



All Taxa

Multiple Species

The ABMI presents three metrics summarizing overall biodiversity—Intactness, Species Richness, Uniqueness—which provide information on the health of biodiversity, the number of species present, and the uniqueness of species composition.

Intactness

To report on the status of biodiversity in Alberta, the ABMI has developed a metric called the Biodiversity Intactness Index. The intactness index, which ranges from 0% to 100%, reflects how modifications to habitat as a result of human activities result in changes to species' abundance. Deviations from intact conditions occur when species become more abundant or less abundant than expected due to habitat modifications. The further the deviation from 100% intact, the larger the impact of human footprint (e.g. agriculture, urban/industrial areas, roads) on species' abundance.

Methods

ABMI's intactness is a measure of how much human footprint has affected species' abundances. We first use habitat models for each species to estimate its relative abundance in the current landbase, and in a reference landbase in which human footprint has been removed and back-filled with the vegetation that was there prior to the footprint. If the species is predicted to be less abundant in the current landbase than in the reference, intactness is defined as $\text{current abundance} / \text{reference abundance} \times 100\%$. An intactness of 80%, for example, would mean that the species is currently at 80% of the abundance expected in the reference landbase with no footprint. If the species is predicted to be more abundant in the current landbase, intactness is calculated as $\text{reference abundance} / \text{current abundance} \times 100\%$. In that case, an intactness of 80% would mean that the species is currently 1.25 times as abundant as expected in the reference landbase ($1/1.25 \times 100\% = 80\%$). Intactness therefore declines as the current abundance differs from the reference abundance, regardless of whether the species is predicted to be less or more abundant currently.

Intactness of birds is simply the average of the intactness of each bird species. Because any difference between current and reference, positive or negative, lowers intactness of a species, species that increase with human footprint do not cancel out species that decrease with footprint.

For intactness maps, we calculate the intactness in each 1 km² pixel covering the province. For tables that summarize intactness for particular regions, we calculate each species' current and reference abundance by summing the 1 km² raster values in the region, then calculate intactness for the species from those totals. Species intactness values are then averaged to give the intactness of the taxon for the region, and the taxa are averaged for biodiversity intactness.

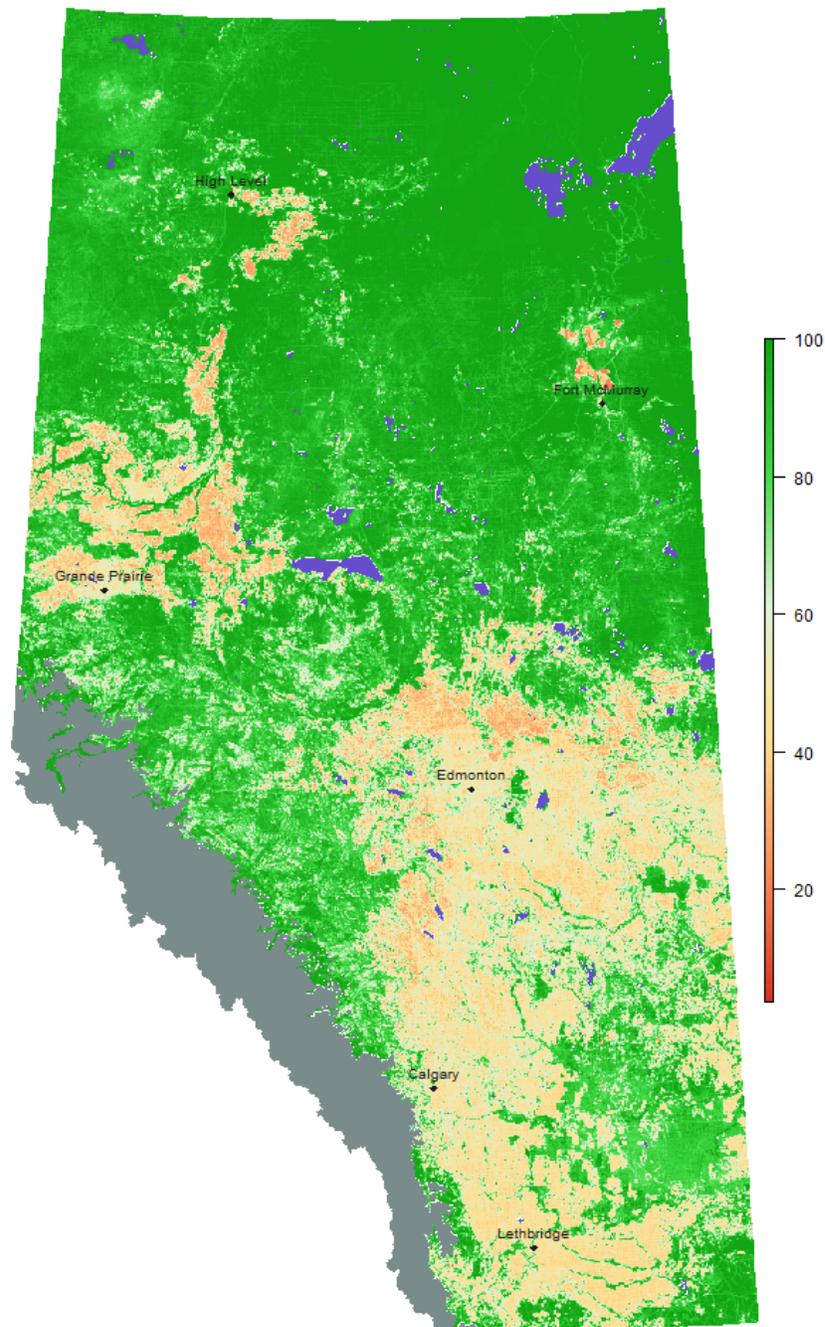
Intactness uses the total current and reference population in a reporting region. One human footprint type can have

