## Potential Supervisors

**Dr Phillip Stansfeld**

One of the fundamental challenges in biological sciences is to visualise biomolecular machines in high-resolution detail. This is notoriously difficult, expensive and time-consuming to achieve by using experimental techniques, especially for proteins that exist in cell membranes, known as Integral membrane proteins (IMPs). These proteins play fundamental roles in cell biology e.g. as processing enzymes, ion channels, drug receptors, and solute transporters.

My group uses computational methods to study IMP structures and currently hosts MemProtMD; a pipeline for inserting experimentally-solved IMP structures into their native bilayer environment and analysing the stability, dynamics and resultant lipid interactions. This resource uses multiscale molecular dynamics (MD) simulations that permit the accurate assembly of an IMP into a membrane at the coarse-grain level, prior to careful assessment of the quality of the IMP structure at atomic resolution.

The MemProtMD pipeline also forms a springboard to studying the dynamics of experimentally solved structures through MD simulations. With the increasing threat of anti-microbial resistance, we are especially interested in bacterial IMPs. Knowledge of the three-dimensional structures of proteins involved in essential processes provides the physical details of potentially viable targets for killing drug-resistant, pathogenic bacteria. By breathing life into these frozen structures we may assess the association of proteins with lipids, drug molecules and other components of the protein complexes.

## Software Tools Developed

MemProtMD - A database of membrane proteins embedded in lipid bilayers.

CG2AT - A fragment-based approach for multi-scale molecular dynamics simulations.

## Involvement of DTC Students

Sophie Williams (DTP) - Molecular simulations of pore-forming proteins.

Daniel Quetschlich (SABS DTC) - Mass Spectrometry and molecular dynamics approaches to protein-lipid interactions.

Michael Horrell (DTP) - Molecular simulations of membrane proteins solved by Cryo-EM

Matt Raybould (SABS DTC) - Molecular understanding of drug binding to the hERG potassium channel.

Tom Newport (SysBio DTC) - Development of MemProtMD for protein-lipid interactions.

## Industrial links

UCB

Oxford Nanopore Technologies