Project title: Advances in cellular barcoding: a combinatorial analysis and toolkit construction

Supervisor: Dr Mark Dukes

New techniques in bio-technology have allowed for what were once thought to be impossible tasks in the world of genetic engineering to become reality. The active tracking of the progeny of cells is important for a variety of reasons, perhaps most notable is the desire to determine the fate of cells that seem to have thrived - for one reason or another - in the presence of some agent or vaccine.

Cellular barcoding is a recently established tool that allows one to do this in several situations. This is, in essence, accomplished by inserting specially constructed segments of base pairs (called codewords or cassettes) into a cell's genome. Certain segments are inserted around the codewords to indicate the start and end of code segments, and the Cre Lox system is one such system that has been employed in the first versions of this technology.

Some of my recent work (Weber et al.[1]) concerns a novel method that allowed for an order of magnitude increase in the barcode diversity through the use of this system and is based on an analysis of the permutations of codewords that are achievable. While this method was a theoretical construct, recent developments have proven the construct is realizable and the outcomes of the theory broadly match with the experimental data so far.

This project will study this novel construction and others from its natural setting: the combinatorics of DNA code-words mechanisms, strand excision, strand inversion, and combinatorial diversity. It will build and examine a theory for these Cre-Lox actions to produce a toolkit that is readily applicable to any similar technologies.

References

[1] T. Weber, M. Dukes, D. Miles, S. Glaser, S. Naik, K. Duffy. Site-specific recombinatorics: in situ cellular barcoding with the Cre Lox system. *BMC Systems Biology*, 10(1):43, 2016.