Alberta Biodiversity
Monitoring Institute

www.abmi.ca

Manual for Estimating Species and Habitat Intactness at the Regional Scale

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Summary

The Alberta Biodiversity Monitoring Institute (ABMI) monitors hundreds of species of vertebrates, invertebrates, plants, lichens and habitat structures at 1656 sites systematically located across the province of Alberta, and at additional targeted sites. One of the main goals of the institute is to provide credible and understandable indices which summarize information on thousands of species and habitat elements to support natural resources management. This document details the statistical methods used to derive reference conditions, and the indices ABMI has developed to assess the intactness (or deviation from reference condition) for individual species, functional guilds, habitat guilds, taxonomic groups and habitat features. The methods presented here are continuously in revision, and updated versions of this document will be released periodically.

1. Background on ABMI

The Alberta Biodiversity Monitoring Institute (ABMI) was initiated in 1997 through a broad partnership of industry, government, and academia. ABMI is tasked with providing an effective way to track status and change to biodiversity at local, regional and provincial scales, and provide relevant and objective information to policy-makers, scientists, and the general public.

The institute collects information on thousands of terrestrial and aquatic species (mammals, birds, fish, invertebrates, vascular plants, lichens, bryophytes, mites, and aquatic macro-invertebrates) and habitat structures at 1656 sites spaced systematically on a 20-kilometre grid across the entire province. Each of the 1656 sites is sampled once every 5 years using a set of scientifically reviewed protocols. The same protocols are used in additional "off-grid" sites targeted to complement the main sites to address species questions, such as the effects of gradients of human disturbance. This standardized data collection is designed to reduce duplication and increase cost efficiency for provincial and regional monitoring commitments, and provide a more complete understanding of cumulative impacts on the environment from multiple industries and human activities.

One of the main goals of the institute is to provide scientifically valid indices of biodiversity intactness for regions within the province and for the entire province of Alberta. These indices identify how the state of biodiversity has changed in comparison to a pre-determined reference condition. All ABMI data (raw species data plus summarized indices) are freely available to everyone through the institutes' website.

This document describes the analysis methods used to estimate species intactness and habitat intactness indices at the regional scale. Species level indices (individual species and species groups), along with important habitat structures, are ABMI's focus because they are the most clearly defined level of biodiversity. However, information is also rolled up to provide indices for species guilds or groups. By focusing on species and guilds, changes in the ecological communities in response to human disturbance is evaluated.

1.1 Information Pyramids

Monitoring biodiversity results in information for thousands of species (Boyd and Murray 2001). This wealth of information leads to difficulty in communicating with public, resource managers, and policy-makers (Cash et al. 2002). To improve management it is necessary to develop integrated measures of biodiversity. Overton et al. (2002) proposed Information Pyramids as a framework for aggregating and simplifying ecological knowledge (Figure 1). In this system, information is integrated into fewer and fewer groups as one "moves up" the pyramid. Each level of the pyramid is expected to be relevant to different stakeholders. For example, scientists might be interested in Level 2 to understand species population trends, while resource managers might be interested in the status of sensitive guilds (i.e. cavity nesters).

Pyramids have high intuitive appeal to both ecologists and decision-makers because they make it easy to communicate and understand the type of data being evaluated and how it is organized. Pyramids demonstrate a bottom up design, where the upper levels of the pyramid are based on

lower levels, and their application is not tied to a particular spatial scale or level of biological organization.

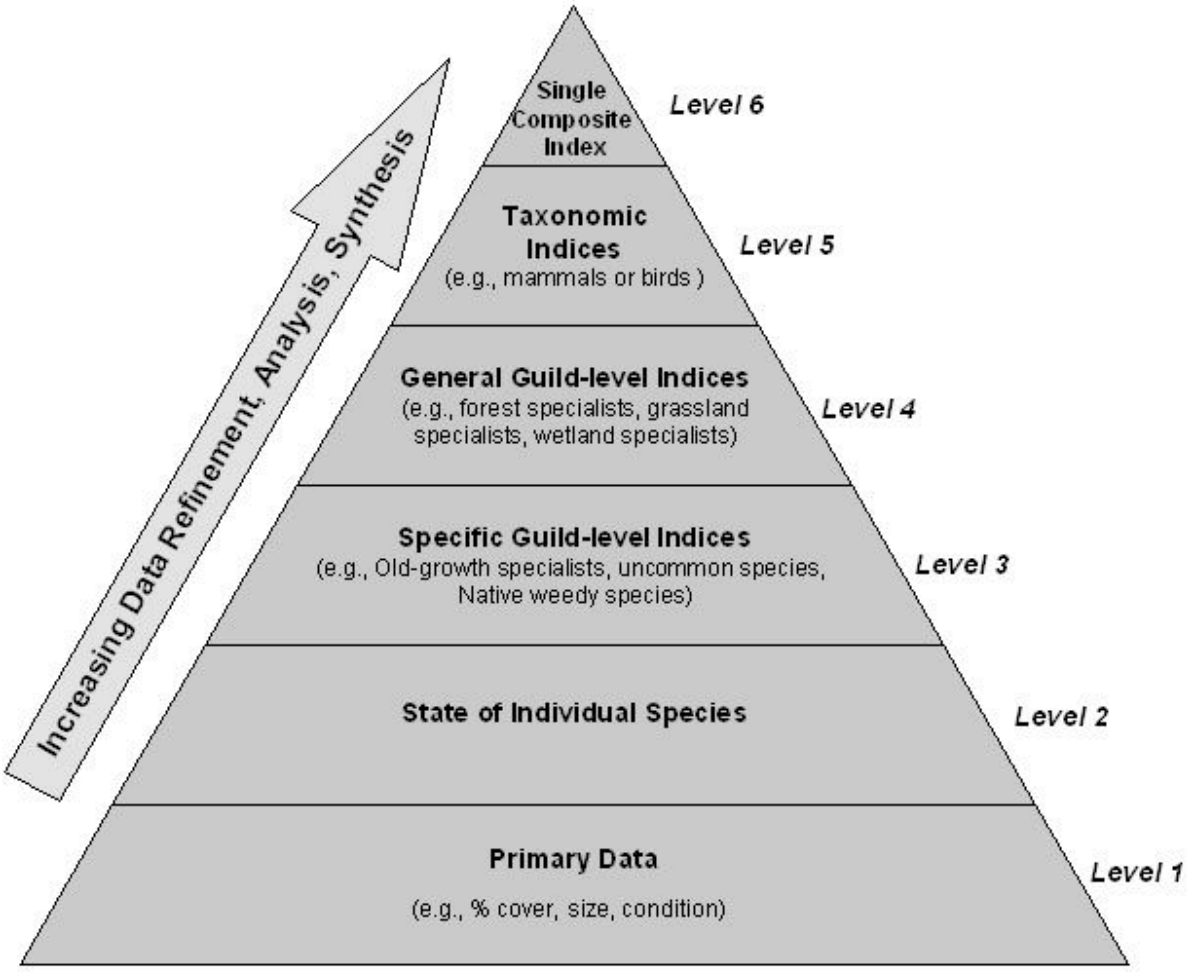

Figure 1. Alberta Biodiversity Monitoring Institute's pyramid for integrating biodiversity indices. Indices can be calculated for any of the levels except primary data (Level 1).

