

# **Project title: Digital twins for histopathology toward personalised cancer treatment**

**Project reference: DT4H\_01\_2023**

**1<sup>st</sup> supervisor: Dr Heba Sailem - Institute of Pharmaceutical Science and Biomedical Engineering**

**2<sup>nd</sup> supervisor: Prof. Claire Wells - Comprehensive Cancer Centre**

## **Aim of the project**

In this project, our primary objective is to create a digital tumour twins model aimed at optimizing cancer treatment through predictive analytics by developing advanced supervised and self-supervised deep learning technologies. The digital tumour twins model will not only consider the patient's medical history and individual characteristics but also incorporate microscopic tumour characteristics derived from histopathological images. Importantly, these models will be age and gender-matched to explore the landscape of disease trajectories in patients with similar profiles. The digital tumour model presents several unique opportunities, including personalized treatment recommendations based on patient-specific data and the identification of tumours with similar characteristics. A key innovation in our approach is the integration of our digital models with corresponding biological models. This integration will be achieved by establishing 3D tumour spheroid and organoid models, enabling the testing of various treatment options in vitro to identify the most effective therapeutic approach. These cellular models will not only serve as a means to validate and refine the accuracy of our digital models but also facilitate the determination of best treatment for the patient.

## **Project description**

Histopathology remains the cornerstone of cancer diagnosis, carrying profound implications for patient prognosis. Pathologists carefully evaluate tissue samples, relying on their expertise to discern changes in cell morphology, cellular organization, and mitotic events while considering the underlying tissue anatomy. While histopathological assessment is generally robust for many cancer types, it can be subjective and susceptible to human error. Moreover, human perception is limited as it only can compare only a handful of parameters at a time. However, within a single histopathological image, there can exist thousands to millions of cells within tumour sections, which can result in large number of potential features.

This is where artificial intelligence (AI) can have huge potential. AI systems have the exceptional capability to systematically identify and extract relevant features from thousands of histopathological images, unveiling clinically significant patterns that might not be apparent to the naked eye. This not only promises a more objective evaluation of existing pathological criteria but also offers the prospect of uncovering novel predictive biomarkers that were previously inconceivable.

Our Digital twins project aims to provide an invaluable tool for advancing cancer therapy. We plan to harness AI-driven insights derived from histopathological images and integration with other omics data. Thus, our digital twins project can offer a wealth of data that can inform tailored treatment strategies and predict disease trajectories with a level of precision and comprehensiveness that was

previously unattainable. The resulting technology would not only reduce the need for animal testing but could also outperform it as it is based on a comprehensive analysis of patient and tumour characteristics and relevant cellular models.

We will combine our digital twins approach with a biobank of advanced cellular models that match our digital tumour models to enable rapid testing of potential treatments to offer more tailored therapy. Importantly, by developing a matched cellular model, we will enrich our digital models and our database. The incorporation of biological validation also gives us the opportunity to test novel pathways that may be highlighted by our comprehensive analysis of tumour cell features, potentially leading to new therapeutic approaches.