a positive effect on a species in a region and another type have a negative effect. These offsetting effects would keep intactness relatively high for that species, even though each footprint type has an effect.

Limitations

Because intactness is based on the models for each species, it incorporates the limitations of those models. However, intactness is an average across many species, making error in individual species' models less important. A main limitation is that intactness is largely a function of human footprint. Maps of intactness are therefore highly correlated with maps of human footprint, regardless of the taxon. Intactness maps differ from human footprint maps only because some footprint types have greater or lesser effects on species in a taxon. Intactness does not show how much species have changed over time because many factors besides habitat change due to human footprint can change species' populations.

Intactness - All Species



Richness

Species richness is simply a measure the number of species within a defined region, and is one of the simplest ways to describe biodiversity (Gotelli and Colwell 2001). The ABMI has created an index of species richness for Alberta, which is a relative measure of the number of **common** native species within each 1 km square area across the province.

Methods

Species richness for each taxon was modelled by stacking predictions from individual species habitat association models. Individual species models were built by relating the species' occurrence data to three sets of environmental variables: vegetation types, human footprint, and geographic location. Using these relationships, the mean occurrence probability of each species was projected for each 1 km² grid cell in the province. The species richness index for each taxon was produced by simply summing these predicted probabilities and scaling the values to range between 0 and 1 by dividing each 1 km² grid cell value by maximum value over all grid cells. For birds, relative abundance was rescaled to probability as $1 - \exp(-\text{abundance})$, the probability of > 0 abundance in a 1 ha area.