Despite their broad application potential, the use of Information Pyramids is limited by the availability of appropriate data and statistical methodology. Using Information Pyramids as a conceptual framework, ABMI has developed an innovative multi-metric approach for aggregating and communicating ecological data (Figure 1). The Species Pyramid described in this report is designed to support natural resource management at large spatial scales (e.g., >0.5 million ha) using the data collected by the ABMI. We use a comparable pyramid to aggregate information on individual habitat structures.

1.2 Species Pyramid Framework

The Species Pyramid contains 6 levels. The upper levels (3–6) are designed to communicate the state of species groups to politicians, policy-makers, managers, and the public. The lower levels

(1 & 2) are expected to be of interest primarily to scientists and environmental organizations for conducting original analysis, or for evaluating species-level trends. This document details how indices are calculated for each of the pyramid levels. The six levels are described below:

Level 1: contains raw data (e.g., number, size, condition, or location) and forms the foundation for all subsequent data analyses.

Level 2: describes the state of individual species or their reporting equivalent (e.g., subspecies or genera). Level 2 aggregates information from Level 1 into a single metric (*SI*) describing the state of a species. Species indices developed in level 2 form the building-blocks for indices in levels 3, 4, and 5.

Level 3: describes the state of a group of species that share a common characteristic (e.g., habitat, behavioural, or life-history). At level 3 in the pyramid, species can reside in none, one, or more than one guild.

Level 4: describes the state of a group of species that share a common habitat type (e.g., forest, grassland, river, or wetland). Guilds in this level also include "habitat generalists" (species common to two or more habitat types) and "non-native species". Level 4 draws directly from level 2 indices. At level 4 in the pyramid, species can only reside in a single guild.

Level 5: describes the state of a species from a particular taxon (e.g., Division, Class, Order, or Family). Level 5 of the pyramid draws directly from indices developed in level 2.

Level 6: is a single value that describes the state of all species from all taxonomic groups. Indices developed in level 5 (for birds, mammals, bryophytes, lichens, vascular plants, mites and aquatic invertebrates) are combined into a single composite index. The average of level 5 indices is used (rather than taking the average of all species indices from level 2) to ensure that particularly species-rich taxa do not disproportionately influence the level 6 index.

1.3 Objectives

Here, we document ABMI's approach to biodiversity indices at multiple levels of organization. The objectives of this document are to explain how:

1) Reference conditions are calculated for each species and habitat structures.
2) Intactness indices are calculated at the species level and for habitat structures.
3) Indices of intactness for species guilds and composite biodiversity are calculated.

2. Statistical Methods

2.1 Reference Condition

A key step in all monitoring programs is to determine the baseline or reference conditions to which the current state of species is compared. Three methods of determining reference condition have been used: 1) desired or target state, 2) time-zero, and 3) protected areas. In desired state, social values determine reference conditions (Young et al., 2004). This method is unfeasible when dealing with hundreds of species for which little ecological

knowledge exists. Under the time-zero approach, a starting date, often the initiation of the monitoring program, is selected to compare against current and future conditions. Since many ecosystems are already degraded at the start of the monitoring, the time-zero benchmarks do not reflect intact conditions. The last approach, protected areas, is problematic because these areas are rarely representative of all ecosystems, and in Alberta many protected areas occur in remote or high elevation regions with low productivity.

A fourth method has been developed by the ABMI (Nielsen et al. 2007). The relationship between a species' abundance and human footprint can be determined based on statistical modeling of ABMI data. This relationship can then be used to determine the expected abundance of a species with no human footprint by "zeroing out" human footprint. A variety of ecosystem or geographic variables can be included as covariates in the models to increase their predictive ability, thus allowing estimates of reference conditions to differ among vegetation types or locations. This reference condition approach removes statistically detectable effects of local footprint. However, it cannot account for any past changes in the species' abundance that are not due to local footprints, including historical exploitation, effects of diseases or introduced species that are not associated with footprint, climate change or past effects outside the province for migratory species.

Nielsen et al. (2007) provided an example of how a modeled reference condition could be determined using one predictor (linear features). However, there are many types of human footprint in a landscape, and as such we have expanded the modeling framework for the ABMI. We use a multi-model approach to include the cumulative effects of human footprint when determining reference condition.

2.2 Statistical Methods

We model the relationship between abundance of each species and human footprint gradients, with covariates representing ecosystem type and spatial location of the sites, and use these models to estimate expected abundance in current landscapes and landscapes with zero human footprint. Abundance is modelled differently depending on the field sampling method for a particular taxa and the resulting statistical distribution (see Terrestrial Field Data Collection Protocols and Wetland Field Data Collection Protocols on the ABMI website, Standards and Protocols tab).

Count data: Count data (number of individuals detected per site) for aquatic invertebrates and some habitat elements are analyzed with negative binomial models:

$$\Pr(y_i \mid x) = \left[\frac{\Gamma(k + y_i)}{y_i!\Gamma(k)}\right]\left(\frac{LP}{LP + k}\right)^{y_i}\left(\frac{k}{k + LP}\right)^{k} \qquad \textbf{eqn. 1}$$

where $\Pr(y_i \mid x)$ is the probability of observing count y_i, given values of the independent variables x, k is the dispersion parameter, and LP is the linear predictor based on the independent variables x using a log link function (i=1,…,m; m is total number of observations).

