BioSyM Seminar by
Prof. Peter J Hunter, FRS
Auckland Bioengineering Institute,
The University of Auckland,
Auckland, New Zealand

Venue: CREATE Theatre, CREATE TOWER, Level 2
Date: 9th Jan 2015
Time: 2.30 pm

Computational Physiology:
Connecting molecular systems biology with clinical medicine

Professor Hunter holds engineering degrees from the University of Auckland and a DPhil (PhD) in Physiology from Oxford University. He is currently a **Professor of Engineering Science and Director of the Bioengineering Institute at the University of Auckland, and co-Director of Computational Physiology at Oxford University.** As co-Chair of the Physiome Committee of the International Union of Physiological Sciences he has been helping to lead the international Physiome Project, which aims to use computational methods for understanding the integrated physiological function of the body in terms of the structure and function of tissues, cells and proteins, and has been developing the standards (CellML and FieldML) to facilitate reproducible multi-scale modeling.

Multi-scale models of organs and organ systems are being developed under the umbrella of the Physiome Project of the International Union of Physiological Sciences (IUPS) and the Virtual Physiological Human (VPH) project funded by the European Commission. These computational physiology models deal with multiple physical processes (coupled tissue mechanics, electrical activity, fluid flow, etc) and multiple spatial and temporal scales. They are intended both to help understand physiological function and to provide a basis for diagnosing and treating pathologies in a clinical setting. A long term goal of the project is to use computational modeling to analyze integrative biological function in terms of underlying structure and molecular mechanisms. It is also establishing web-accessible physiological databases dealing with model-related data at the cell, tissue, organ and organ system levels.

This talk will provide an update on the current state of the standards, databases and software being developed to support robust and reproducible multi-scale models for the VPH/Physiome project. These standards include CellML and FieldML for encoding models and BioSignalML for encoding time-varying signal data, together with model repositories and software tools for creating, visualizing and executing the models based on these standards. Recent work has focussed on the semantic annotation of physiological models in order to link parameters and variables in the models with bio-informatic databases and on new approaches to modelling tissue inhomogeneity.