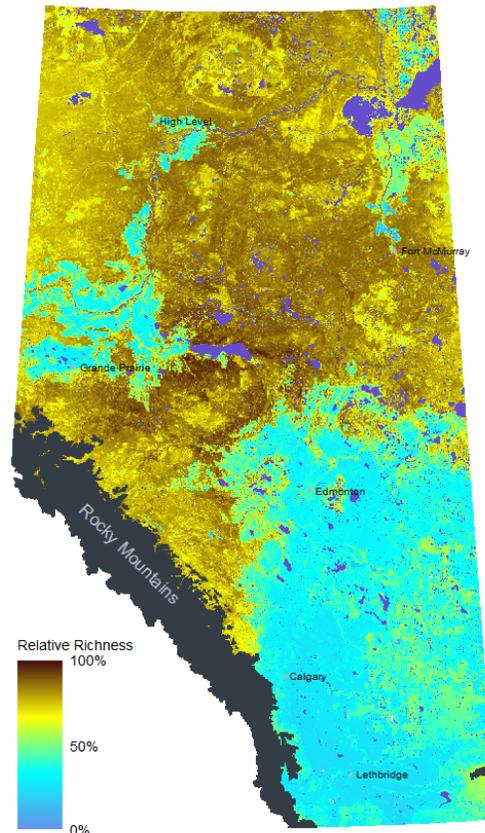
Limitations

The index of richness does not adjust for multiple habitat types occurring within each 1 km² grid cell. For each species probability of occurrence was modeled for each habitat type, and an area-weighted average across habitat types determined for each 1 km² grid cell. By summing across species an index of richness was determined. This estimate was really just the average of point richness throughout each 1 km² grid cell, and did not incorporate the fact that most 1 km² grid cells span multiple habitat types and thus have higher richness than any single type alone, or having higher richness due to edge effects. However, a 1 km² grid cell dominated by habitats having relatively high richness will have higher index than a 1 km² grid cell dominated by habitats with low richness.

Rare species were not included when determining the index of richness. ABMI only models species habitat associations for species that have sufficient data to create robust models. Since the index of richness was created from the species models, the index only includes species with more than the minimum number of detections. It is possible that there are some habitat types may have a disproportionate number of rare species (e.g., possibly some wetland types) and our index of richness that does not incorporate rare species does not capture this.

Spatial irregularities in sampling intensity influence the index of richness. In regions with higher intensity of ABMI surveys, more species will have reached the minimum number of detections required for modeling, and thus more species will have been included in the index of richness. ABMI sampling intensity has been relatively low in the Rocky Mountain natural region, and in northwestern Alberta. Thus, species that are most commonly found in these regions will be less likely to have been included in the index of richness and 1 km² grid cell in these regions may have artificially low indices of richness.

Species Richness of All Taxa
(species common enough to analyse)



Uniqueness

Measuring and mapping biological uniqueness is one way to show similarities and differences in species composition among areas within a defined region. The ABMI has developed a relative index of uniqueness for each Natural Region in Alberta; the index identifies the degree to which species composition in a one km square area is distinct compared to all other pixels within the Natural Region. The uniqueness analysis was conducted separately for each Natural Region because the regional species pool, and their predicted relative abundances differ between these. Relative abundance of each species in each pixel was predicted using habitat association models that relate species abundance to native habitat types. The uniqueness index was calculated based on species co-occurrence (see methods).

Uniqueness of species composition in space is a relative measure and values estimated for specific sites are partly dependent on the scale of study. For example, a given area might be regarded less unique in a relatively homogeneous subset area where it is found but that particular subset area could have high uniqueness compared to a larger scale of study.

Methods

The relative uniqueness measure shows the degree to which species composition in each pixel was distinct compared to all other pixels within the Natural Region. The uniqueness analysis was conducted separately for each Natural Region because the regional species pool and their predicted relative abundances differ between these. Relative abundance of each species in each pixel was predicted using habitat association models that relate species relative abundance to native habitat types. The uniqueness index was calculated based on two patterns of distribution in relative abundance of species: (1) the co-occurrence pattern among species pairs (species dissimilarity matrix) in the region and (2) the degree to which the relative abundance of species was clumped in the region. The species

uniqueness for a given pixel in a region was calculated as:

$$SU_k = \sum_{i=1}^{s-1} \sum_{j=i+1}^{s-1} d_{ij} \sqrt{p_{ik} p_{jk}}$$

where SU_k is the uniqueness value for pixel k , d_{ij} is the dissimilarity between species i and j in the natural region, and p_{ik} and p_{jk} the proportion of species i and j in site k . The species pairwise dissimilarity matrix was calculated using the relative abundance of species in the region and based on Bray-Curtis dissimilarity index. The relative abundance was standardized to species maximum so that rare and common species were equally weighted.

