

Fixation probability in constant-selection evolutionary dynamics on higher-order networks**报告人 Naoki Masuda 教授**Department of Mathematics & Institute for
Artificial Intelligence and Data Science,
State University of New York**主持人：李阿明 助理教授****时 间：6月16日（周五）上午9:30****地 点：力学楼434会议室****报告摘要：**

Population structure substantially affects evolutionary dynamics. Networks that promote the spreading of fitter mutants are called amplifiers of selection, and those that suppress the spreading of fitter mutants are called suppressors of selection. Research in the past two decades has found various families of amplifiers while suppressors still remain somewhat elusive. It has also been discovered that most networks are amplifiers under the birth-death updating combined with uniform initialization, which is a standard condition. In the present talk, we discuss our recent results on constant-selection evolutionary dynamics on two types of higher-order networks: hypergraphs and temporal networks. In contrast to the case of conventional networks, we show that a vast majority of hypergraphs and temporal networks are suppressors of selection. We also show that this suppressing effect is not explained by natural transformations of those higher-order networks into conventional networks (i.e., one-mode projection in the case of hypergraphs and time-averaged static networks in the case of temporal networks). Our results suggest that the modeling framework for structured populations in addition to the specific network structure is an important determinant of evolutionary dynamics.

报告人简介：

Naoki Masuda received his PhD in 2002 from the University of Tokyo. He worked as Lecturer and then Associate Professor at the University of Tokyo, Japan, between 2006 and 2014. Then, he worked as Senior Lecturer and Associate Professor at the University of Bristol, UK, between 2014 and 2019. He moved to Department of Mathematics at University at Buffalo in 2019 as Associate Professor and has been full Professor since 2021. His research interests include network science and mathematical biology, including neuroimaging data analytics. In network science, he is particularly known for his work on temporal networks, models of epidemic processes, random walks on networks, and analysis of biological data.

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