

fuzzySim: an R (+ QGIS) package for analysing fuzzy similarity in species occurrence patterns

A. Márcia BARBOSA <barbosa@uevora.pt>



Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO/InBIO) – Univ. Évora, Portugal

Problem

► There is growing interest in analysing species **biogeographic associations**, **biotic regions** and **β -diversity patterns** (including **spatial and temporal species turnover**, in the past or predicted under future scenarios). Such analyses have important applications in **biogeography**, **community ecology**, **global change biology**, and **biodiversity conservation**.

► However, these studies are commonly **tied to binary comparisons of species presence/absence records**, which are both **incomplete and more categorical than their underlying natural patterns**.

► Moreover, proximity between species' occurrence sites is disregarded, such that **occurrences at adjacent, even interspersed, but not strictly coincident localities** are **considered as dissimilar as occurrences at opposite ends of the study region**.

► This amplifies the **effects of data deficiencies** and the **scale-dependence of such analyses**.

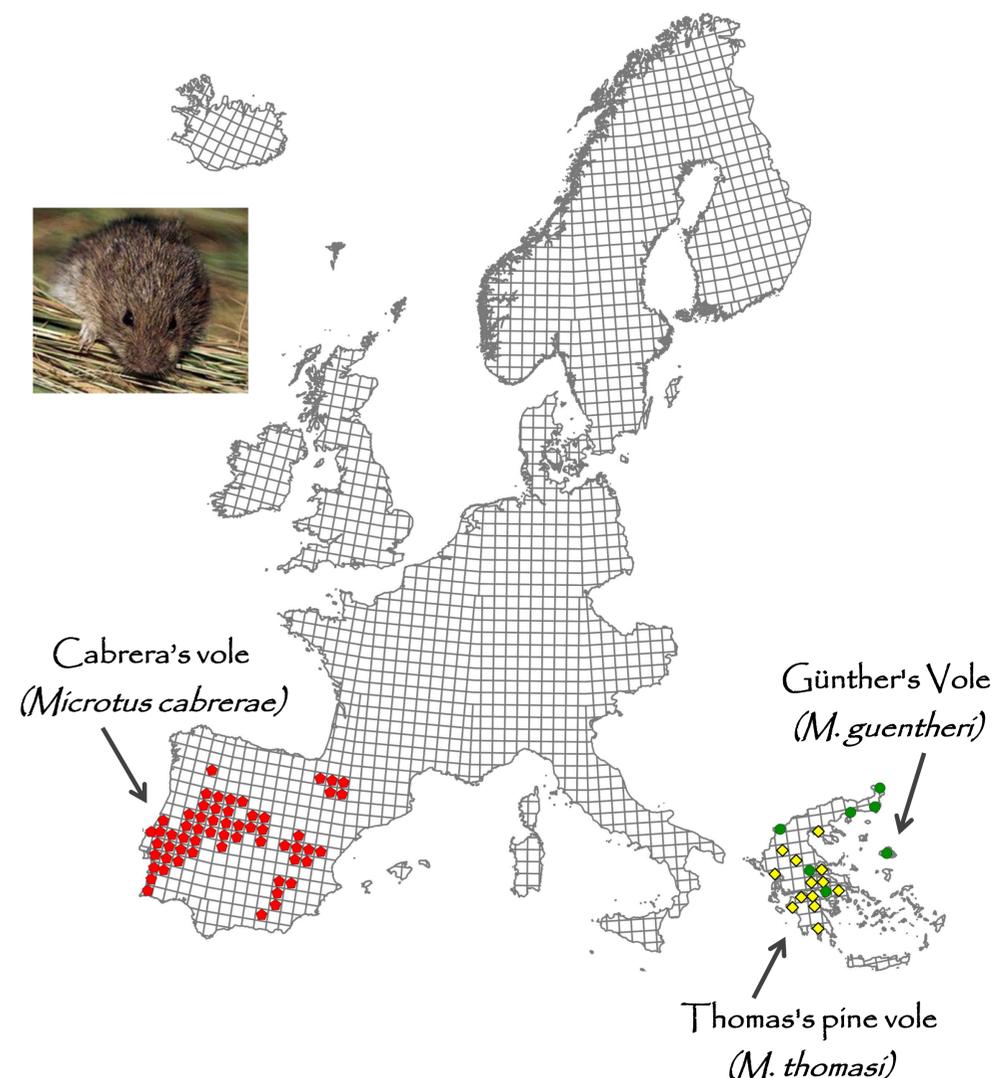
Proposal

The **fuzzySim** package implements **fuzzy versions of species occurrence data and of the binary similarity indices** most commonly used in ecology, so that these can be **directly applied to continuous rather than binary occurrence values**, thus producing more realistic similarity assessments.

Availability

The package is currently **available on R-Forge**. A version for the **QGIS** processing toolbox is also being implemented. An **article** explaining the method and its applications has been **submitted** and should be published soon.

Example



With any of the **commonly used similarity indices**, the **distributions of these 3 species** are all **considered completely different** (zero similarity). Using fuzzy versions of these distributions (obtained e.g. with trend surface analysis, inverse distance interpolation or distribution modelling) and of the similarity indices, **fuzzySim** detects the occurrence areas of **Thomas's and Günther's voles** are **more similar** to each other **than to Cabrera's vole's**.

Advantages

The method is **robust to data source disparities**, gaps or other **errors in species occurrence data**, even for restricted species for which slight inaccuracies can affect substantial parts of their range.