

**PRINCIPLES AND PROCEDURE FOR PLACE-BASED CONSERVATION PLANNING FOR
CANADIAN SPECIES AT RISK**

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ABSTRACT

Place-based biological conservation planning and recovery delineates “places” – spatial extents with favourable conditions for the recovery and management of multiple species simultaneously. Places represent geographic areas where constituent species are more likely to benefit from a specific set of recovery and management actions. Currently, place-based conservation planning is focused on prioritizing already-identified places. Findlay and McKee (2016) propose an approach to identify and delineate places by grouping geographical units based on species-at-risk (SAR) co-localization in (a) geographical, and (b) threat space. The following research is a practical application of the Findlay-McKee Methodology (FMM), using southern Ontario as a case study. I develop a parameterized algorithm to operationalize the design principles laid out in the FMM. I first define metrics to characterize the variation in SAR overlap and the degree to which sets of SAR share common threats. Next, I explore how the spatial extent of places (place size) changes as a function of tolerance for dissimilarity in both measures. The case study allowed me to evaluate the benefits and limitations of the FMM. I conclude that the FMM has the potential to be a defensible method for characterizing places based on SAR community overlap and inter-species threat similarity. However, the FMM's applicability is limited by the availability of datasets at an appropriate resolution for analysis; uncertainty in selecting appropriate thresholds of tolerance for dissimilarity; and the criteria used to designate seed planning units. Given the increasing popularity of multi-species and ecosystem level recovery and conservation management, developing an efficient and effective process to guide place selection is crucially important. I recommend further research focus on empirically determining the number of places in a planning region and identifying at what tolerance thresholds places lose their ability to delineate areas where a comparatively small number of recovery actions will confer widespread benefits.

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TABLE OF CONTENTS

1. INTRODUCTION.....	1
1.1. THE HISTORY OF IMPERILED SPECIES LEGISLATION IN CANADA.....	1
1.2 RECOVERY PLANNING AND CONSERVATION MANAGEMENT.....	3
1.3 SINGLE-SPECIES CONSERVATION AND RECOVERY PLANNING.....	4
1.4 MULTIPLE SPECIES CONSERVATION AND RECOVERY PLANNING.....	6
1.4.1 Surrogate species conservation and recovery planning	8
1.4.2 Systematic place-based conservation and recovery planning	10
1.5 THE FINDLAY-MCKEE METHODOLOGY (FMM)	12
2. RESEARCH OBJECTIVES.....	15
3. METHODOLOGY	16
3.1 - IDENTIFY A PLANNING REGION (PR).....	16
3.2- DEFINE THE MINIMUM PLANNING UNIT (MPU).....	17
3.3 DEFINE AND MAP A SET OF METRICS TO CHARACTERIZE SAR COMMUNITY WITHIN EACH PLANNING UNIT (PU).....	18
3.4. DEFINE AND MAP A SET OF METRICS THAT CAPTURE THE SIMILARITY IN THREAT PROFILES IN SPECIES COMMUNITY WITHIN EACH PU.....	21
3.5 DEFINE AND MAP A SET OF COMPOSITE METRICS.....	22
3.6 TOLERANCE FOR DISSIMILARITY AND PLACE SIZE.....	22
4. RESULTS.....	26
4.1 HEAT MAPPING OF PU.....	26
4.2 PLACE SIZE AND TOLERANCE THRESHOLDS.....	37
5. DISCUSSION.....	41
5.1 HOW THE FMM FITS INTO EXISTING CONSERVATION PLANNING.....	41
5.2 LIMITATIONS, IMPROVEMENTS, AND EXTENSIONS.....	44
5.2.1 RESOLUTION AND AVAILABILITY OF DATASETS.....	45
5.2.2 THE ASSUMPTION OF THREAT UNIFORMITY.....	46
5.2.3 SEED DESIGNATION AND PLACE DETERMINATION.....	47
5.2.4 SELECTING APPROPRIATE TOLERANCE THRESHOLDS	48
6.3 THE COST OF RECOVERY.....	48
6. CONCLUSION.....	51
7. REFERENCES.....	52
APPENDIX A – DATA REQUIREMENTS.....	59
APPENDIX B – CHARACTERIZING SAR COMMUNITY.....	62
APPENDIX C – CHARACTERIZING INTER-SPECIES THREAT DISTANCES	66
APPENDIX D – COMPOSITE METRICS.....	69
APPENDIX E – ADAPTIVE PLACE SIZE.....	70
APPENDIX F – GLOSSARY OF TERMS.....	74
APPENDIX G – BRAY-CURTIS DISSIMILARITY	76
APPENDIX H – ALGORITHM (PYTHON CODE).....	77

LIST OF FIGURES

FIGURE 1:	PLANNING REGION AND SUBREGIONS OF SOUTHERN ONTARIO.....	18
FIGURE 2:	FREQUENCY DISTRIBUTION AND HEAT MAPPING OF RAW SAR RICHNESS.....	26
FIGURE 3:	GEOGRAPHIC VARIATION IN FREQUENCY DISTRIBUTION OF RAW SAR RICHNESS.....	27
FIGURE 4:	FREQUENCY DISTRIBUTION AND HEAT MAPPING OF WEIGHTED SAR RICHNESS.....	28
FIGURE 5:	GEOGRAPHIC VARIATION IN FREQUENCY DISTRIBUTION OF RAW SAR RICHNESS.....	29
FIGURE 6:	WEIGHTED SAR RICHNESS PLOTTED AGAINST RAW SAR RICHNESS.....	30
FIGURE 7:	FREQUENCY DISTRIBUTION AND HEAT MAPPING OF AVERAGE DISTANCE IN SAR THREAT PROFILES.....	31
FIGURE 8:	GEOGRAPHIC VARIATION IN FREQUENCY DISTRIBUTION OF AVERAGE DISTANCE IN SAR THREAT PROFILES.....	32
FIGURE 9:	AVERAGE DISTANCE IN SAR THREAT PROFILES PLOTTED AGAINST RAW SAR RICHNESS.....	33
FIGURE 10:	OUTLIERS OF 6E AND ASSOCIATED GEOGRAPHIC LOCATIONS.....	34
FIGURE 11:	FREQUENCY DISTRIBUTION AND HEAT MAPPING OF COMPOSITE SCORES.....	35
FIGURE 12:	GEOGRAPHIC VARIATION IN FREQUENCY DISTRIBUTION OF COMPOSITE SCORES...	36
FIGURE 13:	“PLACE” SIZE AS A FUNCTION OF INCREASING TOLERANCE THRESHOLDS FOR 5E....	37
FIGURE 14:	“PLACE” SIZE AS A FUNCTION OF INCREASING TOLERANCE THRESHOLDS FOR 6E....	38
FIGURE 15:	“PLACE” SIZE AS A FUNCTION OF INCREASING TOLERANCE THRESHOLDS FOR 7E...	38
FIGURE 16:	AVERAGE PLACE SPATIAL EXTENT AS A FUNCTION OF INCREASING THRESHOLDS FOR TOLERANCE IN DISSIMILARITY FOR INTER-SPECIES THREAT DISTANCE	39

1. INTRODUCTION

1.1 - The history of imperiled species legislation in Canada

In the age of the Anthropocene, a period marked by increased economic development and exponential population growth (Steffen et al., 2015), the escalated demand for resources has put increased pressure on biological populations (WWF, 2018). Natural systems have been negatively impacted by anthropogenic activities (Pimm et al., 2014). Drivers of species decline, including land-use changes, resource exploitation, the introduction of invasive species, pollution, and climate change (UN, 2019), have been causally linked to habitat degradation, fragmentation, and loss (Pimm et al, 2014). According to a recent UN report, species are declining rapidly, at rates unprecedented in human history. Current estimates identify nearly one million species globally are threatened with the risk of extinction (UN SDG, 2019). The need to mitigate this prominent loss of biodiversity is clear.

In 1992, an aggregate of international governments, indigenous groups, and non-government organizations gathered in Rio de Janeiro, Brazil, to participate in the United Nations Earth Summit. The resulting Convention on Biological Diversity (CBD), recognized the need for a global effort to conserve wildlife species by promoting their recovery and persistence (UN Environment, 2017). Canada, as a signatory to the CBD, made an international commitment to protect imperiled species from further declines as well as support their recovery (Broome, 2010). In 2002, the *Species at Risk Act (SARA)* was passed into legislation by the Canadian Federal Government (Government of Canada, 2017). As Canada's response to the commitment made in Brazil (Ecojustice, 2012), SARA is founded on the principles to protect "designatable units (Government of Canada, 2017)" - "subspecies, varieties or geographically or genetically distinct populations (SARA c.29 s.2)", from becoming extinct, and implement recovery strategies for those units identified as threatened or endangered (Green, 2005). SARA recognizes the inherent value of Canadian wildlife, mandating the prevention of species extirpation or extinction

and promoting the recovery of wildlife species that have been impacted by anthropogenic activities.

Affording species protection under SARA is a multi-step process. Initial assessment is conducted by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). This independent advisory board evaluates a species' risk of extinction based solely on the best available scientific evidence (COSEWIC, 2017). Following completion, the status assessments are forwarded to the Minister of Environment and Climate Change. The Minister invariably undertakes a consultation process with potentially affected stakeholders, eventually making a recommendation to the Governor in Council based not only on scientific knowledge, but also considering socioeconomic implications, stakeholder values, and political will (Mooers et al., 2010). A final listing decision is ultimately provided by the Governor in Council, who must render a decision within nine months of receipt of this recommendation (SARA c.29 s.27(1.1)).

Although the listing process in Canada is discretionary, once a critical listing decision (endangered, threatened, or extirpated) is achieved under SARA, legal protection is incurred. Basic prohibitions against "harm, harass, or capture ((SARA c.29 s.32(1)), "possession and trafficking of (SARA c.29 s.32(2)), " and the "destruction of residence (SARA c.29 s.33)" of critically listed species are immediately applied following a protected status. This piece of federal legislation serves as the primary political and legal instrument for identifying and protecting imperiled wildlife in Canada (Mooers et al., 2017).

In Canada, a decision to list under SARA imposes a requirement for the federal government to develop a recovery plan. This two-step process begins with the initial Recovery Strategy (RS) documenting the current status of the population, identifying the series of potential threats faced by the population, and setting distribution targets or goals (SARA c.29 s.41(1)). The RS is followed by a Recovery Action Plan (RAP), quantifying goals, evaluating socioeconomic implications, and initiating measures to meet the outlined objectives (SARA c.29 s.49(1)). SARA mandates that following a critical listing decision, recovery strategies be

proposed within one year for populations granted endangered status and two years of listing for threatened and extirpated status (SARA c.29 s.42). If recovery is deemed feasible by a competent minister, the associated recovery strategy must include - consistent with the information provided by COSEWIC:

- (a) a description of the imperiled population,
- (b) the identification of the threats - barriers to recovery and/or persistence,
- (c) the identification of the extent of a population's critical habitat,
 - (c.1) if critical habitat has not yet been identified, a schedule of studies to determine critical habitat,
- (d) a general description of the recovery and management actions needed to assist in the recovery of imperiled populations,
- (e) any other matters relating to the regulation including goals, objectives, and approaches to recovery planning
- (f) a statement on whether additional information is required, and
- (g) an associated timeline for the completion of associated action plan(s) (SARA c.29 s.41(1(a-g))).

Protections may be applied to single species through targeted individual recovery plans, or be applied at the ecosystem level, incurring recovery strategies for multiple species simultaneously (SARA c.29 s.41(3)).

1. 2 – Recovery planning and conservation management

Wildlife populations are valued both extrinsically - for their direct, indirect, or potential uses, and intrinsically – for their inherent existence (NRC, 1999). The set of values attributed to the persistence of wildlife has given rise to legislation, regulations, and policy targeting the protection of species and natural systems. For example, SARA's purpose mandates for the prevention of ecological extirpation and extinction of wildlife, as well as the recovery of imperiled

populations (SARA c.29 s.6). Processes that increase the risk of ecological extinction and extirpation (i.e. exposure to anthropogenic-induced drivers of habitat alteration) undermine these values. Conversely, actions that mitigate or compensate for these risks (i.e. recovery and conservation management actions) sustain these values. Sustaining the persistence of wildlife populations requires recovery strategies designed to reduce or compensate for the impact of exposure to such threats.

Planning for the recovery of imperiled populations is arguably the most impactful component of legislation enacted to protect at-risk species from further declines. Recovery strategies and conservation action plans integrate quantitative species data with expert analysis to frame recovery criteria and identify management priorities (Bottrill et al, 2008; Schwartz, 2008). Given limited time, resources, and expertise, biological management is a challenging endeavor (Lindenmayer et al., 2007). There is no singular approach to conservation planning and recovery management (William et al., 2013). Conventionally, recovery has focused on specific populations, tailoring recovery plans on a species-by-species basis (Feagan, 2017). With legislative provisions allowing the option to approach recovery through a multi-species or ecosystem lens, advocates have cited the benefits of using a systematic place-based approach to conservation planning (Clark et al., 2002; Findlay and McKee, 2016). Each approach to conservation planning has its advantages and limitations, sparking considerable debate over which approach most appropriately serves to successfully identify protected space for biological conservation.

1.3 Single-species conservation and recovery planning

Strategies centered on the conservation of single species are designed to promote the recovery of a particular imperiled unit or population. Identifying areas for protection or conservation is relatively simple because this type of approach values the persistence of a single, target species. Recovery actions are tied to individual species. Protecting a portion, or the entirety, of

the species' range delineates spatial extents where recovery actions will decrease the risk of ecological extirpation and/or extinction for the species of interest. Protected areas become geographic extents whereby targeting conservation efforts for a single species is expected to confer benefits to the targeted imperilled species or population. This type of approach is most appropriate when the target species occupies a distinct habitat type, has a narrow geographic distribution, and is affected by a unique set of threats (USFWS, 2000).

The benefits of species-specific recovery are illustrated by, for example, the case of *Centrocercus urophasianus*, the Greater Sage Grouse. The Greater Sage Grouse is an imperilled North American grouse species, indigenous to the mixed grassland ecoregion of the Canadian and Western United States prairies (Environment Canada, 2013). Following substantial population declines, the Canadian population was listed as Endangered status under SARA in 2003. Agricultural practices, pipeline construction, and anthropogenic-induced changes to hydrological regimes had altered nearly 80% of the identified critical habitat, threatening the existence of *C. urophasianus* (Environment Canada, 2013). The total adult Canadian population was estimated to be between 93-138 individuals in the amended recovery strategy published in 2012. In an effort to recover the nearly extirpated Canadian subspecies, the Governor in Council issued an *Emergency Protection Order*. This single-species recovery approach restricted activities in areas deemed indispensable to the survival and recovery of *C. urophasianus*. Failure to comply with the restrictions outlined in the order was a violation of SARA, a punishable offence under federal law (SARA c.29 s.97). Following the intervention, male *C. urophasianus* experienced substantial relative growth, with increases reaching 150% in Alberta and 222% in Saskatchewan (Ecojustice, 2016). The state of the Greater Sage Grouse is improving, the direct result of actions informed by a species-specific recovery approach.

Though species-specific recovery actions have the potential to be both biologically and technically feasible, several limitations may inhibit this type of approach. Producing a recovery strategy requires extensive knowledge of preferred habitat, potential threats and other

limitations to persistence, and appropriate conservation actions. Considerable time and financial resources are required to create these documents (Franklin, 1993; Taylor et al, 2005).

Furthermore, recovery strategies focused solely on individual species have the potential to negatively affect co-occurring units or populations. While the benefit of conservation efforts targeting individual species certainly exist, it is not possible to protect all imperiled species in this manner. Approaching conservation on a species-by-species basis exhausts available financial and knowledge resources (Franklin, 1993). Given the limited resources afforded to conservation endeavours, alternative approaches to conservation planning are increasing in popularity (Government of Canada, 2018; WWF, 2005)

1.4 – Multiple species conservation and recovery planning

Attempts to improve the efficacy of conservation efforts have directed conservation managers to develop conservation approaches targeting multi-species simultaneously (Franklin, 1993; Government of Canada, 2018; WWF, 2005). Conservation planning and management for multiple species designs recovery for suites of species under a single, integrated strategy (Lambeck, 1997). Because extinction and/or extirpation risk varies both geographically and among species, promoting the recovery and persistence of several species through a single recovery strategy requires consideration of the suite of barriers impeding their recovery – the threats to which they are exposed. Similarly, geographic range and habitat associations must also be factored into place identification. Protected spaces, under this approach, are defined as geographic extents where favourable conditions exist for the recovery and persistence of several imperiled units (Lambeck, 1997). Targeting recovery and conservation actions to a set of co-occurring species is expected to confer benefits to all. Conservation efforts at this scale are attractive as they can address the tight timelines for completion of recovery plans mandated by SARA (SARA c.29 s.42), and at least in principle – make more efficient use of limited resources (Simberloff, 1998). Advocates support the shift, citing that a multi-species approach

to management reduces the constraints associated with limited time, available funds, and scientific knowledge (WWF, 2005). Implementing multi-species recovery strategies, “if carried out effectively, should provide improved cost effectiveness and greater opportunity for long term success (Tear et al., 1995).”

In the Canadian context, several recovery strategies have been developed explicitly for sets of imperiled species. For example, in 2012, Environment Canada (EC) combined the recovery targeting protection of the Acadian Flycatcher, *Empidonax virescens*, and the Hooded Warbler, *Wilsonia citrina* under a single strategy. The multi-species plan was justified by EC as the species’ distributions overlapped, they exhibited similarities in preferred habitat (identified as deciduous forests of Southern Ontario), and they faced similar threats (primarily anthropogenic-induced habitat degradation and fragmentation). Hence it was argued that within this area, a single set of recovery actions focused on mitigating major threats would benefit both species (Environment Canada, 2012).

While support for multi-species recovery actions has been increasing (Franklin, 1993; Tear et al., 1995; Lambeck, 1997; Groves et al., 2002; Kellner et al., 2011), conservation planning targeting multiple species is more complex (La Roe, 1993). Tailoring recovery strategies to include several species is data intensive. Because protected spaces represent areas where imperiled populations exhibit geographical co-occurrence, similar habitat associations, and face a similar suite of threats (Clark and Harvey, 2002; Findlay and McKee, 2016), geographic distribution, preferred habitat, barriers to persistence, and potential recovery actions must be known for all species. Furthermore, the process is complicated by the complex nature of biological attributes, anthropogenic-species interactions, and prevailing political and social landscapes (Tear et al., 1995). Moreover, the approach exhausts resources. Defining these spatial boundaries is an important challenge in multi-species conservation management as the utility of multi-species recovery planning fails when species are inappropriately grouped (Clark and Harvey, 2002). Selection of the criteria for grouping species

and/or populations is subject to debate among conservation biologists and political players (WWF, 2005)

1.4.1 Surrogate species conservation planning and recovery

Surrogate species conservation planning is one approach used to group species for multi-species recovery. Surrogate, or proxy-based recovery and conservation planning approaches use surrogate species as proxies to confer protection to multiple species (Weins et al., 2008). Common to all surrogate species approaches is the assumption that the proxy adequately represents the ecological needs of multiple species. Because surrogates are presumed to suitably represent other species or aspects of the environment, conservation measures targeted towards protection of the surrogate(s) are assumed to extend protective benefits to geographically co-occurring species (Roberge and Angelstam, 2004). Conservation areas are established by protecting either the entirety - or a significant portion of - the range occupied by the surrogate.

This conservation management framework was applied in the recovery strategy proposed for the Northern Spotted Owl, a species that inhabits late successional stage and old growth forests found in the Pacific Northwest. Its Canadian extent is limited to southwestern British Columbia. Degradation and fragmentation of these conifer forests have resulted in declining population abundance (Chutter et al., 2004). Within the range of *S. caurina*, biologists identified 71 insular (species with ranges confined to that of the surrogate) and 214 co-occurring (species with ranges that overlap, to some extent, that of the surrogate) species (Harper and Miliken, 1994). Protection of the multitude of vertebrates, invertebrates, and plants that occupy the old-growth and late successional stage forest of southwestern British Columbia was addressed in the finalized recovery strategy for *S. caurina* (Chutter et al., 2004). By providing protective measures targeting *S. caurina*'s relatively widespread range, management actions would, it was assumed, indirectly protect insular and co-occurring species. The Northern

Spotted Owl served as a proxy, or umbrella, for the protection of species occupying old growth and late successional stage forests.

Surrogate species conservation planning reduces the complexity of species-rich systems, facilitating recovery by targeting actions on a small number of representative species (Weins et al., 2008). The framework takes a systematic approach to implement, manage, and monitor protected areas (Weins et al., 2008). Although managing the needs of a community, (either partially or in its entirety) by implementing a systematic, proxy-based approach is theoretically possible, evidence supporting the presumption that protection of proxies confers adequate protection to co-occurring species is weak (Andelman and Fagan, 2000).

The assumption that one taxonomic group serves as a reliable proxy across other taxonomic groups is largely unsubstantiated (Fleishman et al., 2001). The ability of a surrogate to effectively protect insular species is affected by scale (Favreau et al., 2006). Surrogate species conservation planning is founded on extrapolation, from surrogates to groups of species. However, grouping numerous species under the protection of a surrogate species reduces consideration of the suite of unique characteristics that drive species distribution and abundance (Carrol et al., 2001). Disparate species' responses to management actions reduces the probability of successful recovery for insular and co-occurring species (Carlisle, 2018). When the extent of a place spans a large geographic area, or the number of insular and co-occurring species is very large, it becomes increasingly difficult for surrogates to adequately represent the variety of taxa present (Caro, 2010) – limiting the likelihood that management actions will confer mutually beneficial results. Moreover, the processes guiding the selection of surrogates' lack frameworks with defined procedures. As a result, little consensus exists concerning what characteristics should be prioritized when deciding on a surrogate (Andelman and Fagan, 2000; Caro, 2010). Particular proxies are largely chosen *ad hoc*, due to their widespread range or charismatic nature (Andelman and Fagan, 2000). Using these indices of selection reduces the relative importance of other scientifically sound criteria, compromising the

efficacy of recovery and management actions (Fleishmann et al., 2001). These limitations reduce the reliability that surrogate-based conservation planning will result in the sustained persistence of co-occurring populations. Several evaluations testing the validity of surrogate-species approaches have concluded its utility as an effective approach to multi-species conservation and management planning is limited (Andelman and Fagan, 2000; Branton and Richardson, 2011; Fleishman et al., 2001; Manne and Williams, 2003).