Plot occupancy data: Abundance of vascular plants and (as of 2009) bryophytes and lichen species are measured by their occurrence in 0 to 4 of 4 quadrats per site, and snow-tracked mammals by their occurrence on 0 to 10 1000-m transect segments per site. Prior to 2009, bryophytes and lichens were measured as presence/absence at the site. Due to concerns about repeatability of counts of individual bird species at point count stations, bird analyses now also use plot-occupancy data, using a 0-9 score for each site based on detections at 0-9 of 9 stations. Although we have counts of mites, we also analyse them as 0 to 4 occurrences in the 4 traps per site, due to the extreme aggregation of some species. Total abundance for these groups is analyzed with a binomial count model:

$$\Pr(y_i \mid x) = \binom{n}{y_i} \bullet p^{y_i} \bullet (1-p)^{n-y_i} \qquad \textbf{eqn. 2}$$

where $\Pr(y_i \mid x)$ is the probability of observing count y_i (0-n) in the n quadrats/segments, given values of the independent variables x, and p is a logistic function of the independent variables x. Covers of vegetation layers and ground substrates are also analysed with a binomial model.

Mammal transects: Data along the linear 10-km mammal snow-track transects is recorded as species occurrence in 250m segments. An older method from the pre-2005 prototype period used triangles with 3-km sides, with presence/absence recorded for each 1-km segment. In order to make data collected from the two methods compatible, we analyse footprint relationships for mammals using binomial presence/absence on 1-km segments (collating four adjacent 250m segments for the linear transects). To recognize the dependence of segments in a transect or triangle, we include a random effect intercept for each transect or triangle, and we use the transect or triangle as the resampling unit for bootstrapping error estimates (see below).

Wetland plants: Unlike upland sampling, sub-transects for plants in wetlands are stratified by wetland zone (open water, emergent vegetation, fen and upland margin). Sampling is not necessarily directly proportional to the area of each zone. To make these subsamples representative of the wetland site, they are treated as a stratified sample, and weighted in proportion to the area of each wetland zone (example in Table 1). The stratified count is then used in a binomial regression, with the total number of subtransects at a site used as the number of trials.

Table 1. Example of calculating a stratified count for a wetland with 3 zones that were not originally sampled in proportion to their area. The site would be analysed as having 5.16 occurrences of the species on 20 sub-transects ('trials').

				Weighted by zone area	
Zone	Subtrans.	Occupied	% Area	→Subtrans.	→Occupied
A	3	2	10	2	1.33
B	7	1	50	10	1.43
C	10	3	40	8	2.40
				20	5.16

2.3 Human Footprint Gradients

ABMI categorizes human footprints into five broad types (Agriculture, Forestry, Industrial Resource Extraction, Urban/Rural Development and Linear Features), eight discrete categories (Table 2), and many finer types.

Table 2. Eight broad footprint categories.

Broad type	Category
Agricultural	1. % area converted for crops and accompanying cultivation
	2. % area converted for pasture
Forestry	3. % area with clear-cut timber extraction
	4. % area with partial retention timber extraction (>20% retention)
Industrial Resource Extraction	5. % area converted for industrial activity with a low density of people (i.e. surface removal: mines, pump stations, well pads, or industrial: refineries, factories, pulp & paper mills)
Urban/Rural Development	6. % area converted for human use with a high density of people (permanent residences, seasonal homes, work places, and related activities like malls, parking lots)
Linear Features	7. % area converted for linear features that are paved or gravel (highways and logging roads)
	8. % area converted for linear features that are grass or natural vegetation after disturbance (pipelines, skid roads)

The location and extent of human footprint at each site is determined from digital Alberta Vegetation Inventory (AVI) and Grassland Vegetation Inventory (GVI) data verified and updated with SPOT data from the available time closest to the sampling date. Footprint is summarized at 4 spatial scales (centred on the site centre): 1) 1-ha square, matching the main central plot, 2) 150m radius circle around each bird point count station, 3) 500m radius circle encompassing all 9 bird point counts, and 4) a 1km* 1km square. Similar information is summarized from a 500m band along mammal tracking transects (250m on each side of the transect). For intactness analyses, we use footprint variables measured at the scale considered most appropriate to the sampling design and biology of the species, currently 1-ha square for plants, lichens, invertebrates and habitat structures, the combined 150m-radius circles around the 9 count stations at a site for birds, and a 250m buffer for mammal transects.

For plants and invertebrates measured in wetland sites, footprint is recorded for a 250m-wide buffer around the open water of the wetland. Intactness for these taxa is therefore assessing the effects of adjacent landuse of the aquatic organisms. We do not currently have direct measures of human impacts in wetlands, because these are typically not visible (fertilizers, pesticides, grazing).

In the long term, ABMI will construct models using these 8 types of human footprint or finer subdivision within some of the 8, and various interactions. With the sites that have been sampled to date, however, there is limited information on some types of human footprint. The available footprint mapping also cannot reliably distinguish urban/rural development from

industrial sites. As a result, we combine the types in a variety of non-exclusive categories, such as:

1) Agriculture (types 1 and 2)
2) Forestry (types 3 and 4)
3) Urban/rural/industrial (types 5 and 6)
4) Hard linear features (type 7)
5) Soft linear features (type 8 above)
6) Successional disturbances which retain native vegetation (types 3, 4 and 8)
7) Alienating development which removes vegetation and disturbs the soil (types 1, 2, 5, 6 and 7)
8) All linear features (types 7 and 8)
9) Non-agricultural alienating features (types 5, 6 and 7)
10) Total human footprint (all eight types)

Different sets of these footprint classes are used in different analyses, depending what types the available data support recognizing. Footprint variables are expressed as a percentage of the site area, but not otherwise transformed, because our expectation is that there will be an approximately linear effect of footprint on many species over much of the footprint gradient.

2.4 Model framework for footprint relationships

For each species, several multiple regression models are created with the human footprint categories, and analysed in an AIC-based multi-model framework. General additive models (GAMs) are used, because they allow flexible spline relationships and the different error distributions. All models include all types of footprint, but grouped in the different ways listed above. For example, one model in the set may include only total human footprint, another alienating + successional, a third agriculture + non-agricultural alienating + successional, and the most complex model agriculture + forestry + urban/rural/industrial + hard linear + soft linear. Interactions among footprint types may be included where there are sufficient sites to support this, generally a sufficient number of sites that have >20% of two footprint types at the scale of analysis. We try to use the same set of models for each taxonomic group within a region, but different sets are sometimes necessary because of the footprint gradients have been sampled differently for different taxa – due either to the different scale for birds and mammals compared to other taxa, or to fewer sites for taxa where surveys began more recently.

Relationships with the gradient of footprint levels are represented by splines of limited flexibility, usually 3 or 4 equivalent degrees of freedom. The splines allow the relationships to be non-linear, including maximum or minimum values at intermediate footprint levels, which could represent local edge effects. Importantly, the splines also allow approximately linear relationships on the probability or count scale, even though the analysis is conducted using log or logit links.

