Measuring biodiversity change – how useful are indices?

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1. What are biodiversity indices?

- Biodiversity indices measure the level of biodiversity through the relationship between species number and abundance.
- Indices are used to compare biodiversity at different sites, habitats or time periods.
- However, usually only one value of an index is calculated for any given site or time period.
- Is this value representative of the site or time period being studied?
- Confidence intervals or standard errors are rarely reported.

The aim of this study is to measure the uncertainty of biodiversity indices and assess their use in detecting biodiversity change through space and time.

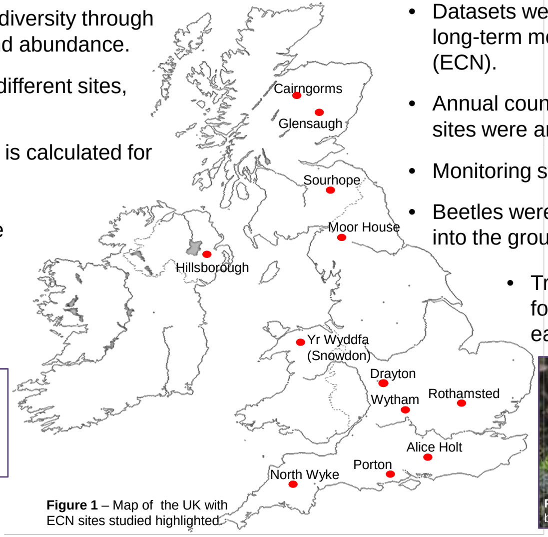

Figure 1 – Map of the UK with ECN sites studied highlighted.

2. The Study System

- Datasets were analysed from sites in the UK (Figure 1) managed by the long-term monitoring programme, the Environmental Change Network (ECN).
- Annual counts of ground beetle species (Figure 2) from 12 terrestrial sites were analysed.
- Monitoring started in 1993 and continues to be implemented.
- Beetles were collected using a pitfall trap method (small pots are placed into the ground to capture the crawling insects)(Figures 3 and 4).
- Traps are set along 3 transects in each site and collected fortnightly. Transects are placed in different habitat types at each site where possible.

Figure 2. A common ground beetle species

Figure 3. Example of pitfall traps along a transect in Cairngorms site

Figure 4. Collecting beetles from the traps

3. Calculating Uncertainty

- The uncertainty of biodiversity indices was calculated using 3 methods to resample the total annual counts of beetle species for each transect per site.
- All methods create 1000 new samples from which biodiversity indices can be calculated.
- The Shannon Weiner Index is a commonly used biodiversity index. The results of this index will be presented here.
- Results from Glensaugh (glen), Alice Holt (alice), and Rothamsted (roth) are focussed on.

a) Non-parametric bootstrap

- Samples of beetle counts for each transect per year were drawn with replacement.
- The mean Shannon index and 90% confidence intervals varied with transect, site and year.
- All transects and years at Alice Holt (Figure 5A) had indices with narrow intervals and overlapping ranges for each transect.
- Glensaugh (Figure 5B) had values with wider confidence intervals, but the values at transect 1 were distinct from transects 2 and 3.

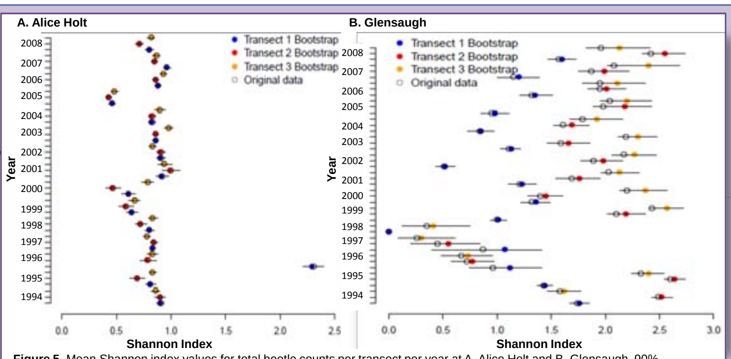

Figure 5. Mean Shannon index values for total beetle counts per transect per year at A. Alice Holt and B. Glensaugh. 90% confidence intervals are shown after a 1000 replicate bootstrap with replacement was performed.

b) Empirical Bayesian - an all species prior

- The bootstrap method used was restricted by the small size of the original sample.
- The data also contained many zeros which the bootstrap method did not model accurately.
- Hence, a Poisson/gamma model was used to improve the resampling.
- The parameters of the gamma prior were calculated from the distribution of the annual beetle counts for all species combined per site and transect.
- The distribution of each species across years was resampled.
- The mean Shannon index values and highest posterior densities show clear distinctions between transects for some sites.
- At Rothamsted (Figure 6A) transect 2 is distinct from transects 1 and 3.
- At Glensaugh (Figure 6B) transect 1 is distinct from transects 2 and 3.

