W0239

Real Space Protein Model Completion: An Inverse Kinematics Approach. Henry van den Bedem, Itay Lotan, Jean-Claude Latombe, Ashley Deacon, Joint Center for Structural Genomics/SSRL, Stanford Linear Accelerator Center, 2575 Sand Hill Rd., Menlo Park, CA 94025 USA.

Rapid structure determination relies greatly on the availability of software that can automatically build a protein model into an experimental electron density map. In favorable cases, the programs ARP/wARP, RESOLVE, MAID, and TEXTAL are capable of building over 90% of the final model. At medium-low resolution, only about 2/3 completeness can be expected. To aid model completion, we have developed an algorithm that combines fast inverse kinematics with a real space, torsion angle refinement procedure to fit a poly-alanine chain to the electron density between two anchor points.

The algorithm has been tested and used to complete initial models generated with RESOLVE v2.03. At 2.0A, it closed gaps of 12 residues in length to within 0.25A all-atom RMSD of the final refined structure. In a 2.8A model, it closed 12 residue gaps to within 0.6A. Tests show that our fragments are well within the convergence radius of standard refinement programs. This new algorithm may thus have an application in extending automation of model building towards lower resolution levels.

Test structures were solved and deposited by the JCSG pipeline (www.jcsg.org). The JCSG is funded by the PSI, NIH NIGMS, SSRL operations by DOE BES, and the SSRL SMB program by DOE BER, NIH NCRR BTP and NIH NIGMS. IL is supported in part by a Siebel Fellowship. IL and J-CL are also funded by NSF ITR grant CCR-0086013 and a Stanford BioX Research Initiative grant.