All models include covariates for vegetation types or soils (section 2.5) and spatial gradients. An initial set of models is typically used to determine the best way to combine vegetation types for

each species. These vegetation type models will include, for example, combining versus keeping separate different forest types, or different broad age classes within forest types. Analyses for particular areas, like a forest management area or the oil sands area include models with interactions between the area and major footprint types, to capture any distinct effects of footprint in the target region. Analyses using 1-km segments of mammal snow-track data include a random intercept effect for each transect.

Note that in this modeling approach, footprint relationships are treated as an additive effect (on the logit- or log-scale). That is, the predicted value of a species at a site with no footprint is determined by the ecosystem and spatial covariates, then that value is modified based on the levels of the different footprint types. The footprint effect is the same, on the logit- or log-scale, for any ecosystem type. We will assess that assumption as enough sites are surveyed to provide full footprint gradients in different ecosystem types.

Models are fitted for all species with detections at a minimum number of sites. Typically species must be detected at ≥15 sites for forest regions, or ≥10 sites for grasslands (which have fewer footprint types and simpler spatial models). The minimum number may be higher when interaction terms are included in the modeling. Species with marginal numbers of detections are sometimes excluded when a majority of the footprint models fail to converge.

Because we require these minimum numbers of detections and we have many species of interest, we fit the footprint models using the datasets from large regions, such as the entire boreal. We use those regional models when we are making predictions for smaller subregions, effectively assuming that the same footprint relationships apply in the smaller subregions (unless we specifically add models with interactions between subregion and footprint).

2.5 Ecosystem types

Ecosystem type is expected to have an effect on abundances of many species, and is included as a covariate in all models. In forested sites, we use a combination of province-wide mapping of broad vegetation types (conifer, deciduous, mixedwood, shrub, grass, wetland, water, barren), a separate layer that delineates wet areas based on several sources and allows us to distinguish lowland forests, a provincial pine layer that lets us separate pine from other upland conifers, and age information from the Alberta Vegetation Inventory (available for ~2/3 of our forested plots) and fire history maps. We use broad age classes for forest (0-40yr, 40-100yr, >100yr). The vegetation types, including age classes, will be refined as further mapping is available, and more sites are surveyed to support estimating more classes.

In the grasslands and parklands, ecosystem types are represented by soil types, classified for each site based on regional soil mapping. Soil types are summarized as loamy, sandy, silty, clay, hardpan, subirrigated and open water.

If the central 1-hectare plot is in open water, the site is omitted from analyses for taxa sampled only in that central plot (i.e., everything except birds). Sites with open water at 5 or more of the 9 point count stations are omitted from bird analyses.

We have not yet developed ecosystem covariates for the wetland analyses, although preliminary analyses showed that surrounding forest type had an effect on biota in boreal wetlands.

2.6 Spatial Distribution of Sites and Subregions

The spatial distribution of sites is included in ABMI intactness models using smoothing splines. Controlling for spatial patterning helps to identify footprint relationships more accurately, removes confounding relationships between human footprint and geographical location, and improves estimation of the precision of relationships. Spatial location is also included in ABMI calculations for user-defined subregions since these are not random samples of the entire dataset, and spatial patterns in species abundances might otherwise be confounded with real responses to human footprint because of geographic trends in human footprint.

For analyses that are conducted for specific subregions, such as large forest management areas (FMA's), additional models that incorporate the subregion as a factor may be added (i.e., whether a site is in or out of the designated subregion). These subregional models may also include hypothesized interactions between footprint variables and subregion to assess effects of management actions that are subregion-specific (e.g., forestry effects that differ inside and outside a large FMA).

2.7 Using sites with more than one visit

Some sites are surveyed more than once within the 5-year sampling interval in order to assess year-to-year variation. These repeat samples are included in intactness models but weighted by the number of repeats (1/n; in other words, each site has the same overall weighting even if some sites include data from more than one survey). During bootstrap analysis (see below), the site is treated as the unit of resampling, such that data from all surveys at a site are resampled together.

2.8 "Off-grid" sites

In addition to the 1656 sites on the systematic grid across the province, ABMI samples many "off-grid" sites. These sites are chosen to complement the systematic sites for the purpose of addressing specific short-term questions, and are sampled with the same protocols as the main sites. A main objective underlying the choice of off-grid sites surveyed to date has been to improve sampling coverage along the gradient of human footprint levels for improved estimation of species-footprint relationships. Off-grid sites have therefore been focused on the end of the footprint gradient that is less common in a region: high footprint sites in the boreal and foothills region, and low footprint sites in the grasslands and parklands. Effort is made to find sites satisfying these conditions while also being widely distributed and representative of the ecosystem types in a particular region (although this is not always possible). Some off-grid sites are chosen to target underrepresented footprint types, such as large industrial sites, or address specific management questions, such as the rate of species recovery in older cutblocks. Because we calculate reference and current abundances of species using complete maps of the region of interest (next section), our intactness results are not affected by the fact that the off-grid sites are not a representative sample of the footprint in the region.

2.9 Calculating predicted reference and current abundance

Reference and current abundances of each species are predicted for each quarter-section (~64ha square) in the region of interest. This gives a complete sample of the footprint across the region,

and which vegetation or soil types and geographic locations it occurs in. Although intactness is intended as a regional index, the use of quarter-sections also allows us to map predicted reference and current abundance of species, and intactness at the quarter-section scale. The 64-ha quarter-sections are larger than the 1-ha analysis units for all taxa except birds and mammals, which combines with our use of non-linear models to create an issue with "downscaling" (next section).

To make the predictions of reference and current abundance at each quarter-section, the AIC_c value (Burnham and Anderson 1998) and associated Akaike weight are calculated for each model. These weights are then used along with each model's prediction under conditions of zero human footprint to calculate the reference condition and with the current footprint to calculate the predicted current abundance. In this procedure, all candidate models are incorporated, with stronger models having more influence on the estimate than weaker ones. This procedure requires information on what vegetation types used to be present in areas with current footprint. We use a "back-filling" procedure that fills in footprint based on adjacent vegetation types and a set of rules about where habitat-specific footprint types (forestry, agriculture) are most likely to occur. Back-filling is not necessary in the grasslands and parklands, where footprint is most extensive, because there we use soil types as the ecosystem covariates, and these are mapped for all areas, including footprint.

