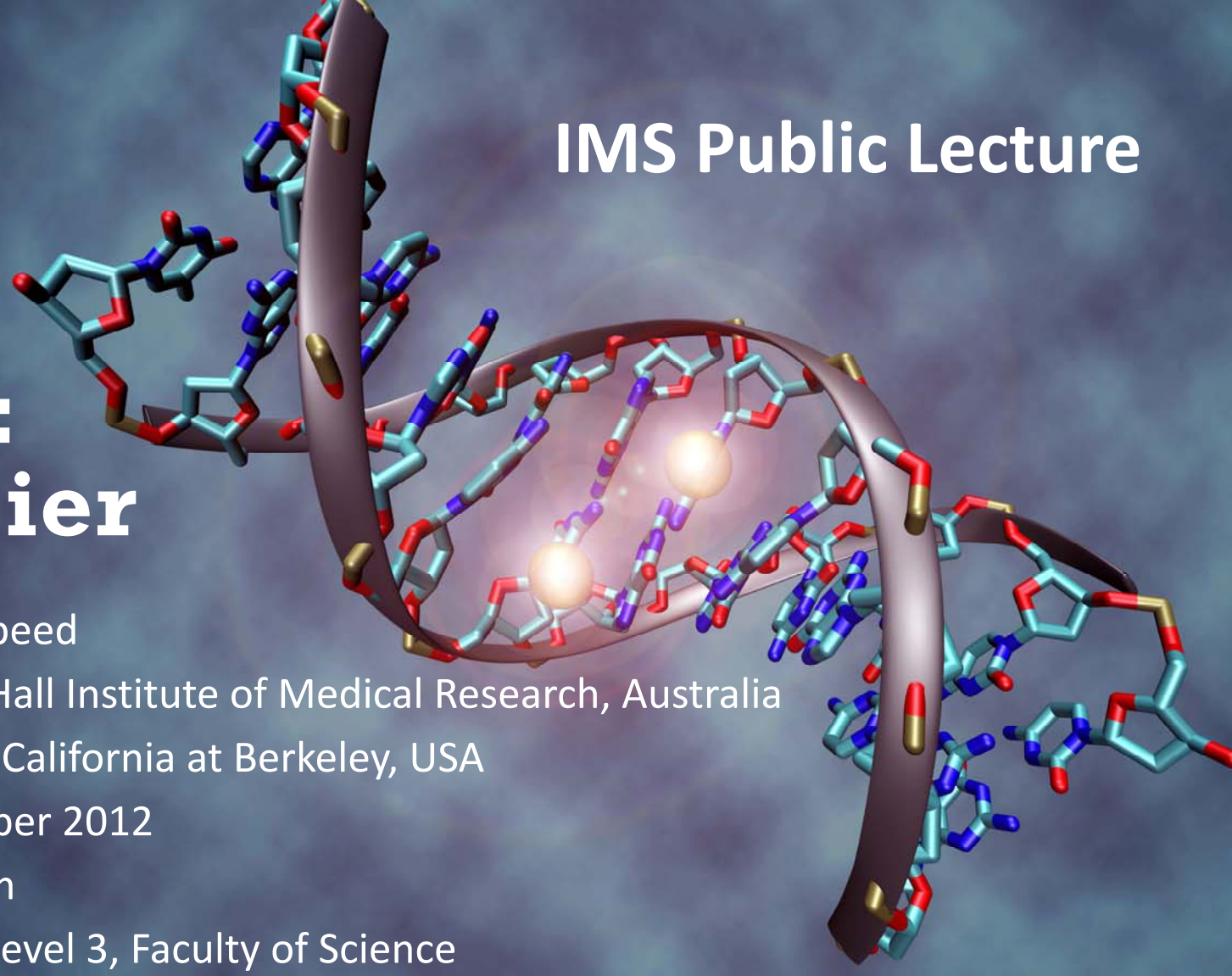
IMS Public Lecture

Epigenetics: A New Frontier



Speaker: Professor Terry Speed
Walter and Eliza Hall Institute of Medical Research, Australia
and University of California at Berkeley, USA

Date: Tuesday, 16 October 2012

Time: 6:30 pm - 7:30 pm

Venue: LT31, Block S16, Level 3, Faculty of Science
National University of Singapore, Singapore 117543

Free Admission

About the Speaker

Terry Speed completed a BSc (Hons) in mathematics and statistics at the University of Melbourne (1965), and a PhD in mathematics at Monash University (1969). He held appointments at the University of Sheffield, U.K. (1969-73) and the University of Western Australia in Perth (1974-82), and he was with Australia's CSIRO between 1983 and 1987. In 1987, he moved to the Department of Statistics at the University of California at Berkeley (UCB), and has remained with them ever since. In 1997, he took an appointment with the Walter & Eliza Hall Institute of Medical Research (WEHI) in Melbourne, Australia, and was 50:50 UCB:WEHI until 2009, when he became Emeritus Professor at UCB and full-time at WEHI, where he heads the Bioinformatics Division. His research interests lie in the application of statistics to genetics and genomics, and to related fields such as proteomics, metabolomics and epigenomics.

Abstract

Apart from a few exceptions the DNA sequence of an organism, that is, its genome, is the same no matter which cell you consider. If we view the genome as a universal code for an organism, then how do we obtain cellular specificity? The answer seems to be via epigenetics, where the Greek prefix *epi* denotes *above* or *on top of*, that is epigenetics is on top of genetics. Epigenetics controls the spatial and temporal expression of genes, and is also associated with disease states. It involves no change in the underlying DNA sequence, and epigenetic marks are typically preserved during cell division.

With the advent of microarrays 15 years ago, these platforms began to be used to give high-throughput information on epigenetics. In the last 5 years, second (also called next-) generation DNA sequencing has been used to study epigenetics, in particular using bisulphite-treated DNA or chromatin immunoprecipitation (ChIP) assays, each followed by massively parallel DNA sequencing. There are now large national and international consortia compiling DNA sequence data relevant to epigenetics, and many statistical challenges are arising.

If we think of the single (reference) human genome, there will be literally hundreds of reference epigenomes, and their analysis will occupy biologists, bioinformaticians and biostatisticians for some time to come. This talk will introduce the topic, outline the data becoming available, summarize some of the progress made so far, and point to future biostatistical challenges.

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