

V19: Protein complexes – Density fitting

(1) We normally assume that various enzymes of a biochemical pathway „swim“ in the cytosol and randomly meet the substrate molecules one after another.

Yet, sometimes multiple enzymes of a pathway associate into large complexes and „hand over“ the substrates from one active site to the next one.

Advantage: avoids free diffusion, increases local substrate density.

(2) Membrane transporters and receptors often form oligomers in the membrane.

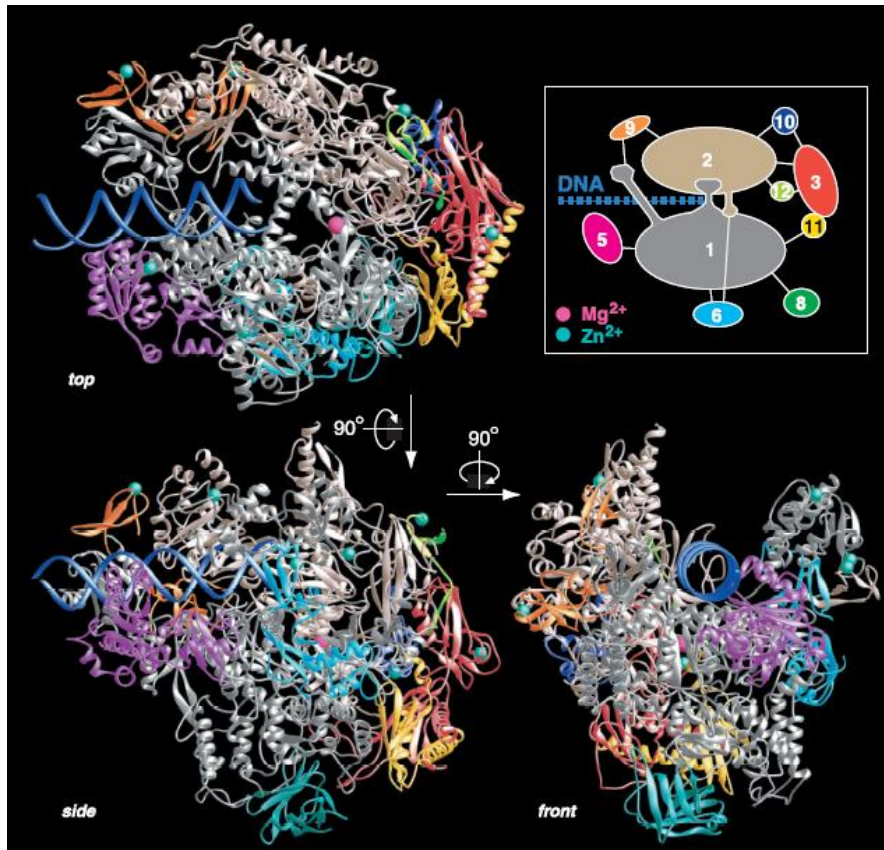
Advantage: (i) large structures are built from small building blocks (simplicity)

(ii) Oligomer formation can be regulated separately from transcription.

(3) Also: complicated structural components of the cell (e.g. cytoskeleton) are built from many small components (e.g. actin)

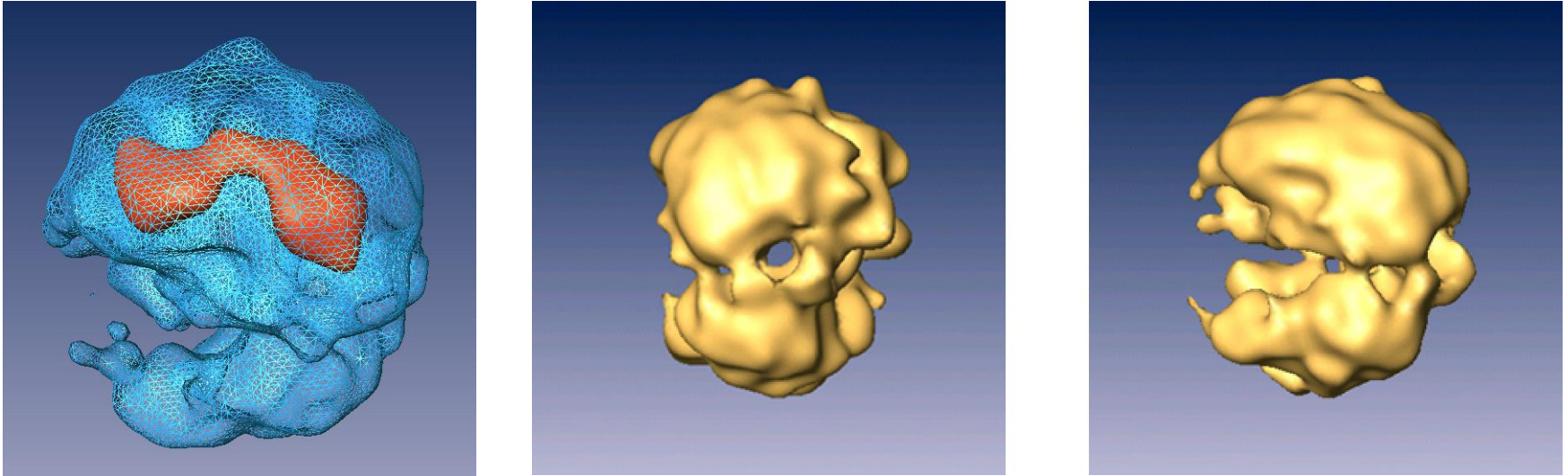
RNA Polymerase II

RNA polymerase II is the central enzyme of gene expression and synthesizes all messenger RNA in eukaryotes.



Cramer *et al.*, Science 288, 640 (2000)

RNA processing: spliceosome



Structure of a cellular editor that "cuts and pastes" the first draft of RNA straight after it is formed from its DNA template.

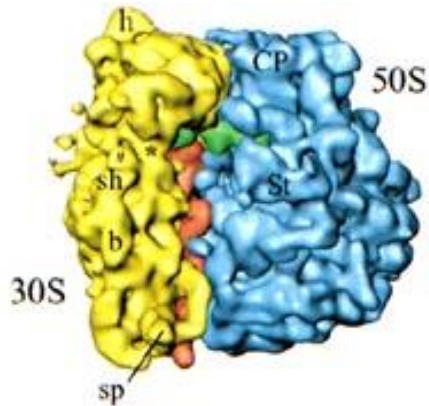
It has two distinct, unequal halves surrounding a tunnel.

Larger part: appears to contain proteins and the short segments of RNA, smaller half: is made up of proteins alone.

On one side, the tunnel opens up into a cavity, which is believed to function as a holding space for the fragile RNA waiting to be processed in the tunnel.

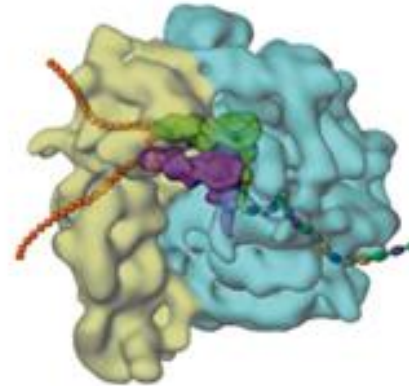
Profs. Ruth and Joseph Sperling
<http://www.weizmann.ac.il/>

Protein synthesis: ribosome



The ribosome is a complex subcellular particle composed of protein and RNA. It is the site of protein synthesis,

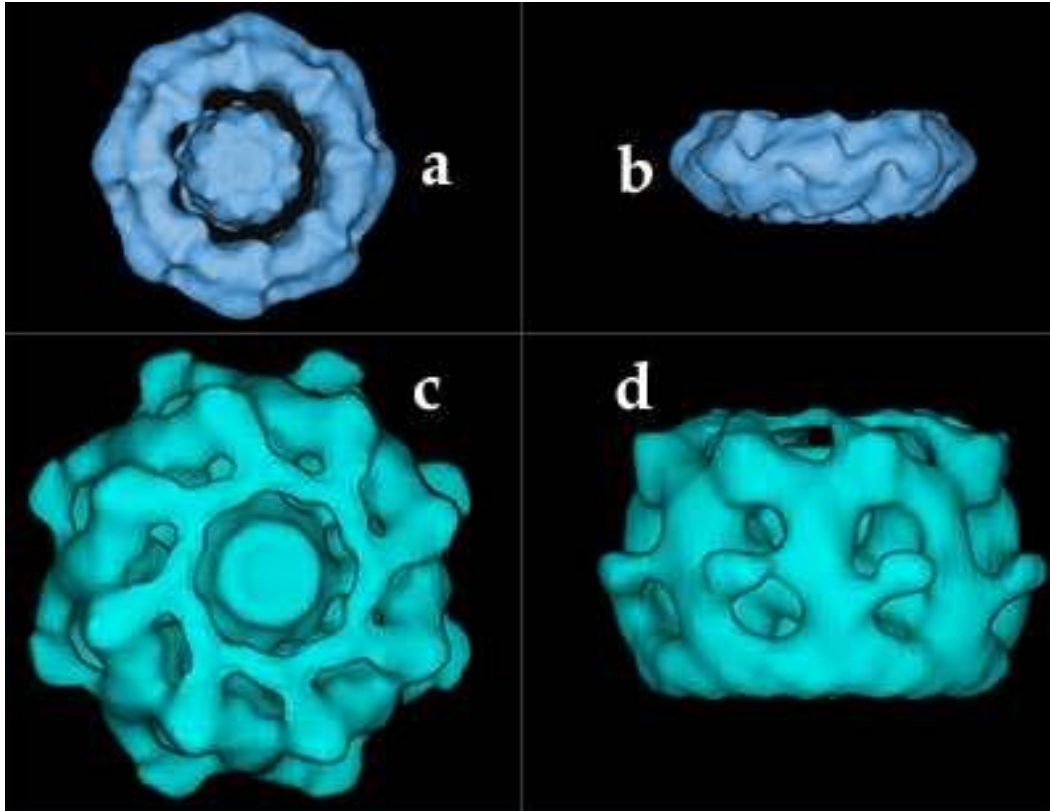
<http://www.millerandlevine.com/chapter/12/cryo-em.html>



Model of a ribosome with a newly manufactured protein (multicolored beads) exiting on the right.

Components of ribosome assemble spontaneously in vitro:
No helper proteins (assembly chaperones) needed

Nuclear Pore Complex



NPC is a 50-100 MDa protein assembly that regulates and controls trafficking of macromolecules through the nuclear envelope.

A three-dimensional image of the nuclear pore complex (NPC), revealed by electron microscopy.

A-B The NPC in yeast.

Figure A shows the NPC seen from the cytoplasm while figure B displays a side view.