1.4.2 Systematic place-based conservation planning and recovery

Alternatively, approaches grouping species can employ a spatially explicit, place-based approach. The processes that undermine imperilled species recovery and persistence may show geographic or spatial variation (Olsen et al., 2013) - i.e., threats driving habitat loss, fragmentation, and/or degradation are often patchily distributed across a species' range (Findlay and McKee, 2016). Similarly, a spatial component is associated with the application of recovery and conservation management actions (Findlay and McKee, 2016; Mason, 2007; Williams et al., 2013). Application of actions to reduce and/or compensate for these threats are likely to generate greater benefits in areas where exposure to threats is high (Findlay and McKee, 2016). Spatially explicit management strategies become a function of "place" - areas where implementing a set of recovery actions reduces the risk of ecological extirpation or extinction (Findlay and McKee, 2016). Assigning value to biological and/or economic attributes delineates places where implementing a comparatively small set of recovery and management actions will likely confer benefits to a large number of species found within its boundaries.

Place-based conservation planning (PBCP) employs a systematic approach to identify and prioritize places for multi species conservation (Ribeiro and Atadeu, 2019). In contrast to conventional species-level conservation planning, systematic conservation planning (SCP) approaches recovery and management through a series of well-defined, spatially explicit steps (Harris et al, 2019; Margules and Pressey, 2000; Pressey and Bottril, 2009). SCP is an

integrated, evidence-based cycle of data collection, decision-making, monitoring and evaluation that identifies and prioritizes places (Harris et al, 2019; Margules and Pressey, 2000). SCP informs conservation decision-making to maximize the effectiveness and efficiency of conservation planning at a multi species or ecosystem level (Margules and Pressey, 2000)

PBCP emphasizes spatially explicit conservation planning (Williams et al., 2013). In PBCP, conservation and recovery actions are not tied to individual species. Instead, conservation actions are tied to geographic areas. Places, in this sense become geographically delineated areas whereby implementing a comparatively small set of recovery and management actions is likely to confer widespread benefits to a number of co-occurring imperilled species (Findlay and McKee, 2016). PBCP first involves identifying and delineating places. Following the initial step, places are prioritized. Next, conservation and recovery actions are implemented. Then, imperilled populations located within place boundaries are monitored and evaluated (Williams et al., 2013; Rao et al., 2007). Currently, PBCP efforts have focused on devising measures and algorithms that prioritize already-defined places (Moore and Wooler, 2004; Roux et al., 2017). These frameworks take, as a given, that places have already been identified, and prioritize conservation targets by weighing the value of ecological and economic attributes (Rao et al., 2007). The question in place-based planning becomes how should these places be delineated, and how should the associated set of conservation actions be characterized to maximize the cumulative benefit to imperilled species?

PBCP frameworks have proposed specialized methodologies to identify potential places for conservation, based on ecological criteria including habitat loss, endemism, diversity, richness, or the value of ecological services (Rao et al., 2007). However, widespread place-based planning requires an integrated systematic operational methodology to characterize the set of places – delineate place boundaries – and the set of species for which conservation actions are likely to confer widespread benefits.

1.5 - The Findlay-McKee Methodology (FMM) for place-based conservation planning.

In a recent report, Findlay and McKee (2016) proposed a general approach to systematically aggregate geographical units to identify place boundaries. The delineation of places using the FMM framework, is driven by the application of foundational metrics characterizing the geographic variation in species-at-risk (SAR) community composition and quantifying the degree of variation in processes linked to increased risk of extirpation and/or extinction. The methodology builds on current PBCP by integrating attributes quantifying SAR richness, the degree of co-localization in species' assemblages, the degree of shared or common threats, and the similarity in required recovery or conservation actions (Findlay and McKee, 2016). At least in principle, under the Findlay-McKee Methodology, for a given geographic unit, one can identify the set of SAR found within its boundaries, the degree of similarity in shared or common threats to which these species are exposed, and the set of conservation actions that would mitigate these threats. Places, under the FMM, can be defined as geographically delineated areas whereby a comparatively small set of conservation actions is likely to benefit a comparatively large group of SAR because these actions target common threats (Findlay and McKee, 2016).

Species' geographic distribution is determined by a unique set of environmental preferences and anthropogenic influences (Verberk, 2011). The result is a considerable geographic variation in SAR community composition. This compositional variation is a central component in the identification of favourable places for multi-species conservation, insofar as areas with the same SAR community composition should have more similar conservation management efforts than areas with different SAR communities. Geographic areas with similar species composition are *more likely* to benefit from a specific set of recovery and management actions than areas with very different SAR community composition. As such, similarity in SAR community composition is an important consideration in the geographical delineation of places for conservation management (Findlay and McKee, 2016).

All imperiled populations face a set of threats, limiting their potential for recovery and persistence by, increasing the risk of extirpation and/or extinction (Clark and Harvey, 2002). Successful recovery actions reduce exposure to, mitigate, or compensate for these threats (Novacek and Cleland, 2001). When geographically co-occurring species are affected by a similar suite of threats, recovery and management actions targeting the set of common threats is expected to confer benefits to all. Conversely, when SAR communities exhibit little threat similarity, specific mitigation measures are less likely to have widespread benefits (Clark and Harvey, 2002; Findlay and McKee, 2016). *SAR threat distance* metrics, derived to characterize the degree of overlap in shared threats within SAR assemblages, provide an index of threat similarity. A second important attribute of places for multi-species conservation then pertains to the extent to which the SAR community share common threats (Findlay and McKee, 2016).

It seems clear then, that place characterization should integrate these two sets of metrics in order to identify and prioritize areas where a comparatively small set of conservation management and recovery actions is likely to provide widespread benefits to the entire SAR community. “Places”, according to the FMM¹ are thereby defined as:

“spatially contiguous geographical areas within which are found approximately the same species at risk (SAR) community, to which are exposed approximately the same set of threats and for which recovery or management involves approximately the same set of recovery or management actions (Findlay and McKee, 2016).”

The FMM provides a way of delineating places based on the compositional variation in SAR assemblage and inter-species threat distance. Heat mapping, in this context, serves as a useful tool to identify “hotspots” - places where the SAR community, the set of species, is (spatially) homogenous, and inter-species threat similarity is relatively high. If administrative, jurisdictional, hydrological, geological, and socioeconomic boundaries are ignored, the spatial extent of places

¹ Going forward, the Findlay-McKee methodology will be referred to as the FM Method or FMM

depends on the degree of spatial dissimilarity permitted in SAR community composition and inter-species threat distances. If no variation is tolerated (i.e. places are characterized by a spatially homogenous SAR community, members of which are exposed to an identical set of threats), “places” will generally be small. As tolerance increases, i.e. so that more spatial variation in SAR community composition and/or greater divergences in threat profiles among species is tolerated, places become larger (Findlay and McKee, 2016).

2. RESEARCH OBJECTIVES

The FMM is designed to geographically characterize places for place-based conservation. At least in principle, under the FMM, for a given planning unit one can identify the set of SAR found in it, the degree of similarity in the set of threats to which the co-occurring species are exposed, and the set of conservation actions that would mitigate these threats. The framework can be applied on a local, regional, or national scale. In Canada, it has the potential to inform the three federal agencies responsible for imperiled species recovery in Canada: Environment and Climate Change Canada (ECCC), Parks Canada (PC), and the Department of Fisheries and Oceans (DFO), as well as provincial and territorial agencies involved in endangered species protection. The FMM may also be used to inform conservation planning outside Canada.

The issue, at present, concerns its operationalization. To address this issue, here I apply the FMM method to Southern Ontario, a hotspot for imperiled species' richness (Kerr and Cihlar, 2004). I develop and implement a spatially explicit method for operationalizing the design principles laid out in the FMM. I define and apply metrics characterizing SAR community, the degree of geographic variation in species' assemblages (SAR community overlap), and the degree of similarity in shared threats among sets of SAR. I then explore how the spatial extent of places changes as the degree of tolerance for variation in SAR community composition and/or inter-species threat distance increases. For a given tolerance, using geographic information software (GIS), I employ a parameterized algorithm to identify places of particular value for multi-species conservation. This research evaluates the benefits and limitations of the FMM in delineating places for place-based recovery and conservation management.

3. METHODOLOGY

The FMM framework for identifying and prioritizing favourable places for the recovery and conservation management of multiple imperiled Canadian wildlife was operationalized and evaluated using the procedure described below. The procedure requires, for a specified planning region, six different datasets:

- (1) A planning region shapefile that delineates the geographical boundaries of the planning region of interest (Appendix A.1);
- (2) Species distribution maps for the set of SAR of interest (Appendix A.2);
- (3) Measures of extinction risk (here operationalized as COSEWIC status designations), for the set of SAR of interest (Appendix A.3);
- (4) A habitat/ land cover map (Appendix A.4);
- (5) A habitat association profile (HAP), elements of which give the suitability of a given habitat/ land cover class in (4) for a particular species (Appendix A.5); and
- (6) A threat profile (TP), element of which minimally denotes whether a particular species is exposed to a specific threat or threat class (Appendix A.6).

Here I use ArcGIS 10.6.1 software to integrate and manipulate datasets (1) - (6) to identify and delineate places in southern Ontario. Statistical analysis was performed through Microsoft Excel (For Office 365, Version 1903).

3.1 - Identify a planning region (PR)

As the FMM can, in theory, be applied on a local, regional, or national scale, it is necessary to specify an appropriate geographic area of interest for the purpose of recovery or management actions. The *planning region* defines the geographical areas within which places will be delineated (Findlay and McKee, 2016). Southern Ontario, a region of high endangered species density (Kerr and Cihlar, 2004), is the *planning region* of interest in this case study. The region, as determined by census data (FED-DEV Ontario, 2014), was subdivided into three *planning*

subregions (PSR), on the basis of their ecoregion designation: (5E) Georgian Bay Ecoregion – the northernmost subregion; (6E) Lake Simcoe-Rideau Ecoregion – the mid subregion; and (7E) Lake Erie- Lake Ontario Ecoregion – the southernmost subregion (Ministry of Natural Resources and Forestry, 2018). The planning region was isolated and extracted to form a new layer, containing only the planning region and subregions of interest (Figure 1).

3.2 - Define the *minimum planning unit* (mpu)

Planning subregions are divided into square polygons (cells). Each cell is referred to as a *planning unit (PU)*. These PU represent the *minimum size of a place* - where recovery and management actions will, in theory, successfully sustain multiple imperiled species. The appropriate PU size is a function of the size of the planning region (with larger regions having larger PU); the geographic range of species within the planning region (with areas having SAR with narrow ranges having smaller PU); and the availability of resources (dividing a planning region into smaller PU requires greater computational resources (Findlay and McKee, 2016). For this case study, cell size (minimum PU size) was set to 100km². The procedure was then:

- a) A 100km² PU grid was created for the entire planning region;
- b) PU (10kmX10km polygons) not entirely contained within the planning region were eliminated from the analysis (n = 237);
- c) PU comprised of more than 50% water (as determined by MODIS landcover data, Appendix B.1) were eliminated from the analysis (n = 226);
- d) PU in which were found (based on SAR range maps) 1 or fewer SAR (see Appendix B.2) were eliminated from the analysis (n = 75);
- e) All remaining PU (N = 1426) were partitioned among planning subregions – with the location of the PU centroid determining to which planning subregion the PU belonged (N_{5E} = 356; N_{6E} = 785; N_{7E} = 285). This ensured that every PU was assigned only to one planning subregion (Figure 1).

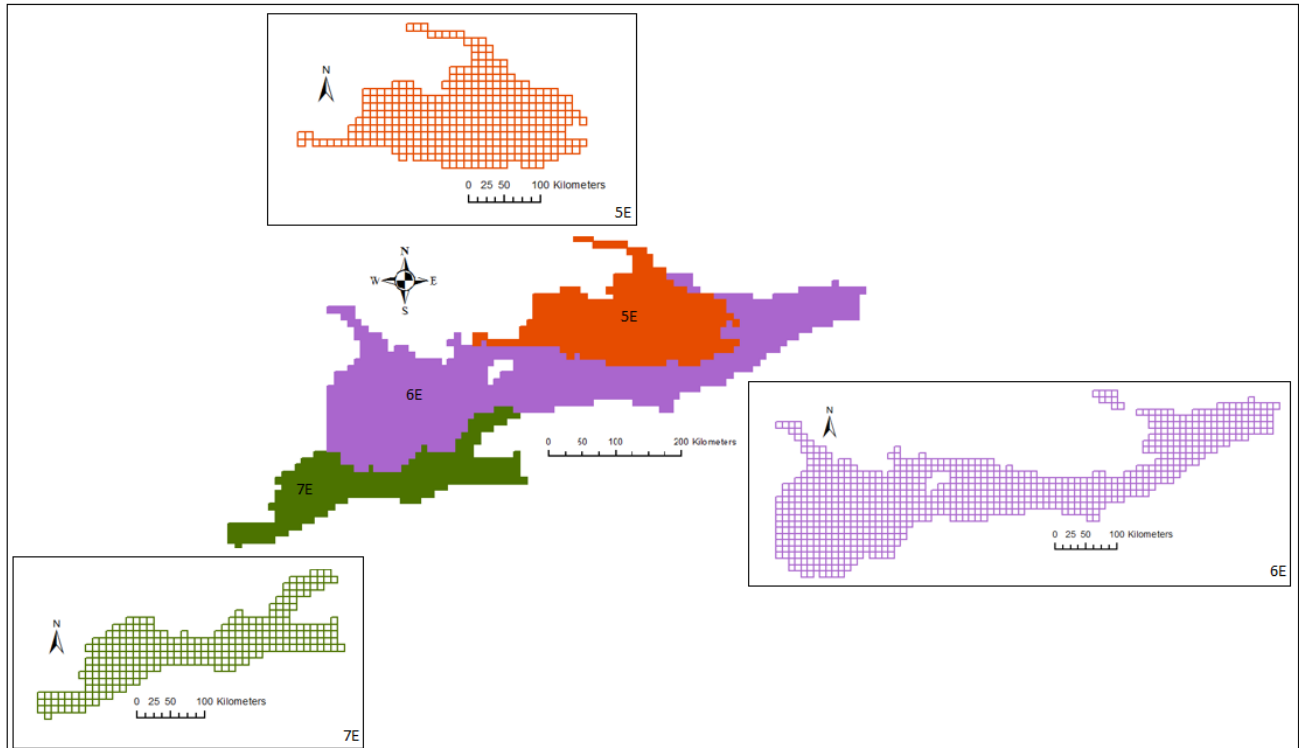


Figure 1. Planning Region and Subregions of Southern Ontario. The planning region (PR), Southern Ontario (delineated by census divisions obtained through FED-DEV) and planning subregions (PSR) determined by ecoregion. The southernmost PSR, 7E (Lake Erie - Lake Ontario) is contained within the deciduous Niagara region of the Mixedwood Plains ecozone. PSR 6E (Lake Simcoe – Rideau) is also part of the Mixedwood Plains ecozone as it stretches from Lake Huron to the Ottawa River, including most of the Lake Ontario shoreline and Ontario St. Lawrence. The northernmost PSR, 5E (Georgian Bay) is part of the Canadian Shield Ecozone. For each PSR, the minimum planning unit grid is highlighted. Each planning unit is a 10km by 10km polygon square with the total number of polygons, $N = 1426$ [$N(5E) = 356$; $N(6E) = 785$; $N(7E) = 285$].

3.3 - Define and map a set of metrics to characterize SAR community *within* each planning unit (PU)

To represent the set of species notionally present (the SAR community) in each PU j within the planning region, the procedure requires the definition of metrics (*SAR community metrics*) quantifying:

- a) A raw (unweighted) presence score S for species k in PU j , S_{kj} , for each of the SAR of interest (Appendix B.1);
- b) A raw (unweighted) species richness score SR for PU j , SR_j , for each PU of interest (Appendix B.2);
- c) A habitat suitability score P for each species k in PU j , P_{kj} , for each of the SAR of interest (Appendix B.3);

- d) An extinction risk index, ER , associated with species k , ER_k , for each of the SAR of interest (Appendix B.4);
- e) A weighted presence score, S^* for species k in PU j , S^*_{kj} – species presence weighted by habitat suitability score (c) and extinction risk (d) for each of the SAR of interest (Appendix B.5); and
- f) A weighted species richness score SR^* for PU j , SR^*_j - richness score weighted by habitat suitability (c), and extinction risk (d) for each PU of interest (Appendix B.6).

I used the following procedure to calculate and apply *SAR community metrics* within the planning region of interest:

- (1) Species distribution maps for the number of terrestrial species listed under Schedule 1 of SARA, ($N = 454$), were projected into the desired coordinate system (GCS_North_American_1983) and clipped to the planning region. The subset of species whose distribution includes at least one PU constitutes the set of SAR (SAR pool) of the planning region ($N = 134$).
- (2) The distribution of each SAR within the *planning region* ($N = 134$) was refined by habitat association in order to increase the granularity of notional species presence (see Appendix B.1):
 - i. For each SAR, MODIS land cover data was overlaid atop the distribution map - generating a detailed distribution map with MODIS land cover classes;
 - ii. Using HAPs, areas within a SAR's distribution with land cover classes NOT associated with a species' suitable habitat were eliminated. This operation was performed by specifying (with an SQL statement) that only areas with suitable landcover classes be included in the refined distribution map. This procedure eliminated 11 SAR as their associated

suitable habitat(s) did not occur in the planning region, leaving $N=123$ SAR in the regional pool.

(3) For every PU ($N = 1426$) within the planning region:

- i. Raw (unweighted) species presence scores S_{kj} , (Appendix B.1) for each of the SAR within the regional pool was calculated. If a SAR's distribution included all or part of the PU, the species was assigned a score of 1; otherwise it was assigned a score of zero. For each PU, the SAR community is the set of SAR with presence scores equal to 1;
- ii. Raw (unweighted) species richness, SR_j , (Appendix B.2) was determined by summing the number of species notionally present (the SAR community) in the PU, as determined in (i);
- iii. For each member of the PU SAR community, as determined in (i), habitat suitability scores, P_{kj} , (Appendix B.3) reflect the proportion of the PU which – notionally at least – constituted suitable habitat for the SAR in question. If the PU contained no suitable habitat, the habitat suitability score was 0. By contrast, if the entire PU was suitable habitat, the score was 1. Species with high (low) habitat suitability scores are considered to have a higher (lower) probability of occurrence in the PU;
- iv. For each member of the PU SAR community, as determined in (i), extinction risk based on COSEWIC status, ER_k , (Appendix B.4) was assigned;
- v. For each member of the PU SAR community, as determined in (i), weighted species presence scores, S^*_{kj} , were calculated. These scores are simply the raw presence scores weighted by habitat suitability (iii) and extinction risk (iv) (Appendix B.5);

- vi. Weighted species richness, SR^*_j , (Appendix B.6) was determined by summing the weighted species presence scores, as determined in (v), for all members of the SAR community in the PU

Heat mapping of species richness scores in the planning region of interest revealed, for both raw/unweighted (SR_j , a measure of the number of members in the SAR community of the PU) and weighted (SR^*_j , which takes into account both the proportion of suitable habitat and extinction risk for each member of the PU's SAR community) "*hot planning units*." In the case of raw richness, these "hot" PU comprise a relatively large SAR community. Alternatively, in the case of weighted richness, "hot" PU are dominated by SAR with a high extinction risk, especially for those SAR who are more likely to be found within - occupy a notionally larger percentage of - the PU. Conversely, "*cold planning units*" identified PU with relatively small SAR communities (raw/unweighted richness), and PU where SAR have a comparatively lower extinction risk, and/or notionally occupy a smaller proportion of the unit.

3.4 - Define and map a set of metrics that capture the similarity in threat profiles in species community within each PU

The extent to which threats are shared among species in a PU can be determined by measuring the distance in threat space between pairs of threat profiles, producing, over the set of species, a set of pairwise threat distances. One can then define various measures over this set of distances, for example, the mean distance between species in threat space. For the purpose of this case study, I used the root mean square (RMS) distance (σ) between SAR in threat space (see Appendix C) – small RMS indicating that, on average, threat profiles for the set of SAR are very similar ($\sigma = 0$ corresponding to the case where all SAR have identical profiles), and large σ indicating comparatively large distances in threat profiles (where the set of SAR have greater dissimilarity in their threat profiles). PU are considered "hot" when interspecies threat distances are low - when SAR community member exhibit high similarity in their threat profiles. "Hot" PU

identify places where mitigation of a comparatively small number of threats, is expected to have positive impacts on a comparatively large number of species, since they share a similar set of threats. By contrast, “cool” areas are those for which, because threat profiles differ considerably among species, mitigation of a particular set of threats is likely to benefit comparatively few species.

3.5 - Define and map a set of composite metrics that integrates the SAR composition and inter-species threat distances within each PU

Composite SAR community metrics are obtained by combining estimates of SAR community richness with inter-species threat distances (Appendix D). Here we use a particular metric which weights species richness by the distribution of inter-species threat distances. Under this formulation PU with a comparatively large number of SAR exhibiting high similarity in shared threats (small RMS distance in threat space) are “hotspots.” By contrast, PU with comparatively few SAR sharing few common threats represent “coldspots.”

3.6 - Determine how tolerance for compositional variation in SAR community and inter-species threat distance affects the spatial extent of “places”

The steps identified in (3.3) – (3.5) above were initially applied to each PU. However, places may comprise multiple PU. The spatial extent of a place (i.e. the number of contiguous PU making up the delineated place) depends on the threshold tolerance assigned to the (1) differences in SAR communities between adjacent PU, and (2) the degree of inter-species threat distance similarity (Findlay and McKee, 2016). I explored how the size of places changed when thresholds for tolerance (of both SAR compositional variation and inter-species threat distances) increased (Appendix E) – developing an algorithm (using Python code, Appendix G) to systematically iterate through PU, starting at seed (initial) PU.

