representative (Accurate)

We created a nonmetric multidimensional scaling (NMDS) ordination for the pooled species across all surveys (hereafter referred to as total species) as well

as the data collected by each team employing each survey type (6 ordinations total) at two scales and four intensities. We used Procrustes permutation tests to determine whether multivariate patterns in each survey were significantly correlated to those in the total species data (Peres-Neto and Jackson 2001, Appendix 3.1). We used the metaMDS and protest functions from the ©R package vegan (Oksanen et al. 2011, R Development Core Team 2011), with a maximum of 100 random starts and two axes in the NMDS, the Sørensen similarity metric (identical to the Bray-Curtis metric when species abundance data are used), and 999 Procrustes permutations. While the Sørensen metric is thought to underestimate true similarity as compared to Chao's corrected indices (Chao et al. 2005) it has proven robust in multivariate analyses and is widely used (Legendre and Gallagher 2001, McCune and Grace 2002) allowing comparison of our results to other studies. The Sørensen similarity measure is also the inverse of pseudoturnover as calculated by Nilsson and Nilsson (1985), another metric used in repeatability studies

Criterion Two: Surveys should be Inclusive

We estimated inclusiveness as the percent of total richness diversity at the site captured by each dataset. To examine the effect of plot area on inclusion, we constructed sample-based species accumulation curves and converted the species richness estimates to % total richness by dividing by site-level total richness. Both the number of quadrants (area) and the % total richness were log transformed to linearize the relationship. To determine the effect of survey type, team, and stand type on the slope and intercepts of the log-log SACs, we constructed linear mixed-effects models. We used the lmer function from the lme4 package (Bates et al. 2011) with maximum likelihood approximation and treatment contrasts in R (R Development Core Team 2011, version 2.13.2). Model construction started with the maximal model, containing all possible fixed factors (log(area), collection team, survey type, and stand type), their interactions, as well as a random intercept for site. The model was simplified by removing the variables with the smallest effect and largest standard error. Corrected Akaike Information Criterion (AIC_c) was used to compare models following Burnham and Anderson (2002).

Criterion Three: Surveys should be Repeatable (Precise)

We compared the NMDS ordinations of survey types conducted by different teams using permutational Procrustes analysis to determine whether one survey type was more repeatable than the other. To examine the relative effect of team versus survey- and stand-type on detection of species, we modelled species detection with generalized linear mixed-effects models with a binomial family and a logit link using the `glmer` function from the `lme4` package (Bates et al. 2011), with Laplace approximation. We started with a maximal model, and tested hypotheses around random factors, then interaction terms, and finally fixed factors following Bolker (2009). An ideal survey would be robust to observer error (species detectability wouldn't vary by observer, and the interaction between survey type and team wouldn't be significant) and would perform similarly in different stand types (the interaction between survey type and stand type wouldn't be significant). Species were considered missed during a survey if detected by any of the other surveys in a quadrant, including the floristic TU survey. Fixed effects were modelled nested within the random factors quadrant and site. We first modelled detection error at the quadrant scale. Using the best model parameterization for quadrant, we then modelled detection error at the scale of the site.

Criterion Four: Surveys should be Efficient

We compared the ratio of the number of specimens collected to species recorded for each survey type. A specimen equalled either a sample sent for expert identification, a voucher, or a record of a species identified by the technician. For example, if the technician recorded *Sphagnum warnstorffii* from a sample and sent a packet of *Sphagnum* sp. to the expert whom identified it as *Sphagnum warnstorffii*, this would count as two specimens to reflect the full cost of processing.

A second expense incurred is processing time. Composite sample bags are economical in the field but incur a greater laboratory expense. Even if two survey types had similar specimen numbers, if one survey type results in a larger volume of composite material, it may require more time to sort and identify in the lab. To

examine laboratory processing time of the samples from each survey, we parameterized a maximal balanced linear mixed-effect model, with four factors (survey type, collector, cumulative hours sorting [range of 0 to 300] by the laboratory technician when starting the sort of a given collection, and total specimens [range 106 to 337]) and random intercepts for sites. Processing time showed evidence of autocorrelation at lag one with weak oscillations thereafter, but they didn't approach $\alpha=0.05$ so weren't incorporated into the modeling. We created five models to test the importance of each fixed term and the interaction term.

Results

The influence of plot size on microhabitat diversity

A survey area of 0.3 ha or five 625 m² blocks captured an example of all occupied microhabitats present at a site (**Figure 3.2**). As expected, heterogeneous sites tended toward steeper microhabitat rarefaction slopes, indicating the greater β diversity of microhabitats present at those sites.

Completeness of sampling

Occurrence-based species-accumulation curves declined in slope but did not asymptote (**Figure 3.3**). We don't present estimates of richness for each site because we argue that floristic sampling doesn't provide the appropriate information. Rarefactions traditionally are assembled using collections that are 'blind', i.e., where all individuals irrespective of their species identity have an equal chance of inclusion. The efficiency of floristic sampling is derived from violating this assumption: the collector can be selective and only sample individuals that differ from individuals already collected. As a result, common species are underrepresented in these samples as compared to their true cover or abundance in the community, and the species richness estimating functions likely overestimate the rate of accumulation and subsequent extrapolated site richness. Regardless, the declining slopes suggest that our sampling provided a good representation of each site.

While comparisons with other studies are difficult due to differences in plot size, geographic location, and site history, we compiled species lists from published studies that were either extensive or employed large plots in similar boreal stand types. Vitt and Belland (1995) reported 109 spp. in their study of 100 homogeneous bogs and fens using relevés, and we recorded 56 of those species. Of the 53 spp. we didn't record, 36 spp. were exclusively found in fens, and of the 17 species found in bogs but absent in our study, 7 were rare liverworts (found in $\leq 11\%$ of sites), 6 were *Sphagnum* spp., and 3 were *Drepanocladus* spp. Belland and Vitt (1995) reported 50 spp. in their study of 65 bogs using 5x5 m relevés, and we recorded 39 of these species. Of the 11 spp. we didn't record, 4 were *Sphagnum* spp., 6 were liverworts and the last was a *Brachythecium*. Caners (2010) recorded 135 spp. in 24 0.13 ha plots in replicate mixedwood forests that had been partially harvested at different intensities, and we detected 97 of those species. Of the 38 spp. we didn't record, 15 were liverworts, 4 were *Splachnum* spp., and 5 were *Brachythecium* or *Bryum* species. We didn't find any comparable studies on pine stands as published surveys were restricted to understory vegetation. Carleton (1982) recorded 23 spp., and we observed all of these except *Dicranum ontariense* (then *D. drummondii*). Similarly, we recorded all 10 spp. Kotelko et al. (2008) recorded in pine stands in Manitoba, all 8 spp. recorded by Carroll and Bliss (1982) and all 18 spp. recorded by Ostafichuk and Laroi (1983) in pine forests in northeastern Alberta. In comparison, we recorded 29 species (20% of the 147 species recorded) that were not reported in any of the above studies.

Ability of novice technicians to detect a diversity of bryophytes

In total, the surveys resulted in 6,557 bryophyte specimens and detection of 147 species across the six 1ha sites (**Appendix 3.2, Table 3.2**). Of the bryophytes detected, 46% are species tracked by the province (ranked as critically imperiled [10 spp.], imperiled [14 spp.] or vulnerable [44 spp.], Alberta Conservation Information Management System 2011, NatureServe 2012). Liverworts comprised 27% (39 spp.) of the total species list: 28% in bog-

dominated stands (33 of 118 spp.), 24% in mixedwoods (24 of 99 spp.), and 17% in pine-dominated stands (14 of 83 spp.). Our mixedwoods liverwort proportion was 4% lower than observed by Caners (2010, 39 liverworts or 28% of species detected in unlogged mixedwoods) and our bog proportions were 6% lower than Belland and Vitt (1995, 17 liverworts or 34% of species detected in intact bogs).

Technicians captured diversity within genera that are both species-rich and morphologically difficult to separate (**Appendix 3.2**). For example, 15 *Brachythecium*, 13 *Sphagnum*, 10 *Dicranum*, and 2 *Orthotrichum* spp. were collected. The common *Orthotrichum* spp. were both detected at five sites, and at those sites, detectability within each quadrant averaged 0.7 (*O. speciosum*) and 0.8 (*O. obtusifolium*), respectively. It is more difficult to infer the detectability of different *Sphagnum* species, as they also proved to be the genus most prone to identification error by the sorting technician (**Appendix 3.3**). *Dicranum* spp. were a better comparison as were identified accurately in the laboratory and multiple species occurred at all 6 sites. Collectors detected 60% (average of 6 site averages of 5 surveys) of the *Dicranum* species known to be present at a site, with detection probabilities ranging from 0.33 in the heterogeneous mixedwoods where they were species-poor and sparse (3 spp., 9 specimens total), to 0.77 in the heterogeneous bog where they were twice as diverse and 16 times as abundant (7 spp., 143 specimens total).

Optimizing survey design

Criterion One: Surveys should be Representative (Accurate)

All NMDS ordinations exhibited stress of 0.15 or less, which equated to a high correspondence ($R \geq 90\%$) between samples in ordination space and true species resemblance space. All Procrustes correlations between two ordinations of the same data set were 0.99 ($P \leq 0.002$), indicating stable solutions were found.

At the smallest scale ($n=24$ 0.25 ha quadrants) all survey ordinations were highly correlated to their respective total ordinations ($P < 0.001$, Procrustes symmetric $m^2 \geq 0.81$, **Figure 3.4**), indicating they were representative of the total community composition. Data from Team Two (mean $m^2 = 0.83$) were less

representative than those from Team One (mean $m^2=0.87$) regardless of survey type, but a 2-way ANOVA without replication was unable to detect a difference between survey teams or survey types (both $P>0.08$). The TU floristic survey ordination had the highest correlation ($m^2=0.95$) to the total ordination.

At the scale of the 1 ha site ($n=6$ 1 ha sites, 4 surveys per site), all surveys were less representative of the total species pool. Because of the small number of sites, we tested 1-dimensional solutions against 2-axis solutions; the 2-axis solution significantly reduced stress in each situation, so 2 axes were kept for all ordinations. Regardless, none of the ordinations exhibited correlations greater than 0.8 ($0.64 \leq m^2 \leq 0.79$). Only one correlation to the total, Team One systematic TL survey, was significant ($m^2=0.79$, $P=0.033$). Both teams and both survey types resulted in similar correlations (2-way ANOVA without replication, both $P>0.23$). To determine if this was a sample size effect, we conducted the same analysis on a subset of the 0.25 ha floristic TU (6 NE quadrants); the subsets were highly correlated to the total ($m^2=0.98$, $P=0.001$), indicating the decreased correlation was not due to sample size. To test whether this was due to increased inclusiveness or 'regionality' of the large plots, we compared the mean Sørensen similarity the 1 ha sites to the mean similarity between NE quadrant of each site (0.25 ha scale). The similarity between different 1 ha stand types averaged 0.63 ± 0.08 SD, 17% higher than similarity between 0.25ha quadrants (0.52 ± 0.10 SD).

Increasing the intensity of the survey increased correlation with the total richness for both survey types and team, but it didn't completely remove the observer effect (**Figure 3.5**). Pooling samples resulted in all correlations being highly statistically significant ($P \leq 0.001$). The increased similarity and correlation with the total was in part an artifact of pooling samples, particularly for the dataset that pooled both teams and surveys, because pooling increased the overlap between the resultant dataset and the total. However, the average number of occurrences recorded in the floristic TU survey (363) was approximately equal to the average number of occurrences recorded by the floristic TL (188) and systematic TL (176) surveys combined, and the correlation was higher for the

floristic TU survey. Increasing intensity increased similarity of a dataset to the total community more than increasing plot size (**Figure 3.5**).

Criterion Two: Surveys should be Inclusive

Over the study, each survey type captured approximately equal numbers of species not captured by other surveys (floristic TU captured 13, floristic TL surveys captured 11, and systematic TL captured 10 unique species). While we couldn't include the floristic TU surveys in the model, they captured on average $43.5 \pm 4.4\%$ (SD) of a site's total species richness within the first 0.25 ha quadrant, as compared to $28 \pm 6.1\%$ and $31 \pm 5.2\%$ for the floristic and systematic TL respectively.

Systematic TL surveys recorded 5% more total species richness on average than floristic TL surveys, but model selection didn't support separate slopes (capture rate with increasing survey area, all values and SEs are back-transformed: floristic TL intercept = $31.12 \pm 1.05\%$ (SE), systematic TL intercept = $32.61 \pm 1.03\%$, **Table 3.3, Figure 3.6**). This effect was most pronounced for Team Two, as their species capture increased when conducting systematic TL surveys by 7% in mixedwoods, 15% in bogs, and 20% in pine, while Team One SACs were similar between the two survey types. Collector had a larger effect on overall capture, with Team One capturing 35% more species on average than Team Two (Team One intercept = $31.12 \pm 1.05\%$, Team two intercept = $20.92 \pm 1.13\%$), but the data didn't support separate capture rates in the most parsimonious model. Capture rates varied between stand types, and the % total species richness captured by the first quadrant varied by stand type, team and survey type. On average, the % total species richness captured by the first quadrant was 29% and quadrants 2 through 4 added 10%, 8% and 6% respectively, until on average, a team had recorded 54% of the total diversity at the site. Mixedwoods, with their patchy distribution of bryophytes and heavily vegetated understory, had the smallest SAC slopes regardless of survey type or team (**Figure 3.6**).

Doubling the intensity (i.e., doing two surveys in each quadrant) increased the average % total species richness captured by the first to final quadrant to 43-

74% and 36-63% for Team One and Two respectively, while quadrupling the effort (pooling results from both team's TL surveys, four surveys total) increased the capture to 53% in the first quadrant to 88% in the fourth quadrant (**Figure 3.7**).

Criterion Three: Surveys should be Repeatable (Precise)

Both survey types provided similar correlated community representation between teams (floristic TL: Procrustes symmetric $m^2=0.84$, $P= 0.001$, systematic TL: Procrustes symmetric $m^2=0.82$, $P= 0.001$, $n=24$ quadrants).

We modelled 4,644 detections/non-detections of 147 species over 24 quadrants at 6 sites (**Appendix 3.2**). Our results suggest that variation in detectability of each individual species differed more between sites than between collectors or survey types (**Figure 3.8, Table 3.4 A**). Stand type did interact with survey type, largely due to the 15% higher detection probability in systematic TL surveys in the pine stands (**Table 3.4 A**). The interaction between survey type and collector was marginal, and the data didn't provide support for an effect on detectability (**Table 3.4 B**).

Overall detectability was most affected by collector, with Team Two detection probability averaging 37% lower than Team One, and systematic TL surveys resulting in 13% higher overall detection probability (**Table 3.4 C**, model C1, estimated overall $p(\text{det})$: Team One=0.27, Team Two=0.17). Mosses were 19% more likely to be detected than liverworts. The interaction plots suggest that detectability was constant across survey type and microhabitat richness for Team Two, but declined with microhabitat richness for Team Two, particularly using the floristic TL survey. The same pattern is evident for species richness, with the exception that Team One achieved higher than average detection using systematic TL surveys at low richness, but detection declined as species richness increased as with Team Two. However, the inclusion of species richness, microhabitat richness, or stand homogeneity did not substantially improve model fit (**Table 3.4 C**).

We ran the best supported model again, but parameterized it with data for detection/non-detection at the 1 ha scale. Parameter estimates resulted in very

similar effect sizes, except the intercept was higher (Team One=0.47, Team Two=0.31). Descriptively, when we excluded relatively uncommon species (recorded in <10% of the 24 quadrants surveyed, inclusive of all 3 survey types, n=104), average observed detections rose 10-15% (means, all SE=0.03, floristic TL: Team One=0.56, Team Two=0.45, systematic TL: Team One=0.63, Team Two=0.50). When we group the two survey types together, average observed detection rose a further 12% (means, all SE=0.03, Team One=0.75, Team Two=0.62).

Criterion Four: Surveys should be Efficient

Systematic TL surveys were significantly more efficient, resulting in approximately 6.5% fewer specimens for processing and identification while simultaneously detecting 7.5% more species (systematic TL surveys mean ratio 0.29 specimens:species less than floristic TL surveys, **Table 3.5**). If we estimate the identification costs per specimen at \$5, this increased efficiency would result in a saving of \$755 or \$126 per site. Team Two was also more efficient, but their efficiency came at a cost of lower species capture (Team Two mean ratio on average was 0.22 specimens:species less than Team One).

For laboratory processing time, the model with the most support suggested collector didn't affect sorting time, but the maximal model and the model without survey type were also well supported (**Table 3.6**), so we provide effect estimates from the maximal model (adjusted $R^2=0.72$ for linear model equivalent). The best predictor of sorting time was the number of specimens; on average every additional specimen added 2.4 minutes to the sorting time. The second best predictor of sorting time was the cumulative hours of sorting the technician had completed when he started processing a sample. On average, every extra hour of experience decreased sorting time of the next collection by almost a minute - this seems insignificant, but it represents a mean decrease of 4.5 hours per survey over the four month duration of the sorting. Collections from systematic TL surveys and Team One took the longest time to sort; systematic TL surveys required on average 1.19 more hours to sort and Team One samples required on average 0.72 hours more to sort, although these effects do not contribute greatly to model fit.

While we couldn't include the unreplicated floristic TU surveys in the models, the mean ratio was 6.4 specimens:species, 43% and 34% higher than the systematic and floristic TL surveys respectively. At the site level, the floristic TU surveys resulted in 363 specimens on average (twice as many as the TL surveys) and 55 species (28% and 22% more than the floristic TL and systematic TL surveys respectively) per site and required 16.6 hours to sort.

Discussion

Our analyses suggest observer and survey intensity (effort per unit area) can have as much impact as plot size on the species recorded in a survey. Even with high detection bias, however, all surveys had highly correlated multivariate structure, suggesting that novice technicians collected the dominant species characterizing each site. Our results suggest that if individual species or metrics such as species richness are of interest, a plot size of 0.1-0.3ha, with survey intensity of at least 25m²/min and a systematic TL survey will optimize species capture with relatively few duplicates that inflate processing costs, while resulting in more homogeneity between teams, however, detection error is likely to be substantial. If more specific microhabitat information is required for each specimen, it can be incorporated at a cost of 5-20% decrease in the number of species recorded in a 20-25 minute survey, depending on the collector. For the ABMI, which has allocated 2.5 hours for surveying bryophytes, this survey intensity translates to a maximum survey area of 0.375ha. We recommend dividing this survey area into multiple plots to create a relative abundance metric (e.g., Hylander and Dynesius 2006) or to use in detection modelling to statistically correct for high detection error. This will also keep surveys within each plot short enough so that technicians can better track what they've collected.

Ability of novice technicians to detect diversity

The species composition recorded by novices was similar to other extensive studies of boreal bryophytes conducted by more experienced or expert bryologists. The species groups that were consistently under-collected were the small leafy liverworts such as the *Cephalozia* and *Cephaloziella*, and diverse

genera with morphologically similar species such as *Sphagnum*. Conversely, there was a diverse group of 44 bryophytes which were present in $\leq 33\%$ of quadrants but were detected with a probability of 0.8 or greater. Cryptogam detection for novice technicians is almost certainly related to the autecology of each species, including size of colony, growth form, colour, and microhabitat-related features such as contrast with the background substrate. Bryologists may be able to employ correction factors analogous to those commonly used by avian ecologists as a post-hoc method to improve estimates of species occupancy. These include the maximum detection distance employed by Partners in Flight (Rich et al. 2004) and habitat-specific effective detection radius (Matsuoka et al. In press). Just as additional factors such as weather and time of day can be incorporated into bird detectability (Wolf et al. 1995), survey-specific factors such as weather during or just prior to survey (moisture absorption causes many species to swell in size and become more conspicuous), density of the understory, and tree density could be included in modelling of bryophyte detectability.

More error is attributed to botanists overlooking species than misidentifying species in vascular plant detectability studies (Nilsson and Nilsson 1985, Archaux et al. 2009, Chen et al. 2009, Vittoz et al. 2010, Moore et al. 2011), and our data suggest this disparity is even greater for bryophytes. Overlooking is more complicated in cryptogam studies because of disconnect between collection and identification in the laboratory, so we suspect experience will improve detection, but not mitigate it to the degree expected in vascular plants. More research is needed in this area, and an important first step is reporting detection probabilities. Aside from this study, we found a single set of detection probabilities reported in the literature; Archaux et al. (2009) reported the detections of 7 bryophyte species recorded in a floral survey that included vascular plants. Because detection likely varies by microhabitat, we relegate this discussion to a future publication.

Plot size

Our data suggests for bryophyte surveys in boreal Alberta, a plot size of 0.1-0.3 ha is large enough to contain most occupied representative microhabitats.

Conversely, a plot size of 1 ha may contain too much natural heterogeneity, increasing the similarity to other sites and making it difficult to detect site-specific changes. The microhabitat curves are likely specific to this region, thus researchers are advised to calculate their own curves as microhabitats may be more patchily distributed or sparse in their region. We caution against using small plot sizes (e.g., less than 5 m²) for floristic monitoring. In addition to the recognized issue of small plots capturing little microhabitat diversity, small plots also may be overly sensitive to natural temporal variation in cover by cryptogams, which has been shown to fluctuate at the scale of a single tree even when undisturbed (Zechmeister et al. 2007). For example, Snäll et al.(2005) documented extinction and colonization of a rare bryophyte at the scale of individual trees, and suggested that bryophyte metapopulation dynamics can be affected by very localized factors such as connectivity to other trees (Löbel et al. 2006) .

Optimizing survey design

When examining the repeatability of ordinations at the 0.25 ha scale, survey type and collector had a negligible impact on how representative a single survey was to the total bryophyte community. At the 1 ha scale, the average similarity between stands of different types increased 17% as compared to the same metric at the 0.25ha scale, and increased similarity was seen even between different types of homogenous stands (e.g., pine and mixedwoods). Studies employing floristic programs need to be explicit about the level of regionality they desire in their plots, and to explore whether the increased natural variation contained within a large plot comes at a cost of statistical power to detect changes due to anthropogenic impacts.

Both TL surveys provided repeatable representation of community structure. If the goal is to track individual species, however, the systematic TL survey resulted in higher detectability than the floristic TL survey for both collection teams. Detection was doubled when quadrant surveys were pooled and occurrence and detection error examined at the 1 ha scale. Collector affected overall detectability, but collector didn't impact relative detectability of a species

within a site as much as stand type. We interpret this as follows: species detections were in part driven by their abundance in each habitat, which was in turn driven by well-known niche differences between species. Observers may have had higher or lower probability of detecting diversity, but the overall pattern or relative detectability within a site was correlated between observers.

The overall detectability attained by each survey type varied by stand by $\pm 7\%$, but this effect was approximately a quarter the magnitude of the observer effect and half the magnitude of the survey effect. Detectability was lowest overall in the lowest diversity habitat, the pine stands. This is the opposite of what we expected and suspect it may be due to the patchy and sparse nature of the bryophyte coverage in these stands. Lower overall cover and abundance resulted in lower overall detectability, but as alluded to already, this isn't a perfect correlation, and there are species that are perfectly detected yet are relatively uncommon.

At the site level, TL surveys provided on average 75% of the species detected by the TU survey in about a quarter of the field time (1.3 hours for TL surveys vs. 4-6 hours for TU surveys) and half the number of specimens for sorting. While we don't have expert data to compare, we think this is driven by the novice nature of the collectors, and contains a fundamental lesson when field sampling is conducted by novices. While time-unlimited surveys may be perceived as the best solution to avoid potential time limit biases, simply removing the time limit doesn't have the same impact on a novice as it may on an expert, particularly in large plots. Collectors indicated they struggled to remember what they had sampled, and given the motivation to measure diversity and the inability to identify most specimens in the field, collected species repeatedly. Some lichen and bryophyte species can exhibit strong phenotypic variation, and this also contributed to the number of duplicates. These effects were amplified by increases in plot size and survey duration.

A second efficiency of the systematic TL survey was its predictability. Once a site's microhabitat diversity was known, the number of collection bags expected was also known, and this helped when processing and verifying the large

volume of samples. It was more difficult to ensure all samples were accounted for with the floristic TL and TU methods, where multiple bags were created per microhabitat. Simplicity becomes more valuable the larger the extent of the collection program.

Additional recommendations & future research

Train to homogenize detectability across technicians.

While repeating surveys may be the most effective way of both estimating and ameliorating detection bias, it is also very costly, particularly given the diminishing returns repeat surveys provide in terms of species capture. Repeat surveys also are likely to increase the probability of extirpating uncommon species from the plots (Richard Caners, personal observation). We hypothesize that a modified training program could help mitigate observer effects. Even if technicians cannot perform surveys as a team, training may be able to improve the search images of each individual, particularly if trainees are repeatedly assessed throughout the training, and then matched with someone with competence in collecting the species or genera being under-sampled. Each day technicians could collect both individually and as a pair to assess their improvement. We hope to test this hypothesis by integrating it into the ABMI technician training. At present, bryophyte-collection training occurs during a week-long training period and is interspersed with training for other protocols. Trainers focus on the importance of sampling across the breadth of microhabitats available within a plot, morphological variation in features to focus on in the field, and the breadth of species within each morphologically-similar group of bryophytes (e.g., *Sphagnum*). More formal lecture and specimen review, including time with microscopes, are interspersed with field work and practise sessions. Technicians conduct the protocol a minimum of four times during the training period, providing ample opportunity for feedback.

Follow the Goldilocks Principle of sample size

Whenever sites are permanent or monitored for other taxa, it is critical to minimize the chances of local species extirpations because of sampling. We

instructed technicians to aim for samples that fit in the palm of the hand (but to never take more than half of a specimen/colony/weft). This proved large enough to include incidental species such as small leafy liverworts, but small enough so that all collected material could be processed economically.

Report time spent sampling and experience level of field staff

While it is standard protocol to report on some experimental design attributes such as plot size or alpha used in statistical analyses, it is rare that researchers report the time spent surveying field sites or the level of experience of their practitioners, partly because time-limited surveys are uncommon. Our data suggest that observer and intensity effects can have a greater impact than plot size on the species recorded in a survey. We recommend that both attributes be reported, even if researchers believe their survey to be a time-unlimited census.

Conclusion

Bryophyte studies focused on diversity can benefit from adopting many of the ideas of floristic habitat sampling, which uses the biology of the target organisms to maximize species capture (Belland and Vitt 1995, Newmaster et al. 2005). Our research provides guidance for incorporating floristic practises into a standardized survey design, and how to optimize repeatability and inclusiveness when collecting is conducted by novices. Our results should aid in the design of other studies and highlight species or genera that require more survey effort to record repeatably (**Appendix 3.2**).

In studies of faunal diversity, repeated-measures and models incorporating imperfect detection such as mark-recapture models have long been the standard (Krebs 1999, White and Burnham 1999). When the biology of the organism drives detectability, it has become standard protocol to allocate extra effort to minimize sample bias. In comparison, in floristic studies where all species physically present at a given point in time are supposedly available for observation (not taking into account phenology), it appears that botanists have been slower to acknowledge how their background experience and visual acuity affects survey results, and subsequently, correct for that. That is changing for

vascular plants (e.g., Garrard et al. 2008, Alexander et al. 2009, Archaux et al. 2009, Chen et al. 2009, Vittoz et al. 2010), and we suspect it will change for bryophytes and other cryptograms as well, but practitioners in these fields may need different tools to deal with detectability because of the disconnect between laboratory and field work. Because sampling is not 'blind' like many invertebrate sampling methods, SACs may not be the appropriate answer either as floristic studies violate the assumption that each individual has an equal chance of representation in a sample. Much more research is needed before researchers can comfortably apply 'corrections' that reduce error rather than inflate it (Johnson 2008).

Our research was prompted by the needs of a regional monitoring initiative in our area. Large-scale biodiversity monitoring programs face a fundamental conundrum (e.g., Nichols and Williams 2006, Magnusson et al. 2008, Lindenmayer and Likens 2009, Haughland et al. 2010). While many scientists and environmentalists see the utility of large-scale, long-term monitoring of multiple taxa in the face of climate change, pollution, and human-caused habitat loss (e.g., Lubchenco et al. 1991, Sutherland et al. 2009), others question their utility, cost and probability of success (e.g., National Research Council 1995, but see Nielsen et al. 2009). Research such as ours that compare the magnitude of the various sources of sampling error will help programs such as the ABMI communicate the level of inference their data allow, and the strengths and weaknesses of their data in comparison to more traditional research. This transparency is essential in any scientific program, and is the foundation upon which trust in the results is built.

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Table 3. 1 Strata for bryophyte surveys. Each stratum contains one or more microhabitats. When time and survey type permitted, additional characteristics of sampled microhabitats were recorded, as indicated by asterisks below.

Logs and Stumps (at least 1 m long if possible) *Note if log or stump, species, diameter, and decay stage	
LS – Soft stumps and logs	Sample on logs and stumps >10 cm diameter (decay classes 3-5)
LH – Hard stumps and logs	Sample on logs and stumps >10 cm diameter in decay classes 1-2
Wetlands and Peatlands *Note if treed or not, if has standing water or not, and if a shore, if on mineral or organic	
WMF – Wetlands, marshes, and fens with or without trees and shrubs	Sample the water's edge within the wetland both under and away from trees
WSB – Shores/banks of wetlands, ponds, lakes, and streams	Sample on soil (organic or mineral) starting adjacent the water's edge
WDS – Moist depressions/seasonal wetlands dry at time of survey	Sample sides and bottom from an area most greatly influenced by water
WPW – Peatlands with or without standing water at the surface	Sample an area that includes both standing water and vegetation if possible; sample all sides, top and bottom of peat hummocks
Trees * Note species, DBH, and if dead, decay stage	
TD – Exposed roots, tree bases, trunks, and branches of live deciduous trees	Sample all sides of the roots, bases, trunks, and branches of live trees
TC – Exposed roots, tree bases, trunks, and branches of live coniferous trees	Sample all sides of the roots, bases, trunks, and branches of live trees
Human Structures * Note type (fence, house)	
HB – Buildings and structures	Sample on vertical and horizontal parts of the structures
Disturbed Soils *Note cause of disturbance of mineral soil from other causes	
DT – Tip-ups	Sample the hollow, the roots, and the soil that has tipped up
DC – Agricultural cultivation	Sample within the cultivated area
DM – Mineral soil from any other causes	Sample on mineral soil with little humus
Undisturbed Upland Soils * Note if mainly shaded or open, wet or dry	
UH – Humus soils with or without tree/shrub cover	Sample an area that includes a diversity of cover (shaded, partly shaded, open)
Animal matter	
AM – Dung or Bones	Sample on and around the animal matter
Rocks and Boulders *Note type of rocky area, and position of samples	
BC – Boulders (>50 cm diameter), cliffs, and ledges including crevices	Sample from all surfaces (top, sides, and around base) from the soil upwards
RR – Rocks (<50 cm diameter) tops, sides, and bases	Sample from the top, all sides, and around the base of the rocks

Table 3. 2 Mean alpha (α , Whittaker 1972) and total diversity of the 6 sites.

	mean α [0.25 ha quadrant]	Total site diversity [all surveys, 1 ha site]
Homogeneous stands		128
Pine OJ	37	58
Mixedwoods OM	49	75
Lowland bog BB	58	93
Heterogeneous stands		124
Pine OP	40	70
Mixedwoods OA	48	73
Lowland MB	60	87

Table 3. 3 Linear mixed-effect model comparisons of factors affecting species capture as measured by percent of total species richness. Maximal fixed factor parameterization included the following: $\log(\%total) \sim \log(area) * team * survey\ type * stand\ type$. All models included random factors for *site*. Model simplification stopped when all parameters had large effect sizes relative to their SE and removal of the smallest effect sizes reduced model fit.

	K	AICc	Δ AICc	Model Likelihood	AICc Weight	Log Likelihood
3. Area*stand type + survey type+ team	15	-186.34	0.00	1.00	0.89	111.17
2. Area*team*stand type + survey type	18	-181.28	5.06	0.08	0.07	113.08
4. Area*mixedwood* [bog+pine]+survey type+ team	11	-179.84	6.50	0.04	0.03	102.49
1. Maximal model	26	-173.01	13.34	0.00	0.00	122.68

Table 3. 4 Generalized linear mixed-effect model comparisons of factors affecting species detectability. Maximal fixed factor parameterization included the following: *moss/liverwort+ team+ survey type+ stand heterogeneity+ stand type+ standardized spp richness+ standardized microhabitat richness+ survey type:stand type+ survey type:stand homogeneity+ team:survey type*. All models included random factors for *site/quadrant*. The parameterization with the most support at a given level was used in subsequent levels.

	K	AICc	ΔAICc	Model Likelihood	AICc Weight	Log Likelihood
A. Random factor exploration using maximal fixed factor model						
A1. Random spp. intercepts & slopes by site	36	5278.84	0.00	1.00	1.00	-2603.13
A2. Random spp. intercepts & slopes by observer	18	5689.82	410.97	0.00	0.00	-2826.83
A3. Random spp. intercepts	16	5690.48	411.64	0.00	0.00	-2829.18
A4. Random spp. intercepts and slopes by survey type	18	5694.28	415.43	0.00	0.00	-2829.06
B. Interaction exploration using random intercepts and slopes for each species by site and maximal fixed factor parameterization						
B1. Survey results vary by stand type	34	5277.05	0.00	1.00	0.69	-2604.27
B2. Survey results vary by collector	35	5279.08	2.02	0.36	0.25	-2604.26
B3. Survey results vary by stand heterogeneity	33	5281.73	4.68	0.10	0.07	-2607.62
C. Fixed factor exploration using random intercepts and slopes for each species by site and interaction between survey results and stand type						
C1. Moss/liverwort+survey type+stand type+observer	31	5273.04	0.00	1.00	0.44	-2605.30
C2. No effect of microhabitat richness	33	5275.02	1.99	0.37	0.16	-2604.27
C3. No effect of stand heterogeneity	33	5275.08	2.04	0.36	0.16	-2604.30
C4. No effect of species richness	33	5276.34	3.30	0.19	0.08	-2604.93
C5. No effect of survey type	34	5277.05	4.02	0.13	0.06	-2604.27
C6. Maximal model	34	5277.05	4.02	0.13	0.06	-2604.27
C7. Moss & liverworts detected equally	33	5278.14	5.10	0.08	0.03	-2605.83
C8. No effect of observer	33	5346.99	73.95	0.00	0.00	-2640.25

Table 3. 5 Linear mixed-effect model comparisons of factors affecting efficiency of species capture, as indicated by the ratio of specimens collected to species richness at each time limited survey across 24 quadrants at 6 sites. Maximal model: *specimen:species~collector*surveytype+quadrant/site[random]*

	K	AICc	ΔAICc	Model Likelihood	AICc Weight	Log Likelihood
No interaction between Survey type & collector	6	70.42	0.00	1.00	0.76	-28.74
Maximal model	7	72.74	2.33	0.31	0.24	-28.73
No effect of Survey type	5	80.18	9.77	0.01	0.01	-34.76
No effect of collector	5	87.13	16.71	0.00	0.00	-38.23

Table 3. 6 Linear mixed-effect model comparisons of factors affecting laboratory processing time, as indicated by the number of hours required to sort composite collection bags and identify common species for each survey from 6 sites. Maximal model: *hours~collector+surveytype+cumulative hours experience+total specimens+site[random]*

	K	AICc	ΔAICc	Model Likelihood	AICc Weight	Log Likelihood
No effect of collector	6	110.94	0.00	1.00	0.64	-47.00
No effect of survey type	6	113.09	2.15	0.34	0.22	-48.07
Maximal model	7	114.42	3.47	0.18	0.11	-46.71
No effect of cumulative sorting experience	6	116.96	6.01	0.05	0.03	-50.01
No effect of number of specimens	6	127.30	16.36	0.00	0.00	-55.18

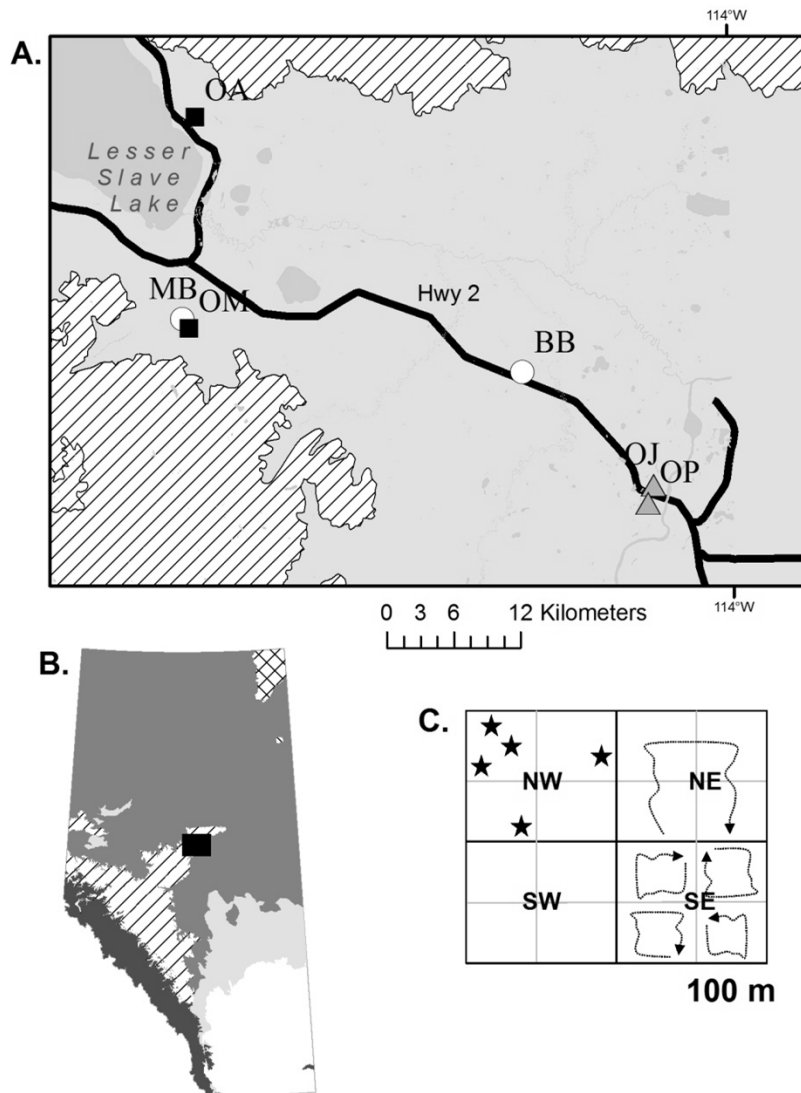


Figure 3.1 A. Map of the study area. Natural regions are represented by different shading (Natural Regions Committee 2006). Circles = bogs, triangles = pine stands, and black squares = mixedwoods. The corresponding letters are the site codes, used on subsequent figures. B. Extent of study area in Alberta, Canada, indicated by the black rectangle. C. Extent of coverage provided by each survey type within a 1ha site. Floristic time-limited sampling is illustrated in quadrant NW (collectors went directly to examples of microhabitats they perceived to be diverse), systematic time-limited sampling in NE (collectors were required to cover a predetermined transect but could deviate to visit diverse microhabitats encountered on either side), and floristic time-unlimited sampling in the SE (collectors covered each subquadrant systematically, collecting at each microhabitat encountered).

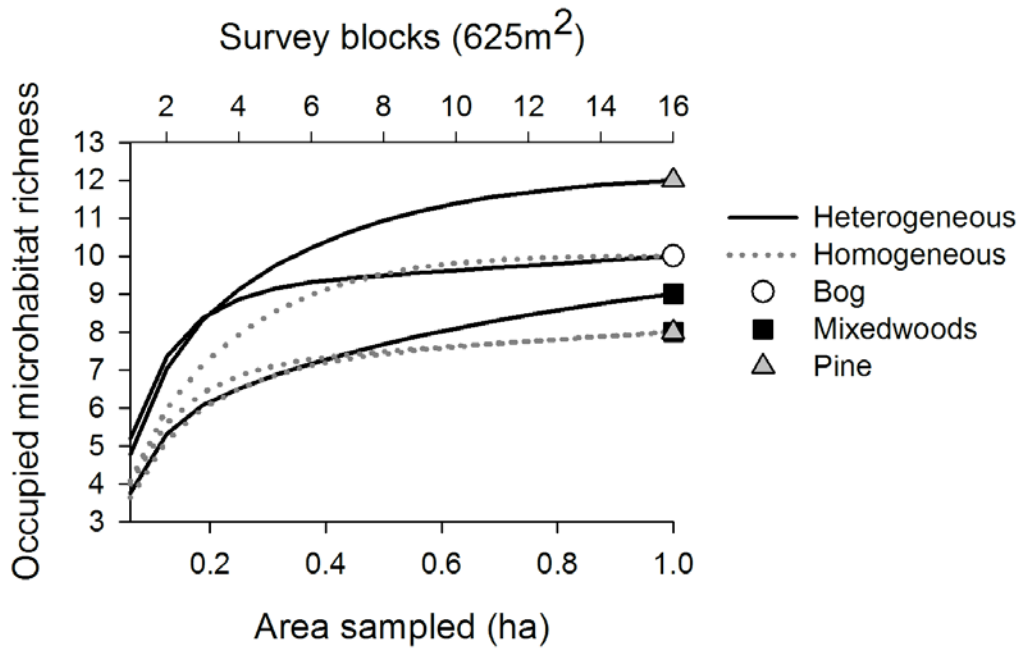


Figure 3. 2 Effect of plot size on occupied microhabitat diversity.

