MODERATE RESOLUTION FITTING – A DISCUSSION

Moderate Resolution

- Rigid body fitting
- Flexible fitting
- Feature Extraction
- Using Other Restraints

Information obtained from: http://3dem.ucsd.edu/SI_Table1_ver2.pdf

Rigid Body Fitting

- 3SOM
  - http://www.russelllab.org/3SOM/
  - Fitting of atomic structures to low resolution electron density maps by surface overlap maximization.
- BCL::EM-Fit
  - http://meilerlab.org/index.php/servers/show?s_id=6
- Emfit
  - http://bilbo.bio.purdue.edu/~viruswww/Rossmann_home/softwares/emfit.php
  - Fitting criteria includes the sum of densities at atomic sites, the lack of atoms in negative or low density, the absence of atomic clashes between symmetry-related positions of the atomic structure, and the distances between identifiable features in the map and their positions on the fitted atomic structure, etc.
  - Can handle symmetry

Rigid Body Fitting

- Chimera
- GMFit
  - https://pdbj.org/gmfit/
  - GMFit superimposes several subunit atomic models into a low resolution EM using a Gaussian Mixture Model.
- MultiFit
  - http://modbase.compbio.ucsf.edu/multifit/
  - Simultaneously fitting atomic structures of components into their assembly EM map.
- Situs
  - A package for the modeling of atomic resolution structures into low-resolution density map s e.g. from electron microscopy, tomography, or small angle X-ray scattering

Flexible Fitting

- DireX
  - http://www.schroderlab.org/software/direx/ef2-1.avi
  - DireX performs efficient geometry-based conformational sampling of protein structures under experimental restraints. It combines prior structural information with experimental data through the Deformable Elastic Network (DEN) approach which drastically reduces over-fitting.
- Flex-EM
  - http://topf-group.ismb.lon.ac.uk/flex-em/
  - The method includes a rigid fitting stage followed by a refinement stage, either conjugate gradients minimization (CG) or simulated annealing molecular dynamics (MD)

Flexible Fitting

- iModFit
  - http://chaconlab.org/hybrid4EM/imodfit
  - Efficient tool for flexible fitting of atomic structures into EM maps based on Normal Mode Analysis in internal Coordinates.
- MDFF
  - http://www.ks.uiuc.edu/Research/mdff/
  - Flexibly fit atomic structures into density maps. The method consists of adding external forces proportional to the gradient of the density map into a molecular dynamics simulation of the atomic structure. Other data can be added as additional restraints.

Flexible Fitting

- NMFF
  - http://mmtsb.org/software/nmff.html
  - Flexible multi-resolution fitting of large atomically detailed structures into electron density maps from cryo-EM, tomography and related lower resolution methods.
- NORMA
  - http://www.sciences.univ-nantes.fr/elnemo//NORMA/
  - NORMA searches along few lowest frequency modes to minimize the URO misfit parameter using a multiple-dimension simplex-minimization with optional simulated annealing. Minimization calculations are performed in reciprocal space, which reduced density segmentation bias.

Feature Extraction

- Gorgon/Pathwalker
  - http://gorgon.wustl.edu/
  - Gorgon is an interactive molecular modeling system specifically geared towards cryo-EM and other low resolution structures of macromolecular complexes. Gorgon's de novo modeling procedure couples sequence-based secondary structure prediction with feature detection and geometric modeling techniques to generate initial protein backbone models.
- Chimera
  - Watershed segmentation

Integrative Modelling

- IMP
  - https://integrativemodeling.org/about.html
  - IMP's broad goal is to contribute to a comprehensive structural characterization of biomolecules ranging in size and complexity from small peptides to large macromolecular assemblies, by integrating data from diverse biochemical and biophysical experiments.