To evaluate the variation in SAR composition between PU, I applied the Bray-Curtis Dissimilarity (Appendix F). In ecological studies, the Bray-Curtis Dissimilarity Index is often used

to quantify differences in species' composition between two areas of equal size (Scheiner, 2012). Output values are bounded by 0 – which signifies the two sites of interest share identical species composition, and 1 – signifying sites exhibiting complete dissimilarity in species composition (no species overlap) (Scheiner, 2012). Here I use habitat suitability scores quantifying the proportion of each PU with suitable habitat (Appendix B.3) as proxies for species' abundance.

The variation in inter-species threat distances between PU was evaluated using root mean square (RMS) distance (Appendix C). The mean distance between species in threat space was calculated using the combined SAR pool (the set of SAR found in the two PU being compared). Smaller RMSs indicate high similarity in shared threats between the SAR of the two PU of interest. Larger values, indicate that threat similarity between species is low – the set of SAR being compared share few threats.

The analysis of threshold-induced spatial extents was conducted by the series of steps outlined below:

- (1) In each planning subregion, a set of “seed” PU were identified (Appendix E.1). Seed designation followed the following process:
 - i. A maximum number of places is decided. Each seed PU represents the minimum geographic extent of a place. In this particular experiment, $N=12$ seeds were chosen for each planning region - the number of seeds constant between regions (in this case study $N_{5E} = 4$; $N_{6E} = 4$; $N_{7E} = 4$);
 - ii. Seed designation criteria is selected. Seeds were designated based on 2 criteria: (a) composite score (Appendix D), and (b) minimum distance between PU;
 - iii. PU composite scores were arranged from highest to lowest;
 - iv. The first seed is assigned to the PU with the largest composite score;

- v. The second seed is the PU with the second highest composite value that is separated by at least (a minimum of) one PU;
- vi. This process continued until all seed PU had been assigned - the number of seed PU equal the maximum number of places;

(2) All immediately adjacent PU are assessed with respect to (a) SAR community overlap with the SAR community of the seed PU; and (b) the RMS distance among all members of the SAR community present in the seed and the PU in question (that is, the union of the set of SAR present in the seed and PU in question) (Appendix E.2).

- a) SAR community overlap thresholds reflect the maximum allowable dissimilarity in SAR composition between the two PU being compared. As the tolerance threshold increases, a greater dissimilarity in SAR composition is allowed between units – with a tolerance of 0 corresponding to the case where SAR compositions must be identical. Here, I set *SAR overlap thresholds* at 0.15, 0.20, and 0.25 – reflecting 15%, 20%, and 25% dissimilarity in overlap, respectively;
- b) Similarly, threat distance thresholds reflect the maximum allowable variation in threat profiles, averaged over the set of SAR present in both PU. As the tolerance threshold increases, PU with sets of SAR exhibiting lower threat similarity (larger RMSs) are included. Here, I set *threat distance thresholds* at ($\sigma = 0.24, 0.25, 0.26, 0.27, 0.28, 0.29, \text{ and } 0.30$);

(3) If the overlap in SAR species composition between the seed and the adjacent PU is less than (falls below) the threshold for tolerance, the PU may potentially be added to the place. Similarly, if the addition of the SAR present in an adjacent PU results in a distribution of inter-species threat distances, for which the RMS of this (new) distribution does not exceed the tolerance threshold, the adjacent PU is not added to the place. If it does not exceed this threshold, this PU may potentially be added to the place. A PU is

added to a place only if it satisfies both conditions – variation falls below tolerance threshold values for both (a) SAR community overlap and (b) average threat distance (see Appendix E.2);

- (4) Steps (2) and (3) are repeated for each candidate PU that is adjacent to the developing boundary of the place (Appendix G). Thus, at each step, the size (spatial extent) of the place defined by the PU may increase, i.e. the place grows by accretion of adjacent PU to the seed unit. If at some point, none of the PU adjacent to the place boundary satisfy the tolerance criteria for (a) and/or (b), the process terminates. The final place is then delineated by the set of PU that have been added to the initial seed PU.

The number of places defined in a subregion under this algorithm is determined by the number of seeds. The consequence is, then, that depending on the threshold tolerances set and the number of initial seed PU, many PU may not be associated with any place. For example, if tolerances are set very low (i.e. such that PU must have near-identical SAR community composition and/or high similarity in shared threats), then places will necessarily be small, and most PU will not be associated with any place. Conversely, as tolerances become increasingly forgiving (higher thresholds), a greater number of PU are incorporated into each place, and the number of PU not associated with a place decreases. Similarly, if only a few seed PU are chosen, fewer places exist and, many PU may not be associated with any place. Conversely, as the number of seed PU increases, the number of places increases, and the number of PU not associated with a place decrease.

4. RESULTS

4.1 - Heat mapping of PU within the PR

Heat mapping of PU based on unweighted (raw) SAR species richness illustrates a trend of increasing SAR richness from north to south within the planning region (Figure 2). PU farther south (in the southernmost ecoregion – planning sub-region (PSR) 7E) had a greater estimated number of average SAR per PU (mean = 25, SD = 4.9; Figure 3) when compared to estimates for the mid-subregion, PSR 6E (mean = 19, SD = 4.3; Figure 3) and northernmost sub-region, PSR 5E (mean = 14, SD = 4.2; Figure 3).

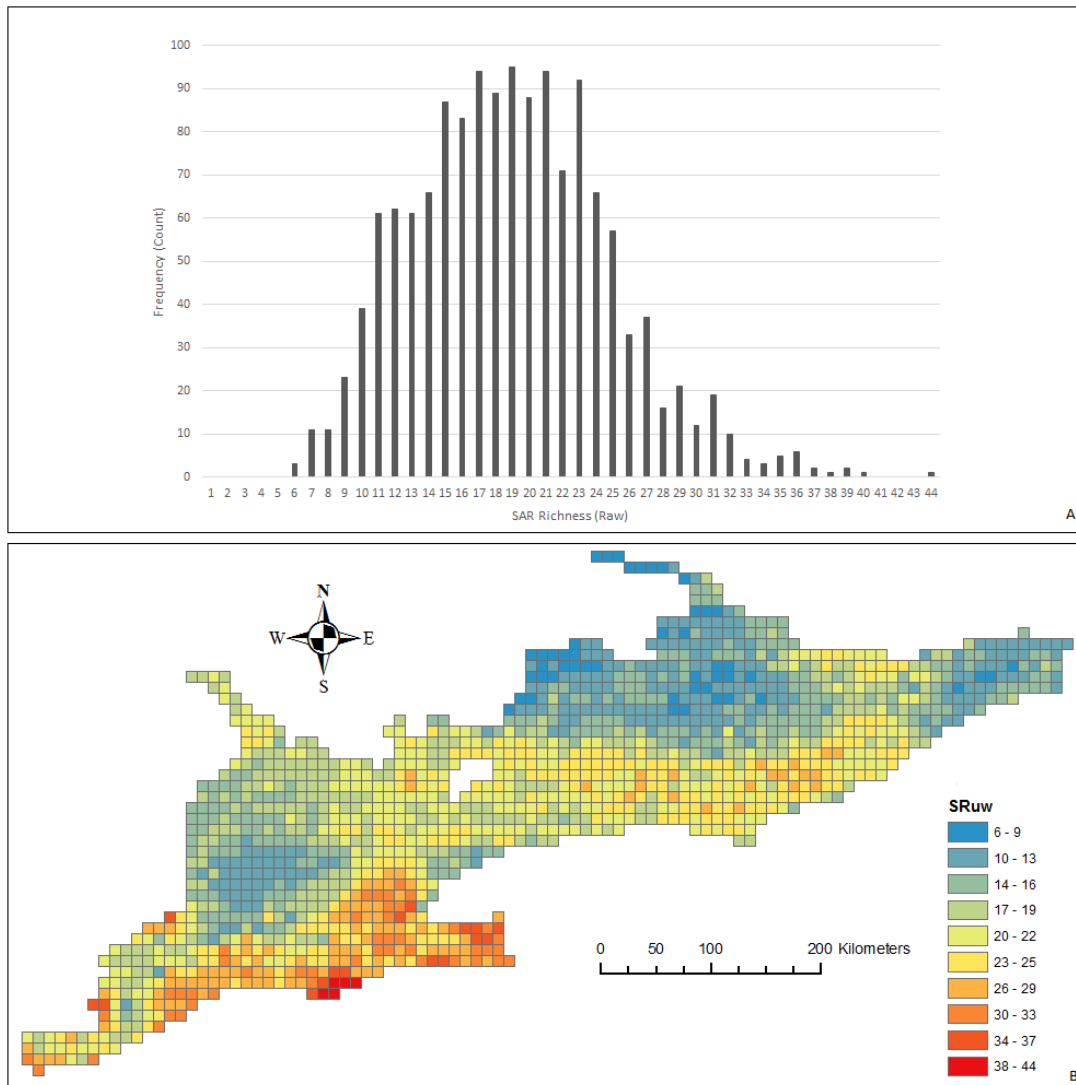


Figure 2. Frequency distribution (A) and heat mapping (B) of unweighted (raw) Species at Risk (SAR) species richness in the study region at the individual planning unit scale (N = 1426). Over the entire region, average unweighted richness was 19, SD = 5.87.

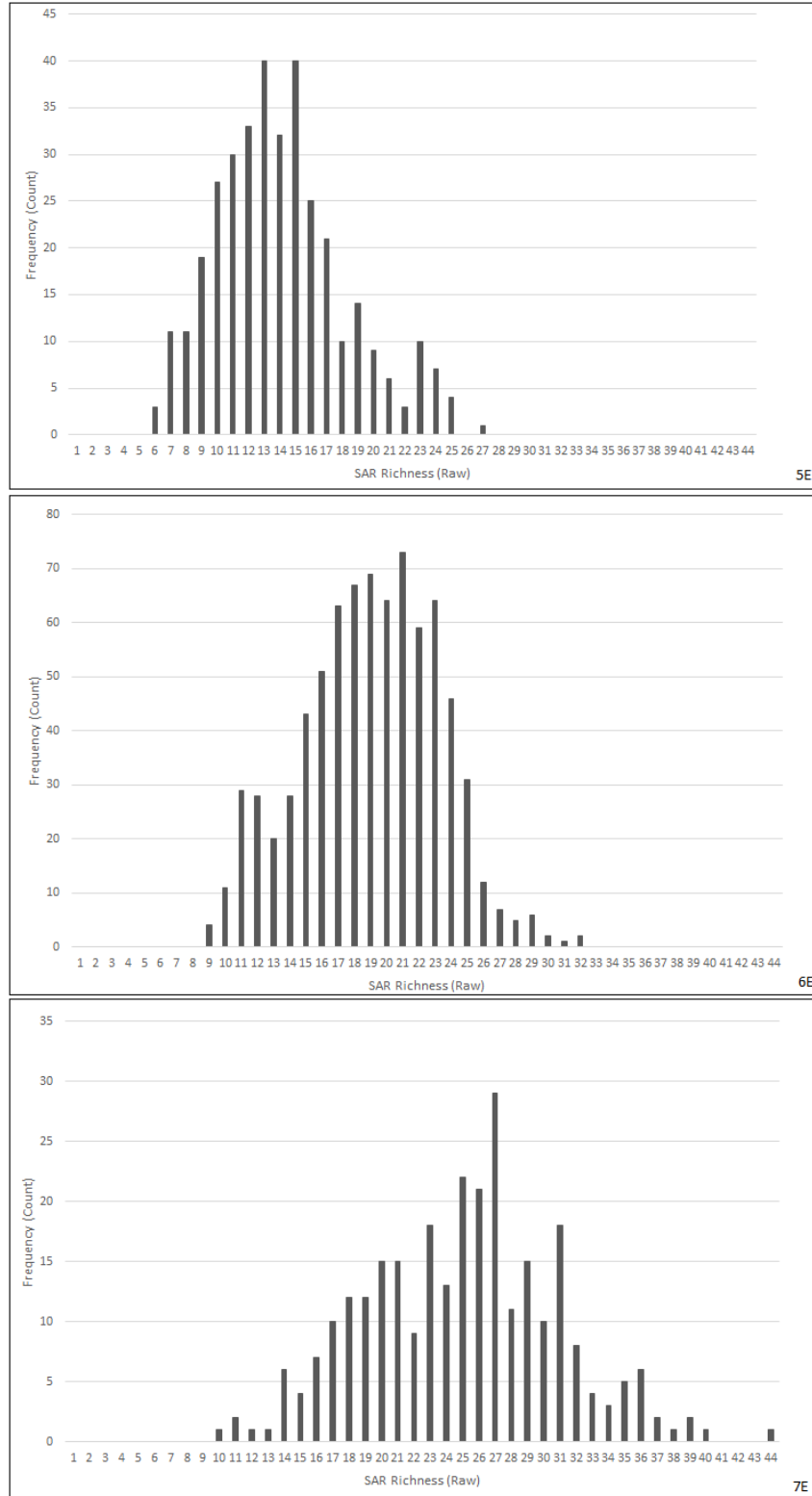


Figure 3. Frequency distribution of unweighted (raw) Species at Risk (SAR) species richness in the study planning subregions (PSR) at the individual planning unit scale. (Top): PSR 5E: n = 356; mean = 14 ± 4.2 ; (Middle): PSR 6E: n = 785; mean = 19 ± 4.3 ; (Bottom): PSR 7E: n = 285; mean = 25 ± 4.9

Heat mapping of SAR species richness weighted by habitat suitability and extinction/extirpation risk illustrates a similar pattern (Figure 4) – with southernmost PSR (7E) having a greater estimated weighted SAR richness (mean = 6.29, SD = 1.53; Figure 5) than mid-region (6E: mean = 5.14, SD = 1.17; Figure 5) and northern (5E: mean = 3.34, SD = 1.21; Figure 5) PSRs. It is important to note that, with respect to SAR species richness (both raw and weighted), PU cannot be considered independent. This is due to the large positive spatial autocorrelation in species distribution, i.e. if species *x* is present in PU *y*, it is also very likely to be present in adjacent PU. However, it is very clear, from Figures 3 and 5, that means and variances of the distributions in planning sub-regions are different.

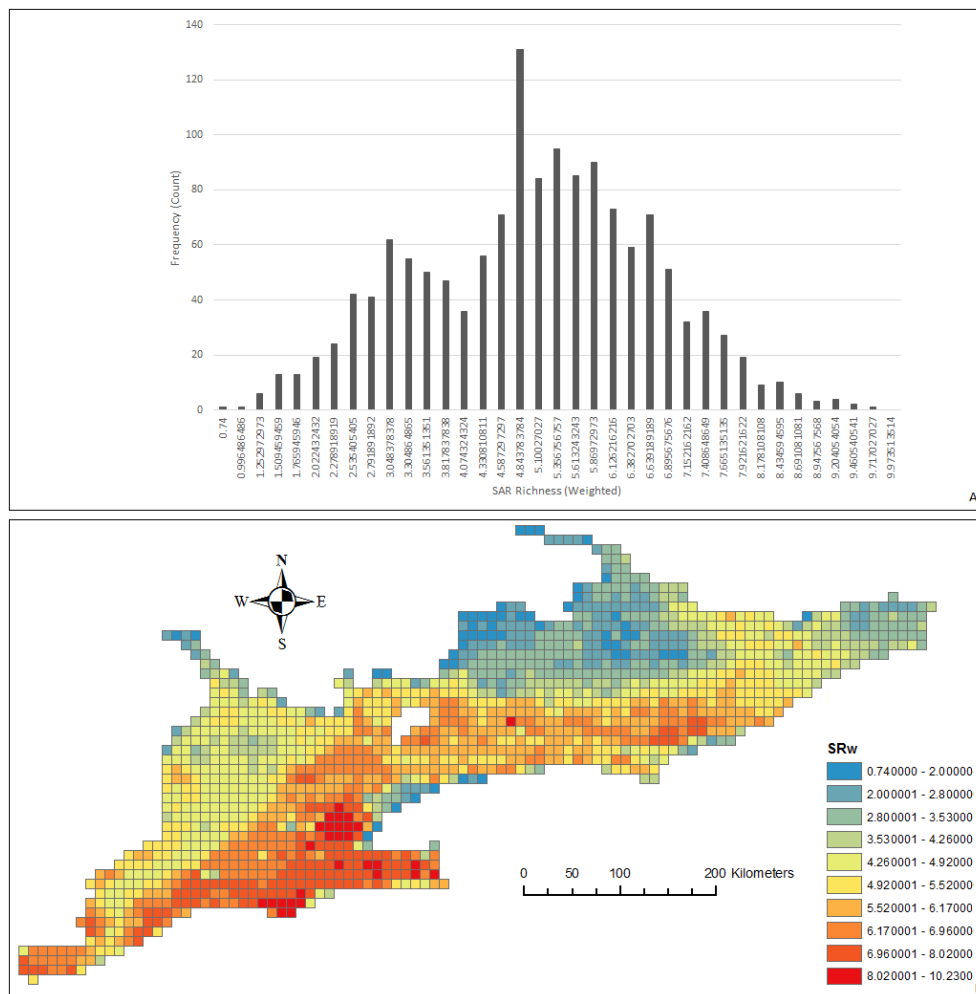


Figure 4. Frequency distribution (A) and heat mapping (B) of weighted (by HAP and Extinction Risk) Species at Risk (SAR) species richness in the study region at the individual planning unit scale (N = 1426). Over the entire region, average unweighted richness was 4.92, SD = 1.62.

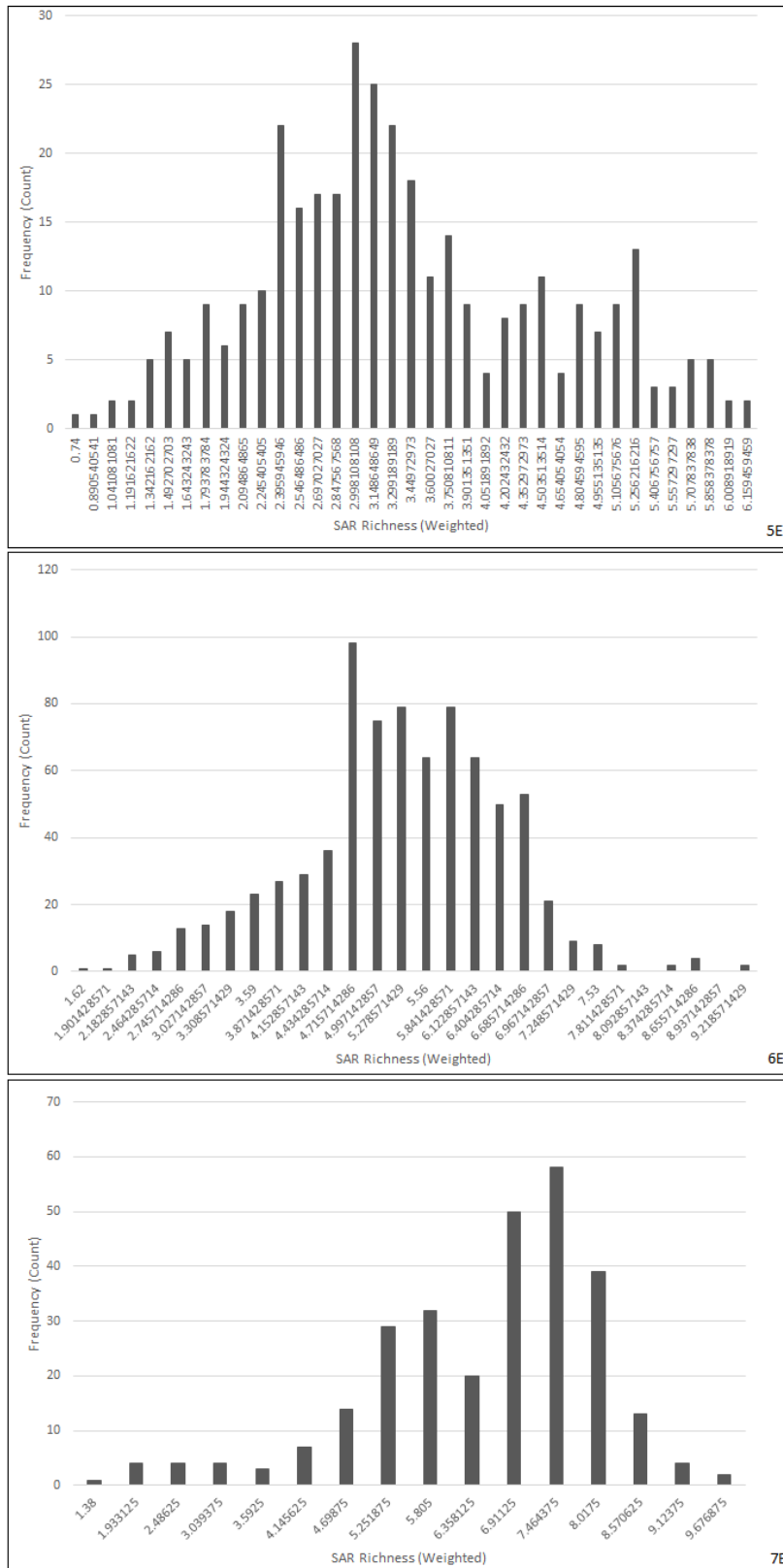


Figure 5. Frequency distribution of weighted (by HAP and Extinction Risk) Species at Risk (SAR) species richness in the study planning subregions (PSR) at the individual planning unit scale. (Top): PSR 5E: n = 356; mean = 3.34 ± 1.21 ; (Middle): PSR 6E: n = 785; mean = 5.14 ± 1.17 (Bottom): PSR 7E: n = 285; mean = 6.29 ± 1.53

When weighted SAR species richness is plotted against raw SAR species richness (Figure 6) we observe, in general, a positive correlation ($r = 0.77$). This positive correlation is much weaker in the mixed wood plains ecoregions (6E, $r = 0.56$; and 7E, $r = 0.63$) when compared to the northern Ontario shield ecoregion (5E, $r = 0.83$), suggesting that, for a given raw SAR species richness, a larger number of PU in the mixed wood plains ecoregion have an unusually high or low weighted richness – indicating higher or lower (respectively) than average proportion of species at high/low extinction risk and/or above/below average habitat suitability.

