Research groups

Heath Laboratory (http://www.birmingham.ac.uk/schools/biosciences/staff/profile.aspx?ReferenceId=9657&Name=professor-john-heath) : Structure and function of growth factors and their receptors

We are interested in how the specificity and dynamics of growth factor signalling is controlled in human cells. This is a central problem in understanding a wide variety of human disease states such as cancer, inflammation, tissue repair and infertility.

Our research relies heavily on advanced techniques for studying and manipulating the formation and dynamic distribution of protein complexes including mass spectroscopy/proteomics, optical imaging, computational modelling and structural biology. Funding for the research comes from Cancer Research UK and the **EC Endotrack programme (http://www.endotrack.org/)** .

Kreft Laboratory (http://www.biosciences-labs.bham.ac.uk/kreftlab/index.html) : Individual-based Modelling of Biofilms

We are interested in the dynamics of interaction between 'parts' (e.g. individual organisms) and how these interactions give rise to emergent behaviour on the next higher level of organisation (e.g. the population). Research is focused on competition, cooperation, and communication of microbes in spatially structured systems such as biofilms.

Research interests include: cooperation and communication of microbes in biofilms, metabolic division of labour, individual-based modelling, systems biology.

Winn Laboratory (http://www.birmingham.ac.uk/schools/biosciences/staff/profile.aspx?ReferenceId=9918&Name=dr-peter-winn) : Understanding Cellular Organisation at the Atomic Level

The group is interested in the physical and chemical processes important for biological organization. In particular, how does this influence **protein (http://en.wikipedia.org/wiki/Protein)** evolution? Cellular function comes from organized processes of events, often in response to external stimuli. The aim of the group is to use mathematical models of the processes involved to understand better these biological process. Areas of more general interest include: Protein conformation, protonation states and function; Prediction of protein interactions; Understanding how higher protein organization leads to specific functionality; Fast predictions of protein flexibility and conformation; Discovery of small molecule inhibitors.

Jabbari Group: Mathematical modelling of gene regulation networks

We specialise in the mathematical modelling of gene regulation networks, incorporating experimental data to parameterise the models and test model-driven hypotheses. Circuits of interacting genes, proteins and signals are employed to ensure a cell is undergoing the most appropriate behaviour in its environment at any given time. Understanding these structures enables the prediction, prevention or exploitation of a cell's fate. For instance, identifying the central genes governing toxin production by the so-called superbug Clostridium difficile will reveal much-needed novel drug targets, while investigating networks in a closely related bacterium, Clostridium acetobutylicum, will assist us in forcing these bacteria to "over-produce" solvents which can be used as biofuels. Focusing primarily on prokaryotic organisms, the aim is to use a genuinely interdisciplinary approach to predict bacterial behaviour.

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