**Aim:** Prediction is a central application in many real-world data analyses. In this project, we will aim to apply classification techniques for predicting novel kinase-substrates.

**Background:** Protein post-translational modifications (PTMs), which can activate or inhibit protein function/activity, have emerged as key regulators of various signalling pathways. Phosphorylation is a common type of PTM that is characterised by the addition of a phosphate group by a protein kinase to a serine, a threonine, or a tyrosine residue on a substrate protein. Recent advances in mass spectrometry (MS)-based technologies make it possible to profile proteome-wide phosphorylation events *in vivo* for investigating signal transduction cascades. A key goal is to identify the set of kinases and their corresponding substrates that underlie key signalling events over a course of time.

The time-course phosphoproteome profiling of insulin stimulated fat cells (3T3-L1) conducted by Humphrey et al. (2013) provides a unique opportunity to reveal previous unknown aspects of insulin pathways, a key for treating type II diabetes. Previous knowledge suggests that Akt and mTOR are central kinases involved in the insulin signalling in fat cells. It is known that kinases regulate their substrates by recognising substrate peptide sequence motif and substrates of the same kinase often have similar response profile. To this end, we aim to predict novel substrates of Akt and mTOR by using and/or extracting learning features from temporal phosphoproteomics data (and, if possible, combining these features with kinase-substrate recognition sequence motif).