



學術報告

Mapping the Ecological Networks of Microbial Communities

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时间：4月17日 星期二 下午 3:00

地点：浙江大学工控新楼501室

Biography: 肖延东，现为国防科技大学系统工程学院博士研究生。2015年10月至2017年10月在哈佛大学医学院联合培养两年。2012年获得国防科技大学信息工程专业工学学位。研究兴趣侧重于网络控制、系统动力学在微生物系统的应用研究。以第一作者在《Nature Communications》、《Physical Review E》等杂志发表SCI论文7篇，2014年获全国复杂网络大会最佳学生论文奖。

Mapping the ecological networks of microbial communities is a necessary step toward understanding their assembly rules and predicting their temporal behavior. However, existing methods require assuming a particular population dynamics model, which is not known a priori. Moreover, those methods require fitting longitudinal abundance data, which are often not informative enough for reliable inference. To overcome these limitations, here we develop a new method based on steady-state abundance data. Our method can infer the network topology and inter-taxa interaction types without assuming any particular population dynamics model. Additionally, when the population dynamics is assumed to follow the classic Generalized Lotka–Volterra model, our method can infer the inter-taxa interaction strengths and intrinsic growth rates. We systematically validate our method using simulated data, and then apply it to four experimental data sets. Our method represents a key step towards reliable modeling of complex, real-world microbial communities, such as the human gut microbiota.