

Linking statistical and ecological theory: Hubbell's unified neutral theory of biodiversity as a hierarchical Dirichlet process ¹

Keith Harris¹, Todd L Parsons², Umer Z Ijaz³, Leo Lahti⁴, Ian Holmes⁵, Christopher Quince^{6,*}

¹ School of Mathematics and Statistics, University of Sheffield, Sheffield, UK

² Laboratoire de Probabilités et Modèles Aléatoires, CNRS UMR 7599, UPMC Univ Paris 06, Paris, France

³ Infrastructure and Environment Research Division, School of Engineering, University of Glasgow, Glasgow, G12 8LT, UK

⁴ Department of Veterinary Biosciences, University of Helsinki, Helsinki, Finland & Laboratory of Microbiology, Wageningen University, Wageningen, Netherlands

⁵ Department of Bioengineering, University of California, Berkeley, California, USA

⁶ Warwick Medical School, University of Warwick, Coventry, CV4 7AL, UK

* E-mail: c.quince@warwick.ac.uk

Abstract

Neutral models which assume ecological equivalence between species provide null models for community assembly. In Hubbell's Unified Neutral Theory of Biodiversity (UNTB), many local communities are connected to a single metacommunity through differing immigration rates. Our ability to fit the full multi-site UNTB has hitherto been limited by the lack of a computationally tractable and accurate algorithm. We show that a large class of neutral models with this mainland-island structure but differing local community dynamics converge in the large population limit to the hierarchical Dirichlet process. Using this approximation we developed an efficient Bayesian fitting strategy for the multi-site UNTB. We can also use this approach to distinguish between neutral local community assembly given a non-neutral metacommunity distribution and the full UNTB where the metacommunity too assembles neutrally. We applied this fitting strategy to both tropical trees and a data set comprising 570,851 sequences from 278 human gut microbiomes. The tropical tree data set was consistent with the UNTB but for the human gut neutrality was rejected at the whole community level. However, when we applied the algorithm to gut microbial species within the same taxon at different levels of taxonomic resolution, we found that species abundances within some genera were almost consistent with local community assembly. This was not true at higher taxonomic ranks. This suggests that the gut microbiota is more strongly niche constrained than macroscopic organisms, with different groups adopting different functional roles, but within those groups diversity may at least partially be maintained by neutrality. We also observed a negative correlation between body mass index and immigration rates within the family Ruminococcaceae. This provides a novel interpretation of the impact of obesity on the human microbiome as a relative increase in the importance of local growth versus external immigration within this key group of carbohydrate degrading organisms.

Introduction

A key question in ecology is what maintains species diversity in communities. The classical view is that every species occupies a distinct niche and the species observed in a community are then determined by the niches present. The niche itself is viewed as an n -dimensional hyper-volume in a space of abiotic and biotic environmental variables [1]. If two species occupy the same niche then one will outcompete the other [2]. This viewpoint has been challenged by neutral theory. Neutral models of species abundance combine stochastic population dynamics with the assumption of ecological equivalence between species, formally defined as equivalent forms for all *per capita* demographic rates, e.g., birth and death. Ecological equivalence is assumed to operate between species with a similar functional role deriving from the same