Using machine learning to improve data analysis from complex *in vivo* datasets

Supervisory team:
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Project description:
The skeletal system is surprisingly dynamic, undergoing remodelling due to changes in gene expression and or loading throughout life. Changes to either underpin skeletal and joint diseases and over 15 million people in the UK have a musculoskeletal disorder such as osteoporosis or osteoarthritis. Zebrafish are increasingly used as the animal model of choice to study developmental biology and cell behaviour. They offer excellent genetic tractability along with dynamic *in vivo* imaging due to their translucency and the potential to use fluorescent reporters to track cells in the whole animal. Our group has made >20 mutant lines of zebrafish carrying mutations in genes that lead to disease states in humans, along with transgenic lines that allow us to see the cells that make up muscle, cartilage, bone, tendons and the immune system in living fish. We have amassed a large number of 3D datasets that contain data that we currently do not fully extract. This project focuses on developing machine learning strategies to process large, complex, 3D *in vivo* datasets with the aim of using these to develop high throughput systems for testing of new clinically relevant genes and *in vivo* compound screening to test new pharmaceutical strategies. The project is highly interdisciplinary offering the chance to combine advanced *in vivo* skills (CRISPR genome editing, live imaging of transgenic reporters) with computational AI and machine learning approaches to visualise and analyse data. The supervisory team has members from both academia and industry. The project would give the student a highly desirable skill set that is increasingly in huge demand. This project would particularly suit a student with an interest in biological systems and some experience of programming, ideally in Python.