In general, highly restricted species (i.e., species with a patchy distribution) were less likely to occur with other species than were common or widely distributed species. This results in restricted species having relatively larger distance in the species pairwise association matrix. Moreover, by being restricted to a few places, most of the species regional population for a clumped species was concentrated in a few places resulting in the regional abundance of these species being relatively higher in the localities where they occur. The relative uniqueness index for a given locality was calculated by multiplying the distance between all species pairs and their respective regional proportion in the locality, and summing the products for all species pairs in the locality.

Limitations

The uniqueness of species composition is a relative measure and values estimated for specific sites are partly dependent on the scale of study. For example, a given area might be regarded less unique in a relatively homogeneous subset area where it is found but that particular subset area could have high uniqueness compared to a larger scale of study.

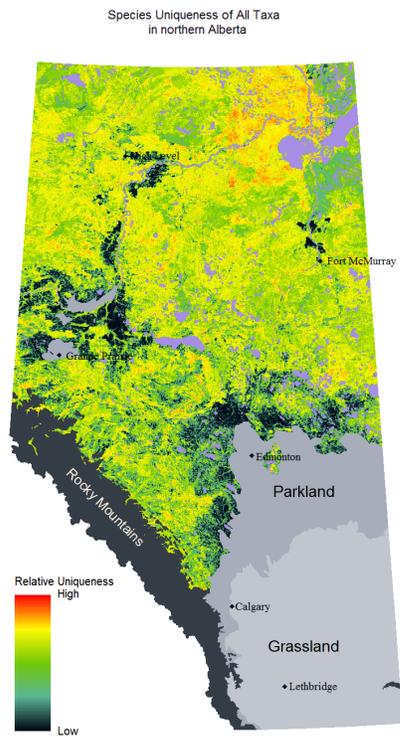
The index of relative uniqueness is not comparable across natural regions. For each taxon, relative uniqueness was estimated for each 1km² grid cell in each natural region, and values were rescaled to 0-1 range by dividing the value by the maximum of all values in the region. Since the maximum values differed among regions, the index was scaled differently among regions and thus is not comparable among different regions. However, the maximums were similar among forested regions (Boreal, Foothills and Shield natural regions), and for the non-forested regions (Parkland and Grassland natural regions). Thus, results have been presented separately for forest and non-forest regions.

The data for uniqueness is based on predictions made using native habitat only. The species habitat association analysis was conducted using native habitats only. This means that the role of other environmental (eg., climate) and spatial variables (e.g., latitude/longitude) were not incorporated in the index.

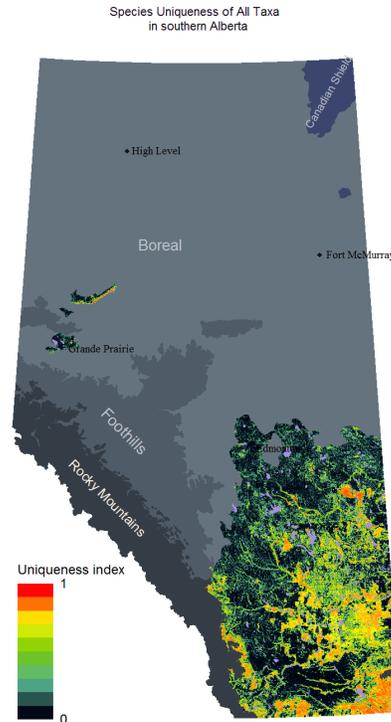
Relative uniqueness is not a measure of species composition. The index of uniqueness identifies the degree to which species composition in a pixel differs from the regional centroid. Pixels with high uniqueness had species assemblages that differed greatly from the average, but this does not mean that they had similar species composition to each other.

Relative uniqueness is sensitive to the dissimilarity measure and data transformation. The index of uniqueness was strongly influenced by species that had clumped distributions. The species dissimilarity matrix was computed using a dissimilarity index that emphasized co-occurrences of species independent of species' rarity and commonness giving all species equal weight.