The biodiversity intactness index (see details below) compares this predicted reference abundance with the abundance expected given current footprint at the sites. For the current value, rather than using the observed species counts at a site, we use the multi-model prediction for each quarter-section when the footprint variables are set to *their observed levels*. This is done for 3 reasons:

1) Measurement error is large for single counts, and substantial even across multiple sites in a subregion. We do not want to compound true footprint-caused species differences and the effects of measurement error.
2) The reference condition is calculated using regression models with a link function (log or logit). The observed condition also needs to be calculated with this link function, to avoid differences due simply to different types of scaling (parallel to the difference between arithmetic and geometric means).
3) This allows us to do the calculations using quarter-sections that cover the entire area of the region, rather than just the small subsample of the area where we have ABMI sites with the direct counts.

Once data from the planned re-surveys of sites become available in the future, additional terms will be added to the models to allow the overall abundance and footprint relationships to differ between initial and subsequent sampling periods. The predicted abundance for the second (or later) measurement cycle can therefore be greater or less than the abundance predicted from footprint alone. Intactness calculations after a second set of samples is begun will include both the footprint effect and any additional changes in the species. This will allow us to attribute changes in species abundances to both the effects of changes in human footprint and other changes unrelated to footprint.

2.10 Downscaling

We fit footprint models for all taxa except birds and mammals with data for the 1-ha plots. These models include non-linear footprint relationships. We apply the models to quarter-sections (~64ha) for mapping. (We can't apply the models to each 1-ha unit across the province because of computer limitations.) This change in scale can bias our predicted current abundances at intermediate footprint levels when there are non-linear footprint relationships (Figure 2).

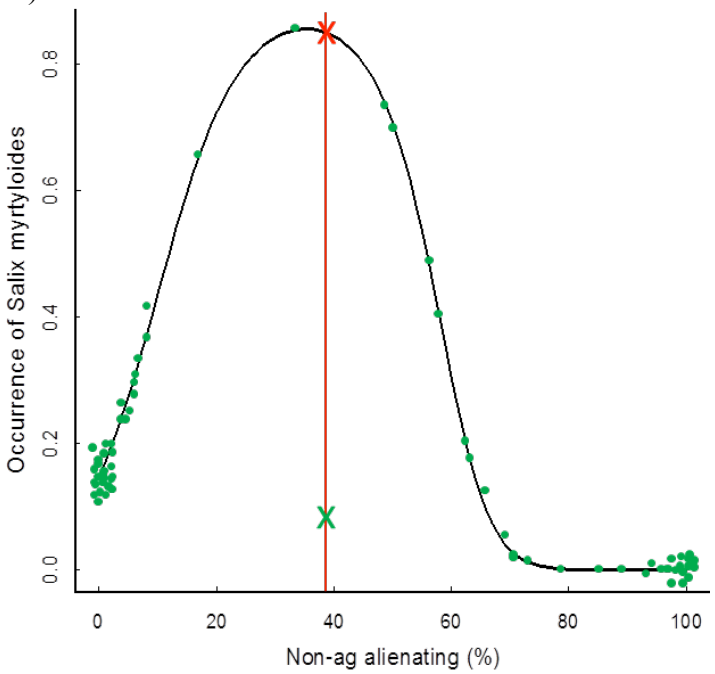

Figure 2. How applying 1-ha scale models to 64-ha quarter-sections can bias predicted current abundance. In the example, the red X is the species' naively predicted abundance in a quarter-section at 38% footprint. However, that quarter-section is actually composed of 64 1-ha units, most of which have nearly 0 or nearly 100% footprint. The green points are the predictions for each 1-ha unit. The green X is the average of those predictions for 1-ha units, which is the correct prediction for the quarter-section.

To address this problem, we also apply the footprint models to one 1-ha unit within each quarter-section, so that we have predicted current abundances at a large number of pairs of 1-ha units and quarter-sections. We then calculate the difference in the predicted current abundance between the two scales on the logit scale. We model this scale difference as a multiple regression with different footprint types (e.g., for the boreal, third-order polynomials of successional and alienating footprint, and a second-order polynomial of linear features). This downscaling model is then used to predict the difference between the 1-ha scale and quarter-section scale abundances for each quarter-section, which is used to adjust the quarter-section scale abundance to the expected value for the 1-ha scale. The corrected ("downscaled") current abundance is then used along with the reference value (which doesn't have this issue since there is no footprint involved) to calculate intactness.

As an example, sarsaparilla (*Aralis nudicaulis*) shows a modestly non-linear response to successional footprint, and a close to linear response to alienating footprint. As a result, the 1-ha

scale predicted abundances at intermediate successional footprint are somewhat higher than the quarter-section scale abundances (because the low and high end of the footprint relationship are higher than the middle) (Figure 3). There is little scale difference with alienating footprint. Predicted abundances at intermediate successional footprint on the quarter-section scale would therefore be adjusted upward to down-scale to 1-ha scale abundances.

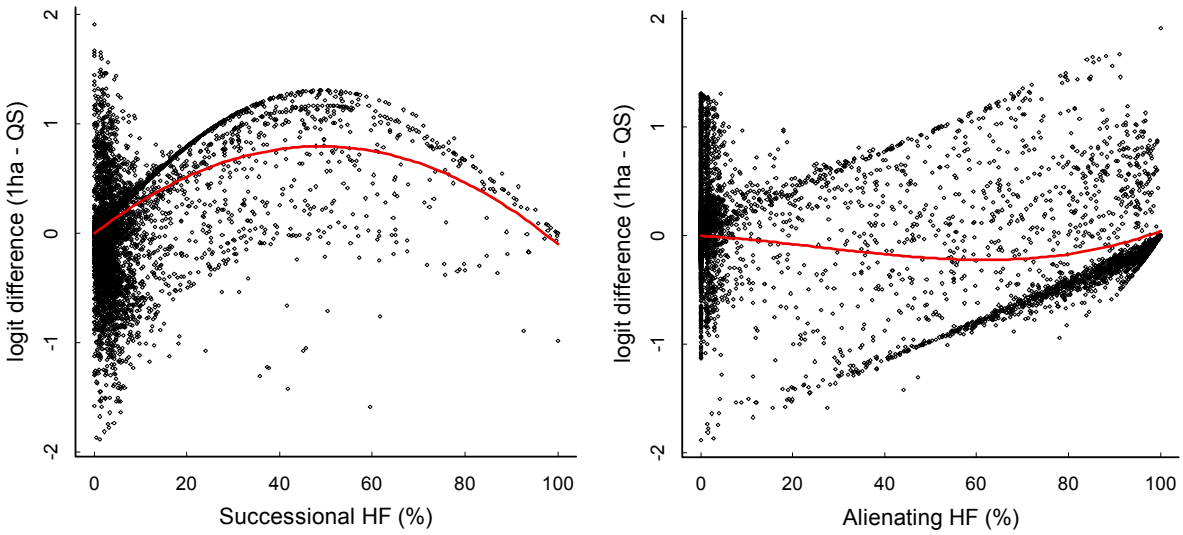

Figure 3. Example of down-scaling relationship. Logit-scale difference in predicted current abundance at 1ha versus quarter-section scale for *Aralia nudicaulis* as a function of successional footprint (left) and alienating footprint (right). The upper and lower bounds in the right-hand figure clearly show 1-ha units with 0% footprint and 100% footprint respectively (these are near each other in the left-hand figure, because of the U-shaped footprint relationship). Scatter at the low end of the y-axis is because of different levels of the other footprint types.