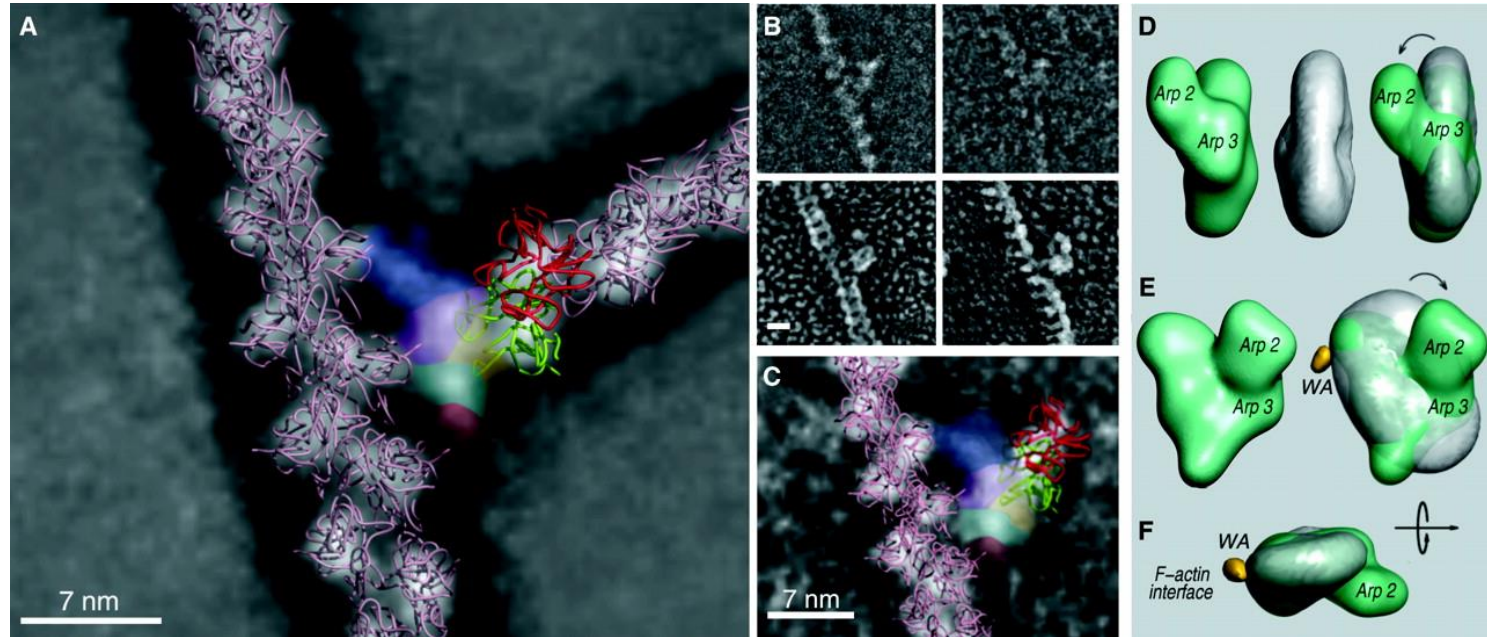
C-D The NPC in vertebrate (Xenopus).

http://www.nobel.se/medicine/educational/dna/a/transport/ncp_em1.html

Three-Dimensional Architecture of the Isolated Yeast Nuclear Pore Complex: Functional and Evolutionary Implications, Qing Yang, Michael P. Rout and Christopher W. Akey. Molecular Cell, 1:223-234, 1998

**Molecular structure:
lecture V22**

Arp2/3 complex

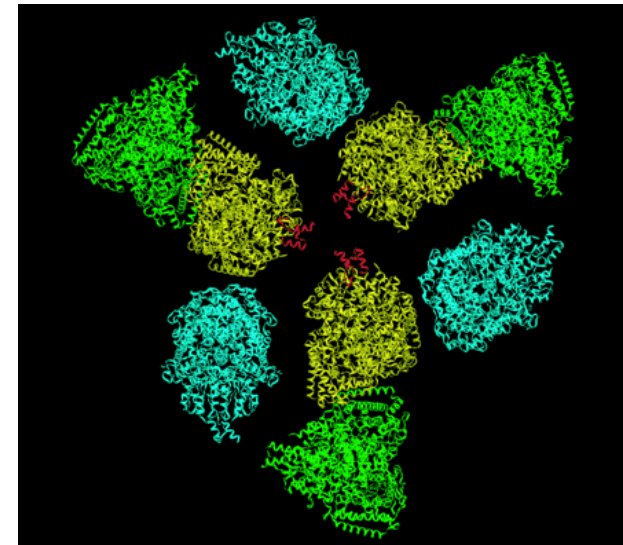
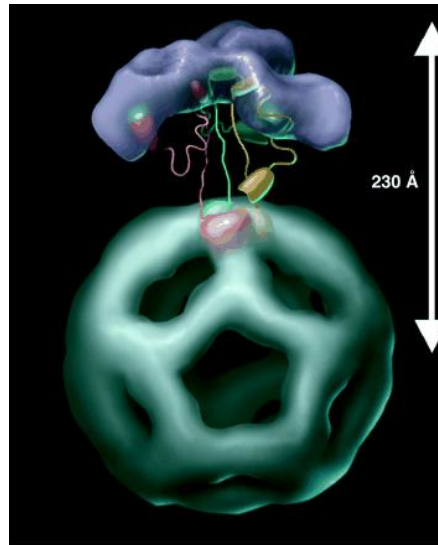
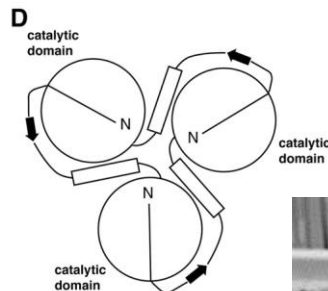
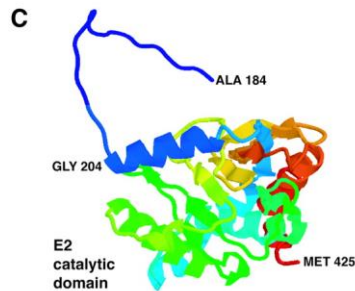
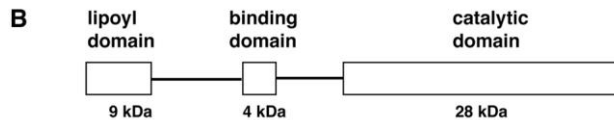
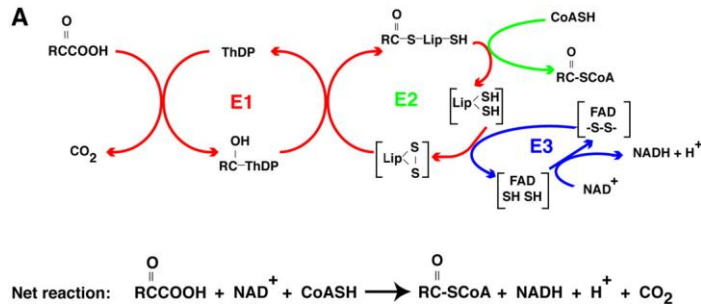


The seven-subunit Arp2/3 complex choreographs the formation of branched actin networks at the leading edge of migrating cells.

(A) Model of actin filament branches mediated by *Acanthamoeba* Arp2/3 complex. (D) Density representations of the models of actin-bound (green) and the free, WA-activated (as shown in Fig. 1D, gray) Arp2/3 complex.

Volkman *et al.*, Science 293, 2456 (2001)

icosahedral pyruvate dehydrogenase complex: a multifunctional catalytic machine

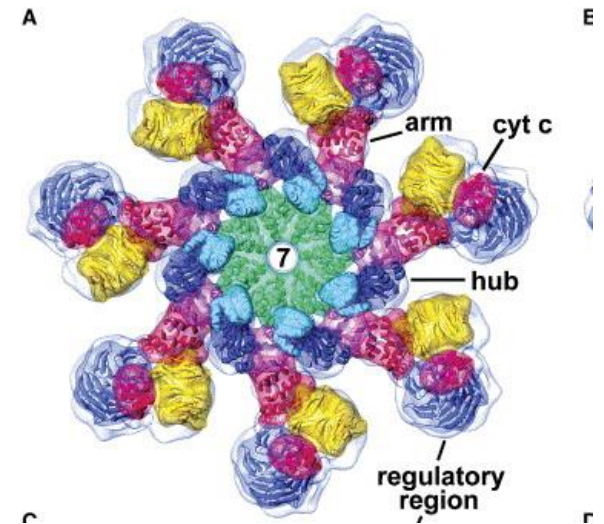
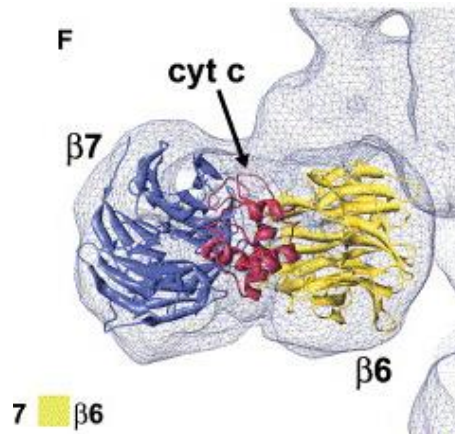
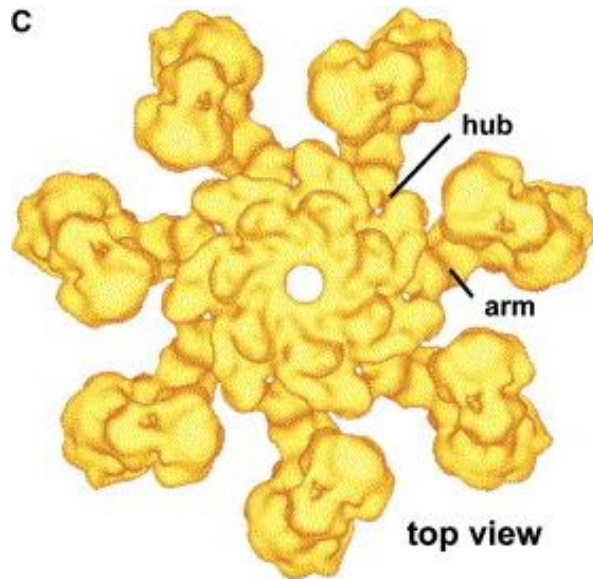


Model for active-site coupling in the E1E2 complex. 3 E1 tetramers (purple) are shown located above the corresponding trimer of E2 catalytic domains in the icosahedral core. Three full-length E2 molecules are shown, colored red, green and yellow. The lipoyl domain of each E2 molecule shuttles between the active sites of E1 and those of E2. The lipoyl domain of the red E2 is shown attached to an E1 active site. The yellow and green lipoyl domains of the other E2 molecules are shown in intermediate positions in the annular region between the core and the outer E1 layer. Selected E1 and E2 active sites are shown as white ovals, although the lipoyl domain can reach additional sites in the complex.

Milne *et al.*, EMBO J. 21, 5587 (2002)



Apoptosome



Apoptosis is the dominant form of programmed cell death during embryonic development and normal tissue turnover. In addition, apoptosis is upregulated in diseases such as AIDS, and neurodegenerative disorders, while it is downregulated in certain cancers. In apoptosis, death signals are transduced by biochemical pathways to activate caspases, a group of proteases that utilize cysteine at their active sites to cleave specific proteins at aspartate residues. The proteolysis of these critical proteins then initiates cellular events that include chromatin degradation into nucleosomes and organelle destruction. These steps prepare apoptotic cells for phagocytosis and result in the efficient recycling of biochemical resources.

In many cases, apoptotic signals are transmitted to mitochondria, which act as integrators of cell death because both effector and regulatory molecules converge at this organelle. Apoptosis mediated by mitochondria requires the release of cytochrome c into the cytosol through a process that may involve the formation of specific pores or rupture of the outer membrane. Cytochrome c binds to Apaf-1 and in the presence of dATP/ATP promotes assembly of the apoptosome. This large protein complex then binds and activates procaspase-9.

Determining molecular 3D structures

Experimental techniques:

Dimensions

proteins: 1 – 5 nm

atoms: 0.1 – 0.5 nm

bond stability

covalent ca. 300 kJ/mol

H-bonds: ca. 5 – 20 kJ/mol

X-ray crystallography

NMR

electron microscopy

FRET

AFM pulling



- applicability

- resulting information

- resolution

- distortions

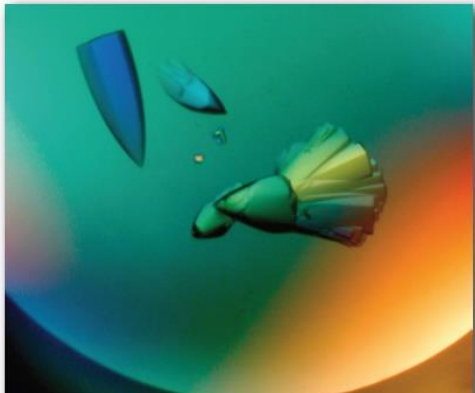
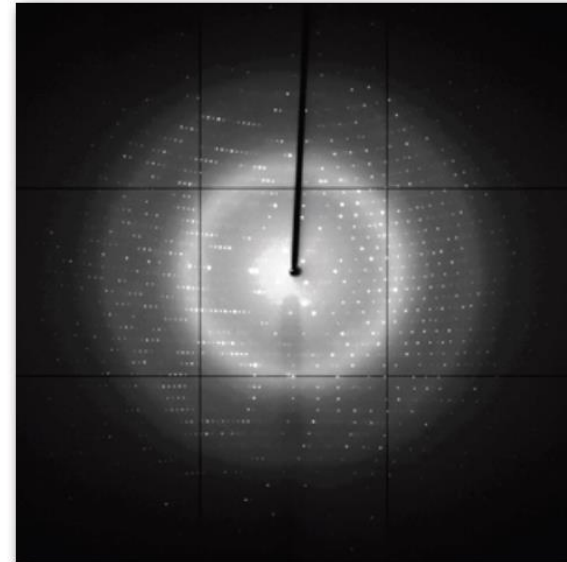
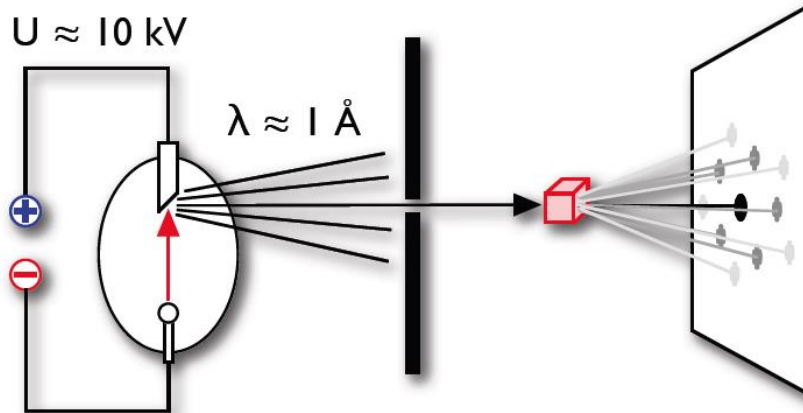
- effort/cost ...