Northern Alberta



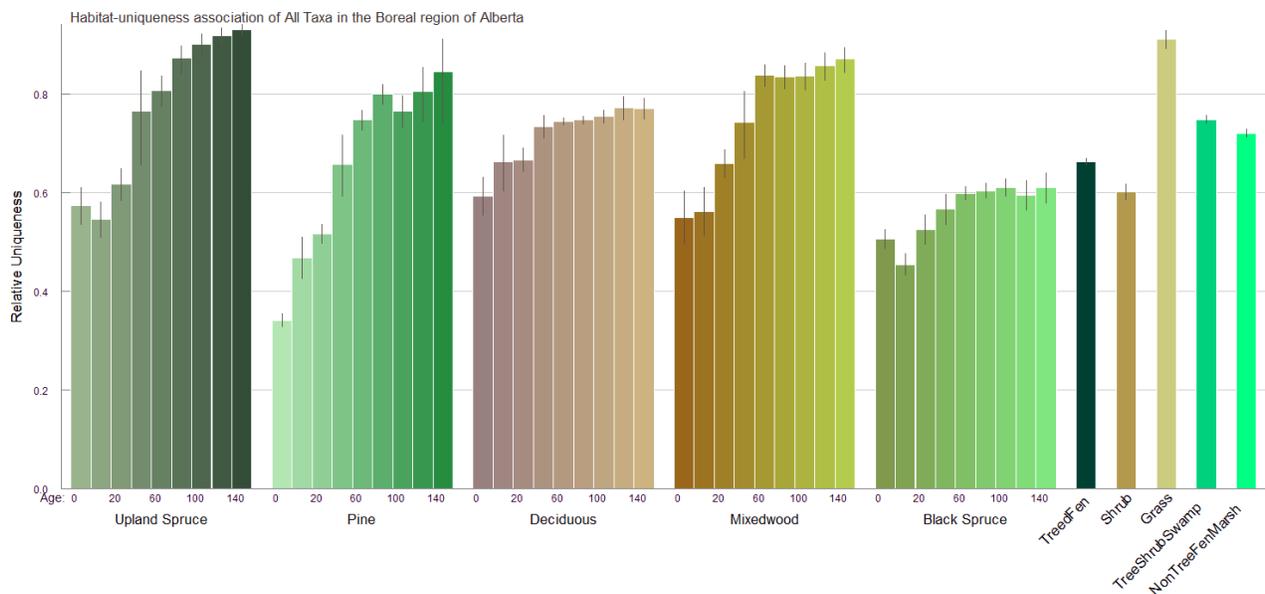
Southern Alberta



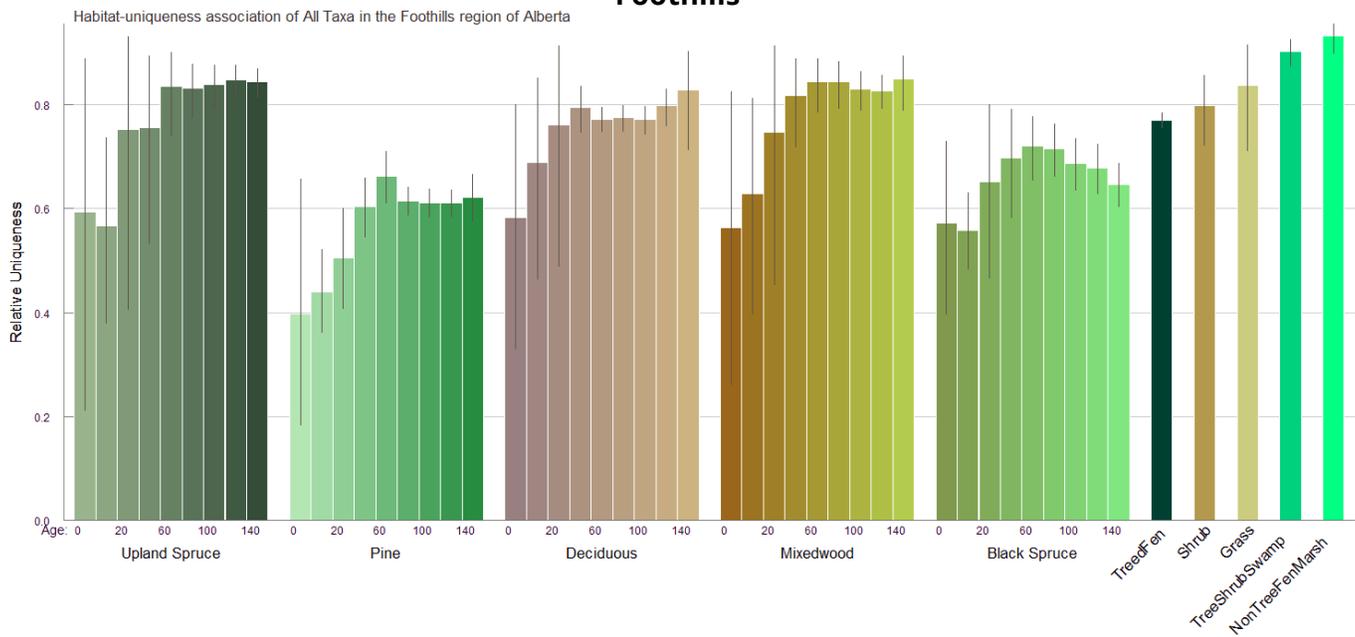
Habitat Associations by Natural Regions

The relative uniqueness measure shows the degree to which species composition in each pixel was distinct compared to all other pixels within the Natural Region. The uniqueness analysis was conducted separately for each Natural Region because the regional species pool and their predicted relative abundances differ between these. Relative abundance of each species in each pixel was predicted using habitat association models that relate species relative abundance to native habitat types (read methods and limitations).

