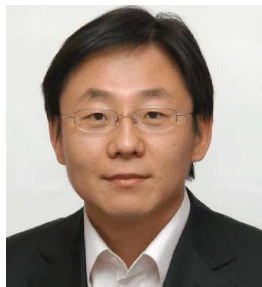




Transforming biomedicine with AI: Enabling data-driven biomedical discovery with machine learning techniques



报告人: Prof. Jiangning Song 宋江宁教授
Monash University 澳大利亚蒙纳士大学

报告时间: 5月14日周三 9:30-10:30

报告地点: 生命学院3-105会议室

邀请人: 欧竝宇 教授

报告人简介:

宋江宁担任澳大利亚蒙纳士大学医学院生物医学发现研究所教授，博士生导师，基于数据驱动的生物信息学和生物医学实验室主任，兼任澳大利亚研究理事会高等分子成像卓越研究中心高级研究员，兼任蒙纳士大学微生物抗生素耐药性研究中心的创始成员及研究中心科研主管。在生物信息学、生物医学、机器学习、高通量基因组序列分析、模式识别、蛋白质结构与功能预测、特征工程、海量异源数据驱动的人工智能系统开发等交叉学术研究领域发表了SCI论文超过330篇，影响因子大于7以上论文150余篇，其中第一作者论文30多篇、通讯作者论文120多篇；包括Cell、Nature Methods、Nature Sustainability、Nature Computational Science、Nature Communications、Lancet Oncology、Lancet Planetary Health、Science Immunology、Science Advances、Cell Genomics、Nucleic Acids Research、等杂志。担任生物信息学领域国际顶级核心期刊IEEE Journal of Biomedical and Health Informatics、Genomics, Proteomics and Bioinformatics等多家国际SCI杂志的副主编或编委。

报告摘要:

The exponential growth of molecular data has created a paradigm shift in biology, necessitating data-driven computational frameworks that can efficiently and accurately decode sequence-structure-function relationships across diverse biomolecules. To meet this challenge, we developed machine learning-based platforms capable of systematic feature extraction and integrative analysis of multi-dimensional molecular data—from sequences to 3D structures. Our tools empower researchers to uncover latent biological mechanisms, derive actionable hypotheses, and accelerate discovery. Through case studies spanning whole-genome sequencing, high-resolution histopathology, and multi-omics integration, we demonstrate how advanced machine learning extracts biologically meaningful insights from heterogeneous data.

热烈欢迎各位老师和同学参加!