

**Are you a student doing research in Computational Biology or Bioinformatics?**

**Do you share our aspiration to advance current understanding of the life sciences using computer science or mathematics?**

Meet and have a casual drink with other students like you at the:

# Computational Biology and Bioinformatics Seminar followed by Wine and Cheese

**Date:** Tuesday 27<sup>th</sup> of November, 5:30pm - 6:30pm

**Venue:** Brown Theatre, Level 1  
Department of Electrical and Electronic Engineering (Building 193)  
University of Melbourne  
Map: <http://www.pb.unimelb.edu.au/CampusMaps/Parkville.pdf>

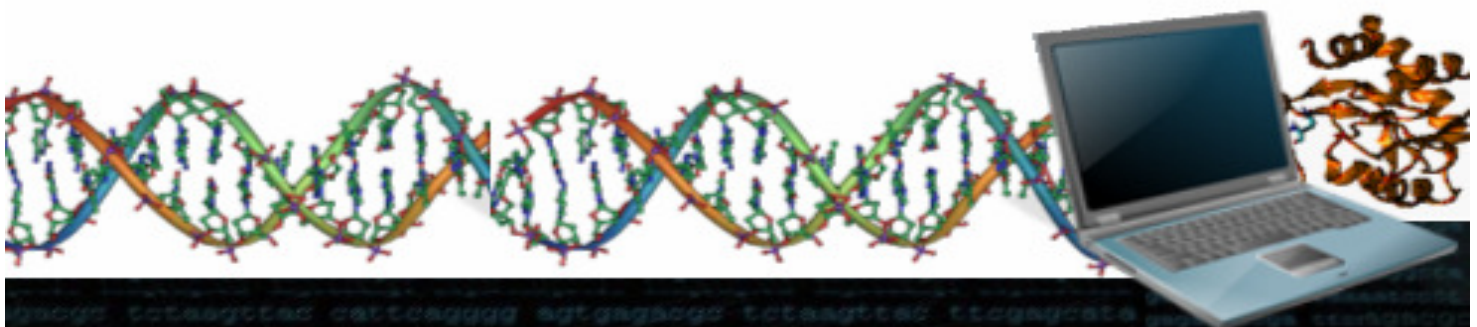
**Program:** 30 mins seminar by **Prof. Terry Speed** + 30 mins discussion and drinks

**Abstract:** **Ten reasons why I like to do bioinformatics** (by Terry Speed @ WEHI): **1.** I've always wanted to do biomedical research. **2.** I was a disaster in chem and bio labs. **3.** I like chemistry in general, and biomolecules in particular - in theory. **4.** I don't want to get rich or famous. **5.** I was o.k. at maths and stats. **6.** I like collaborative research. **7.** I like interdisciplinary research. **8.** I prefer being in neglected minorities to being mainstream (i.e. I'm a neurotic introvert). **9.** Some people in other countries say it's important. **10.** It might get properly funded in Australia one day.

**It's a rapidly moving field. I might change these reasons before November 27, so come along and find out.**

**Bio:** Terry Speed splits his time roughly 50:50 between the Department of Statistics at the University of California, Berkeley (Jan-May) and WEHI (June-Dec) each year. His research and teaching interests cover many aspects of the application of statistics to genetics and molecular biology, including biomolecular sequence analysis, the mapping of genes in experimental crosses and human pedigrees, and the analysis of gene expression data. His major interests within this area are in the mapping of genes in mice and humans, including disease genes and genes contributing to the variation of quantitative traits. The Human Genome Project was a stimulus for a number of the problems he has investigated with his students. Other areas of interest include the analysis of DNA and protein sequences, for example, finding genes or motifs in DNA sequence, and the analysis of microarray data. He is currently on the editorial board of the Journal of Computational Biology, JASA, Bernoulli and the Australian and New Zealand Journal of Statistics.

**Registration by the 23rd November is essential, RSVP to [combiogroup@yahoo.com.au](mailto:combiogroup@yahoo.com.au)**



This event is organized by **ICT for Life Sciences Forum Students Chapter**, an initiative designed to convene the community of interest at the convergence of the Life Sciences and Information and Communication Technology disciplines for the purpose of knowledge sharing, fostering collaboration and innovation.