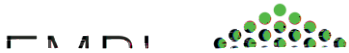

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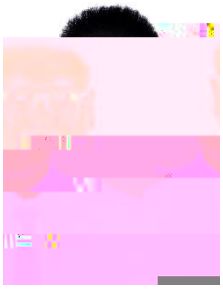

Dr Fuyi Li

Fuyi is a Professor at the College of Information Engineering, Northwest A&F University, China, and an Honorary Research Fellow at the Peter Doherty Institute for Infection and Immunity, the University of Melbourne. With a background in software engineering and expertise in bioinformatics, Fuyi has developed a series of data-driven machine learning-based algorithms and tools to address open complex biological problems. His research interests focus on the development of machine learning-based bioinformatics approaches to functionally interpret massive heterogeneous biology datasets involving genomics, proteomics, and 3D structural data.

Leveraging AI and big data in bioinformatics: exploring opportunities, tackling challenges, and driving innovation.

Advancements in high-throughput technologies have enabled the collection of vast amounts of biological data, providing an opportunity for data-driven discoveries in biology. However, the complexity and scale of these data present significant challenges for traditional data analysis methods. The field of bioinformatics aims to address these challenges by developing computational tools and algorithms to analyse biological data. In recent years, the application of artificial intelligence (AI) has revolutionized the field of bioinformatics, enabling new approaches for data analysis and interpretation. In this presentation, I will discuss the opportunities and challenges of using AI-driven bioinformatics approaches to analyse large and complex biological datasets. I will showcase examples of AI-driven bioinformatics research, including our work on developing machine learning-based approaches for understanding open biological questions. I will also discuss the potential applications of AI-driven bioinformatics in drug discovery, personalized medicine, and agriculture. Finally, I will highlight future directions in the field and the importance of interdisciplinary collaborations between computer scientists and biologists to tackle the challenges of the era of big data in biology.

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Dr Piyushkumar Mundra

Dr Piyushkumar Mundra is a Senior Research Officer at the Garvan Institute of Medical Research in Sydney, Australia. He holds a PhD in Computer Engineering, which he earned from Nanyang Technological University in Singapore. His PhD thesis was highly impactful, resulting in three publications in leading computational journals. After his PhD and short stint as a research fellow at NTU, Dr Mundra went on to work in the Metabolomics lab at Baker Institute in Melbourne, Australia. There, he conducted advanced lipidomics research on clinical trial samples, which led to numerous publications, including in the prestigious journal . To expand his experience in genomics, he moved to the Molecular oncology lab at Cancer Research UK Manchester Institute. During his tenure there, he worked on several melanoma studies using both preclinical and clinical samples. His research resulted in publications of ten manuscripts, with the first or joint-first author papers in highly respected journals such as and . Through his research, he was able to gain a fundamental understanding of the impact of ultraviolet radiation on melanomagenesis and developed a novel signature for immunotherapy response. Since 2020, Dr Mundra has returned to Australia, where he is currently working on developing a genetic compendium of germline mutations in sarcomas. He recently co-authored a manuscript in , describing two novel pathways implicated in sarcomas. Dr Mundra specializes in bioinformatics analysis of various -omics datasets and his expertise has enabled him to make significant contributions to the field of computational biology through several high-impact publications (Google h-index :26).

Deciphering oncogenesis through genomic biomarker discovery.

High-throughput -omics technologies such as genomics, transcriptomics, proteomics, and metabolomics have revolutionised the way we study cancer biology and make treatment decisions. Genomic biomarker discovery approaches can help identify key genetic changes that are associated with cancer development, progression and therapy response. In this presentation, multiple case-studies will be presented discussing how biomarkers could be identified from tumour as well as blood samples to decipher cancer evolution. Using genomics and transcriptomics approaches on a induced melanoma preclinical model, melanoma tumours were classified into groups by mutation signatures, and ten recurrently mutated UVR signature genes were identified that predict patient survival. In response to anti-PD-1 treatment, stromal and proliferation signatures were associated with prolonged response. Both of these studies are corroborated in multiple independent melanoma patient cohorts. In rare disease such as sarcomas, whole-genome sequencing on blood samples could play a pivotal ro4.23 506.35 0 0 1 183.9

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