3. Biodiversity Indices

3.1 Species Intactness (based on total abundance)

The species intactness index compares the model-fitted relative abundance of each species across all sites in the province, region or subregion to the predicted abundance for that species under zero human footprint in the same region. This measure of intactness is scaled between 0 and 100, with 100 representing species abundance expected under reference conditions, and 0 representing species abundance as far from reference condition as possible. Both over- and under-abundances are viewed as deviations from intact conditions. The index is estimated as:

$$SI_s = \left[\frac{\min(O_s, R_s)}{\max(O_s, R_s)}\right] \bullet 100 \qquad \textbf{eqn. 3}$$

where SI_s is the species intactness index for species s, O_s the abundance of species s under observed footprint levels, and R_s the predicted abundance for species s under reference conditions. Equivalently, SI_s is O_s/R_s when $O_s<R_s$ ("decreaser" species) and R_s/O_s when $O_s>R_s$ ("increaser" species). A value of 50%, for example, means that the species is either half as abundant as the reference condition, or twice as abundant.

Non-native plants: A different approach is used for non-native plants, which are treated as a disturbance agent, similar to human footprint (see footprint manual). We assume that the reference condition is 0 for these species, then calculate a species' intactness as: SI_s = 100% - percent occurrence of the species. Percent occurrence is calculated at the quadrat (50m x 50m) level. For example, a non-native species that occurred in 20% of quadrats would have an intactness value of 80%.

3.2 Guild Intactness (Pyramid Level 3-5)

Species are combined into guilds at levels 3-5 of the information pyramid. Guild intactness (*GI*) is calculated as the average (simple arithmetic mean) of species intactness for all species in the guild. *GI* has the same scale as *SI,* from 0 for completely degraded conditions to 100 for intact conditions, and measures the average intactness of the species in the guild relative to that expected when the landscape has zero human footprint.

Guilds intactness at level 3-5 of the pyramid, is calculated as:

$$GI_i = \frac{1}{N}\Sigma SI_j \qquad \textbf{eqn. 4}$$

where GI_i represents intactness of guild i, N the number of species in the guild, and SI_j the intactness score for species j.

Note that because the intactness index for individual species decreases from 100% with either downwards or upwards differences from reference conditions, an "increaser" species does not cancel out a "decreaser" species in the guild. Instead, both contribute to lowering the average guild intactness.

We considered many other ways of combining species intactness results, but decided that a simple mean is the most appropriate. Geometric, harmonic or other types of averages have undesirable properties, including giving excessive weight to individual species with extreme values, which were often the most poorly estimated results (for rare or highly aggregated species). Alternatives that weighted species by the precision of their intactness estimate are biased toward common species. More complicated methods that statistically correct for the expected relationship between abundance and precision could be used to remove this bias with precision-weighted averages. However, the loss of transparency and ease of understanding the results was considered to outweigh any possible statistical benefits of such a procedure.

Non-native plants: For non-native species, it does not make sense to calculate an average intactness, because the more rare non-native plant species that are included, the higher the intactness. For example a non-native species that is observed once in a region with 100 sites sampled has an intactness of 99%, and another non-native that is observed at 50 sites has an intactness of 50%. If these intactness values were simply averaged, the first record of a newly invading non-native species would raise the mean intactness, which is not a sensible result. For that matter, potential non-native species that have not yet been detected would have an intactness of 100%, and would raise the average intactness for the overall group even higher. Instead, we calculate the overall intactness of all non-native plants as 100% - percent occurrence of any non-

native species on a quadrat. This value is simply the percent of quadrats on which no non-native species was detected in a region.

3.3 Biodiversity Intactness (Pyramid Level 6)

All of the major taxa being monitored (birds, mammals, mites, aquatic invertebrates, vascular plants, bryophytes, and lichens) are considered equally important measures of biodiversity. As such, biodiversity intactness is calculated as the simple average of the level 5 taxonomic intactness (eqn. 5):

$$BI = \frac{1}{N}\Sigma GI_i \qquad \textbf{eqn. 5}$$

where BI represents biodiversity intactness, N the number of taxa, and GI_i the intactness score for each taxon i at level 5 of the pyramid.

3.4 Bootstrapping and confidence intervals

The sampling distribution of species- and guild-level intactness indices are estimated using bootstrapping, in which the original data are resampled with replacement and the entire analysis repeated 100 times. The bootstrap replicates are used to calculate the median reference condition and confidence intervals (based on percentiles of the 100 resampled values). Bootstrapping is required, rather than an analytical formula, because the current abundances and reference conditions are not independent, and the intactness calculation is complicated for the multi-model approach with different weighting of revisited sites. A blocked bootstrap is used, in which the resampling is done within pre-defined spatial blocks to preserve some of the spatial structure of the sample design. For mammal snow-tracking, the transect or triangle is used as the unit of resampling.

3.5 Multi-species corrections

When results are generated for multiple species, sampling error ensures that estimates of intactness for some species will be higher or lower than the true values. With many species monitored by the ABMI, chance deviations for species with the most extreme intactness values can be substantial. This provides a misleading impression of change, particularly for the most extreme species which are often the focus of subsequent interpretation. Additionally, the intactness index decreases with any deviation, up or down, from the reference condition, so that the effect of chance deviations is to bias the average intactness index downwards. For example, if all species were truly intact, with a score of 100%, some would appear to be below reference condition because of sampling error and some would appear to be above – both situations would produce an intactness less than 100%. A procedure is being developed to correct the intactness estimates for each species when multiple species are analysed (Appendix 1). With this correction, values for individual species can be interpreted directly without having to worry about effects of sampling error exaggerating extreme results, and the corrected values can simply be averaged to calculate the value for guilds, taxa or biodiversity overall, without the downward bias.

4. Habitat Intactness

Intactness analysis for habitat elements is the same as for species, including the multi-model approach, footprint model set and covariates. Counts of discrete habitat elements (trees, snags and logs) in size, species and decay classes are analysed with a negative binomial model. Habitat elements expressed as percent cover are analysed directly with logistic regression models. As with individual species, these analyses provide reference conditions and expected abundances of the habitat elements with current footprint levels.

