

# **MURPA Seminar Friday 23 September 2011 at 9am: Compute- and Data-Intensive Analyses in Bioinformatics**

Venue: Seminar Room 135, Building 26 Monash Clayton

Presenter: Dr Wayne Pfeiffer, San Diego Supercomputer Centre

Abstract:

The advent of high-throughput DNA sequencers has produced a flood of genomic data. How big is this flood, and what are the computational requirements for analyzing the data? These questions will be addressed for three common types of bioinformatics analyses: read mapping (including pairwise alignment), de novo assembly, and phylogenetic tree inference. Use of the TeraGrid for phylogenetic analyses via the CIPRES gateway will also be summarized

Bio:

Wayne Pfeiffer is a Distinguished Scientist at SDSC and has been with the center since its inception in 1985, serving as Deputy Director for many years. The gateway Wayne works on currently accounts for 25% of all TeraGrid (now XSEDE) users. He is currently doing research in supercomputer performance analysis, an area of long-standing interest to him. Previously he was principal investigator for NSF- and DARPA-funded studies to evaluate a novel computer with multithreaded architecture. Before that he co-lead the Joint NSF-NASA Initiative on Evaluation of scalable parallel computers.

During most of his tenure at SDSC, he has held various senior management positions - for several years as Deputy Director of NPACI, the NSF-funded national partnership led by SDSC. In that capacity he coordinated the resources activities of NPACI.

Before helping found SDSC, he worked at General Atomics as a computational physicist in fission and fusion energy research and development. He has a PhD in engineering science from the California Institute of Technology and belongs to the American Physical Society and IEEE Computer Society.