智能·研究·探索·创新

ACADEMIC FORUM

受中国矿业大学人工智能研究院陈兴副院长邀请，美国埃默里大学秦昭晖教授在我校举行学术报告，欢迎广大师生踊跃参加！

iPath: 利用单样本的基于通路的整体基因表达作为预测临床预后的生物标志物

2022/5/31 周二上午10:00
ZOOM会议ID： 642 216 1915
密码：333

主讲人：**秦昭晖**

报告摘要

Identifying biomarkers to predict the clinical outcomes of individual patients is a fundamental problem in clinical oncology. Multiple single-gene biomarkers have already been identified and used in the clinics. However, multiple oncogenes or tumor-suppressor genes are involved during the process of tumorigenesis. Additionally, the efficacy of single-gene biomarkers is limited by the extensively variable expression levels measured by high-throughput assays. In this study, we hypothesize that in individual tumor samples, the disruption of transcription homeostasis in key pathways or gene set plays an important role in tumorigenesis and has profound implications for the patient's clinical outcome. We devised a computational method named iPath to identify, at the individual sample level, which pathways or gene sets significantly deviate from their norms.

秦昭晖博士现任美国埃默里大学生物统计与生物信息学教授。秦昭晖1994年本科毕业于北京大学。2000年在密西根大学获得统计学博士学位。秦博士在生物信息学，计算生物学，基因组学及统计遗传学等领域有丰富研究经验。目前已发表一百多篇同行评议的研究论文。秦博士目前的主要研究兴趣在高通量组学数据分析，以及利用统计建模和机器学习等方法进行组学大数据的数据挖掘。

主办单位：中国矿业大学人工智能研究院

邀请人： 陈兴 副院长