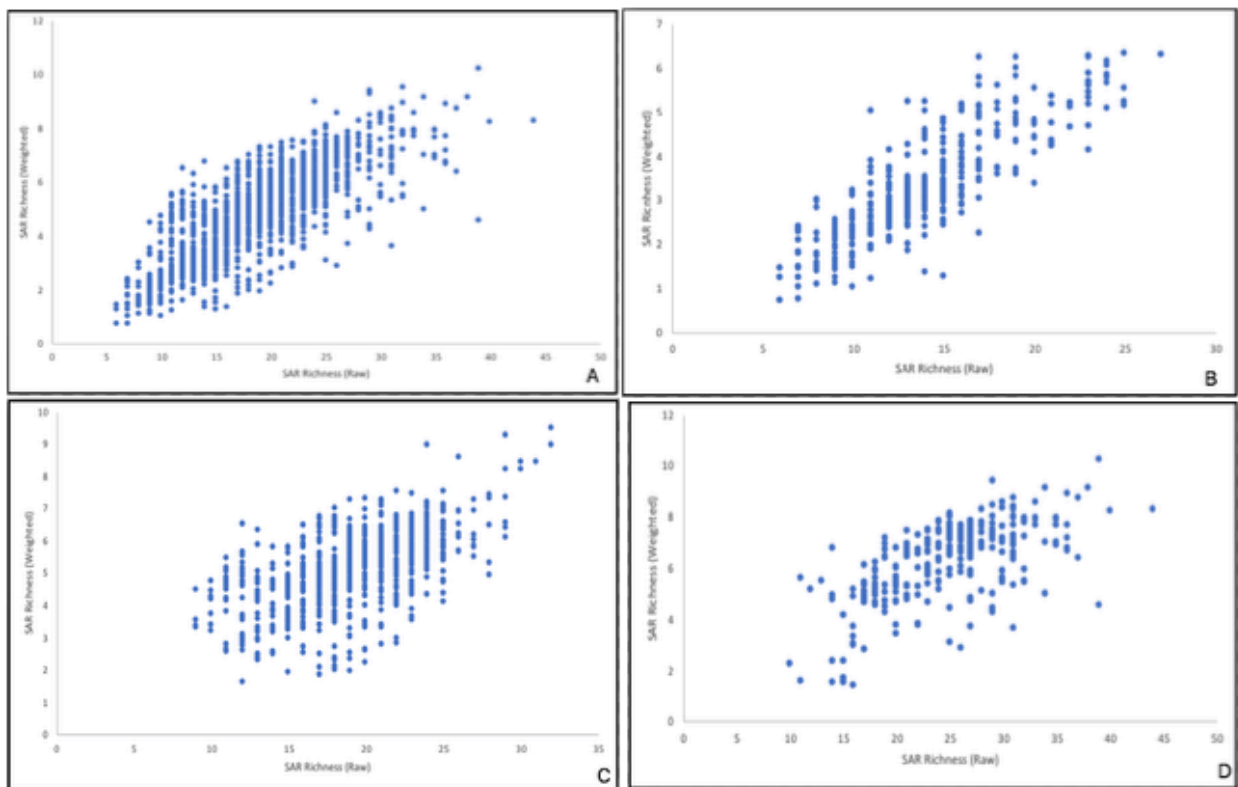


Figure 6. Weighted Species at Risk (SAR) species richness plotted against unweighted (raw) Species at Risk (SAR) species richness at the individual planning unit scale richness for (A) the entire study region ($n = 1426$; $r = 0.77$); (B) Planning subregion, PSR 5E ($n = 356$; $r = 0.83$); (C) PSR 6E ($n = 785$; $r = 0.56$) and (D) PSR 7E ($n = 285$; $r = 0.63$).

Heat mapping of PU based on average SAR threat distance (σ) illustrates a north – south trend (Figure 7), whereby more southerly areas (PSR 7E) have smaller distances – a greater threat similarity- (mean = 0.30, SD = 0.04; Figure 8) when compared to mid-region (PSR 6E: mean = 0.34, SD = 0.05; Figure 8) and northernmost areas (PSR 5E: mean = 0.52, SD =

0.06; Figure 8). This indicates that SAR communities further south are, on average, exposed to a more similar set of threats than in the north.

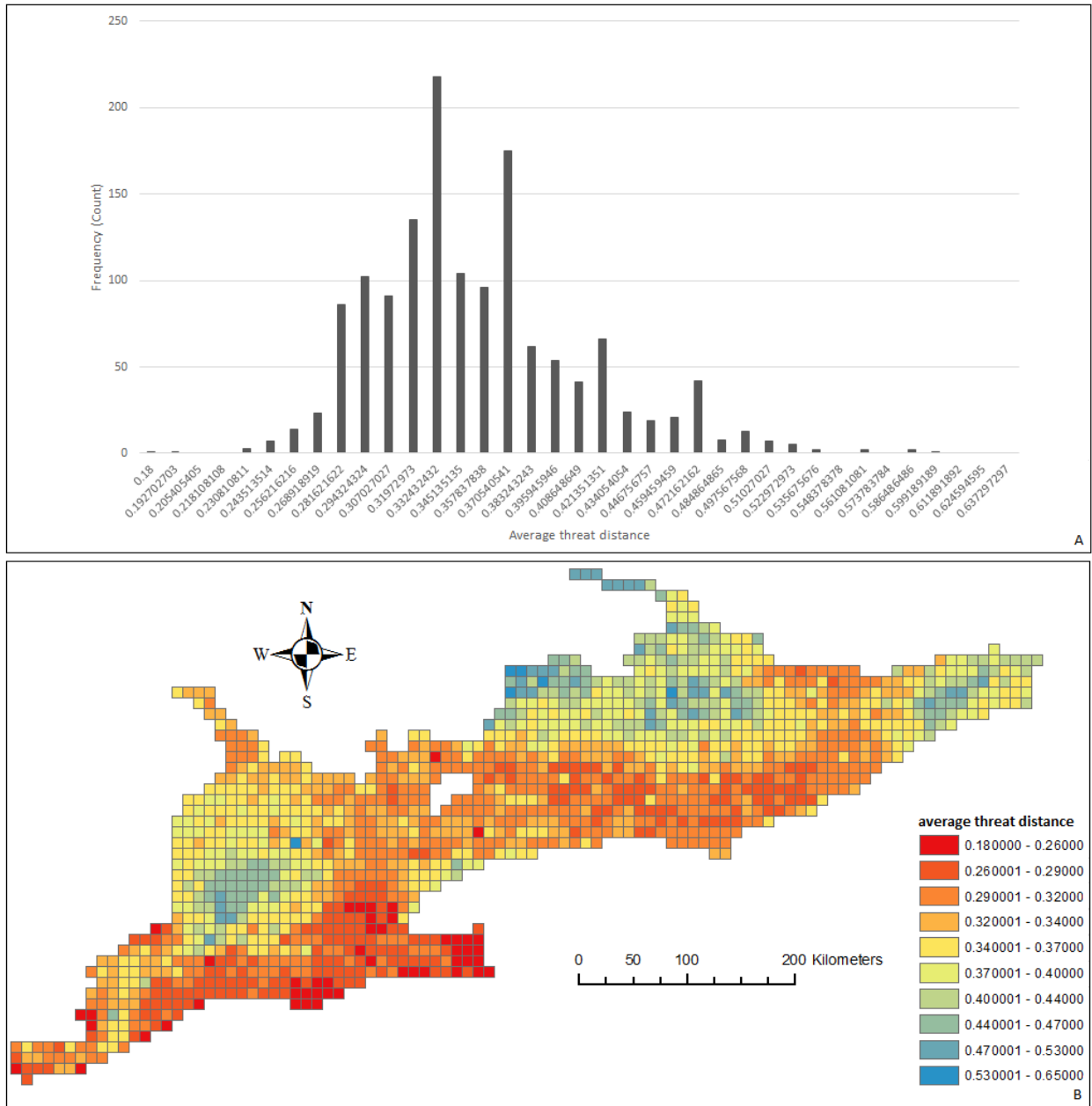


Figure 7. Frequency distribution (A) and heat mapping (B) of the average distance in threat profiles of Species at Risk (SAR) species in the study region at the individual planning unit scale (N = 1426). Over the entire region, average threat distance was 0.35, SD = 0.06.

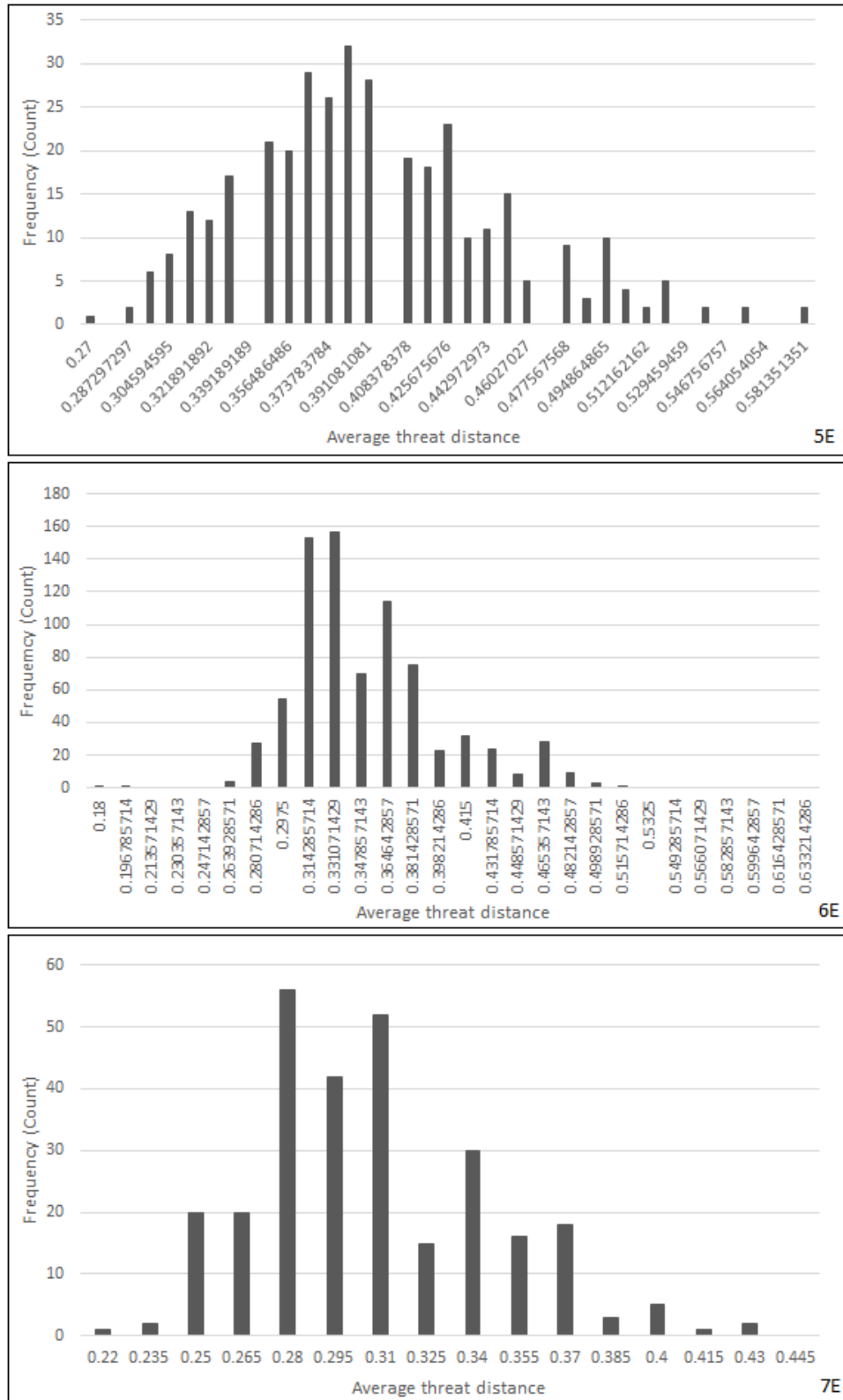


Figure 8. Frequency distribution of the average distance in threat profiles of Species at Risk (SAR) in the study planning subregions (PSR) at the individual planning unit scale. (Top): PSR 5E: n = 356; mean = 0.52 ± 0.06; (Middle): PSR 6E: n = 785; mean = 0.34 ± 0.05 (Bottom): PSR 7E: n = 285; mean = 0.30 ± 0.04.

Plotting average threat distance against raw (unweighted) SAR species richness reveals strong positive relationships ($r = 0.92$; Figure 9) for all PSRs (7E: $r = 0.96$; 6E: $r = 0.92$; 5E: $r = 0.94$). As estimated PU SAR species richness increases, similarity in shared threats increases (threat distance, σ , decreases). This relationship suggests that in southern Ontario, where SAR species richness is greatest, so too is the similarity in threat profiles. Six outliers identified in PSR 6E (Figure 10) reveal PU where, for a given raw SAR species richness, the SAR community shares an unusually high, or low similarity in shared threats.

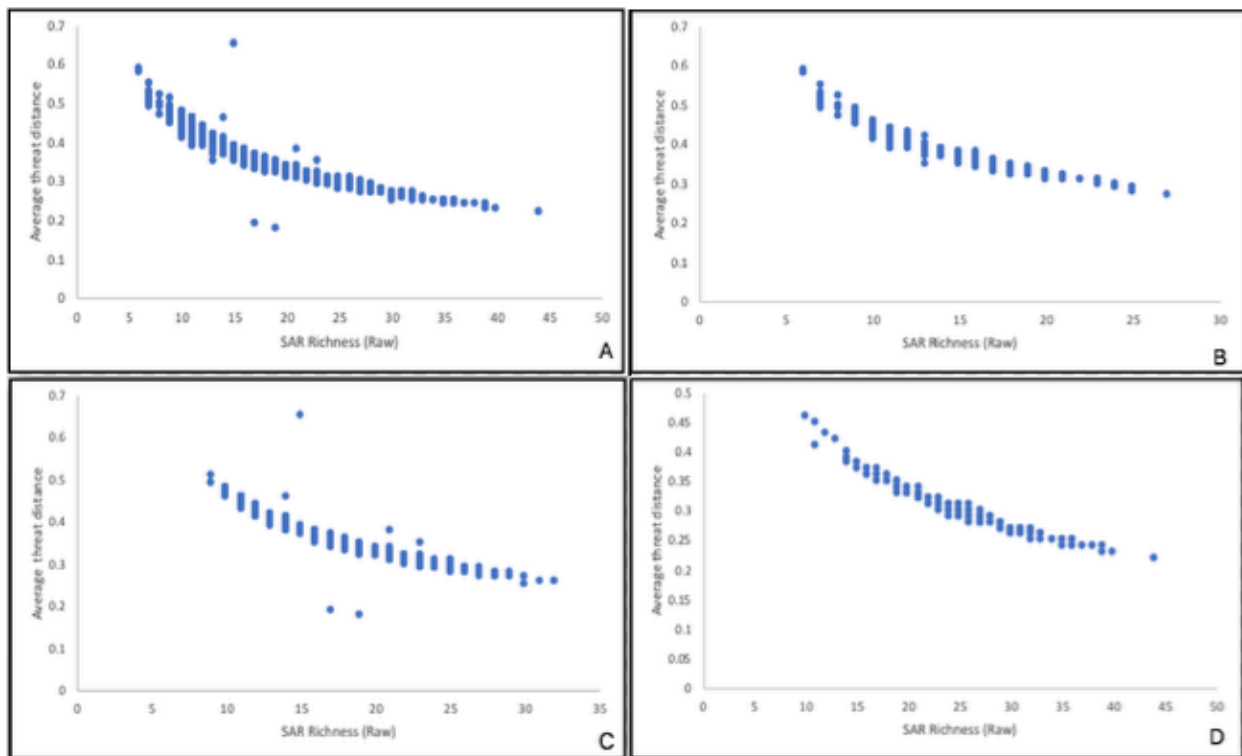


Figure 9. Average distance in threat profiles of Species at Risk (SAR) species plotted against unweighted (raw) Species at Risk (SAR) species richness at the individual planning unit scale richness for (A) the entire study region ($n = 1426$; $r = 0.92$); (B) Planning subregion, PSR 5E ($n = 356$; $r = 0.96$); (C) PSR 6E ($n = 785$; $r = 0.92$) and (D) PSR 7E ($n = 285$; $r = 0.94$).

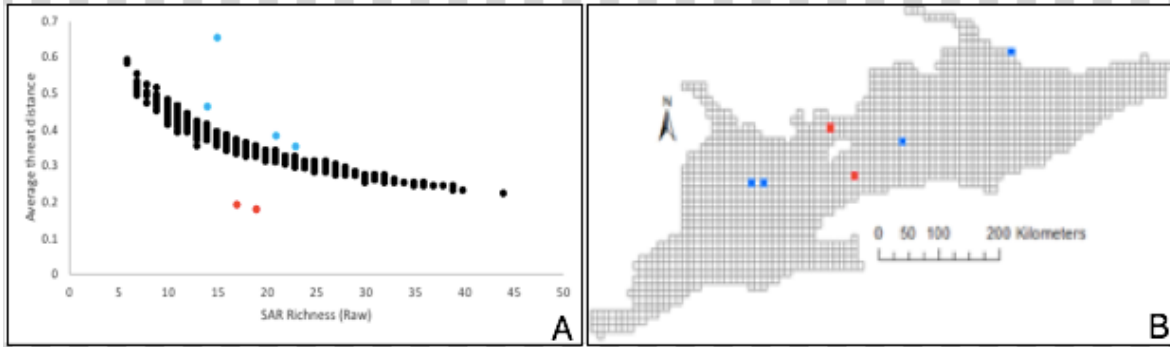


Figure 10. Planning Unit (PU) outliers (in red, $n = 6$) in ecoregion 6E when average distance in threat profiles of Species at Risk (SAR) species plotted against unweighted (raw) SAR species richness, (A) and associated geographic location of PU outliers (B). PU with higher threat similarity are denoted in red (Z45: SAR richness 17, $\sigma = 0.19$; S41: SAR richness 19, $\sigma = 0.18$) and PU with lower threat similarity in blue (AA28: SAR richness 15, $\sigma = 0.65$; AA30: SAR richness 21, $\sigma = 0.38$; H71: SAR richness 14, $\sigma = 0.46$; U53: SAR richness 23, $\sigma = 0.35$).

Composite scores integrate weighted SAR species richness (SR_w) with the inverse of threat distance measures (σ^{-1}). As expected, heat mapping of PU based on composite scores illustrates a similar north - south trend within the planning region (Figure 11), as is reflected by both SAR species richness (Figure 4), and threat distance (Figure 7) heat maps. Composite values are higher in southern PU (7E: mean = 21.43, SD = 6.86; Figure 12) than in mid region (6E: mean = 15.44, SD = 4.86; Figure 12), and northernmost PSRs (5E: mean = 9.13, SD = 4.42; Figure 12).

