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Diversity analysis

Diversity indices

Theory **R functions** Examples Exercise 

R functions

- **specnumber (library vegan)** - calculates species richness for individual samples, optionally number of species for different groups of samples. Applies on sample x species matrix of abundances, presences absences or other type of data (calculation of richness does not consider species abundances). Argument `group` allows to calculate group-based species richness (i.e. number of species occurring in samples classified into given group). Just a little more clever than simple `rowSums (x > 0)`.
- **diversity (library vegan)** - calculates **Shannon and Simpson index**. Applies on the sample x species matrix, where cells are species abundances. Argument `index` is either `shannon` (calculates Shannon entropy), `simpson` (calculates Gini-Simpson index, i.e. 1-Simpson, since Simpson index decreases with richness), and `invsimpson` (calculates reciprocal Simpson 1/D, which in fact is Simpson diversity - effective number of species calculated from Simpson's concentration index). Argument `base` can modify the base of the logarithm which is used to calculate Shannon (default is natural logarithm, some prefer to use `base = 2`). The function works also if data are not genuine counts of individuals (abundances), but other measures (dominance, cover); in that case, the interpretation is not "randomly chosen individual" (Shannon) or "two randomly chosen individuals" (Simpson), but e.g. "randomly chosen bit's of biomass".
- **d (library vegetarian)** - calculates **Hill numbers** for alpha, beta and gamma diversity. Applies on sample x species matrix of abundances (or biomass, cover etc.). Argument `q` modifies the coefficient q of the Hill numbers; default is `q = 1`, which is Shannon diversity (effective number of species calculated from Shannon's entropy). `q` can be any real number (also negative, although that makes not sense since this would give high weight to rare species). Allows to estimate confidence intervals via bootstrapping. For `level = 'alpha'` it calculates diversity on the level of individual rows (samples), for `level = 'gamma'` on the level of the whole dataset. `level = 'beta'` calculates beta richness.

From:

<https://anadat-r.davidzeleny.net/> - **Analysis of community ecology data in R**

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