For most summaries, the results for particular size classes of trees, snags and logs are then converted to basal areas of stems or volume of downed woody debris using the quadratic mean diameter of pieces in each size class. This allows us to combine size, species and/or decay classes into broader habitat variables and ultimately a composite index of intactness of habitat structure. The approach of conducting the analyses on the count data, then converting the resulting reference and current values into basal area or volume, allows us to properly recognize the underlying count-based statistical distribution of the data, while providing intactness values based on basal area or volume which are more familiar to managers and tie in more directly to published habitat requirements for many species.

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Appendix 1. Correcting for effects of error in multiple species' results

When interpreting results, we naturally focus on the most extreme species when many species are analysed (e.g., the strongest trends or the greatest deviations from intactness). However, at least some of that "extremeness" is due to sampling error – even if no species deviated from 0%/yr trend or 100% intact, sampling error would ensure that the most extreme of a group of species would deviate substantially from these null values. The goal in the correction procedure developed here is to adjust estimates of intactness or trend for multiple species to remove the "bias towards extremeness", while retaining results that are truly different from the null values. This correction is particularly important for intactness, where any deviations from reference condition lower intactness scores.

The current approach to correcting results from multiple species uses the bootstrapped distribution of each species' result to calculate the quantile of the null value (100% intact, 0%/yr trend, or alternatively the mean of these values across all species), then compare this observed quantile to the quantile expected from the species' rank under the null model. If the observed and expected quantiles are similar, the species' deviation is no more than expected by chance (given its rank among all species), and the species' result is corrected strongly (see description below) towards the null value. In contrast, if the observed quantile is much more in the tail of the distribution than the expected null quantile, the result shows strong evidence of real deviations from the null, and it is corrected minimally. This procedure preserves species results that deviate strongly from the null, while removing deviations that are no more than those expected from chance alone. The approach is explained for intactness calculations, but will also apply to trend results when these are available in the future.

Details of the approach

1. Bootstrap results are summarized as a parametric distribution: The bootstrap results for each species' intactness on the 0-200 scale are transformed as logit(x/200), then summarized as the mean and SD of a normal distribution. This logit-transformation was efficient at normalizing the bootstrap distributions for species centred near 100% intact and for those away from 100%, as well as for precisely and imprecisely estimated species. It constrains the distribution to be between 0 and 200, and is appropriate for the symmetrical ratio scale of SI.
2. The parametric distribution is centred on each bootstrap result and used to calculate the quantile of the null value (=100% intact) → "observed quantile". For each bootstrap iteration and each species, a normal curve is established centred on the logit-transformed bootstrap value, with the species' logit-scale SD. The quantile of the null value of 100% intact (0 on the logit scale) is then calculated for this normal curve. For example, a value of 90% intact (-0.201 on the logit scale) for a species with a SD of 0.1 on the logit scale would produce a quantile of 0.022. (i.e., 2.2% of the distribution of the logit-normal curve centred on 90% intact, with the observed SD, is >100%). This is the "observed quantile". A small deviation from 100% intact for a very precisely estimated species could produce the same observed quantile as a large deviation for an imprecisely estimated species.
3. The species' quantile for each bootstrap iteration is ranked relative to the other species → "expected quantile". The observed quantile for that species is then ranked relative to the observed quantiles for all the other species in that bootstrap iteration. The null expectation

quantile for the species at that rank is (rank–0.5)/$n_{species}$. [1] For example, if there were 60 species and the example observed quantile of 0.022 was the 5th lowest, its rank quantile would be 4.5/60 = 0.075. For the example species, the results for step 2 and 3 indicate that that species' result is moderately more extreme than the expectation from chance alone for a species at that rank.

Figure A1.1 shows the randomization quantiles and the null expectation quantiles based on rank for 67 bird species from a single bootstrap iteration. If results for all species were just those expected by chance, the points would lie along the dashed red 1:1 line (with some kind of random error). In the example iteration in the figure, about half the decreasers and some of the increasers are very near to the 1:1 line – their results are just those expected if the species were really 100% intact but had variation due to sampling error. A few decreasers and several increasers are a moderate distance from the 1:1 line, suggesting reasonably strong evidence for real deviations, with some additional contribution from the sampling error. Finally, 6-9 decreasers and about 12 increasers are well over an order of magnitude off the 1:1 line, showing deviations that are well beyond those expected by chance, even given the many species being analysed here.

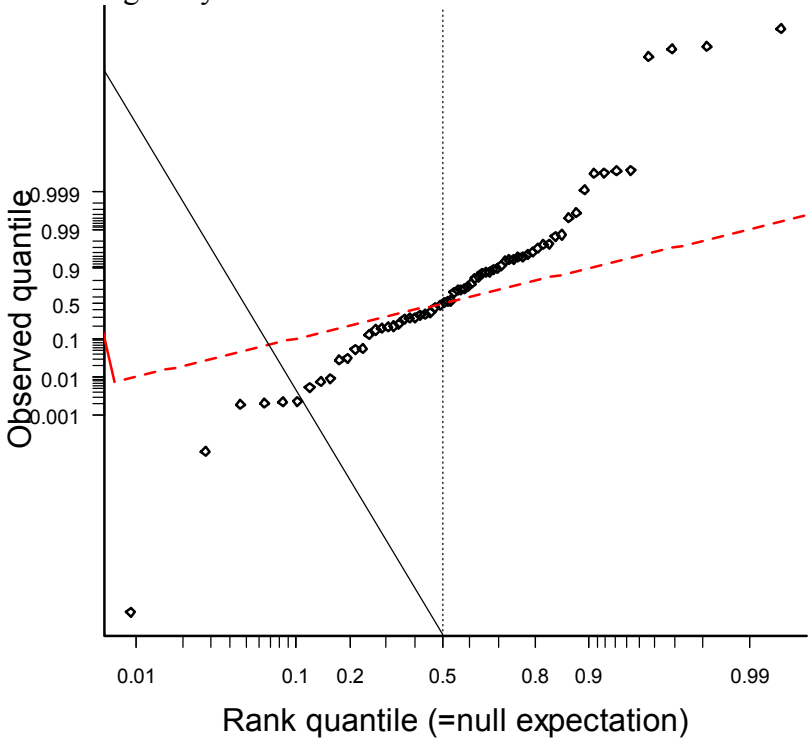

Figure A1.1. Distribution of the observed quantiles versus the null expectation distribution for 67 bird species in 1 bootstrap iteration. Note that the axes are spread out at the ends (logit scale) to show values near 0 and 1 better. The dashed red line is 1:1, the expectation if all species' deviations from 100% intact were purely due to chance.

