Applications of normal modes in structural dynamics

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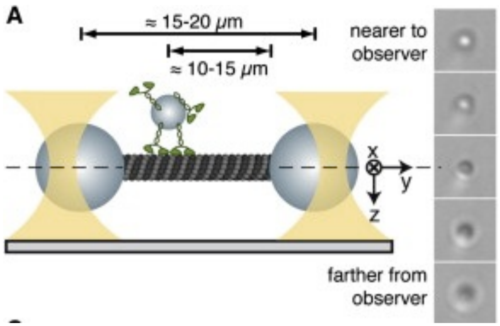
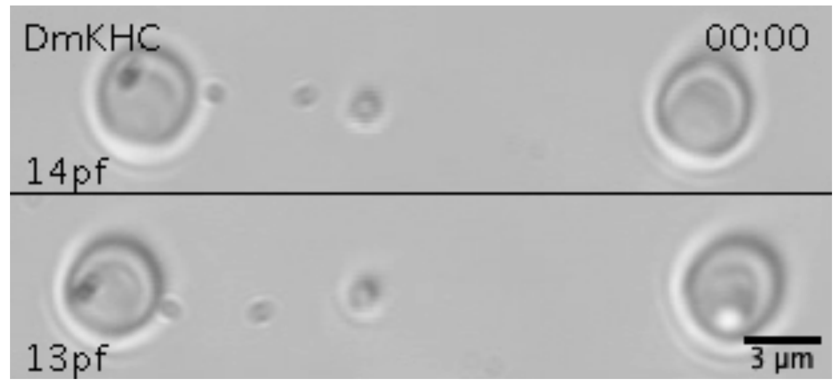
Real-time motion of kinesin on a microtubule





~10 μ m/10s = 1nm/ms

Brunnbauer et al. Mol Cel 46:147 (2012).

Approximating the protein free energy landscape

Rough and funnel-shaped energy landscape that is function of atomic coordinates

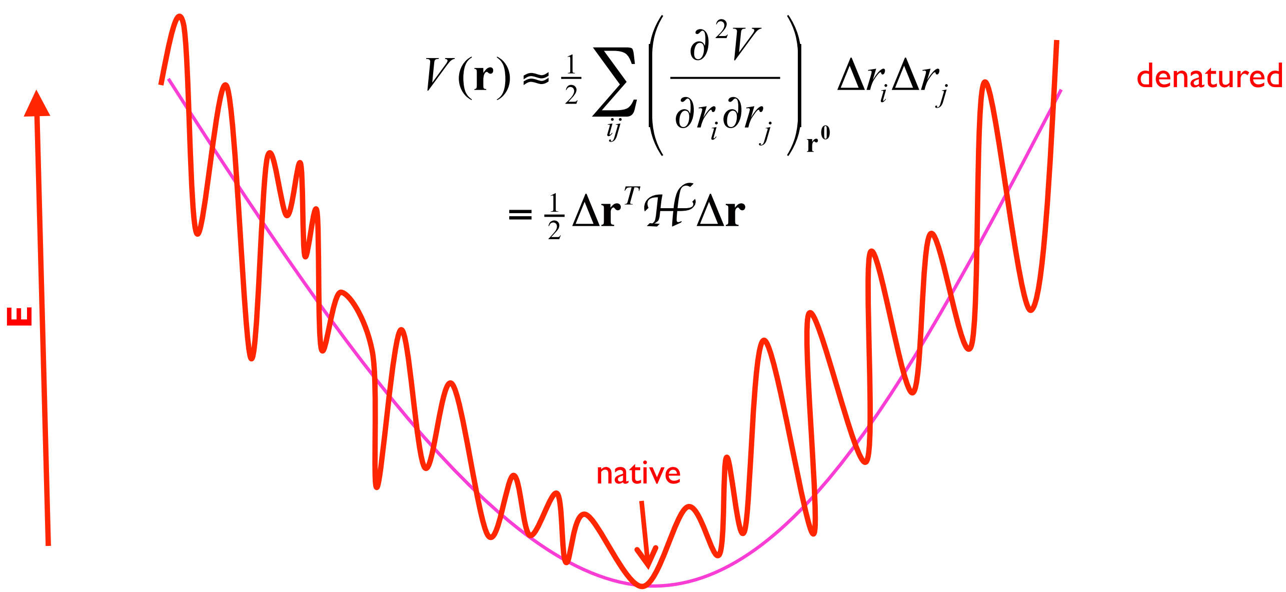
$$\mathbf{r} = (x_1, y_1, z_1, \ldots, x_N, y_N, z_N)^T$$

