R-Package: Richness

Asymptotic estimations of species richness from spatial abundance data

Two functions richnessEstsCov.R and bootRichnessEsts.R that respectively return point estimates (observed richness, Chao1, Chao2, ACE, Jackknife-abundance, Jackknife-incidence, Ω_0 , and Ω_T) and bootstrapped estimates for estimator precision/uncertainty quantification. These functions take in data matrix with species as columns, spatial units (e.g., transects or quadrats) as rows, and individual counts as values. A wrapper function estimateRichness.R allows the user to provide community data as a matrix, data.frame, list, or array. Lists or arrays can be input to compare multiple communities, such as a time series.

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URL: https://github.com/EWTekwa/RichnessEstimator/tree/main/Richness

Citation: Tekwa, Whalen, Martone, O'Connor, Theory and application of an

improved species richness estimator. bioRxiv.

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