Seminar: Friday 11 October 2013:Monash Undergraduate Research Projects Abroad (MURPA) and Queensland Undergraduate Research Projects Abroad (QURPA).

The annual MURPA/QURPA program exposes final year undergraduate students to an international research experience within a leading research laboratory.

On Friday 11 October Dr Mark Miller will present his seminar "Embedding CIPRES Science Gateway Capabilities in Phylogenetics Software Environments" live to audiences in Melbourne and Brisbane.

Melbourne Date: Friday 11 October Time: 10.00 - 11.00am Location - Monash University: Seminar Room G12A, Building 26, Clayton Campus Enquiries: Caitlin Slattery (Faculty of IT)

Brisbane Date: Friday 11 October Time: 9.00 - 10.00am Location - University of Queensland: Seminar Room 505A, Building 47 (Axon), St Lucia Campus Enquiries: Sharon Cook (Research Computing Centre)

San Diego Date: Thursday 10 October Time: 4.00pm - 5.00pm Location: 5004 Meeting Room Enquiries: Teri Simas

Abstract: Embedding CIPRES Science Gateway Capabilities in Phylogenetics Software Environments

Mark Miller, San Diego Supercomputer Center

The explosive growth in DNA sequence data over the past decade makes it possible to clarify evolutionary relationships among all living things at unprecedented levels of resolution. However, The phylogenetic inference codes required to accomplish this goal are computationally intensive, so turning this wealth of DNA sequence data into new insights about evolution requires access to high performance computing (HPC) resources. The CIPRES Science Gateway (CSG) was designed to meet this need by providing browser-based access to phylogenetic codes run on XSEDE compute resources. The CSG has accelerated discovery by supporting more than 6,100 users and enabling more than 600 publications over the past three years. This talk will describe plans to take access to a new level, by creating a set of RESTful CSG web services that can be accessed programmatically by any developer through a public API. The public API will make it possible to embed access to XSEDE resources in well-established community phylogenetics software packages, leveraging investments by developers who create these rich work environments and by users who use them. The public API will also allow any developer with modest scripting skills to access and use CSG capabilities outside of the current browser interface. This talk will describe design of the CSG web services, identify potential issues to be addressed in exposing programmatic access to HPC resources, and describe plans to embed the CSG web services in eight popular community applications.