C O N T R A

Computational Oncology Training Alliance

ESR 13 - Integrated image and genomics

Research project	Tumours are intrinsically heterogeneous. Cancer cells have the ability to remodel and adapt to microenvironmental pressure according to Darwinian theory. Understanding such a dynamic phenomenon that occurs both in time and space is central to our capacity to deliver precision medicine with maximum therapeutic efficacy and minimal drug resistance. Thus far, we are limited by current approaches to study this process in human tumours. Cancer genetic heterogeneity and evolution are often studied without the spatial context. Just like in ecology where spatial organisation of the ecosystem is critical for understanding functioning, it is becoming increasingly evident that we need to use a similar spatial approach to study cancer. The development of a new type of methodology that combines diagnostic pathology with next-generation sequencing, thereby enabling simultaneous spatial mapping of morphological and molecular tumour heterogeneity and microenvironmental characteristics, could change the way we study cancer and enhance our ability to deliver precision medicine. The aim of this project is to develop deep learning methods to integrate these data types in breast cancer. The student will develop skill sets and gain experience in implementing algorithms using image analysis, deep learning and bioinformatics. This is a highly multidisciplinary project linking cancer biodiversity with ecosystem spatial context in human tumours through the interactions with pathology, genomics and machine learning.
Supervisor	name Yinyin Yuan e-mail Yinyin.Yuan@icr.ac.uk website yuanlab.org
Host institution ICR	The Institute of Cancer Research, United Kingdom Centre for Evolution and Cancer, Division of Molecular Pathology
PhD program	Centre for Evolution and Cancer, Division of Molecular Pathology
Expected results	1) The development of new image analysis software to superimpose multiple pathological images 2) The implementation of spatial statistic algorithms to identify distinct tumour sub-regions (habitats) 3) A computational analysis platform for deciphering tumour evolution as a process of interaction between genetically defined, heterogeneous cancer subclones and microenvironmental features 4) The identification of new biomarkers that inform treatment sensitivity
Planned secondments	1) UCAM-Markowetz for spatial genomics 2) UVIGO-Posada for cancer evolutionary dynamics 3) KTH-Lagergren for machine learning (3 months)
Required profile	Statistics, machine learning, or bioinformatics