

## **MURPA Seminar: Friday 14 September 2012, 9am**

### **The CIPRES Science Gateway: Enabling High-Impact Science for Phylogenetics Researchers with Limited Resources**

**Speaker:** Dr Mark Miller

**Venue:** Seminar Room 135, Building 26, Clayton Campus, and Seminar Room H7.84, Caulfield Campus, Monash University

#### **Abstract:**

In the past decade, the rate of DNA sequence accumulation has increased more rapidly than the number of floating point operations on a computer processor core (i.e. Moore's law). The rapid accumulation of DNA sequences makes it possible to ask broader and deeper questions about evolutionary relationships, but the problems are computationally difficult, and can only be answered by scientists with access to substantial computing resources. In other words, scientists in lesser resourced laboratories find it difficult to ask big questions. The CIPRES Science Gateway (CSG) was created to provide browser-based access to the resources required for modern phylogenetic research. The Gateway currently provides 5 parallel phylogenetic codes run on large compute clusters. The toolkit is modest, yet more than 4000 users have run more than 100,000 parallel tree inference jobs on XSEDE resources since December, 2009. The talk will describe the process of creating a highly successful Gateway, the challenge that by a rapidly growing user base, and the impact of the Gateway on discovery in Biology.

#### **Biography:**

Mark Miller leads the Next Generation Tools for Biology Group at the San Diego Supercomputer Center. He currently leads the CIPRES Science Gateway and the Next Generation Biology Workbench projects at SDSC. His current professional focus is providing enabling tools and capabilities for Biology, but his interests are broad and includes publications in many areas of biochemistry and structural biology. He holds a PhD in Biochemistry from Purdue University.