

Victorian Centre for Biostatistics**Seminar**

**Thursday 26th June
9.30am to 10.30am
Seminar Room 2, Level 5
Alfred Centre
99 Commercial Road, Prahran**

Normalization**Professor Terry Speed**

**Division of Bioinformatics
Walter & Eliza Hall Institute**

Normalization is a term that has come to describe a range of adjustments done to data prior to carrying out conventional statistical analyses. Usually it is not model-based. It first came to my attention with microarray data, but is now used for a wide range of "omic" data (genomic, proteomic, metabolomic,...) and beyond. In this talk I'll describe some of my experiences with this notion. Along the way, I'll explain why and how people normalize data, and how it affects their ultimate results. My main story will be from microarray gene expression data, but I'll also mention RNA-seq data. My view now is that it can be model-based.

Professor 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.

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