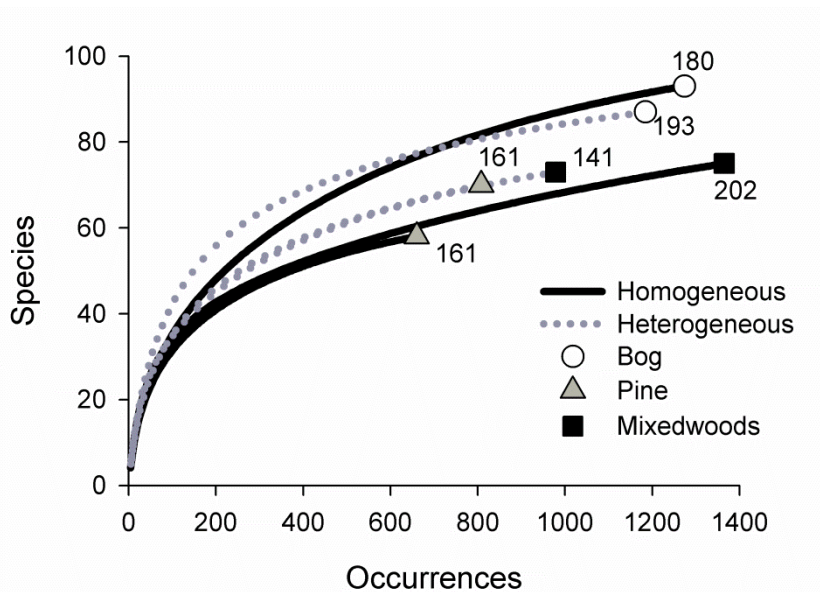


Figure 3. 3 Occurrence-based rarefactions for six 1ha forested sites. An occurrence is a recorded presence of a species in a collection bag. Sample units were collection bags from all surveys. β diversity was higher in heterogeneous stands (dashed grey lines) vs. homogenous stands (solid black lines), and in bogs (circles) vs. pine (grey triangles) and mixedwoods (black squares). The number of collection bags per site is indicated beside each site symbol.

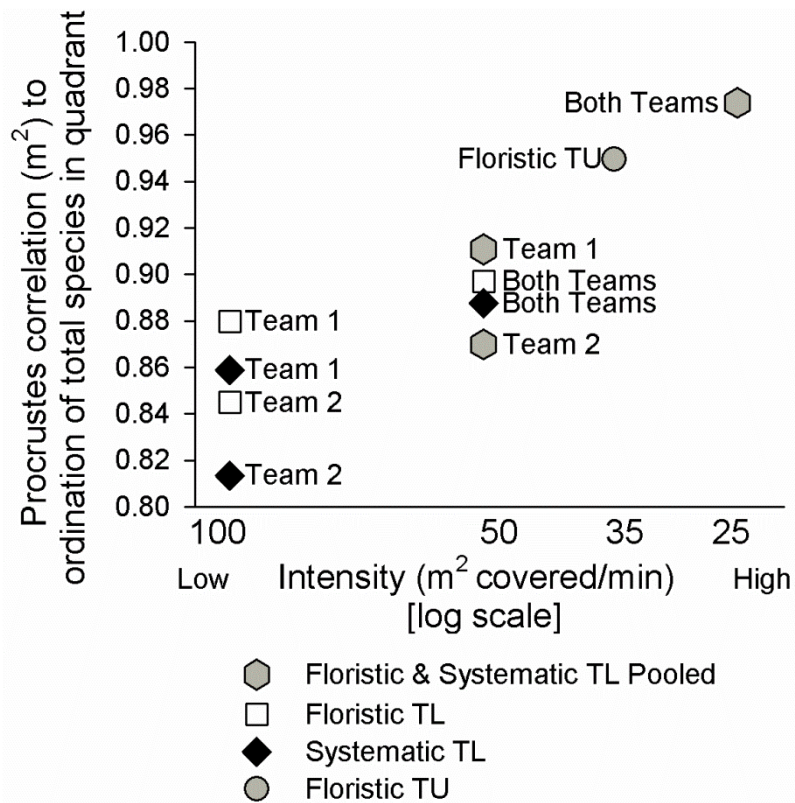


Figure 3. 4 Procrustes correlations to total species in quadrant for two survey types and two teams of observers, at various survey intensities. TL=Time limited, TU=Time unlimited. Floristic surveys were directed to diverse examples of each microhabitat present and involved more time packaging and recording substrate data. Systematic surveys were based on a standard transect and only microhabitat information was recorded.

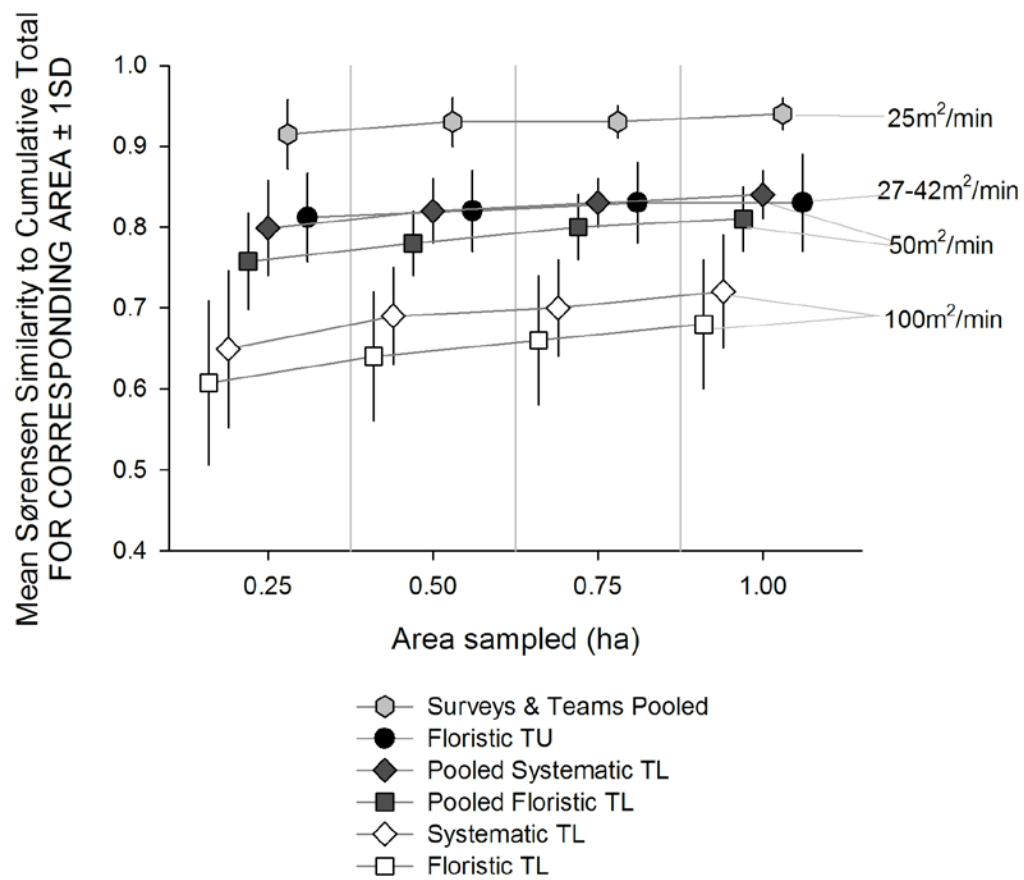


Figure 3. 5 Sørensen similarity between total species and samples of the total species pool across four scales and four survey intensities.

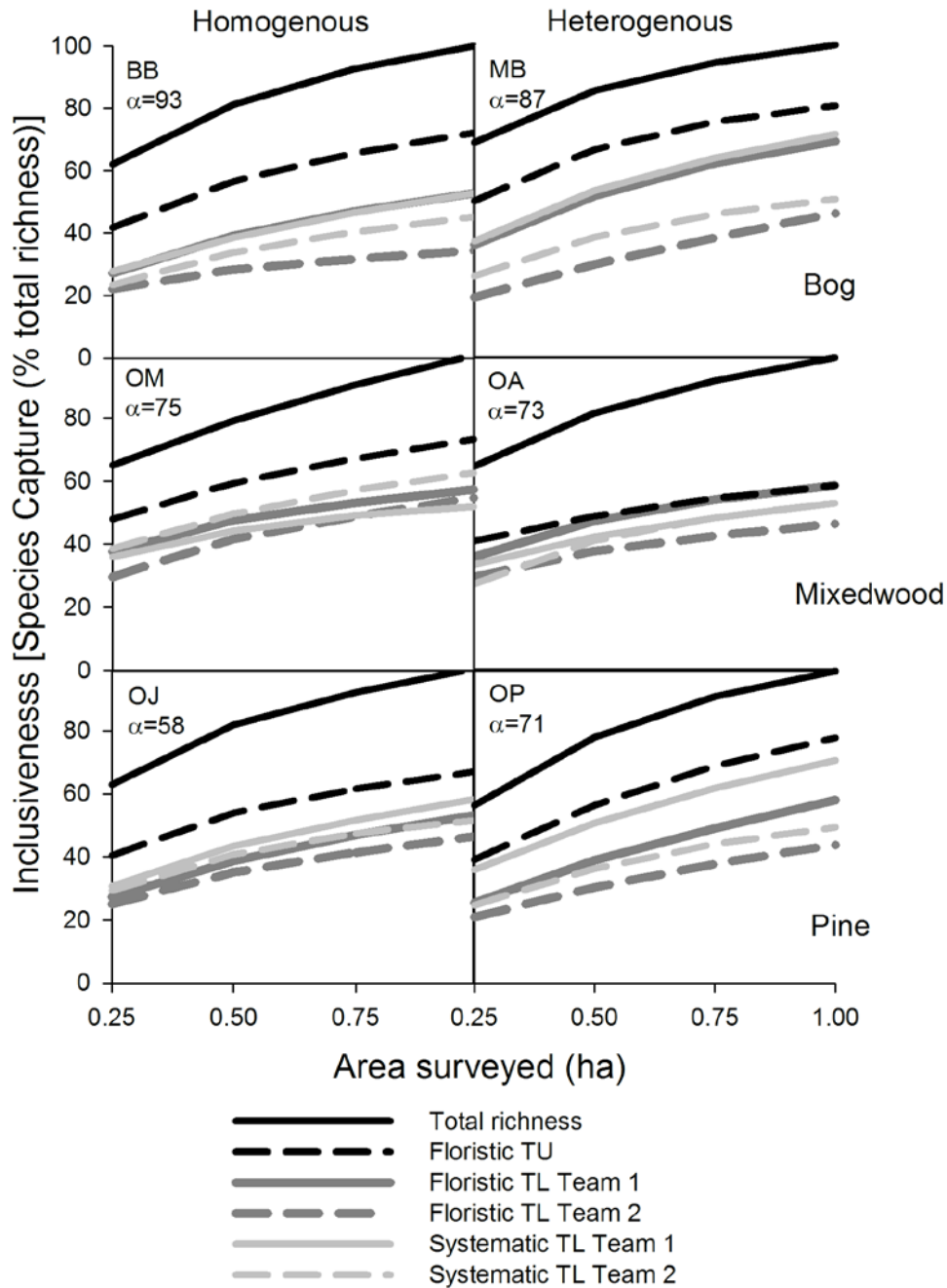


Figure 3. 6 Comparison of sample-based rarefactions for different surveys. Species capture was standardized to a % total species richness to enhance comparisons between sites. TL=time limited, TU=time unlimited. Floristic surveys were directed to diverse examples of each microhabitat present and involved more time packaging and recording substrate data. Systematic surveys were based on a standard transect and only microhabitat information was recorded. The site code and α diversity at each site are noted in the top left corner of each plot.

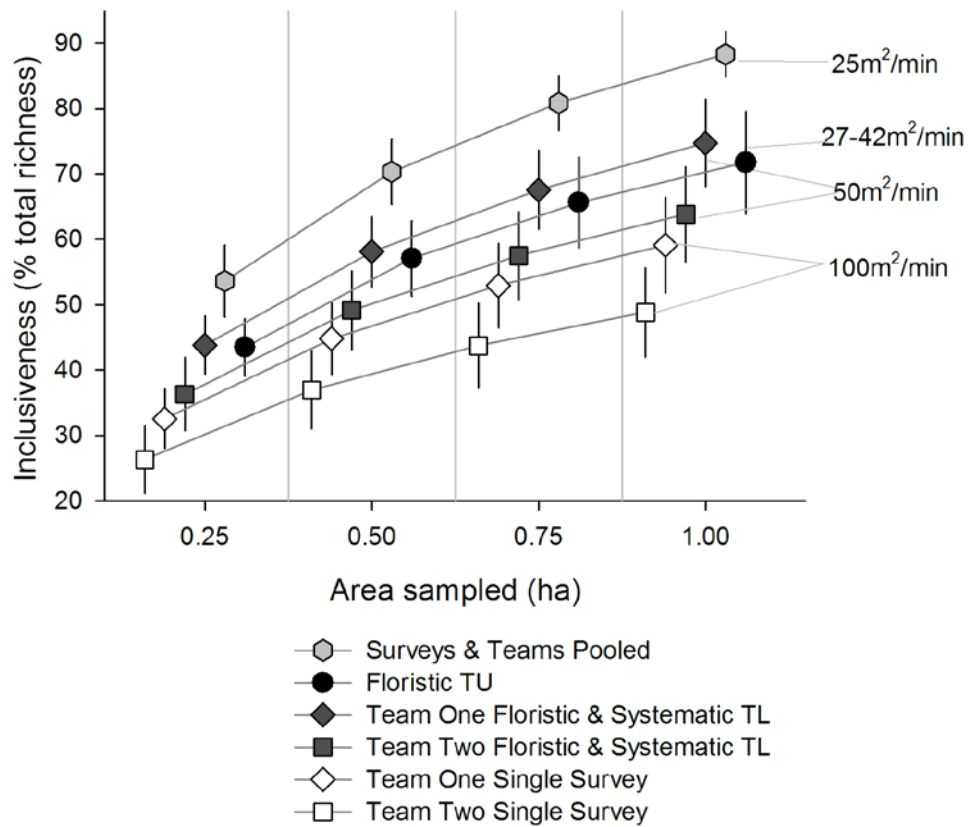


Figure 3. 7 Comparison of mean \pm 1SD sample-based rarefactions of species occurrence as captured by different survey intensities. Species capture was standardized to a % total species richness to enhance comparisons between sites. TL=time limited, TU=time unlimited. Single surveys n=12, all other curves n=6.

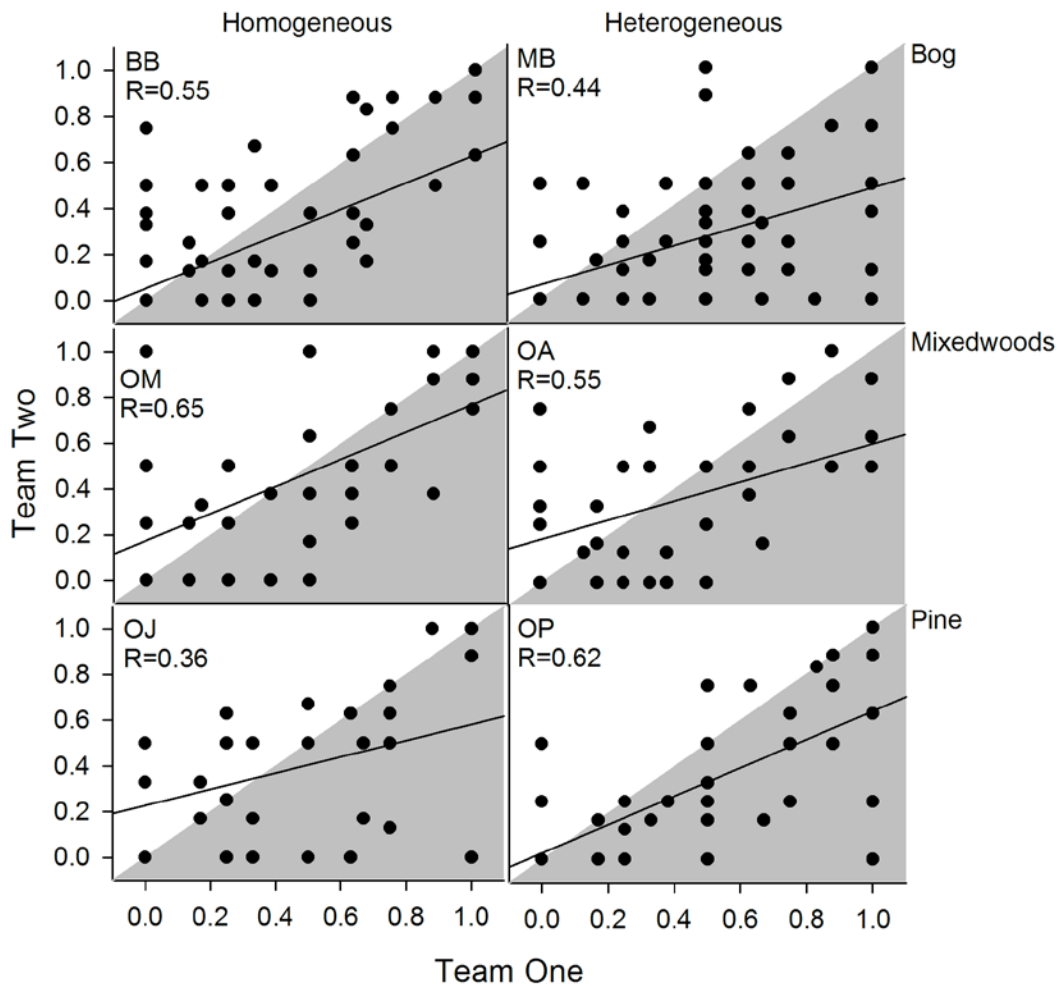


Figure 3. 8 Correlation between two collection teams' observed detection probabilities. Each data point represents the average detectability of a species across the four quadrants of the respective site. Detectability within each quadrant was calculated as the proportion of time-limited surveys a team collected the species. A detectability of 0 indicates the species was recorded during the time-unlimited survey, but not during any of the time-limited surveys.

Appendix 3.1 Methods for assessing the accuracy or representativeness of a sample to a more complete community dataset

Because assessing the accuracy of community data appears to be relatively uncommon and we encountered conflicting advice, here we compare the questions addressed by the breadth of analytical options.

Option 1 - Comparison of similarity in multidimensional space.

Multivariate Analysis of Variance (ANOVA) based on dissimilarity matrices permits comparisons of the mean dissimilarity between different levels of a factor (D_A) to the mean dissimilarity within each factor level (D_W). A robust implementation of this is available in the R library *vegan* (function *adonis*, analogous to an analysis of similarity); it uses sequential permutations to test the ratio of $D_A:D_W$. If we simplify our question to one factor with levels A and B, the question addressed by this method would be: are the similarities between samples of A consistently higher than the similarity between sample of A and B? A statistically significant result would therefore suggest that the cloud of samples of each level is distinguishable within the overall sample cloud. With regards to this study, it's critical to note that this compares the similarity of the samples, which are incomplete representations of what we estimate to be the true bryophyte community. A comparison of an ordination of the quadrant totals to an ordination of totals in combination with the surveys makes this difference clear (**Figure A3.1.1**).

Option 2 - Comparison of accuracy along a univariate gradient. Given a known environmental or sampling gradient of interest, an ordination can be constructed using a training dataset. If there is one parameter of particular interest, then the ordination axis correlated with your parameter of interest becomes a univariate gradient. The survey data can then be scored onto the training ordination space, and the accuracy of each survey along the gradient or axis of interest calculated using a version of McCune's accuracy equation

(McCune et al. 1997, McCune and Grace 2002):

$$Accuracy = 100 - \left| 100 \frac{survey\ score - total\ score}{gradient\ length} \right|$$

Gradient length is the distance between the minimum and maximum score along the axis of interest. Accuracy scores for each survey can then be arcsin square-root transformed and analysed in a traditional ANOVA to answer the question, are different survey types more accurate than others. If the experimental design is unbalanced or has multiple error strata, then a mixed effect model framework may be preferable.

As a variant of this approach, Pythagorean theorem can be used to calculate the difference between a test sample's predicted ordination score and a single corresponding training sample ordination score on multiple axes (McCune and Grace 2002). In this case the distance can't be standardized by a common denominator and instead the Euclidean distances themselves are analyzed in an ANOVA or mixed model framework. The only negative aspect of this approach is that the distances are not relative to the gradient length in the training dataset as in Option 2 which permitted an interpretation of the magnitude of any inaccuracies in comparison to the variability within the training dataset.

Option 3 - Comparison of training & test ordination. A second approach based on the same training ordination allows comparison of surveys to their total using Euclidean distance. In this case, an ordination is created for each total dataset and sample dataset. Pythagorean theorem is used to calculate interpoint distances within each dataset on the number of desired axes. Redundancy between the two matrices can be summarized and a Mantel test (Mantel 1967) used to assess the significance of the correlation between the two matrices of interpoint distances (McCune and Mefford 2011). Alternatively a Procrustes analysis can be used, and has shown to be more statistically powerful when matrix correlations are low (Peres-Neto and Jackson 2001). This approach is useful if accuracy alone is the principle concern, regardless of what environmental variable each ordination axis represents.

Option 4 - Comparison of similarity to *a priori* established samples.

Rather than relying on an ordination to summarize the dominant patterns of sites in multivariate space, the similarity between a survey and the corresponding total can be calculated directly. How the results of this option differ from Option 3 depend on the nature of the data, i.e., whether data are abundances or presence/absence, the collinearity between species, and the resultant reduction of the complexity of the dataset through ordination. In general, Option 3 better addresses the similarity of a subsample or survey to the total in terms of dominant patterns of community structure. Option 4 confounds the number of species captured by a survey from the total species pool (which we analyze as inclusiveness) with the accuracy in representing community structure, particularly when data are limited to occurrence.

When dissimilarity is the focus of the investigation, this is termed pseudoturnover (Lynch and Johnson 1974, Nilsson and Nilsson 1985). Pseudoturnover is the number of unpaired or unique species records in each survey divided by the sum of the total species detected by each survey. Numerically, pseudoturnover as calculated by Nilsson and Nilsson (1985) is equivalent to 1-Sørensen similarity for presence/absence data.

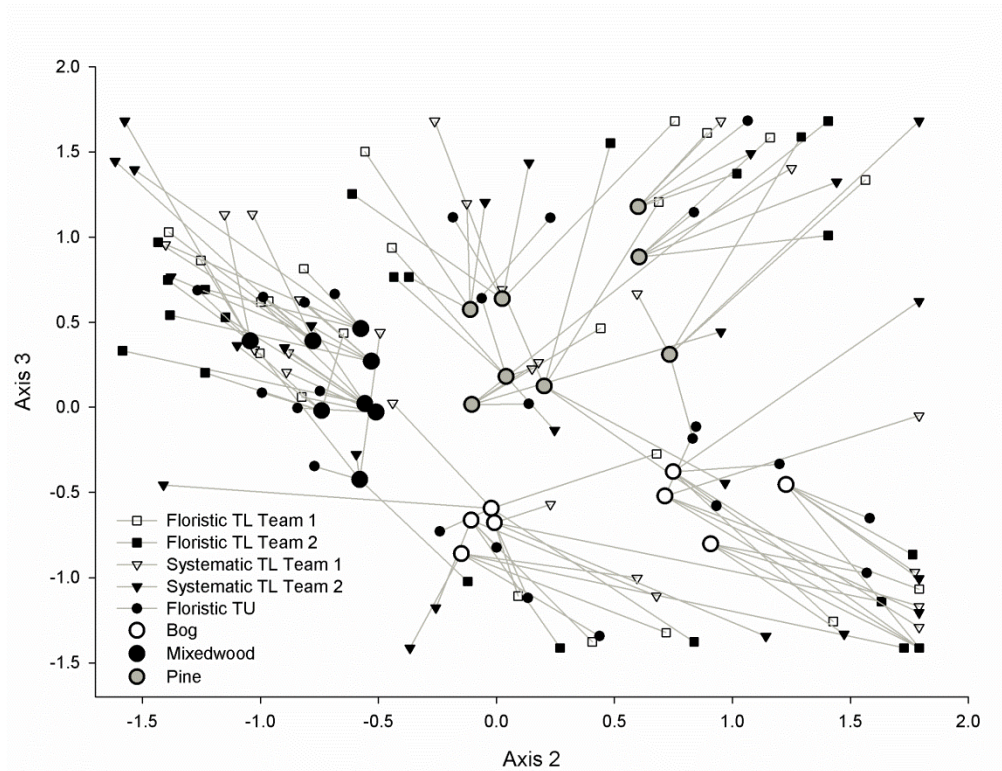


Figure A3.1. 1 Nonmetric multidimensional scaling of the total bryophyte community in each of the four quadrants of 6 1ha boreal forest stands (large circles, $n=24$). The best solution has three axes, and we show axes 2 and 3 here because they provided the clearest visual separation of the points. The best NMDS solution was used to predict the ordination scores of the 5 different surveys done in each quadrant ($n=120$). The grey lines connect each survey to their respective quadrant.

Appendix 3.2 Bryophyte occupancy and detectability by forest type for time-limited surveys.

Species detectability for each stand type is estimated as follows. Four time-limited surveys were conducted per quadrant per site. The numbers in the Quadrant columns indicate the number of TL surveys the species was recorded in. Zeros indicate that the species was detected in the time-unlimited survey for that quadrant, but not in any of the time-limited surveys. The mean detection is the average % of surveys a species was detected in ($\# \text{ detections}/4 \times 100$), first by site, and then by stand type. Species recorded in only 1 site by one team or during the time-unlimited survey are marked with an asterisk and a T1 (Team One), T2 (Team 2) or TU.

Table A3.2. 1 Percent of surveys that species were detected in as estimated by repeat sampling of two 1 ha bog sites near Lesser Slave Lake, Alberta. Letters after the stand heterogeneity correspond to the site names in Figure 3.1.

Species	Homogeneous-BB				Mean	Heterogeneous-MB				Mean	Bog	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
Liverworts												
1 <i>Anastrophyllum helleranum</i>	1				25	0				0	13	
2 <i>Barbilophozia attenuata</i> *TU		1		0	13						13	
3 <i>Blepharostoma trichophyllum</i>	1			0	13	1	0		1	17	15	
4 <i>Calypogeia muelleriana</i>	1	1	1		25		0			0	13	
5 <i>Calypogeia sphagnicola</i>	3	3	3	4	81	2	1		1	33	57	
6 <i>Cephalozia catenulata</i>		2		1	38	3	2		1	50	44	
7 <i>Cephalozia connivens</i>	3	4	1	3	69				1	25	47	
8 <i>Cephalozia loitlesbergeri</i>		1		1	25	1	1		1	25	25	
9 <i>Cephalozia lunulifolia</i> *TU		0			0						0	
10 <i>Cephalozia pleniceps</i>		1		2	38						38	
11 <i>Cephaloziella elachista</i>	1	2	2	3	50						50	
12 <i>Cephaloziella hampeana</i>	1	1	3	2	44		0		2	25	34	
13 <i>Cephaloziella rubella</i>	3	4	3	3	81	1	2		2	42	61	
14 <i>Cephaloziella subdentata</i>	2	2	0	1	31						31	
15 <i>Chiloscyphus pallescens</i>	1				25						25	
16 <i>Conocephalum conicum</i> *T1						1				25	25	
17 <i>Jamesoniella autumnalis</i>		1	1		25	1	1	2	1	31	28	

Species	Homogeneous-BB				Mean	Heterogeneous-MB				Mean	Bog	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
18 <i>Lepidozia reptans</i>	0			0	0	2	4	1	3	63	31	
19 <i>Lophocolea heterophylla</i>	1			1	25						25	
20 <i>Lophozia badensis</i>	1	2	1	1	31	1	2	0	2	31	31	
21 <i>Lophozia heterocolpos</i>		1		1	25				1	25	25	
22 <i>Lophozia obtusa</i> ^{*T1}			1		25						25	
23 <i>Lophozia ventricosa</i>	2	3	1		50	1	3	2	1	44	47	
24 <i>Marchantia polymorpha</i>	4	1		4	75	0	0			0	38	
25 <i>Mylia anomala</i>	2	1	2	2	44	0	0	0	1	6	25	
26 <i>Plagiochila asplenioides</i>				0	0	0	0	1		13	6	
27 <i>Pleuroclada albescens</i> ^{*T1}		1			25						25	
28 <i>Ptilidium ciliare</i>								1		25	25	
29 <i>Ptilidium pulcherrimum</i>	1	2	3		50	4	4	4	4	100	75	
30 <i>Scapania glaucocephala</i>		0		0	0	0		1		13	6	
31 <i>Scapania irrigua</i>				0	0						0	
32 <i>Scapania paludicola</i> ^{*TU}									0	0	0	
33 <i>Tritomaria exsectiformis</i> ^{*T1}	1				25						25	
Mosses												
1 <i>Amblystegium humile</i>		1			25				1	25	25	
2 <i>Amblystegium serpens</i>	1	0		0	8	2	2	1	1	38	23	
3 <i>Aulacomnium palustre</i>	4	4	4	4	100	4	4	1	4	81	91	
4 <i>Barbula convoluta</i>				0	0						0	
5 <i>Brachythecium campestre</i>	1				25	1	1	1	1	25	25	
6 <i>Brachythecium erythrorrhizon</i>						1	0	1	1	19	19	
7 <i>Brachythecium mildeanum</i>						1	2	0	0	19	19	
8 <i>Brachythecium nelsonii</i> ^{*TU}	0			0	0						0	
9 <i>Brachythecium plumosum</i>	1			1	25	1	0		1	17	21	
10 <i>Brachythecium salebrosum</i>				0	0	2	1	3	1	44	22	
11 <i>Brachythecium starkei</i>									2	50	50	
12 <i>Brachythecium velutinum</i>	0	0	1		8	2	1	2	3	50	29	
13 <i>Bryohaplocladium microphyllum</i>									0	0	0	
14 <i>Bryum pseudotriquetrum</i>	0	0	1		8						8	
15 <i>Bryum weigelii</i>	0				0				2	50	25	
16 <i>Calliargon cordifolium</i>									3	75	75	
17 <i>Calliargon giganteum</i> ^{*T2}									1	25	25	
18 <i>Campylium hispidulum</i>	0	1		1	17	1	1	1	2	31	24	
19 <i>Campylium radicale</i>	0			0	0						0	
20 <i>Campylium stellatum</i>				1	25						25	
21 <i>Catoscopium nigratum</i> ^{*T1}				1	25						25	
22 <i>Ceratodon purpureus</i>	4	4	4	4	100	3	2	2	2	56	78	
23 <i>Climacium dendroides</i>							1		3	50	50	

Species	Homogeneous-BB				Mean	Heterogeneous-MB				Mean	Bog	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
24 <i>Dicranum elongatum</i>								2	1	38	38	
25 <i>Dicranum flagellare</i>	1				25	3	2	2	2	56	41	
26 <i>Dicranum fragilifolium</i>						0	1	3	1	31	31	
27 <i>Dicranum fuscescens</i>								1		25	25	
28 <i>Dicranum montanum</i>		1	1	0	17	1	1	2	2	38	27	
29 <i>Dicranum polysetum</i>	2	1	2		42	4	2	2	3	69	55	
30 <i>Dicranum undulatum</i>	3	3	4	4	88	3	3	1	3	63	75	
31 <i>Ditrichum flexicaule</i>				1	25						25	
32 <i>Drepanocladus aduncus</i>	0		1	1	17		0		1	13	15	
33 <i>Entodon brevisetus</i>	1				25						25	
34 <i>Eurhynchium pulchellum</i>						2	1	3	1	44	44	
35 <i>Funaria hygrometrica</i> ^{*TU}							0			0	0	
36 <i>Hamatocaulis vernicosus</i>	1				25						25	
37 <i>Helodium blandowii</i>	3	1	1	2	44						44	
38 <i>Hylocomium splendens</i>	3	3	3	1	63	4	4	4	4	100	81	
39 <i>Hypnum cupressiforme</i>	1			1	25						25	
40 <i>Hypnum pratense</i>	1	0		0	8	1	2		1	33	21	
41 <i>Isopterygiopsis pulchella</i> ^{*T1}				1	25						25	
42 <i>Leptobryum pyriforme</i>	3	1	0	3	44	1	1			25	34	
43 <i>Mnium spinulosum</i>						1	1	1		25	25	
44 <i>Oncophorus wahlenbergii</i>	0	1	1	0	13			1		25	19	
45 <i>Orthotrichum obtusifolium</i>	1				25	2	4	3		75	50	
46 <i>Orthotrichum speciosum</i>						2	4	2	1	56	56	
47 <i>Plagiomnium cuspidatum</i>						1	1	2	1	31	31	
48 <i>Plagiomnium drummondii</i>	0		1		13		1	1		25	19	
49 <i>Plagiomnium ellipticum</i>						2	1	0	4	44	44	
50 <i>Plagiomnium medium</i>						1			1	25	25	
51 <i>Plagiothecium denticulatum</i>	0	1	1	1	19			1		25	22	
52 <i>Plagiothecium laetum</i>		1			25	1	0			13	19	
53 <i>Platydictya jungermannioides</i>	1	1	1	0	19						19	
54 <i>Platygyrium repens</i>						3	3	3	2	69	69	
55 <i>Pleurozium schreberi</i>	4	4	4	4	100	4	4	4	4	100	100	
56 <i>Pohlia cruda</i> ^{*TU}			0		0						0	
57 <i>Pohlia nutans</i>	4	4	4	4	100	4	4	3	3	88	94	
58 <i>Pohlia sphagnicola</i>	1	1		2	33	1				25	29	
59 <i>Polytrichum commune</i>							1	1		25	25	
60 <i>Polytrichum juniperinum</i>	0		1	1	17	2	0	2	1	31	24	
61 <i>Polytrichum strictum</i>	4	4	4	4	100	3	2	1	4	63	81	
62 <i>Ptilium crista-castrensis</i>	0	1	0	3	25	4	4	4	4	100	63	
63 <i>Pylaisiella polyantha</i>	0	0	0	0	0	2	1	2		42	21	

Species	Homogeneous-BB				Mean	Heterogeneous-MB				Mean	Bog	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
64 <i>Rhizomnium gracile</i>	1				25	1				1	25	25
65 <i>Rhizomnium pseudopunctatum</i>							2			2	50	50
66 <i>Sanionia uncinata</i>	3	3	3	3	75	3	4	3	4	4	88	81
67 <i>Sphagnum angustifolium</i>	4	4	4	4	100	2	1		1	33	67	
68 <i>Sphagnum capillifolium</i>	1	0	1		17	4	2	1	4	69	43	
69 <i>Sphagnum centrale</i>	1			1	25				1	25	25	
70 <i>Sphagnum fallax</i> *T1		1		1	25							25
71 <i>Sphagnum fuscum</i>	2	3	3	2	63	1	0		1	17	40	
72 <i>Sphagnum girgensohnii</i>	0	2	0	1	19	2		1	2	42	30	
73 <i>Sphagnum magellanicum</i>	4	4	4	3	94	2	1		1	33	64	
74 <i>Sphagnum rubellum</i> *TU	0		0		0							0
75 <i>Sphagnum russowii</i>				0	0	1	1			25	13	
76 <i>Sphagnum squarrosum</i>			1	0	13							13
77 <i>Sphagnum teres</i> *T1				1	25							25
78 <i>Sphagnum warnstorffii</i>	3	2	3	4	75	2	4	1	4	69	72	
79 <i>Sphagnum wulfianum</i>	1	0			13				0	0	6	
80 <i>Tetraphis pellucida</i>			1		25		1		1	25	25	
81 <i>Tetraplodon mnioides</i>							0	0	0	0	0	0
82 <i>Thuidium recognitum</i>						0	1		1	17	17	
83 <i>Tomentypnum nitens</i>	3	2	3	4	75	4	1		1	50	63	
84 <i>Warnstorfia exannulata</i> *TU		0			0							0
85 <i>Warnstorfia fluitans</i>			1	0	13							13

Table A3.2. 2 Percent of surveys that species were detected in as estimated by repeat sampling of two 1 ha pine sites near Lesser Slave Lake, Alberta. Letters after the stand heterogeneity correspond to the site names in Figure 3.1.

Species	Homogeneous-OJ				Mean	Heterogeneous-OP				Mean	Pine	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
Liverworts												
1 <i>Barbilophozia barbata</i> *TU			0		0							0
2 <i>Blepharostoma trichophyllum</i>				1	25		0		1	13	19	
3 <i>Cephaloziella elachista</i>			1	1	25			1		25	25	
4 <i>Cephaloziella hampeana</i>			0	1	25						25	
5 <i>Cephaloziella rubella</i>			1	1	25	3	3	0	2	50	38	
6 <i>Cephaloziella subdentata</i>			0	0	0				0	0	0	
7 <i>Chiloscyphus polyanthos</i>									1	25	25	
8 <i>Geocalyx graveolens</i>				0	0							0
9 <i>Jamesoniella autumnalis</i>		1	1		25			1	1	25	25	
10 <i>Lophozia badensis</i>					1	25		1	2	33	29	
11 <i>Lophozia ventricosa</i>							0			0	0	
12 <i>Marchantia polymorpha</i>								4		100	100	

Species	Homogeneous-OJ				Mean	Heterogeneous-OP				Mean	Pine	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
13 <i>Ptilidium ciliare</i>	1				25			0		0	13	
14 <i>Ptilidium pulcherrimum</i>	3	3	2	3	69	3	4	4	4	94	81	
Mosses												
1 <i>Abietinella abietina</i> ^{*T2}				1	25							25
2 <i>Amblystegium humile</i>			1		25							25
3 <i>Amblystegium serpens</i>	1	0	3	3	44	1	1	3	3	50	47	
4 <i>Aulacomnium palustre</i>	1			2	38		1	4	1	50	44	
5 <i>Brachythecium campestre</i>				1	25		1			25	25	
6 <i>Brachythecium erythrorrhizon</i>	1			1	25			1	1	25	25	
7 <i>Brachythecium mildeanum</i>								1		25	25	
8 <i>Brachythecium oedipodium</i> ^{*TU}				0	0							0
9 <i>Brachythecium plumosum</i>	0			1	13	1	2	2		42	27	
10 <i>Brachythecium salebrosum</i>	2	1	3	1	44	1	1	1	2	31	38	
11 <i>Brachythecium starkei</i>	1		1	1	25		1	2	1	33	29	
12 <i>Brachythecium velutinum</i>	2	2	1	2	44	1	3	0	4	50	47	
13 <i>Bryohaplocladium microphyllum</i>			1	3	50		0	1	0	8	29	
14 <i>Bryum pseudotriquetrum</i>	1	1	1	2	31			1		25	28	
15 <i>Campylium chrysophyllum</i>							0	1		13	13	
16 <i>Campylium hispidulum</i>	1		1		25	1		1		25	25	
17 <i>Campylium polygamum</i>							1			25	25	
18 <i>Campylium radicale</i>				1	25						25	
19 <i>Campylium stellatum</i>	1		1	0	17						17	
20 <i>Ceratodon purpureus</i>	4	3	4	4	94	2	4	4	3	81	88	
21 <i>Cinclidium stygium</i> ^{*T1}								1		25	25	
22 <i>Climacium dendroides</i>								1		25	25	
23 <i>Dicranum acutifolium</i>							0		1	13	13	
24 <i>Dicranum elongatum</i>		1			25	0	2		0	17	21	
25 <i>Dicranum flagellare</i>	2	2	0	0	25	3	4	3	4	88	56	
26 <i>Dicranum fuscescens</i>		1	1	1	25						25	
27 <i>Dicranum montanum</i>	2				50	0	3		2	42	46	
28 <i>Dicranum polysetum</i>	4	4	4	3	94	4	4	4	4	100	97	
29 <i>Dicranum scoparium</i> ^{*T1}	1	1		0	17						17	
30 <i>Dicranum spadiceum</i>						0	0		1	8	8	
31 <i>Dicranum undulatum</i>	1	3	2	1	44	3	3	3	2	69	56	
32 <i>Drepanocladus aduncus</i>				0	0			4	0	50	25	
33 <i>Eurhynchium pulchellum</i>	3		1	1	42		2	0	3	42	42	
34 <i>Hamatocaulis vernicosus</i>									1	25	25	
35 <i>Helodium blandowii</i>								2		50	50	
36 <i>Hylocomium splendens</i>	4	1	4	3	75	4	4	4	4	100	88	
37 <i>Hypnum cupressiforme</i>			1		25						25	
38 <i>Hypnum pallescens</i>	1	1	1		25						25	
39 <i>Hypnum pratense</i>								1		25	25	
40 <i>Leptobryum pyriforme</i>								1	1	25	25	
41 <i>Mnium spinulosum</i>	1	1		0	17		2		2	50	33	
42 <i>Oncophorus wahlenbergii</i>		1	1	0	17	2	0	1	0	19	18	
43 <i>Orthotrichum obtusifolium</i>	3	0		4	58				4	100	79	
44 <i>Orthotrichum speciosum</i>	3	0		4	58			2	3	63	60	
45 <i>Plagiomnium cuspidatum</i>	2				50		0		3	38	44	

Species	Homogeneous-OJ				Mean	Heterogeneous-OP				Mean	Pine	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
46 <i>Plagiomnium drummondii</i>	1			0	13			0		1	13	13
47 <i>Plagiomnium ellipticum</i>								4	1	63	63	
48 <i>Plagiothecium laetum</i>								0		0	0	
49 <i>Platydictya jungermannioides</i>	3	1		1	42			1	1	25	33	
50 <i>Platygyrium repens</i>	1			1	25	2	3	3	3	69	47	
51 <i>Pleurozium schreberi</i>	4	4	4	4	100	4	4	4	4	100	100	
52 <i>Pohlia nutans</i>	4	4	4	3	94	3	4	3	3	81	88	
53 <i>Polytrichum juniperinum</i>	4	4	4	3	94		3		2	63	78	
54 <i>Polytrichum piliferum</i>	1	3	4	2	63	4	3		3	83	73	
55 <i>Polytrichum strictum</i>							0	2	1	25	25	
56 <i>Ptilium crista-castrensis</i>	4	4	4	3	94	3	3	3	4	81	88	
57 <i>Pylaisiella polyantha</i>	3	0	4	3	63			2	3	63	63	
58 <i>Rhizomnium gracile</i>								1		25	25	
59 <i>Sanionia uncinata</i>	3	2	1	2	50	2	1	4	4	69	59	
60 <i>Sphagnum angustifolium</i>								0		0	0	
61 <i>Sphagnum capillifolium</i>								1		25	25	
62 <i>Sphagnum squarrosum</i>								0		0	0	
63 <i>Sphagnum warnstorffii</i>								0		0	0	
64 <i>Tayloria serrata</i> ^{*TU}								0		0	0	
65 <i>Tetraplodon angustatus</i>				1	25	1	2			38	31	
66 <i>Tetraplodon mnioides</i>				1	25						25	
67 <i>Thuidium recognitum</i>				0	0	0	2			25	13	
68 <i>Tomentypnum nitens</i>							0	4		50	50	
69 <i>Warnstorfia fluitans</i>							0		0	0	0	

Table A3.2. 3 Percent of surveys that species were detected in as estimated by repeat sampling of two 1 ha mixedwoods sites near Lesser Slave Lake, Alberta. Letters after the stand heterogeneity correspond to the site names in Figure 3.1.