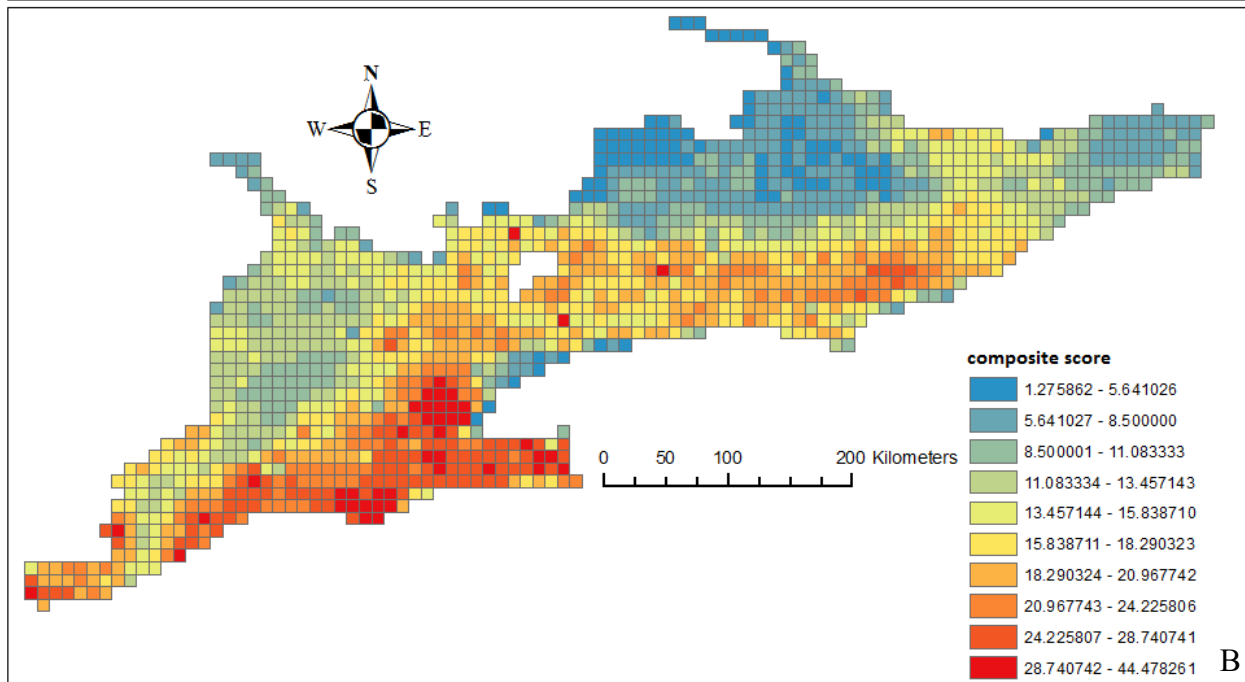
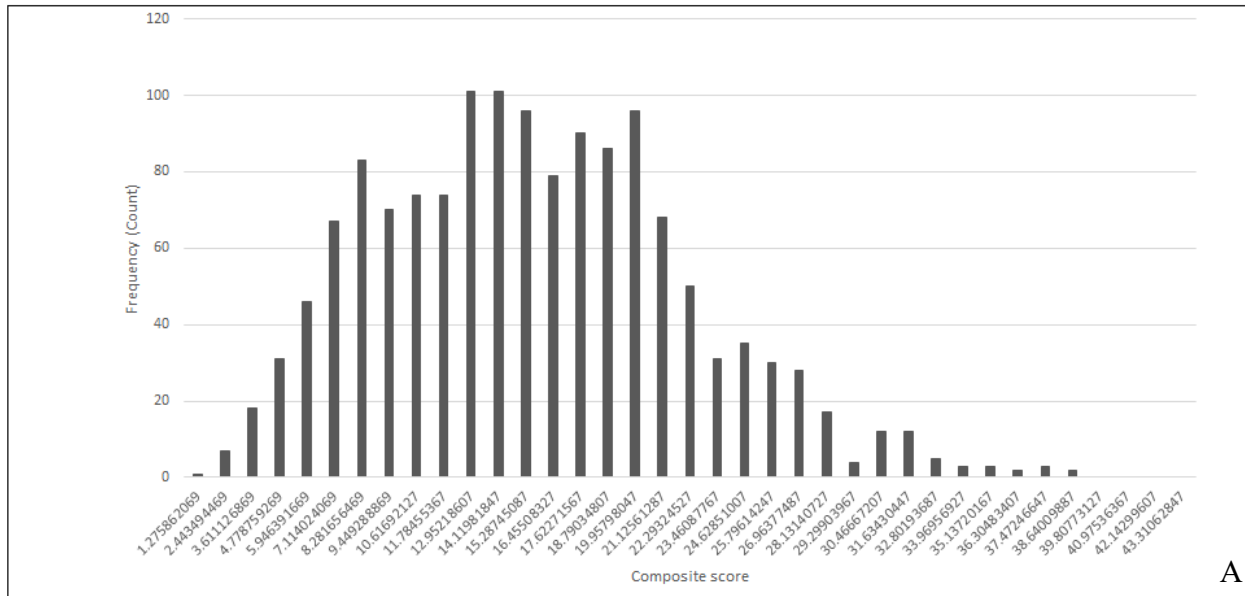


Figure 11. Frequency distribution (A) and heat mapping (B) of the composite scores (integrating average threat distance and weighted species richness of Species at Risk (SAR) species in the study region at the individual planning unit scale (N = 1426). Over the entire region, average composite score was 0.35, SD = 0.06.

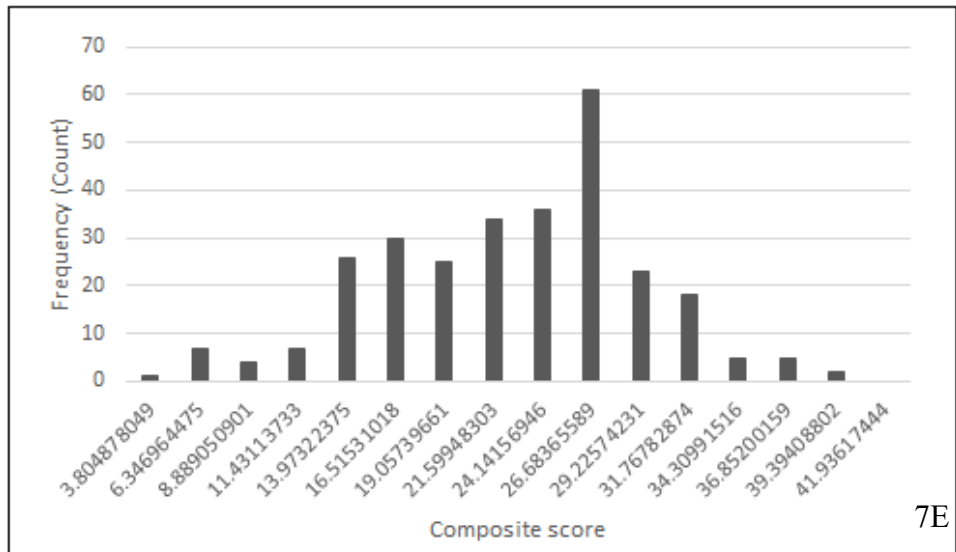
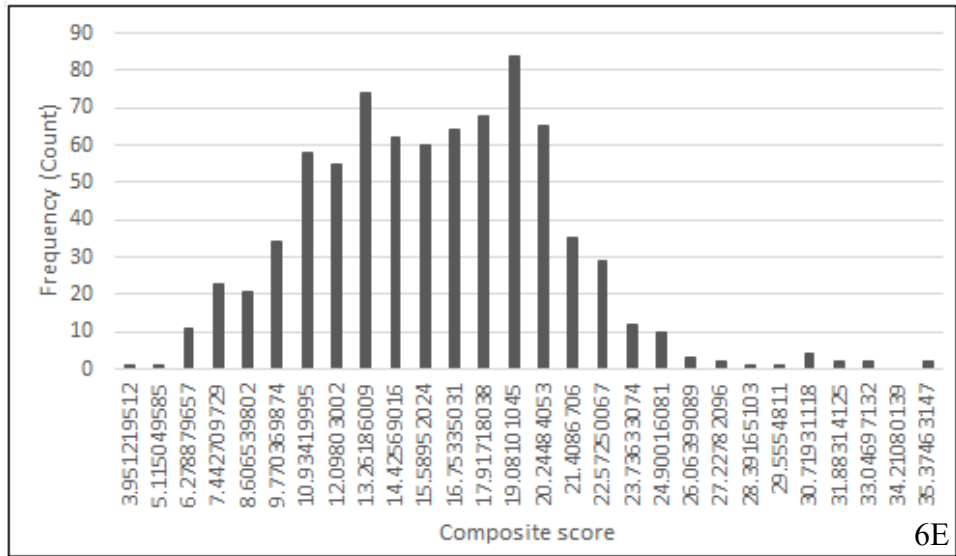
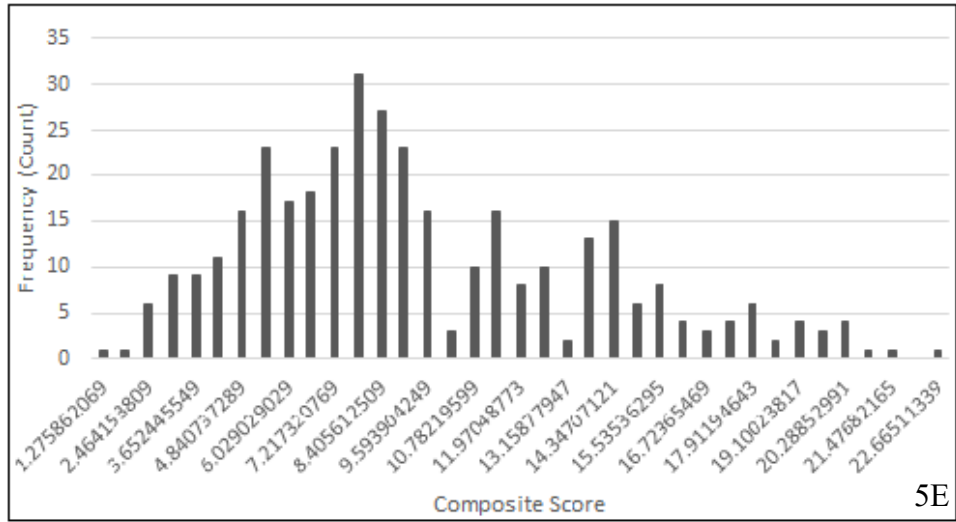


Figure 12. Frequency distribution of the composite scores of Species at Risk (SAR) in the study planning subregions (PSR) at the individual planning unit scale. (Top): PSR 5E: n = 356; mean = 9.13 ± 4.42; (Middle): PSR 6E: n = 785; mean = 15.44 ± 4.86 (Bottom): PSR 7E: n = 285; mean = 21.43 ± 6.86.

4.2 - Place size and tolerance thresholds

Place characterization incorporated two measures of interest (a) SAR overlap, and (b) inter-species threat distances. Only if both the overlap in SAR species composition and the resultant distribution of inter-species threat distance between the seed and adjacent PU fell below the tolerated thresholds for dissimilarity was the PU added to the place. For each measure, as thresholds of tolerance for dissimilarity relaxed (became increasingly tolerant), the number of candidate PU – PU that fall below the tolerance threshold in (a) or (b) and may potentially be added to a place – increased. Similarly, by increasing the tolerance for dissimilarity in SAR community composition overlap and/or differences in SAR threat profiles the average size of places increased, in all planning subregions, as a greater number of PU were added to the initial seed PU (5E Figure 13; 6E Figure 14; 7E Figure 15). It is important to note that as tolerances are relaxed - and a greater dissimilarity in measures (a) and/or (b) is accepted it is possible for individual PU to belong to several places. This was observed in all three PSR (and is denoted by a cross-hatched design - 5E Figure 13; 6E Figure 14; 7E Figure 15).

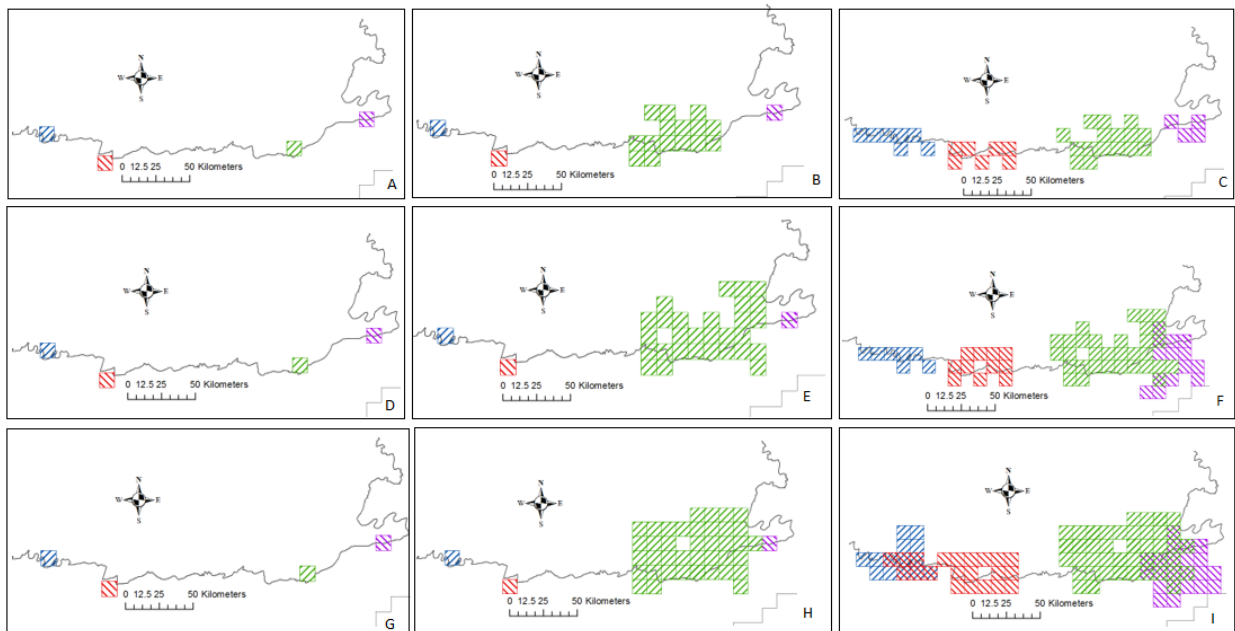


Figure 13. “Place” size as a function of increasing tolerance thresholds for *community overlap* (BC_d) and *average inter-species threat distance* (σ) in ecoregion 5E (Georgian Bay). Tolerance for *compositional overlap* increases top to bottom. Tolerance for *threat distance* increases left to right. (A) $\sigma = 0.26$, $BC_d = 0.15$; (B) $\sigma = 0.28$, $BC_d = 0.15$; (C) $\sigma = 0.30$, $BC_d = 0.15$; (D) $\sigma = 0.26$, $BC_d = 0.20$; (E) $\sigma = 0.28$, $BC_d = 0.20$; (F) $\sigma = 0.30$, $BC_d = 0.20$; (G) $\sigma = 0.26$, $BC_d = 0.25$; (H) $\sigma = 0.28$, $BC_d = 0.25$; (I) $\sigma = 0.30$, $BC_d = 0.25$. Each place ($n = 4$), as characterized by a seed planning unit, is denoted by a different colour. Areas where places overlap - and planning units are shared by two places are denoted by a hatched design.

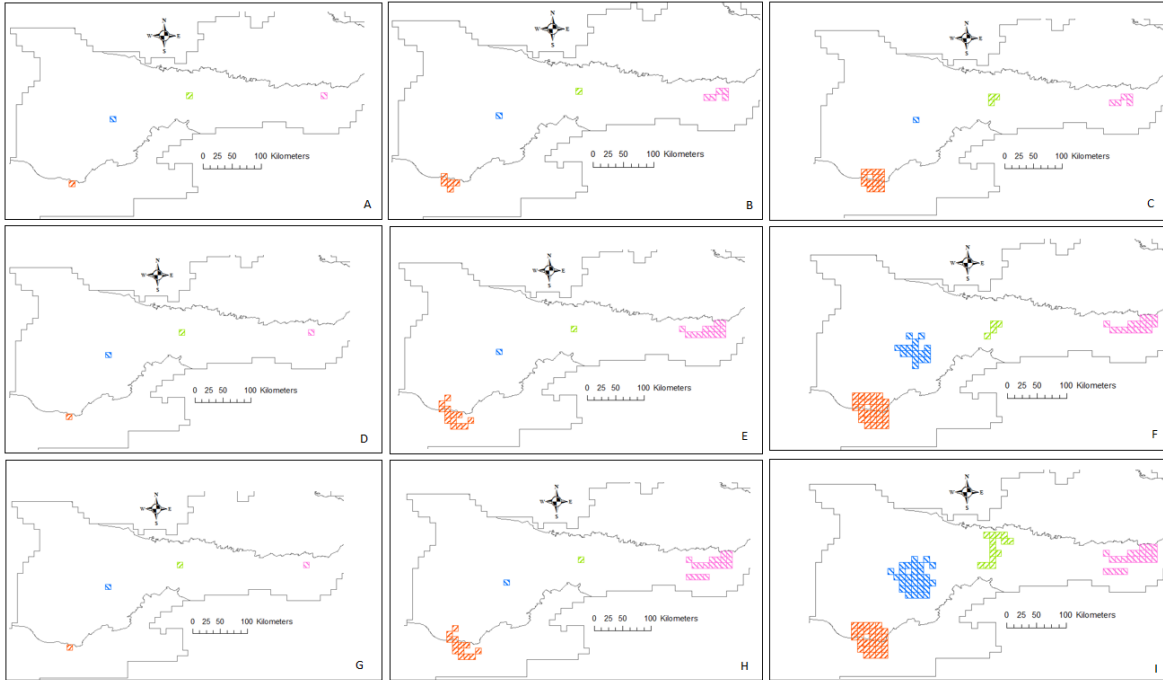


Figure 14. “Place” size as a function of increasing tolerance thresholds for *community overlap* (BC_d) and *average inter-species threat distance* (σ) in ecoregion 6E (Lake Simcoe - Rideau). Tolerance for *compositional overlap* increases top to bottom. Tolerance for *threat distance* increases left to right. (A) $\sigma = 0.26$, $BC_d = 0.15$; (B) $\sigma = 0.28$, $BC_d = 0.15$; (C) $\sigma = 0.30$, $BC_d = 0.15$; (D) $\sigma = 0.26$, $BC_d = 0.20$; (E) $\sigma = 0.28$, $BC_d = 0.20$; (F) $\sigma = 0.30$, $BC_d = 0.20$; (G) $\sigma = 0.26$, $BC_d = 0.25$; (H) $\sigma = 0.28$, $BC_d = 0.25$; (I) $\sigma = 0.30$, $BC_d = 0.25$. Each place ($n = 4$), as characterized by a seed planning unit, is denoted by a different colour. Areas where places overlap - and planning units are shared by two places are denoted by a hatched design.

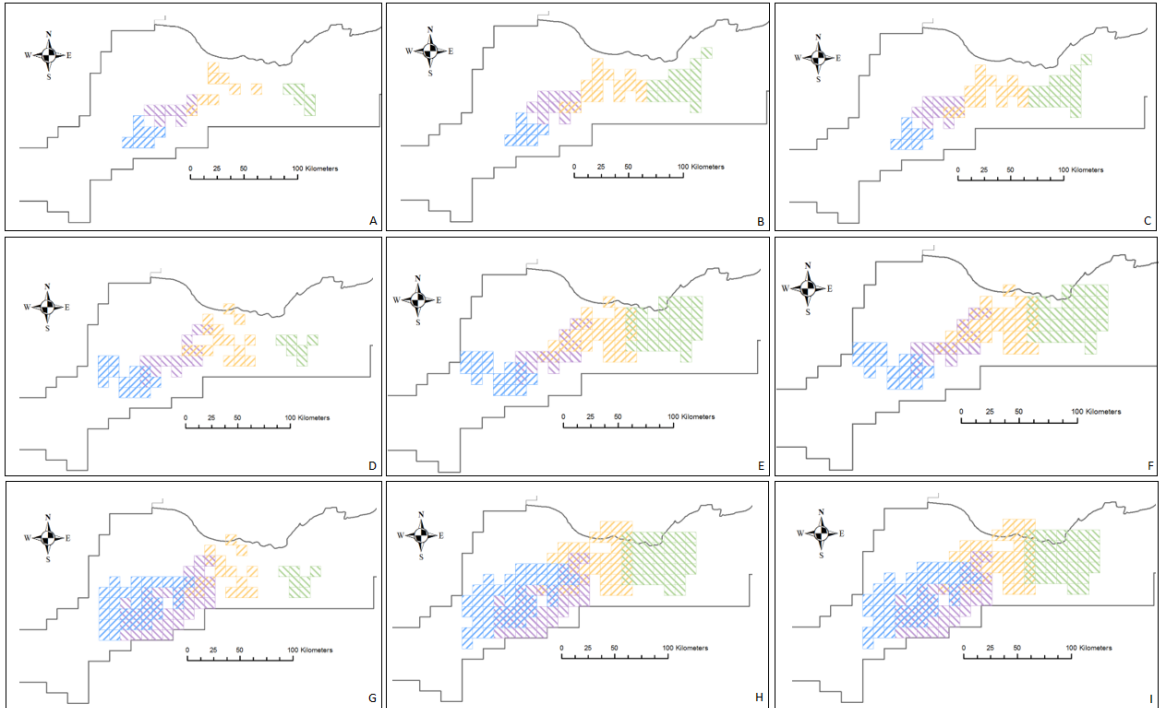


Figure 15. “Place” size as a function of increasing tolerance thresholds for *community overlap* (BC_d) and *average inter-species threat distance* (σ) in ecoregion 7E (Lake Erie - Lake Ontario). Tolerance for *compositional overlap* increases top to bottom. Tolerance for *threat distance* increases left to right. (A) $\sigma = 0.26$, $BC_d = 0.15$; (B) $\sigma = 0.28$, $BC_d = 0.15$; (C) $\sigma = 0.30$, $BC_d = 0.15$; (D) $\sigma = 0.26$, $BC_d = 0.20$; (E) $\sigma = 0.28$, $BC_d = 0.20$; (F) $\sigma = 0.30$, $BC_d = 0.20$; (G) $\sigma = 0.26$, $BC_d = 0.25$; (H) $\sigma = 0.28$, $BC_d = 0.25$; (I) $\sigma = 0.30$, $BC_d = 0.25$. Each place ($n = 4$), as characterized by a seed planning unit, is denoted by a different colour. Areas where places overlap - and planning units are shared by two places are denoted by a hatched design.

Thresholds for threat distance were increased until a *critical threshold* was surpassed – places were of very large size. At this critical threshold, the tolerance for dissimilarity is so forgiving that even PU with comparatively low levels of threat similarity are included in the same place. A similar effect was observed as tolerance for SAR community composition dissimilarity increased. In practice, if thresholds for place characterization are set above the critical threshold, mitigation measures, individual recovery efforts are unlikely to confer widespread benefits. On the other hand, if place characterization requires PU be identical in SAR overlap and/or threat exposure, places, in all PSR, are limited to a single PU (seed PU).

The effect of the observed geographic variation in the distribution of average PU threat distance (Figure 7 & Figure 8) on place size was evaluated at greater depth. Keeping SAR overlap thresholds constant (at 25% dissimilarity), areal extents of places at increasing threat distance thresholds were compared between PSRs (Figure 16). Ecoregional variation is evident. For a given threat distance tolerance threshold, average place size in the southernmost PSR, 7E, is larger than in mid-range (6E), and northern (5E) PSRs. This pattern is (likely) linked to the lower average threat distances measured in PSR 7E (Figure 8).

