

## **W0064**

**Maximum Likelihood Molecular Replacement in Phaser.** Randy Read, Airlie McCoy, Laurent Storoni, CIMR, Univ. of Cambridge, Hills Rd., Cambridge CB2 2XY, UK.

The Phaser software for molecular replacement has been developed with the twin aims of providing improved search algorithms and of being highly automated. The novel molecular replacement ensembling, rotation and translation function algorithms have been developed using maximum likelihood and multivariate statistics, and have proved to be significantly better than traditional methods for discriminating correct solutions from noise. The molecular replacement functionality has been linked to packing and rigid body refinement functionality to provide automated tree-searches, giving solutions where the patience and job-tracking abilities of users would be exhausted. Phaser is also our platform for the future development of improved phasing methods and their release to the crystallographic community.