Species	Homogeneous-OM				Mean	Heterogeneous-OA				Mean	Mix	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
Liverworts												
1 <i>Anastrophyllum helleranum</i>	1	4	1	1	44	1	1	1	1	25	34	
2 <i>Blepharostoma trichophyllum</i>	0				0	0	1	1	1	19	9	
3 <i>Calypogeia muelleriana</i>			0		0						0	
4 <i>Cephalozia catenulata</i>			0		0	1	3			50	25	
5 <i>Cephalozia connivens</i>	1		1		25						25	
6 <i>Cephalozia pleniceps</i>				0	0				0	0	0	
7 <i>Cephaloziella elachista</i>							1			25	25	
8 <i>Cephaloziella rubella</i>		1	1		25	0		1	1	17	21	
9 <i>Cephaloziella subdentata</i>						0	1			13	13	
10 <i>Chiloscyphus pallescens</i>	0				0		1			25	13	
11 <i>Chiloscyphus polyanthos</i>			1		25						25	
12 <i>Cladopodiella fluitans</i>							1			25	25	
13 <i>Geocalyx graveolens</i>						0		1		13	13	
14 <i>Jamesoniella autumnalis</i>	4	4	2	4	88	4	2	3	2	69	78	
15 <i>Lophocolea heterophylla</i>						1	1	1		25	25	

Species	Homogeneous-OM				Mean	Heterogeneous-OA				Mean	Mix	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
16 <i>Lophocolea minor</i> ^{*T2}							1			25		25
17 <i>Lophozia badensis</i>	2	4	1	2	56	2				50		53
18 <i>Lophozia heterocolpos</i>		0	1		13	3	2	1	2	50		31
19 <i>Lophozia ventricosa</i>		1			25							25
20 <i>Plagiochila asplenioides</i>	1		0		13							13
21 <i>Ptilidium pulcherrimum</i>	4	4	4	3	94	4	4	4	3	94		94
22 <i>Riccardia palmata</i> ^{*TU}			0		0							0
23 <i>Scapania glaucocephala</i>	1	1	0	1	19	2	0	2	4	50		34
24 <i>Scapania irrigua</i>						1				25		25
Mosses												
1 <i>Amblystegium humile</i>	1	2	1	2	38							38
2 <i>Amblystegium riparium</i>				0	1	13						13
3 <i>Amblystegium serpens</i>	4	4	4	3	94	4	4	3	4	94		94
4 <i>Aulacomnium palustre</i>		0	3	0	25	1	0			1		17
5 <i>Barbula convoluta</i>										1		25
6 <i>Brachythecium acuminatum</i> ^{*T2}				1	25							25
7 <i>Brachythecium albicans</i> ^{*T1}							1		1	25		25
8 <i>Brachythecium campestre</i>	3	2	1	3	56	1	1	1		25		41
9 <i>Brachythecium erythrorrhizon</i>	1	0	1	0	13	1	1	1	1	25		19
10 <i>Brachythecium mildeanum</i>							2	1		38		38
11 <i>Brachythecium plumosum</i>	1	2	3	0	38	2	1		3	50		44
12 <i>Brachythecium populeum</i> ^{*TU}							0	0		0		0
13 <i>Brachythecium reflexum</i> ^{*T1}								1		25		25
14 <i>Brachythecium rivulare</i> ^{*T2}			1		25							25
15 <i>Brachythecium salebrosum</i>	4	4	4	3	94	3	3	3	4	81		88
16 <i>Brachythecium starkei</i>	4	2	3	3	75	2	1		2	42		58
17 <i>Brachythecium turgidum</i> ^{*T2}						1	0		1	17		17
18 <i>Brachythecium velutinum</i>	4	2	4	4	88	3	4	4	4	94		91
19 <i>Bryohaplocladium microphyllum</i>	3	1	2	4	63	3	4	4	4	94		78
20 <i>Bryum pseudotriquetrum</i>									1	25		25
21 <i>Calliergon cordifolium</i>			0		0							0
22 <i>Campylium chrysophyllum</i>	1		2	1	33							33
23 <i>Campylium hispidulum</i>	3	4	3	2	75		2	3	1	50		63
24 <i>Campylium polygamum</i>			1		25			1	2	38		31
25 <i>Campylium radicale</i>						0				0		0
26 <i>Campylium stellatum</i>						1			1	25		25
27 <i>Ceratodon purpureus</i>	1	2	2	2	44	2	1	3	3	56		50
28 <i>Climacium dendroides</i>			3		75							75
29 <i>Dicranum acutifolium</i>				0	0							0
30 <i>Dicranum elongatum</i>				1	25							25
31 <i>Dicranum flagellare</i>	1	1	3	2	44	0		1	1	17		30
32 <i>Dicranum fragilifolium</i>	1	0	2		25							25
33 <i>Dicranum montanum</i>		1			25	1				25		25
34 <i>Dicranum polysetum</i>	2	2	3	1	50	1	0		0	8		29
35 <i>Dicranum undulatum</i>			1	1	25							25
36 <i>Ditrichum flexicaule</i>							1	1		25		25
37 <i>Drepanocladus aduncus</i>						1	1	1		25		25
38 <i>Entodon brevisetus</i>						1				25		25

Species	Homogeneous-OM				Mean	Heterogeneous-OA				Mean	Mix	Mean
	NE	SE	SW	NW		NE	SE	SW	NW			
39 <i>Eurhynchium pulchellum</i>	4	3	3	4	88	4	4	3	2	81		84
40 <i>Herzogiella turfacea</i> *T1							1	1		25		25
41 <i>Hylocomium splendens</i>	4	4	4	4	100	4	2	2	3	69		84
42 <i>Hypnum cupressiforme</i>									2	50		50
43 <i>Hypnum pratense</i>	0	1	2		25	1	0	0	1	13		19
44 <i>Leptobryum pyriforme</i>				1	25			1		25		25
45 <i>Leskea polycarpa</i> *TU						0				0		0
46 <i>Mnium spinulosum</i>	3	4	4	4	94	2			1	38		66
47 <i>Oncophorus wahlenbergii</i>	4	4	3	3	88	3	3	3	2	69		78
48 <i>Orthotrichum obtusifolium</i>	4	4	3	4	94	4	2	3	4	81		88
49 <i>Orthotrichum speciosum</i>	4	4	3	4	94	2	3	3	4	75		84
50 <i>Plagiomnium ciliare</i> *T1								1		25		25
51 <i>Plagiomnium cuspidatum</i>	4	4	4	4	100	4	4	3	4	94		97
52 <i>Plagiomnium drummondii</i>	4	4	3	3	88	4	4	3	4	94		91
53 <i>Plagiomnium ellipticum</i>			1		25							25
54 <i>Plagiomnium medium</i>	2	1	2	1	38			1		25		31
55 <i>Plagiothecium laetum</i>			1		25							25
56 <i>Platydictya jungermannioides</i>				1	25	2	2	1		42		33
57 <i>Platygyrium repens</i>	4	4	4	4	100	4	4	3	2	81		91
58 <i>Pleurozium schreberi</i>	4	4	4	2	88	4	2	3	2	69		78
59 <i>Pohlia nutans</i>	1	2	3	1	44	1	0	1	1	19		31
60 <i>Polytrichum juniperinum</i>	0	1	0	0	6	2			0	25		16
61 <i>Polytrichum strictum</i>			2		50		1			25		38
62 <i>Ptilium crista-castrensis</i>	4	3	4	4	94	4	4	2	3	81		88
63 <i>Pylaisiella polyantha</i>	3	3	2	2	63	4	4	3	4	94		78
64 <i>Rhizomnium gracile</i>				1	25							25
65 <i>Rhizomnium pseudopunctatum</i>							1			25		25
66 <i>Rhytidiadelphus triquetrus</i> *T2		1			25							25
67 <i>Sanionia uncinata</i>	4	4	4	4	100	3	4	4	4	94		97
68 <i>Sphagnum angustifolium</i>		0			0							0
69 <i>Sphagnum capillifolium</i>			1		25							25
70 <i>Sphagnum girgensohnii</i>			0		0							0
71 <i>Sphagnum squarrosum</i>			4		100							100
72 <i>Sphagnum warnstorffii</i>			1		25							25
73 <i>Tetraphis pellucida</i>	1	1	1	0	19	0				0		9
74 <i>Thuidium recognitum</i>			2	0	25	0	1	0	1	13		19
75 <i>Warnstorffia fluitans</i>				0	0			1		25		13

Appendix 3.3 Misidentification rates for 8 liverwort and 51 moss species identified at least once by the sorting technician

Using the accuracy rate per species and applying it to the number of unchecked specimens, we estimate the overall error due to misidentification to be 9.9% if we assume the error of our expert to be negligible. If we estimate our expert's error to be 5%, the overall misidentification error increases to 11.7%.

Table A3.3. 1 Accuracy was estimated using the vouchers checked by the expert, and then extrapolated to the unchecked specimens. Accuracy estimates greater than 75% are bolded and shaded; between 50 and 75% are italicized and lightly shaded; less than 50% normal font, no shading.

Species	# Specimens not checked/Vouchers checked	Accuracy (%) based on Vouchers	Estimated # Specimens Incorrect
Liverworts			
<i>Blepharostoma trichophyllum</i>	11/3	100	0
<i>Calypogeia sphagnicola</i>	0/1	0	0
<i>Geocalyx graveolens</i>	0/2	<i>50</i>	0
<i>Lepidozia reptans</i>	17/2	<i>50</i>	8.5
<i>Lophozia heterocolpos</i>	1/1	0	1
<i>Lophozia ventricosa</i>	0/1	100	0
<i>Marchantia polymorpha</i>	31/2	<i>50</i>	15.5
<i>Ptilidium pulcherrimum</i>	273/6	<i>67</i>	90.09
Mosses			
<i>Abietinella abietina</i>	0/1	100	0
<i>Amblystegium serpens</i>	99/3	<i>67</i>	32.67
<i>Aulacomnium palustre</i>	249/6	100	0
<i>Brachythecium salebrosum</i>	59/4	<i>50</i>	29.5
<i>Bryohaplocladium microphyllum</i>	69/5	100	0
<i>Bryum pseudotriquetrum</i>	10/1	100	0
<i>Campylium stellatum</i>	6/1	0	6
<i>Ceratodon purpureus</i>	253/6	100	0
<i>Climacium dendroides</i>	13/3	100	0
<i>Dicranum flagellare</i>	85/7	100	0
<i>Dicranum fragilifolium</i>	19/3	100	0
<i>Dicranum polysetum</i>	148/6	100	0
<i>Dicranum scoparium</i>	6/1	0	6
<i>Dicranum undulatum</i>	81/5	100	0

Species	# Specimens not checked/Vouchers checked	Accuracy (%) based on Vouchers	Estimated # Specimens Incorrect
<i>Drepanocladus aduncus</i>	10/5	40	6
<i>Eurhynchium pulchellum</i>	116/6	100	0
<i>Funaria hygrometrica</i>	0/1	100	0
<i>Helodium blandowii</i>	25/2	100	0
<i>Hylocomium splendens</i>	241/6	100	0
<i>Hypnum pratense</i>	17/1	100	0
<i>Leptobryum pyriforme</i>	28/4	75	7
<i>Mnium spinulosum</i>	48/7	100	0
<i>Oncophorus wahlenbergii</i>	67/6	100	0
<i>Orthotrichum obtusifolium</i>	120/8	88	14.4
<i>Orthotrichum speciosum</i>	125/5	100	0
<i>Plagiomnium cuspidatum</i>	195/6	83	33.15
<i>Plagiomnium drummondii</i>	99/4	100	0
<i>Plagiomnium ellipticum</i>	30/2	50	15
<i>Plagiomnium medium</i>	12/2	50	6
<i>Plagiothecium denticulatum</i>	5/1	100	0
<i>Platygyrium repens</i>	193/12	58	81.06
<i>Pleurozium schreberi</i>	463/9	89	50.93
<i>Pohlia nutans</i>	323/14	69	100.13
<i>Polytrichum juniperinum</i>	66/1	100	0
<i>Polytrichum piliferum</i>	41/1	100	0
<i>Polytrichum strictum</i>	115/4	100	0
<i>Ptilium crista-castrensis</i>	207/7	100	0
<i>Pylaisiella polyantha</i>	112/7	71	32.48
<i>Rhizomnium pseudopunctatum</i>	3/1	100	0
<i>Rhytidiadelphus triquetrus</i>	0/1	100	0
<i>Sanionia uncinata</i>	287/10	90	28.7
<i>Sphagnum angustifolium</i>	51/4	50	25.5
<i>Sphagnum fuscum</i>	13/1	100	0
<i>Sphagnum magellanicum</i>	46/2	50	23
<i>Sphagnum squarrosum</i>	4/3	100	0
<i>Sphagnum warnstorffii</i>	42/5	20	33.6
<i>Tetraphis pellucida</i>	4/5	100	0
<i>Tetraplodon angustatus</i>	1/2	100	0
<i>Tetraplodon mnioides</i>	2/2	100	0
<i>Thuidium recognitum</i>	12/5	100	0
<i>Tomentypnum nitens</i>	54/4	100	0

CHAPTER FOUR

Parataxonomists can conquer the taxonomic impediment of routine identification with experience and quality control: a macrolichen case study

Introduction

'[. . .] ecologists are often ill informed of both the value and the problems of systematics. That is true even though ecologists have long been parasitic on taxonomists' (Ehrlich 1997, p. 23).

The taxonomic impediment (Tayler 1983, New 1984) refers to the dearth of money and expertise for the "discrimination, description, and identification" of specimens (Weeks and Gaston 1997), and continues to present a paradox for biologists and managers. While demand for biodiversity research and monitoring continues to increase, funding and personnel to tackle the resulting taxonomic workload are increasingly difficult to secure (e.g., Lindenmayer 1999, Packer et al. 2009). The issue is particularly relevant for lesser-known taxa such as invertebrates, bryophytes, fungi, and lichens. These taxa compose a significant proportion of Earth's biodiversity, yet most are diminutive, cryptic and often difficult to develop expertise in. Because many species cannot be identified in the field, specimens are instead collected for later identification *en masse* in the laboratory (de Carvalho et al. 2005, de Carvalho et al. 2007). The bulk of the specimens collected (which can number in the tens of thousands) often represent common species. When species-level identifications are required, already over-worked taxonomists can be impeded by having to repeatedly make these 'routine' identifications (Gaston and O'Neill 2004). While technology may tackle this impediment in the future (e.g., automated identification, Gaston and O'Neill 2004, Newmaster 2009), a solution that can be implemented immediately is the use of novice parataxonomists, sometimes termed parataxonomists (Janzen 1991), to process specimens and identify common species.

'Parataxonomist' has been used to describe a range of positions from volunteers to part-time field parataxonomists to career collectors from diverse

backgrounds working full-time. Parataxonomists and apprentices as originally described (chosen from a larger cohort for their potential, provided training, given collection and sorting responsibilities, and part of a larger team that includes specialists) are proving invaluable in Costa Rica (Janzen 1991), Papua New Guinea, Guyana (Basset et al. 2000), and India (Steven Newmaster, University of Guelph, personal communication). However, there are legitimate concerns about lack of consistency between parataxonomists, high overlooking rates (defined as the failure to discriminate among similar-looking taxa or to recognize and record a species presence), and high misidentification rates relative to a specialist (Krell 2004, Ahrends et al. 2011). For a long-term, large-scale biodiversity monitoring program, these concerns are amplified by the number of specimens, turnover in personnel, and the need for temporal consistency in the quality of taxonomy.

We think at least part of these concerns arise from a failure to differentiate **parataxonomists** (a vocation) from **parataxonomy** (sorting of specimens without regard for traditional taxonomy, variously termed 'Recognizable Taxonomic Units' (RTUs, Oliver and Beattie 1993), 'morphospecies', 'Operational Taxonomic Units' (Sokal and Rohlf 1970) or as we shall use from here on in, 'Parataxonomic Units' or PUs (Krell 2004). PUs can be useful when community characterization is the goal (sensu Colwell and Coddington 1994, Longino and Colwell 1997), however, many studies want to record more than richness or morphospecies abundance distribution (Krell 2004, Lamb et al. 2009). To assess the status and trends of biological species, compare species trends with other jurisdictions, and contribute autoecological knowledge, monitoring programs benefit from traditional taxonomy and strict inventory (Longino and Colwell 1997).

Most studies examining the accuracy or feasibility of using PUs actually examined the efficacy of **parataxonomy**, where 'intelligent ignoramuses' (after Sokal and Rohlf 1970, i.e., intelligent individuals with little experience in taxonomy) are the only individuals engaged in source of sorting and identification to PUs, and PUs are the base unit for further analyses. The most common measure of efficacy is the congruence between PU richness and species richness or some other measure of community structure (Krell 2004 and references

within). Most studies of parataxonomy have dealt with invertebrates (but see Oliver and Beattie 1993, [bryophytes in part], Abadie 2008 [vascular plants], and Giordani et al. 2009, [lichens]). The success of parataxonomists as Janzen envisioned (Janzen 1991, Janzen 2004), conducting traditional taxonomy as part of a larger team that includes specialists, has apparently not been examined (Basset et al. 2000).

Questions

Here we address the following questions using data from three years of work with parataxonomists responsible for identifying macrolichens: How accurate are parataxonomists when applying traditional taxonomy? Are there particular macrolichens that are problematic for parataxonomists, and what traits do these species share? What is the magnitude of the variation in error rate and rate of improvement between parataxonomists? Do all parataxonomists improve at approximately the same rate, or is there a correlation between an individual's initial error rate and rate of improvement (e.g., Hinze et al. 2009)? In addition, we investigated the effects of proximal factors (e.g., days or years of experience, day of the week, volume of sorting accomplished) and gender, as these factors are common to any study employing parataxonomists and the magnitude of their effect can be used to direct quality control.

Methods

Field methods

We briefly summarize the field methods to illustrate the nature of the samples parataxonomists worked on in the laboratory. Lichen sampling was conducted as part of a larger set of terrestrial biodiversity monitoring protocols conducted by the Alberta Biodiversity Monitoring Institute (ABMI, Chapter One, www.abmi.ca). The foundation of ABMI's monitoring is a systematic 20 x 20 km grid of 1,656 1 ha sites located across the province of Alberta. Specimens were collected only after a survey of the potential lichen microhabitats (**Table 4.1**) at the site. Working from a predetermined and prioritized list of microhabitats, one

parataxonomist documented the availability of each microhabitat within each of the four 0.25 ha quadrants of the 1 ha plot. The parataxonomist also mapped species-rich examples of each microhabitat as they were encountered while completing other field protocols such as tree measurements and vascular plant surveys.

Prior to 2009, the parataxonomist then spent between 90 and 120 minutes searching for and collecting specimens from up to 6 examples of each microhabitat present at the 1 ha site. At each microhabitat example searched, the parataxonomist collected examples of all specimens that appeared unique into one brown paper collection bag. If multiple examples of a microhabitat (e.g., conifer trees) were within a 10m radius, the parataxonomist searched those as well, adding unique samples to the same collection bag. From 2009 onwards, four 25 x 15 m plots (0.15 ha total) within the 1 ha site were surveyed separately to increase the effort per unit area and the repeatability of surveys (Chapter One, **Figure 1.2**). One parataxonomist spent up to 35 minutes in each of the four plots (maximum total 140 minutes) collecting specimens from different microhabitat strata. Species-rich strata (downed woody material, trees and other vertical structures and rocks) were searched within the plot: less diverse strata (soils and lowland substrates) were searched in 50 x 2m belt transect along two sides of the quadrant. Specimens were placed in one composite brown collection bag per stratum per quadrat (20 bags per site). Specimens were dried and shipped to the Royal Alberta Museum, Edmonton, Alberta Canada for cataloguing and sorting.

Laboratory and quality control methods

From 2007 to 2010, all collections were sorted during the month of August, by groups of parataxonomists working side by side with a more experienced supervisor. Here we provide a brief overview of that training; more details are available online (<http://www.abmi.ca/abmi/reports/reports.jsp?categoryId=0&subcategoryId=63>). Parataxonomists were trained and tested on procedures and identification for five days. If additional training was necessary it was provided for up to an additional five days. This training built on field and laboratory training that had occurred prior to the field season. Parataxonomists

that continued to struggle to efficiently reach quality control targets (see below) were reassigned to other non-taxonomic tasks. Species that are both common and relatively easy to identify were identified to species by the parataxonomists: these species typically account for 40-60% of lichens specimens collected at a site (**Figure 4.1, 4.2**). Other specimens were isolated, identified to genus where possible and sent to experts for species-level identification. Any specimens that could be identified to species were made into reference specimens and placed in envelopes for curation at a later date. Once good quality reference specimens had been collected, additional examples of this species from other collections at the site were identified and recorded but were not put into envelopes for curation. Instead, after being recorded, these 'duplicates' were returned to the collection bag as residual material. Specimens that could not be identified to species were identified to genus or subgenus and were sorted into envelopes for identification by experts.

Parataxonomists were supervised by someone that had a) a minimum of one year of experience collecting and identifying macrolichens, b) trained under a more experienced taxonomist or specialist, and c) passed a test in the laboratory administered by a more experienced lichenologist. Parataxonomists were expected to process the collections from 13-18 sites during their month in the laboratory. The lab supervisor verified the reference specimens from every site, all genus or morphological-level identifications from the first two sites sorted, and from five collection bags from every fifth site sorted by a parataxonomist thereafter. In addition, they checked all the residuals from the first two sites and from five collection bags from every fifth site to ensure that species were not overlooked and duplicates in residual material bags were not misidentified. Where necessary, for each species for each parataxonomist, the supervisor continued to verify species-level identifications until five consecutive correct identifications were made. This addressed easily identified yet localized species that the parataxonomists were responsible for identifying but which may not occur with regularity across all sites and thus may not be addressed in the bulk of the quality control. Parataxonomists were expected to achieve $\geq 95\%$ accuracy for

identified species and record $\geq 80\%$ of the species in each sample bag (either to species or to genus for later identification by experts). Importantly, a lab supervisor was present every day that sorting occurred to conduct both quality control and to serve as a source of encouragement and expertise for the parataxonomists.

Explanatory factors and statistical methods

Errors recorded during quality control were coded as erroneous identification (for both species- or genus-level identifications), overlooked species, or processing error (e.g., correctly identifying a species but forgetting to record it in the database). Specimens that underwent quality control were treated as binomial trials, with 1 representing an error. Our data were observational and non-orthogonal; not all parataxonomists were followed in all years as not all parataxonomists were employed in every year.

To test these hypotheses while taking into account the variation caused by repeated measures on each parataxonomist, we used the program R (R Development Core Team 2011, version 2.12.2) to generate generalized linear mixed-effects model with a binomial family and a logit link. We used the lmer function from the lme4 R package (Bates et al. 2011) with Laplace approximation and treatment contrasts. For all models, model construction started with the maximal model, containing all possible random and fixed factors of interest. Models with different random factor formulation were examined first, holding the fixed factors constant, followed by model comparison for the fixed factors using the random factor formulation with the most support. Corrected Akaike Information Criterion (AIC_c) was used to compare models following Burnham and Anderson (2002). Prior to analyses, variables were checked for collinearity using variance inflation factors (VIFs, Quinn and Keough 2002) and R code described in Zuur et al. (2009): all VIFs were below 2, which is considered the most stringent cutoff in identifying potentially ecological-effect obscuring collinearity. Apparent outliers were identified using the methods of Zuur et al. (2009), checked for accuracy, and when accurate, kept in the dataset.

Errors were modeled as daily errors (all trials conducted on a given day were analyzed together). We conducted the modeling on all errors regardless of error type.

Daily Errors

Each parataxonomist's errors were summed for each day in their regular work week and analyzed as the number of errors (numerator) over the number of quality control trials (denominator): this allowed the number of trials to accurately weight the binomial models (Crawley 2007). Four fixed factors were explored. First, experience was quantified as cumulative consecutive weekdays of experience. Unless a parataxonomist had relevant experience at the beginning of their first year with ABMI, experience started at 1 on the first day of training and incremented by 1 for each additional day of experience. For parataxonomists that returned in multiple years, experience each year started accumulating again from experience gained the previous year. Second, the total number of specimens sorted and/or identified in a day was tallied to investigate whether more errors were made when the rate of sorting accelerated. Third, day of the week was investigated. Research in other fields have found accuracy to be affected by day of the week (Elsheikh et al. 2010), and understanding this pattern could focus quality control and training. Fourth, we looked for cohort effects by including the standard deviation in experience level amongst the parataxonomists each year. To explore possible curvilinear relationships of error rate with experience and day of the week, we constructed orthogonal polynomials using the `poly` function in R. We estimated the degree of polynomial to construct based on exploratory analyses using generalized additive models (`gam` function) in the R package `mgcv` (Wood 2011). Orthogonal polynomials allow better estimation of regression coefficients because they are not collinear with each other (Kennedy and Gentle 1980).

We included parataxonomist as a random factor and our maximal model included correlated random intercepts and slopes for each random factor level. We did not include year as a random factor because our data were limited to 3 factor levels (Bolker et al. 2009 recommend random factors have at least 5-6

levels for proper estimation of variation between levels) and it was collinear with cohort effect

Gender

The selectivity model of information processing (Meyers-Levy 1989, Meyers-Levy and Maheswaran 1991) postulates that women pay more attention to subtle clues, are more detail-oriented, and are less likely to overlook information that contradicts their original conclusion. This hypothesis has been supported by experiments in fields such as accounting (Chung and Monroe 1998) and advertising (Darley and Smith 1995) therefore we hypothesized that women would be slower but more accurate parataxonomists. Because returning parataxonomists were largely female, gender was not included in the daily error rate modeling. Instead, generalized linear mixed-effects models examining the data subset for days of experience ranging from 1 to 17 were run, with or without the addition of a gender fixed factor.

Cost-benefit analysis

We estimated the benefits of doing quality control by estimating our statistical power to detect a -3% annual trend in species occurrence over two 5-year monitoring cycles (10 years total), monitoring 5 sites from a panel of 25 sites per year, using the β estimates in Chapter Five (Nielsen et al. 2009). We chose a small number of sites and a short time period as statistical power is generally low for this scenario, and therefore the most gains can be made. We first estimated power using the prevalence and detectability estimates calculated using the same methods and datasets as Nielsen et al. (2009), which were available for 20 of the 23 species parataxonomists were responsible for. To estimate the increase in power as a result of quality control, we interpreted the change in error rate in the laboratory as an increase in detectability. For each species we calculated the improved detectability as follows: original probability of detection from field work and unsupervised identification + (post-quality control error probability - original error probability). We then predicted statistical power with the new detectability values while holding all other parameters constant.

Taxonomy and curation

Following the suggestions of Bortolus (2008), here we provide information on the specialists and taxonomic resources involved in this project. Lichenologist Janet Marsh (e.g., Marsh 1996), provided an initial list of Alberta-dwelling species she thought were both common and distinct enough to be identified by a non-specialist. This list was refined based on experience with parataxonomists in the lab (see **Table 4.2** for final list). For these species, a list of definitive traits (Goward et al. 1994, Goward et al. 1995, Goward 1999, Brodo et al. 2001), similar species and their distinguishing features, along with photographs and illustrations (illustrations were reproduced with permission from Goward et al. 1994, Goward 1999) showing key features were compiled by the senior author (available in pdf format upon request to the senior author). This document underwent substantial revision by the senior author and was reviewed by Janet Marsh (contractor) and Trevor Goward (Curator of Lichens, University of British Columbia and Enlichened Consulting) prior to the 2008 field season, and continues to be revised annually to reflect small changes in protocols and taxonomy.

Nomenclature follows Esslinger (2010). Specimens pertaining to the data analyzed here are either identified (2008; identified by Janet Marsh) or currently are undergoing expert identification (2009-2010, by the senior author). Specimens are being curated and will be deposited in a special collection in the PMAE herbarium at the Royal Alberta Museum, Edmonton, Alberta, Canada. ABMI data (lichen and otherwise) from the prototype (2003-2006) and first two years of data collection (2007-2008) are available at www.abmi.ca. Each record in the raw data file indicates the determiner in the columns entitled "Identification Analyst" and "Advanced Identification by". The two specialists are indicated as follows: Janet Marsh by either "J. Marsh" or the initials "JM", and Jim Case by the initials "JC" (Case Biomanagement Consulting). All other initials in these columns are those of parataxonomists.

Results

From 2008 to 2010, we tracked error rates for 17 parataxonomists (largely undergraduate students) over three summers; experience level ranged from one to five summers (hereafter referred to as years) of field collection and laboratory sorting of lichens, mostly with the ABMI (we accounted for prior experience by giving equivalent 'credits' when calculating a parataxonomist's experience). We truncated our analysis to 45 days of experience or less, as there was only one parataxonomist with more experience. The minimum amount of experience was a complete month (i.e., 17-18 sorting days). Three parataxonomists were removed from the analyses: two were high school volunteers who spent 5 days in the lab, and the third was a field supervisor who only conducted lab sorting sporadically. All parataxonomists were new in 2008 (all values hereafter are means \pm 1 SD), while in 2009 there were equal numbers of new and returning parataxonomists (1.7 ± 0.7 years experience). In 2010, 75% of parataxonomists had 2-4 years of experience (2.2 ± 1.1 years experience). In total, we analyzed 273 parataxonomist days of quality control for 14 individuals, spread approximately equally between the three years of data collection (2008-2010). On average, there were 25 ± 14 quality control trials for each parataxonomist that underwent quality control on any given day, and parataxonomists on average underwent quality control during $96\pm 4\%$ of their workdays.

Over the three Augusts, conservatively 22,247 specimens were sorted and identified to species or genus/PU by the parataxonomists. Parataxonomists identified 38% of these specimens to species (8,524 specimens). The overall average error rate was 9.2% (8,558 trials, 787 errors- and genus/PU-level errors for all 17 parataxonomists).

Twenty-three species were routinely identified by parataxonomists (**Table 4.2, Figure 4.1, 4.2**). Nine of those species usually were only identified by more experienced individuals and are here-after referred to as difficult species. Initial error rates provide an estimate of the error rates that would exist if supervisors did not conduct formal quality control or correct discovered errors, but were present to answer questions and to train. These error rates averaged $8.8\pm 8.2\%$. The most

common type of error was overlooking or detection error (66% of all errors), followed by misidentification (29% of all errors) and processing errors such as forgetting to record a specimen packet (5% of all errors). After we removed the errors corrected by quality control, we extrapolated the overall error rates to the specimens that had not undergone quality control (Error %, **Table 4.2**), and then again using species-specific error rates for each parataxonomist (Error% IW [Individually Weighted], **Table 4.2**).

If we disregard the differences between individual parataxonomists, and assume that error rates are constant, we estimate that $4.0 \pm 3.4\%$ of the specimens identified to species by parataxonomists are incorrectly identified. If we consider each species and parataxonomist individually, that rate further decreases to $2.5 \pm 3.4\%$. When accounting for individual parataxonomists, all 14 species identified by all parataxonomists and 7 of the 9 difficult species meet the ABMI's $\geq 95\%$ accuracy goal.

When examining species that have higher error rates, one pattern is readily apparent: parataxonomists struggled to differentiate the small, pale, appressed foliose lichens. We observed that parataxonomists struggled to differentiate soredia (vegetative propagules consisting of fungal hyphae and algal cells) and isidia (corticate vegetative propagules formed from outgrowths of the thallus) in the lab, contributing to the error rates in discriminating the sorediate *Parmeliopsis* and isidiate *Imshaugia* species (**Figure 4.2**).

If individuals vary in their natural ability to identify lichens, we hypothesized that individuals with low initial error rates would also improve the most quickly. When examining the cumulative daily error rate, the model with the greatest support had random intercepts and slopes for each of the 14 parataxonomists (**Table 4.3 A**). However, the model with only random intercept was within 2 AIC_c units, suggesting that the evidence for highly variable individual improvement rates over time/with experience was weak. The strong support for random intercepts indicates that parataxonomists vary strongly in their initial error rates, however, the lack of support for the correlations between slopes

and intercepts again suggests that in general, all parataxonomists improve at a similar rate.

We expected that returning parataxonomists not only would make fewer errors themselves, but that they also would mitigate the high error rate of new parataxonomists by conducting informal quality control for their peers (shown to be an effective training strategy in medicine, e.g., Van Bruwaene et al. 2009). The simplest hypothesis is that error rates decrease with increasing experience, both within and across years. We looked for polynomial trends as well because the literature on skill acquisition suggests that relatively inexperienced individuals can become overconfident (e.g., Bjork 1999). If new parataxonomists lack the caution that experienced individuals develop, we hypothesized individual error rates would increase at some point in their development. Error rates changed in a non-linear pattern as parataxonomists became more experienced. The model with third-order polynomials for consecutive days of experience had greater support than the model with only a linear term and slightly less support than the model with a second-order polynomial (**Table 4.3 B**). The second order polynomial resulted in a slightly lower predicted peak error rate and a higher intercept, but in general, the predictions were similar as were the parameter estimates for other variables, so we present the third-order polynomial predictions part of model B1. In general, parataxonomists started out with relatively low error rates. Error rates increased until approximately two weeks (70-80 hours) of experience was gained, and then decreased (**Figure 4.3**). Experienced parataxonomists made fewer errors and also appeared to decrease error rates in new parataxonomists working alongside them (**Table 4.3, Figure 4.3**), as evidenced by the poor support for a model without the overall group experience factor.

To investigate a more proximal cause of error, we also determined whether error rates varied throughout the week. We investigated three possible mechanisms. If fatigue and boredom caused error rates as the week progressed, we hypothesized error rates would increase linearly from Monday to Friday. In contrast, if skill level back-slid over the weekend, something that is plausible given the parataxonomists' inexperience, error rates may be highest on Monday

and decline linearly with practice until Friday. Finally, if individuals were more prone to errors during the middle of the week, perhaps because Wednesday (the day furthest from the weekend) appears to be the most 'unhappy' day of the week (Dodds and Danforth 2010), we hypothesized a quadratic relationship with error rates peaking mid-week. Our results show that error rates were highest on Fridays, an effect that was most pronounced in 2008 when all of the parataxonomists were new. Mondays and Thursdays were the next most error-prone days. There was good support for this non-linear relationship, as evidenced by the low weight of the model with a linear day-of-the-week factor and the model lacking a day-of-week factor (**Table 4.3, Figure 4.4**).

The second proximal source of error we considered was volume of specimens sorted in a day. There is considerable pressure to sort all of the samples collected. Increased stress may reinforce skill acquisition (e.g., Yacef and Alem 1997), but it may also cause higher error rates in novices (e.g., Beilock et al. 2008). However, the most supported model didn't include volume, suggesting that it didn't affect error rate significantly. In case this was confounded by the last week of sorting, when volume of sorting often decreases as completion nears and parataxonomists begin doing more difficult identification, we re-ran model B1 and B3 using data from only the second and third weeks of August from all three years. As with the full dataset, adding volume to the model reduced fit (reduced B1[full model without volume] AICc=230.21, log likelihood=-99.78, reduced B3[maximal model] AICc=232.87, log likelihood=-99.91, n=173 days of quality control).

The final source of error we examined, gender of the parataxonomist, also proved largely inconsequential. Contrary to our predictions, male parataxonomists (n=4) had lower error rates than female parataxonomists (n=9). The effect was small however, and the model without the gender term had almost as much support as the model with gender (**Table 4.3**).

The biggest statistical power gains were seen for species where quality control reduced the error rate by more than 5% and for species that have intermediate levels of prevalence (neither extremely common nor rare). On

average, we estimate that quality control will increase our statistical power to detect a trend of decreasing occurrence over time by a minimum of $5.3 \pm 3.7\%$ for the 20 species examined. We estimate this to be the minimum estimate as these analyses do not allow us to separate the effect of having an experienced supervisor present from the effect of the official quality control that the supervisor conducted. An alternative strategy to increase power to detect change over time is to monitor more sites. Using the original prevalence and detectability, we reran the models, increasing the number of sites visited per year by 1 until the average power increased by 5%. To get the same increase in power as quality control is estimated to have achieved, we would need to monitor 7 additional sites per year in our scenario, increasing the sites monitored yearly from 5 to 12, more than doubling the original number of sites monitored per year from 25 sites to 60 sites. The cost of hiring someone to conduct quality control varied between years depending on whether the supervisor was working as in-kind support, an employee already drawing a wage, or a contractor, but we estimate the costs to average \$6000 per season. The cost of monitoring more than double the number of sites in a year would be at least an order of magnitude higher than \$6000.

Discussion

This is the first study we know of to examine skill acquisition in taxonomy, and we suggest there are three main lessons for biodiversity research and monitoring specifically, and taxonomy in general. First, when provided quality control, parataxonomists were able to efficiently and accurately identify a moderate diversity of macrolichens: errors were negligible over the average 77 identifications each parataxonomist completed per day. Second, parataxonomists made the most mistakes after they had logged over 40 hours of practice, and errors peaked around 60-80 hours of practice. This suggests that quality control is most needed when least expected, i.e, after parataxonomists have developed a routine and performed more than 300 species or genus-level identifications on average. Lastly, when parataxonomists had experience they more than halved both their error rates and the error rates of their inexperienced peers.

Our data suggest that with focused training, supervision, and quality control, non-experts can identify macrolichens with high accuracy. Even higher accuracy can be achieved if we consider the behavioral biology of parataxonomists. First, the bulk of errors were made after parataxonomists had sorted at least one site and their volume sorted per day was reaching its maximum. We hypothesize that this is due to overconfidence, complacency, and/or pressure to start working faster after the initial (and necessary) relatively slow days; additional studies are needed to determine whether this is a general patterns, and if so, establish a mechanism. Increased stress may reinforce skill acquisition (e.g., Yacef and Alem 1997), but it may also cause higher error rates in novices (e.g., Beilock et al. 2008). Regardless of the mechanism, quality control could be targeted to that period to ensure that accuracy is consistently high across samples.

Our models also suggest that error rates peak on Friday, suggesting that boredom, fatigue, or again, pressure to complete the current sample resulted in higher errors. The small magnitude of this effect likely doesn't warrant additional quality control. Instead, we suggest simply informing parataxonomists of this trend: our experience suggests that most parataxonomists are highly motivated to be accurate. Education should be effective even if motivation is more pragmatic (i.e., desire to avoid resorting samples if they're found to have a high error rate) than ethical or moralistic (i.e., desire to generate accurate data for science and conservation).

