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## ACADEMIC FORUM

受中国矿业大学人工智能研究院邀请，安徽大学郑春厚教授在我校举行学术报告，欢迎广大师生踊跃参加！

# Integrative Analysis of Multi-Dimensional Cancer Genomics Data

## 2020/08/24周一上午9:00

## 腾讯会议（会议号571 534 741）

**主讲人：郑春厚**

## 报告摘要

Understanding the mechanisms of cancer development and uncovering actionable target genes or disease-related pathways is essential for cancer treatment. With rapid advances in high-throughput sequencing technologies, some large scale cancer genomics projects, such as TCGA and ICGC, have produced a sea of multi-dimensional and different omics data. And it is widely accepted that genes or pathways are often function cooperatively by interaction network in cancer progression. So we can investigate cancer progression mechanism by integrating multi-omics based on network. How do we distinguish driver genes or important pathways from passengers? In this talk, I will give the network-based computational methods to discover driver genes and cancer subtype. In addition, I will introduce two models which are designed to solve maximum weight submatrix problem based on mutation data to identify driver pathway.

郑春厚，安徽大学计算机科学与技术学院教授、博士生导师，安徽省学术和技术带头人后备人选。近年来，在Bioinformatics、Neural Computation、Pattern Recognition、IEEE/ACM Transactions 系列会刊等国内外重要学术刊物与国际会议上发表论文100余篇，论文总被引2000余次。主持国家自然科学基金重点项目1项（联合重点），面上项目3项、省部级课题多项。2007年获中国科学院王宽诚博士后工作奖，2010年获安徽省自然科学一等奖（第二完成人），2016年获教育部自然科学一等奖（第二完成人），2019年获安徽省自然科学二等奖（第一完成人）。

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