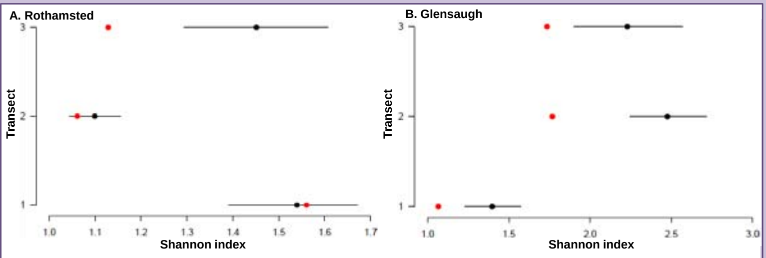

Figure 6. The mean Shannon index values (black circles) from the predicted posterior distribution and the associated highest posterior densities obtained from an empirical Bayesian analysis with an all species combined prior. A. Rothamsted and B. Glensaugh. The red circles are the mean Shannon Index values from the original data.

c) Empirical Bayesian – specific common species prior

- In Figure 6, the Shannon index calculated from the original data was not always within the range of the predicted values.
- Therefore, the same method as in (b) was applied, but using a different prior only for the species with high counts.
- The parameters for the prior were estimated using the distribution of the original data for each common species.
- The mean Shannon index from the new simulations has decreased (Figures 7A &B).
- The highest posterior densities for transects increased making distinctions between transects unclear.
- The mean Shannon index for the original data is close to the mean from the simulated datasets or within the highest posterior density range.

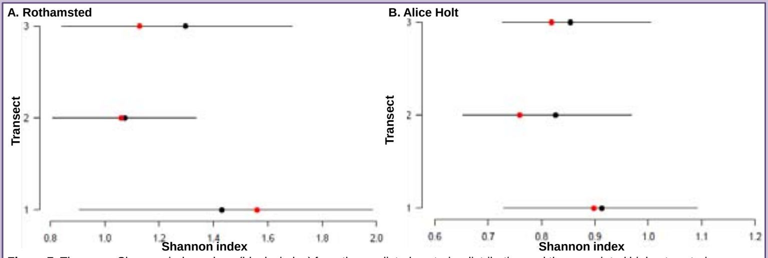

Figure 7. The mean Shannon index values (black circles) from the predicted posterior distribution and the associated highest posterior densities obtained from an empirical Bayesian analysis with a species specific prior. A. Rothamsted and B. Alice Holt. The red circles are the mean Shannon index values from the original data.

4. Habitat comparison

- The results from method (c) show that transects have different Shannon index values within a site even with the larger uncertainty values.
- The habitat type was examined as a cause of the difference in Shannon index values (Figure 8).
- All transects in woodland areas at Alice Holt have a range of index values that are distinct from the values at transects in a peat habitat.
- The grassland habitat has a range of values that are generally lower than those from the peat habitat.

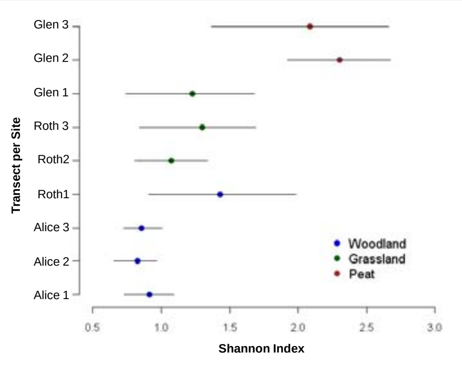

Figure 8. The mean Shannon index values and highest posterior densities calculated from method (c) and displayed by the habitat type of each transect.

5. Conclusions

1. Uncertainty in biodiversity indices can be calculated by several methods.
2. Each method has limitations depending on the type of data collected.
3. Samples with a high number of zero values and/or a few dominant species require a better resampling method.
4. The Shannon index can be used to detect differences between areas possibly due to habitat type.
5. The larger uncertainty values observed in sampling methods (b) & (c) may be due to the variation in species number with time.

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