Returning parataxonomists are critical because of their ability to lower error rates in even their novice co-workers. The ABMI's goal is to retain a minimum of 50% of their parataxonomists from year to year. To encourage retention, ABMI offers pay raises and bonuses to returning parataxonomists, and to parataxonomists that complete the entire summer of employment. These analyses suggest that this money is well spent. Mechanistically, it is likely that novice parataxonomists use their more experienced peers as resources, and put themselves through unofficial quality control more often when experienced peers are present. This is more evidence that the collaborative environment that is created in the lab is beneficial. Some biodiversity programs ship their samples to

individuals working in different labs - our results suggest that if logistically feasible, accuracy advantages may be had by hosting an identification workshop or "ID bee" or "curation blitz".

While we found no published research on taxonomic skill acquisition, there is a body of research on skill acquisition in other disciplines, including education (e.g., Anderson 1982, Rayner et al. 2001), medicine (e.g., Van Bruwaene et al. 2009), and sports (e.g., Beilock et al. 2008, Fiore et al. 2008). We predict that learning taxonomy involves a combination of motor skill learning, language comprehension, visual perception and adequate working memory. Motor-skill learning can be divided into three phases (Fitts and Posner 1967): cognition (comprehension of the steps of the task), association (practice), and autonomy (the skill becomes automatic and no longer requires cognitive awareness). Autonomy is the difference between an experience taxonomist knowing at a glance what species a specimen belongs to, and a novice requiring a dichotomous key and illustrated glossary to come to the same conclusion. Research on reading skills suggests that success depends in part on the capacity of an individual's working (previously called short-term) memory, and taxonomy has parallel requirements (Just and Carpenter 1992); an experienced taxonomist 'reads' a specimen (sensu Goward 2010), integrating multiple cues and idiosyncrasies to arrive at an identification. We think there are some exciting opportunities for future collaborative research on taxonomic skill acquisition: at a time when taxonomic expertise is both in decline and increasing demand (Tayler 1983, Gaston and May 1992, Godfray 2002, Packer et al. 2009), it would be beneficial to better understand how to teach and acquire this complex skill.

With regards to data quality, while quality control in ecology tends to be "largely intuitive and unreported" (McCune and Grace 2002), we think the value of reporting accuracy and bias is great. It provides transparency. It allows analyses to be weighted in favor of more accurate species identifications, when concerns about accuracy are large. It highlights to members of the ecological community which taxa are problematic. Other fields such as medicine and

manufacturing have rigorous quality control, perhaps because of consequences of unmitigated error are greater (e.g., Van Bruwaene et al. 2009). However, taxonomic error in ecological studies can be insidious in that it is likely to go unnoticed (Bortolus 2008). It is unlikely that key results will be revisited if large taxonomic errors are detected after publication, and as a result, these errors can propagate through ecological theory (Bortolus 2008). Finally, when taxonomy is used to inform legal land management decisions, explicit quality control is just as critical as documentation around effect size and error in statistical analyses (e.g., Mapstone 1995).

Alternatives

Previous research has clearly shown observer effects are a large contributor to sample variation in the field, so should we focus our efforts on minimizing species overlooking rates in the field? There is a small but growing body of literature addressing inter-observer variability in field sampling, both between experts and novices (McCune et al. 1997, Giordani et al. 2009) and between different experts (e.g., Archaux et al. 2009). Archaux and colleagues have examined various contributors to error rates in plant monitoring (Archaux et al. 2006, Archaux et al. 2007, Archaux and Berges 2008, Archaux 2009, Archaux et al. 2009). These studies found that even experienced specialists make relatively high numbers of overlooking and misidentification errors. Given the variability between experts, minimizing overlooking of parataxonomists likely is a more difficult endeavor (Chapter Two). High environmental variability may interact with the natural variability in the skill-level of the parataxonomists in sometimes unpredictable ways. Fortunately, many lichen samples are of mixed colonies and contain more species than the sampler recognizes in the field.

Another alternative would be to send samples directly to an expert for identification. Even at the economical price of \$5 per specimen, the 8,524 specimens identified by the parataxonomists would cost over \$42,600, and take time that could be better spent by expert lichenologists. If we restricted the parataxonomists to packaging specimens, it would also result in a slower process and more specimens sent for identification, as all specimens would have to be

packaged for expert identification (2,562 vouchers were made of the 8,524 specimens identified - the remainder were left as duplicates in the residual material). Additional efficiencies to be had by involving parataxonomists include the detection of species that experts may have overlooked. They also create the database and populate it with preliminary data, again saving experts' time.

Finally, there is the technological alternative. While DNA barcoding (Hebert et al. 2003) has just begun to be explored for lichens (Kelly et al. 2011), Newmaster et al. (2006) proposed it as a solution to the routine identification of plants. Should DNA barcoding become a common method of species identification in lichens, we envision parataxonomists as complementary rather than redundant. Parataxonomists in partnership with experts provide efficiencies that allow new technologies to improve taxonomy (Wheeler 2004). In this situation, parataxonomists in collaboration with experts can do much of the specimen processing, while also identifying common things that don't need to be barcoded at a great savings of time and money. Parataxonomists who persist and advance to become experts themselves will maintain the crucial knowledge of taxonomy that can't be addressed molecularly, such as morphological and descriptive taxonomy and systematic classification (Lipscomb et al. 2003, Wheeler 2004).

Future research

We have a unique opportunity at the Royal Alberta Museum, Edmonton, Canada to extend these analyses to bryophytes, aquatic invertebrates, and oribatid soil mites and determine whether the patterns we have observed among lichen parataxonomists are common across taxa, or whether some taxa are intrinsically more difficult. Collections of these taxa undergo a similar process, where parataxonomists are responsible for the initial sorting and identification of selected common species.

Conclusion

Often in ecological studies there is an implicit assumption that species identifications are without error, or more precisely, that the error is not large

enough to bias interpretation of results. For many model structures, however, such as presence-only and presence-absence habitat modeling, false positives may cause as many problems as false negatives. We see increasing recognition of this, such as the addition of a module to deal with false-positive error rates in the detection modeling software PRESENCE (Hines 2006).

Parataxonomists as described by Janzen (Janzen 1991, Janzen 2004) need not be limited to sorting specimens into parataxonomic units (Krell 2004). Because taxonomy has progressed to the point where it's largely the domain of highly trained experts (Pearson et al. 2011), parataxonomists often are judged as inadequate when they are perfectly adequate at filling their particular niche. In return, large-scale monitoring and research programs reciprocate by filling the void left by many universities as they move away from teaching basic identification and taxonomy skills (Dayton 2003). Many university-trained biology students are hungry to contribute to a project that has more longevity than their term papers. Including these students as parataxonomists will educate and encourage these students as they become better acquainted with what are often lesser-known but more diverse taxa. We are confident that some of those students will eventually take real strides towards taxonomic expertise, and in the interim, their efforts are alleviating the taxonomic impediment of routine identification.

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Table 4. 1 Lichens were sampled from microhabitats in five strata.

Stratum #1: Logs and Stumps (samples in 1 bag)
LS: Soft stumps & logs (decay classes 3-5) - sample roots and all sides
LH: Hard stumps & logs (decay classes 1-2) - sample roots and all sides
Stratum #2: Trees and Other Vertical Structures (samples in 1 bag)
TD: Deciduous Trees - all sides of the roots, bases, trunks, and branches of both live and dead deciduous trees
TC: Coniferous Trees - all sides of the roots, tree bases, trunks, and branches of both live and dead coniferous trees
TS: Shrubs - all sides of the roots, bases, stems, and branches of live & dead shrubs
HB: Human Structures - vertical and horizontal parts of the structures (survey from the ground)
Stratum #3: Wetlands and Peatlands (samples in 1 bag)
WMF: Wetlands, marshes, & fens - within the wetland survey both under and away from trees
WSB: Shores/banks of wetlands, ponds, lakes, & streams - survey on organic or mineral soil adjacent the water's edge
WDS: Moist depressions/seasonal wetlands dry at time of survey - sample sides and bottom in the area influenced by water
WPW: Peatlands with or without standing water - survey both standing water and vegetation hummocks
Stratum #4: Rocks and Cliffs (samples in 1 bag)
BC: Boulders (>50 cm diam.) - survey all surfaces (top, sides, and base) from the soil upwards
RR: Rocks (<50 cm diam.) - survey all surfaces (top, sides, and base) from the soil upwards
CL: Cliffs (steep high rock face) - survey all of the faces, ledges, and crevices that can be accessed safely
Stratum #5: Upland Soils (samples in 1 bag)
UC: Humus soils under trees/shrubs (shaded by canopy) - survey as large a variety as possible
UO: Humus soils without trees/shrubs (open to sunlight) - survey as large a variety as possible
DC: Agriculturally cultivated soils
DM: Mineral soil in upland areas from any causes

Table 4. 2 (Next page) Error rates for each lichen species parataxonomists identified. # Correct & # incorrect: specimens undergoing quality control determined to be either correct or incorrect. # Unverified: specimens identified to species by the parataxonomists that did not undergo quality control. Total: sum of the columns 1- 3. Initial error %: $\frac{\text{incorrect}}{\text{correct} + \text{incorrect}}$. # Estimated errors in unverified specimens: initial error x # unverified. Error %: $\frac{\text{estimated errors}}{\text{total}}$. IW columns: same as previous columns, but first calculated for each parataxonomist using individual species-specific error rates and number of unverified specimens. Error rates higher than 5% are shaded grey.

Scientific name	# Correct	# Incorrect	# Unverified	(% Misidentified/overlooked/process Error)	Total	Initial error (%)	# Errors in unverified specimens	Error (%)	# Errors in unverified specimens IW	Error (%) IW
Species identified by all parataxonomists										
<i>Letharia vulpina</i>	19	0	2	0, 0, 0	21	0.0	0	0.0	0	0.0
<i>Cladonia stellaris</i>	14	3	3	67, 0, 33	20	17.6	1	2.6	0	0.0
<i>Evernia mesomorpha</i>	436	18	458	22, 72, 6	912	4.0	18	2.0	8	0.9
<i>Vulpicida pinastri</i>	510	24	571	4, 88, 8	1105	4.5	26	2.3	16	1.4
<i>Hypogymnia physodes</i>	496	31	488	45, 45, 10	1015	5.9	29	2.8	18	1.8
<i>Cladonia botrytes</i>	145	14	87	29, 64, 7	246	8.8	8	3.1	4	1.8
<i>Tuckermannopsis americana</i>	265	23	261	22, 74, 4	549	8.0	21	3.8	12	2.1
<i>Ramalina dilacerata</i>	223	29	202	17, 79, 3	454	11.5	23	5.1	10	2.2
<i>Peltigera neckeri</i>	59	5	29	60, 20, 20	93	7.8	2	2.4	2	2.6
<i>Parmelia sulcata</i>	600	40	799	25, 63, 13	1439	6.3	50	3.5	40	2.8
<i>Parmeliopsis ambigua</i>	326	49	337	22, 71, 6	712	13.1	44	6.2	24	3.4
<i>Parmeliopsis hyperopta</i>	171	33	158	28, 72, 0	362	16.2	26	7.1	18	5.0
<i>Imshaugia aleurites</i>	105	22	104	32, 68, 0	231	17.3	18	7.8	12	5.1
<i>Phycia adscendens</i>	209	45	205	29, 71, 0	459	17.7	36	7.9	24	5.1

Scientific name	# Correct	# Incorrect	# Unverified	(% Misidentified/overlooked/process Error)	Total	Initial error (%)	# Errors in unverified specimens	Error (%)	# Errors in unverified specimens IW	Error (%) IW
Species identified by experienced parataxonomists										
<i>Peltigera malacea</i>	14	0	24	0, 0, 0	38	0.0	0	0.0	0	0.0
<i>Flavocetraria cucullata</i>	7	0	3	0, 0, 0	10	0.0	0	0.0	0	0.0
<i>Cladonia rangiferina</i>	92	1	147	0, 100, 0	240	1.1	2	0.7	0	0.0
<i>Cladonia cornuta</i>	38	4	96	50, 50, 0	138	9.5	9	6.6	1	0.5
<i>Peltigera leucophlebia</i>	89	5	85	60, 40, 0	179	5.3	5	2.5	3	1.9
<i>Cladonia cenotea</i>	42	11	28	55, 45, 0	81	20.8	6	7.2	3	3.8
<i>Peltigera aphthosa</i>	44	5	51	80, 20, 0	100	10.2	5	5.2	5	5.3
<i>Physcia aipolia</i>	26	6	32	83, 17, 0	64	18.8	6	9.4	6	10.1
<i>Flavocetraria nivalis</i>	22	11	23	27, 73, 0	56	33.3	8	13.7	8	14.0
Total	3952	379	4193	29, 66, 5	8524	8.8	341	4.0	215	2.5

Table 4. 3 (Next page) Generalized linear mixed model comparisons of factors affecting cumulative daily error rate. Maximal fixed factor parameterization included the following: *3rd order orthogonal polynomial for Day of Experience + 2nd order orthogonal polynomial for Day of Week + SD of Cohort Years of Experience + Volume of Sorted Specimens*). Maximal random factor parameterization (A3) included the following: *intercepts, slopes and correlations between intercepts and slopes for each parataxonomists for the 3rd order orthogonal polynomial for Day of Experience*. The random factors from the model with the highest support in part A [shaded grey] were used in part B. The model with the highest support in part B [shaded grey] contained all fixed factors except *Volume of Sorted Specimens*.

	K	AICc	Δ AICc	Model Likelihood	AICc Weight	Log Likelihood
A. Random factor exploration using maximal fixed factor model						
A1. Uncorrelated random intercepts and slopes for each parataxonomist	15	348.00	0.00	1.00	0.60	-158.07
A2. Random intercepts only	9	348.92	0.92	0.63	0.38	-165.12
A3. Correlated random intercepts and slopes	18	354.56	6.56	0.04	0.02	-157.94
B. Fixed factor exploration using uncorrelated random intercepts and slopes for each parataxonomist						
B1. No effect of volume	14	345.88	0.00	1.00	0.42	-158.13
B2. Unimodal effect of days of experience	11	346.68	0.80	0.67	0.28	-161.84
B3. Maximal model	15	348.00	2.12	0.35	0.14	-158.07
B4. Linear effect of day-of-week	14	349.55	3.67	0.16	0.07	-159.96
B5. No effect of day-of-week	13	349.82	3.94	0.14	0.06	-161.21
B6. Linear effect of days of experience	13	350.61	4.73	0.09	0.04	-161.60
B7. No effect of cohort experience	14	374.84	28.96	0.00	0.00	-172.61
C. Gender fixed factor exploration using uncorrelated random intercepts and slopes for each parataxonomist and maximal fixed factor model minus volume fixed factor. Days of experience truncated to ≤ 17						
With gender	15	273.34	0.00	1.00	0.59	-120.16
Without gender	14	274.09	0.75	0.69	0.41	-121.73



Figure 4. 1 (previous page) Examples of macrolichens identified by parataxonomists. Names followed by "*" are difficult species for more experienced parataxonomists. 1) *Letharia vulpina*, 2) *Peltigera aphthosa**, 3) *Parmeliopsis hyperopta*, 4) *Tuckermannopsis americana*, 5) *Peltigera malacea**, 6) *Cladonia stellaris*, 7) *Hypogymnia physodes*, 8) *Imshaugia aleurites*, 9) *Vulpicida pinastri*, 10) *Cladonia botrytes*.

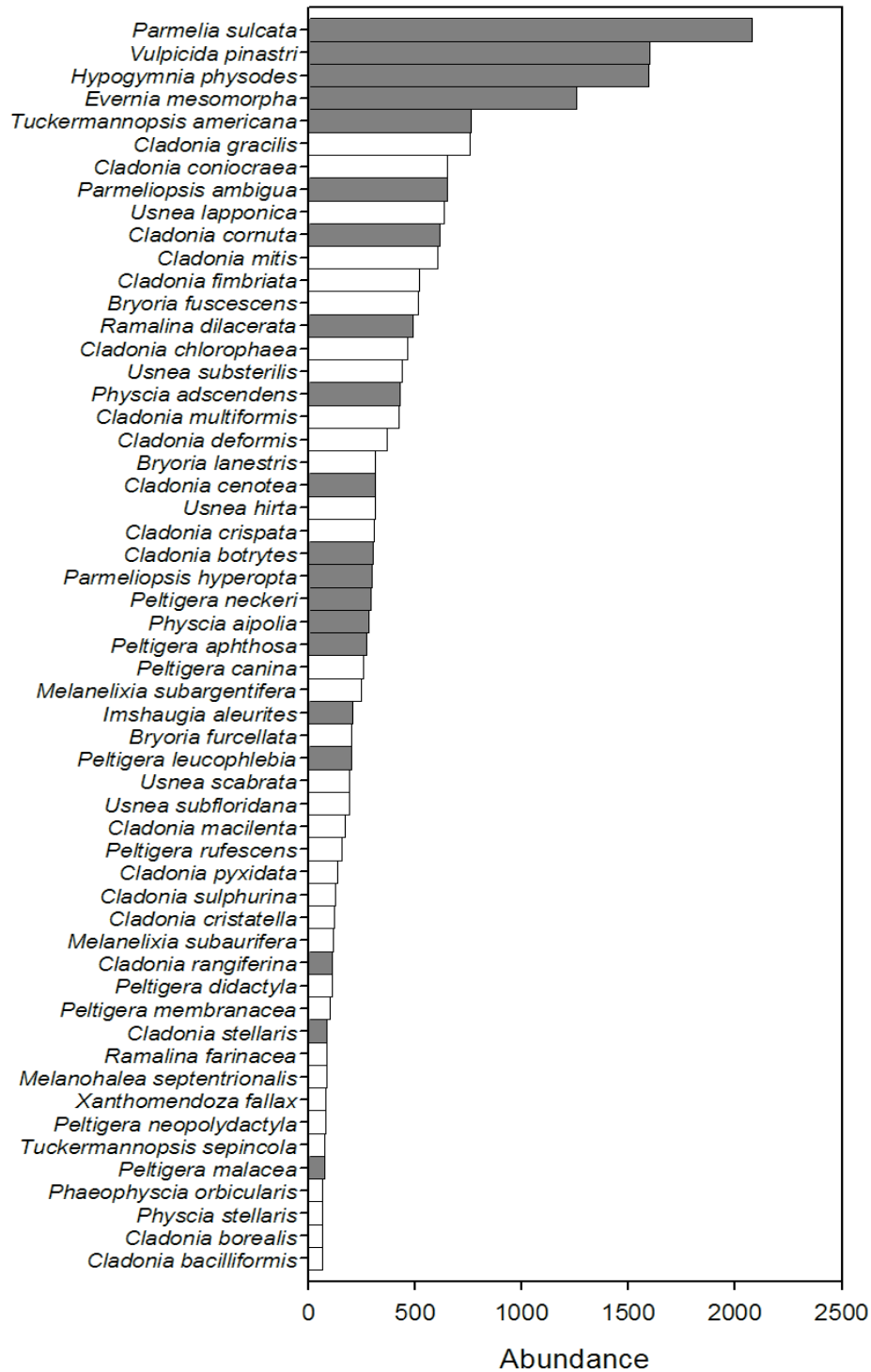


Figure 4. 2 Rank-abundance curve for lichens collected from 2003-2008. The 56 species shown make up 90% of the specimens collected. Grey bars indicate species identified by parataxonomists. Other species identified by parataxonomists but present in low numbers and excluded from the graph are: *Flavocetraria cucullata* (12), *Flavocetraria nivalis* (32), and *Letharia vulpina* (5)

Figure 4. 3 Individual experience and the level of experience of the cohort affect the probability of error by parataxonomists. Model parameterization from model B1 (Table 4.3); day-of-the-week was held constant at Wednesday for all curves.

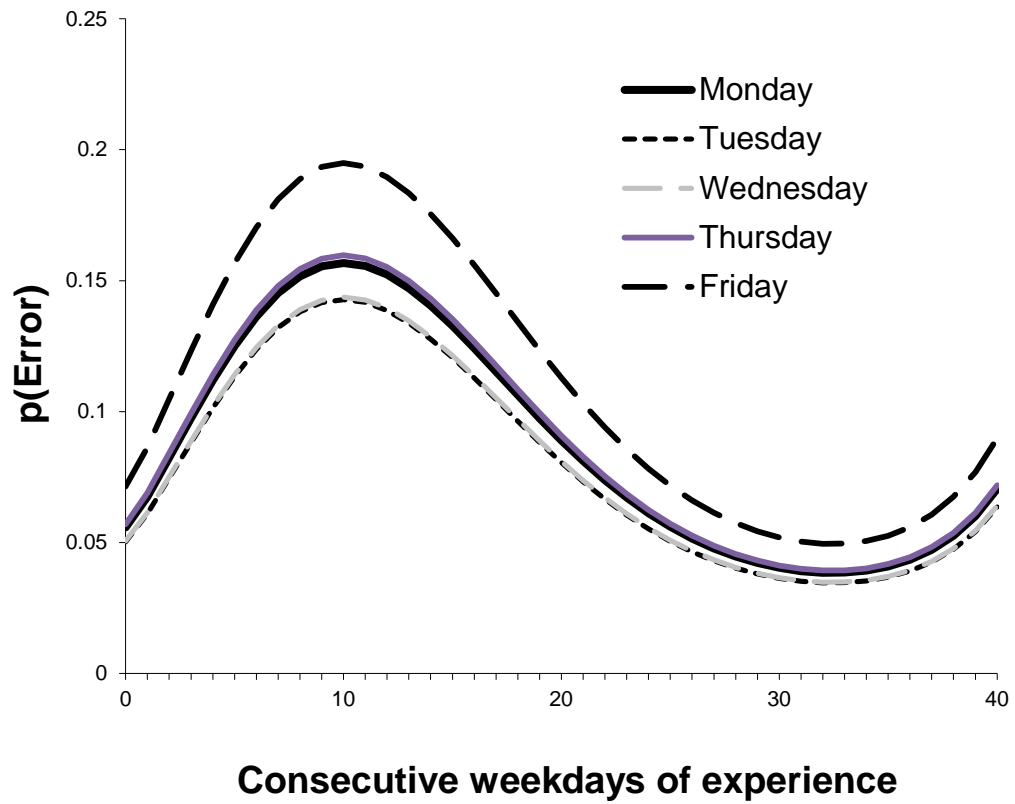


Figure 4. 4 Day-of-the-week effects on error rates. Model parameterization from model B1 (Table 4.3); group experience was held constant at SD=0 years' experience (100% Novice).

CHAPTER FIVE

Capacity of large-scale, long-term biodiversity monitoring programs to detect trends in species occurrence

A version of this chapter is published:

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Summary

There is a critical need for monitoring programmes to assess change or trends in species status to inform conservation. A key aspect in developing such programmes is evaluating their statistical power—the ability to detect a real change. Here we examine the capacity of a broad-scale biodiversity monitoring programme in Alberta, Canada to measure changes in species prevalence. Using observed variation in detectability and prevalence for 252 species monitored at 85 sites, we simulated 3% annual declines and evaluated sample size (6 different sizes) and length of monitoring (5 different durations) necessary to detect change with a 90% certainty (power) at an α of 0.1. Our results suggest that after four monitoring cycles (e.g., 20 years for a 5-year cycle) a power of 90% can be expected for 99% of species when monitoring 1,625 sites, 65% of species for 300 sites, 27% of species for 75 sites, and 8% of species for 25 sites. We found that 66% detectability and 50% prevalence were needed to ensure that 3% annual change is detected at 50 sites over a 20-year period. Our results demonstrate that broad-scale monitoring programmes cannot effectively detect trends in all species at all spatial scales. The time period and spatial scale necessary to detect a real change at a specified level needs to be provided to stakeholders to ensure the short-term success of biodiversity monitoring programmes and to ensure that the most robust indicators of biodiversity are selected.

Introduction

Many countries are striving to reduce the rate of biodiversity loss by 2010 (Secretariat of the Convention on Biological Diversity 2005). To achieve this target, signatories require monitoring programmes capable of measuring trends in biodiversity. However, biodiversity cannot be measured in its entirety, forcing the use of surrogates. Biodiversity monitoring sometimes relies on coarse filter surrogates, such as habitat quantity or quality, measured via remote sensing or field mapping (Duro et al. 2007; Lengyel et al. 2008a). However, habitats may persist even though key elements of biodiversity are lost (Huggard et al. 2006) making habitat an inappropriate measure of status for some species. For instance, in Africa numerous mammals were displaced through hunting activities not correlated with human density and land use, while exotic species contributed to losses of mammals in Australia (Ceballos and Ehrlich 2002). To ensure coarse filter surrogates of biodiversity do not overlook important on-the-ground changes it is necessary to monitor biota.

Approaches to monitoring biota can be categorized as either targeted or surveillance monitoring (Nichols and Williams 2006). Targeted monitoring tends to be hypothesis-driven, stressor-specific, and restricted to a few well-studied, charismatic, or rare species. Surveillance monitoring is taxonomically-broad, species-rich, and most frequently hypothesis-free (Yoccoz et al. 2001; Nichols and Williams 2006). Although targeted monitoring appears to be an attractive short-cut for indexing biodiversity condition, indicator species are rarely reliable surrogates for larger groups of species or other taxa (e.g., Prendergast et al. 1993; Simberloff 1998; Lindenmayer et al. 2002; Favreau et al. 2006). Accurate measures of biodiversity necessitate that more than a few indicator species be considered. Designing a monitoring programme to measure and detect trends for multiple species and taxa is, however, challenging. Benefits gained by monitoring large numbers of species need to be weighed against the loss of precision and accuracy associated with rapid-assessment survey protocols.

Prospective power analyses has become standard practise when determining how to allocate monitoring effort, but most published reports

describe how to optimize effort for single species (Taylor and Gerrodette 1993) or a single taxon (Roy et al. 2007; Van Strien et al. 1997; Archaux and Bergès 2008; Manley et al. 2004, 2005). The design attributes that affect statistical power for a single species or taxon are the same for taxonomically-broad monitoring programs, including: number of sites monitored, duration of monitoring, process and sample variability, statistical method, choice of α and β levels, and effect size (Fox 2001; Field et al. 2004; Legg and Nagy 2006). The difference lies in the constraints faced by taxonomically-broad programmes. Monitoring effort cannot be optimized for all species simultaneously. When multi-stakeholder monitoring is designed to be large-scale and long-term, the often-prescribed solution of monitoring a few sites intensively and many sites superficially is not desirable (e.g., reduced-effort schemes, Roy et al. 2007). It is better to focus on minimizing and understanding sampling error and employing design attributes that allow the programme to make robust inferences to the population of sites, such as a random or systematic sampling design.

At present, few programmes have been implemented over long enough periods or at large enough scales to gauge their capability to identify biodiversity loss. We report here on the prospective capacity of a large-scale taxonomically-broad monitoring programme to identify trends in the prevalence of species (proportion of monitoring sites a species was detected) using a combination of real-world field data from Alberta, Canada and numerical simulations. Species prevalence was chosen as our measure of abundance because it is simple to communicate and measure, although it may have lower statistical power than other metrics such as relative abundance or density (Purvis and Hector 2000). Our objectives were to: (1) determine the number of monitoring sites and duration of monitoring necessary to detect a 3% annual change in species prevalence; (2) evaluate the degree to which detectability and prevalence influence statistical power; (3) develop a simple predictive model to estimate how statistical power was affected by species prevalence, detectability, number of monitoring sites, number of repeated visits, and an α of 0.1; and (4) determine whether certain assemblages are more effective at detecting trends than others.

Methods

Study area and monitoring design

We simulated statistical power for a large-scale, long-term biodiversity monitoring initiative recently initiated in Alberta, Canada by the Alberta Biodiversity Monitoring Institute (ABMI; Stadt et al. 2006). ABMI's monitoring design consists of 1,656 sites evenly spaced across Alberta using a 20-km grid. Site locations are permanent with exact GPS coordinates recorded, so they can be surveyed repeatedly over time. Sites have been randomly divided into five panels with each panel to be surveyed once every 5 years. During 2003–2005, prototype data for ABMI were collected at 85 of the 1,656 permanent monitoring sites, primarily in central Alberta's boreal forest (**Figure 5.1**). Ten of the 85 sites were re-surveyed each year for 3 years to allow assessments of the reliability of monitoring protocols, including species detectability.

Survey methods

At each of the 85 monitoring sites, the presence–absence (detected/non-detected) and relative abundance of songbirds, vascular plants, and bryophytes were recorded (ABMI 2007). Songbirds were surveyed using single-visit point counts to each monitoring site during the breeding season (June). An omnidirectional microphone was used to digitally record singing birds for 10 min at each of nine stations. The stations were spaced 300 m apart in a 3 x 3 grid. All audio recordings were interpreted by a single expert in a standardized laboratory setting. Vascular plants and bryophytes were surveyed within a 1-ha square plot that was centred on a permanent ABMI site marker. The 1-ha plot was flagged into four 0.25-ha sub-plots, and vascular plants were surveyed during July for each sub-plot using area-restricted, 20-min. searches. Species not identified in the field were collected for expert identification in the laboratory. During the same visit in July, presence–absence of bryophytes was determined using time-limited searches of microhabitats. Technicians searched the 1-ha plot and created a list of all pre-defined microhabitats found (types of lowland and upland substrates, trees and stumps, downed woody material, and rocks). A technician then searched

microhabitats for bryophytes over a two hour period. Samples of each moss and liverwort that appeared distinctive were collected for identification by expert bryologists in the laboratory. The cumulative list of species observed over all sub-samples (bird points, sub-plots, or microsites) was used as our measure of presence–absence for the monitoring site.

Simulations and analysis of trends

We simulated 3% annual declines in the prevalence of each species for those with an initial prevalence where detected of 0.1 or greater. Although 3% is arbitrary, a 3% annual decline for 10 years would result in a 27% overall decline, which was viewed as a meaningful change by managers in Alberta. The prevalence of each species at the 85 sites we sampled in ABMI was used to populate our simulation at year t . In our simulation, species prevalence was tracked each year at each site. We then “sampled” from this known population as per the systematic sampling design used by the ABMI. Declines in prevalence were modelled as a deterministic reduction in the number of sites where a species occurred by reducing the number of occupied sites by 3% each year. Sampling variation at sites where species were present was introduced to the simulations by detection probabilities (i.e. probability that a species is detected given that it is present). Detectability was estimated from the mean occurrence of a species at each of the ten sites that were re-surveyed for each of the three years. Species detectability for each site ranged from 0.33 (recorded only once during the three years) to 1 (recorded all three years). A uniform random number was generated at each step in the simulation to determine whether a species was detected at a site given that it was present. If the random number was less than the species detectability value, the simulation treated that site as an absence (zero) in subsequent analysis (i.e. false negative). As ABMI sites were permanent and protocols constant, the detectability value we used in simulations represents a combination of observer/method-associated variability. It also includes natural inter-annual variation that could have included short-term seasonal changes or year-to-year variation in occurrence or detection probability at a site.

A total of 500 simulations at 3% annual declines in species prevalence were generated for each of 252 species and 30 scenarios representing six sample sizes (25, 50, 75, 100, 300, and 1,625 sites; **Table 5.1**) and five time-horizons for monitoring (10, 20, 30, 40, and 50 years). All sample sizes and monitoring periods were divisible by 5, as Alberta protocols call for grouping sites into five panels that are each re-monitored in a single year (**Table 5.1**). Given the number of species and scenarios examined, 7,560 unique estimates of statistical power were determined based on 3,780,000 data points (500 replicates per scenario).

For each species and scenario combination we assessed the power of detecting a trend in the species prevalence when simulated using population-averaged panel-data via Generalized Estimating Equation (GEE) in STATA 9 (StataCorp 2005). GEEs allow for direct identification of data correlations associated with longitudinal measurements and observations that are clustered around a common group or panel (Liang and Zeger 1986). Each simulated monitoring site was randomly grouped into one of five panels and each panel ‘surveyed’ during a different year. This mimicked the ABMI monitoring design consisting of five rotating panels where surveys were completed once every 5 years. Year of simulation was set to identify a longitudinal data series. A binomial family and logit link GEE with an autoregressive order 1 within-group correlation structure for panels was used to account for temporal autocorrelation of grouped monitoring sites and the variable year tested for a trend. To efficiently estimate models and manage the results of simulations, we used the `STATSBY` command in STATA where GEE models were repeated for each of the 500 simulations per scenario and species combination and the statistics from each model collected (saved). We recorded the number of times a trend parameter for year exceeded the critical F-value assuming an α of 0.1. Because the consequences of either declaring a spurious change significant (type I error) or overlooking a significant change (type II error) can be equally undesirable (Fairweather 1991; Mapstone 1995; but see Field et al. 2004), we balanced α (type I error) and β (type II error) by setting β at 0.1. Therefore, when 90% of simulations in a species-monitoring

scenario (number of monitoring sites and length of monitoring) exceeded the critical α of 0.1, we recorded the scenario as correctly detecting a trend.

Influence of number of monitoring sites and length of monitoring on statistical power

Power of detecting change for monitoring scenarios were plotted as taxa-specific means (± 1 SD) based on sample size and length of monitoring. We also recorded the percent of species within an assemblage that correctly identified a trend ($\beta = 0.1$, $\alpha = 0.1$). To guide evaluation of monitoring effectiveness, we report the sample size and monitoring period necessary to correctly identify a trend for 50, 75, and 100% of monitored species.

Influence of prevalence and detectability on statistical power

Statistical power was compared among assemblages (songbirds, vascular plants, and bryophytes) using a Kruskal-Wallis rank sum test for the sample size and monitoring period of 50 sites and 20 years (scales chosen at what appeared to be the most pronounced differences among taxa). Power was estimated for each scenario and species combination as the proportion of the 500 simulations exceeding the critical F-value at an α of 0.1. Using species prevalence, detectability, panel sample size (number of sites monitored each year or 20% of the total sample size), number of monitoring cycles (years/5), we estimated a generalized linear model with a logit link and robust variance estimators (StataCorp 2005) to predict the statistical power of the monitoring program. Variables were standardized to a mean of zero and standard deviation of one and the model re-parameterized to estimate standardized coefficients (β Z-StanVar) to evaluate the relative importance of individual predictors. Percent change in odds ratio for a standard deviation increase in covariate X (%StdX) was also used to evaluate variable contribution. Prior to model estimation data from simulations were partitioned into a model training and model testing data set using a 75-25% allocation respectively. Training and testing sets were systematically selected based on the ranked order relative to species prevalence and detectability. Every fourth species (in ranked order) was removed from the training dataset and

retained for later evaluation. Predictive accuracy of model estimates were determined by regressing observed power against predicted power for the testing (removed) dataset and the regression fit tested for a slope of 1 and intercept of 0 using an F-test (Haefner 2005).

To explore how statistical power would increase in the short-term if we accepted a greater probability of error by including rare, cryptic species, we re-ran simulations for two scenarios. The first represented statistical power for common, easily-detected species, while the second represented statistical power for rare, difficult to detect species. Each scenario was simulated for a 10-year period, an α and β of 0.2, and for the same six sample sizes used previously and outlined in **Table 5.2**.

Results

Monitored species

A total of 663 species (119 bird species; 166 bryophytes and 378 vascular plants) were detected at 85 monitoring sites. Bird species detected include 85% of the 87 Passeriformes known to inhabit Alberta's boreal forest (J. Schieck, unpublished data), as well as one introduced species (domestic chicken). Bryophytes detected represent 37% of 219 boreal species (R. Belland, unpublished data), while vascular plants detected represent 39% of 854 species (Moss 1994; J. Gould, unpublished data) previously recorded in Alberta's boreal. In addition to species native to the boreal, we recorded 26 vascular plant species introduced to North America and 20 plant species native to Alberta, but not previously recorded in the boreal ecoregion. We detected a total of 61 species considered to be sensitive (13 bird species), potentially at risk (1 bird species), or of conservation concern (41 bryophyte and 6 vascular plant species; Alberta Natural Heritage Information Centre Tracking Lists 2006). Of 663 species detected, 252 were present at 10% or more of the sites. Prevalence and detectability data from these 252 species were used to examine statistical power.

Influence of number of monitoring sites and length of monitoring on statistical power

Using average statistical power by species within assemblages for monitoring scenarios (number of sites and length of monitoring period), species within all three assemblages achieved an average power of 90% when 1625 sites were monitored over 20 years and for 300 sites monitored over 30 years (**Figure 5.2**). In fact, when considering the percent of species within an assemblage, all but one species (a bryophyte) achieved a 90% power after 20 years of monitoring on 1625 (provincial scale) sites with the majority of species reaching 90% power after only 10 years of monitoring (**Table 5.3**). Assuming 300 monitoring sites (the approximate scale of natural regions in Alberta), 50 years of monitoring resulted in at least 90% power for all sampled species. More than 75% of the species reached 90% power within 30 years and the majority of species achieved this target after 20 years (**Figure 5.2**). We found that 50 years of monitoring were required to achieve an average of 90% power if 75 or fewer sites were monitored for songbirds and vascular plants and if 50 or fewer sites were monitored for bryophytes (**Figure 5.2**). The majority of species reached 90% power after 40 years of monitoring at 75 sites and 50 years of monitoring at 50 sites (**Table 5.3**). When monitoring was restricted to 25 sites (the approximate scale of forest management areas in Alberta), about one-third of all species tested reached 90% power after 50 years and about one-tenth reached 90% power after 20 years of monitoring (**Table 5.3**).

Influence of prevalence and detectability on statistical power

Assuming 50 monitoring sites and a 20-year period of monitoring, no difference in statistical power was evident among assemblage ($\chi^2 = 1.11$, $df = 2$, $P = 0.575$). Prevalence and detectability both influenced statistical power, although the influence of prevalence was dependent on the level of detectability. At 60% detectability or less, prevalence had little effect on statistical power (**Figure 4.3**). However, at high levels of detectability (i.e. >60%), power was positively related to species prevalence, especially when prevalence ranged between 0.4 and 0.6

(**Figure 5.3**). All taxa had species with high prevalence and detectability making no particular group more statistically powerful than another.

Predicting monitoring power for species presence-absence

The model that best described statistical power for monitoring changes in species prevalence included number of monitoring sites per panel, length of monitoring period (number of monitoring cycles), prevalence of the species, and detectability. The model accounted for 87% of the deviance in the original data (r^2 calculated following Menard (2000), **Table 5.4**). As would be expected, statistical power increased in a non-linear manner as number of monitoring sites, length of monitoring, prevalence, and detectability increased. Interaction terms among detectability and prevalence and number of monitoring sites per panel and the number of monitoring cycles were also important determinants of statistical power (**Table 5.4**). Based on Z-standardized β coefficients and the percent change in odds ratio for a standard deviation increase in each variable (**Table 5.4**), the factors most influencing on statistical power were programme design variables with the most important being an interactive effect between the number of monitoring sites and length of monitoring (number of monitoring cycles) followed by the individual factors of number of monitoring sites and length of monitoring. For example, even if detectability and prevalence were at unity, if monitoring was restricted to five sites per panel and two monitoring cycles (10 years), power reached a maximum of 0.88. However, even with minimal detectability and prevalence (0.33 and 0.1, respectively), the desired power (0.9) was exceeded when monitoring 325 sites per panel for three monitoring cycles (15 years). The most important species variables were the interaction between prevalence and detectability (**Table 5.4**).

There was high correlation ($r^2=0.91$) between predicted and observed power for species withheld during model building (25% of total), indicating excellent model prediction. However, the slope and intercept between predicted and observed power differed from 1 and 0 respectively ($F=52.88 > F_{2,1853}=2.99$), suggesting slight biases in predictions over some ranges of data. This may reflect an artifact of non-converged GEE models for scenarios with small sample size

and short monitoring periods on species with low prevalence and detectability. The consequence was an over-estimate of statistical power for these scenario combinations.

Influence of alpha and beta

For rare, cryptic (low detectability) species, power to detect change over a 10-year monitoring period increased by approximately 10%, when α was doubled to 0.2. This increase in power was consistent regardless of number of monitoring sites assessed (**Figure 4.4**). Power reached a maximum of 0.6 ($\beta \sim 0.4$) when the number of monitoring sites was 1625. Minimum β was therefore approximately twice as large as α at the scale equal to the province of Alberta. For common, easily detected species, larger α also resulted in increased power, although the difference between the two levels of α diminished as power approached 100% (**Figure 4.4**). Using an error probability of 0.1, 60 sites per panel were required to reach a power of 90% (i.e., to have $\alpha = \beta$) for common species, while 10-15 sites per panel were required to reach a power of 80% when using an α of 0.2.

