

Collaboration opportunity

AI-based multiplex image analysis of pathology slides (SANDI)

The Institute of Cancer Research, London, is seeking licensees or collaborators for an AI-based method enabling the automated, rapid and accurate identification and classification of single cells from multiplexed pathology slides.

The technology could help accelerate research into how different cell types within the tumour microenvironment influence tumour behaviour, prognosis and response to treatment.

Key features

- Universal and quantitative automation of single-cell detection from multiplex pathology slides with minimal human input.
- Agnostic to the antigen detection method and imaging platform used to stain and visualise tissue samples.
- Pioneering use of AI in digital pathology.

Intellectual property

The Institute of Cancer Research (ICR) has filed a PCT patent application (PCT/EP2022/061941) covering the AI-based quantitative method for single-cell detection and classification in pathology slides, requiring minimal human input.

Commercial opportunity

The ICR team is now seeking licensees and commercial development partners looking to apply this technology in R&D programmes.

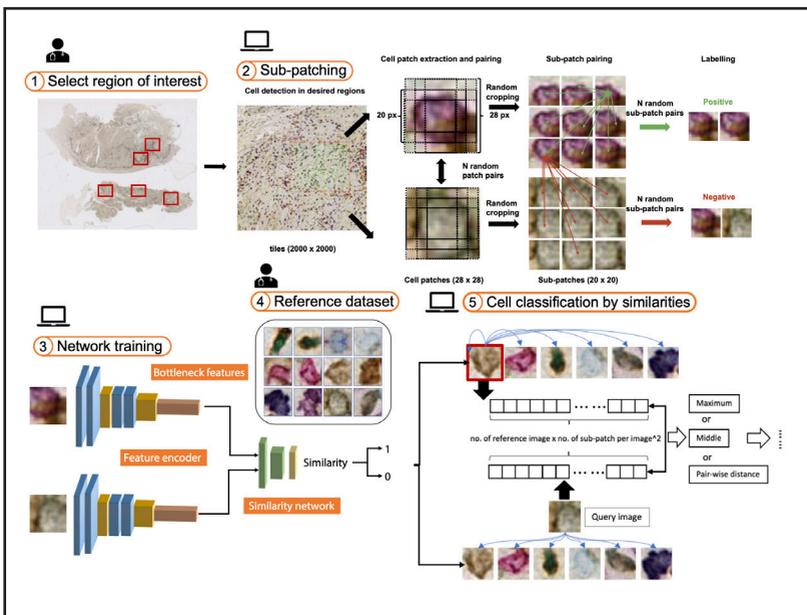
About the programme

Digital pathology is an emerging field. It uses sophisticated computing tools and AI to diagnose disease and guide treatments faster and more easily – offering exciting opportunities for understanding cancer in novel ways.

The Computational Pathology and Integrative Genomics Team at the ICR, led by Professor Yinyin Yuan, has created an AI-based approach that provides rapid accurate and reliable analysis of multiplex histopathology slides at a single cell level with minimal human input.

Self-supervised Antigen Detection AI (SANDI) involves scanning slides stained with multiplexed labels into digital images and using an AI algorithm to analyse the images automatically at a single-cell level.

Developed and validated using datasets from normal and tumour samples (breast, ovarian cancer and myeloma), the technique is agnostic to the antigen detection method or imaging platform used. In principle, it should detect an unlimited number of antigens within the same cell and work across all types of cancer and cell types.



Schematic to illustrate the five steps of the SANDI pipeline. 1) Selection of region of interest. Regions in the whole slide images containing various cell types are picked. 2) Data preparation process. Single-cell patches of 28 × 28 pixel are retrieved from manually picked regions and are randomly paired and cropped into 20 × 20 pixel sub-patches. Sub-patch pairs originated from the same patch are labelled as positive, otherwise negative. 3) Model training. Pairs of sub-patches are processed by two identical encoders to generate a feature vector of 32. The encoded features are concatenated as inputs for the similarity model, which learns to discriminate between similar and dissimilar pairs. 4) Reference dataset. 1-2 representative cell images per type were selected as references. 5) Classification of unknown cells based on similarity score. The query images are compared with each of the reference based on the similarity score and classified into the type of the most similar reference.

Lead scientists/inventors

Professor Yinyin Yuan and Hanyun Zhang

Professor Yinyin Yuan leads the Computational Pathology and Integrative Genomics team, which uses techniques from a broad range of scientific fields to formulate unique approaches for linking genetic mutations, pathological observations and patient treatment.

Hanyun Zhang is a PhD student in the team currently working on this project.



More information

For more information on the background to the programme and on our other projects available for licensing and collaboration, use the contact details below or visit

<https://icr.portals.in-part.com>.

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