Prediction techniques:

Homology modelling, correlation based fitting, ab-initio modelling

X-ray crystallography

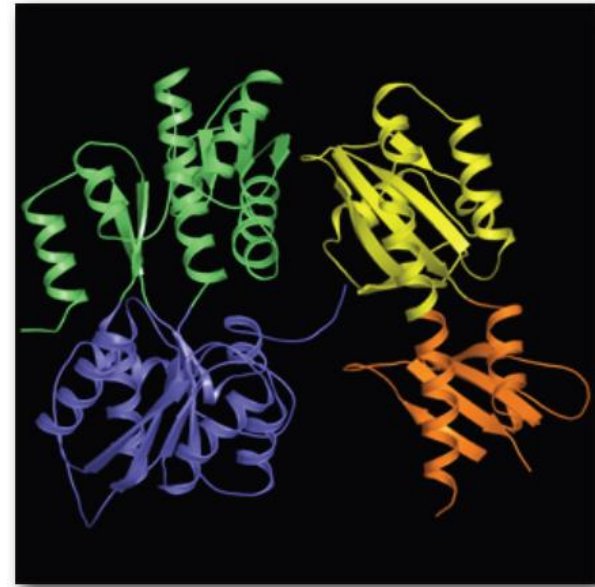
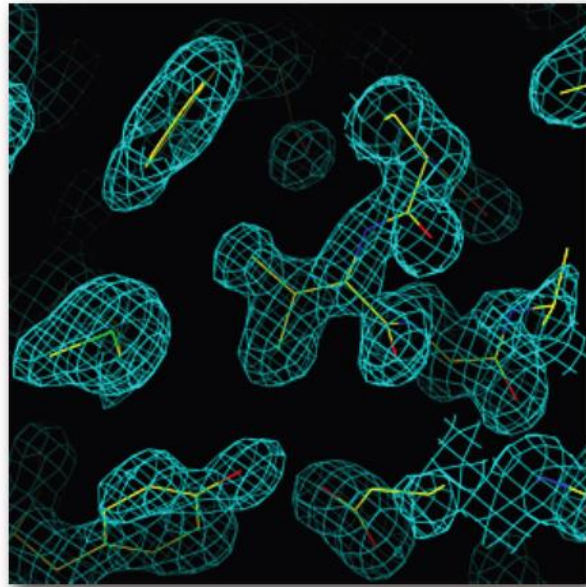
Beam of photons (no mass),
need high energy, method
needs relatively large samples



Crystallize proteins, record diffraction patterns
of X-rays (scatter at the electron clouds)
 \Rightarrow reconstruction

$$1 \text{ keV} \approx 10^5 \text{ kJ/mol}$$

X-ray reconstruction



Reconstruct electron density maps from diffraction patterns at multiple wavelengths and orientations, refine structure computationally

Main problem: proteins do not like to crystallize (especially membrane proteins)

PDB: experimental technique == X-Ray: 43138 results

X-Ray && "in the membrane": 1232 results

<http://www.molbio.princeton.edu/macro/about.html>

Nuclear magnetic resonance

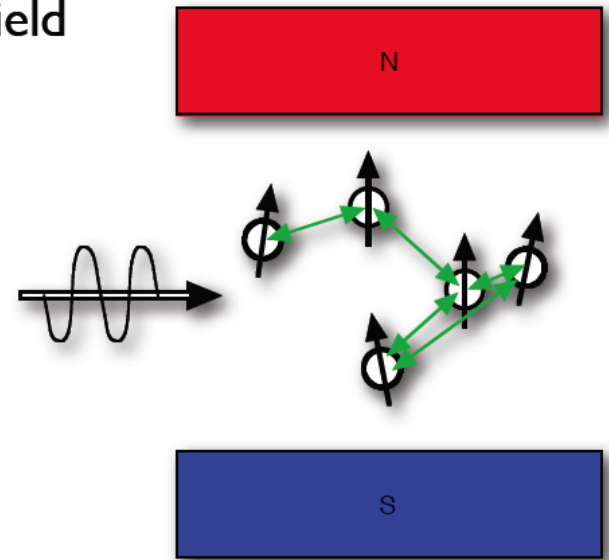
Place sample with the proteins into strong magnetic field
=> nuclei with non-zero magnetic moment
(^1H , ^{13}C , ^{15}N) align

Apply electromagnetic RF field

=> resonances of the nuclear spins depending on

- atom type
- chemical environment

=> extract distances between close by ^1H atoms
(distance constraints)

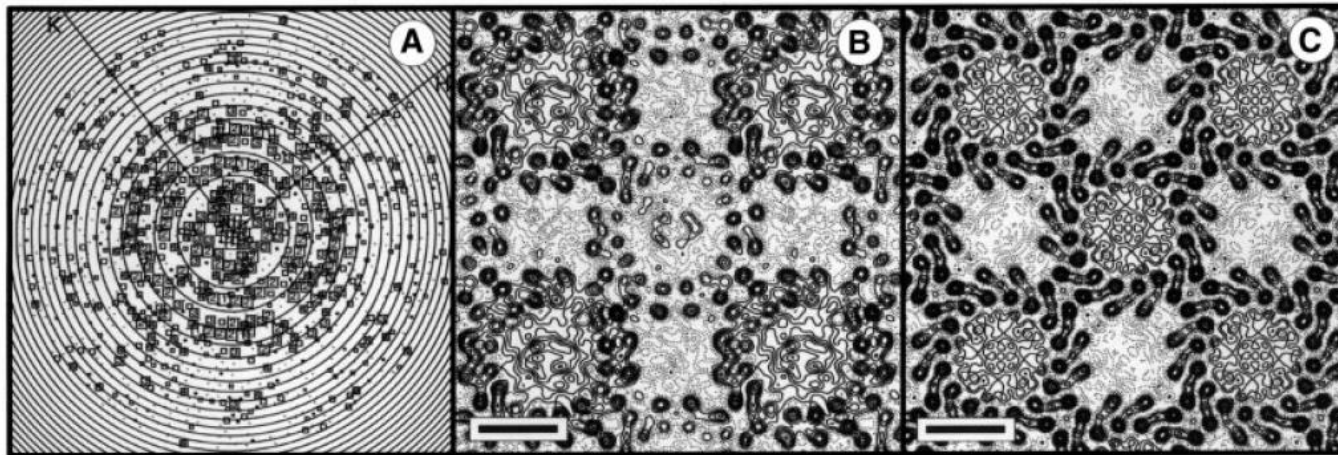


- + no crystallization required, proteins in physiological environment
- + atomic resolution
- too much overlap for larger proteins (≥ 15 kDa)

Electron microscopy

- Like X-ray crystallography, but with electrons (electrons have mass)
- => much stronger interaction with electron clouds
- => works already on 2D crystals (membrane proteins!)
- => strong radiation damage of the sample
- => resolution limited (keep electron energy low) (longer wavelength)

For 3D tomography: rotate sample

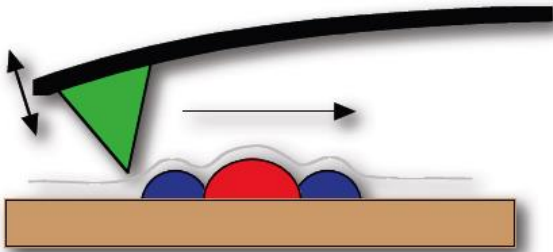


Cryo-EM images
of the LHI-RC
core complexes
of *Rhodospirillum
rubrum* at 8.5 Å
resolution

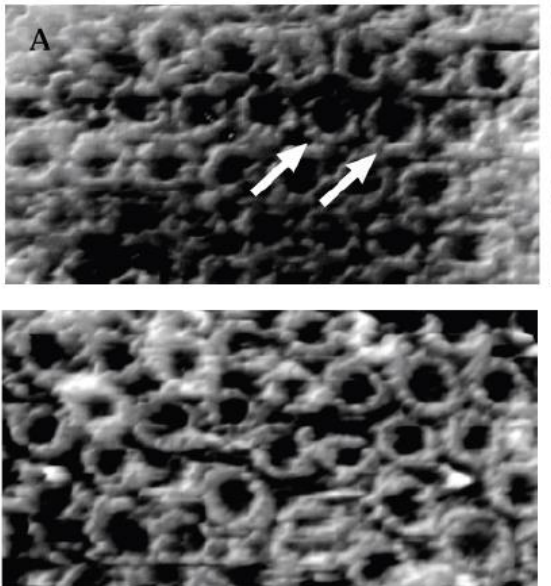
Fig. 3. (A) Representation of amplitudes of Fourier components calculated for one image of a glucose-embedded tetragonal crystal. Numbers and box sizes correspond to the spot IQ value, with spots of the highest signal-to-noise ratio having an IQ of 1 (Henderson *et al.*, 1986). Spots are shown to a resolution of $1/6 \text{ Å}^{-1}$. (B) 8.5 Å resolution projection map calculated from five averaged images of glucose-embedded tetragonal crystals, assuming $p1$ symmetry. Contouring is at 0.5 r.m.s. density with density above mean (protein) represented by solid contours. Scale bar: 50 Å. (C) As (B), with $p42_12$ symmetry applied.

Jamieson et al, *EMBO J* **21** (2003) 3927

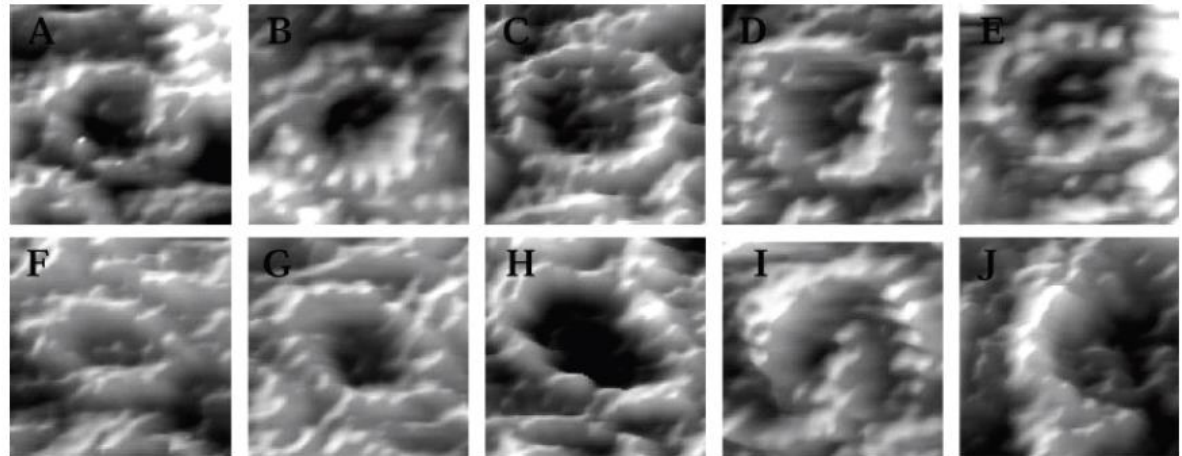
Atomic force microscopy



Scan membrane with proteins
(in physiological conditions)
=> protein arrangement (coarse view)
=> protein shape (high resolution)