Discussion

Monitoring programmes having the goal of detecting trends or changes in species populations have traditionally focused on measures of local abundance (count-based monitoring), with area-occupied and presence–absence monitoring only more recently gaining popularity (Marsh and Trenham 2008). Despite a reduction in local information, presence–absence is viewed by many as a good indicator of change in population size and species range (Gaston 1994), especially in heterogeneous environments (Karr and Chu 1999). In contrast to count-based (abundance) monitoring of a few select species or single assemblage, much less is known about the effectiveness of monitoring trends in presence–absence for taxonomically-broad monitoring programmes that have numerous species within numerous assemblages. In Alberta, Canada, a large-scale (1,656 sites with 20-km spacing), long-term (100-year) systematic biodiversity monitoring programme managed by ABMI (Stadt et al. 2006) is attempting to detect 3% annual declines

in species prevalence (presence–absence across multiple sites) over a 20-year period and ideally at spatial scales as small as forest management areas.

Based on our simulations and sampling design, we found that 3% annual declines were detected for all but 1 of 252 species over a 20-year period of monitoring at a provincial scale (1,656 sites) and that declines could be detected for the majority of species (65%) at the level of a natural region (300 sites). However, at a forest management scale (25 sites) short-term trends were detected for only 8% of the species examined (species with a prevalence of 10% or more). Because our measure of detectability was across years, not within a season, change may have occurred during the period of monitoring making our estimates conservative. Detectability was also based on only ten permanent monitoring sites surveyed each year over a three year period resulting in detectability rates of species for any one site being either 33%, 66%, or 100% (low, moderate, or high). In contrast to detectability, prevalence was based on 85 monitoring sites where surveys were completed in at least one of the three years. Since our intent was to evaluate how changes in monitoring design variables (number of monitoring sites and duration of monitoring) and species variables (detectability and prevalence) affected statistical power for a long-term monitoring programme using species parameterized by best-available data, we do not see these limitations as problematic. Indeed, prevalence and detectability could have been randomly assigned to simulated species using some pre-defined distribution. This, however, would have compromised our goals of determining whether differences existed among assemblages and whether the ABMI programme had sufficient power to detect short-term trends at local scales.

Our results are similarly to those of Manley et al. (2004, 2005) who detected ($\alpha = 0.2$, power = 0.8) a 20% one-time change in species occurrence for 66% of Lake Tahoe vertebrates at ~2,760 sites using the United States Forest Service Multiple Species Inventory and Monitoring protocol. In the short-term, statistical power for Manley et al. (2004) was slightly higher than what we found due to the large number of sites surveyed (higher grid density) and higher α . Choice of α is arbitrary. An *a priori* discussion of what should be deemed a

statistically significant trend needs to be agreed upon prior to implementation of a biodiversity monitoring programme. Grid density, on the other hand, can be modified to improve short-term detection of trends. ABMI has a low systematic grid density (20-km spacing) and although it would be impractical to increase density for the entire province due to monitoring costs and logistics, certain regions of the province that are more threatened could be delineated and density of sites increased to improve short-term detection of biodiversity trends.

Indeed, one of the strengths of a systematic sampling design is that users can draw inferences about trends at different spatial scales. However, as the spatial scale decreases, so does the power to detect trends over short periods of monitoring. Prevalence of the species is also important. Detecting trends in rare species, especially in localized regions, is more difficult than for common species, resulting in fewer short-term indicators. We suggest that detectability needs to be at least 66% and species prevalence above 50% to detect short-term (~20 year) changes at relatively few sites (~25 sites). Using this rule-of-thumb, 11% of the 252 species evaluated (all common species) would be considered candidates for monitoring short-term trends in a localized region (i.e., a forest management area of Alberta). No single taxon (songbirds, bryophytes, and vascular plants) had a statistical advantage for detecting change. Assuming similar rates and encompassing all taxa included in ABMI (vascular plants, mosses, fungi, lichens, phytoplankton, birds, mammals, fish, springtails, mites, zooplankton, and benthic invertebrates), we estimate that 200 species could be used as short-term indicators for regional assessments. For some taxa where sub-samples are collected at a site, statistical power would likely improve if subsamples were used as units of replication (with a random effect for site).

One possible solution for monitoring short-term trends in rare species is to extrapolate trends from common species to rare species who share ecological similarities or vulnerabilities (Edwards et al. 2004; MacKenzie et al. 2005a). However, if the emphasis of the monitoring programme is ecosystem-wide, long-term biodiversity monitoring, then taxonomically-broad surveillance techniques that emphasize common species should be supported. Monitoring common

species does not presently fit the priorities of most conservation groups or existing monitoring programmes (for instance the Red List Index by Butchart et al. 2005). However, recent work suggests that even small proportional declines in common species can result in significant modifications to ecosystem structure, function, and services (Gaston and Fuller 2008). We suggest that species-based monitoring programmes need to include the complete range of species, including common species, and that long-term, ecosystem-wide monitoring cannot be used as a replacement for existing monitoring initiatives focused on rare species (e.g., Canada's Species At Risk Act) or specific management concerns.

Regardless of the prevalence of species being monitored, modifications can be made to the monitoring and analytical designs of the programme to enhance statistical power. This may include one or more of the following changes: (1) reduce observer error through staff training and modify survey protocols to increase detection probabilities; (2) account for detection probabilities of less than one through statistical analyses; (3) augment the traditional rotating panel survey design with monitoring sites that are visited repeatedly to account for natural annual variation; (4) stratify monitoring sites to better account for variance; (5) use community-level information to evaluate trends rather than analyses of individual species; and (6) integrate raw information or estimates from other monitoring programmes. Below we discuss possible advantages of each modification and practical challenges for implementation in a monitoring programme like that of the ABMI.

If a species has low detectability, it may be possible to modify survey methods to improve detectability and consequently increase power. Methods to reduce observer error will also boost detectability and increase statistical power (Strand 1996; Thompson and Mapstone 1997; Lotz and Allen 2007). For example, better training of field staff may be a cost-effective approach to minimizing observer error and increasing detectability. Gains from increased training however, may be limited for some taxa. For instance, even highly trained experts failed to detect 33% of lichen species that were known to occur at a site (McCune et al. 1997). Reducing observer error through modifications of survey methods or

increased staff training should clearly be a priority for monitoring programmes, but should not be considered the only solution for monitoring species with low detectability.

In addition to increased training and modification of survey methods to reduce observer error, statistical approaches can be used to account for low species detectability when sites are resurveyed within a single monitoring period (MacKenzie et al. 2005b). However, revisiting sites on a different date would substantially increase monitoring costs (double the cost for one revisit and triple the cost for two revisits) making these methods improbable for large-scale monitoring programmes that occur in remote locations such as the ABMI programme. Reduced-effort schemes that select only a sub-set of sites for intense, repeated sampling (Roy et al. 2007) may provide one compromise assuming that intensely-sampled sites were representative of reduced-effort sites. Repeat visits, however, assume a ‘closed’ status where occupancy does not change between repeated surveys (MacKenzie et al. 2005b). For sedentary species (i.e. vascular plants), increasing the sample effort (i.e. time spent surveying) to enhance detectability will often be more cost-effective than returning to a site on a different date because of travel costs (Drapeau et al. 1999). In some cases, re-sampling existing data may act as a surrogate for repeated visits, although this changes the definition of the spatial and/or temporal scale of sampling. For instance, bird songs are permanently recorded as 10- min surveys in the ABMI programme allowing re-sampling of the surveys into sub-samples for estimation of detection probabilities and corrections of occupancy at a site. For other taxa, use of multiple, independent observers during a single survey visit may prove to be a cost-effective solution to estimating detection probabilities.

Another approach to boosting statistical power of monitoring programmes that are based on rotating panel or serially alternating monitoring designs is to incorporate an augmented design. In augmented designs, a select set of sites (typically 20–50% of total) are repeatedly visited during a monitoring cycle (either in consecutive years for multiple panels or one panel selected for annual surveys) to measure and account for natural annual variation. By accounting for

annual variation in augmented designs, trends can be documented more effectively for a set number of monitoring sites than if the same effort was spent visiting new sites (Urquhart and Kincaid 1999). Since in our example the number of monitoring sites was fixed and the detectability and prevalence of species was critical to short-term detection of trends, we expect that an augmented rotating panel design will result in only small gains in power, yet substantially increase monitoring costs. Our expectation has not been tested.

When there is *a priori* knowledge about a species preferred habitats, stratified sampling that emphasizes important habitats can be employed to increase statistical power at any given level of effort. Rare species are often associated with particular habitats making stratified surveys especially effective for these species. However, stratified designs are problematic for long-term biodiversity monitoring programmes, since stratification must remain constant in the presence of natural and anthropogenic-induced ecosystem change (climate change, natural disturbances, etc.). In the presence of these changes, the extent and location of strata will change resulting in the loss of initially optimized statistical power. Although a systematic sampling grid may not initially be as optimal for detecting trends in some species as compared to a stratified design, the systematic monitoring design will not be dependent on initial conditions and will maintain its power over time. Systematic designs are therefore often favoured over stratified designs for long-term monitoring initiatives.

An alternative to analysis of trends for individual species is the integration of analyses among species. Relationships between biota and environmental conditions often are stronger for community-level analyses than for single species analyses (e.g., McCune et al. 1997) and the inclusion of additional species strengthens relationships for single species analyses (Plattner et al. 2004; Clarke and Murphy 2006). Metrics of species intactness (Buckland et al. 2005; Nielsen et al. 2007) can also be considered. For example, Lamb et al. (2009) found species intactness to be more effective for detecting trends than common measures of community diversity (i.e. Shannon or Simpson diversity) or multivariate analyses (i.e. Mantel test) of community change. As such, community analyses that build

upon statistical models of intactness are expected to better elucidate changes for rare species than individual analyses of species using prevalence.

Statistical power of monitoring programmes can also be enhanced by integrating raw information or parameter estimates from other monitoring programmes (Henry et al. 2008; Lengyel et al. 2008b). Analytical techniques, such as meta-analysis or weighted analysis, can be used to combine information from other monitoring programmes allowing for more immediate assessments of biodiversity change (Henry et al. 2008). Critical to this integration is clear definitions of survey methods. In the long-term, creation of a standardized, international monitoring network or a common set of biodiversity monitoring protocols is needed to facilitate direct comparisons and reporting of biodiversity trends (Henry et al. 2008; Lengyel et al. 2008b).

Conclusion

In summary, we advocate that biodiversity monitoring programmes include a continuum of species from rare to common. The inclusion of rare species will build support for the monitoring programme because loss of rare species is easily understood by the general public (Biggs 2000). However, large-scale biodiversity monitoring programmes cannot be expected to be a replacement for existing monitoring programmes that focus on rare species, since detectability and observer error from more general survey methods are likely to compromise detection of trends. Furthermore, emphasis on rare species may be misplaced ecologically since even small reductions in abundance of common species will have profound effects on ecosystems (Gaston and Fuller 2008), making such species important components of monitoring programmes. Inclusion of common species should also increase statistical power of the programme and facilitate community-based metrics of biodiversity. We think that taxonomically-broad monitoring programmes will be of great value to managers and increase in value with time. For instance, it will be possible to evaluate the effects of climate change on species distribution (geographic range) using information from long-term, large-scale monitoring programmes that measure a broad spectrum of species. Taxonomically-broad monitoring is also more likely to facilitate a

proactive monitoring and management approach to conservation by recognizing trends early on and thereby maintaining common species while being common, as opposed to a reactive monitoring and management paradigm that focuses on rescuing rare species that have already declined markedly.

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Table 5. 1 Number of monitoring sites and panel sizes (number of monitoring sites within panel) considered in assessments of statistical power for detecting 3% annual changes in species occurrence. Scales represented in Alberta based on a 20-km by 20-km systematic grid are provided.

Number of monitoring sites	Panel size	Area (km ²)	Regional scale represented
25	5	10,000	Forest management agreement
50	10	20,000	↓
75	15	30,000	Natural sub-region
100	20	40,000	↓
300	60	120,000	Natural region
1625	325	650,000	Province of Alberta

Table 5. 2 Prevalence and detectability of species used in simulations, as measured at selected ABMI monitoring sites in the boreal natural region of Alberta.

Taxonomic group	Number of species	<i>Prevalence</i>		<i>Detectability</i>	
		Mean	St. Dev.	Mean	St. Dev.
Birds	62	0.41	0.25	0.59	0.20
Bryophytes	65	0.42	0.23	0.63	0.16
Vascular plants	125	0.35	0.24	0.69	0.22

Table 5.3 Percent of species where 3% annual declines were detected at a power of 90% ($\beta = 0.1$) and an $\alpha = 0.1$ for combinations of sample size (number of monitoring sites) and period of monitoring (years and number of re-visits) by assemblages. Light and dark grey shading represents scenarios where at least 50% and 75% of species respectively reached desired power. A box outlines those scenarios that reached an optimal success of 100% of species.

Taxa	Years	Number of re-visits	Number of monitoring sites (Number per panel)					
			25 (5)	50 (10)	75 (15)	100 (20)	300 (60)	1625 (325)
Birds (62 spp.)	10	2	0	3	6	13	18	62
	20	4	11	18	21	27	64	100
	30	6	16	29	39	55	80	100
	40	8	21	42	60	66	97	100
	50	10	31	58	69	77	100	100
Bryophytes (65 spp.)	10	2	0	2	2	6	23	70
	20	4	6	18	23	40	71	98
	30	6	18	37	48	60	91	100
	40	8	23	48	68	71	97	100
	50	10	37	66	74	85	100	100
Vascular plants (125 spp.)	10	2	0	2	5	12	34	66
	20	4	8	28	32	38	62	100
	30	6	26	36	46	54	82	100
	40	8	30	45	56	63	95	100
	50	10	32	53	65	76	100	100
			10000	20000	30000	40000	120000	650000
			Spatial scale (km ²) at 20-km spacing					

Table 5. 4 Estimated coefficients (β_i), standard errors (SE), P values (Wald z statistic), percent change in odds ratio per unit increase in covariate X (%), coefficients for Z-standardized variables (β Z-StdVar), percent change in odds ratio for a standard deviation increase in covariate X (%StdX), and standard deviation of X (SDofX) for estimating the power of a monitoring program ($\alpha = 0.05$, $df = 5665$, 190 clusters, $r^2=0.87$).

Variable	Unstandardized variables				Standardized variables		
	β	SE	P	(%)	β Z-StdVar	%StdX	SDofX
<i>Program design variables</i>							
Number of monitoring sites per panel	0.025	0.002	<0.001	37.7	2.85	1624	113.2
Number of monitoring cycles	0.624	0.035	<0.001	68.7	1.77	485	2.8
Number of monitoring sites per panel squared	-0.770 [†]	0.048 [†]	<0.001	36.8	-2.97	-94.9	38660
Number of monitoring cycles squared	-0.027	0.002	<0.001	35.8	-0.95	-61.3	34.6
<i>Species variables</i>							
Prevalence	3.036	0.180	<0.001	766	0.70	101.4	0.231
Detectability	0.273	0.214	0.202	48.3	0.06	5.7	0.204
Prevalence squared	-3.432	0.304	<0.001	1.2	-0.74	-52.3	0.216
Detectability squared	1.035	0.189	<0.001	104	0.28	32.5	0.272
<i>Interaction terms</i>							
Detectability and prevalence	4.314	0.339	<0.001	2751	1.00	172.4	0.232
Number of monitoring sites per panel and number of monitoring cycles	0.508 [*]	0.066 [*]	<0.001	37.0	3.95	5103	777.5
Constant	-4.534	0.161	<0.001	0.4	2.89		

[†] coefficients and SE 10000 times original value, ^{*} coefficients and SE 100 times original value

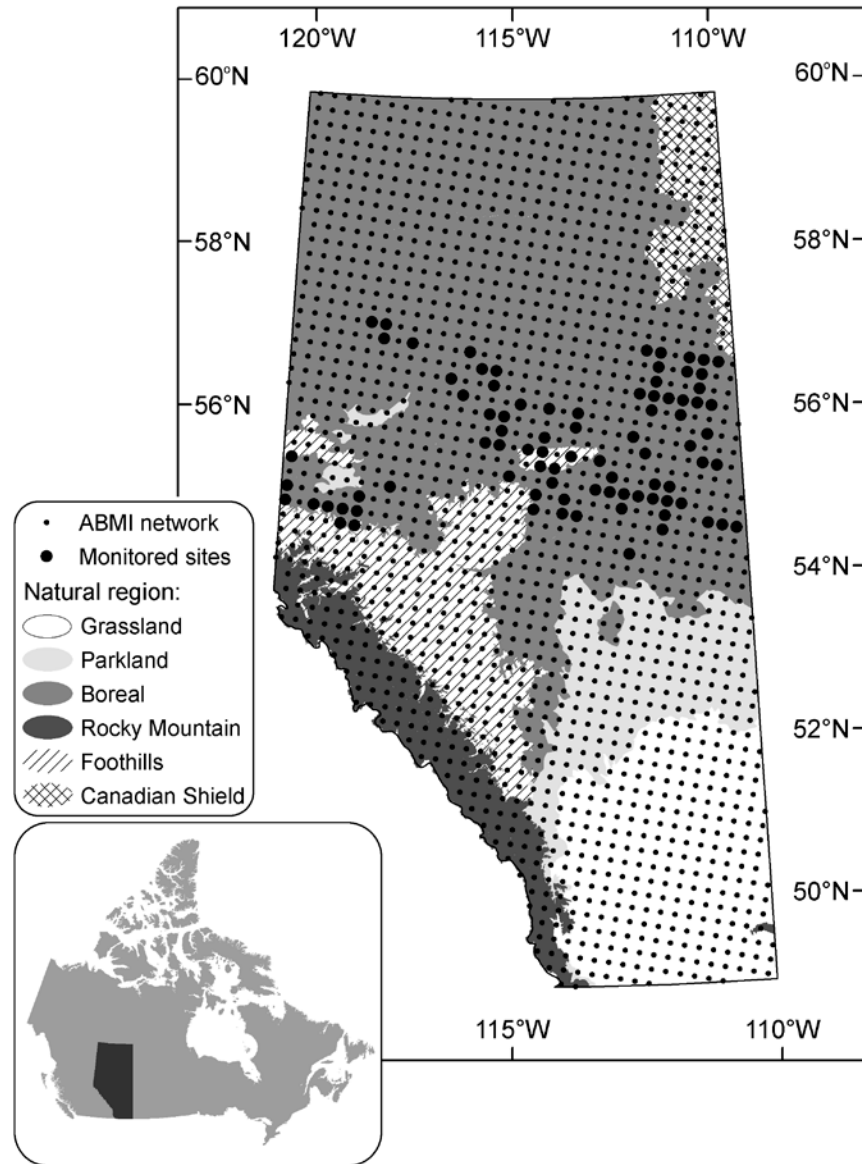


Figure 5. 1 Location of sites from the Alberta Biodiversity Monitoring Institute (ABMI) used to evaluate program monitoring power. The ABMI network is a 20-km by 20-km systematic grid. Location of Alberta in Canada depicted in the lower left figure.

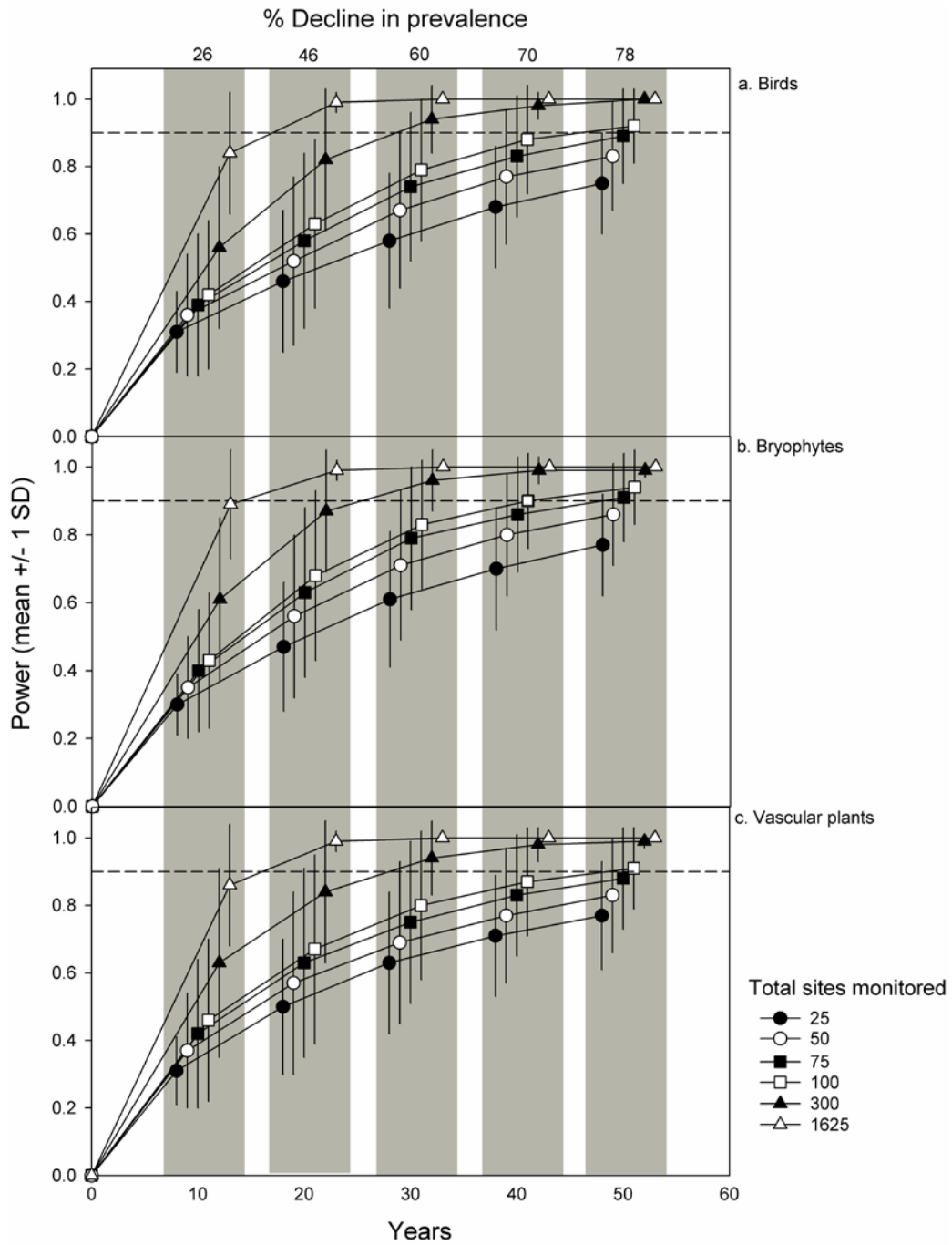


Figure 5. 2 Power curves by assemblage (a.birds, b. bryophytes, c. vascular plants) for six sample sizes across sampling period.

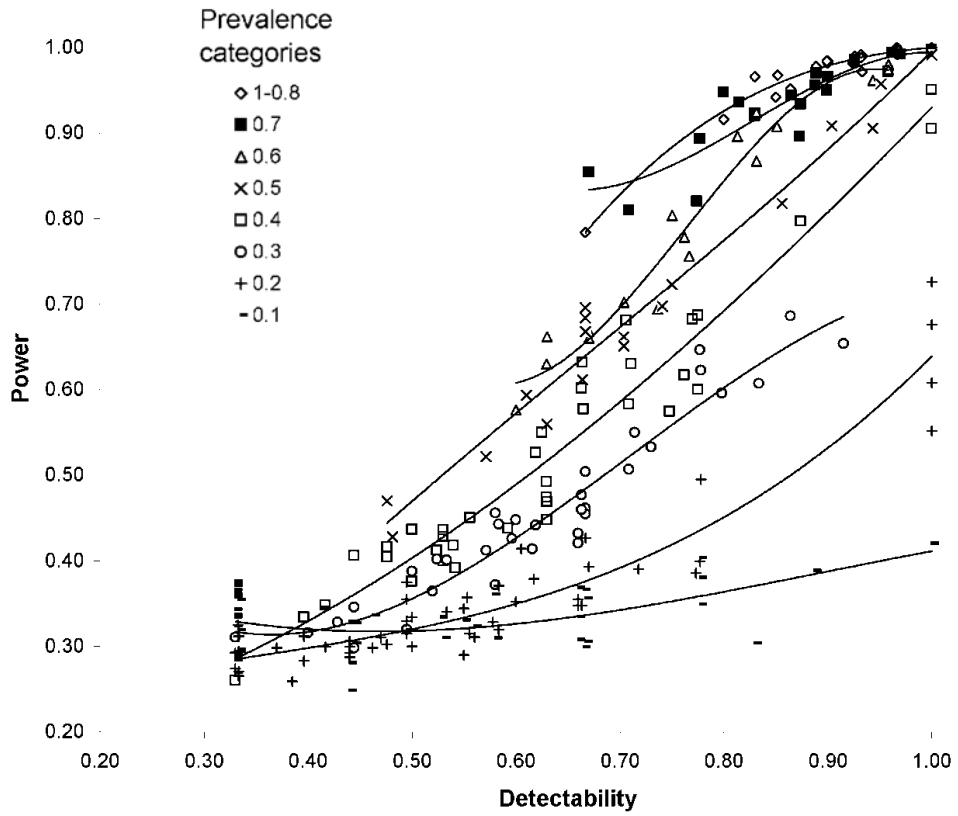


Figure 5. 3 Relationship between statistical power and species prevalence and detectability at a -3% annual trend, 50 monitoring sites, and 20 years of monitoring.

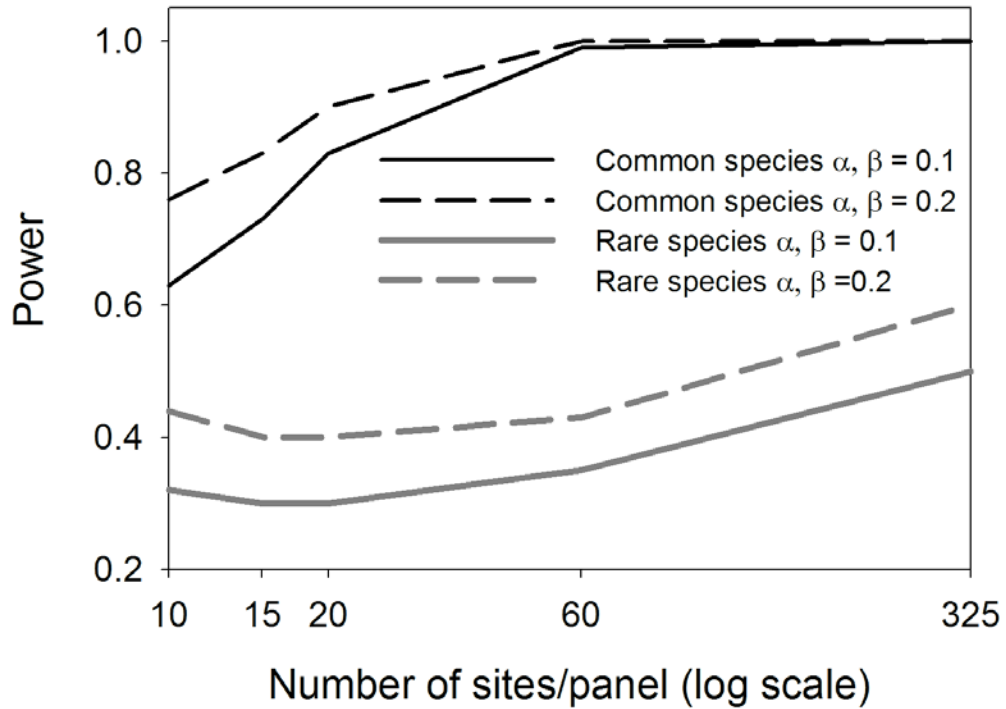


Figure 5. 4 Power to detect change over time for $\alpha = \beta$ at 0.1 and 0.2. These analyses were conducted for a common, easily-detected species (prevalence = 0.74, detectability = 0.89) and a rare, difficult to detect species (prevalence = 0.13, detectability = 0.33).

CHAPTER SIX

What is the value in monitoring multiple assemblages? A boreal forest case study

Introduction

Biodiversity in many regions is subject to multiple, overlapping anthropogenic disturbances, including climate change, forestry, agriculture, and non-renewable resource extraction. Understanding the impacts of these diverse disturbances on biodiversity is difficult; the traditional approach of relying on a either a single assemblage or single species as an indicator of change or surrogate for other components of biodiversity is neither theoretically nor empirically supported (e.g., Saetersdal and Gjerde 2011). Recent meta-analyses found that agreement or concordance between richness of different assemblages typically is weak, particularly at the ecosystem scale (Wolters et al. 2006, Rodrigues and Brooks 2007 Heino, 2010 #2916). Rather than continue to look for indicators, cost-effective or otherwise (Gardner et al. 2008), the inverse approach may be more fruitful for understanding biodiversity change. Given that multiple ecological and disturbance gradients simultaneously determine species' distributions, ecologists may be better served by a suite of assemblages that provide highly complementary rather than concordant information on biodiversity change. Examining the value of complementarity is often difficult in traditional small-scale research, where time and money constraints typically mean diversity can only be incorporated for one aspect: biota, habitat types, or disturbance types. Recent large-scale multi-taxon monitoring initiatives provide a means of redressing this difficulty.

The Alberta Biodiversity Monitoring Institute (ABMI) tracks the status and trends in occurrence and/or relative abundance of over 2,000 species across the province of Alberta, Canada (an area of 661,848 km²), estimates species' ranges of natural variation in intact habitat, detects when species are outside the range of natural variation with a predetermined statistical probability, and correlates those shifts to changes in the environment, including climate change.

The assemblages monitored by ABMI were chosen using a variety of criteria including pragmatism (availability of experts for identification and unbiased rapid assessment protocols that could be employed by field technicians), ecology (known sensitivity to environmental gradients and/or anthropogenic disturbance), efficiency (potential to record a relatively high number of species in a short survey period), and appeal to the public. The ABMI currently includes (but is not limited to) oribatid soil mites, bryophytes, vascular plants, and breeding birds amongst its suite of measured attributes (background information is available at www.abmi.ca and in Chapter One and Two).

Despite their apparent sensitivity to environmental gradients, both natural and anthropogenic (e.g., Gignac 1992, Vitt and Belland 1995, Jonsson and Jonsell 1999, Frego 2007, Cole et al. 2008, Gergocs and Hufnagel 2009, Caners et al. 2010, Dechene and Buddle 2010, Sylvain and Buddle 2010), oribatid soil mites and bryophytes are not commonly included in biomonitoring. They appear to have limited appeal to the public, and there are relatively few specialists for species identification. In contrast, vascular plants and birds are two of the most commonly monitored assemblages, and are very appealing to both scientists (e.g., Pereira and Cooper 2006) and society (as evidenced by the abundance of field guides for their identification).

Here we assess both the complementarity and the concordance of these four terrestrial assemblages monitored by the ABMI. We compared the response of oribatid soil mites, breeding birds, vascular plants, and bryophytes to three natural gradients (space, climate, and nutrient-moisture conditions) as well as anthropogenic disturbance gradients as measured by changes in stand structure and in extent of area disturbed by different anthropogenic land uses. We compare the sensitivity of each assemblage to anthropogenic disturbance as estimated by changes in species richness, as well as indicator species analysis for different intact forest stands and disturbed forest stands. We also compare the number of species monitored within each assemblage, and the completeness of the methods in recording diversity within each assemblage. The boreal forest is an interesting biome for such analyses because the majority of the world's intact and unmanaged

forests are boreal forests (United Nations Environmental Programme (UNEP) 2002). Increasingly however, the boreal is subject to fragmentation and habitat alteration due to extraction of non-renewal resources, forestry, and agriculture (Alberta Environmental Protection 1998, Timoney 2003, Schneider and Dyer 2006, Ruckstuhl et al. 2008).

Methods

Study area & survey design

ABMI's monitoring design consists of 1,656 permanent sites evenly spaced across Alberta on a 20 x 20 km grid (**Figure 1.1**, Chapter One). The ABMI began data collection during a prototype phase from 2003-2006. From 2007 onwards, groups of 9 sites were visited as part of a predetermined rotation or set of sites across Alberta. During 2007-2010, additional supplementary sites were surveyed using ABMI protocols. We included sites from the Boreal Plains ecozone of Alberta in this analysis (Environment Canada 2008, **Figure 6.1**). The data were collected from across an area of 381, 357 km² (**Figure 6.1**). The elevation range is 192-1560 m above sea level, and elevation is strongly correlated with latitude and longitude, decreasing from the foothills of the Rocky Mountains in the southwest to the edge of the Canadian Shield in the northeast (**Figure 1.1**, Chapter One). The forested area is characterized by a patchy mosaic of habitats, ranging from dry, nutrient-poor sites dominated by pine trees (*Pinus banksiana* and *P. contorta*) to wet, nutrient-rich sites dominated by small black spruce (*Picea mariana*), larch (*Larix laricina*) and/or birch (*Betula*) shrubs. The most common ecological condition however, is mesic moderately nutrient-rich mixedwoods dominated by poplar (*Populus tremuloides* and *P. balsamifera*) and conifers, predominantly white spruce (*Picea glauca*).

Field methods

Here I briefly describe the methods used to collect field data, but more detailed information can be found online (e.g., Alberta Biodiversity Monitoring Institute 2010), and in **Figure 1.2**, Chapter One. Additional taxonomic

information is available in **Appendix 6.1**. To survey songbirds, technicians conducted point counts during a single visit to each monitoring site during the breeding season (late May to June). Starting within 30 minutes of sunrise, technicians used omni-directional microphones to digitally record singing birds for 10 minutes at each of nine pre-determined locations. Locations were spaced 300 m apart. All audio recordings were interpreted by an expert in a standardized laboratory setting, and the number of individuals heard of each species enumerated. Mites were collected from soil cores collected approximately 7 m from the outer corners of the 4 quadrants of the 1 ha plot. At each coring location, a minimum of 4 cores were taken in a standardized pattern until 500 mL of the litter-fermentation-humus soil layers was sampled. The soil was kept cool and transferred to the lab within 7 days of collection, where the living mites were extracted using Berlese funnels for 7 days. All mites $\geq 300\mu\text{m}$ in length were identified and enumerated. The abundance of each species at each site is the sum of the individuals observed over all samples.

Vascular plants were surveyed at each monitoring site during July using 20-minute circular transect searches on each of four 0.25 ha plots. Species that could not be identified in the field were collected for expert identification in the laboratory. During the same visit in July, the relative abundance of bryophytes was determined using time-limited searches of microhabitats. From 2003-2008, the presence of microhabitats was determined prior to the searches, and a 1.5-2 hour search for bryophytes was conducted at as many examples of each microhabitat as possible throughout the 1 ha site. Microhabitats included lowland and upland substrates, trees and stumps, downed woody material, and rocks (**Table 3.1**, Chapter Three). From 2009 onwards, four 25 x 15 m plots (0.15 ha total) within the 1 ha site were surveyed separately to increase the effort per unit area and the repeatability of surveys (Chapter Three). Species-rich strata (downed woody material, lowland substrates, and rocks) were searched within the plot: less diverse strata (upland soils and trees and other vertical substrates) were searched in 50 x 2m belt transect along two sides of the quadrant (**Table 4.1**, Chapter Four). One technician spent up to 35 minute in each of the four plots (maximum

total 140 minutes) collecting specimens from different microhabitat strata. Technicians collected samples of each moss and liverwort that appeared distinctive for later identification by expert bryologists in the laboratory or students under expert supervision (Chapter Four). **Appendix 6.2** presents a preliminary comparison of the two survey methods. For vascular plants, relative abundance was calculated as the number of quadrants a species was recorded in. For bryophytes, we limited the analysis to detection/non-detection at the site due to the methodological change.

Covariate estimation

Climate

We used mean annual temperature (MAT), mean annual precipitation (MAP), and growing degree days exceeding 5 degrees Celsius (GDD5) to model climate gradients. These data were estimated from the Alberta Climate Model (Alberta Environment 2005), and reflect average conditions from 1961-1990.

Space & geography

Latitude and longitude in 10 TM universal transverse mercators (LAT and LONG), as well as elevation (ELEV) were included to account for spatial gradients in species distributions.

Anthropogenic disturbance/land use

Using a combination of updated geographic information system (GIS) layers and satellite imagery, the area affected by human activity was classified and quantified within a 3x6 km polygon around each site using ArcGIS software and SPOT satellite imagery (Alberta Biodiversity Monitoring Institute 2011). The age of disturbance was not available for some features so initial layers were vetted by eye; any disturbance no longer visible to a technician in the 2007 satellite imagery was removed from the disturbance layer, and additional polygons of physical disturbance were added (Hird et al. 2009). The final layers were combined, clipped to different scales and summarized as the total percent of area disturbed. The two scales used herein are the 1 ha square (HA_PTOT), and 500 m radius (HKM_TOT) circle centered on the 1 ha site. Within the 1 ha, disturbance

was categorized as the percent area impacted by industrial (e.g., well pads, gravel pits, pumping stations, oil and gas plants, HA_PIND), hard linear features (e.g., roads), soft linear features (e.g., seismic lines, power lines, and pipelines and other vegetated right-of-ways, HA_PSLIN), forestry (HA_PFOR), and agriculture (HA_PAG). The total disturbance at each scale was expressed as a percentage of the area disturbed. Correlation between the scales of disturbance was high ($r > 0.85$), so we used the least correlated subset of these variables using a variance inflation factor cut-off of ≤ 3 : HA_PTOT, HA_PAG, HA_PFOR, HA_PSLI, HA_PIND (Zuur et al. 2009).

Stand structure and nutrient-moisture conditions

Fifty-three covariates describing current stand structure at each site were available. For trees and snags, we created three synthetic variables to reduce the original 53 variables to the strongest underlying gradients using non-metric multidimensional ordination (TREEA1-3, NMDS, **Appendix 6.3**). Downed woody material (DWMVOL) volume was calculated as the sum of the volume of DWM size classes, summed over the four DWM transects. An index of vertical complexity (VCOMPLEX) was created by counting vegetation layers present at a site, including short and tall shrubs, and small (≤ 7 cm diameter at 1.3 m height [DBH]), medium (7.1-24.9 cm DBH), and large (≥ 25 cm DBH) deciduous and coniferous trees. Depth of the organic soil layer was estimated as the overall average of two soil transects at each site (DEPTHORG). The average percent cover of shrubs greater than 1.3 m tall (TSHRUB_C) and less than 1.3 m tall (SSHUB_C) were estimated in 10 m² plots in each quadrant. The estimated areal extent of wetland (WETLAND) was a composite metric, compiled from landcover classes from GIS layers as well as digital elevation models. The dominant nutrient and moisture conditions (NM) at each site were included using binary dummy variables. Rare NM conditions were grouped with similar ecosites. The four NM conditions used were 1) nutrient-medium to -poor xeric sites dominated by pine or black spruce (NM_PX), 2) nutrient-medium mesic sites dominated by poplar or mixedwoods (NM_MM), 3) nutrient-medium to -rich hygic sites dominated by poplar and white spruce (NM_RG), and 4) nutrient-

poor to –rich hydric sites dominated by black spruce and larch (NM_PD).

ABMI's boreal classification system is a simplified version of published ecosite descriptions (e.g., Beckingham and Archibald 1996, Willoughby et al. 2006). We classified disturbed sites by their historical NM as a measure of their potential ecological traits. Stand structure was used as a proximate metric of the effect of disturbance as measured through geographic information systems (see below).

Site selection

We *a priori* excluded sites in open water, as well as marshes and fens dominated by shrubs. We excluded sites that burned in the last 30 years to avoid confounding natural and anthropogenic disturbance. To represent gradients at undisturbed sites, we selected sites with $\leq 1\%$ disturbance in the central 1 ha square, and excluded sites that had been revisited multiple times, which left 105 unique sites. To represent highly disturbed sites, we chose sites with $\geq 80\%$ disturbance in the central 1 ha. To approach the number of intact sites we used all 91 disturbed sites fitting the above criteria as well as 3 sites with lower disturbance (mean of 67% disturbance), for a total of 199 sites located across the boreal ecozone (**Figure 6.1**). Most surveys were conducted on core ABMI grid sites. Of the 51 supplementary sites, 20 were distributed across the boreal and were surveyed by the senior author, 13 sites were surveyed in Alberta's Central Mixedwood subregion in cooperation with Alberta Pacific Forestry and the remaining 18 sites were surveyed in Alberta's Foothills natural region by ABMI (provincial natural regions are outlined in Alberta Environment et al. 2005).

Breeding birds, vascular plants, and bryophytes were surveyed at all 199 sites, while oribatid soil mites were added to the program in 2007 and subsequently were included in 149 of the 210 sites. Bird surveys were complete (all 9 point counts conducted) at 98% of sites included here; 4 sites are missing 1-2 point counts due to bear encounters, impassible geography or technical difficulties

Statistical methods

We used indirect gradient analyses (or free gradient analyses) to infer the relative importance of different climatic, spatial, environmental, and anthropogenic disturbance variables in structuring assemblages. We used non-metric multidimensional scaling (NMDS) to ordinate spatial, climatic, anthropogenic disturbance, and current stand structure covariates, as well as the assemblages themselves. We chose NMDS because it has proven powerful at extracting underlying gradients in relatively few synthetic axes, and it allows the use of non-normal, nominal, categorical and quantitative data simultaneously, given the appropriate data standardization (McCune and Grace 2002).

