Summer 2009 internship projects

High Performance Computing for Computational Biology

Supervisor
Mark Williams

Project Description
The current major trend in computer hardware is toward multi-core computing. Quad core CPUs have recently become common place, and will soon be replaced by 8 or 16 cores. The PS3 games console currently has 6 cores and there will probably be 32 cores in the PS4. GPUs with hundreds of parallel computational units are coming into mainstream use. We have a strong interest in using these parallel computer architectures to accelerate computations of the interactions and motions of biological molecules.

Several possible projects are available to implement and test algorithms on these architectures. Previous experience of C/C++ is essential, some knowledge of SIMD programming would be desirable.

A Web-based Server for Biophysical Data Analysis

Supervisor
Mark Williams

Project Description
The analysis of data on the interactions of biological molecules from a variety of physical techniques, e.g. circular dichroism, fluorescence or UV-visible spectroscopy, isothermal and differential scanning calorimetry, is generally carried out using the different proprietary software packages supplied with each instrument. Learning many separate types of software presents a barrier to new users of the instrumentation and also makes it difficult to carry out a unified analysis of data obtain by several methods applied to the same molecules. This duplication is both expensive and unnecessary as many of the analyses require use of similar mathematical and computational methods (often the same equations). Further, the manufacturer's software often does not perform the latest types of analysis that have been described in the scientific literature, such as Monte Carlo error estimation or global analysis.

In this project the intern would develop a web-based server that would allow researchers or students anywhere in the world to carry out a variety of common analyzes of biophysical data using the latest methods. The server would be developed using the Mathematica technical computing system. Previous programming experience and/or strong mathematical skills are desirable.

References
Cliff MJ, Williams MA, Brooke-Smith J, Barford, D & Ladbury JE (2005). Molecular recognition via coupled folding and binding in a TPR domain. *J. Mol. Biol*. 346, 717-732

Molecular interactions in the cytoplasm

Supervisors
Tina Daviter & Mark Williams

Project Description
Whereas, the interactions of many protein domains are now well understood at 25°C in dilute solution, the present quantitative understanding of how these might be modified inside cells is very poor. Protein complex formation in the dense soup of the cellular cytoplasm depends not only on the intrinsic capacity for interaction of proteins, but on the chemical constituents of the local environment, particularly on salt and small molecule concentrations and on crowding effects due to surrounding proteins that are not part of the reaction.

We seek to examine the influence of several physical features of the cytoplasm that may be important in the thermodynamic properties and kinetics of protein-protein interactions. We intend to investigate the thermodynamic and kinetic consequences of such effects in detail by mimicking the cytoplasmic environment in the test-tube.

References
Ladbury JE & Williams MA (2004). The extended interface: measuring non-local effects on binding. *Curr Opin Struct Biol* 14:562-569.

Minton AP (2001). The influence of macromolecular crowding and macromolecular confinement on biochemical reactions in physiological media. *J Biol Chem* 276, 10577-10580.