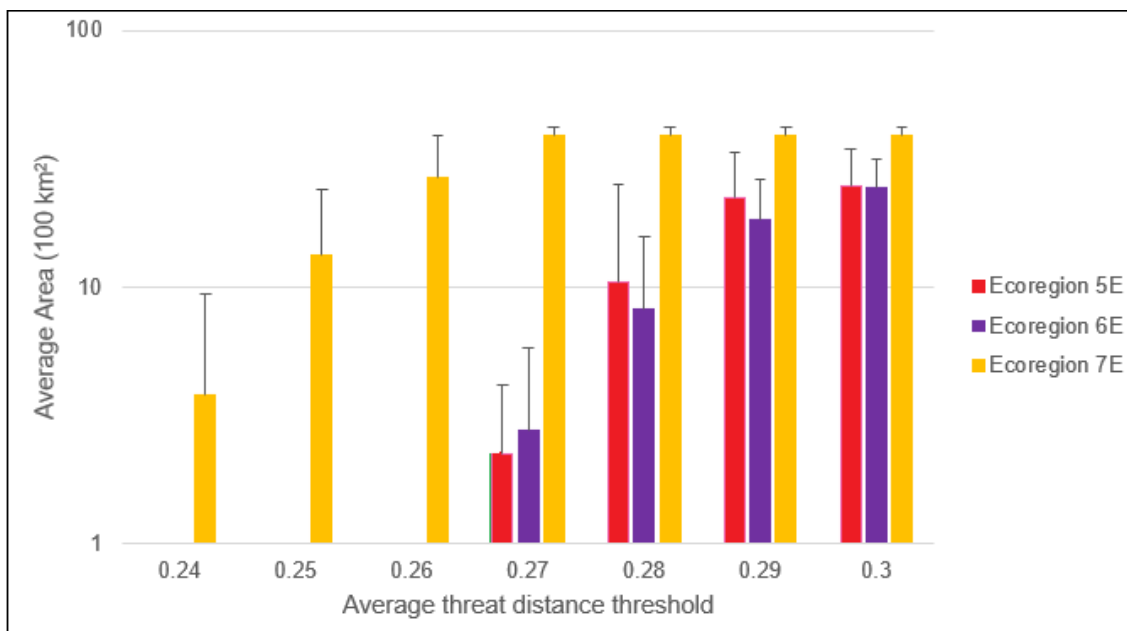


Figure 16. Average place spatial extent (Area, in km²) as a function of increasing thresholds for tolerance in dissimilarity or *interspecies threat distance* (σ), separated by ecoregion (5E with $n = 4$; 6E with $n = 4$; 7E with $n = 4$). Compositional variation (SAR overlap) tolerance for all trials was constant ($BC_d = 0.25$) Standard deviation bars are shown.

Place characterization is not only a function of tolerance thresholds, but also of seed designation. Because, in this exercise, the criterion of choosing seeds with the highest composite score identifies seed PU with both comparatively high SAR richness and high degree of threat similarity, in general seeds will be at the southern edge of the PSRs – giving rise to places along the southern edge. Assigning seeds based on other criteria, or randomly, would produce a different set of places. Given the condition that seeds need only be one PU apart, places are more likely to be closer together. Geographic overlap in place spatial extents was observed in all PSR– due partially to increasing threshold tolerance, and partially to spatial proximity of seed PU (Figures 13; 14; & 15). Furthermore, the majority of PU were not included in any place. First, we must consider the underlying principle - the number of seeds determines the number of places. In this exercise, I set the maximum number of places per PSR at four. Assigning a greater number of seed PU would increase the number of places, and in all likelihood, a greater number of PU would be assigned to a place. Secondly, by setting higher tolerances for dissimilarity in (a) SAR overlap, and/or (b) threat distance, a greater number of PU would be assigned to places.

5. DISCUSSION

5.1 - How the FMM fits into existing conservation planning

The approach (FMM) outlined here identifies and delineates places based on SAR co-localization in (a) geographical; and (b) threat space. The idea that conservation efforts should prioritize geographical areas based on species composition has a long-standing history in conservation. Setting conservation priorities based on measures of species richness, and community composition is a common theme in conservation management (Daru et al, 2018; Groves et al., 2002; Ricketts et al., 1999; Wilson et al., 2011). Myers (2000) advocated the identification of global biodiversity hotspots based, in part, on biological community richness and composition (the latter with a focus on endemism). Similarly, Carrara (2017) defined diversity hotspots on the basis on species richness, and measures of range size rarity (narrow vs expanse geographic distribution). Franklin (1993) rationalized a shift towards ecosystem-level conservation management, stating the potential for successful recovery (of constituent species) by delineating areas (ecosystems) displaying a high congruency in species composition. Furthermore, geographical overlap of SAR has been cited as a criterion for developing multi-species plans under SARA (Environment Canada, 2013; Environment Canada and Parks Canada Agency, 2016; Parks Canada Agency, 2006).

In the same manner, the idea that multi-species recovery plans should include species with a high degree of threat overlap has underlain much of multi-species conservation planning. The United States Fish and Wildlife Service (USFWS) recommends that SAR be combined into multi-species plans primarily on the basis of threat similarity (Clark and Harvey, 2002). Grouping SAR on the basis on threat similarity leads to recovery strategies aimed at reducing common threats (Lessard, 2002). Clark and Harvey (2002) argue that grouping SAR based on threat similarity is the key to successful multi-species recovery and management planning. This position is supported by several advocates – who stress the importance of considering the commonality of identified threats when developing recovery and conservation management

strategies, plans, and actions (Clark and Harvey, 2002; Cunnington et al., 2003; Moore and Wooler, 2004).

The place-based approach to conservation developed by Findlay and McKee (2016) is an appealing procedure to inform the process selecting sites for multi-species conservation and recovery. The application of the method allows the user to define (1) the set of PU that belong to the same (delineated) place; and (2) the set of PU that do not belong to any (delineated) place. With respect to (1), the places so defined will vary in the richness of the SAR community and the extent to which members thereof share similar threats. Thus, places (as defined in (1)) can be ranked – “hot” places are those which have comparatively high richness and comparatively large similarity in shared threats. These are places where (assuming all else being equal) a comparatively small set of threat mitigation strategies are most likely to yield widespread conservation benefits to the set of SAR. By contrast, “cool” places – those with comparatively low SAR community richness, whose set of SAR share fewer common threats – are areas where the conservation benefits of a small set of threat mitigation strategies are expected to have smaller (less widespread) conservation benefits.

Indeed, the method suggested by Findlay and McKee makes the distinction between “ecosystem” and “multi-species” plans/strategies largely arbitrary. In the latter, the focus is on threat co-localization: one first defines the set of species based on their threshold threat dissimilarity, and once this set of SAR is defined, the place then becomes the areas where these species occur. Note that in this case, these areas may not be geographically contiguous, and there is no need to restrict management prescriptions/proscriptions to areas where the species co-occur. By contrast, for “ecosystem” plans, the direct focus is on geographical co-localization. That is, we define places by considering thresholds in geographical co-localization and habitat distribution. Here, an ecosystem is defined by the threshold one sets for SAR community dissimilarity in contiguous geographical areas. In this case, places are

geographically contiguous, with management prescriptions/proscriptions applying to all areas within the defined place

The FMM provides a systematic method for determining (a) precisely what species will be included in multi-species recovery plans - under the method, the SAR that are included are those which have some degree of co-localization in both geographic and threat space and; (b) provides a systematic method for determining the geographical boundaries of ecosystem recovery plans/strategies, in the same way. Managers can define the threshold of co-localization (geographic and/or threat) as they deem appropriate. In the case that 100% overlap is required in both measures of interest, SAR overlap and threat similarity, the result is a set of places of minimum size. As tolerance for dissimilarity in one and/or both measures increase, a greater number of PU are added to places – and place size increases. In southern Ontario, inter-species threat distances are, on average, much smaller in the south. Even though there are more SAR in the south (as indicated by higher average estimated SAR richness) there is a greater similarity in shared threats than in the north, i.e. in the north, more threats are “idiosyncratic.”

The value of the FMM lies in its design. The FMM builds on current PBCP approaches by incorporating a threat exposure dimension into the analysis for delineating places. Threat assessment is an integral component of conservation planning methods prioritizing places (Groves et al., 2002) but is often excluded from methodologies designed to identify and delineate places (Rao et al., 2007). The FMM integrates ecological criteria with threat assessment - addressing the limitations of current platforms by providing a defensible rational, and repeatable process for place characterization (identification and delineation). Systematically grouping SAR based on measures of interest, metrics distinguishing compositional variation (SAR community overlap) and the degree of threat commonality similarity SAR of interest, provides a quantitative tool for determining the set of SAR that might be included in a multi-species recovery plan. This place-based approach shifts conservation management goals away

from a locus focused on individual (populations and/or species) persistence, targeting recovery at the community level. Here, cumulative benefit is assessed (Findlay and McKee, 2016). While specific species within delineated places may still require species-specific management, the FMM approach identifies places where targeted threat mitigation recovery actions are most likely to result in widespread conservation benefits.

The FMM has several advantages over other place-based approaches for determining the geographical boundaries of ecosystem or multi-species recovery plans. First it reduces the potential for cultural, political, or social bias which has been associated with the selection of surrogate species (Andelman and Fagan, 2000; Lindenmayer et al, 2002; Roberge and Angelstam, 2004; Tear et al, 1995). Second, there is no built-in presumption that surrogate-specific threat mitigation confers additional conservation benefits on other geographically co-occurring SAR (Simberloff, 1998, Carroll et al, 2001). Third, it provides a general framework. Providing a general framework allows for flexibility in the attributes used to group together planning units. For example, to delineate places based on the degree of similarity in recovery actions, one would simply substitute, or add, the data into the analysis. By providing a general framework the FMM reduces time and monetary constraints often associated with developing (labour-intensive) plans targeting the recovery and persistence of an explicit set of SAR. Lastly, because the data required to apply the FMM are available and sufficient, at least at the coarsest level of resolution, concerns regarding the inapplicability of a process subject to disproportionate and/or unavailable data are addressed (Fleishman et al., 2001; Freudenberger and Booker, 2004).

5.2 – Limitations, improvements, and extensions

To operationalize the FMM, I developed a spatially explicit parametrized algorithm. I fixed certain parameters, including the planning region and planning unit size. I allowed other parameters to remain variable – including tolerance thresholds for SAR composition and inter-

species threat similarity. This case study provided a means by which to evaluate the benefits and limitations of the FMM. The FMM has the potential to be a defensible method for characterizing places. However, its applicability is limited by (1) the resolution and availability of datasets; (2) the assumption of spatial and temporal uniformity in threat exposure; (3) the criteria used in seed planning unit designation; (4) the arbitrary determination of the maximum number of places; and (5) the selection of appropriate tolerance thresholds.

5.2.1 Resolution and availability of datasets

Place-based management planning through the FMM requires, minimally, the knowledge of SAR distributions and their associated threats. The FMM is scale independent. Given the availability of datasets at the appropriate resolution, the methodology can theoretically be operationalized at a global, regional, or local scale. The datasets required to operationalize the FMM are sufficient and available – but currently only at the coarsest level of resolution. This narrows the scale at which analysis can be operationalized, limiting its applicability at a local scale. Range map quality varies on a per species basis - a function of the quality and spatial resolution of the raw data used in production (Findlay and McKee, 2016). For certain species, critical habitat range maps are available, but often, these maps are incomplete and include only a portion of the identified critical habitat. Critical range maps were not used in this exercise. However, if critical habitat maps are completed, they would further increase the reliability of species-presence estimates. Furthermore, habitat association data, in binary vector format, does not distinguish between primary or secondary habitat uses and cannot provide life cycle association (Findlay and McKee, 2016). Introducing this type of data would improve the reliability of the output from an FMM analysis but would also increase the computational data requirements necessary for application. Moreover, it is important to note that the datasets used in this analysis are not sacred. For example, I used MODIS data because it was readily

available at the required resolution. However, it would be possible to build habitat association profiles from other classification systems.

Place characterization, in this context, required measures for (a) SAR overlap, and (b) average threat distance of the SAR community (single PU or the union of two PU). In characterizing threat space, I used the RMS to determine the distance between threat profiles. This metric quantifies the extent of shared threats but tells us nothing about which threats are shared. This process could be improved by looking at threat commonality – the degree to which certain threats are shared among a set of SAR, i.e. if there are N species, which threats are shared by all N species? a subset of N species? Alternatively, place characterization may be based on distances in habitat space. Using land-use or land-cover classifications, habitat profiles may be developed for the set of SAR of interest – based on the proportion of land within every PU of interest that is in a certain land-use or land-cover class. Distances in habitat space could then be used as a measure of interest for place characterization – with places characterized by contiguous PU that satisfy some threshold distance. Moreover, given the availability of recovery action and/or land-value data, it would be possible to incorporate these parameters to group planning units into places.

5.2.2 The assumption of spatial and temporal threat uniformity

Data identifying processes threatening the persistence of imperilled populations is the second fundamental requirement of the FMM. Determining the causality linked to species decline is a complex endeavour as threatening processes rarely act in isolation (Simberloff, 1998). Threat exposure varies both spatially and temporally. Presenting threat profiles as binary vectors removes these considerations. Using binary data, we assume that threat exposure does not vary in space nor time. Threat data are not geographically specific, but clearly, the intensity and magnitude of a threat may vary across the species' distributions, especially for those with large ranges. It is important that, when implementing recovery actions, these variations be

considered. Furthermore, classifying threat exposure through binary vectors assumes all threats are equal. If threat exposure data were prioritized – from most important to least (given the availability of such information), distances in threat space and/or threat overlap could be limited to only “important” threats, improving the accuracy of threat distance metrics.

5.2.3 – Seed PU designation and arbitrary determination of maximum number of places

How seeds are chosen (criteria for seed designation), and how many seeds are chosen (thus determining the maximum number of places) may be based on whatever attributes - measures of interest - are considered to be “important”, ultimately leading to some sort of ordination or ranking of seed PU. Given this prioritization, and the tolerance thresholds set, the output is a set of places. Specific to this particular exercise, places were implicitly prioritized through seed designation. Using composite scores as the criterion to designate seed PU implicitly prioritizes PU with large SAR community and/or high degree of threat similarity. Given the importance of threat similarity in successful multi-species recovery (Clark and Harvey, 2002), one might consider prioritizing places by designating seeds based solely on the criterion of inter-species threat distance. Alternatively, planning units with a high degree of similarity in required recovery actions or low land values might be prioritized if these attributes align with conservation targets.

In this case study, the maximum number of places per planning subregion was determined arbitrarily (n=4) and kept as a fixed parameter. The result was a large number of planning units not included in any place until large tolerance thresholds (a greater dissimilarity) were allowed. The FMM inherently limits conservation initiatives only to those planning units found within a place. Omitting the majority of planning units from recovery and conservation actions based on an arbitrary decision could significantly reduce the potential of this framework to inform conservation managers. Future research should focus on empirically determining the

maximum number of places, which in turn, will determine the number of seeds chosen per planning region.

5.2.4 – Selecting appropriate tolerance thresholds

Tolerance for dissimilarity is considered an adjustable parameter in place characterization under the FMM. Places may be comprised of one, or several PU, depending on the allowed threshold (level) of dissimilarity. Places were characterized by adding adjacent, or candidate PUs to seed PUs. In order to be added, candidate PUs had to satisfy (fall below) both species overlap and threat similarity tolerance thresholds. The size of a place is a direct function of these tolerance thresholds. As tolerance for dissimilarity increases, place spatial extents increase, incorporating increasingly dissimilar PU until places no longer represent areas where recovery actions are likely to provide widespread benefits. The question now becomes – at what tolerance threshold do places lose their ability to delineate areas where recovery actions successfully provide co-benefits to the SAR assemblage within? Further research should be focused on examining the relationship between specific tolerance thresholds with respect to the potential benefit of place designation.

5.3 – The cost of recovery

One putative advantage of multispecies and ecosystem level recovery plans is cost reduction (La Roe, 1993). Utilizing a single species recovery and conservation management approach quickly exhausts funding resources, and time (Franklin, 1993). In light of limited resources, development of multi-species plans seems like a reasonable alternative to approach biological conservation (La Roe, 1993; Tear et al., 1995). Multi-species plans are considered favourable when two or more SAR (of the same genus) exhibit both geographic and threat co-localization (Clark and Harvey, 2002; Jewell 2000). While support for multi species recovery actions has been increasing (Franklin, 1993; Groves et al., 2002; Kellner et al., 2011; Lambeck, 1997; Tear

et al., 1995), there are concerns about the effectiveness based on analysis of such plans compared to single species plans.

A study conducted by Boersma et al (2001) found that, under the United States' *Endangered Species Act (ESA)*, SAR listed under individual or single-species recovery plans were 4X more likely to be improving in status, than SAR listed under multi-species recovery plans. Why are single species recovery strategies seemingly more effective? While it is possible that single species recovery plans provide a better foundation for recovery efforts, Clark and Harvey (2002) identified that often, SAR are inappropriately grouped under multi-species plans. Though SAR listed under multi-species plans are habitually grouped by taxonomic similarities and geographic co-occurrence, insufficient consideration is given to common threats. Their analysis concluded that in nearly half of multi-species plans, threat similarity was not significantly different than for randomly selected groups of SAR – of different taxa, inhabiting different geographic regions (Clark and Harvey, 2002). Moreover, developing multi-species and/or ecosystem-based recovery strategies without a systematic process can be a complex, time-consuming, and resource-draining endeavour (Canadian Wildlife Service, 2002). Without a specified procedure or set of guidelines, developing efficient and effective multi-species plans under the timelines mandated by SARA is a challenging task.

Intended to be a practical conservation tool for decision makers, the FMM addresses some of these concerns – providing a systematic set of guidelines to delineate geographic boundaries for effective multi-species management. The systematic method for place characterization provided through the FMM has the potential to reduce time constraints associated with producing multi-species recovery strategies – increasing the feasibility of producing efficient and effective multi-species plans under the timelines mandated in SARA. As the FMM can be applied on a national, regional, or local scale (given the sufficiency and availability of data) the process is applicable to conservation managers at all levels of government. Furthermore, the FMM provides a set of guidelines for appropriately grouping sets

of SAR. Sufficient consideration is given to threat similarity when grouping PU into places, if priority is given to metrics quantifying the extent and/or overlap in threat space between SAR of interest. Triaging PU based on such measures of interest results in places where constituent SAR share a high commonality in threats. By addressing some of the concerns associated with current multi-species recovery and management strategies, the FMM will likely contribute to efficient and effective multi-species conservation and management.

6. CONCLUSION

Given the current state of natural systems and severe declines in diversity (UN SDG, 2019), the need for effective protective and restorative conservation actions is evident. If the goal is to minimize the net loss of species, conservation management requires a systematic process of procedures to inform the identification and delineation of places – spatial extents where implementing a set of recovery actions will confer widespread benefits to the constituent SAR community. This exercise – which evaluated the FMM’s ability as a place-based approach to multi-species conservation in a case study of southern Ontario – determined the process and procedures defined by the FMM could successfully delineate geographic boundaries of places. Place characterization, under the FMM, is a function the criteria determining seed designation, as well as a function of thresholds of tolerance for dissimilarity in (a) SAR overlap, and/or (b) inter-species threat distance. Moreover, place size increases as a greater tolerance for dissimilarity in these measures is allowed. The FMM approach has great potential to contribute to effective and efficient place-based multi-species conservation and management. Further research should focus on selecting the appropriate criteria for seed planning unit designation, empirically determining the maximum number of places, and examining the relationship between tolerance thresholds and place size in greater detail, specifically identifying critical tolerances – thresholds above which the resultant output, geographic boundaries delineating a set of places, no longer reflect areas where recovery actions are likely to provide co-benefits to the constituent SAR community. Such contributions would improve the reliability of this framework as a place-based approach to multi-species conservation and management.

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APPENDIX A. DATA REQUIREMENTS

Given that data are available and complete (at the level required for analysis), the Findlay-McKee Methodology (FMM) may be applied at a local, regional or national scale. The required datasets do not depend on the scale of analysis; however, the resolution of the required data is scale-dependent. For example, analysis conducted at a local scale will require data of finer resolution than analysis conducted at a regional and/or national scale. Essential datasets for the application of the FMM are described below.

A.1 – Planning Region Shapefile (Vector format):

In order to operationalize the FMM we must first identify a planning region, within which “places” are delineated. Vector-format data delineating potential *planning regions* of interest can be downloaded from Scholar’s Geoportal (or comparable websites). Ontario provincial outline and ecoregion shapefiles (.shp) were retrieved from (<http://geo2.scholarsportal.info>), projected in GCS_North America_1983. To isolate southern Ontario data, census divisions were retrieved from FEDDEV – the federal economic development agency. The northernmost census divisions formed the northern boundary of the area of study. The shapefiles were then clipped (using ArcGIS software) to the area of study.

A.2 – SAR Distribution Range Maps (Vector format):

Species’ ranges can be represented geographically through digitized distribution maps (shapefile, vector format). A national dataset of imperiled species ranges is available through Environment and Climate Change Canada. Range data is collected through field inventories, and distribution modelling. Access to digitized distribution maps for terrestrial SAR listed as schedule 1 under SARA ($N = 454$) was granted by the ECCC and projected to the same coordinate system as the shapefiles delineating the area of study – planning region (GCS_North America_1983).

A.3 – Extinction Risk Data (Vector format):

In Canada, the initial assessment on the status of wildlife populations is conducted by COSEWIC, an independent advisory board. Evaluations result in designated statuses, based on the risk of extinction (from Not at Risk to Endangered/Extirpated). Because COSEWIC follows quantitative criteria and guidelines, the status assigned to wildlife populations can be used as an index of extinction risk. Data on all COSEWIC-assessed populations is freely-accessible available through the Government of Canada, at: <https://www.canada.ca/en/environment-climate-change/services/species-risk-public-registry.html>. Using the information extracted from the website, COSEWIC statuses were given ordinal designations, creating an index for extinction risk (Not at Risk = 0; Special Concern = 1; Threatened = 2; Endangered = 3; and Extirpated = 4). An excel spreadsheet was created listing: Latin name, common name, population, COSEWIC ID, and listing status.

A.4 – Land Cover Data (Raster format):

Based on Moderate Resolution Imaging Spectroradiometer (MODIS) satellite imagery, it is possible to produce maps classifying land cover. Depending on the classification scheme and the level of resolution, physical land types such as forests, wetlands, impervious surfaces, and urban developments are identified, in pixelated, raster data. These datasets are required to

provide greater spatial resolution of species distributions within planning regions, according to habitat suitability. The required resolution is dependent upon the scale of analysis, with smaller planning regions requiring higher spatial resolution imagery.