Prior to ordination, we removed species that were present at $\leq 5\%$ of the sites because we were most interested in uncovering strong compositional gradients. Ordinations for assemblages were constructed for 1 to 6 dimensions, and then a final ordination re-run using the dimension beyond which further reductions in stress were proportionately small. Raw abundance data for mites and birds were $\log(x+1)$ transformed prior to analysis, and Bray-Curtis (Sørensen) distance used to construct distance matrices for mites, birds, and plants, while Jaccard distance was used for bryophytes. Different metrics produced very similar ordinations. No mites, bryophytes, or vascular plants were *a priori* excluded, but we excluded raptors as well as shorebirds and waterfowl associated with open water or recorded mainly as fly-overs from the bird recording data. We also removed all records for specimens not identified to species except the bryophyte genera *Bryum* and *Brachythecium*. These genera are not routinely identified to species by ABMI, so all species in each respective genus were grouped for analyses.

Environmental ordinations were estimated for 2 axes because the number of variables in each ordination was limited to between 3 and 8. Variables were examined for collinearity, standardized to z-scores with a mean of 0 and standard deviation of 1 prior to analysis, and Euclidean distance was used to construct distance matrices. Space was represented simply as the z-transformed LAT and LONG of each site. Our metric of space was simple, but as our purpose was to

examine the relative effect size between taxa rather than derive an absolute measure of spatial variation, it should suffice. In addition, more complicated methods often do not perform any better (Gilbert and Bennett 2010).

For each assemblage we compared assemblages to each other based on composition within sites and to the four gradients using Procrustes-based Protest with 9,999 permutations to assess significance (Jackson 1995, Peres-Neto and Jackson 2001). This provides a measure of correlation (m^2) in structure between two ordinations. In addition, we examined the correlations of each independent variable to the assemblage ordination axes, again using 9,999 permutations to estimate the significance of the goodness-of-fit statistic r^2 . Because multiple metrics of concordance are recommended (Gioria et al. 2011), we also conducted Mantel tests (Mantel 1967, Smouse et al. 1986) using Spearman ranks and 9,999 permutations to assess significance of correlations in the raw distance matrices. We examined whether assemblages at undisturbed sites varied significantly by nutrient-moisture conditions using permuted multivariate analysis of variance of distance matrices with function `adonis` in the R package `vegan` (Anderson 2004, Oksanen et al. 2011). Because significant differences may be caused by differences in composition and/or heterogeneity in multivariate dispersions, we also ran a permuted test for homogeneity using function `permutest` in `vegan` (based on Anderson 2006). Both tests were run with 9,999 permutations to assess significance.

To compare the completeness of the samples as well as α (alpha) and γ (gamma) diversity for each assemblage and each disturbance class using all species, we constructed sample-based species area curves (SAC) (Colwell and Coddington 1994, Colwell et al. 2004). We compared species density (number of species rarefied by sample size) because it reflects both species richness and species distribution within sites (Buddle et al. 2005). We calculated the species turnover between undisturbed sites vs. disturbed sites by pooling species in each category and comparing the two species pools with 1-Jaccard similarity coefficient for occurrence. Finally, we conducted indicator species analyses (ISA, Dufrêne and Legendre 1997) using 9,999 permutations to assess significance for

each assemblage. We conducted ISA for undisturbed sites to compare the proportion of species tightly linked to specific NM conditions, as well as at all sites by disturbance category.

We ranked the assemblages from highest (1) to lowest (4) in each of the following categories: species richness, diversity sensitivity, community composition sensitivity, concordance with other assemblages, numbers of indicator species and relative effort required to reach the level of completeness. Effort was not enumerated in dollar amounts, rather the number of hours required to gather field samples and process and identify those samples was compared. Availability of expertise considered general availability of skilled taxonomists in North America. For example, while ABMI employs an excellent acarologist at present, should he retire, ABMI would be extremely hard pressed to find a replacement as he is one of a few people in North America with these skills (**Appendix 6.1**). In contrast, there are many more skilled botanists and ornithologists. Surveys requiring less effort were given higher ranks. Concordance was ranked by first ranking all correlations in **Table 6.3**, and then summing the ranks for each assemblage. The assemblage with the lowest summed rank was considered to have the highest overall cross-taxon concordance.

Rarefactions, species richness and sample similarity estimates were calculated in either EstimateS (Colwell 2009) or R (R Development Core Team 2011), mainly with the vegan (Oksanen et al. 2011) and BiodiversityR package (Kindt 2012). Multivariate analyses were done in PC-ORD (McCune and Mefford 2011) and with the R vegan package.

Results

Assemblage composition

The final stress of all NMDS ordinations was between 10-20, and the configurations were highly comparable between runs and when conducted in either PC-ORD or R. Two-axes solutions were chosen for all assemblages as three axes provided minimal gains in stress-reduction (**Figure 6.2**). Space and

climate gradients were highly correlated, as expected given the latitude and elevation gradients in Alberta's boreal forest (**Table 6.1, Figure 1.1**).

Anthropogenic disturbance, measured directly as areal extent or indirectly as stand structure, was either not correlated or weakly correlated with space. As a result, the influence of these two sets of gradients (climate-space) and (areal disturbance-stand structure) could be considered independently.

Oribatid mites were the only assemblage where climate was the strongest correlative environmental gradient, although mites also were moderately correlated with stand structure (**Table 6.2**). Community composition of breeding birds, vascular plants, and bryophytes were most correlated with stand structure, followed by climate for birds and anthropogenic disturbance for plants and bryophytes (**Table 6.2**). Cross-taxon correlations were approximately 20-25% stronger than the strongest environment-assemblage correlations (**Table 6.3**). Bryophytes exhibited the highest cross-taxon concordance to other taxa.

Vascular plant community composition appeared to be the most responsive to multiple gradients, as the ordination axes were significantly correlated at $P < 0.01$ with 17 of 24 covariates (**Table 6.4**). Vascular plant community composition varied the most between nutrient-moisture (NM) site classifications, although all four assemblages varied significantly between NM conditions (permuted multivariate anova - plants: $F_{3,101}=13.15$, $P < 0.001$, $r^2=0.28$ vs. mites: $F_{3,61}=2.96$, $P < 0.001$, $r^2=0.13$, birds: $F_{3,101}=5.74$, $P < 0.001$, $r^2=0.15$, or bryophytes: $F_{3,101}=5.89$, $P < 0.001$, $r^2=0.15$). For birds and bryophytes, these differences were due largely to compositional shifts (permuted test of homogeneity - mites: $F_{3,61}=2.22$, $P=0.098$, birds: $F_{3,101}=1.25$, $P=0.3$). However, flora were heteroscedastic (permuted test of homogeneity - plants: $F_{3,101}=11.57$, $P < 0.001$, bryophytes: $F_{3,101}=4.87$, $P=0.006$). Examination of multivariate dispersion plots and Tukey post-hoc tests suggest PD sites were more heterogeneous than the MM and RG upland sites for bryophytes. This may be due to the simplified classification system that grouped forested nutrient-poor and nutrient-rich hydric sites together (PD) rather than a real difference in beta diversity between NM classifications. Vascular plants sites formed two post-hoc

groups, MM-RG and PD-PX. Of the four anthropogenic disturbance types, agriculture had the strongest effect on community composition of all four assemblages (**Table 6.4**).

Species richness

The surveys for fauna appear to have captured a larger percentage of the predicted species richness as compared to the flora, but the lower completeness of the floral surveys may be due to methodological differences (occurrence in plots as the base metric rather than the abundance of individuals (Chapter Three, **Table 6.5, 6.6**). Overall, the surveys have recorded >80% of the species expected at undisturbed sites, and >73% of the species expected in disturbed sites. Species richness varied little by NM groups in intact sites, but the trend in species richness in response to disturbance varied by NM classification and assemblage (**Figure 6.3**). Of the four disturbance types, agriculture had the strongest effect on richness, diminishing richness of species in all groups except birds, where additional species found only in disturbed sites increased species richness (**Table 6.5, 6.6**). Upland sites (PX, MM, RG) generally decreased in richness with disturbance, while the lowland site (PD) tended to increase in richness (**Figure 6.3**).

Species turnover between disturbed and undisturbed species pools

Turnover was highest in vascular plants (0.406), followed by bryophytes (0.378), mites (0.315), and birds (0.195). Turnover in plants was the result of 141 additional species populating disturbed sites and a loss of 85 species restricted to undisturbed sites, while 332 species were shared. Bryophyte turnover resulted from the loss of 54 species only detected in undisturbed sites, and the addition of 13 disturbed site species, while 96 species were shared. Turnover in mites was due to the loss of 31 species found in undisturbed sites and the gain of 13 species found only in disturbed sites. For birds, 91 species were shared between disturbed and undisturbed sites; 4 undisturbed species were lost while 18 additional species were found in disturbed sites.

Indicator species

When considering species that occurred at $\geq 5\%$ of sites, bryophytes and plants had the highest percentage of ecological indicator species (**Figure 6.4**). The nutrient-moisture classifications with the most significant indicator species were the wetter ecosites, PD and RG. Bryophytes also had the highest proportion of undisturbed site indicators, followed by mites, plants and birds. Plants had the highest proportion of disturbance indicators overall. More birds exhibited high fidelity to agriculture, while mites, bryophytes and plants had a greater proportion of indicator species for soft linear features such as power lines and pipelines (**Figure 6.4**).

Discussion

Overall, vascular plants and oribatid soil mites were ranked higher in diversity, sensitivity to ecological and anthropogenic gradients, and logistical feasibility than birds or bryophytes (**Table 6.7**). Mites and plants could be considered to form a complementary suite of species for programs desiring to assess changes in biodiversity, although the availability of taxonomists for mites certainly will be a limiting factor. Bryophytes were also responsive to ecological gradients, particularly for lowland forests, and were highly concordant with other taxa. However, bryophytes require the most effort in the laboratory as species are not identified in the field and composite sample bags require sorting prior to identification (Chapter Three). Ranks for birds suggest that the other assemblages surpass them as indicators or surrogates in every metric except the level of completeness. However, given that birds are allocated more field effort (approximately 4 hours vs. 2.5 hours for plants, 2.5 hours for bryophytes, and approximately an hour for mites), and they are the lowest diversity assemblage, it is not surprising that these surveys have recorded almost all species predicted to occur in the region. Our summary suggests if only one survey could be performed, vascular plants would be the best ecological and logistical choice.

We know of no other study that has performed these comparisons for these assemblages, or compared the response of these assemblages over multiple

gradients. In general, comparisons of concordance between studies are of limited utility because of the different gradients, gradient lengths, and disparate suite of assemblages each study examines. In addition, the pragmatic logistic parameters vary greatly between research programs, including the money available for surveys, costs to conduct surveys given a region's terrain and accessibility, and the availability of taxonomic expertise. Rather, we hope to illustrate an approach that other biomonitoring programs can employ to compare the information each assemblage provides and prioritize the allocation of effort and money.

Gardner et al. (2008) examined the ability of 14 assemblages to act as 'high-performance indicator taxa', i.e., taxa that were both good indicators of some ecological measure of integrity and were cost effective to sample. While they determined dung-beetles and birds were the best indicators, they also cautioned that their study examined a single anthropogenic gradient in a single region. Our approach differs from that of Gardner et al. (2008) in that we examined multiple ecological and anthropogenic disturbances, and we sought complementarity as well as concordance. The utility of the additional information gained by monitoring complementary assemblages will vary according to the research question; if the question involves assessing the response of biodiversity in any broad sense (not biodiversity of a predetermined assemblage or guild) to a given disturbance or gradient, we argue that monitoring complementary assemblages is a more productive route than seeking concordance.

There are conflicting recommendations regarding the utility of examining change in a group of species by individual-species-based indices or by community-level-indices when detection error varies. Lamb et al. (2009) found that indices based on averaging individual species indices of abundance were favoured over diversity indices or multivariate indices, particularly when species had low detectability. McCune et al (1997) also concluded that metrics such as species richness were not consistent between observers, but differences in ordination space were highly robust to observer error. We found that multivariate ordinations were sensitive methods for examining an assemblage's response to different gradients, but that species richness was also sensitive for certain taxa,

namely mite and bryophytes. We suggest this variation is due to non-random species loss, and variation in different assemblage's ability to repopulate or persist in disturbed areas. However, we didn't calculate indices of biotic integrity for individual species, and this would be an interesting comparison to make in future research.

Future research

Future work should examine guilds within each assemblage to better understand the biological mechanisms behind composition change and declines in species richness. For example, liverworts are known to be more sensitive to forestry than bryophytes (Baldwin and Bradfield 2007, Caners et al. 2010). Grouping them in analyses alters the interpretation of their response to anthropogenic disturbance. Of course, each species will respond in a slightly different way to disturbance, and the ABMI is developing individual-based indices of biotic intactness (Nielsen et al. 2007, Alberta Biodiversity Monitoring Institute 2009). The challenge with individual species is that ABMI methods have relatively high detection error for many species (Chapter Three, Five), making inference more difficult at that scale. It may be that guilds or functional groups provide the best balance of robustness to detection error and sensitivity to environmental perturbation. In addition, it would be interesting to replicate these analyses for the remaining terrestrial taxa, including macrolichens and winter-active mammals.

At present, the ABMI has collected 32% of the sites in the boreal and foothills natural regions. As a consequence of the plot size as well as the size class distribution of disturbed areas, most sites surveyed to date are undisturbed at the 1 ha scale, and relatively few sites span the intermediate-to-high disturbance gradient. As the ABMI completes its first rotation, and as additional supplementary sites are collected to fill in the disturbance gradients, an additional metric that should be considered is species turnover. Species turnover between sites is high because of the long gradients and the number of non-detections, so a proper turnover metric will likely involve a rarefaction /resampling statistic to

pool data across similar sites for comparison with contrasting ecological or anthropogenic site groups.

Recommendations & Conclusion

The value in monitoring multiple assemblages is a more complete understanding of the effects of anthropogenic activity on human disturbance. In our study, vascular plants were excellent all-around indicators. However, bryophytes were highly indicative of wetter forests, and responsive to a variety of anthropogenic disturbance through altered community composition and loss of species. While lowland forests are not threatened by agriculture or forestry, they are threatened by climate change. In addition, lowlands forests are susceptible to oil and gas activities that changes the hydrological flow in an area as well as reclaim impacted lowlands to upland stand types (Rooney et al. 2012). Oribatid mites were highly sensitive to agriculture and industrial developments such as oil and gas facilities which remove or alter the humus soil layers. Monitoring oribatid soil mites can provide inference into the underground decomposer community health, as well as provide a highly sensitive metric of when an impacted site may be considered rehabilitated. The weak results for breeding birds were not particularly surprising, given the high dispersal ability of birds and the variability in neotropical bird populations due to migration and habitat alteration in their wintering grounds. Monitoring programs include birds because they are relatively well-understood and they appeal to the public, as well as being a diverse vertebrate guild, but their inclusion perhaps should be justified as such. Programs using breeding birds as indicators should be aware of the potentially misleading inference that could be made by monitoring this assemblage alone. For example, bird species richness increased in response to agriculture, while all other taxa decreased (**Table 6.5, 6.6**), and birds as an assemblage had a lower proportion of indicator species than either of the more diverse flora.

All biota have intrinsic value, and ethically many would agree that we have a responsibility to protect and preserve species we impact. If multi-taxon monitoring programs can afford to monitor multiple assemblages, ethically and ecologically, that choice is justifiable, particularly given the variety of responses

of different assemblages to different types of disturbance (**Table 6.7**). When funds are very limited, studies such as ours are useful in providing some justification for the choice of assemblage to monitor as an indicator of terrestrial biodiversity. Of course, if ABMI had not adopted a multi-taxon approach, this study would not be possible. To that end, we recommend that large-scale monitoring programs attempt to incorporate breadth into their first monitoring rotation. After each site has been visited at least once, complementarity and concordance can easily be examined and the program can be stream-lined if desired. Another possibility to continually increase ecological knowledge would be to trade taxa after the first rotation, and to monitor some taxa only every second rotation.

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Table 6. 1 Correlations between environmental gradients in Alberta's boreal forest. Correlations between ordinations are indicated with the m^2 statistic, and Spearman correlations between distance matrices are indicated with an r statistic. Significance of both statistics was tested using 9,999 permutations.

		Climate	Stand structure	Area disturbed
Stand structure	m^2	0.159*		
	r	0.010		
Area disturbed	m^2	0.137*	0.300***	
	r	0.002	0.240***	
Space	m^2	0.666***	0.196***	0.118
	r	0.617***	0.036	-0.004

Table 6.2 Correlations between community composition and environmental gradients for four assemblages in Alberta's boreal forest. Correlations between ordinations are indicated with the m^2 statistic, and Spearman correlations between distance matrices are indicated with an r statistic. Significance of both statistics was tested with 9,999 permutations. Highlighted cells indicate the gradient with the highest correlation for each assemblage.

		Climate	Stand structure	Area disturbed	Space
Oribatid soil mites n=144 sites	m^2	0.431***	0.419***	0.332***	0.359***
	r	0.235***	0.266***	0.272***	0.165***
Breeding birds n=199 sites	m^2	0.404***	0.511***	0.315***	0.239***
	r	0.236***	0.298***	0.280***	0.180***
Vascular plants n=199 sites	m^2	0.236***	0.517***	0.314***	0.297***
	r	0.108**	0.309***	0.288***	0.050*
Bryophytes n=199 sites	m^2	0.292***	0.497***	0.317***	0.227***
	r	0.143***	0.310***	0.300***	0.096**

Table 6.3 Correlations between community composition of four assemblages in Alberta's boreal forest. Correlations between ordinations are indicated with the m^2 statistic, and Spearman correlations between distance matrices are indicated with an r statistic. Significance of both statistics was tested with 9,999 permutations. Highlighted cells indicate the gradient with the highest correlation for each assemblage.

		Oribatid soil mites	Breeding birds	Vascular plants
Breeding birds	m^2	0.652***		
	r	0.419***		
Vascular plants	m^2	0.573***	0.688***	
	r	0.430***	0.499***	
Bryophytes	m^2	0.617***	0.730***	0.709***
	r	0.457***	0.562***	0.591***

Table 6. 4 Correlations between gradient metrics and NMDS ordination axes for four boreal assemblages. Each ordination had 2 axes; n=144 for mites, n=199 for all other taxa. See methods for descriptions of variables.

Variable	Oribatid soil mites		Breeding birds		Vascular plants		Bryophytes	
	r ²	P	r ²	P	r ²	P	r ²	P
Nutrient-moisture conditions (NM coded as dummy variables)								
NM_PX	0.075	0.005	0.080	0.001	0.033	0.036	0.073	0.001
NM_MM	0.042	0.049	0.147	0.000	0.194	0.000	0.181	0.000
NM_RG	0.084	0.003	0.051	0.006	0.072	0.001	0.042	0.015
NM_PD	0.058	0.015	0.197	0.000	0.505	0.000	0.287	0.000
WETLAND	0.111	0.000	0.107	0.000	0.316	0.000	0.144	0.000
Space								
LAT	0.155	0.000	0.195	0.000	0.135	0.000	0.124	0.000
LONG	0.120	0.000	0.002	0.856	0.046	0.010	0.005	0.608
ELEV	0.182	0.000	0.121	0.000	0.021	0.124	0.069	0.001
Climate								
MAT	0.137	0.000	0.184	0.000	0.155	0.000	0.108	0.000
MAP	0.141	0.000	0.054	0.004	0.005	0.584	0.044	0.012
GDD5	0.330	0.000	0.244	0.000	0.041	0.016	0.138	0.000
Area disturbed anthropogenically								
HKM_PTOT	0.225	0.000	0.447	0.000	0.324	0.000	0.389	0.000
HA_PTOT	0.153	0.000	0.344	0.000	0.384	0.000	0.339	0.000
HA_PIND	0.003	0.802	0.057	0.004	0.207	0.000	0.066	0.003
HA_PSLI	0.001	0.944	0.009	0.420	0.023	0.099	0.005	0.644
HA_PAG	0.520	0.000	0.451	0.000	0.451	0.000	0.399	0.000
HA_PFOR	0.002	0.884	0.018	0.159	0.096	0.000	0.013	0.282
Stand structure								
TREEA1	0.138	0.000	0.359	0.000	0.442	0.000	0.367	0.000
TREEA2	0.247	0.000	0.331	0.000	0.284	0.000	0.293	0.000
TREEA3	0.254	0.000	0.302	0.000	0.296	0.000	0.158	0.000
DWMVOL	0.054	0.020	0.202	0.000	0.432	0.000	0.125	0.000
DEPTHORG	0.072	0.007	NA	NA	NA	NA	NA	NA
VCOMPLEX	0.244	0.000	0.412	0.000	0.401	0.000	0.410	0.000
TSHRUB_C	0.022	0.211	0.064	0.002	0.069	0.001	0.111	0.000
SSHRUB_C	0.047	0.034	0.101	0.000	0.139	0.000	0.184	0.000
Number of r ² ≥0.2	6		9		11		8	

Table 6.5 Summary of alpha and gamma diversity and survey completeness for two faunal assemblages assessed throughout the boreal forest of Alberta. Shaded rows indicate the disturbance type exhibiting the greatest change in % of intact richness.

	Number of sites surveyed	Number of individuals collected/recorded	Total observed species	Estimated true spp richness ¹	Completeness	Sample-based rarefied spp density ²	Average alpha diversity per site	Average individuals collected per site	% of intact richness ³
Oribatid soil mites	149	6,533	140						
INTACT	66	3,667	126	140	90	64	14	56	
DISTURBED (1 ha ≥80%)	83	2,866	107	129	83	43	8	34	66
- agriculture	13	166	12	15	81	10	2	13	16
- forestry	43	1,735	83	112	74	42	10	40	66
- soft linear	9	412	60	77	78	60	12	46	93
- heavy industrial	18	513	54	68	80	38	7	29	58
Breeding birds	199	25,000	113						
INTACT	105	12,218	95	105	90	63	23	116	
DISTURBED (1 ha ≥80%)	94	12,782	109	132	82	71	27	136	113
- agriculture	14	2,123	82	94	87	74	28	152	117
- forestry	52	7,267	94	106	89	67	28	140	106
- soft linear	9	1,057	69	83	83	69	28	117	110
- heavy industrial	19	2,335	76	82	93	65	26	123	103
DISTURBED (500m r circle ≥80%)	24	2,886	94	111	84	72	24	120	115

1. As estimated by the average of the ACE, Chao1 and Jack1 species richness estimates in EstimateS.

2. Species density estimated at the lowest number of sites for any disturbance category (n=9).

3. Based on rarefied species densities.

Table 6. 6 Summary of alpha and gamma diversity and survey completeness for two floral assemblages assessed throughout the boreal forest of Alberta. Shaded rows indicate the disturbance type exhibiting the greatest change in in % of intact richness.

	Number of sites surveyed	Number of occurrences recorded ⁴	Total observed species	Estimated true spp richness ¹	Completeness	Sample-based rarefied spp density ²	Average alpha diversity per site	Average occurrences per site	% of intact richness ³
Vascular plants	199	27,274	559						
INTACT	105	13,785	418	483	86	174	47	131	
DISTURBED (1 ha ≥80%)	94	13,489	473	544	87	201	54	144	116
- agriculture	14	947	151	184	82	117	25	68	67
- forestry	52	8,281	347	413	84	161	57	159	93
- soft linear	9	1,564	223	265	84	223	71	174	128
- heavy industrial	19	2,697	279	322	87	209	60	142	120
Bryophytes	199	5,297	225						
INTACT	105	3,246	204	253	81	97	31	NA	
DISTURBED (1 ha ≥80%)	94	2,051	161	221	73	72	22	NA	73
- agriculture	14	94	39	73	53	30	7	NA	31
- forestry	52	1,328	143	218	66	75	26	NA	77
- soft linear	9	242	88	119	74	88	20	NA	90
- heavy industrial	19	387	88	115	76	67	20	NA	68

1. As estimated by the average of the ACE, Chao1 and Jack1 species richness estimates in EstimateS.

2. Species density estimated at the lowest number of sites for any disturbance category (n=9).

3. Based on rarefied species densities.

4. Occurrences for vascular plants range from presence in 1-4 quadrants per site, while occurrences for bryophytes reflects detection at the site.

Table 6.7 Summary of assemblage complementarity and concordance across the metrics calculated herein. Assemblages with the highest diversity, concordance, proportion of indicators, or lowest effort required to survey them, and level of completeness are given the highest rank (1).

			Mites	Birds	Vascular Plants	Bryophytes
Diversity	Species richness	Species richness	3	4	1	2
		Species turnover	3	4	1	2
	Change in species richness with different disturbance types	Agriculture	1	4	3	2
		Forestry	1	4	3	2
		Soft Linear	4	2	1	2
		Industrial	1	4	3	2
Community composition	Natural gradients	Climate	1	2	4	3
		Space	1	3	2	4
		NM r ²	1	2	1	2
	Anthropogenic gradients	Area disturbed	1	3	4	2
		Stand structure	4	2	1	3
	# correlations with community composition	All variables	4	2	1	3
Correlations with other assemblages		4	2	3	1	
Indicator species	Nutrient-moisture conditions	% of common species	4	3	2	1
		# NM with indicator species	1	2	1	1
	Anthropogenic disturbance	% of common species	4	3	1	2
		# disturbances with indicator species	4	2	1	3
Logistics	Survey parameters	Completeness	1	1	3	4
		Field effort	1	4	2	2
		Lab effort	3	2	1	4
		Availability of expertise*	4	2	1	3
Sum of ranks			51	57	40	50
Number of metrics ranked 1st			10	1	11	3

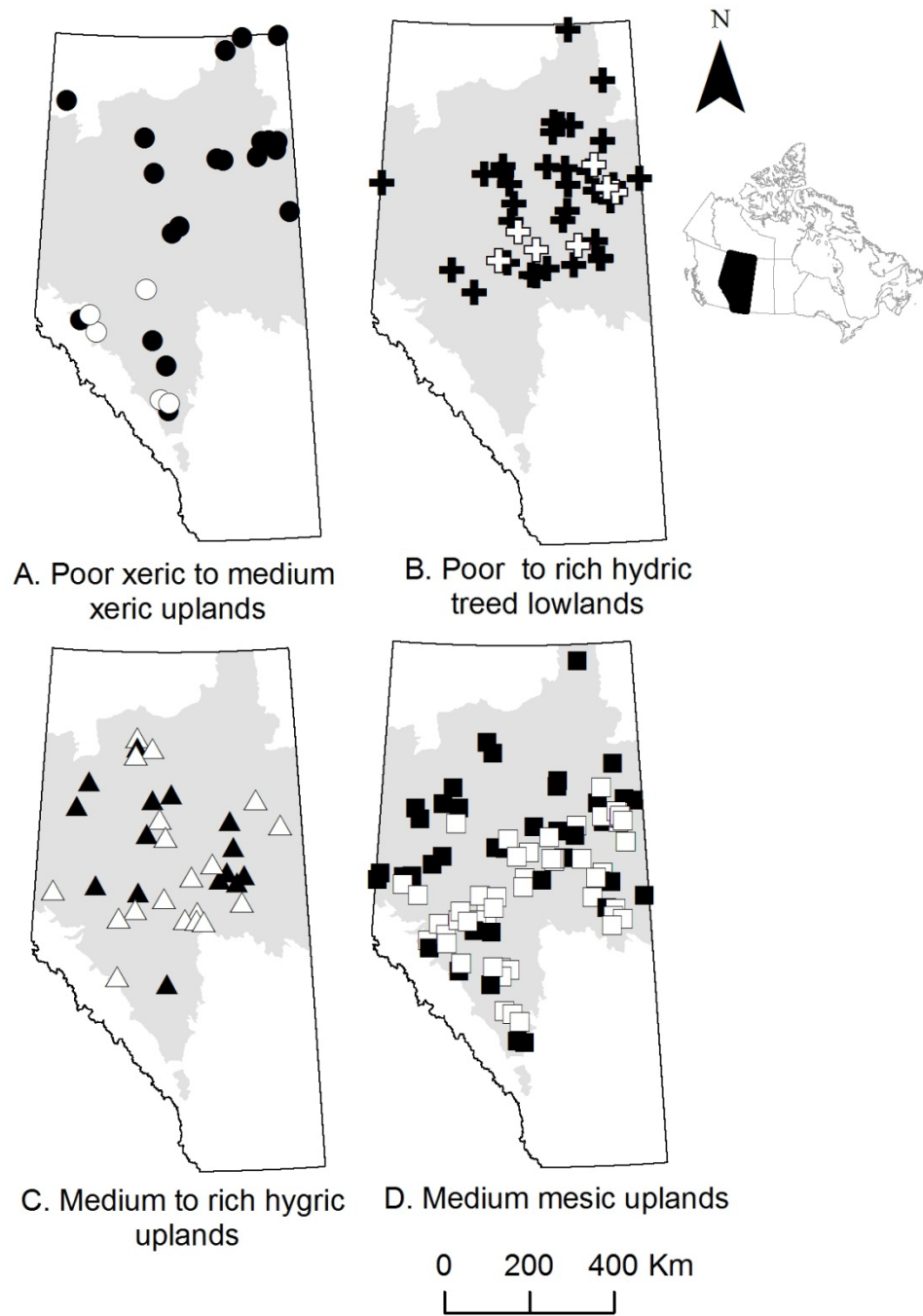


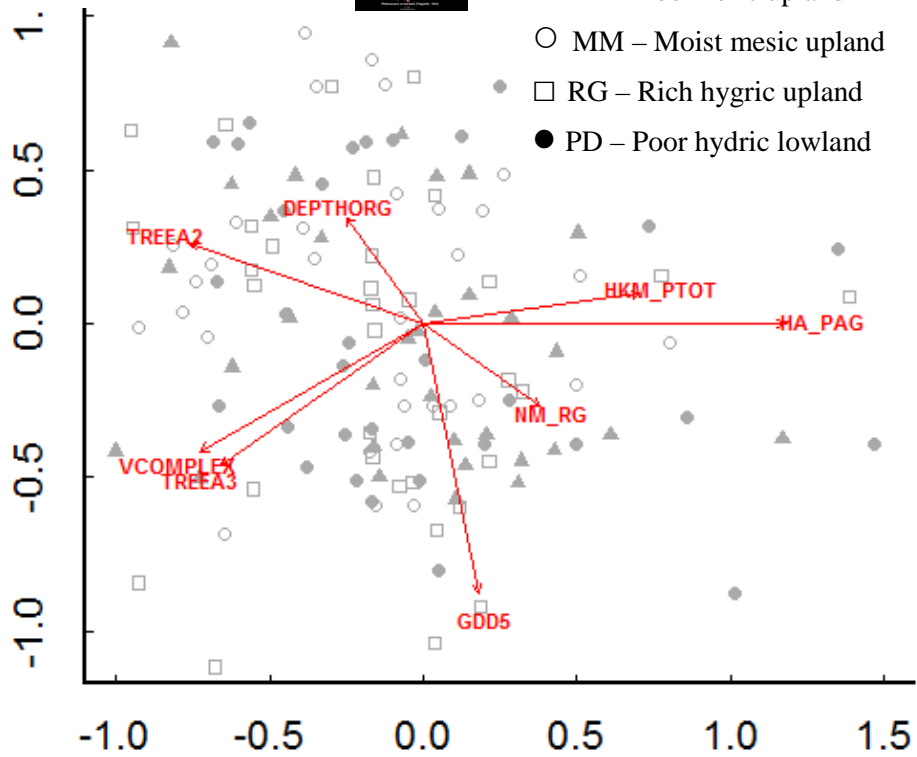
Figure 6. 1 Distribution across Alberta, Canada of undisturbed and anthropogenically disturbed sites analyzed herein. Each map corresponds to a simplified nutrient-moisture classification. Black symbols represent undisturbed habitat (e.g., ▲), white symbols represent highly disturbed habitat (e.g, △). The grey shaded region is the Boreal Plains ecozone (Environment Canada 2008)

A. Oribatid soil mites
i. Site biplot

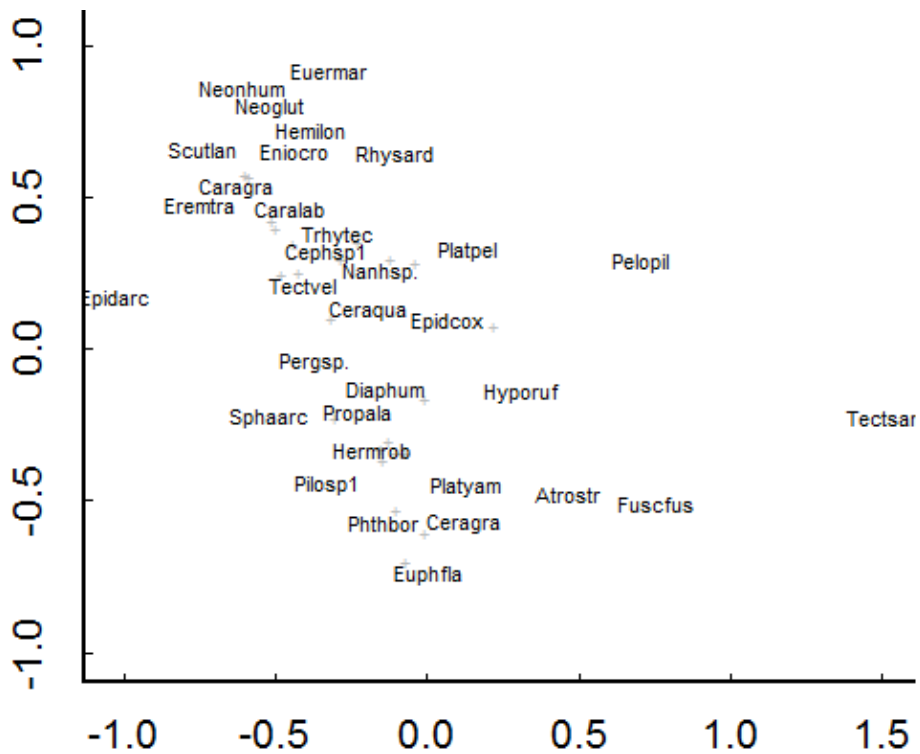


Site Nutrient-Moisture Codes

- ▲ PX – Poor xeric upland
- MM – Moist mesic upland
- RG – Rich hygric upland
- PD – Poor hydric lowland

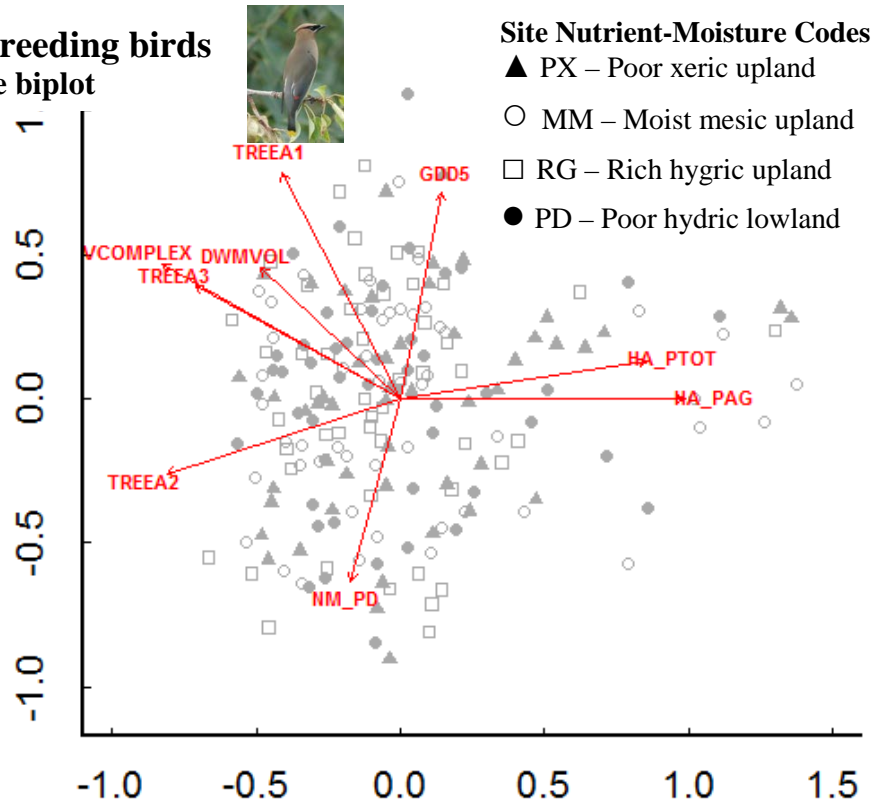


ii. Abundant species plot

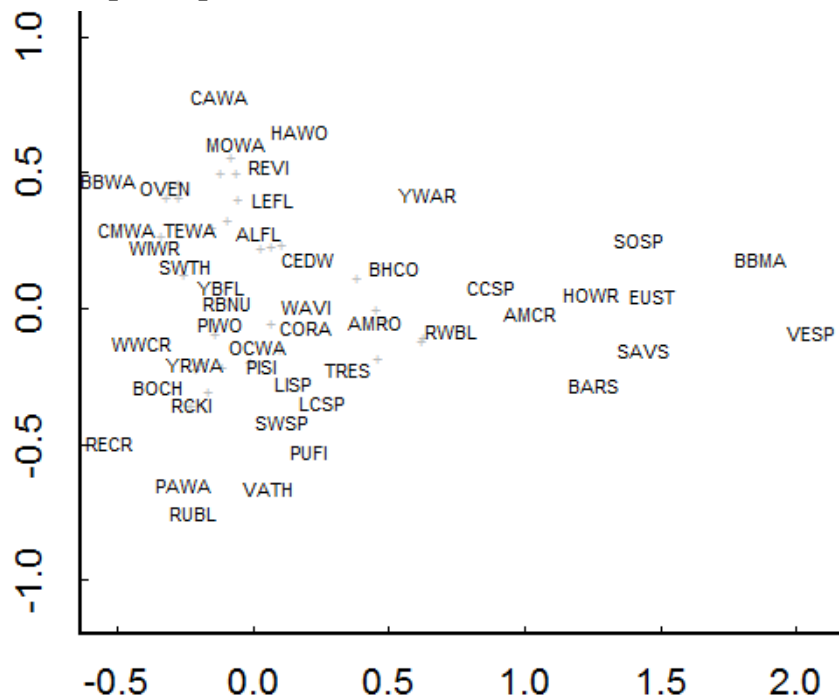


B. Breeding birds

i. Site biplot



ii. Abundant species plot

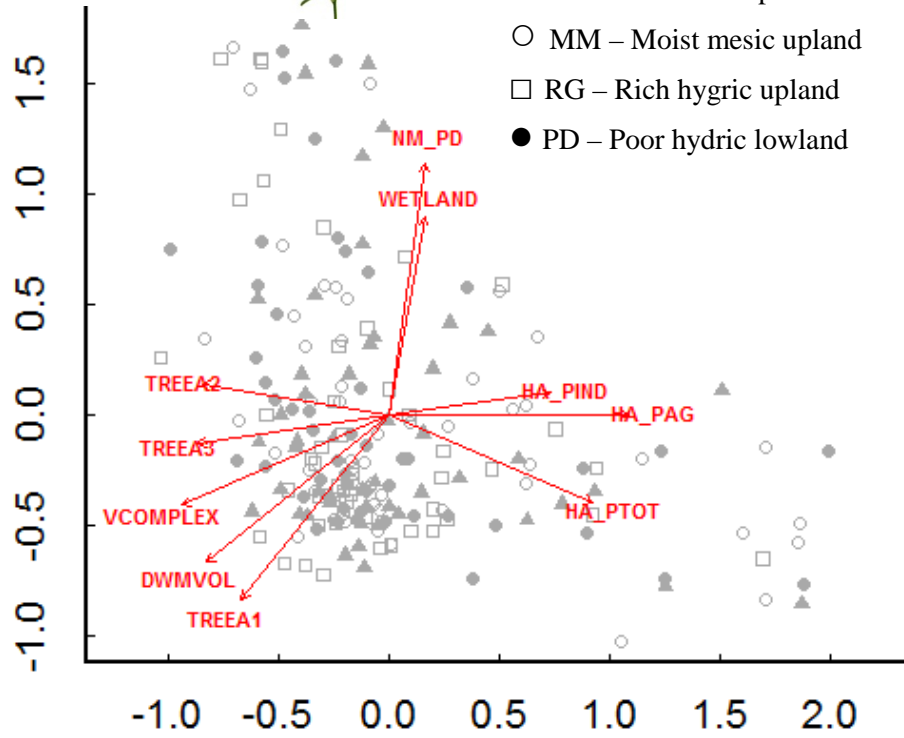


C. Vascular plants
i. Site biplot

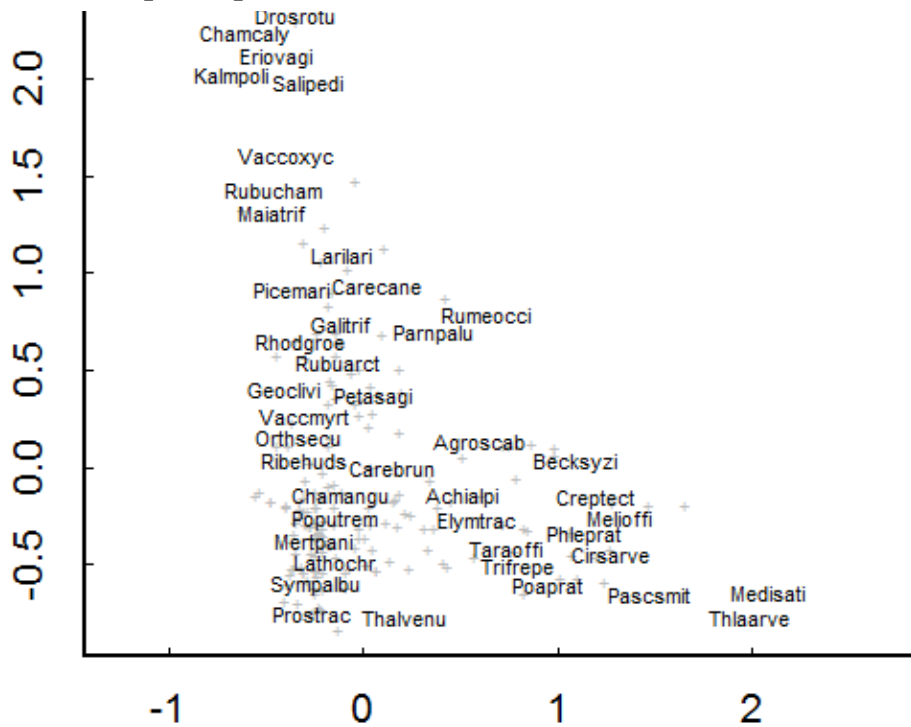


Site Nutrient-Moisture Codes

- ▲ PX – Poor xeric upland
- MM – Moist mesic upland
- RG – Rich hygric upland
- PD – Poor hydric lowland