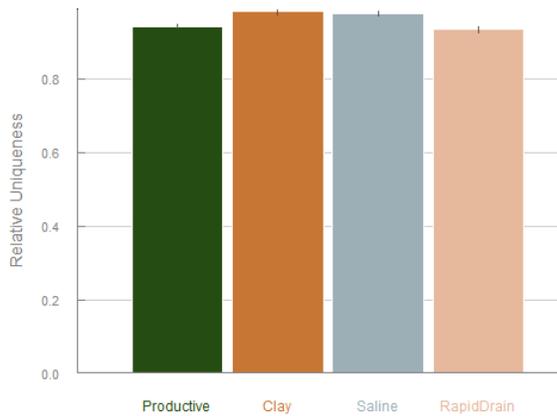
Boreal



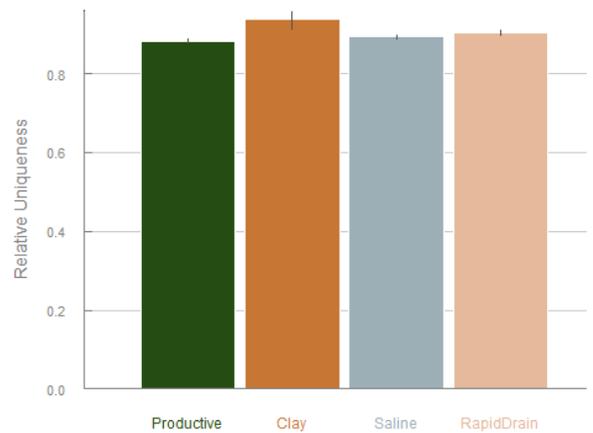
Foothills



Parkland



Grassland



References & Credits

References

Gotelli, N.J. and R.K. Colwell. 2001. Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. *Ecology Letters* 4:379-391.

Data Sources

Data collected by ABMI.

Recommended Citation

Alberta Biodiversity Monitoring Institute. 2017. Multiple Species Analysis: All Taxa.

ABMI Website: <http://abmi.ca/home/data-analytics/biobrowser-home/multi-species/multiple-species-alltaxa>.