通 知

中華民國 107 年 12 月 20 日
聯絡人：彭振昌、楊宗鑫
聯絡電話：271-7161～3

主旨：本處校務研究組訂於 107 年 12 月 27 日（四）辦理「大數據應用議題演講」，歡迎校內師生同仁踊躍參加。

說明：

一、配合 107 年度高等教育深耕計畫辦理「大數據應用議題演講」。
二、主講人：國立清華大學統計學研究所趙蓮菊教授。
三、參加對象：校內師生同仁。
四、演講地點：本校蘭潭校區理工大樓 8 樓多功能視聽教室（A16-808）。
五、演講日期：107 年 12 月 27 日（四）13：20 至 15：10。

<table>
<thead>
<tr>
<th>時 間</th>
<th>議 程</th>
</tr>
</thead>
<tbody>
<tr>
<td>13：00～13：20</td>
<td>現場報名、簽到</td>
</tr>
<tr>
<td>13：20～14：50</td>
<td>【演講主題】稀釋與外插：如何標準化樣本以公平客觀比較生物多樣性（演講摘要如附件）</td>
</tr>
<tr>
<td>14：50～15：10</td>
<td>座談與討論</td>
</tr>
</tbody>
</table>

六、報名方式：請當日逕至會場報名參加。
七、惠請各單位協助轉達所屬師生同仁週知。
八、本通知已公告於本校首頁，並傳送至各單位及師長電子信箱。

此致

各單位、教職員工生

研究發展處  敬啟
The goal in many biodiversity analyses is to make a fair comparison and assessment of diversity measures (e.g., species richness, taxonomic diversity, phylogenetic diversity and functional diversity) among multiple assemblages. For most measures, it is well known that the empirical diversities in a sample are dependent on sample size or sampling efforts. When samples are incomplete, standardization via rarefaction and extrapolation is needed; rarefaction and extrapolation methods allow for fair and meaningful comparison of diversity estimates for standardized samples on the basis of sample size or sample completeness. In this talk, two types of standardization methods are reviewed: (1) Sample-size-based rarefaction and extrapolation methods aim to compare diversity estimates for equally-large samples determined by samplers. (2) Coverage-based rarefaction and extrapolation methods aim to compare diversity estimates for equally-complete samples; the sample completeness in this method is measured by sample coverage (the proportion of the total number of individuals that belong to the species detected in the sample), a concept originally developed by Alan Turing and I. J. Good in their cryptographic analysis during World War II. Contrary to intuition, sample coverage for the observed sample, rarefied samples, and extrapolated samples can be accurately estimated by the observed data themselves. These two types of standardization methods allow researchers to efficiently use all available data to make robust and detailed inferences about the sampled assemblages, and also to make objective comparisons among multiple assemblages. Hypothetical and real examples are presented for illustrating the use of the online software iNEXT (iNterpolation/EXTrapolation) to compute and plot seamless rarefaction/extrapolation sampling curves based on several diversity measures.