上海交通大学自动化系
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系统控制与信息处理教育部重点实验室
Key Laboratory of System Control and Information Processing, Ministry of Education

学术报告会

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Edge biomarker for precision medicine

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Abstract:

Edge biomarkers are a reliable form to characterize phenotypes or diseases in contrast to individual molecules. However, to obtain edges or correlations among molecules requires the measurement of multiple samples, which are not generally available for each individual in clinic practice. Thus, it is strongly demanded to diagnose a disease by edge biomarkers on the basis of a single sample for one individual, which actually represents the majority of the clinic cases. We developed a new computational framework and method, i.e., EdgeBiomarker, to distinguish phenotypes or diseases by both edge biomarkers and node biomarkers for each single test sample, in particular, detect early and advanced stages of lung and breast cancers based on big biomedical data. The new framework of edge biomarkers in this work opens us a new way to analyze and diagnose diseases as well as their molecular mechanisms by edges or networks even with individual samples, which also provides a powerful tool for precision medicine or big-data medicine.

Biography:

陈洛南，博士，研究员。1984年获华中科技大学电气工程学士学位；1988年获日本东北大学系统科学硕士学位；1991年获日本东北大学系统科学博士学位。1997年起任日本大阪产业大学副教授；2000年起任美国加州大学洛杉矶分校访问教授；2002年起任日本大阪产业大学终身教授；2006年起任日本科学振兴机构（JST）复杂生命系统研究组负责人；2009年4月起任日本东京大学兼职研究教授；2009年10月至今任中科院系统生物学重点实验室执行主任，研究员。2009年获中科院-诺和诺德长城教授奖。目前，在计算系统生物学领域的主要国际学术期刊中担任重要工作，如 *BMC Systems Biology* Section Editor，*IEEE/ACM Trans. On Computational Biology and Bioinformatics* Associate Editor，*Neural Processing Letters* Associate Editor，*Journal of Theoretical Biology* 编委，*IET Systems Biology* 编委，*Mathematical Biosciences* 编委，*Int. J. of Systems and Synthetic Biology* 编委，*Int. J. of Data Mining and Bioinformatics* 编委，*J. of Systems Science and Complexity* 编委，《系统生物学百科全书》编辑，IEEE-SMC《系统生物学委员会》主席，中国运筹学会《计算系统生物学分会》理事长。