For this analysis, I used 2010 MODIS land cover data at 250m resolution (a 250m pixel size). These data are available for all of North America and was retrieved from <http://www.cec.org/tools-and-resources/north-american-environmental-atlas/north-american-land-change-monitoring-system>. The dataset uses the Land Cover Classification System (LCCS) developed by the UN Food and Agricultural Organization (Table 1) to identify 19 land-use classes (FAO, 2000).

Table 1. MODIS land cover classifications as characterized by the LCC

Numerical Value	Land Cover Classification
1	Temperate or sub polar needleleaf forest
2	Sub-polar taiga or needleleaf forest
3	Tropical or sub-tropical broadleaf evergreen forest
4	Tropical or sub-tropical broadleaf deciduous forest
5	Temperate or sub-polar broadleaf deciduous forest
6	Mixed forest
7	Tropical or sub-tropical shrubland
8	Temperate or sub-polar shrubland
9	Tropical or sub-tropical grassland
10	Temperate or sub-polar grassland
11	Sub-polar or polar shrubland-lichen-moss
12	Sub-polar or polar grassland-lichen-moss
13	Sub-polar or polar barren-lichen-moss
14	Wetland
15	Cropland
16	Barren land
17	Urban and built-up
18	Water
19	Snow and ice

A.5 – Habitat Association Profiles (Vector format):

Distribution maps are often produced at coarse resolution – delineating the boundaries of species’ ranges. The reliability of such maps to predict species occurrence can be increased by restricting the distribution within these delineations to habitats associated with the species. Species-specific habitat associations were extracted from COSEWIC status reports (which specify habitat *use*, *requirements* and *distribution*) to create a dichotomous habitat association profile (HAP) depending on whether the MODIS land cover class is suitable (score = 1) or unsuitable (score = 0) for the species in question. HAP designation was based on a condensed

land cover classification system, with 11 land-use classes (Table 2). An excel table was created combining information for all species in the planning region: Latin name, common name, population, COSEWIC ID, and associated suitable MODIS land cover classes.

Table 2. HAP land-use classes

HAP designation	FAO Land Cover Classification (numerical value)
Coniferous	Temperate or sub polar needleleaf forest (1)
	Sub-polar taiga or needleleaf forest (2)
	Tropical or sub-tropical broadleaf evergreen forest (3)
Deciduous	Tropical or sub-tropical broadleaf deciduous forest (4)
	Temperate or sub-polar broadleaf deciduous forest (5)
Mixed Forest	Mixed forest (6)
	Tropical or sub-tropical shrubland (7)
	Temperate or sub-polar shrubland (8)
Shrub/Early Successional*	Tropical or sub-tropical grassland (9)
	Temperate or sub-polar grassland (10)
Lichen/Mosses	Sub-polar or polar shrubland-lichen-moss (11)
	Sub-polar or polar grassland-lichen-moss (12)
	Sub-polar or polar barren-lichen-moss (13)
Wetland	Wetland (14)
Cultivated	Cropland (15)
Bare Areas	Barren land (16)
Urban	Urban and built-up (17)
Waterbodies, Snow and Ice	Water (18)
	Snow and ice (19)

* The herbaceous land-cover classification was grouped in with shrub/early successional categorization.

A.6 – Species Threat Profiles (Vector format):

Imperiled populations are exposed to a range of threats. Threats can be categorized at varying degrees of granularity, as reflected in the IUCN Threats Classification. For the purpose of this exercise, we construct threat profiles for individual species based on IUCN Threat Classification Version 3.2 Tier 1 classes. Using data extracted from the most recent COSEWIC status reports, dichotomous threat profiles (binary vector data) were created for each Tier 1 threat class. A species was scored as either 1 (indicating that, in the report, a threat associated with the Tier 1 threat class was explicitly identified) or 0 (indicating that no threat in the associated Tier 1 class was explicitly identified).

APPENDIX B. CHARACTERIZING THE SAR COMMUNITY WITHIN EACH PLANNING UNIT.²

The following procedure outlines how the set of species at risk (SAR community), potentially present at each planning unit (PU), j , within planning region, R , was determined.

B.1 – Notional Species Presence Score, S_{kj} , (Raw/Unweighted).

To begin, we define the set of SAR (the SAR community) $SI = \{S_k, k = 1, \dots, S_R\}$ that have some probability of occurrence within a planning region $R = \{PU_j, j = 1, \dots, M_R\}$ defined by a set of PU (cells) of a specified size. The size of the PU will be determined by a number of factors, including the scale of analysis and resolution of available data. Operationally, it is the minimum size of an area over which a fixed suite of recovery or management actions would be implemented – in this case, each PU is a 10km² cell.

Here we assume that for R , there exists distribution or range maps for the set of SAR of interest. To generate the set SI :

- (1) We define the boundaries of the planning region on a base map;
- (2) Determine the set of PU, R , that lie within the planning region (Figure B.1.1);
- (3) Restrict range/distribution maps of candidate species to include only areas, within these delineations, that are associated with habitat suitable to the species (as determined by HAPs) (Figure B.1.2);
- (4) Overlay range/distribution maps of candidate SAR onto planning region, R . The subset of species for whose distribution includes at least part of at least one PU in R constitutes SI , the planning region SAR pool (Figure B.1.1);
- (5) For each PU within the planning region, overlay the range maps of each species in the planning region SAR pool and determine whether the range includes some portion of the PU. The set of species that satisfy this condition constitutes the potential SAR community for the PU in question (Figure B.1.1);

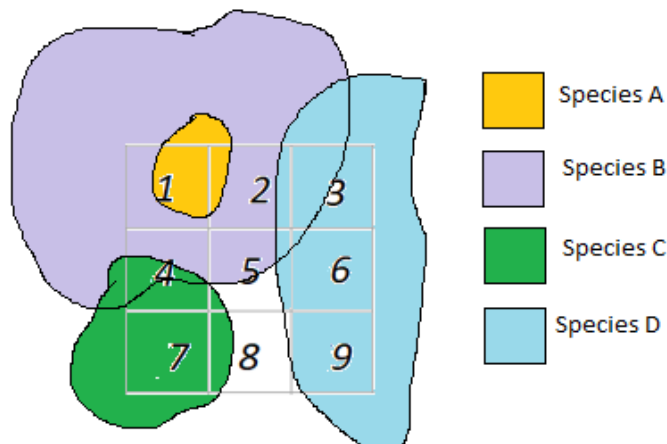


Figure B.1.1. In the hypothetical example above, the planning region, R , comprised of 9 PU, overlaps with the geographical distributions of four species, forming the regional SAR pool $\{A, B, C, D\}$. These SAR are potentially present in the planning region but not in all PU. For example, PU 9 falls in the range of only one species $\{D\}$, while PU 1 is within range of two SAR $\{A, B\}$.

² Adapted from Findlay and McKee, 2016

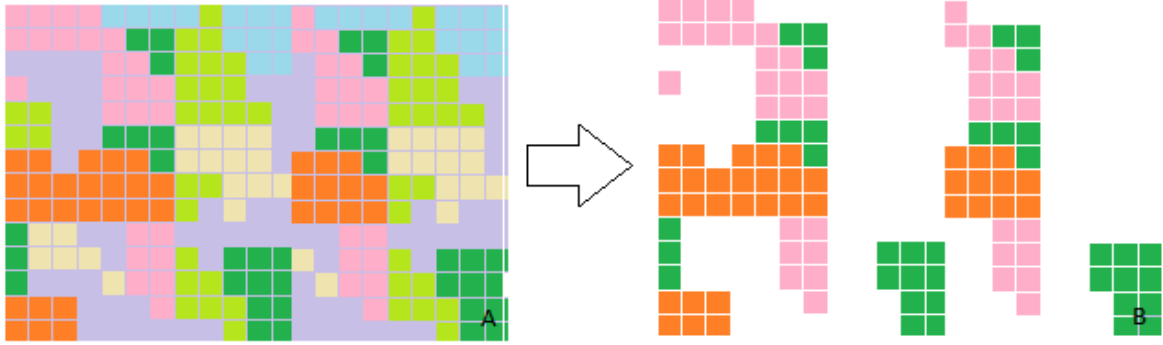


Figure B.1.2. Consider a hypothetical situation where the distribution or range map of Species A line is overlaid on MODIS land cover data (A). Every square cell represents a pixel at which landcover is assessed. The different pixel colours represent different land cover classifications, i.e. blue = water, orange = deciduous forests, dark green = mixed wood forests, etc. The HAP of Species A identifies its suitable habitats as those land cover classifications denoted by pink, orange, and dark green. Even though the distribution map consists of multiple landcover classes, Species A is not likely to be found in unsuitable habitats. We can increase the resolution of the distribution map by restricting the range to only those pixels with suitable land cover classes. (B) represents the restricted distribution of Species A.

- (6) The SAR community in PU j can be represented by a *species presence vector* $S_{kj} = (S_{1j}, S_{2j}, \dots, S_{SR})$ whose elements give a score S for the presumed presence of species k in PU j . In its crudest form, S_{kj} is a binary vector, with $S_{kj} = 1$ if j lies within the range (restricted by habitat suitability) of the species k and zero otherwise (if no part of j lies within the species' range).

B.2 – Species Richness, SR_j or (Raw/Unweighted)

We begin with the binary species presence vector $S_{kj} = (S_{1j}, S_{2j}, \dots, S_{SR})$ for PU, j (see B.1 (6)). Unweighted, or raw species richness, SR_j , is simply the number of SAR species in PU j for which $S_{kj} = 1$, and is obtained by counting the number of elements in $S_{kj} = (S_{1j}, S_{2j}, \dots, S_{SR})$ that satisfy this condition.

B.3 – Habitat Suitability Score, P_{kj}

Within each PU, we consider the proportion of habitat suitable to each species of interest. Distribution maps were restricted to include only those habitat (land-cover classes) suitable for the species of interest (as determined by HAPs, Figure B.1.2). For each PU it is possible to determine the proportion of the PU potentially occupied by each species in the SAR community. This habitat suitability score, P_{kj} – the proportion of suitable habitat for species k , within PU j is given by:

$$P_{kj} = A_{kj} / A_j$$

Where A_{kj} is the area occupied, notionally by species k in PU j , and A_j is the total area of PU j . In this manner we generate a habitat suitability score between 0 and 1 for each SAR within a PU. We can interpret P_{kj} as an index of the relative amount of potentially suitable habitat in PU j for species k , which may vary dramatically among SAR species whose range includes the PU in question. If, for a given PU a species has a score close to 1, then virtually all of the area within the PU is suitable habitat. By contrast, for those with scores near zero the amount of potentially suitable habitat is negligible.

B.4 – Extinction Risk Index, ER_k

It is also possible to weight species presence vectors by an index of extirpation/extinction risk. One such index is the status assigned by COSEWIC, with weight increasing with threat status. The index is then described by:

$$ER_k = (T_k \ln 2) / (4 \ln 2)$$

if we assign T_k as the extinction risk value associated with the assigned COSEWIC status of species, then $T_k = 0$ if status is not at risk, $T_k = 1$ if status is Special Concern, $T_k = 2$ if status is Threatened, $T_k = 3$ if status is Endangered, and $T_k = 4$ if status is Extirpated.

B.5 – Species Presence Score S^*_{kj} , (Weighted by Habitat Suitability and Extinction Risk).

The approach determining species presence as described in B.1 assumes a binary presence, wherein each vector is either a 1 or a 0 – either a species is present (score = 1) or a species is absent (score = 0) from the PU of interest. Such scoring does not take into account the uncertainty in the inference that indeed, the species in question is present or absent. In general, uncertainty is incorporated into scoring systems by weighting scores (in this case, binary scores) by their uncertainty – based on information that is independent of the initial score. Weights increase with decreasing uncertainty, so that large weights are attributed to highly certain estimates, low weights highly uncertain estimates.

It is possible to refine the species presence vector $S_{kj} = (S_{1j}, S_{2j}, \dots, S_{SR})$ (see B.1(6)) for a set of SAR (SAR community) in PU j by weighting the score by habitat suitability (B.3) and extinction risk (B.4). We can use *habitat suitability scores* as a weight for species presence, the underlying rationale being that species for which P_{kj} is high and are more likely to be present in the planning region than those for which P_{kj} is low. Under this interpretation, species presence scores S for species k in PU j are represented by $S^*_{kj} = (P_{1j}, P_{2j}, \dots, P_{SR})$ is now a ratio-valued vector with elements $P_{kj} \in [0, 1]$ corresponding to habitat suitability scores.

Similarly, another possibility is to weight elements of species presence vector by some measure of the importance of the PU to the recovery of the species in question – in this case, extinction risk, ER_k . Then we can generate a weighted species presence vector whose elements are given by the product of the habitat suitability index and an extirpation/extinction risk ratio:

$$S^*_{kj} = P_{kj} [(T_k \ln 2) / (4 \ln 2)]$$

(Note that this is the interpretation of S^*_{kj} used in this particular experiment)

The decision as to what information to use in determining weights, and how to combine weights in composite weighting schemes will depend on particular circumstances. The particular metrics used in this case study may not be fully applicable in other circumstances depending on the availability and resolution of data. However, the following principles are strongly recommended by Findlay and McKee – and were adhered to in this exercise.

1. *Direct comparisons between planning regions requires that the weighting scheme be applied in all regions.* Identical weighting schemes and metrics were applied to all planning subregions.
2. *Care must be taken to avoid unduly penalizing species for which little information exists.* Weighting schemes were designed for the coarsest available data to avoid up-weighting between SAR.

3. *Any weight for species presence be normalized to the unit interval [0, 1].* This was the case for the weighting schemes defined for habitat suitability and extinction/extirpation risk. In producing weighted species presence data, each weighting factor is accorded the same implicit weight.
4. *In computing composite metrics, care must be taken to avoid “double counting.”* For example, we assume that habitat suitability indices, and extinction risk weights are pairwise independent. This assumption can be evaluated by evaluating the correlation matrix (derived from the distribution of weights among species in the SAR community in PU j) for the set of candidate weights and, if strong correlations exist, producing composite weights defined by the first couple of principle components in a standard decomposition.

B.6 – Species Richness, SR_j^ (Weighted by Habitat Suitability and Extinction Risk)*

We begin with the species presence vector, $S_{kj} = (S_{1j}, S_{2j}, \dots, S_{SR})$ (see B.1(6)) and weight the vector by habitat suitability and extinction risk (B.5), resulting in a ratio-valued presence vector $S_{kj}^* = (S_{1j}^*, S_{2j}^*, \dots, S_{SR}^*)$, for PU j .

In calculating a weighted species richness, SR_j^* , we sum weighted species presence vectors, S_{kj}^* over the set of SAR species:

$$SR_j^* = \sum_{k=1}^{SR} S_{kj}^*$$

Since in the case of no weighting whatsoever, $S_{kj} = (0, 1)$, it follows that:

$$SR_j \leq SR_j^*$$

that is, weighted species richness will always be less than or equal to the unweighted species richness. Heat mapping of this metric distinguishes areas that have a comparatively large number of SAR, each with a high prevalence (hot areas), and/or a high extinction risk (i.e. endangered species), from areas with fewer species with comparatively lower prevalence and/or a lower extinction risk (i.e. special concern).

APPENDIX C. CHARACTERIZING INTER-SPECIES THREAT DISTANCES.³

To begin, we define a set of threats (the threat pool) $T_j = \{T_{kj}, k = 1, \dots, T_{Nj}\}$ to which at least one member of the SAR community in the planning region $R = \{PU_j, j = 1, \dots, M_R\}$ is exposed.

Let S_j be the set of SAR found in planning unit (PU) j (i.e. the SAR community), and let $\mathbb{T}_{kj} = (T_{1k,j}, T_{2k,j}, \dots, T_{Nj})$ be a binary threat vector for species k in PU j , with $T_{ik,j} = (0,1) \forall i, j, k$ with $k \in S_j$, where a value of 1 or 0 denotes a threat to which species k in PU j is, or is not (respectively) exposed, and N is the total number of possible threat classes. For this exercise, IUCN level 1 threat classes are used to define threat profiles, $N = 11$. Summing over species in the SAR community in PU j yields:

$$T_{ij} = \sum_{k \in S_j} T_{ik,j}$$

The set of threats to which at least one SAR in PU j is exposed is just the subset of threats for which $T_{ij} > 0$ (Figure C.1)

	IUCN Level 1 threats										
Species	1	2	3	4	5	6	7	8	9	10	11
A	0	0	0	1	1	0	0	1	0	0	0
B	0	0	1	1	1	1	0	0	0	0	0
C	0	1	0	0	1	1	0	0	0	0	0
D	0	0	0	1	1	0	0	1	1	0	0
E	0	0	0	1	0	0	0	1	0	0	0
Sum	0	1	1	4	4	2	0	3	1	0	0

Figure C.1. In this hypothetical situation, the SAR community in PU j includes 5 species at risk (A-E) whose binary threat profiles based on IUCN level 1 threat classification are shown in rows. Summing over species within a threat class gives a score T_{ij} for each threat class i . Four threat classes (1, 7, 10, and 11) have $T_{ij} = 0$; the threat pool for PU j is then $T_j = \{2, 3, 4, 5, 6, 8, 9\}$ with $N_{T_j} = 7$ being the size of the threat pool.

We can then compute a reduced threat profile which eliminates all threat classes to which no species in the SAR community in PU j are exposed (Figure C.2).

	IUCN Level 1 threats						
Species	2	3	4	5	6	8	9
A	0	0	1	1	0	1	0
B	0	1	1	1	1	0	0
C	1	0	0	1	1	0	0
D	0	0	1	1	0	1	1
E	0	0	1	0	0	1	0
Sum	1	1	4	4	2	3	1

Figure C.2. Here the threat profiles for each member of the hypothetical SAR community shown in Figure C.1 have been reduced to exclude those threat classes (1, 7, 10, 11) to which no

³ Adapted from Findlay and McKee, 2016

member in PU j is exposed. Each row now represents the reduced threat profile for species k in PU j .

For the purpose of this case study, we used the root mean square (RMS) distance (σ) between SAR in threat space as a metric to compute distances among SAR in threat space. To compute the RMS distance among SAR community members, we first determine the *threat pool* for the unit. This is just the set of threats to which at least one species in the SAR community for the PU in question is exposed. We then define the threat profile centroid, a vector whose elements are given by:

$$\bar{T}_{ij} = \frac{1}{N_j} \sum_{k \in \mathbb{S}_j} T_{ik,j}$$

The RMS distance in (reduced) threat space is then given by:

$$\sigma_j(T) = \frac{1}{N_j} \sqrt{\sum_{j=1}^{N_j} \sum_{k \in \mathbb{S}_j} (T_{ik,j} - \bar{T}_{ij})^2}$$

This can be understood as the average (Euclidean) distance between each reduced threat vector and the vector which defines the group centroid (Figure C.3, C.4), The greater this distance, the more different, on average are the reduced threat profiles of members of the SAR community in PU j . If each member has an identical reduced threat profile, then:

$$T_{ik,j} = \bar{T}_{ij}$$

for all l and all k , in which case $\sigma_j(T) = 0$, that is, the distance between any pair of SAR community members is zero.

Species	IUCN Level 1 threats							Sum of squared deviations
	2	3	4	5	6	8	9	
A	0	0	1	1	0	1	0	0.52
B	0	1	1	1	1	0	0	1.52
C	1	0	0	1	1	0	0	2.12
D	0	0	1	1	0	1	1	1.12
E	0	0	1	0	0	1	0	1.12
Centroid	0.2	0.2	0.8	0.8	0.4	0.6	0.2	
							Sum over species	6.40
N _j	5							
$\sigma(T)$	0.51							

Figure C.3. Example calculation for the root mean square distance in threat space. For a given threat class, the value of the centroid is just the column average. For example, for threat class 2, the value of the centroid is $(0+0+1+0+0)/5 = 0.20$. For a given species, the sum of squared deviations is calculated by subtracting each threat value from the corresponding centroid value, squaring it, and summing over all threats. So, for example, for species A, this is given by $(0 -$

$$0.2)^2 + (0 - 0.2)^2 + (1 - 0.8)^2 + (1 - 0.8)^2 + (0 - 0.4)^2 + 1 - 0.6)^2 + (0 - 0.2)^2 = 0.52. \sigma(T) \text{ is then } (1/5) \sqrt{6.40} = 0.51$$

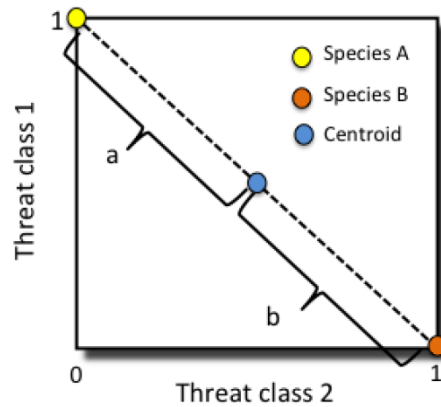


Figure C.4 Schematic representation of distance in threat space. In this simple example, two species (A and B) are defined by binary threat vectors in a two-dimensional threat space (Threat 1, Threat 2). The profile for species A is (0,1), for species B (1, 0). The centroid is then located at (0.5, 0.5), with each species' profile being the same distance from the centroid, with distances given by length of line segment a and b for species A and B respectively. Because in this simple example, each species is located equidistant from the centroid, the root mean square distance is simply the length of a (or b).

APPENDIX D. COMPOSITE METRICS INTEGRATING COMPOSITIONAL VARIATION AND INTER-SPECIES THREAT DISTANCES⁴

In Appendix B, we develop a set of species richness metrics that characterize the SAR community in a planning unit (PU), either (raw) unweighted (SR_j) or weighted by habitat suitability and extinction/extirpation risk (SR_j^*). In Appendix C we develop a set of metrics that characterize the variation in distance among threat profiles, using root mean square distance. We now produce a composite metric (M_{mj}) for the set of SAR in a given PU:

$$M_{mj} = SR_j^* \times \frac{1}{\sigma_j(T)}$$

Under this formulation, PU with a comparatively large weighted species richness (SR_w) and little variation in threat profiles among members of the SAR community $\sigma_j(T)$ will have a comparatively large value of the composite metric, M_{mj} . By contrast, PU with few SAR species with large differences in threat profiles will have comparatively small values of M_{mj} .