4. <u>The ratio of observed to expected quantile is used to correct the calculated value towards the null value.</u> The ratio of the observed quantile (0.022 in the example) and the null expectation rank quantile (0.075) is then calculated (0.022/0.075=0.293). For increasers (intactness >100

[1] Because the lowest species by chance would be between its 0/$n_{species}$ and 1/$n_{species}$ quantiles, the second between 1/$n_{species}$ and 2/$n_{species}$, etc. Hence the quantile distribution from chance alone would be 0.5/$n_{species}$, 1.5/$n_{species}$…($n_{species}$-0.5)/$n_{species}$.

on the 0-200 scale; or, equivalently, observed quantile >0.5), 1 minus each quantile is used (i.e., (1-observed quantile)/(1-null expectation quantile), to indicate how far into the upper tail the result is compared to expectation. The observed bootstrap result is then adjusted that proportion of the way towards 100. In the example, the observed value of 90% is adjusted to 92.93 (which is 0.293 of the way from 90% to 100%). This is effectively saying that there is fairly good evidence that there is an effect beyond that expected from chance alone (given the species' rank), but that some of the observed effect is probably due to chance.

This correction approach is ad hoc and does not yet have any strong statistical underpinning, but it is sensible in the extreme cases. If the null of 100% is far in the tails of the bootstrap distribution, the ratio of the observed quantile to null expectation rank quantile will be very near 0, so the observed value stays almost exactly the same – the observed effect is clearly well beyond that expected by chance, even with many species analyzed, so the result is presented as is. At the other end, if a species' result is just where it would be expected by chance given its rank, then it is adjusted all the way back to 100% - there is no evidence that the deviation from intactness is anything more than chance, again given that many species are being analysed. However, there is no particular rationale for why the correction is linear with the quantile ratio between those extremes. This is a focus for future development of the method.

5. The whole procedure is done for each species in each bootstrap iteration, giving a distribution of corrected values for each species. These are then summarized as the median and percentiles, or aggregated into higher guild-level results.

The observed and corrected results for birds for the central boreal (results through 2008) are shown below. A few bird species remain as decreasers with the correction. Note that these are not just the species with the greatest original decreases – precisely estimated species with modest decreases in intactness, like Swainson's thrushes and yellow-rumped warblers, also have corrected estimates of intactness that are less than 100%. Species with similar original intactness estimates are corrected more if they have wider confidence intervals. About 7 species remain as clear decreasers and 20 bird species remain as clear increasers, and these results seem sensible from natural history.

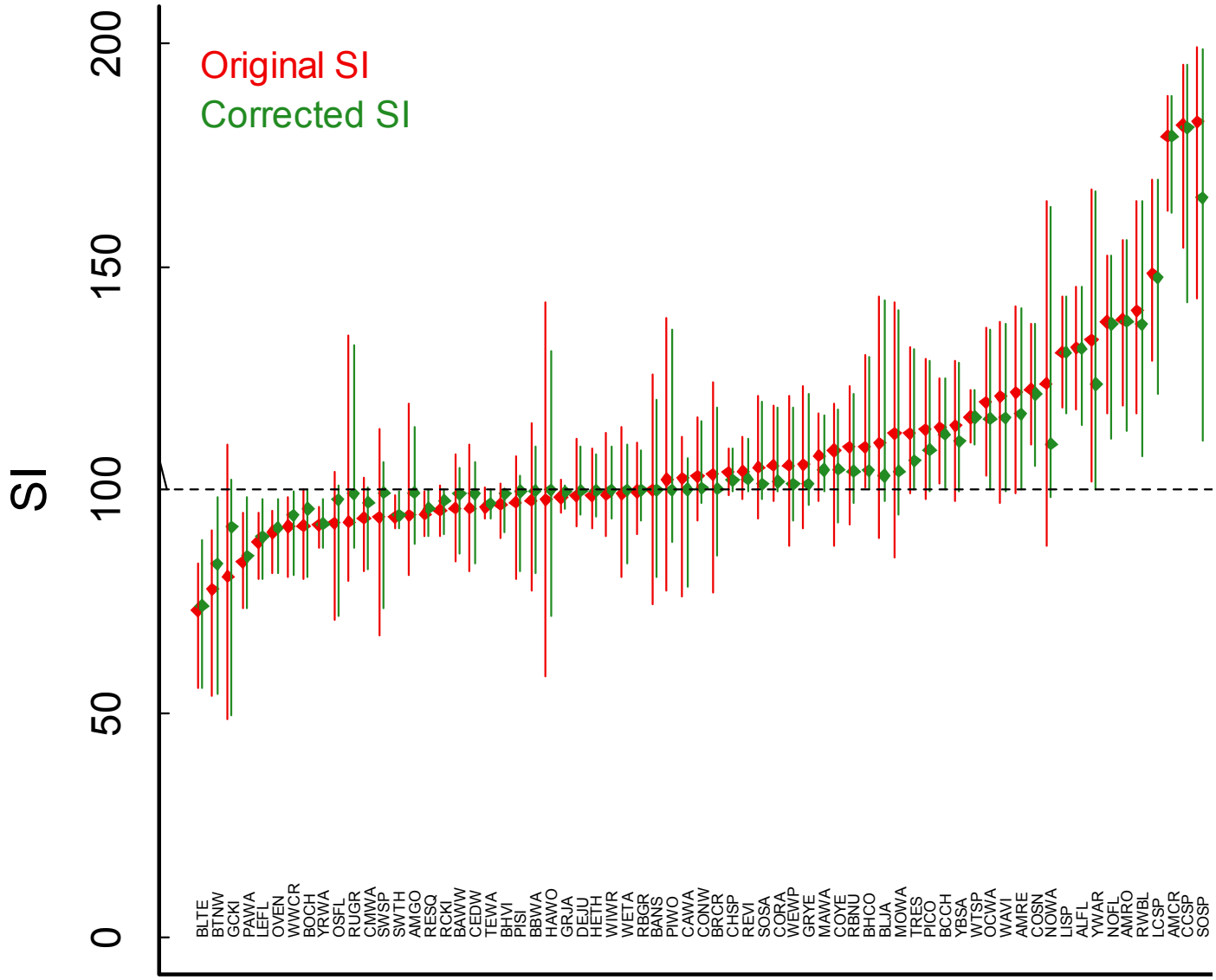

Figure A1.2. Example of original calculated SI and corrected values for 67 bird species in the central boreal region.