Shapes and sizes of monomeric
LHI from purple bacteria

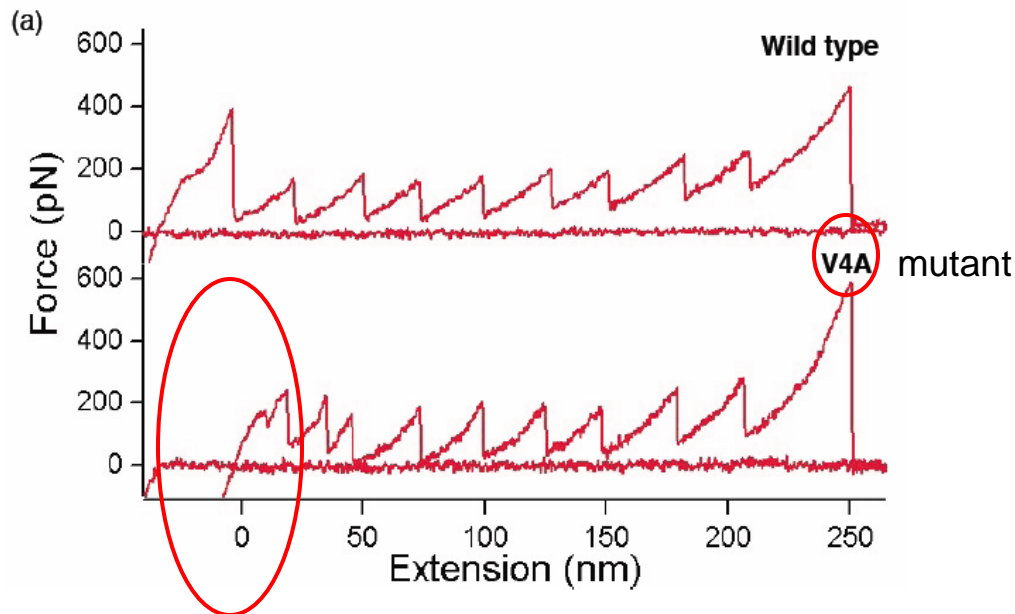


Bahatyrova et al, *J Biol Chem* **279** (2004) 21327

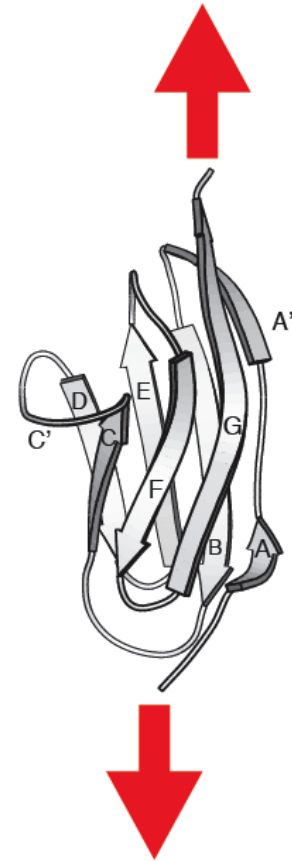
AFM pulling

Mechanical Unfolding of a Titin Ig Domain: Structure of Unfolding Intermediate Revealed by Combining AFM, Molecular Dynamics Simulations, NMR and Protein Engineering

Susan B. Fowler¹, Robert B. Best¹, José L. Toca Herrera¹
Trevor J. Rutherford¹, Annette Steward¹, Emanuele Paci²
Martin Karplus^{2,3} and Jane Clarke^{1*}



Can also be applied to
protein complexes



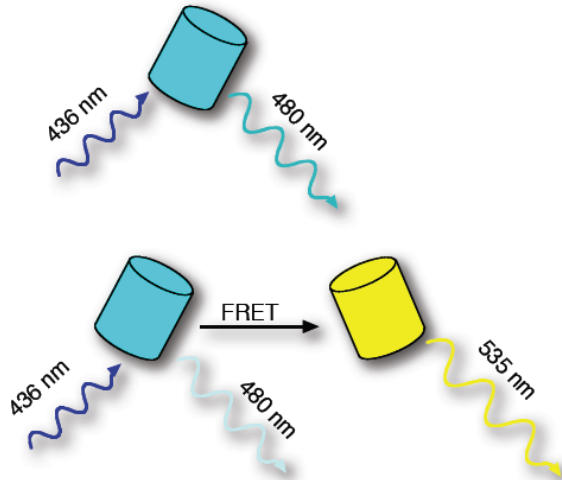
J. Mol. Biol. **322** (2002) 841–849

Fluorescence energy transfer

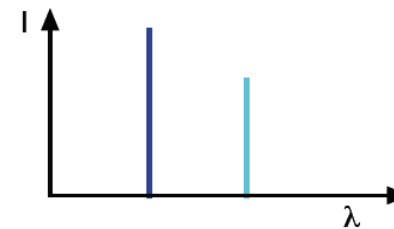
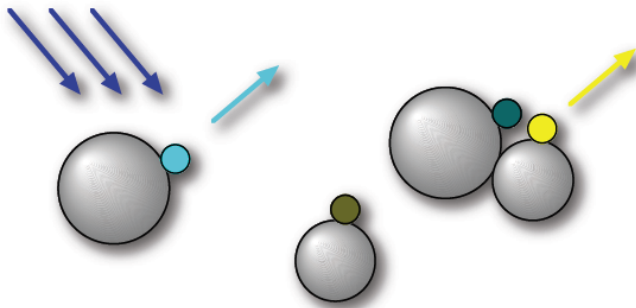
Chromophore of the cyan fluorescent protein (CFP) absorbs at 436 nm and emits at 480 nm, YFP absorbs at 480 nm and emits at 535 nm.

=> **resonant** (non-radiative) energy **transfer** from CFP onto YFP when both are close enough

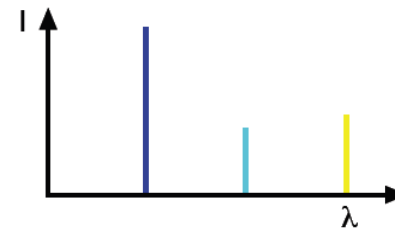
Resonant Förster transfer $\propto d^{-6}$



Tag two potential **complex partners** with CFP and YFP and measure **fluorescence spectrum**:



Observed when CFP and YFP are far away



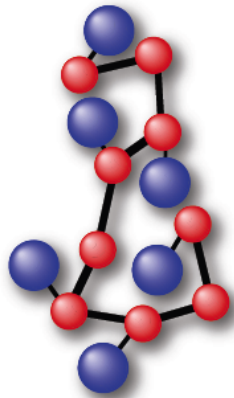
Observed when CFP and YFP are close

Structural techniques - overview

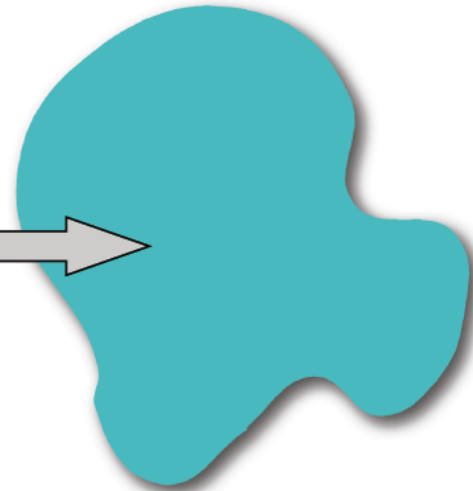
	X-ray crystallography	NMR	EM/ tomography	AFM	FRET	Y2H	TAP	MS
Structure $\leq 3\text{\AA}$	X	X						
structure $\geq 3\text{\AA}$	X	X	X	X				
contacts	X	X	X		X	X	X	X
proximity	X	X	X		X	X		
stoichiometry	X	X					X	X
complex symmetry	X	X	X	X				

Fitting atomistic structures into EM maps

Atomistic structure of
a part of the complex

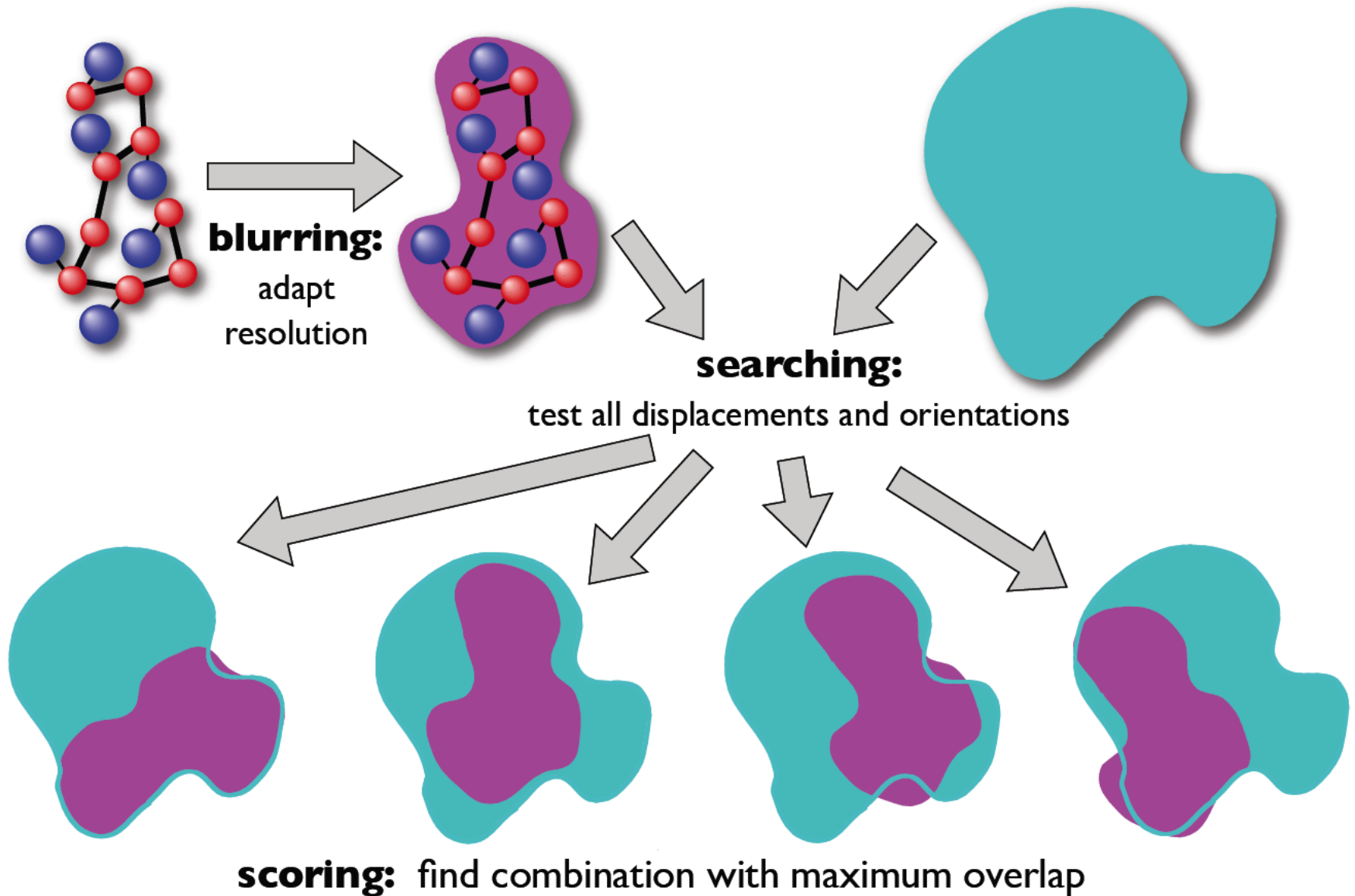


Coarse EM structure of
the whole complex



- same resolution for both structures
- exhaustive search with scoring
- choose best pose(s)

The procedure



Step 1: blurring the picture

Mathematically:

