DockEM2 (and ShapeEM)

Part 1 – (YESTERDAY)
Introduction

Using with UCSF Chimera
UCSF Chimera options

Practical example
Run you own domain

Part 2 – tomorrow-more detailed analysis of solutions
DockEM2 (and ShapeEM)

There will be a GUI soon.

Directed input, error trapping

Part 2 – today

Finish practical example

Run you own domain

More detailed analysis of solutions

Approaches to multidomain fitting

Validation of solutions

Displaying correlation maps in Chimera
DockEM uses the FLCF

- Fourier implemented Fast Local Correlation Function, or locally normalised correlation coefficient.

As described in:


Summary

• Normalised fast local correlation function is a Fourier real space method
• Costs 3 x
• Advantages are flying mask and optimal local normalisation
• Don’t need to define boundaries
• Equivalent to least squares matching of voxels, with scale optimisation.
Apo GroEL at 8 Å resolution
3D objects, 3D masks
Search object density ff8, with pdb
Mask around search object density
Mask around search object density
Fig 3. Move domain. Save relative to map.
DockEM2 solution compared to the full heptamer, pdb coordinates 1grl
Docked domains, with oligomer pdb:1grl
ShapeEM

• Same algorithm and concepts
• Entry point is density object
• Output is extracted densities aligned to match the search object.
Important factors

• Correct magnification scale for target map and search objects (DockEM2 can do a scale search)

• Match resolution ranges

• Fourier amplitude scaling check, match (DockEM2 will have a utility for this in the next release)
Validation

• Symmetry related domains don’t clash
• Multiple domains don’t clash
• Chains could be linked between domains
• The model will predict function of mutations
• (However allow for possible flexing of rigid bodies)
COLLAGEN VI
Hsc70-induced changes in clathrin-auxilin cage structure suggest a role for clathrin light chains in cage disassembly.

Young et al. Traffic 2013; 14(9) 987–996
Three-dimensional reconstruction of Heterocapsavcircularisquama RNA virus by electron cryo-microscopy
Chimera to examine correlation maps
More complicated schemes: Use and edit masks to define allowed regions

- Fit best domain first.
- Don’t allow next domains to intersect
- A) visually reject in Chimera
- B) use solution of 1 to mask the cccmap
- C) More specific procedure: Use Makedensity to turn pdb hit file into density model. See if this density is compatible with your current model, by checking for intersection. E.g. Using a spider script.
Notes will be provided

Documents

• SlidesDay1.pdf
• SlidesDay2.pdf
• INSTRUCTccpem-tutorial.pdf
• DockEM2.0-Instructions.pdf

We will prepare a package (including the programs) you can take with you tomorrow.
Viruses and the Development of Quantitative Biological Electron Microscopy

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Jo Butler, Samantha Wynne, John Berriman