New Likelihood-based Phasing Methods in *Phaser*

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We have been developing a new program, *Phaser*, to apply likelihood to solving macromolecular crystal structures by molecular replacement and experimental phasing methods.

Initial experiences with molecular replacement using brute-force likelihood targets in the program *Beast* [1] showed that likelihood had greater power to discriminate correct solutions, but the brute-force approach was prohibitively slow. To address this problem we have developed likelihood-based fast rotation [2] and fast translation [3] functions. The combination of these fast targets in *Phaser* with powerful automation strategies makes it possible to solve many difficult molecular replacement problems routinely.

More recent developments in *Phaser* focus on experimental phasing. The program includes new likelihood targets for phasing by SAD [4], as well as by MAD or MIRAS (unpublished). Completion of the heavy-atom substructure is accomplished through the automated interpretation of log-likelihood-gradient maps.

Applications of *Phaser* to difficult structure solutions will be discussed, along with plans for future development.

[1] Read R.J., *Acta Cryst.*, 2001, **D57**, 1373. [2] Storoni L.C., McCoy A.J., Read R.J., *Acta Cryst.*, 2004, **D60**, 432. [3] McCoy A.J., Storoni L.C., Read R.J., *Acta Cryst.*, 2005, **D61**, *in press*. [4] McCoy A.J., Storoni L.C., Read R.J., *Acta Cryst.*, 2004, **D60**, 1220.

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