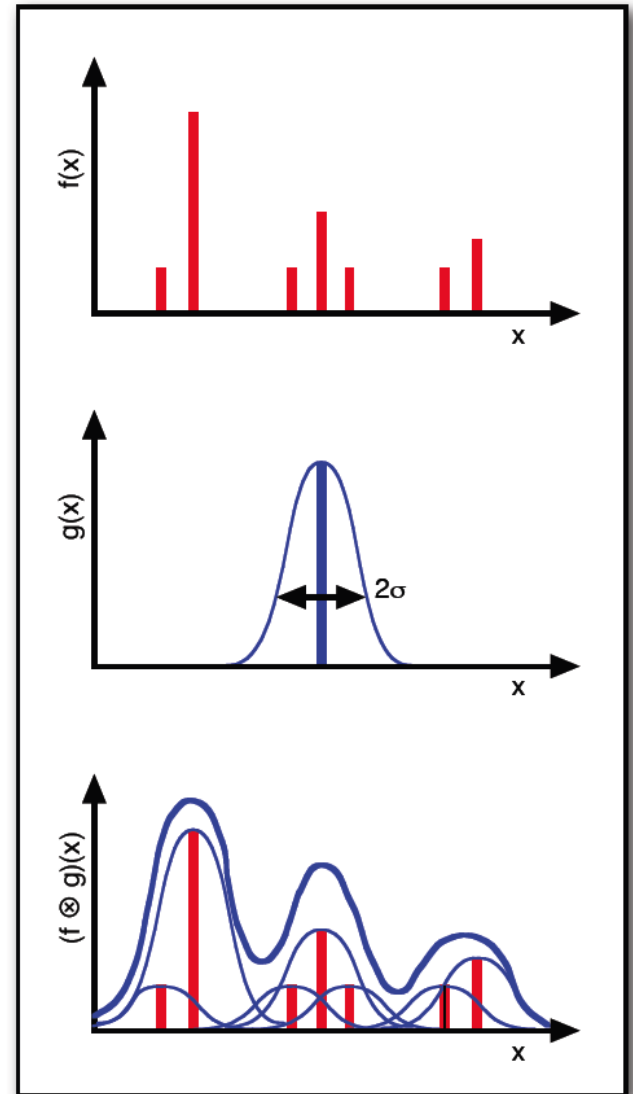
convolution of (exact) atomistic structure $f(x)$
with experimental resolution $g(x)$

$$\tilde{f}(x) = (f \otimes g)(x) = \int dz f(z) g(x - z)$$

Diagram illustrating the convolution equation:

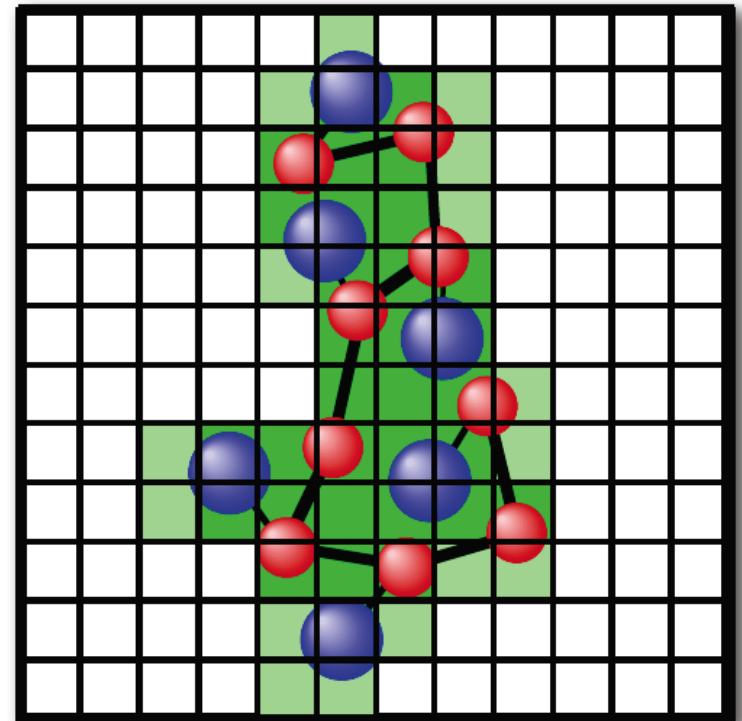
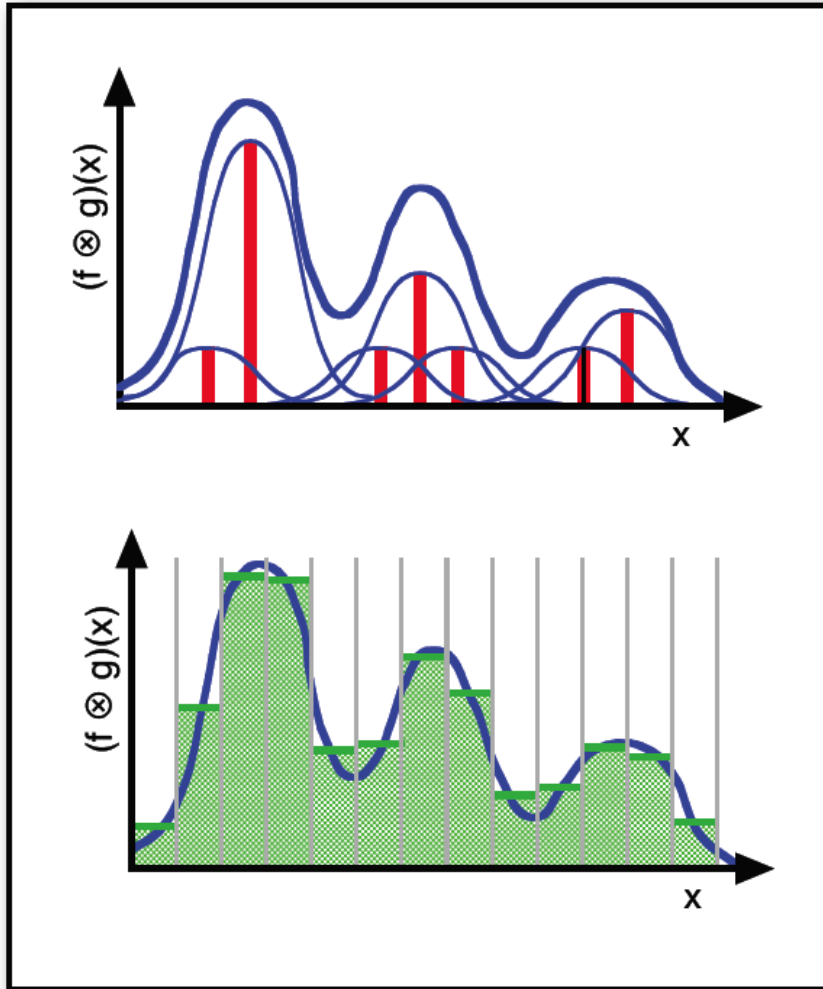
- $\tilde{f}(x)$ is labeled "original data seen through the imaging apparatus".
- $f(z)$ is labeled "original signal".
- $g(x - z)$ is labeled "'kernel' => what is the image of a single point? (=delta signal)".

Often: blurring with gaussian



Put it on a grid

Discretize:



Fourier Transformation

Forward

$$F(k) = \int_{-\infty}^{\infty} dx e^{-ikx} f(x)$$

and inverse Fourier transform

$$f(x) = \frac{1}{2\pi} \int_{-\infty}^{\infty} dk e^{ikx} F(k)$$

with $e^{ikx} = \cos(kx) + i \sin(kx)$

=> convert between real and frequency (Fourier) space

short distances \Leftrightarrow high frequencies

long distances \Leftrightarrow low frequencies

Shift of the Argument

$$\begin{aligned} FT[f(x + \Delta x)] &= \int_{-\infty}^{\infty} dx e^{-ikx} f(x + \Delta x) \\ &= \int dy e^{-ik(y - \Delta x)} f(y) \\ &= e^{ik \Delta x} \int dy e^{-iky} f(y) \\ &= e^{ik \Delta x} FT[f(x)] \end{aligned}$$

Variable transformation:
 $y = x + \Delta x$

change name of
integration variable
back from y to x

Convolution

$$\tilde{f}(x) = (f \otimes g)(x) = \int dz f(z) g(x - z)$$

Apply FT on both sides:

$$FT[\tilde{f}(x)] = FT[(f \otimes g)(x)] =$$

=

=

$$= FT[f(x)] FT[g(x)]$$

Integration in real space
is replaced by simple
multiplication in Fourier
space.

But FTs need to be
computed.

What is more efficient?

If the same width $g(x)$ is used for multiple displaced datasets
=> do $FT[g(x)]$ only once

Fourier on a Grid

On a finite grid: => maximum wavelength = length of grid
 => minimum wavelength = grid spacing
 => sum instead of integral

$$F_k = \sum_{j=0}^{N-1} e^{-2i\pi j k/N} f_j \qquad f_k = \frac{1}{N} \sum_{j=0}^{N-1} e^{+2i\pi j k/N} F_j$$

FFT by Danielson and Lanczos (1942)

Danielson and Lanczos showed that a discrete Fourier transform of length N can be rewritten as the sum of two discrete Fourier transforms, each of length $N/2$.

One of the two is formed from the even-numbered points of the original N , the other from the odd-numbered points.

$$\begin{aligned} F_k &= \sum_{j=0}^{N-1} e^{-2\pi i k \frac{j}{N}} f_j \\ &= \sum_{j=0}^{\frac{N}{2}-1} e^{-2\pi i k \frac{2j}{N}} f_{2j} + \sum_{j=0}^{\frac{N}{2}-1} e^{-2\pi i k \frac{2j+1}{N}} f_{2j+1} \\ &= \sum_{j=0}^{\frac{N}{2}-1} e^{-2\pi i k \frac{j}{N}} f_{2j} + e^{-2\pi i k \frac{1}{N}} \sum_{j=0}^{\frac{N}{2}-1} e^{-2\pi i k \frac{j}{N}} f_{2j+1} \\ &= F_k^e + e^{-2\pi i k \frac{1}{N}} F_k^o \end{aligned}$$

F_k^e : k -th component of the Fourier transform of length $N/2$ formed from the even components of the original f_j 's

F_k^o : k -th component of the Fourier transform of length $N/2$ formed from the odd components of the original f_j 's

FFT by Danielson and Lanczos (1942)

The wonderful property of the Danielson-Lanczos-Lemma is that it can be used recursively.

Having reduced the problem of computing F_k to that of computing F_k^e and F_k^o , we can do the same reduction of F_k^e to the problem of computing the transform of **its** $N/4$ even-numbered input data and $N/4$ odd-numbered data.

We can continue applying the DL-Lemma until we have subdivided the data all the way down to transforms of length 1.

What is the Fourier transform of length one? It is just the identity operation that copies its one input number into its one output slot.

For every pattern of $\log_2 N$ e's and o's, there is a one-point transform that is just one of the input numbers f_n

$$F_k^{eoeoeoeo...oe} = f_n \quad \text{for some } n$$

FFT by Danielson and Lanczos (1942)

The next trick is to figure out which value of n corresponds to which pattern of e's and o's in

$$F_k^{eoeeoeo...oe} = f_n$$

Answer: reverse the pattern of e's and o's, then let $e = 0$ and $o = 1$, and you will have, in binary the value of n .

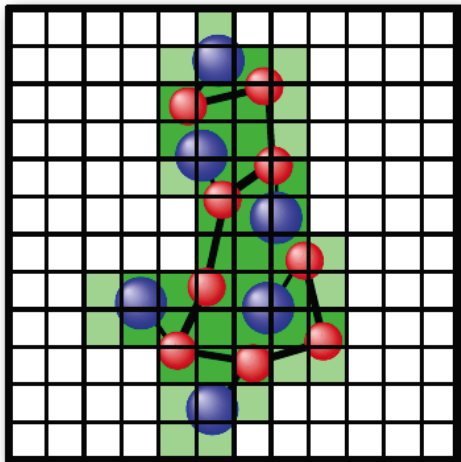
This works because the successive subdivisions of the data into even and odd are tests of successive low-order (least significant) bits of n .

Thus, computing a FFT can be done efficiently in $O(N \log(N))$ time.