⁴ Adapted from Findlay and McKee, 2016

APPENDIX E. ADAPTIVE “PLACE” SIZE⁵

Here I describe the general procedure for the determination of places of different sizes within a planning region:

E.1 – Seed Determination

- 1) For a given planning region, one defines a PU size – based on the scale of analysis and resolution of available data;
- 2) A maximum number of “places” is defined. The number of places in a planning region is determined by the number of seeds chosen, i.e. if, for planning purposes, we are interested in three places, then three seeds are chosen;
- 3) For the planning region, the associated table of attributes – with average threat distance (σ), unweighted (raw) SAR species richness (SR_{uw}), weighted SAR species richness (SR_w), and composite scores (M_{mj}) – with each row identifying a different PU within the region, is generated
- 4) Seed designation criteria is selected. For the purpose of this experiment, seed designation was based on two criteria – composite score, and minimum distance between seed PU:
 - a. Composite scores, in the attribute table, were arranged from highest to lowest
 - b. The first seed is the PU with the largest composite score
 - c. The second seed is the PU with the second highest composite value that is separated by at least (a minimum of) one PU
 - d. This process continues until all seed PU have been assigned – the number of seed PU equals the maximum number of places.

For this particular exercise, 4 seeds were chosen for each planning subregion (N = 12 places).

- 5E (n = 4): S77, T55, U72, V59
- 6E (n = 4): W45, W68, AA32, AL25
- 7E (n = 4): AM20, AN27, AP16, AS14

It is important to note that the criterion of choosing seeds with the highest composite scores (based on richness measures and average threat distance) means that, in general seeds will be at the southern edge of sub-planning regions. Given the condition that seeds need only be one PU apart, they will often be close together.

E.2 – Place characterization

- 1) We begin by establishing geographical dissimilarity tolerance thresholds for (a) SAR overlap and (b) average threat distance for the set of SAR – considered as adjustable parameters in place characterization;

⁵ Adapted from Findlay and McKee, 2016

2) For each measure of interest, as (a) and (b) are analyzed separately, beginning with the seed PU, I assessed the neighbouring units (using the algorithm in Appendix G) to see whether they fall within the specified dissimilarity tolerance limits (Figure E.2.1);

- If, the neighbouring unit fall below the threshold (tolerance limit) they are added to the seed unit
- If the neighbouring unit does not fall below the threshold then it is *not* added, and instead determines a boundary for the “place” based on that specific measure of interest

A1	A2	A3	A4	A5	A1	A2	A3	A4	A5
B1	B2	B3	B4	B5	✗	✓	✗	B4	B5
C1	C2	C3	C4	C5	✗	C2	✓	C4	C5
D1	D2	D3	D4	D5	✗	✓	✓	D4	D5
E1	E2	E3	E4	E5	E1	E2	E3	E4	E5

Figure E.2.1. In this hypothetical figure, the planning region is comprised of 25 equal-sized PU. The maximum number of places is one, and the seed unit (yellow; left panel) had been identified by its high composite score. Analysis with the algorithm (right panel) reveals units that fall below the tolerance thresholds (green checkmark) for the measure of interest (a) - SAR overlap, and are thus added to the seed unit. PU that exceed the tolerance limit are not included, and instead form a boundary.

3) I then take the next set of surrounding PU and conduct the same tolerance analysis. Again, if a PU falls below the tolerance threshold, they are added to the seed. If not, they determine a boundary of the output seeded by the original PU. This continues until either (1) all PU, within a planning region, have been assessed or (2) boundaries prohibit any further analysis. It is important to note that new PU are being compared to the seed PU always (Figure E.2.2);

✗	✗	A3	A4	A5	✗	✗	✗	✓	✓	A1	A2	A3		
✗		✗	✓	B5	✗		✗		✗	B1		B3		B5
✗	C2		✓	C5	✗	C2			✗	C1	C2			C5
✓			✗	D5				✗	✗				D4	D5
✓	✗	✓	✓	E5		✗			✗		E2			E5

Figure E.2.2. The results of analysis with algorithm for measure of interest (a) SAR overlap, in the hypothetical situation described in Figure E.2.1. The yellow PU the right panel indicate the

list of PU in the planning region that fall under the tolerance threshold – when compared to the seed.

- 4) The same analysis processes, using the same starting seed PU, is conducted for the second measure of interest (b) average threat distance – the output: a list of PU that fall within the tolerance threshold when compared to the seed unit (Figure E.2.3). Note that tolerance threshold need not be the same between measures of interest but must remain constant throughout the analysis;

A1	A2	A3	A4	A5
B1			B4	B5
C1	C2			C5
D1				
E1	E2	E3		

Figure E.2.3. The results of the analysis described in steps (2) and (3) conducted for the second measure of interest (b) average threat distance. Note that although the tolerance threshold may differ from the first measure of interest (a) the seed PU remains the same and the tolerance threshold for the particular measure of interest is kept constant.

- 5) Because both measures (a) SAR overlap, and (b) threat distance are considered in place characterization, place size is determined by the intersect of the outputs from steps (3) and (4). Only those PU that fall below the tolerance thresholds for BOTH measures of interest are included in a “place” and place size becomes a multiple of the size of the minimum PU (Figure E.2.4)

A1	A2	A3		
B1		B3		B5
C1	C2			C5
			D4	D5
	E2			E5

A1	A2	A3	A4	A5
B1			B4	B5
C1	C2			C5
D1				
E1	E2	E3		

A1	A2	A3	A4	A5
B1	B2	B3	B4	B5
C1	C2	C3	C4	C5
D1	D2	D3	D4	D5
E1	E2	E3	E4	E5

Figure E.2.4. The output of analysis, described by the hypothetical situation in Figures E.2.1 – E.2.3 for measures of interest (a) SAR overlap [left, yellow], and (b) threat distance [middle, blue] and the resultant place size [right, green] as the intersect of the two outputs – at specified tolerance thresholds.

- 6) Steps (2) – (5) are repeated for ALL seed PU at ALL tolerance thresholds (determined in step (1)). In the case of this exercise three tolerance thresholds were analyzed for (a) SAR overlap - 0.15, 0.20, and 0.25 (15%, 20%, and 25% dissimilarity, respectively) and

five tolerance thresholds were analyzed for (b) threat distance – 0.22, 0.24, 0.26, 0.28, and 0.30. As one increases the tolerance for dissimilarity, in one and/or both measures of interest, the size of delineated places increases.

APPENDIX F. GLOSSARY OF TERMS

Candidate Planning Unit (candidate PU) – Planning units adjacent to (1) the seed planning unit or (2) a planning unit that has been added to a place during an analysis. These planning units are analyzed to evaluate if they satisfy the conditions required to be added to a place.

Critical habitat – Under the federal *Species at Risk Act (SARA)*, critical habitat is the habitat that is necessary for the survival or recovery of listed extirpated, endangered, or threatened species, as identified as in a recovery strategy or action plan.⁶

Designatable Unit – It is widely recognised that status assessments and the conservation of biological diversity require that units below the species level (using “species” in the accepted sense of the taxonomic hierarchy) be considered when appropriate. The Species at Risk Act includes “subspecies, varieties or geographically or genetically distinct population” in its definition of wildlife species. This recognizes that conservation of biological diversity requires protection for taxonomic entities below the species level (i.e. designatable units or DUs), and gives COSEWIC a mandate to assess those entities when warranted.⁷

Inter-species threat distance – A measure quantifying the degree of similarity in shared or common threats within a specified set or group of species-at-risk (SAR)

Place – Defined by the FMM as a geographically delineated area whereby a comparatively small set of conservation actions is likely to benefit a comparatively large group of SAR because these actions target common threats

Place-based conservation planning (PBCP) – A type of systematic conservation planning approach that groups species on the basis of spatially explicit attributes. Generally, the approach involves identifying and delineating geographic areas (places) that are suitable for conservation.

Planning Region (PR) – The geographic area within which places are identified and delineated. The planning region defines the geographic scope of analysis.

Planning Unit (PU) – Equally sized, geographic unit of analysis within a planning region; size depends on the scale of analysis and resolution of data; the minimum possible size of a place

Recovery Action – Specific conservation intervention, implemented to reduce or mitigate the effect of processes that limit a species’ ability to persist

Seed Planning Unit (seed PU) – Planning units where the algorithm starts.

Species-at-Risk (SAR) – In this analysis, a distinct population, species’ or subspecies that has been granted extirpated, endangered, or threatened status under the *Species At Risk Act*.

⁶ Definition taken from Environment and Climate Change Canada. Available at: <https://www.canada.ca/en/environment-climate-change/services/species-risk-public-registry/critical-habitat-descriptions/identification-toolbox-guidance.html>

⁷ Definition taken from COSEWIC. Available at: <http://cosewic.ca/index.php/en-ca/reports/preparing-status-reports/guidelines-recognizing-designatable-units>

SAR composition – The set of species-at-risk found within (1) a single planning unit or (2) an aggregate of planning units (place)

Tolerance Threshold – The upper limit for degree of dissimilarity allowed in a parameter of interest

Threat – A process that restricts or limits a species' ability to persist or recovery; i.e. pollution, habitat loss...

APPENDIX G. BRAY-CURTIS DISSIMILARITY AND “PLACE SIZE”

The Bray-Curtis Dissimilarity (BC_d) is an index often used in ecology as a measure of β -diversity as it quantifies the degree of variation, or dissimilarity, in species' composition between two sites of equal area. The general formula is given by:

$$BC_d = \frac{\sum_{n=1} | (X_{ni} - X_{nj}) |}{\sum (x_{ni} + x_{nj})}$$

where i and j are the sites, planning regions, being compared. Note that the Bray-Curtis Dissimilarity assumes equal area and/or volume of sites.

X_{ni} is the abundance of species n at the sites i and;
 x_{nj} is the abundance of that same species n at site j

The index is calculated by summing the differences in species' abundances between sites of interest and dividing by the total abundances at both sites. If a species is absent from a site its abundance is effectively recorded as 0.

The metric produces a measure of dissimilarity between sites of interest. It is bounded, on the lower end, by 0 – signifying 0% dissimilarity in species' composition (presence and abundance). A BC_d value of 0 indicates two identical sites. Conversely, a value of 1, the highest possible value, indicates two sites exhibiting complete dissimilarity in species composition. By setting a threshold for tolerance based on BC_d , we can quantify the degree to which compositional variation is tolerated. Setting low thresholds requires that PU be nearly identical in their SAR communities to be included within a “place.” As the tolerance for compositional dissimilarity increases, PU that share a lower percentage of species will be included in the same “place,” increasing its spatial extent.

APPENDIX H. ALGORITHM (PYTHON CODE)

The algorithm (named polygons.py) below was developed, using Python, for ArcGIS 10.6.1, to iterate through the series of PU, as described in Appendix E, starting with a designated initial seed PU. The process for applying the algorithm is described below:

- (1) To load access to the algorithm, in ArcGIS python window;
import polygons
from polygons import polygons
- (2) Specify the environment – whereby the environment is the location of the cells representing the PU;
Arcpy.env.workspace = "*location of planning unit shapefiles*"
- (3) Set parameters for algorithm;
p = polygons ('X' , 'Y' , 'Z')
p.mainAlgorithm

With the general formula ('X' , 'Y' , 'Z') where:

X represents the seed ID (the starting PU),
Y is the threshold value (when PU are assessed, only those with values that are equal to or fall below this threshold are added to the output list and,
Z is the analysis/ measure of interest being analyzed with (1) for SAR overlap using the Bray-Curtis dissimilarity, and (2) inter-species threat distance using the root mean square distance

- (4) The output is a list of PU that are included in the place, at a given threshold, with a given seed, for a measure of interest.

The algorithm (polygons.py):

```
import random
import numpy as np
import math
import arcpy
```

```
class polygons:
    def __init__(self, seed, thresh, type):
        self.seedList = [seed]
        self.threshold = thresh
        self.type = type
        self.features = {}

    def __getitem__(self, index):
        return self.Matrix[index]

    def __setitem__(self, index, value):
        self.Matrix[index] = value

    def getIndex(self, seed):
```

```

if (len(seed) == 2):
    yCoord = ord(seed[0]) - 64
    xCoord = int(seed[1])
if (len(seed) == 3):
    if (ord(seed[1]) < 65):
        yCoord = ord(seed[0]) - 64
        xCoord = int(seed[1]) * 10 + int(seed[2])
    else:
        yCoord = ord(seed[1]) - 64 + 26
        xCoord = int(seed[2])
if (len(seed) == 4):
    yCoord = ord(seed[1]) - 64 + 26
    xCoord = (int(seed[2]) * 10) + int(seed[3])
# print(xCoord, yCoord)
return xCoord, yCoord

def getStringLiteral(self, x, y):
    if (y > 26):
        yString = "A" + chr(y + 64 - 26)
        # print(yString)
    else:
        yString = chr(y + 64)
        # print(yString)
    # print(yString + str(x))
    return yString + str(x)

def getNeighbourStrings(self, x, y):
    print(self.getStringLiteral(x - 1, y - 1) + " "
          + self.getStringLiteral(x, y - 1) + " " + self.getStringLiteral(
            x + 1, y-1))
    print(self.getStringLiteral(x-1, y) + " " + self.getStringLiteral(x, y)
          + " " + self.getStringLiteral(x+1, y))
    print(self.getStringLiteral(x-1, y+1) + " " + self.getStringLiteral(
            x, y+1) + " " + self.getStringLiteral(x+1, y+1))

def analyzeNeighbourString(self, seed1, x, y):
    if self.getStringLiteral(x-1, y-1) in self.features:
        if self.getStringLiteral(x-1, y-1) not in self.seedList:
            self.analysis(self.seedList[0], self.getStringLiteral(x - 1, y - 1))
    if self.getStringLiteral(x, y-1) in self.features:
        if self.getStringLiteral(x, y-1) not in self.seedList:
            self.analysis(self.seedList[0], self.getStringLiteral(x, y - 1))
    if self.getStringLiteral(x+1, y-1) in self.features:
        if self.getStringLiteral(x+1, y-1) not in self.seedList:
            self.analysis(self.seedList[0], self.getStringLiteral(x + 1, y-1))
    # y row
    if self.getStringLiteral(x-1, y) in self.features:
        if self.getStringLiteral(x-1, y) not in self.seedList:
            self.analysis(self.seedList[0], self.getStringLiteral(x-1, y))
    if self.getStringLiteral(x, y) in self.features:
        if self.getStringLiteral(x, y) not in self.seedList:

```

```

        self.analysis(self.seedList[0], self.getStringLiteral(x, y))
    if self.getStringLiteral(x+1, y) in self.features:
        if self.getStringLiteral(x+1, y) not in self.seedList:
            self.analysis(self.seedList[0], self.getStringLiteral(x+1, y))
# y + 1 row
if self.getStringLiteral(x-1, y+1) in self.features:
    if self.getStringLiteral(x-1, y+1) not in self.seedList:
        # print("analyze",self.getStringLiteral( x-1, y+1))
        self.analysis(self.seedList[0], self.getStringLiteral(x-1, y+1))
if self.getStringLiteral(x, y+1) in self.features:
    if self.getStringLiteral(x, y+1) not in self.seedList:
        # print("analyze",self.getStringLiteral(x, y+1))
        self.analysis(self.seedList[0], self.getStringLiteral(x, y+1))
if self.getStringLiteral(x+1, y+1) in self.features:
    if self.getStringLiteral(x+1, y+1) not in self.seedList:
        # print("analyze",self.getStringLiteral(x+1, y+1))
        self.analysis(self.seedList[0], self.getStringLiteral(x+1, y+1))

def analysis(self, seed1, seed2):
    if (self.type == 1):
        # if (not bool(random.randint(0, 4))):
        r = self.CombineTables(seed1, seed2)
        cent = self.getAllCentroids(r)
        sigmaT = self.calcSigmaT(cent, r)
        print(seed2, sigmaT)
        if (sigmaT <= self.threshold):
            self.seedList.append(seed2)
    if (self.type == 2):
        bcij = self.calcBrayCurtis(seed1, seed2)
        print(seed2, bcij)
        if (bcij <= self.threshold):
            self.seedList.append(seed2)

def mainAlgorithm(self):
    self.features = arcpy.ListFeatureClasses()
    for seed in self.seedList:
        self.analyzeNeighbourString(seed, self.getIndex(seed)[0], self.getIndex(seed)[1])
    print("Final Result List",self.seedList)

def calcCentroid(self, r, index):
    i = 0.0
    tot = 0.0
    for row in r:
        i = i + 1
        tot += int(row[index])
    return tot/i

def calcBrayCurtis(self, seed1, seed2):
    r = set()
    r2 = set()
    # print(seed2)

```

```

rmerge1 = {}
rmerge2 = {}
cij = 0
si = 0
sj = 0
Cursor = arcpy.da.SearchCursor(seed1, ['SpeciesID'])
Cursor2 = arcpy.da.SearchCursor(seed2, ['SpeciesID'])
for row in Cursor:
    r.add(row[0])
for row in Cursor2:
    r2.add(row[0])
rint = list((r.intersection(r2)))
Cursor = arcpy.da.SearchCursor(seed1, ['SpeciesID', 'Proportion'])
Cursor2 = arcpy.da.SearchCursor(seed2, ['SpeciesID', 'Proportion'])
for row in Cursor:
    if (not row[1] is None):
        si += row[1]
    # print(row[0])
    if (row[0] in r.intersection(r2)):
        rmerge1[row[0]] = (row[1])
for row in Cursor2:
    if (not row[1] is None):
        sj += row[1]
    # print(row[0])
    if (row[0] in r.intersection(r2)):
        rmerge2[row[0]] = (row[1])
for ent in range(len(r.intersection(r2))):
    if (rmerge1[rint[ent]] < rmerge2[rint[ent]]):
        cij += rmerge1[rint[ent]]
    else:
        cij += rmerge2[rint[ent]]
# print(cij, si, sj)
return 1 - ((2 * cij) / (si + sj))

def CombineTables(self, seed, seed2):
    r = set()
    r2 = set()
    r3 = set()
    Cursor = arcpy.da.SearchCursor(seed, ['SpeciesID'])
    Cursor2 = arcpy.da.SearchCursor(seed2, ['SpeciesID'])
    for row in Cursor:
        if (not row[0] is None):
            r.add(row)
    for row in Cursor2:
        if (not row[0] is None):
            r2.add(row)
    for rowset in r.difference(r2):
        # print(r.difference(r2))
        expression = arcpy.AddFieldDelimiters(seed, 'SpeciesID') + '=' + str(rowset[0])
        Cursor = arcpy.da.SearchCursor(seed,
['SpeciesName', 'SpeciesID', 'IUCN1_RCD', 'IUCN2_AG', 'IUCN3_EPM', 'IUCN4_TSC', 'IUCN5_BR

```

```

U','IUCN6_HIM','IUCN7_NSM','IUCN8_IOP','IUCN9_POL','IUCN10_GE','IUCN11_CCSW' ],
where_clause = expression)
    for row in Cursor:
        # print(row)
        if (not row[1] is None):
            r3.add(row)
    for rowset in r2.difference(r):
        # print(r2.difference(r))
        expression = arcpy.AddFieldDelimiters(seed2, 'SpeciesID') + '=' + str(rowset[0])
        Cursor = arcpy.da.SearchCursor(seed2,
['SpeciesName','SpeciesID','IUCN1_RCD','IUCN2_AG','IUCN3_EPM','IUCN4_TSC','IUCN5_BR
U','IUCN6_HIM','IUCN7_NSM','IUCN8_IOP','IUCN9_POL','IUCN10_GE','IUCN11_CCSW' ],
where_clause = expression)
        for row in Cursor:
            # print(row)
            if (not row[1] is None):
                r3.add(row)
    for rowset in r.intersection(r2):
        expression = arcpy.AddFieldDelimiters(seed, 'SpeciesID') + '=' + str(rowset[0])
        expression2 = arcpy.AddFieldDelimiters(seed2, 'SpeciesID') + '=' + str(rowset[0])
        Cursor = arcpy.da.SearchCursor(seed,
['SpeciesName','SpeciesID','IUCN1_RCD','IUCN2_AG','IUCN3_EPM','IUCN4_TSC','IUCN5_BR
U','IUCN6_HIM','IUCN7_NSM','IUCN8_IOP','IUCN9_POL','IUCN10_GE','IUCN11_CCSW' ],
where_clause = expression)
        Cursor2 = arcpy.da.SearchCursor(seed2,
['SpeciesName','SpeciesID','IUCN1_RCD','IUCN2_AG','IUCN3_EPM','IUCN4_TSC','IUCN5_BR
U','IUCN6_HIM','IUCN7_NSM','IUCN8_IOP','IUCN9_POL','IUCN10_GE','IUCN11_CCSW' ],
where_clause = expression2)
        for row in Cursor:
            # print(row)
            for row2 in Cursor2:
                # print(row2)
                rtuple =
(row[0],row[1]|row2[1],row[2]|row2[2],row[3]|row2[3],row[4]|row2[4],row[5]|row2[5],row[6]|row2[6]
,row[7]|row2[7],row[8]|row2[8],row[9]|row2[9],row[10]|row2[10],row[11]|row2[11],
row[12]|row2[12])
                r3.add(rtuple)
    return r3

def calcSigmaT(self, cent, r):
    SumOverSpecies = 0.0
    totSpecies = 0
    rList = list(r)
    for rEntry in rList:
        s = 0
        for i in range(11):
            s += (rEntry[i+2]-cent[i])**2
        # print(s)
        SumOverSpecies += s
        totSpecies += 1
    # print(SumOverSpecies)

```

```
    return math.sqrt(SumOverSpecies)/totSpecies

def getAllCentroids(self, r):
    cent = {}
    for i in range(0, 11):
        cent[i] = self.calcCentroid(r, i+2)
    return cent

# def braeCurtisDissim(self, seed1, seed2):
#     return braycurtis(seed1,seed2)
```