One of the grand challenges in biomedical informatics is the large, complex, high-dimensional and often weakly structured datasets. This “big data” challenge can be described as volume, variety, velocity and, veracity. Simultaneously there is a trend toward precision medicine (that is predictive, preventive, participatory, personalised) and an explosion in the amount of generated biomedical datasets. Biomedical datasets include patient data (e.g. from cardiology, neurology, oncology, vascular), and “omics” data. With increasingly integrative approaches that combine datasets using rich networks of specific relationships, new methods and strategies of visualisation are essential. In a discussion by world leading researchers from Imperial College London this lecture examines these challenges for 21st Century medicine.

This inaugural lecture is presented by the UNSW STEAM Initiative, a collaboration between the faculties of Art & Design and Medicine.
Never Stand Still

Professor Jeremy K. Nicholson
PhD FMedSci. Head of the Department of Surgery and Cancer
Director, MRC-NIHR National Phenome Centre
Faculty of Medicine, Imperial College London, UK

UNSW is pleased to welcome Professor Jeremy Nicholson as a UNSW Visiting Professor 2015–2018

Professor Nicholson became Head of Biological Chemistry at Imperial College London (1998) and then Head of the Department of Surgery and Cancer (2009-present) which has recently expanded and is now named as the Department of Surgery, Oncology and Interventional Medicine. He is the Director of the MRC-NIHR National Phenome Centre and the Imperial-Institute of Cancer Research joint Centre for Systems Oncology and Director of the Centre for Gut and Digestive Health (Institute of Global Health Innovation at Imperial). He also has a new coordinating role as Director of the Institute of Translational Medicine and Applied Therapeutics which bridges the Imperial AHSC and the Faculty of Medicine research programmes in Stratified Medicine for optimising patient safety and healthcare delivery. Nicholson has authored over 600 peer-reviewed papers on metabolic biochemistry, molecular aspects of complex system failure and systems medicine. A major research focus is on microbiome-host metabolic signalling and the role of the microbiome-host interactions in personalised healthcare and disease risks for diabetes, autism and cancer. He is an ISI Highly-Cited Researcher (2014) in Pharmacology and Toxicology (ISI H index = 100). His work has been recognised by international awards including: The Royal Society of Chemistry Silver (1992) and Gold (1997) Medals for Analytical Science and Analytical Chemistry respectively; The Chromatographic Society Silver Jubilee Medal (1994); The Pfizer Prize for Chemical and Medicinal Technology (2002); The RSC medal for Chemical Biology (2003); The RSC Interdisciplinary Prize (2008); The RSC Theophilus Redwood Lectureship (2008); The Pfizer Global Research Prize for Chemistry (2006); The NIH Stars in Cancer and Nutrition Distinguished Lecturer (2010) and The Semmelweis-Budapest International Prize for Biomedicine (2010). In 2010 he was elected Fellow of The UK Academy of Medical Sciences; elected as an Honorary Lifetime Fellow of the International Metabolomics Society (2012); elected Honorary Member of the US Society of Toxicology (2013); elected as an Albert Einstein Honorary Professor of the Chinese Academy of Sciences (2014). He currently holds honorary professorships at 8 other international Universities. He is also a founder director of Metabometrix, an Imperial spin-off company (founded 2001) specializing in molecular phenotyping, toxicological screening and clinical diagnostics.


Changes in climate and population densities and distribution plus increasing socioeconomic stresses placed on healthcare systems pose a unique series of challenges in 21st Century medicine. A tension exists between the development of new investigative, diagnostic and prognostic technologies and the ability of scientists and healthcare professionals to deliver effective translational solutions. Systems biology tools can be applied at both individual and population levels to understand integrated biochemical function in relation to disease pathogenesis but there are still barriers to the clinical actionability of these modelling tools that present barriers to translation. The complex gene-environment interactions that create individual and population disease risks are also responsible for the expression of metabolic phenotypes in different body compartments and fluids. Thus metabolic phenotyping offers an important window on human systemic activity and spectroscopic tools can be employed to help characterize personalised profiles, disease processes and responses to therapy (1). We have developed new scalable and translatable strategies for “phenotyping the patient journey” (2) using top-down systems biology tools that capitalize on the use of metabolic datasets (3) for diagnostic and prognostic biomarker generation to aid clinical decision-making at point-of-care. These have been shown to be of value in the development of prognostic marker models for both clinical efficacy and drug toxicity in cancer patients. Such approaches, including those for near real-time applications as in surgery, molecular pathology, oncology and critical-care, can be extremely sensitive for the detection of diagnostic and prognostic biomarkers in a variety conditions (4,5). These methods also provide a powerful adjunct to conventional procedures for disease assessment that are required for future developments in “precision medicine” including understanding of the symbiotic influences on patient state (6). Finally, the “Metabolome Wide Association Study” (7) concept provides powerful new tool to generate disease risk biomarkers (e.g. for cancer or cardiometabolic diseases) from epidemiological sample collections. Such population risk models can also link to individual patient healthcare models thus closing the personal and public healthcare modelling triangle. The ultimate challenge is to take complex validated data sets and models on human biology and to visualise these in engaging formats and forms that clinically actionable in an ever changing background of human health.

Dr Robert Plumb
Division Surgery and Oncology, Imperial College London
Director of Metabolic Phenotyping and Stratified Medicine
in the Waters Health Sciences Business Operations Division, Milford, Massachusetts, USA

Dr Plumb is the Director of Metabolic Phenotyping and Stratified Medicine in the Waters Health Sciences Business Operations Division, based in Milford, Massachusetts. Dr Plumb has published over 100 papers on the subject of HPLC/MS and NMR for bioanalysis, metabolomics and metabolite identification. He is a recognized expert in the use of liquid chromatography with mass spectrometry, capillary scale LC, purifications scale LC and metabonomics, giving many invited papers at international meetings around the world. After obtaining an honors degree in Chemistry from the University of Hertfordshire in 1992, he started work in at Glaxo Research and Development Drug Metabolism Department. During his time at Glaxo and later GlaxoWellcome he continued his research in liquid chromatography combined with NMR and mass spectrometry for metabolite identification and bioanalysis obtaining his PhD in 1999. Dr Plumb continued his work for GlaxoWellcome with the responsibility of metabolite identification using HPLC/MS/NMR and new analytical technology development. In 2001 he moved to Waters Corporation in Milford, MA, USA where he was responsible for the Life Science Chromatography group and latterly LC/MS applications in the Pharmaceutical Market Development Group before becoming the Director of Metabolic Phenotyping. He is currently a visiting Professor in Analytical Chemistry at Kings College London, visiting Professor at Imperial College in the Dept Surgery and Cancer and a Fellow of the Royal Society of Chemistry. In 2014 he was awarded Highly Cited Researcher by Thompson Reuters.

When Is a BioMarker Not a Biomarker: Training The Medical Community Of The Future

The analytical challenges that face global systems biology in an animal study or a human population environment are many fold; These include the detection of all of the analytes in the samples, the accurate measurement of their relative concentrations, data reduction, the identification of effected biological pathways, all this must be achieved in a short time frame to allow rapid the processing of thousands of samples. The detection of endogenous metabolites requires a high resolution, high sensitivity instrumentation such as chromatography and mass spectrometry system. This is especially true in biological samples such as plasma, urine and bile, where the matrix is particularly complicated. The results from these studies can be confounded by factors such as diet, prescription medicine, OTC medication and environmental exposure. In this presentation we discuss the analytical tools and visualization processed required to discover and verify new biomarkers of disease as well as how clinician and researchers of the future are trained to understand limitations and potential for investigating disease and public health.