Bacterial chemotaxis is the biasing of bacterial movement in response to chemical stimuli. Chemotaxis in *E. coli* is one of the best characterised signalling pathways in biology. There is a large amount of experimental data on this pathway has lead to extensive mathematical modelling of this system. This relatively simple pathway has helped to conceptualize the signalling pathway of general sensory systems. However, with an increasing number of sequenced bacterial genomes it becomes apparent that the chemotactic sensory mechanism of many bacteria is much more complex.

We are applying control theory to guide the rational design of experiments to elucidate the network structure of the more complex chemotaxis pathways of *R. sphaeroides*. The presence of multiple potential signalling pathways that are spatially separated in the cell produces different possible feedback networks – a multi-input, multi-output control system (as opposed to possessing only one feedback loop and one sensing cluster in the *E. coli*). Putative network structures have been investigated by model invalidation to determine potential network architectures. The implications of these architectures on the system robustness and performance are examined.