ii. Abundant species plot

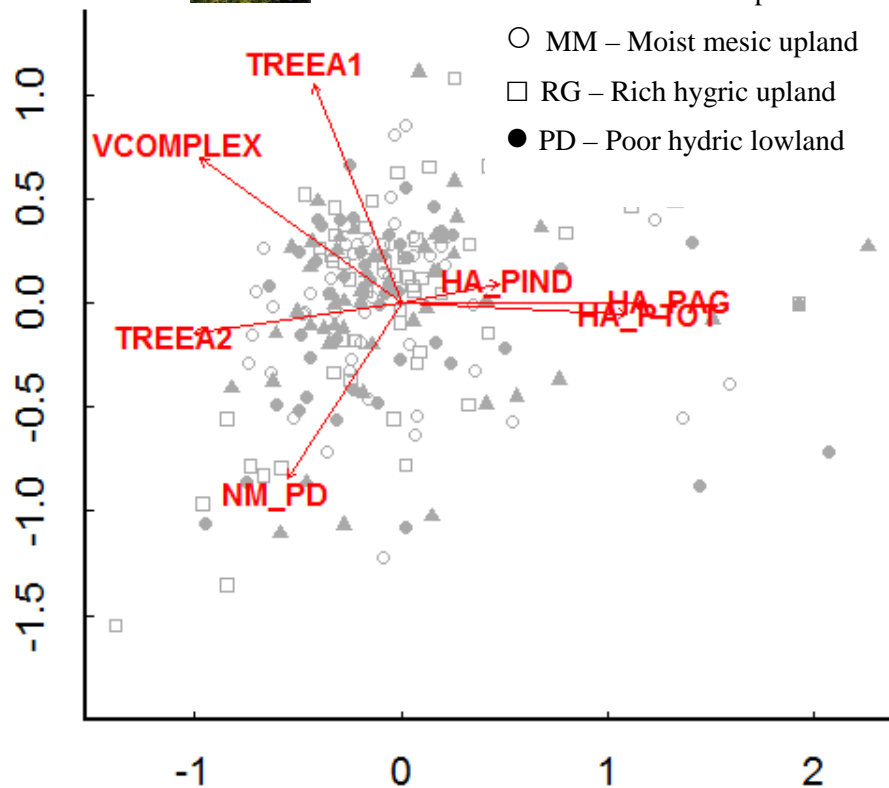


D. Bryophytes
i. Site biplot



Site Nutrient-Moisture Codes

- ▲ PX – Poor xeric upland
- MM – Moist mesic upland
- RG – Rich hygric upland
- PD – Poor hydric lowland



ii. Abundant species plot

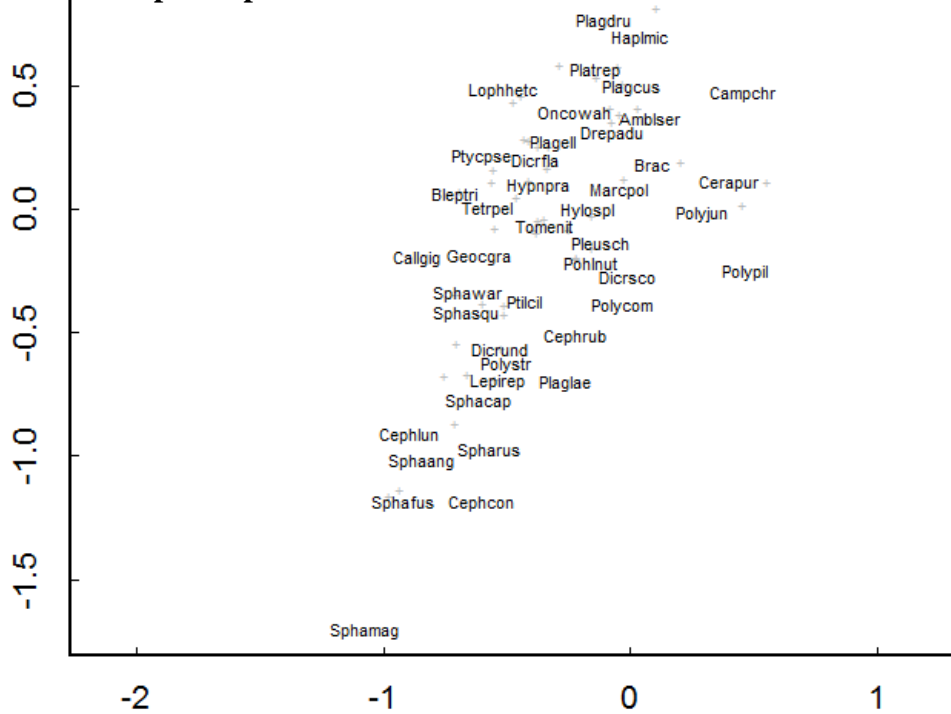


Figure 6. 2 (previous pages) Biplots and species abundance plots from 2-axes non-metric multidimensional scaling ordination of A) Oribatid soil mites, B) Breeding birds, C) Vascular plants, and D) Bryophytes. All plots were rotated according to HA_PAG. Vector lengths are proportional within each graph to their r^2 . In the 'biplots (A-Di), environmental gradients represent the linear correlation of that gradient with the ordination axes. Only axes with an $r^2 \geq 0.2$ at $P \geq 0.01$ are shown. Goodness-of-fit statistics are in **Table 6.4**. In the 'abundant species' plots (A-Dii) not all species are shown – species labels were prioritized by species' abundances and only added if they didn't obscure a more-abundant species. Species codes correspond to scientific names in **Appendix 6.4**, and environmental vector codes are described in the methods. Images: Soil mite *Phthiracarus nr borealis* © David Walter and the Royal Alberta Museum, Cedar Waxwing *Bombycilla cedrorum*, Alfalfa *Medicago sativa*, Knight's Plume moss *Ptilium crista-castrensis*, D.L. Haughland.

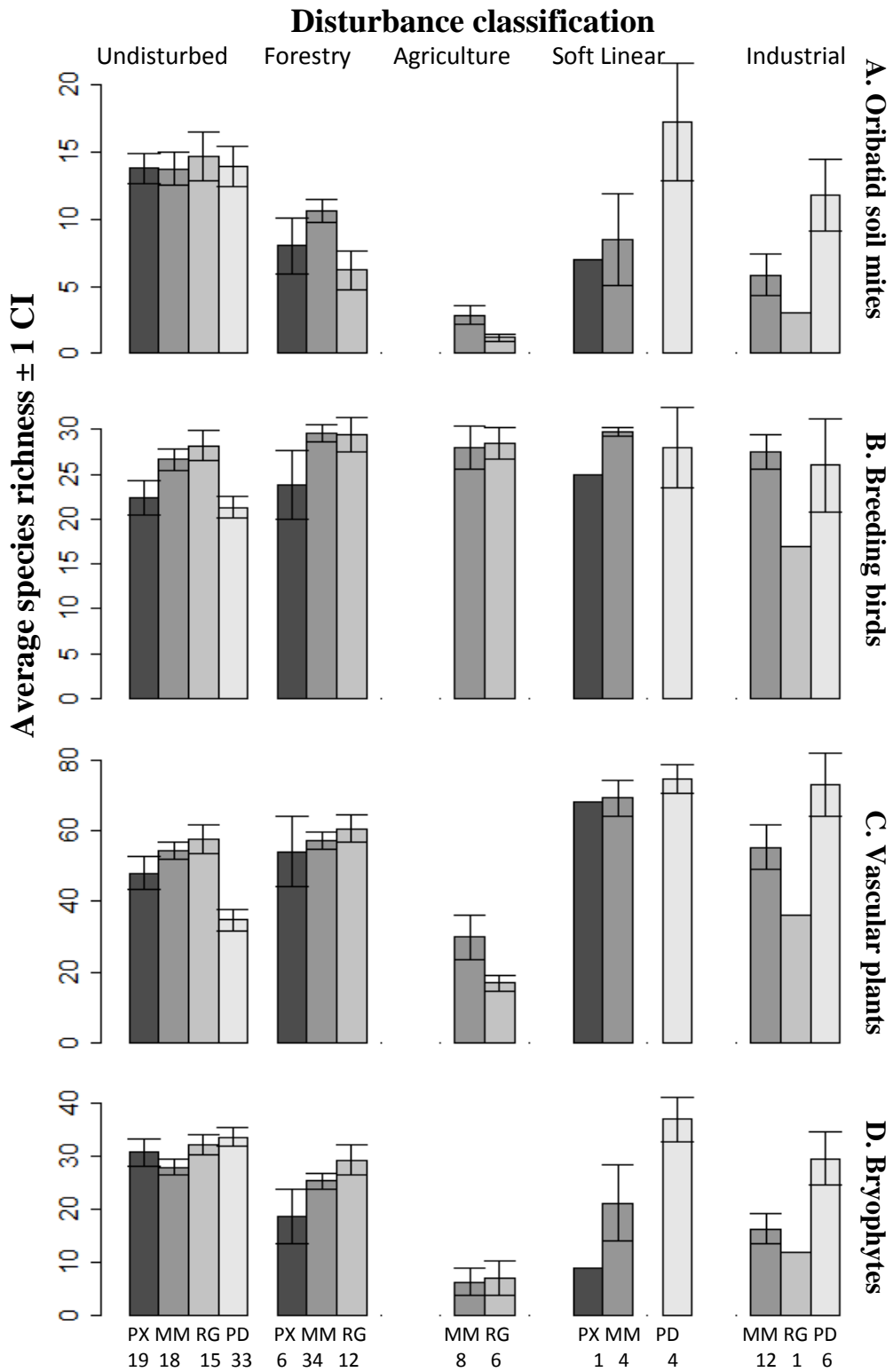


Figure 6.3 Average species richness (\pm 1 CI) by nutrient-moisture classification and disturbance classification. See methods for more information on classifications.

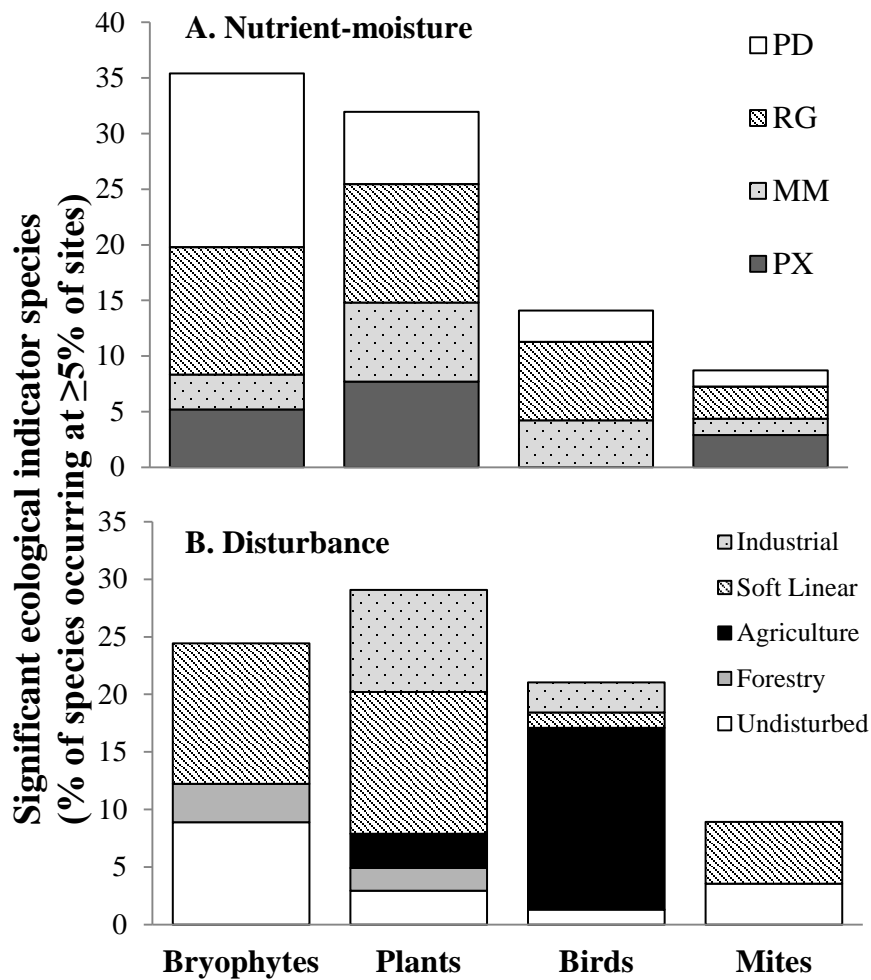


Figure 6. 4 Proportion of common species (occurring at $\geq 5\%$ of sites) from four boreal assemblages with significant indicator species values for A) Nutrient-moisture site classification, and B) Disturbance classification.

Appendix 6.1 Naming species: a brief overview of taxonomy and taxonomic expertise for select assemblages surveyed by the ABMI

All ABMI data can be downloaded freely from www.abmi.ca. Supplementary data I collected will be available freely from the website in the near future. Here I outline the taxonomy and taxonomists of the assemblages discussed in this thesis. This is not an exhaustive list. It does not elaborate on ABMI protocols, which are discussed throughout the thesis. Further inquiries about contractors can be addressed to Dr. Tyler Cobb (Curator of Invertebrate Zoology, Director of the ABMI Processing Centre at the Royal Alberta Museum).

Oribatid soil mites (Animalia, Arthropoda, Arachnida, Sarcoptiformes)

Dr. David Walter (Acarologist, ABMI Taxonomic Advisor, ABMI Processing Centre at the Royal Alberta Museum, Edmonton, Alberta) and a small number of students under his supervision identified all individual mites. All mites $\geq 300 \mu\text{m}$ in size are identified and quantified. Dr. Walter's identification resources and species concepts can be found in the "Almanac of Alberta Oribatida", online at www.abmi.ca or www.royalalbertamuseum.ca (Walter et al. 2010). Wherever possible, an individual of each species found at each site has been deposited to the Invertebrate Zoology collection at the Royal Alberta Museum.

Song birds (Animalia, Chordata, Aves)

ABMI's terrestrial song bird protocols are focused on perching birds (Passeriformes) and woodpeckers (Piciformes), as these are the birds most likely to be conduct auditory territorial behaviour in early spring. Secondary species are also detected, most commonly ducks and geese (Anseriformes), pigeons (Columbiformes), grouse (Galliformes) and owls (Strigiformes). Bird recordings are interpreted by a small group of contracted experienced ornithologists. Most ABMI recordings have been interpreted by contractor Todd Hunter. In 2010 and 2011, additional contractors Cindy McCallum and Theresa Hannah were employed. A library of representative bird calls is maintained by the ABMI

Information Centre and added to each year as new regions are visited and new contractors employed.

Vascular plants (Plantae)

All vascular plants are included in ABMI surveys, including horsetails (Equisetopsida), ferns (Filicopsida), monocots (Liliopsida), clubmosses (Lycopodiopsida), dicots (Magnoliopsida), and conifers (Pinopsida). The majority of common vascular plants are identified by field technicians *in situ*. ABMI selects technicians with strong plant identification skills, and conducts additional training prior to plant surveys. The focus of the training is to reduce misidentification by ensuring technicians "know what they know" and collect samples of everything else. Samples that cannot be easily identified in the field are collected for identification in the laboratory. Dr. Graham Griffiths (decd., contractor, Athabasca, Alberta) conducted the advanced plant identification from 2003 to 2008. Identification from 2009 to present was conducted in part by Tim Chipchar (currently Vascular Plant Specialist and Laboratory Coordinator at the ABMI Processing Centre at the Royal Alberta Museum) and by Dr. Marshall Mackenzie and Dr. Jay Woosaree (Native Plant Development and Restoration, Alberta Innovates-Technology Futures, Vegreville, Alberta). I identified most plants I collected during supplementary site surveys. Dr. Joyce Gould (Science Coordinator, Parks Division, Alberta Tourism, Parks and Recreation, Adjunct Professor, Department of Renewable Resources, University of Alberta) verified and corrected a subset of those identifications, and Dr. Graham Griffiths identified approximately 60 specimens collected in 2007. Taxonomy follows the Flora of North America (Flora of North America Editorial Committee 1993+). Specimens have not been deposited to the PMAE Herbarium at the Royal Alberta Museum but are in storage at the museum.

Non-vascular plants (Plantae, Bryophyta)

All non-vascular plants are included in ABMI bryophyte and lichen surveys, including rock mosses (Andreaeopsida), sphagnum (Sphagnopsida), true mosses (Bryopsida), haircap mosses (Polytrichopsida), 4-toothed peristome mosses (Tetraphidopsida), and liverworts (Jungermanniopsida and

Marchantiopsida). Jennifer Doubt (currently Chief Collections Manager, Botany Section, Canadian Museum of Nature) conducted training and expert identification of bryophytes from 2003 to 2008. Eleanor Edye (former Bryologist, ABMI Processing Centre at the Royal Alberta Museum) supervised parataxonomist identifications from 2007 to 2011 and conducted all other identification from 2009 to 2011. Taxonomy of bryophytes follows the Bryophyte Flora of North America while taxonomy of liverworts follows Tropicos (Missouri Botanical Gardens 2012). Specimens have not been deposited to the PMAE Herbarium at the Royal Alberta Museum but are in storage at the museum.

Lichens (Fungi, Ascomycota)

All macrolichens, dwarf fruticose and squamulose lichens are included in ABMI bryophyte and lichen surveys, including the majority of macrolichen genera (Lecanoromycetes) and mycocalicioid dwarf fruticose lichens (Eurotiomycetes). Dr. Janet Marsh (contractor) conducted training and expert identification of bryophytes from 2003 to 2008. I supervised parataxonomist identifications from 2007 to 2011. I am currently completing all other identification from 2009 to 2011 with a small group of trainees. Taxonomy of lichens follows the North American Lichen Checklist (Esslinger 2010) and Myconet (Lumbsch and Huhndorf 2010). Specimens have not been deposited to the PMAE Herbarium at the Royal Alberta Museum but are in storage at the museum.

Appendix 6.2 Preliminary comparison of community-level results from original and revised bryophyte survey methodology

ABMI bryophyte and lichen protocols changed in 2009 to better link the field results to anthropogenic disturbance at the site and to increase survey repeatability (see **Figure 1.2** for position of plots in revised protocol, Chapter One). Briefly, for bryophyte-rich substrates, (lowland ground cover, rocks and cliffs, and downed woody material) the search area was restricted to four plots of 25x15 m each (total of 0.15 ha vs. the entire 1 ha site), and time limits were given for each plot (25 minutes maximum vs. 90 minutes for the entire 1 ha). Less-diverse substrates (trees and vertical substrates and upland soils) are now surveyed for 10 minutes along 2 25 x 2 m belt transects bordering each plot (vs. surveyed as part of the 90 minute survey of the entire 1 ha). Anthropogenic disturbance and microhabitat availability are recorded for each plot at the site.

While experimental work suggested this change should minimally impact estimates of species richness or microhabitat availability (and the resultant bryophyte community available for surveying, Chapter Three), here I briefly compare species richness and multivariate ordination scores for ABMI sites at which both the original and revised protocol were carried out. The original protocols were conducted from 2003-2007 during the prototype period, while the revised protocols were carried out at the same sites in 2009 during the first monitoring rotation. Ancillary data indicate these sites were not significantly disturbed, either through natural or anthropogenic causes, between the two survey dates, but it is likely that metapopulation dynamics and year effects altered the bryophyte community between surveys. Since I cannot separate differences caused by the time between surveys and the survey methods in this analysis, I am explicitly assuming that the changes due to year effects are relatively small, random in direction, and can be compensated by the large plot sizes employed in both protocols. To further that comparison, I restrict my analysis to presence-absence data to avoid confounding temporal shifts in relative abundance with revised methodology. All species were included in subsequent analyses.

While an average of 4-5 more species were recorded in the 2009 revised surveys (**Table A6.3.1**), species richness did not differ significantly by methodology (**Figure A6.3.1**, paired 2-tailed t-test with unequal variance $t_8=1.8$, $P=0.109$). The multivariate difference between sites was greater than the difference between surveys at the same sites (2-factor permuted multivariate analysis of variance using Jaccard distance matrix, site: $F_{8,8}=2.59$, $P=0.001$, method: $F_{1,8}=2.09$, $P=0.036$, function adonis in the R package vegan, Oksanen et al. 2011). However, method did explain a small but significant amount of the difference between sites (site: $R^2=0.67$, method: $R^2=0.07$). The Procrustes correlation between non-metric multidimensional scaling (NMDS) ordinations of sites based on the original vs. the revised methods was also high (Figure A6.3.2, $m^2=0.855$, $P=0.001$, 9,999 permutations, 2-axes for NMDS, functions metaMDS and protest in R package vegan, Oksanen et al. 2011). This suggests that both methods provide similar measures of dominant bryophyte community composition. More detailed work is needed to compare the effects of the revised methods on individual species dose-response models currently used by ABMI (e.g, Nielsen et al. 2007, Alberta Biodiversity Monitoring Institute 2009).

Table A6.2. 1 Sites surveyed using original ABMI bryophyte methodology and resurveyed with revised methods in 2009. All sites are in the Central Mixedwoods natural sub-region except site 697 (Lower Boreal Highlands, Alberta Environment et al. 2005) and are situated from 56.156345 to 56.703514 10TM UTM latitude and -1111.656158 to -115.698334 10TM UTM longitude.

ABMI Site	Species richness original	Species richness revised	Dominant nutrient-moisture conditions	Year of original survey(s)
507	25	40	Hydric lowland to mesic upland transition	2006
538	26	34	Mesic upland	2006
539	34	34	Mesic upland	2006
559	41	40	Hydric lowland to mesic upland transition	2005
560	40	47	Hydric lowland to mesic upland transition	2005
570	18	34	Hydric lowland	2005
697	33	31	Mesic upland	2005
760	47	42	Mesic upland	2003
761	32.5	35	Mesic upland	2003-2006 ¹

¹The 2006 survey is used in multivariate comparisons. The average richness of all four surveys is used in comparisons of species richness.

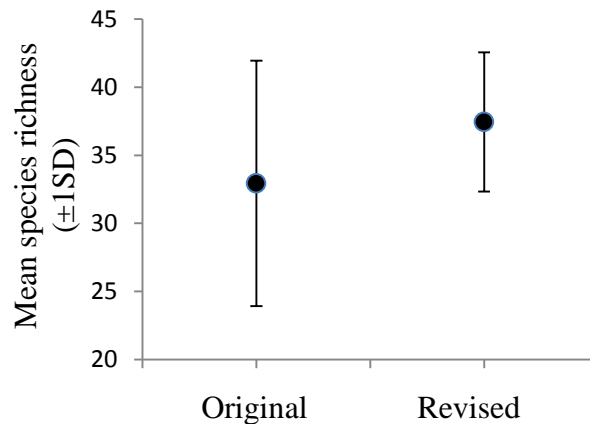


Figure A6.2. 1 The species richness of 9 paired sites as ascertained from original and revised ABMI protocols are not significantly different.

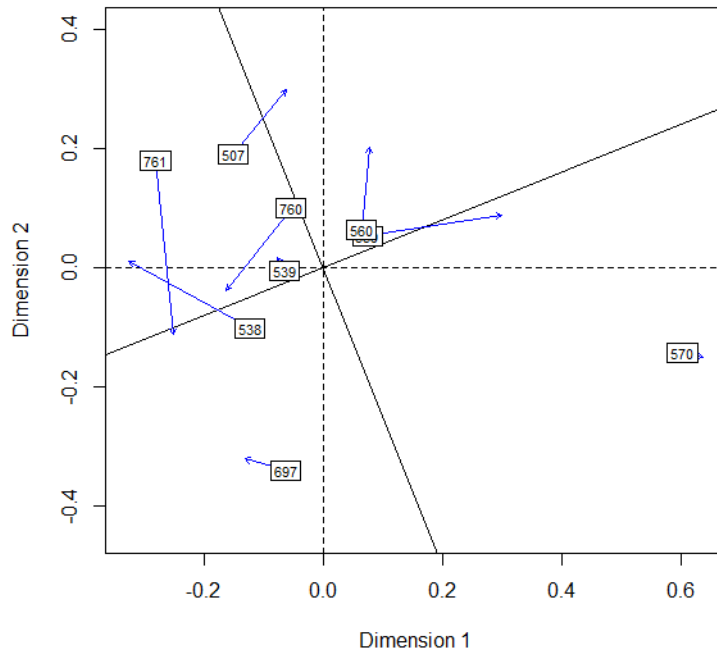


Figure A6.2. 2 Procrustes errors from comparison between a non-metric multidimensional scaling ordination (NMDS) of the 9 sites with the original methods (2003-2006) and an NMDS ordination of the same 9 sites resurveyed with revised methods in 2009. The length of the vector is proportional to the dissimilarity between survey results. Boxes with site numbers represent the position of the sites in the original survey ordination while vectors point to their position in the revised methods ordination.

Appendix 6.3 Reduction of 53 tree and snag variables to three synthetic axes using non-metric multidimensional scaling

ABMI protocols resulted in 53 measures of tree and snag density, productivity (basal area), canopy closure, and age and height of dominant trees (www.abmi.ca, **Table A6.3.1**). We created an additional 4 variables to reflect the dominant nutrient and moisture conditions recorded in the field (site categorization depicted in **Figure 6.1**). To reduce the number of candidate variables for ordinations of assemblages, we ran non-metric multidimensional scaling (NMDS) in PC-ORD ver. 6 (McCune and Mefford 2011) on 105 different undisturbed boreal sites. Tree and snag densities, basal areas, and tree age were $\log(x+1)$ transformed prior to analysis to reduce the highly skewed nature of these data. Additional information on site selection is presented in Chapter Six. Two surveys were removed from further analyses due to high outlier scores and overly strong influence on preliminary NMDS structure. Eight outliers were not removed as they didn't appear to have undue influence on NMDS structure, but rather we hypothesize they represent transitions between two nutrient-moisture conditions. We ran NMDS using Euclidean distance, a random starting configuration, 250 iterations with real data, and ties were not penalized (the 'slow and thorough' setting in PC-ORD). Dimensionality was assessed using a Monte Carlo randomization test. We chose a 3-dimensional solution as it reduced stress from 28 (axis 1) to 16 (axis 2) to 10 (axis 3, all $P=0.004$). A fourth axis reduced stress nominally (to 8, $P=0.004$). Final instability in the solution was less than 0.00000001. The degree of correspondence between plot positions in ordination space and true space (commonly referred to as r^2 or variance represented, McCune and Grace 2002) was 89.2%, with 63%, 15% and 11% attributable to axes 1 through 3 respectively.

Correlations between the 57 measures and the three synthetic axes suggest that axis one represents a nutrient moisture gradient of large-tree-dominated stands with closed canopies (positive values) to lowland forests with open canopies and high densities of small coniferous trees (**Figure A6.3.1**). Axis two is positively associated with medium-sized conifer tree density and high conifer

basal areas, characteristics of more mature xeric pine and spruce stands. Axis three is correlated with small deciduous trees and small coniferous and deciduous snags, so may represent an early successional gradient in upland forests.

To estimate the scores for highly disturbed sites, we used a predictive algorithm in PC-ORD based on ordination of the undisturbed sites and the same 57 tree and snag measures (**Figure A6.3.2**). We fit the data from 95 disturbed sites to the 3 axes of the NMDS ordination simultaneously (5 sites were visited in 2, 4, or 5 field seasons). While we could have ordinated disturbed and undisturbed sites simultaneously, we felt our approach better indicated how disturbed stands compared to the natural variability in undisturbed boreal stands.

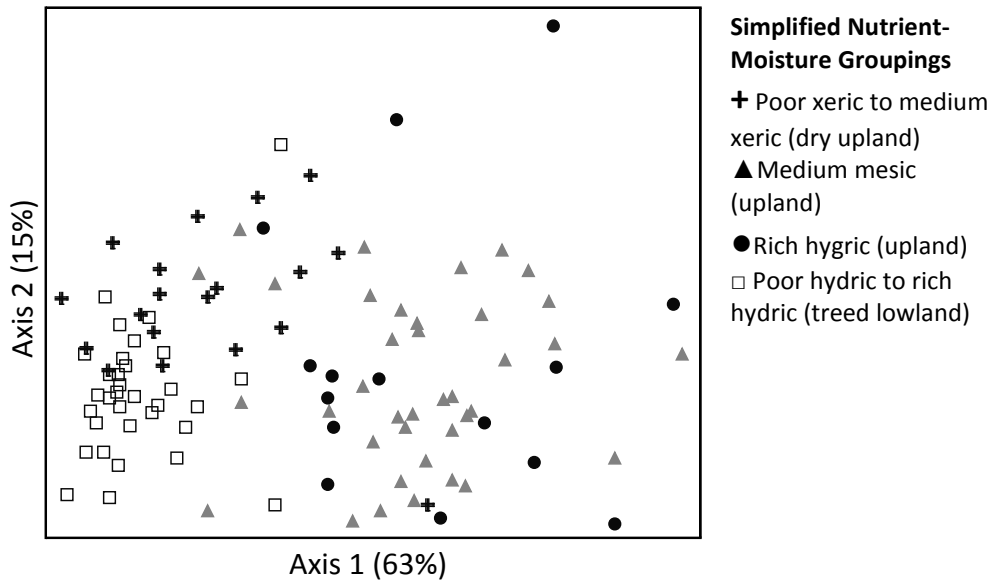
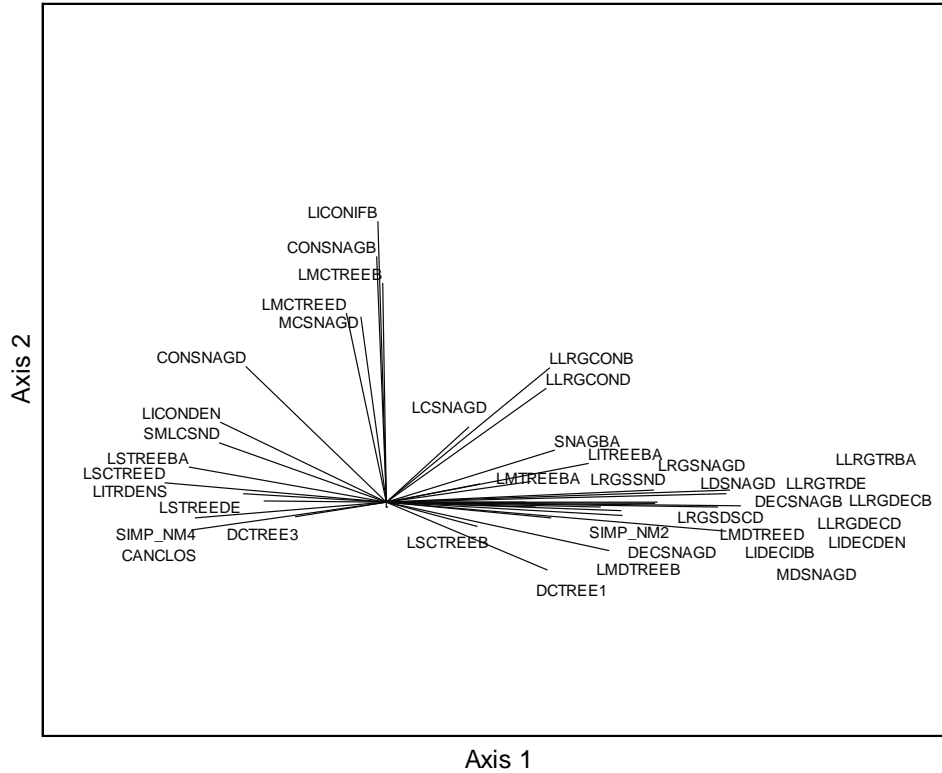


Figure A6.3. 1 Reduction of 57 metrics to two synthetic axes using NMDS ordination (total $r^2=89.2\%$). Codes are described in Table A6.3.1. Convex hulls and symbols indicate the modified nutrient-moisture classification of the sites, simplified from the field classification system. Scaled vectors represent depict variables with an r^2 or 15% or greater.

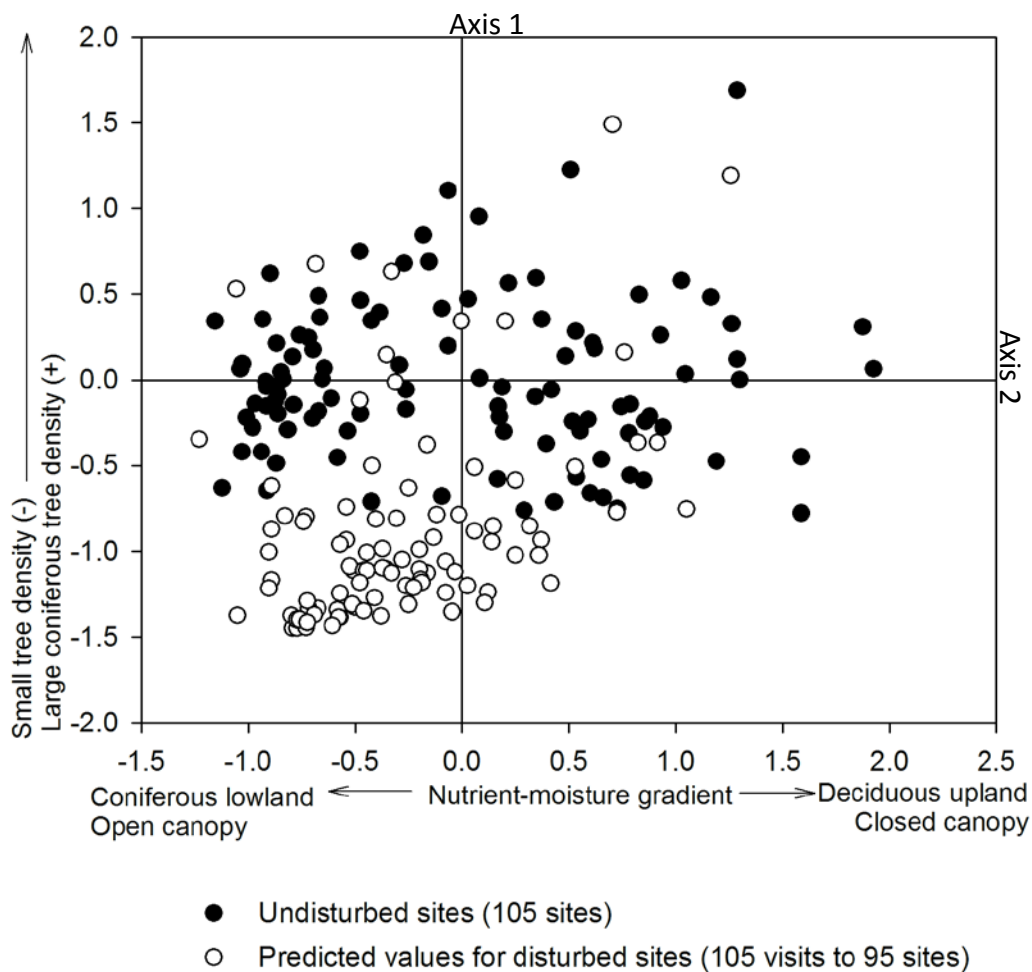


Figure A6.3. 2 Predicted position of highly disturbed sites along the first two synthetic axes of a non-metric multidimensional scaling ordination. The ordination was derived from tree-related measures of undisturbed sites.

Table A6.3. 1 Summary of variables used in stand structure ordination, and codes corresponding to Figure A6.3.1 (n=199 boreal sites)

Variable	Code	Mean	1SD
Dominant tree in canopy (count of binary dummy variables)			
<i>Populus tremuloides</i>	DCTREE1	65	
None	DCTREE2	54	
<i>Picea mariana</i>	DCTREE3	23	
<i>Picea glauca</i>	DCTREE4	19	
<i>Larix laricina</i>	DCTREE5	15	
<i>Pinus banksiana</i>	DCTREE6	7	
<i>Populus balsamifera</i>	DCTREE7	14	
<i>Pinus contorta</i>	DCTREE8	9	
<i>Betula papyrifera</i>	DCTREE9	8	
Live tree density (stems/ha) and basal area (BA, m²/ha)			
Live tree density	LITRDENS	4208.5	4648.8
Live tree BA	LITREEBA	13.9	13.9
Live coniferous tree density	LICONDEN	2357.2	3950.5
Live coniferous tree BA	LICONIFB	7.3	9.6
Live deciduous tree density	LIDECDEN	1769.5	3149.2
Live deciduous tree BA	LIDECIDB	6.4	10.1
Live large (≥25 cm DBH) tree density	LLRGTRDE	42.3	82.2
Live large tree BA	LLRGTRBA	4.0	7.7
Live large coniferous tree density	LLRGCOND	16.4	41.9
Live large coniferous tree BA	LLRGCONB	1.7	4.0
Live large deciduous tree density	LLRGDECD	24.8	58.6
Live large deciduous tree BA	LLRGDECB	2.3	5.5
Live medium tree density	LMTREEDE	515.1	633.1
Live medium tree (7-25 cm DBH) BA	LMTREEBA	7.3	9.6
Live medium coniferous tree density	LMCTREED	320.3	516.3
Live medium coniferous tree BA	LMCTREEB	3.9	6.8
Live medium deciduous tree density	LMDTREED	190.8	363.9
Live medium deciduous tree BA	LMDTREEB	3.3	6.6
Live small tree (≤ 7 cm DBH) BA	LSTREEDE	3651.1	4609.9
Live small coniferous tree density	LSTREEBA	2005.1	3680.1
Live small coniferous tree BA	LSCTREED	1.7	3.0
Live small deciduous tree density	LSCTREEB	1569.4	3230.7
Live small deciduous tree BA	LSDTREED	0.9	1.9
Snags			
Snag density	LSDTREEB	506.6	760.7
Snag BA	SNAGBA	3.7	8.5
Coniferous snag density	CONSNAGD	251.5	617.4

Variable	Code	Mean	1SD
Coniferous snag BA	CONSNAGB	1.4	3.8
Deciduous snag density	DECSNAGD	248.8	432.0
Deciduous snag BA	DECSNAGB	2.3	7.2
Large snag density	LRGSNAGD	8.4	18.9
Large coniferous snag density	LCSNAGD	1.5	4.6
Large deciduous snag density	LDSNAGD	6.6	17.5
Medium snag density	MSNAGD	90.6	147.6
Medium coniferous snag density	MCSNAGD	39.6	94.5
Medium deciduous snag density	MDSNAGD	49.8	120.2
Small snag density	SMLSNAGD	407.6	730.6
Small coniferous snag density	SMLCSND	210.5	598.6
Small deciduous snag density	SMLDSND	192.4	390.2
Large soft snag density	LRGSSND	0.7	2.8
Large soft coniferous snag density	LRGSCSND	0.2	1.1
Large soft deciduous snag density	LRGSDSCD	0.4	1.7
Miscellaneous			
Tree height (m)	TREEHT	9.1	9.0
Tree age (years)	TREEAGE	44.8	38.2
Canopy closure (1-96, 96=completely open)	CANCLOS	52.6	31.4

Appendix 6.4 Summary of species occurrence and indicator value results for species occurring at $\geq 10\%$ sites

Codes presented here correspond to species abundance plots in **Figure 6.3**. Indicator species analyses (ISA) were conducted separately for nutrient-moisture categories (n=66 sites for mites, n=105 undisturbed sites for all other assemblages) and disturbance types (n=83 sites for mites and n=199 sites for all other assemblages). Only significant ($P \geq 0.05$) indicator value (IV) results are shown. Four simplified nutrient-moisture conditions were included: MM – moist mesic uplands, RG – rich hygic uplands, PX – poor xeric to mesic uplands, PD – poor to rich treed hydric lowlands. Five anthropogenic disturbance categories were included: Undist – undisturbed, SoftLin – soft linear features, For – Forestry, Agric – Agriculture, Indust – Industrial. See Chapter Six for more information on methods and group descriptions.

