

清華大學、交通大學
統計學研究所
專題演講

題目：Entropy Unifies Molecules and Ecosystems, for Monitoring and Forecasting Diversity

主講人：Emeritus Professor William Bruce Sherwin
(Evolution and Ecology Research Centre, University of New South Wales)

時間：107年11月2日(星期五)上午10:40 - 11:40
(10:20 - 10:40 茶會於統計所821室舉行)

地點：清大綜合三館837室

Abstract

At all scales from molecules to ecosystems, we measure biodiversity to indicate outcomes of natural or artificial processes, and to compare with forecasts under various management schemes. Every biodiversity level has four basic processes – dispersal, adaptation, random change during transmission, and generation of novel variants (eg, new ecosystems, species, alleles) – so approaches are often strikingly similar.

How can we exploit this similarity? Entropy is an obvious choice, being a general forecasting and measurement tool throughout science. It is also a simple transform of many common biodiversity measures, which are based on: Richness; Gini-Simpson; and Shannon. Macroecologists use Shannon for measurement (more than Simpson), and for forecasts use ‘maximum (Shannon) entropy’ and Simpson. In contrast, molecular ecologists have many measures and forecasts for richness and Simpson (heterozygosity, Fst etc), but have only recently begun to measure and forecast molecular Shannon diversity within and between areas (Sherwin et al 2017). Examples and simulations show that Shannon approaches outperform others in some tasks, such as genetic estimates of dispersal for input to metapopulation models, and tracing rangeshift or invasion. Also, analyses of genomic and transcriptomic networks (linkage disequilibrium and expression) already use measures related to Shannon mutual information, and might benefit from using its transform to Shannon differentiation.

Further analyses will profit from three attributes of Shannon: similarity to logit (log-linear) modeling, sensitivity to rare novel variants that are crucial in adaptation, and independence of measures at different hierarchical levels. Thus the stage is set to unify our monitoring and forecasting of processes that are common across all biodiversity levels, using a complete diversity profile that encompasses richness, Shannon and Simpson. This will integrate well with the many entropic methods in chemico-physical studies.

Citation: Sherwin WB et al. 2017. Trends Ecol. Evol. 32:948.

敬請公佈

歡迎參加