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IL MILIONE: a new suite for crystal structure solution

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IL MILIONE is a suite of computer programs devoted to crystal structure solution. It is able to solve crystal structures in the following cases:
a) *ab initio* for small, medium size crystal structures and proteins (SIR2006). Early figures of merit rank the trial phase sets provided by Patterson Methods or Direct Methods; phase extension and refinement has been powered allowing to solve protein structures even if data have quasi-atomic resolution (1.4-1.5Å).
b) SIR-MIR, SIRAS-MIRAS, SAD-MAD data. The program automatically performs the following steps: the structure factor moduli of the substructure constituted by heavy/anomalous scatterers are evaluated, the substructure is located and such information is used to phase protein reflections
c) Molecular Replacement (REMO). An atomic model is oriented and positioned in the protein cell by exploting experimental reflection moduli at limited resolution.
Finally phases are improved via density modification techniques. All the programs are integrated and controlled by means of a friendly GUI used both to provide input data and to monitor run and results by means of (real time updated) diagrams, histograms etc.
IL MILIONE will be available, in executable format, for Linux and Windows systems.

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Ligand Pose Analysis using Fourier ″Difference of Difference″ Analysis

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Current techniques that are used to fit ligands within unoccupied electron density of protein complexes range from manually fitting rigid conformers by eye to automated fitting with conformational flexibility. The techniques for validating these poses primarily rely upon choosing a low energy conformer, and/or selection of a biologically feasible binding mode. Subsequent refinement of the complex is biased by the initial pose selection. We propose an automated validation technique to be used prior or post refinement. Given multiple poses, it ranks them by Fourier difference analysis in the proposed active site. The efficacy of our ″difference of difference″ method is illustrated with examples of difficult ligands or low resolution data. Our method provides a quantitative measure of ligand fitness based upon the diffraction data as well as the protein interaction scoring of the model.