Table A6.4. 1 Oribatid soil mites occurring at 7 or more boreal sites analyzed herein, their occurrence, and indicator species analysis results.

Oribatid Mite Scientific Name	Code	Occurrence at 149 sites	Indicator Group (IV, P)
<i>Achipteria coleoptrata</i>	Achicol	8	
<i>Achipteria sp. 1 DEW</i>	Achisp.	38	
<i>Allosuctobelba gigantea</i>	Allogig	8	
<i>Allosuctobelba sp. 2 DEW</i>	Allosp.	8	PD (19.5, 0.033)
<i>Atropacarus striculus</i>	Atrostr	18	
<i>Camisia biurus</i>	Camibiu	8	
<i>Carabodes granulatus</i>	Caragra	13	PX (34.7, 0.006)
<i>Carabodes labyrinthicus</i>	Caralab	40	
<i>Cepheus sp. 1 DEW</i>	Cephsp1	36	
<i>Ceratoppia quadridentata</i>	Ceraqua	77	
<i>Ceratozetes cuspidatus</i>	Ceracus	13	
<i>Ceratozetes gracilis</i>	Ceragra	66	
<i>Ceratozetes thienemanni</i>	Cerathi	19	
<i>Chamobates cuspidatus</i>	Chamcus	22	
<i>Dentizetes ledensis</i>	Dentled	13	PD (22.6, 0.052) Undist (17.2, 0.032)

Oribatid Mite Scientific Name	Code	Occurrence at 149 sites	Indicator Group (IV, P)
<i>Diapterobates humeralis</i>	Diaphum	44	
<i>Eniochthonius crosbyi</i>	Eniocro	24	Undist (24.9, 0.025)
<i>Eniochthonius minutissima</i>	Eniomin	9	
<i>Epidamaeus arcticola</i>	Epidarc	9	
<i>Epidamaeus coxalis</i>	Epidcox	36	
<i>Epidamaeus floccosus</i>	Epidflo	11	
<i>Epidamaeus sp. 2 DEW</i>	Epidsp2	8	SoftLin (14, 0.046)
<i>Eremaeus translamellatus</i>	Eremtra	24	
<i>Eueremaes marshalli</i>	Euermar	22	PX (31.8, 0.005)
<i>Euphthiracarus flavus</i>	Euphfla	40	
<i>Fuscozetes fuscipes</i>	Fuscfus	13	
<i>Gymnodamaeus ornatus</i>	Gymnorn	17	RG (27.7, 0.023)
<i>Heminothrus longisetosus</i>	Hemilon	34	
<i>Hermanniella robusta</i>	Hermrob	33	
<i>Hypochothionius rufulus</i>	Hyporuf	18	SoftLin (17.1, 0.053)
<i>Mycobates incurvatus</i>	Mycoinc	25	
<i>Nanhermannia sp. 1 DEW</i>	Nanhsp.	32	
<i>Neogymnobates luteus</i>	Neoglut	11	
<i>Neonothrus humicola</i>	Neonhum	22	
<i>Neoribates aurantiacus</i>	Neoraur	14	
<i>Nothrus borussicus</i>	Nothbor	11	
<i>Oribatodes mirabilis</i>	Oribmir	32	
<i>Peloribates pilosus</i>	Pelopil	25	MM (33.5, 0.008)
<i>Pergalumna sp. 1 DEW</i>	Pergsp.	32	
<i>Phthiracarus borealis</i>	Phthbor	22	
<i>Phthiracarus boresetosus</i>	Phthboe	41	
<i>Pilogalumna sp. 1 DEW</i>	Pilosp1	32	SoftLin (24.5, 0.033)
<i>Platynothrus peltifer</i>	Platpel	35	
<i>Platynothrus yamasakii</i>	Platyam	9	
<i>Propelops alaskensis</i>	Propala	67	
<i>Protoribates sp. 1 DEW</i>	Protsp1	8	
<i>Quatrobella montana</i>	Quatmon	24	
<i>Rhysotritia ardua</i>	Rhysard	22	
<i>Roynortonella sp. 1 DEW</i>	Roynsp.	9	
<i>Scheloribates pallidulus</i>	Schepal	39	
<i>Scutozetes lanceolatus</i>	Scutlan	9	
<i>Sphaerozetes arcticus</i>	Sphaarc	16	
<i>Tectocephus sarekensis</i>	Tectsar	29	
<i>Tectocephus velatus</i>	Tectvel	19	

Oribatid Mite Scientific Name	Code	Occurrence at 149 sites	Indicator Group (IV, P)
<i>Trhypochthonius tectorum</i>	Trhytec	38	
<i>Unduloribates diana</i>	Undudia	9	

Table A6.4. 2 Breeding bird species occurring at 9 or more boreal sites analyzed herein, their occurrence, and indicator species analysis results.

Breeding Bird Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Agelaius phoeniceus</i>	RWBL	65	
<i>Ammodramus leconteii</i>	LCSP	40	PD (26.7, 0.004) Agric (21.4, 0.026)
<i>Bombycilla cedrorum</i>	CEDW	68	
<i>Bonasa umbellus</i>	RUGR	37	
<i>Carduelis pinus</i>	PISI	100	
<i>Carduelis tristis</i>	AMGO	36	Agric (44.5, <0.001)
<i>Carpodacus purpureus</i>	PUFI	12	
<i>Catharus guttatus</i>	HETH	138	
<i>Catharus ustulatus</i>	SWTH	160	
<i>Certhia americana</i>	BRCR	12	
<i>Coccythraustes vespertinus</i>	EVGR	13	
<i>Colaptes auratus</i>	NOFL	48	Agric (25.4, 0.018)
<i>Contopus cooperi</i>	OSFL	29	
<i>Contopus sordidulus</i>	WWPE	39	Agric (20.2, 0.04)
<i>Corvus brachyrhynchos</i>	AMCR	46	
<i>Corvus corax</i>	CORA	122	
<i>Cyanocitta cristata</i>	BLJA	31	
<i>Dendroica castanea</i>	BBWA	20	
<i>Dendroica coronata</i>	YRWA	179	
<i>Dendroica magnolia</i>	MAWA	95	
<i>Dendroica palmarum</i>	PAWA	66	
<i>Dendroica petechia</i>	YWAR	58	Agric (37.9, 0.001)
<i>Dendroica tigrina</i>	CMWA	44	
<i>Dendroica virens</i>	BTGW	22	RG (22.9, 0.011)
<i>Dryocopus pileatus</i>	PIWO	35	
<i>Empidonax alnorum</i>	ALFL	90	
<i>Empidonax flaviventris</i>	YBFL	14	
<i>Empidonax minimus</i>	LEFL	102	
<i>Euphagus carolinus</i>	RUBL	10	
<i>Euphagus cyanocephalus</i>	BRBL	14	

Breeding Bird Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Geothlypis trichas</i>	COYE	69	
<i>Hirundo rustica</i>	BARS	18	Agric (31.6, 0.002)
<i>Ixoreus naevius</i>	VATH	12	
<i>Junco hyemalis</i>	DEJU	117	
<i>Loxia curvirostra</i>	RECR	10	
<i>Loxia leucoptera</i>	WWCR	100	
<i>Melospiza georgiana</i>	SWSP	26	PD (21.3, 0.017)
<i>Melospiza lincolni</i>	LISP	145	
<i>Melospiza melodia</i>	SOSP	32	Agric (66.8, <0.001)
<i>Mniotilta varia</i>	BAWW	57	RG (25.3, 0.013)
<i>Molothrus ater</i>	BHCO	56	SoftLin (25.4, 0.021)
<i>Oporornis agilis</i>	CONW	39	RG (27.8, 0.007)
<i>Oporornis philadelphia</i>	MOWA	63	
<i>Oreothlypis celata</i>	OCWA	64	
<i>Oreothlypis peregrina</i>	TEWA	147	
<i>Parkesia noveboracensis</i>	NOWA	38	RG (21.1, 0.024)
<i>Passerculus sandwichensis</i>	SAVS	37	
<i>Perisoreus canadensis</i>	GRJA	166	
<i>Pheucticus ludovicianus</i>	RBGR	88	
<i>Pica hudsonia</i>	BBMA	14	Agric (63.8, <0.001)
<i>Picoides villosus</i>	HAWO	16	MM (13.2, 0.03)
<i>Piranga ludoviciana</i>	WETA	82	
<i>Poecile atricapillus</i>	BCCH	63	MM (30.8, 0.003)
<i>Poecile hudsonica</i>	BOCH	61	Undist (24.7, 0.031)
<i>Poocetes gramineus</i>	VESP	13	Agric (53.2, <0.001)
<i>Porzana carolina</i>	SORA	26	Agric (22, 0.017)
<i>Regulus calendula</i>	RCKI	157	
<i>Regulus satrapa</i>	GCKI	38	
<i>Riparia riparia</i>	BANS	20	Indust (20.7, 0.018)
<i>Seiurus aurocapilla</i>	OVEN	123	
<i>Setophaga ruticilla</i>	AMRE	72	
<i>Sitta canadensis</i>	RBNU	106	
<i>Sphyrapicus varius</i>	YBSA	101	
<i>Spizella pallida</i>	CCSP	74	
<i>Spizella passerina</i>	CHSP	186	
<i>Sturnus vulgaris</i>	EUST	14	Agric (41.1, <0.001)
<i>Tachycineta bicolor</i>	TRES	45	Indust (20.8, 0.046)
<i>Troglodytes aedon</i>	HOWR	26	Agric (41.9, <0.001)
<i>Troglodytes troglodytes</i>	WIWR	64	RG (31, 0.004)
<i>Turdus migratorius</i>	AMRO	114	
<i>Vireo gilvus</i>	WAVI	77	

Breeding Bird Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Vireo olivaceus</i>	REVI	127	
<i>Vireo solitarius</i>	BHVI	55	
<i>Wilsonia canadensis</i>	CAWA	32	MM (16.4, 0.053)
<i>Wilsonia pusilla</i>	WIWA	15	
<i>Zonotrichia albicollis</i>	WTSP	175	

Table A6.4. 3 Vascular plant species occurring at 9 or more boreal sites analyzed herein, their occurrence, and indicator species analysis results.

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Abies balsamea</i>	Abiebal	42	
<i>Achillea alpina</i>	Achialp	36	MM (13.2, 0.038) SoftLin (24, 0.01)
<i>Achillea millefolium</i>	Achimil	126	
<i>Actaea rubra</i>	Actarub	87	
<i>Adoxa moschatellina</i>	Adoxmos	11	
<i>Agrostis scabra</i>	Agrosca	35	Indust (27.6, 0.004)
<i>Alnus incana</i>	Alnuinc	58	RG (46.8, <0.001)
<i>Alnus viridis</i>	Alnuvir	82	
<i>Alopecurus aequalis</i>	Alopaeq	9	
<i>Amelanchier alnifolia</i>	Amelaln	72	MM (32.9, 0.003) For (36.3, 0.001)
<i>Andromeda polifolia</i>	Andrpol	13	PD (39.4, <0.001)
<i>Aralia nudicaulis</i>	Aralnud	91	
<i>Arctostaphylos uva-ursi</i>	Arctuva	42	PX (19.9, 0.04)
<i>Arctous rubra</i>	Arctrub	9	
<i>Arnica cordifolia</i>	Arnicor	39	
<i>Astragalus americanus</i>	Astrame	17	
<i>Astragalus canadensis</i>	Astrcan	9	SoftLin (24.2, 0.004)
<i>Beckmannia syzigachne</i>	Becksyz	19	Indust (45.1, <0.001)
<i>Betula glandulosa</i>	Betugla	25	PD (21.6, 0.017)
<i>Betula neoalaskana</i>	Betuneo	9	
<i>Betula papyrifera</i>	Betupap	105	
<i>Betula pumila</i>	Betupum	43	PD (29.3, 0.004) SoftLin (21.5, 0.026)
<i>Botrychium virginianum</i>	Botrvir	11	
<i>Bromus ciliatus</i>	Bromcil	27	
<i>Bromus inermis</i>	Bromine	28	SoftLin (31.4, 0.001)
<i>Calamagrostis canadensis</i>	Calacan	149	

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Caltha palustris</i>	Caltpal	31	RG (23, 0.011)
<i>Campanula rotundifolia</i>	Camprot	16	PX (13.5, 0.047)
<i>Carex aenea</i>	Careaen	25	Indust (23.3, 0.01)
<i>Carex aquatilis</i>	Careaqu	46	PD (36.5, <0.001) SoftLin (46, <0.001)
<i>Carex aurea</i>	Careaur	19	
<i>Carex bebbii</i>	Carebeb	15	SoftLin (24.5, 0.005)
<i>Carex brunnescens</i>	Carebru	29	
<i>Carex canescens</i>	Carecan	20	SoftLin (27.4, 0.003)
<i>Carex crawfordii</i>	Carecraf	9	
<i>Carex deweyana</i>	Caredew	9	
<i>Carex disperma</i>	Caredis	31	
<i>Carex gynocrates</i>	Caregyn	10	PD (18.1, 0.014)
<i>Carex magellanica</i>	Caremag	11	PD (23.9, 0.003)
<i>Carex siccata</i>	Caresic	11	
<i>Carex utriculata</i>	Careutr	24	SoftLin (30.1, 0.001)
<i>Carex vaginata</i>	Carevag	16	PX (20.9, 0.007)
<i>Castilleja miniata</i>	Castmin	21	
<i>Chamaedaphne calyculata</i>	Chamcal	16	PD (37.5, <0.001)
<i>Chamerion angustifolium</i>	Chamang	164	
<i>Chenopodium album</i>	Chenalb	10	Indust (18.2, 0.009)
<i>Circaea alpina</i>	Circalp	18	RG (33.1, <0.001)
<i>Cirsium arvense</i>	Cirsarv	36	Agric (38.2, <0.001)
<i>Comarum palustre</i>	Comapal	24	PD (20.4, 0.026) Undist (18, 0.032)
<i>Corallorrhiza maculata</i>	Coramac	10	
<i>Corallorrhiza trifida</i>	Coratri	16	
<i>Cornus canadensis</i>	Corncan	161	
<i>Cornus sericea</i>	Cornser	55	RG (27.8, 0.007)
<i>Corylus cornuta</i>	Corycor	12	MM (15.8, 0.016)
<i>Crepis tectorum</i>	Creptec	36	Indust (51, <0.001)
<i>Delphinium glaucum</i>	Delpgla	33	RG (24.5, 0.007)
<i>Deschampsia caespitosa</i>	Desccae	19	SoftLin (28.6, 0.002)
<i>Diphasiastrum complanatum</i>	Diphcom	23	
<i>Drosera rotundifolia</i>	Drosrot	14	PD (28.3, 0.001)
<i>Dryopteris carthusiana</i>	Dryocar	10	RG (24.5, 0.001)
<i>Dryopteris expansa</i>	Dryoexp	23	RG (16.7, 0.043)
<i>Elymus repens</i>	Elymrep	21	
<i>Elymus trachycaulus</i>	Elymtra	37	MM (14.6, 0.039) Indust (34.2, 0.001)
<i>Empetrum nigrum</i>	Empenig	13	PX (15.4, 0.046)

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Epilobium ciliatum</i>	Epilcil	11	
<i>Epilobium glaberrimum</i>	Epilgla	9	
<i>Epilobium palustre</i>	Epilpal	10	
<i>Equisetum arvense</i>	Equiarv	138	
<i>Equisetum fluviatile</i>	Equiflu	25	
<i>Equisetum hyemale</i>	Equihye	10	
<i>Equisetum pratense</i>	Equipra	40	
<i>Equisetum scirpoides</i>	Equisci	42	PX (37.7, <0.001) Undist (24.2, 0.015)
<i>Equisetum sylvaticum</i>	Equisyl	129	
<i>Eriophorum vaginatum</i>	Eriovag	19	PD (40.8, <0.001)
<i>Eurybia conspicua</i>	Eurycon	73	MM (33, 0.002)
<i>Festuca rubra</i>	Festrub	16	Indust (27.8, 0.002)
<i>Fragaria vesca</i>	Fragves	28	
<i>Fragaria virginiana</i>	Fragvir	135	
<i>Galeopsis tetrahit</i>	Galetet	18	
<i>Galium boreale</i>	Galibor	117	
<i>Galium trifidum</i>	Galitrii	23	
<i>Galium triflorum</i>	Galitril	96	
<i>Geocaulon lividum</i>	Geocliv	39	Undist (25, 0.01)
<i>Geranium bicknellii</i>	Gerabic	13	Indust (16.3, 0.021)
<i>Geum aleppicum</i>	Geumale	31	SoftLin (29.9, 0.003)
<i>Geum macrophyllum</i>	Geummac	16	
<i>Geum rivale</i>	Geumriv	24	
<i>Goodyera repens</i>	Goodrep	16	MM (17.9, 0.033)
<i>Gymnocarpium dryopteris</i>	Gymndry	43	RG (21.6, 0.024)
<i>Halenia deflexa</i>	Haledef	15	
<i>Heracleum maximum</i>	Heramax	32	RG (22.1, 0.008)
<i>Hieracium umbellatum</i>	Hierumb	42	
<i>Hordeum jubatum</i>	Hordjub	28	Indust (51.5, <0.001)
<i>Juncus bufonius</i>	Juncbuf	9	
<i>Kalmia polifolia</i>	Kalmpol	10	
<i>Larix laricina</i>	Larilar	63	
<i>Lathyrus ochroleucus</i>	Lathoch	110	
<i>Lathyrus venosus</i>	Lathven	22	RG (15.9, 0.05)
<i>Leymus innovatus</i>	Leyminn	68	MM (26.8, 0.009)
<i>Lilium philadelphicum</i>	Liliphi	16	
<i>Linnaea borealis</i>	Linnbor	139	
<i>Lonicera caerulea</i>	Lonicae	27	SoftLin (18.4, 0.034)
<i>Lonicera dioica</i>	Lonidio	58	For (30.2, 0.006)
<i>Lonicera involucrata</i>	Loniinv	82	

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Luzula parviflora</i>	Luzupar	20	SoftLin (23.5, 0.01)
<i>Lycopodium annotinum</i>	Lycoann	52	
<i>Lycopodium dendroideum</i>	Lycoden	23	
<i>Maianthemum canadense</i>	Maiacan	109	
<i>Maianthemum stellatum</i>	Maiaste	28	
<i>Maianthemum trifolium</i>	Maiatri	50	Undist (39, 0.001)
<i>Matricaria discoidea</i>	Matrdis	21	Indust (37.8, <0.001)
<i>Medicago sativa</i>	Medisat	16	Agric (39.9, <0.001)
<i>Melilotus alba</i>	Melialb	24	Indust (56.3, <0.001)
<i>Melilotus officinalis</i>	Melioff	22	Indust (40.6, <0.001)
<i>Mertensia paniculata</i>	Mertpan	127	
<i>Mitella nuda</i>	Mitenud	117	
<i>Moehringia lateriflora</i>	Moehlat	23	
<i>Moneses uniflora</i>	Moneuni	14	
<i>Orthilia secunda</i>	Orthsec	70	Undist (24.6, 0.026)
<i>Osmorhiza depauperata</i>	Osmodep	17	
<i>Packera paupercula</i>	Packpaup	14	
<i>Parnassia palustris</i>	Parnpal	12	SoftLin (22, 0.007)
<i>Pascopyrum smithii</i>	Pascsmi	12	Agric (20.9, 0.009)
<i>Pedicularis labradorica</i>	Pedilab	19	
<i>Petasites frigidus</i>	Petafri	138	
<i>Petasites frigidus var. sagittatus</i>	Petafris	59	SoftLin (32, 0.004)
<i>Phleum pratense</i>	Phlepra	58	SoftLin (27.6, 0.009)
<i>Picea glauca</i>	Picegla	135	
<i>Picea mariana</i>	Picemar	89	
<i>Pinus banksiana</i>	Pinuban	39	PX (34, 0.001)
<i>Pinus contorta</i>	Pinucon	39	PX (17.1, 0.045)
<i>Plantago major</i>	Planmaj	35	Indust (33.8, 0.001)
<i>Platanthera hyperborea</i>	Plathyp	38	SoftLin (47.4, <0.001)
<i>Platanthera obtusata</i>	Platobt	11	RG (19.4, 0.012)
<i>Platanthera orbiculata</i>	Platorb	10	
<i>Poa interior</i>	Poaint	9	Indust (12.4, 0.051)
<i>Poa palustris</i>	Poapal	43	SoftLin (42.4, <0.001)
<i>Poa pratensis</i>	Poapra	48	Agric (21, 0.033)
<i>Polemonium acutiflorum</i>	Poleacu	13	SoftLin (24.2, 0.004)
<i>Populus balsamifera</i>	Popubal	126	
<i>Populus tremuloides</i>	Poputre	152	
<i>Potentilla norvegica</i>	Potenor	41	Agric (23.8, 0.016)
<i>Prosartes trachycarpa</i>	Prostra	29	MM (16.9, 0.038)

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Prunus virginiana</i>	Prunvir	12	
<i>Pyrola asarifolia</i>	Pyroasa	103	
<i>Pyrola chlorantha</i>	Pyrochl	24	
<i>Ranunculus acris</i>	Ranuacr	15	
<i>Ranunculus gmelinii</i>	Ranugme	13	
<i>Ranunculus lapponicus</i>	Ranulap	10	
<i>Ranunculus macounii</i>	Ranumac	13	
<i>Rhinanthus minor</i>	Rhinmin	19	SoftLin (29.6, 0.002)
<i>Rhododendron groenlandicum</i>	Rhodgro	135	
<i>Ribes glandulosum</i>	Ribegla	54	For (24.7, 0.018)
<i>Ribes hudsonianum</i>	Ribehud	39	
<i>Ribes lacustre</i>	Ribelac	64	RG (26.4, 0.012)
<i>Ribes oxyacanthoides</i>	Ribeoxy	89	
<i>Ribes triste</i>	Ribetri	88	
<i>Rosa acicularis</i>	Rosaaci	140	
<i>Rosa woodsii</i>	Rosawoo	29	PX (27.3, 0.002)
<i>Rubus arcticus</i>	Rubuarc	49	SoftLin (32.9, 0.001)
<i>Rubus chamaemorus</i>	Rubucha	49	
<i>Rubus idaeus</i>	Rubuida	120	
<i>Rubus pedatus</i>	Rubuped	10	
<i>Rubus pubescens</i>	Rubupub	135	
<i>Rumex occidentalis</i>	Rumeocc	12	SoftLin (43.3, <0.001)
<i>Salix arbusculoides</i>	Saliarb	17	
<i>Salix bebbiana</i>	Salibeb	79	
<i>Salix discolor</i>	Salidis	20	
<i>Salix glauca</i>	Saligla	17	PX (25.9, 0.002)
<i>Salix lucida</i>	Saliluc	9	
<i>Salix maccalliana</i>	Salimac	11	PX (17.5, 0.009)
<i>Salix myrtilifolia</i>	Salimyr	22	PX (26.5, 0.002)
<i>Salix pedicellaris</i>	Saliped	12	PD (26.4, 0.001)
<i>Salix petiolaris</i>	Salipet	9	RG (10.6, 0.039)
<i>Salix planifolia</i>	Salipla	37	
<i>Salix pseudomyrsinites</i>	Salipsey	10	PX (15.3, 0.024)
<i>Salix pyrifolia</i>	Salipyr	27	
<i>Salix scouleriana</i>	Salisco	28	
<i>Schizachne purpurascens</i>	Schipur	13	MM (14.5, 0.029)
<i>Scirpus cyperinus</i>	Scircyp	10	Indust (13.7, 0.046)
<i>Scirpus microcarpus</i>	Scirmic	12	Indust (16.9, 0.016)
<i>Scutellaria galericulata</i>	Scutgal	20	
<i>Shepherdia canadensis</i>	Shepcan	73	

Vascular Plant Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Sibbaldiopsis tridentata</i>	Sibbtri	11	PX (18.8, 0.007)
<i>Solidago canadensis</i>	Solican	31	
<i>Sonchus arvensis</i>	Soncarv	16	SoftLin (21.1, 0.011)
<i>Sorbus scopulina</i>	Sorbsco	11	
<i>Spiraea lucida</i>	SpirLuc	13	
<i>Spiranthes romanzoffiana</i>	Spirrom	14	
<i>Stellaria longifolia</i>	Stellonf	43	SoftLin (40.1, <0.001)
<i>Stellaria longipes</i>	Stellonp	11	
<i>Streptopus amplexifolius</i>	Streamp	15	
<i>Symphoricarpos albus</i>	Sympalb	60	MM (28, 0.006) For (26.3, 0.013)
<i>Symphoricarpos occidentalis</i>	Sympocc	14	RG (24.8, 0.002)
<i>Symphyotrichum ciliolatum</i>	Sympcilo	86	
<i>Symphyotrichum laeve</i>	Symplae	14	
<i>Symphyotrichum puniceum</i>	Symppun	41	RG (21, 0.014) SoftLin (19.9, 0.036)
<i>Taraxacum officinale</i>	Taraoff	111	
<i>Thalictrum venulosum</i>	Thalven	17	MM (13.2, 0.034)
<i>Thlaspi arvense</i>	Thlaarv	12	Agric (33.9, 0.001)
<i>Trientalis borealis</i>	Triebor	44	
<i>Trifolium hybridum</i>	Trifhyb	66	
<i>Trifolium pratense</i>	Trifpra	37	Indust (41, <0.001)
<i>Trifolium repens</i>	Trifrep	30	MM (14.3, 0.031) SoftLin (17.4, 0.046)
<i>Typha latifolia</i>	Typhlat	15	Indust (19.9, 0.012)
<i>Urtica dioica</i>	Urtidio	39	RG (25.9, 0.003)
<i>Vaccinium caespitosum</i>	Vacccae	25	
<i>Vaccinium myrtilloides</i>	Vaccmyr	90	
<i>Vaccinium oxycoccos</i>	Vaccoxy	51	Undist (27.2, 0.009)
<i>Vaccinium vitis-idaea</i>	Vaccvit	110	
<i>Viburnum edule</i>	Vibuedu	114	
<i>Vicia americana</i>	Viciame	105	
<i>Viola canadensis</i>	Violcan	57	RG (36.9, 0.001)
<i>Viola renifolia</i>	Violren	60	RG (38.6, <0.001)

Table A6.4. 4 Bryophyte species occurring at 9 or more boreal sites analyzed herein, their occurrence, and indicator species analysis results.

Bryophyte Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Amblystegium serpens</i>	Amblsru	143	MM (29.4, 0.023)
<i>Anastrophyllum hellerianum</i>	Anashel	17	
<i>Aulacomnium palustre</i>	Aulapal	146	
<i>Blepharostoma trichophyllum</i>	Bleptri	35	
<i>Brachythecium</i>	Brac	173	SoftLin (23.9, 0.007)
<i>Bryum</i>	Bryum	130	
<i>Calliergon cordifolium</i>	Callcor	10	
<i>Calliergon giganteum</i>	Callgig	14	SoftLin (14.3, 0.032)
<i>Calypogeia sphagnicola</i>	Calysph	26	PD (33, <0.001) Undist (16.2, 0.038)
<i>Campyliadelphus chrysophyllus</i>	Campchr	11	RG (12.9, 0.044)
<i>Campylium stellatum</i>	Campste	41	
<i>Campylophyllum hispidulum</i>	Camphis	81	
<i>Cephalozia connivens</i>	Cephcon	11	
<i>Cephalozia lunulifolia</i>	Cephzun	23	PD (18.4, 0.039)
<i>Cephalozia pleniceps</i>	Cephple	17	PD (14.7, 0.04)
<i>Cephaloziella hampeana</i>	Cephham	16	SoftLin (22.8, 0.005)
<i>Cephaloziella rubella</i>	Cephzub	32	
<i>Ceratodon purpureus</i>	Cerapur	152	
<i>Chiloscyphus pallescens</i>	Chilpal	23	
<i>Chiloscyphus polyanthos</i>	Chilpol	13	
<i>Climacium dendroides</i>	Climden	39	RG (22.6, 0.017)
<i>Dicranum flagellare</i>	Dicrfla	76	RG (25.6, 0.039)
<i>Dicranum fragilifolium</i>	Dicrfra	42	RG (31, 0.001)
<i>Dicranum fuscescens</i>	Dicrfus	72	
<i>Dicranum montanum</i>	Dicrmon	9	
<i>Dicranum polysetum</i>	Dicrpol	96	PX (28.9, 0.026)
<i>Dicranum scoparium</i>	Dicrsco	37	
<i>Dicranum undulatum</i>	Dicrund	92	PD (35.9, <0.001) Undist (30.9, 0.003)
<i>Drepanocladus aduncus</i>	Drepadu	59	SoftLin (23, 0.025)
<i>Drepanocladus polygamus</i>	Dreppol	9	
<i>Eurhynchiastrum pulchellum</i>	Eurhpul	115	RG (33.4, 0.002)
<i>Funaria hygrometrica</i>	Funahyg	23	SoftLin (19.9, 0.017)
<i>Geocalyx graveolens</i>	Geocgra	20	
<i>Haplocladium microphyllum</i>	Haplmic	55	MM (26.4, 0.004)
<i>Helodium blandowii</i>	Helobla	21	
<i>Herzogiella turfacea</i>	Herztur	22	RG (17.2, 0.029)

Bryophyte Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Hylocomium splendens</i>	Hylospl	151	Undist (26, 0.013)
<i>Hypnum lindbergii</i>	Hypnlin	9	
<i>Hypnum pallescens</i>	Hypnpal	9	
<i>Hypnum pratense</i>	Hypnptra	61	SoftLin (20.6, 0.042)
<i>Jamesoniella autumnalis</i>	Jameaut	75	Undist (21.6, 0.05)
<i>Lepidozia reptans</i>	Lepirep	55	PD (27.9, 0.007)
<i>Leptobryum pyriforme</i>	Leptpyr	75	SoftLin (25.1, 0.019)
<i>Lophocolea heterophylla</i>	Lophhetp	31	
<i>Lophocolea minor</i>	Lophmin	37	
<i>Lophozia ascendens</i>	Lophasc	13	
<i>Lophozia excisa</i>	Lophexc	10	PX (13.7, 0.031)
<i>Lophozia heterocolpos</i>	Lophhetc	21	
<i>Lophozia ventricosa</i>	Lophven	40	
<i>Marchantia polymorpha</i>	Marcpol	31	SoftLin (17.6, 0.046)
<i>Mnium spinulosum</i>	Mniuspi	31	
<i>Mylia anomala</i>	Myliano	35	PD (53.6, <0.001) Undist (25.6, 0.007)
<i>Oncophorus wahlenbergii</i>	Oncowah	91	RG (32.5, 0.003)
<i>Orthotrichum obtusifolium</i>	Orthobt	74	
<i>Orthotrichum speciosum</i>	Orthspe	51	RG (30, 0.003)
<i>Plagiochila asplenioides</i>	Plagasp	16	
<i>Plagiochila porelloides</i>	Plagpor	10	
<i>Plagiomnium ciliare</i>	Plagcil	9	
<i>Plagiomnium cuspidatum</i>	Plagcus	121	RG (35.7, 0.001)
<i>Plagiomnium drummondii</i>	Plagdru	53	MM (26.2, 0.008)
<i>Plagiomnium ellipticum</i>	Plagell	82	
<i>Plagiomnium medium</i>	Plagmed	40	RG (18.4, 0.044)
<i>Plagiothecium denticulatum</i>	Plagden	22	
<i>Plagiothecium laetum</i>	Plaglae	13	
<i>Platydictya jungermannioides</i>	Platjun	11	PX (13.1, 0.031) SoftLin (15.1, 0.022)
<i>Platygyrium repens</i>	Platrep	41	
<i>Pleurozium schreberi</i>	Pleusch	170	For (26.1, <0.001)
<i>Pohlia nutans</i>	Pohlnut	161	Undist (25.8, 0.002)
<i>Polytrichum commune</i>	Polycom	49	For (24, 0.013)
<i>Polytrichum juniperinum</i>	Polyjun	92	PX (21.7, 0.048)
<i>Polytrichum piliferum</i>	Polypil	14	PX (18.7, 0.003)
<i>Polytrichum strictum</i>	Polystr	75	PD (38.6, <0.001)
<i>Ptilidium ciliare</i>	Ptilcil	53	Undist (24.2, 0.015)
<i>Ptilidium pulcherrimum</i>	Ptilpul	140	Undist (28.9, 0.001)
<i>Ptilium crista-castrensis</i>	Ptilcric	139	For (26, 0.034)

Bryophyte Scientific Name	Code	Occurrence at 199 sites	Indicator Group (IV, P)
<i>Ptychostomum pseudotriquetrum</i>	Ptycpse	28	
<i>Pylaisia polyantha</i>	Pylapol	134	RG (32.9, 0.004)
<i>Rhizomnium gracile</i>	Rhizgra	14	SoftLin (13.5, 0.042)
<i>Rhizomnium pseudopunctatum</i>	Rhizpse	9	
<i>Riccardia latifrons</i>	Ricclat	17	
<i>Sanionia uncinata</i>	Saniunc	154	
<i>Sarmentypnum exannulatum</i>	Sarmexa	13	
<i>Scapania glaucocephala</i>	Scapgl	20	
<i>Sphagnum angustifolium</i>	Sphaang	43	PD (62.9, <0.001)
<i>Sphagnum capillifolium</i>	Sphacap	51	PD (33.8, 0.001)
<i>Sphagnum fuscum</i>	Sphafus	36	PD (52.1, <0.001)
<i>Sphagnum girgensohnii</i>	Sphagir	10	
<i>Sphagnum magellanicum</i>	Sphamag	16	PD (36.4, <0.001)
<i>Sphagnum russowii</i>	Spharus	20	PD (15.4, 0.05)
<i>Sphagnum squarrosum</i>	Sphasqu	20	PD (17.8, 0.027)
<i>Sphagnum warnstorffii</i>	Sphawar	34	PD (22.5, 0.011) SoftLin (30.9, 0.001)
<i>Straminergon stramineum</i>	Strastr	22	PD (26.7, 0.002)
<i>Tetraphis pellucida</i>	Tetrapel	32	
<i>Tetraplodon angustatus</i>	Tetrang	9	
<i>Thuidium recognitum</i>	Thuirec	78	
<i>Tomentypnum nitens</i>	Tomenit	72	
<i>Tritomaria exsectiformis</i>	Tritexs	11	

CHAPTER SEVEN

Conclusion

Overview of major findings

The overarching goal of my dissertation was to assess the ability of the Alberta Biodiversity Monitoring Institute to provide robust data to inform land management. Documenting and minimizing sources of sample error, including detection bias, is critical for scientific transparency and necessary before exploring ecological trends in ABMI data. Evidence presented in this dissertation supports the thesis that the ABMI can provide statistically-powerful measures of changing occurrence for multiple assemblages in the medium to long-term (20 years or greater) at the natural region scale (120,000 km²) given the current level of detection error (Chapter Five). Statistically-powerful trend estimates are possible in the short term for common species (occurring $\geq 50\%$ of sites), and should also be possible by utilizing community metrics, which proved robust to detection error for bryophytes (Chapter Three). Detection errors for two assemblages (bryophytes and macrolichens) are predicted to decrease as the revised methods suggested in Chapter Three are implemented. These methods increase survey effort per unit area while maximizing the number of species recorded via a novel floristic approach (e.g., Appendix 6.2), and permit either detection modelling or a metric of relative abundance.

As in this dissertation, however, broad-scale monitoring programs must look in many directions at once, particularly in the early stages of development. Promising trends in 10 years does not ensure survival today. In the interim, ABMI protocols are estimated to have conservatively recorded more than 70% of the soil oribatid mites, breeding birds, vascular plants and bryophytes species predicted to be present before completion of the first monitoring rotation (Chapter Six). This level of completeness for cryptogamic taxa is achieved in part by parataxonomists in the laboratory, where incidental 'bycatch' (species mixed with more dominant bryophyte samples) is detected, and detection error for common species is minimized (Chapter Four). The ABMI can provide compelling insight

into how boreal biodiversity is changing across multiple anthropogenic and natural gradients (Chapter Six). ABMI scientists currently are populating predictive maps with these data, which can be considered analogous to those commonly constructed for predictions of climate change. Besides testing hypotheses around biodiversity change, these tools will also enable managers to explore tradeoffs between conservation and economic opportunity for alternate land-use scenarios (e.g, Schneider et al. 2012). The greater survey intensity of ABMI as compared to climate stations is justifiable due to the higher local variability of terrestrial biodiversity. Terrestrial ecosystems don't mix like atmospheric systems, thus more stations or surveys are needed to provide robust interpolation of trends (e.g., Andreasen et al. 2001).

Anecdotally, the ABMI appears to have been adopted by government and land managers much more readily than by academics. ABMI data represents a freely-available, novel resource, but uptake of that resource by the academic community has been slow. In addition to the recommendations made in Chapter One, ABMI may benefit from hosting yearly workshops for all interested graduate students, particularly in Alberta, not unlike those hosted for students interested in geographic information systems or other university resources. The breadth of data available can be overwhelming for someone unfamiliar with the program and both its strengths and limitations are not always clearly communicated. The ABMI represents an ecological atlas to both address existing questions and form new ones, and an opportunity for many graduate students to better formulate their plans before going into the field.

The role of ABMI in biodiversity conservation

One thing that hasn't changed, of course, is the difficulty ordinary mortals will have reading Ottawa's [...] Monitoring Plan.... Savour, for example, this criticism (or maybe it's praise?) for current monitoring: it "has not had sufficient spatial and temporal sampling coverage to allow discrimination of anthropogenic impacts from natural heterogeneity". This time, however, the problem seems to be that scientists can't write. A few years ago, gobbledygook sometimes had a political purpose – to mask the fact that nothing was being said."

Edmonton Journal, Saturday March 26, 2011 Editorial, Progress on oilsands monitoring, Opinion page A16

The ABMI has become a vital part of a larger initiative to increase our understanding of environmental change in Alberta, particularly in the oil sands regions of northeastern Alberta (Government of Alberta 2012). However, while scientific transparency, quality control and robust estimates of natural and sample variation are important for the scientific integrity of ABMI, it may not be enough to enact change in land management practices. The above quote could have come from many different ABMI documents – it expresses a fundamental aspect of the ABMI, its geographic and temporal breadth - and the fact that is has no meaning to the educated public is concerning. If ABMI restricts its role to data provisioning and analysis, will those involved be content to document decline of boreal biodiversity rather than decrease the rate of loss? The current economic climate is likely to accelerate land-use change, particularly given the recent changes to the environmental impact assessment process at the federal level (The Canadian Press 2012a). To increase the impact of ABMI, I hope to see greater interplay between the public and ABMI in the future, including working with social scientists to understand the public's valuation of biodiversity (e.g, Van Den Born et al. 2001, Simaika and Samways 2010, Bayne et al. 2012).

Alberta has relatively few endemic species, and most species can be found in equal concentration on at least one other location on the globe. This was the recent justification behind Canada's Environment Minister Peter Kent refusal to issue an emergency order to protect woodland caribou (The Canadian Press 2012b), even though recent research has shown that caribou and industrial development are not mutually exclusive (Schneider et al. 2012). If the one strong lever conservationists have for species that are near their tolerance, endangered species legislation, is broken, than will a mite or lichen will have any pull? Perhaps *en masse* - this may be a key benefit of the ABMI's multi-taxon nature. For example, I showed that agriculture was correlated to the greatest reduction in reduced species diversity across four assemblages (Chapter Six) as compared to forestry, soft linear features or industrial well pads and gravel pits. With climate change there is the potential for conversion of parkland and boreal forest to drier

ecotypes more conducive to agriculture (Schneider et al. 2009). The ABMI can help predict and plan for those shifts.

In reality, biodiversity is lost each time a genetically-unique individual or deme is lost. Implicitly, most humans agree that loss at this level is acceptable and even desirable to further other societal values - we exchange a living tree for timber, we exchange soil biota for sub-level basements. However, society has agreed that it is unacceptable to drive species to extinction, and indeed human communities would also rather not extirpate local populations that provide them food, leisure through trapping, hunting, tourism and other life-style related values. If the society and governments allow it, ecosystems such as the boreal forest that sustain large tracts of relatively unscathed habitat may avoid the degree of alteration visited upon other biomes. Biomonitoring programs like the ABMI are one mechanism to improve land management because they remove time lags due to lack of information. They collect real baseline data against which future states can be compared, preventing 'shifting baselines' (Pauly 1995, Sáenz-Arroyo et al. 2005), i.e., the [potential] misconception of future generations that a depauperate boreal is the only boreal that ever existed.

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