有母數

共同物種數估計

出現率資料/區塊數抽樣

依據出現型資料下的共同物種數估計

Estimate the richness of shared species based on incidence data.

# 摘要

兩群落之間的共同物種是一種表示Beta多樣性最簡單且直觀的指標之一。在過去的許多文獻中，以針對不同抽樣方式、調查方法或是資料型態，提出許多針對群落之間共同物種數的估計方法。且在估計方法的建構中，其中一項常見的方式便是使用有母數的估計方式建立估計式。而在過去也有許多研究針對估計單群落中的物種數，在假設物種出現機率為貝他二項分佈 (Beta-binomial distribution) 的情況下使用動差法 (moment mothed) 建立估計式，且都得到良好的估計效果。因此，本文基於貝他二項分佈的模型假設，使用動差法分別針對取後放回與取後不放回兩種抽樣方式，建立三個估計式。並透過多次的電腦模擬，評估估計式的優劣與穩定性。在結果方面，相較於原有的共同種估計方法，本文所提出的方式獲得較小的偏誤，且在RMSE與95%信賴區間涵蓋率 (95% confidence interval coverage, 95% CI coverage) 兩項評估指標上，也相較現有的估計方法具有更好的表現。最後，將其應用至實例資料中，比較本篇所提出的估計式與現有估計式的結果差異，在計算群落共同種時，本文所提出的估計結果會高於現有估計式。

關鍵字：物種豐富度、共同物種、貝他二項分佈、動差法

The shared species between two communities is a simple and direct index for measuring Beta diversity. Previous research has proposed various methods to estimate shared species, considering different sampling methods, survey approaches, or data characteristics. In the development of these estimation methods, a common approach is to use parametric estimation methods to construct the estimator. Many studies have focused on estimating species richness within individual communities, assuming that the probability of species occurrence follows a Beta-binomial distribution. These studies have utilized the method of moments to derive estimators, consistently achieving reliable estimation results. Therefore, this study is based on the assumption of the Beta-binomial distribution model and utilizes the method of moments to develop three estimation methods for sampling with and without replacement, respectively. Through extensive computer simulations, the study assesses the efficacy and stability of these estimators. The results indicate that compared to the original method for estimating shared species, the approach proposed in this study exhibits lower bias. Additionally, it demonstrates superior performance in terms of RMSE and 95% confidence interval coverage compared to existing estimation methods. Finally, the proposed estimators are applied to real-world data to compare their results with those of existing estimators. When calculating shared species between communities, the estimation results from this study are higher than those from the existing estimator.

Keywords: Species richness, shared species, Beta-binomial distribution, moment method.