Discretization and Convolution

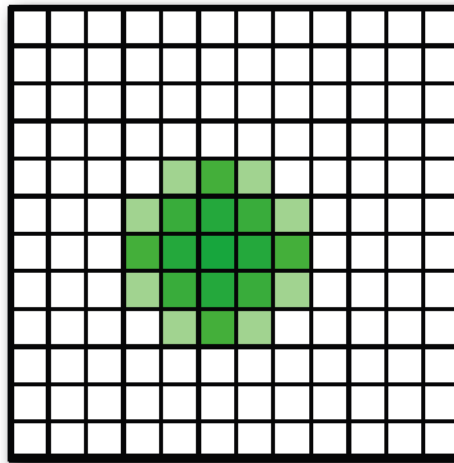
For practical applications:

=> first put atomistic data onto the grid, then blur with FFT



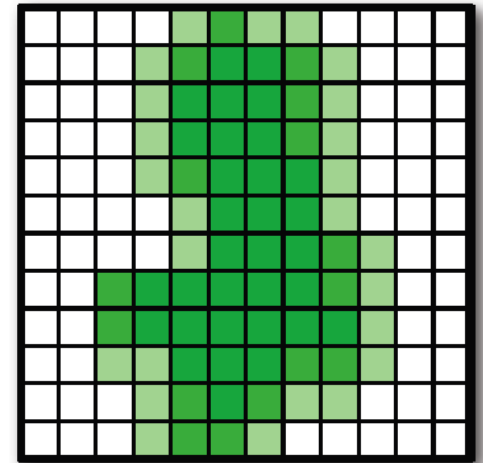
discretized hi-res data

\otimes



blurring kernel

=

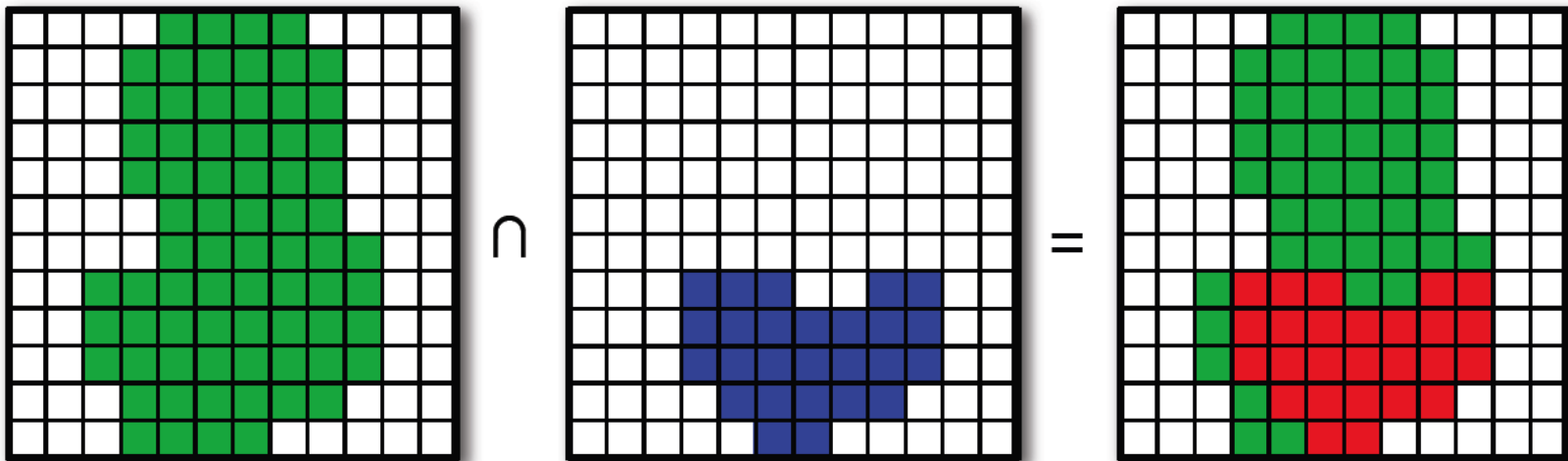


low-res image

Step 3: Scoring the Overlap

Most simple case:

- apply density threshold and count overlapping voxels
 - displace images relative to each other, recount
- => find displacement with maximum overlap



In matrix form with displacements x, y :

$$c(x, y) = \sum_{l=1}^N \sum_{m=1}^N a_{l,m} b_{l+x, m+y}$$

Cross Correlation

Generalization: maximize cross correlation of grided densities with respect to displacement (and orientation)

$$C_{x,y,z} = \sum_{l=1}^N \sum_{m=1}^N \sum_{n=1}^N a_{l,m,n} \times b_{l+x,m+y,n+z}$$

Note: maximize the cross-correlation \Leftrightarrow minimize the squared difference

On a grid with N^3 gridpoints $\Rightarrow N^3$ possible displacements
 \Rightarrow runtime $O(N^6)$

Further complication: the convolution

$$C_{x,y,z} = \sum_{l=1}^N \sum_{m=1}^N \sum_{n=1}^N a_{l,m,n} \times (g \otimes b_{l+x,m+y,n+z})$$

Correlation and Fourier

Apply Fourier transformation to both sides of

$$C_{x,y,z} = \sum_{l=1}^N \sum_{m=1}^N \sum_{n=1}^N a_{l,m,n} \times b_{l+x,m+y,n+z}$$

=> matrix multiplication

$$FT[C] = FT[A]^* \times FT[B]$$

Runtime of 3D FFT = $O(N^3 \log^3(N)) \ll N^6$

=> all possible displacements tested simultaneously

Note: $FT[A]$ only calculated once initially

=> two FFTs per orientation

=> scan orientation via Euler angles

<== Step 2: exhaustive search

Include convolution

Maximize

$$C_{x,y,z} = \sum_{l=1}^N \sum_{m=1}^N \sum_{n=1}^N a_{l,m,n} \times (g \otimes b_{l+x,m+y,n+z})$$

In Fourier space:

Insert convolution

$$FT[f \otimes g] = FT[f] \times FT[g]$$

Into correlation:

$$\begin{aligned} FT[C] &= FT[A]^* \times FT[G \otimes B] \\ &= FT[A]^* \times (FT[G] \times FT[B]) \\ &= \underbrace{(FT[A]^* \times FT[G])}_{\text{can be precomputed}} \times FT[B] \end{aligned}$$

2 FFTs + 1 matrix multiplication

Katchalski-Kazir algorithm

Proc. Natl. Acad. Sci. USA
Vol. 89, pp. 2195–2199, March 1992
Biophysics

Molecular surface recognition: Determination of geometric fit between proteins and their ligands by correlation techniques

(protein–protein interaction/surface complementarity/macromolecular complex prediction/molecular docking)

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Contributed by Ephraim Katchalski-Katzir, October 24, 1991

Developed for protein-ligand docking

<=> same techniques applicable for docking "on the inside"

Discretization for docking

Next, to distinguish between the surface and the interior of each molecule, we retain the value of 1 for the grid points along a thin surface layer only and assign other values to the internal grid points. The resulting functions thus become

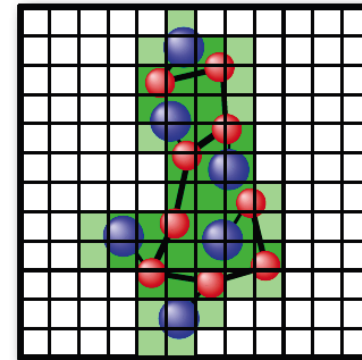
$$\bar{a}_{l,m,n} = \begin{cases} 1 & \text{on the surface of the molecule} \\ \rho & \text{inside the molecule} \\ 0 & \text{outside the molecule,} \end{cases} \quad [2a]$$

and

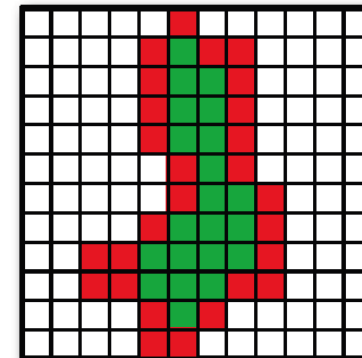
$$\bar{b}_{l,m,n} = \begin{cases} 1 & \text{on the surface of the molecule} \\ \delta & \text{inside the molecule} \\ 0 & \text{outside the molecule,} \end{cases} \quad [2b]$$

where the surface is defined here as a boundary layer of finite width between the inside and the outside of the molecule. The parameters ρ and δ describe the value of the points inside the molecules, and all points outside are set to zero. Two-

Typical values: $\rho = -15$, $\delta = 1$
=> penalty for overlap of volumes

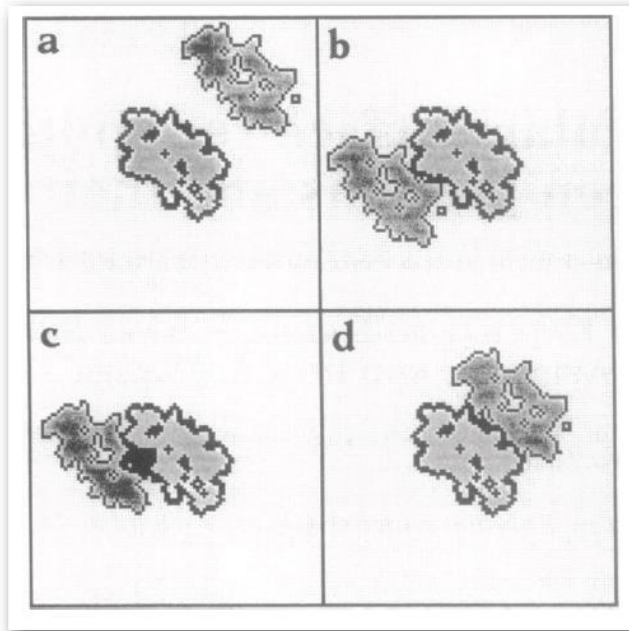


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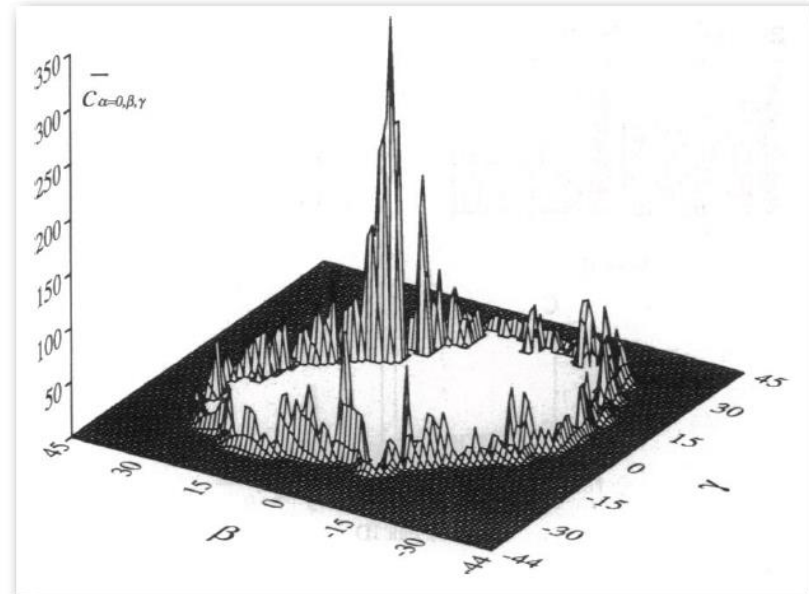
Docking the hemoglobin dimer

2D cross sections at $l = 46$ ($N = 90$)



- a) no contact
- b) limited contact
- c) overlap (black area)
- d) good geometric match

Correlation at $\alpha = 0$



highest peak corresponds to native dimer arrangement

The algorithm

The entire procedure described above can be summarized by the following steps:

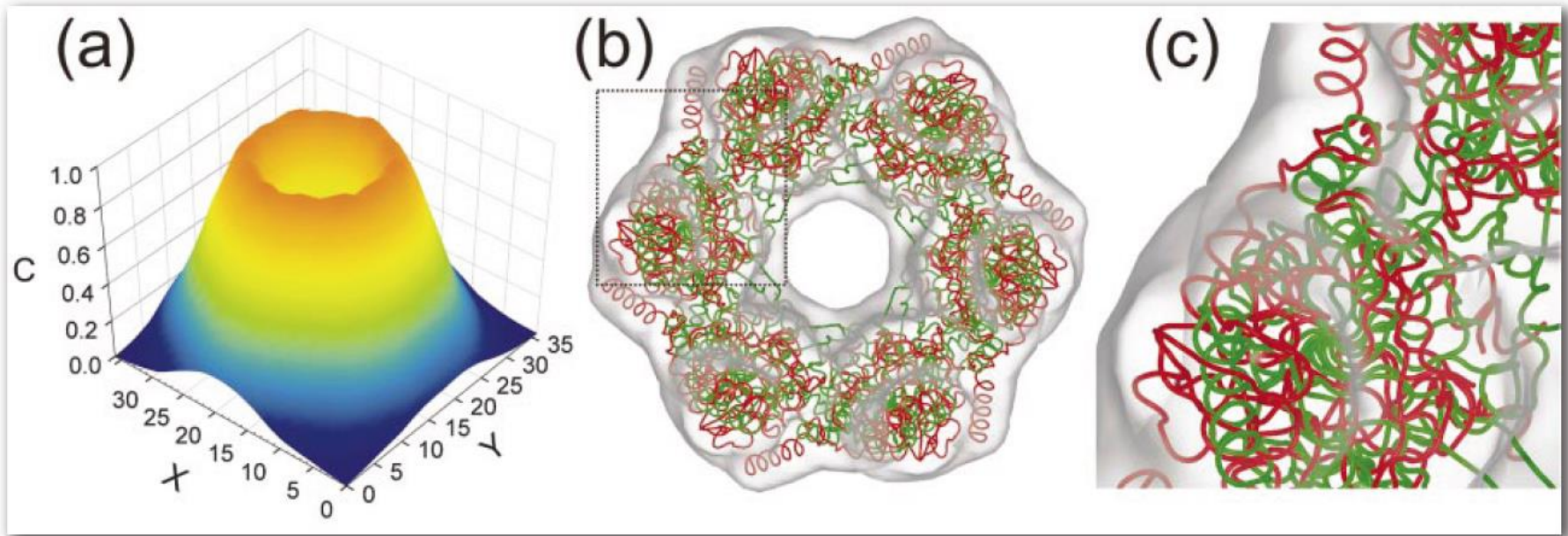
- (i) derive \bar{a} from atomic coordinates of molecule **a** (Eq. 2),
- (ii) $A^* = [\text{DFT}(\bar{a})]^*$ (Eq. 4),
- (iii) derive \bar{b} from atomic coordinates of molecule **b** (Eq. 2),
- (iv) $B = \text{DFT}(\bar{b})$ (Eq. 4),
- (v) $C = A^* \cdot B$ (Eq. 5),
- (vi) $\bar{c} = \text{IFT}(C)$ (Eq. 6),
- (vii) look for a sharp positive peak of \bar{c} ,
- (viii) rotate molecule **b** to a new orientation,
- (ix) repeat steps *iii–viii* and end when the orientations scan is completed, and
- (x) sort all of the peaks by their height.

Each high and sharp peak found by this procedure indicates geometric match and thus represents a potential complex. The relative position and orientation of the molecules within each such complex can readily be derived from the

Katchalski-Kazir et al. 1992

Algorithm has become a workhorse for docking and density fitting.

Problem I: limited contrast



Docking of the RecA helicase monomer into simulated EM density of the hexamer at 15 Å resolution
(exhaustive 6D search with 5Å / 9° steps plus off-lattice optimization)
=> multiple fits with similar correlations

Chacón, Wrighers, *J. Mol. Biol.* **317** (2002) 375

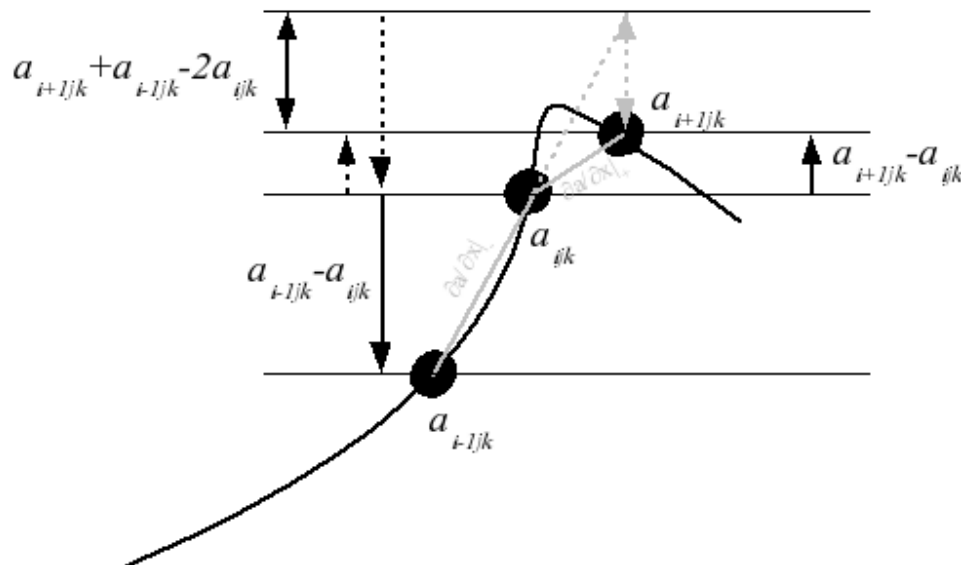
Laplace filter

Evaluate $\nabla^2 = \frac{d^2}{dx^2} + \frac{d^2}{dy^2} + \frac{d^2}{dz^2}$

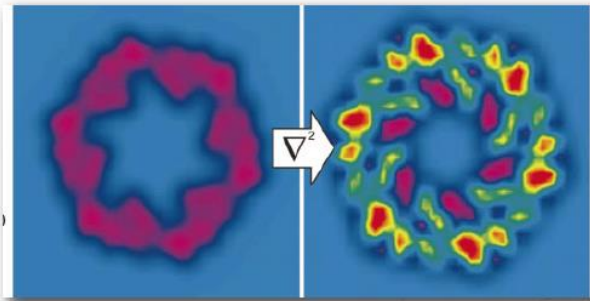
on a grid: $\nabla^2 a_{l,m,n} = -6a_{l,m,n} + a_{l+1,m,n} + a_{l-1,m,n} + a_{l,m+1,n} + a_{l,m-1,n} + a_{l,m,n+1} + a_{l,m,n-1}$

Correlation:

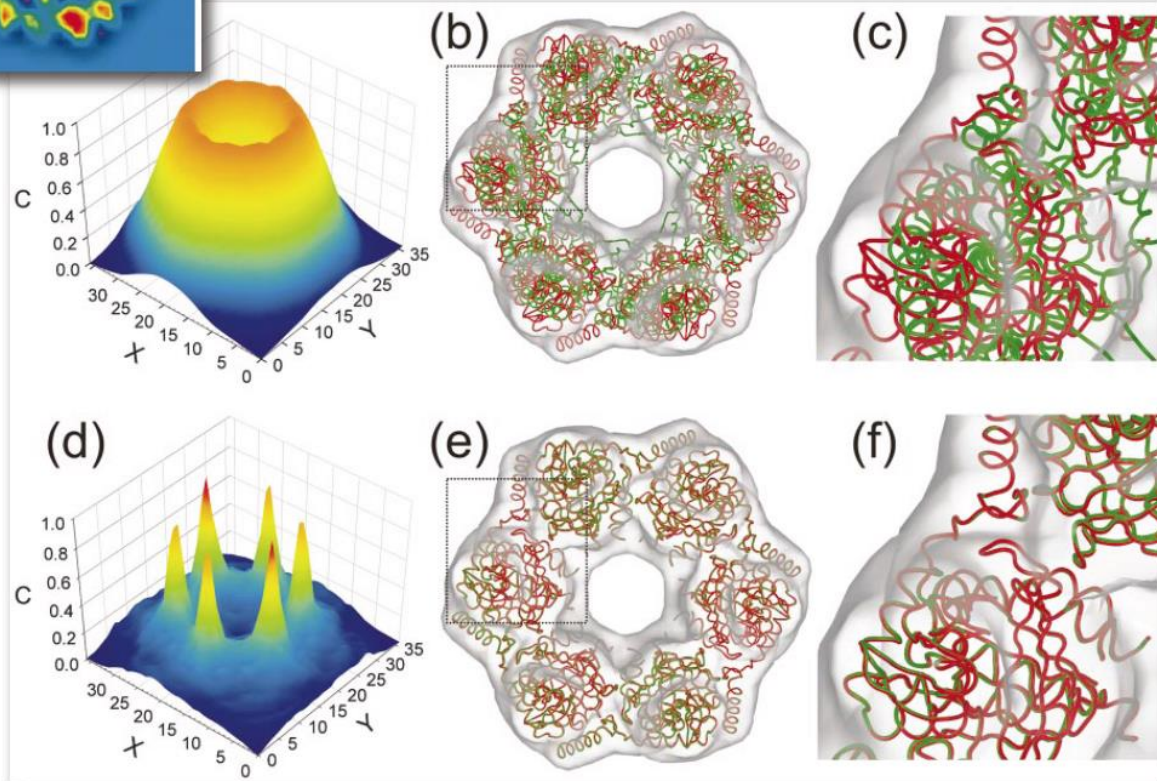
$$C_{x,y,z} = \sum_{l=1}^N \sum_{m=1}^N \sum_{n=1}^N (\nabla^2 \otimes a_{l,m,n}) \times (\nabla^2 \otimes g \otimes b_{l+x,m+y,n+z})$$



Enhanced contrast → better fit



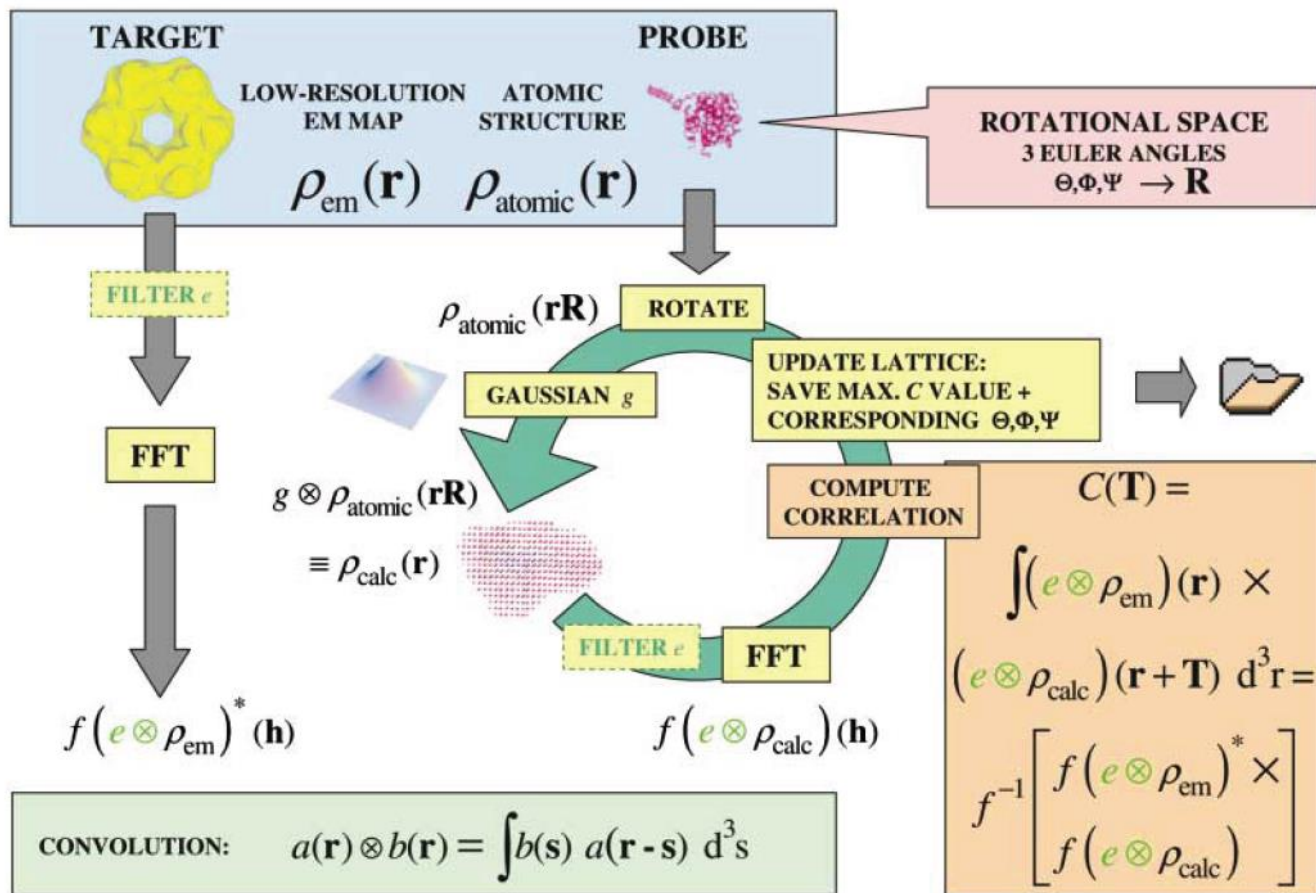
With the
density alone:



With the
Laplacian filter:

Chacón, Wrigger, *J. Mol. Biol.* **317** (2002) 375

The big picture



Wriggers, Chacón, *Structure* **9** (2001) 779

Problem 2: more efficient search

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Structural bioinformatics

ADP_EM: fast exhaustive multi-resolution docking for high-throughput coverage

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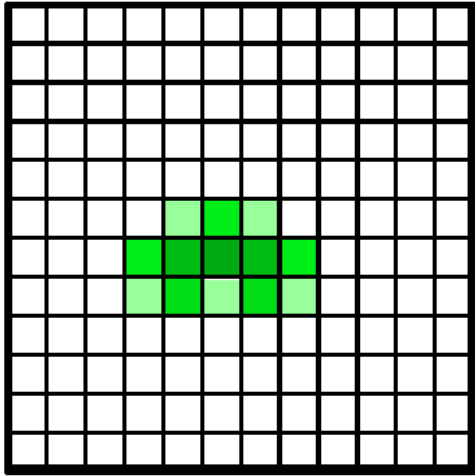
Advance Access publication December 6, 2006

Associate Editor: Alex Bateman

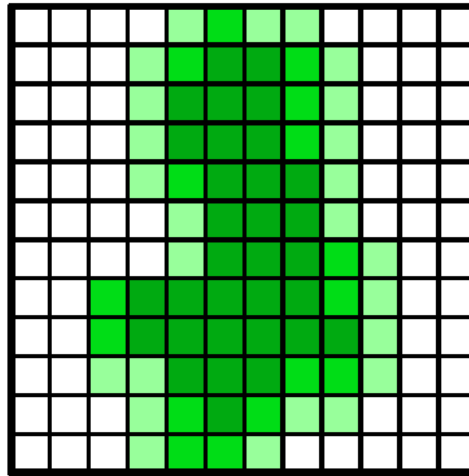
Observations:

- many displacements can be excluded a priori (FFT alg. calculates them all)
- FFT idea makes more sense for rotations (no simple limit on rotations)

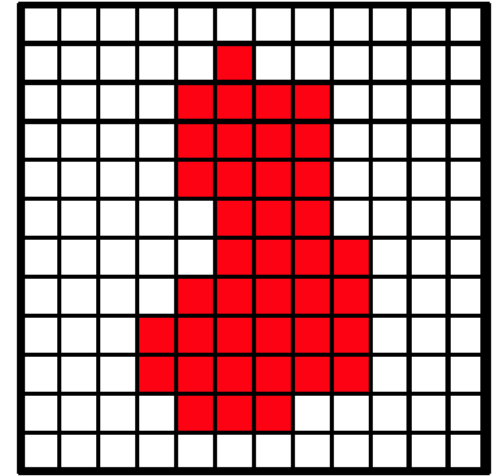
Masked displacements



Probe



Target



Mask =
potential hits

Search space for displacements =
(inside of the target molecule) – (extent of the probe)

Rotational search

Express densities in spherical harmonics on "onion shells"

$$\rho_{\text{low}}(r, \beta, \lambda) = \sum_{l=0}^{B-1} \sum_{m=-l}^l C_{lm}^{\text{low}}(r) Y_{lm}(\beta, \lambda) \quad \rho_{\text{high}}(r, \beta, \lambda) = \sum_{l=0}^{B-1} \sum_{m=-l}^l C_{lm}^{\text{high}}(r) Y_{lm}(\beta, \lambda),$$

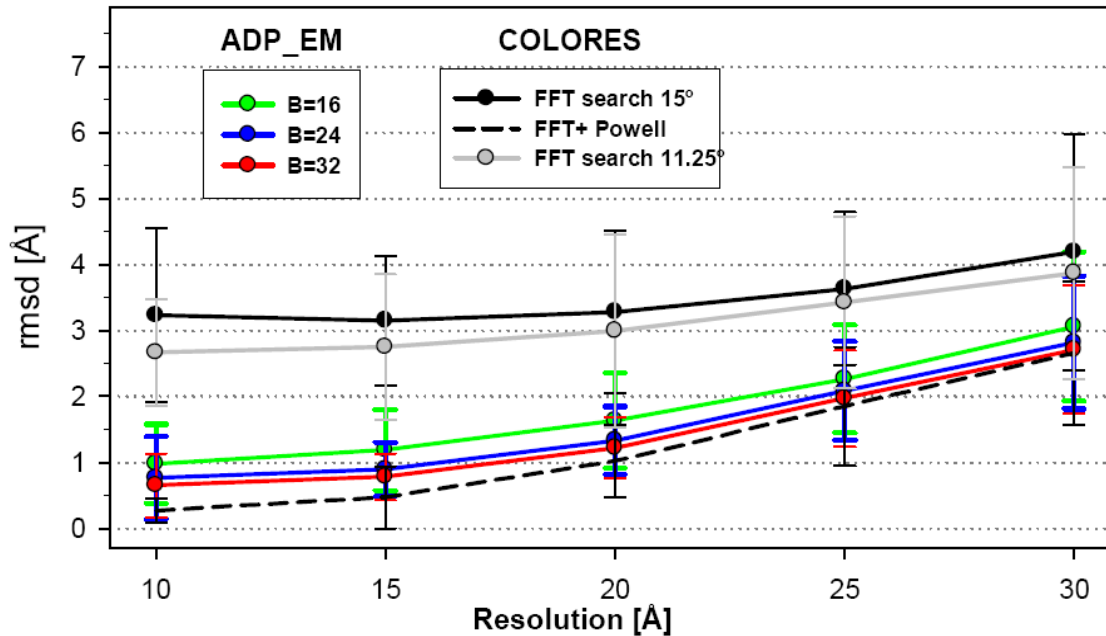
Y_{lm}	$l=0$	$l=1$	$l=2$	$l=3$
$m=-3$				$\sqrt{\frac{35}{64\pi}} \sin^3 \vartheta e^{-3i\varphi}$
$m=-2$			$\sqrt{\frac{15}{32\pi}} \sin^2 \vartheta e^{-2i\varphi}$	$\sqrt{\frac{105}{32\pi}} \sin^2 \vartheta \cos \vartheta e^{-2i\varphi}$
$m=-1$		$\sqrt{\frac{3}{8\pi}} \sin \vartheta e^{-i\varphi}$	$\sqrt{\frac{15}{8\pi}} \sin \vartheta \cos \vartheta e^{-i\varphi}$	$\sqrt{\frac{21}{64\pi}} \sin \vartheta (5 \cos^2 \vartheta - 1) e^{-i\varphi}$
$m=0$	$\sqrt{\frac{1}{4\pi}}$	$\sqrt{\frac{3}{4\pi}} \cos \vartheta$	$\sqrt{\frac{5}{16\pi}} (3 \cos^2 \vartheta - 1)$	$\sqrt{\frac{7}{16\pi}} (5 \cos^3 \vartheta - 3 \cos \vartheta)$
$m=1$		$-\sqrt{\frac{3}{8\pi}} \sin \vartheta e^{i\varphi}$	$-\sqrt{\frac{15}{8\pi}} \sin \vartheta \cos \vartheta e^{i\varphi}$	$-\sqrt{\frac{21}{64\pi}} \sin \vartheta (5 \cos^2 \vartheta - 1) e^{i\varphi}$
$m=2$			$\sqrt{\frac{15}{32\pi}} \sin^2 \vartheta e^{2i\varphi}$	$\sqrt{\frac{105}{32\pi}} \sin^2 \vartheta \cos \vartheta e^{2i\varphi}$
$m=3$				$-\sqrt{\frac{35}{64\pi}} \sin^3 \vartheta e^{3i\varphi}$

Correlation for **all orientations** at a given displacement:

$$C(R) = FT_{m,h,m'}^{-1} \left[\sum_l d_{mh}^l d_{hm'}^l \int_0^\infty C_{lm}^{\text{low}}(r) \overline{C_{lm'}^{\text{high}}(r)} r^2 dr \right]$$

Known Fourier
coefficients of
spherical harmonics Y_{lm} .

Accuracy



rmsd with respect to known atomistic structure of target.

Registration accuracy on simulated EM maps of 28 structures for bandwidths (number of angular sampling points) of $B = 16, 24, 32$ ($11^\circ, 8^\circ, \sim 6^\circ$) compared to Wriggers' COLORES (situs package – Katchalski-Katzir algorithm + local Powell optimization)

Performance

Table 1. Timing results, in seconds, obtained with the benchmark described in Figure 1

	Sampling B/°	10Å	15Å	Resolution 20Å	25Å	30Å
ADP_EM	16/11°	28	31	35	34	38
	24/8°	100	108	119	118	123
	32/6°	226	220	225	216	221
FFT search	−/15°	1697	1926	2341	5028	6681
Powell minim	−/15°	375	918	1747	3739	6597

ADP_EM (Another Docking Platform for EM) is much faster

- only limited spatial region is scanned
- fast evaluation of the orientational correlation via FFT
- spherical harmonics allow for better rotational representation
=> higher accuracy

Some examples

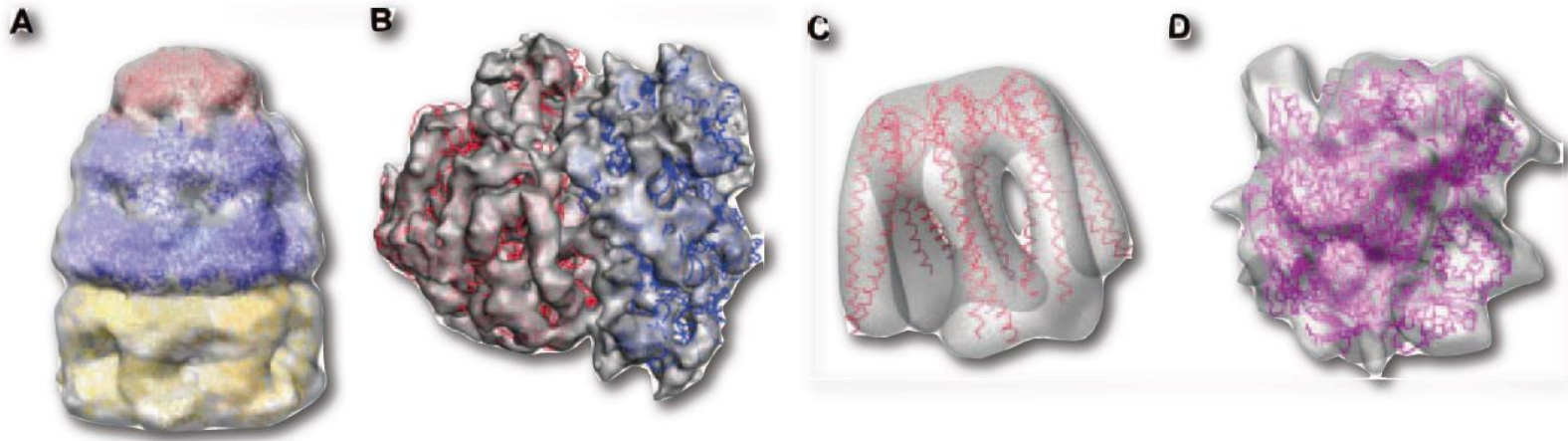


Fig. 2. Docking results with experimental EM data. (A) *E. coli* GroES-ADP7-GroEL-ATP7 from *E. coli* at 23.5 Å (EMD ID 1046, PDB: 1ml5); ADP and ATP GroEL subunits have been docked independently to reconstruct the cis and trans heptameric rings of the complex. For GroES the whole heptamer was used. (B) Docking of 30S and 50S subunits into *E. coli* ribosome map at 14 Å (EMD ID 1046, PDB: 1gix/1giy). Single-molecule docking of prefoldin (C) at 23 Å (Martin-Benito *et al.*, 2002), PDB: 1l6h, and of yeast RNA polymerase II (D) at 15 Å (Craighead *et al.*, 2002), PDB: 1fxk.

Summary

Today:

Docking into EM maps

- Discretization
- Correlation and blurring via FFT => Katchalski-Katzir algorithm
- Laplace filter => enhances contrast
- ADP_EM: FFT for rotations, scan displacements => better performance

Next lecture V20:

using connectivity information for complex assembly