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# Rarefaction

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## R functions

- **iNEXT** (library `iNEXT`) calculates abundance- and incidence-based rarefaction of species on number of individuals (or sites) or on sample coverage (a measure of completeness). The name stems from interpolation-extrapolation, since the function allows both inter- and extrapolation of the rarefaction curve (extrapolation works up to 2 times of max number of individuals or samples). Function `plot` draws the rarefaction curves (optionally with confidence intervals) for any combination of number of individuals (or samples) x number of species x sample coverage (modified by the argument `type` in the function `plot` applied on `iNEXT` object, see `?plot.iNEXT`).
- **estimated** (library `iNEXT`) - rarifies number of species per common number of individuals or sites, or per common level of coverage (completeness). Does not only for species richness ( $q = 0$ ), but also for Shannon and Simpson diversity, respectively ( $q = 1$  and  $q = 2$ ).
- **rarefy** (library `vegan`) - calculates abundance-based rarefaction. Applies on sample x species matrix (cells must be genuine abundances, i.e. counts of individuals) or vector of abundances.
- **rarecurve** (library `vegan`) - draws rarefaction curve for each row in the data. No confidence intervals calculated.
- **specaccum** (library `vegan`) - calculates accumulation curve on the community data matrix (one curve per matrix); `plot` draws the result (optionally with confidence interval).

From:

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

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