$$\Delta\mathbf{r} = \mathbf{r} - \mathbf{r}^0$$

$$V(\mathbf{r}) = V(\mathbf{r}^0) + \sum_i \left(\frac{\partial V}{\partial r_i}\right)_{\mathbf{r}^0} \Delta r_i + \tfrac{1}{2}\sum_{ij}\left(\frac{\partial^2 V}{\partial r_i \partial r_j}\right)_{\mathbf{r}^0} \Delta r_i \Delta r_j + \tfrac{1}{6}\sum_{ijk}\left(\frac{\partial^3 V}{\partial r_i \partial r_j \partial r_k}\right)_{\mathbf{r}^0} \Delta r_i \Delta r_j \Delta r_k + \ldots$$

$$V(\mathbf{r}) \approx \tfrac{1}{2}\sum_{ij}\left(\frac{\partial^2 V}{\partial r_i \partial r_j}\right)_{\mathbf{r}^0} \Delta r_i \Delta r_j$$

$$= \tfrac{1}{2}\Delta\mathbf{r}^T \mathcal{H} \Delta\mathbf{r}$$



Equations of Motion

$$\mathbf{M}\Delta\ddot{\mathbf{r}} = -\mathcal{H}\Delta\mathbf{r}$$

Newton

$$\begin{cases} \mathbf{q} = \mathbf{M}^{1/2}\Delta\mathbf{r} \\ \mathbf{H} = \mathbf{M}^{-1/2}\mathcal{H}\mathbf{M}^{-1/2} \end{cases}$$

Mass-weighted coordinates

Mass-weighted Hessian

$$\begin{aligned} \ddot{\mathbf{q}} &= -\mathbf{M}^{-1/2}\mathcal{H}\mathbf{M}^{-1/2}\mathbf{q} \\ &= -\mathbf{H}\mathbf{q} \end{aligned}$$

$$\begin{cases} \mathbf{q}(t) = \mathbf{q}\mathrm{e}^{-i\omega t} \\ \ddot{\mathbf{q}}(t) = -\omega^2\mathbf{q}(\mathrm{t}) \end{cases}$$

Oscillatory solution

$$\mathbf{H} = \mathbf{V}\mathbf{\Lambda}\widetilde{\mathbf{V}}$$

$$\Lambda_{ij} = \omega_i^2\delta_{ij}$$

Goldstein, Ch. 10

Anisotropic Network Model

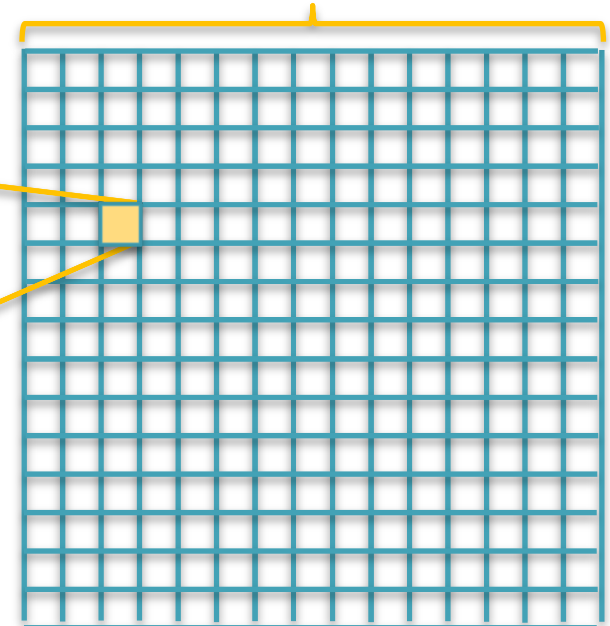
$$V(\mathbf{r}) = \tfrac{\gamma}{2}\sum_{i=1}^{N}\sum_{j>i}\underbrace{\left(\left|\mathbf{r}_{ij}\right|-\left|\mathbf{r}_{ij}^{0}\right|\right)^{2}}_{\text{Harmonic}}\ \underbrace{\Theta\left(R_{c}-\left|\mathbf{r}_{ij}^{0}\right|\right)}_{\text{Step function}}$$

$$\left(\frac{\partial^{2}V}{\partial x_{i}\partial y_{j}}\right)_{\mathbf{r}^{0}} = -\frac{x_{i}^{0}y_{j}^{0}}{\left|\mathbf{r}_{ij}^{0}\right|^{2}}$$

Hessian is calculated directly from structure

$$\mathbf{H}_{\mathbf{ij}} = -\frac{\gamma}{\left(R_{ij}^{0}\right)^{2}}\begin{bmatrix}\left(x_{ij}^{0}\right)^{2} & x_{ij}^{0}y_{ij}^{0} & x_{ij}^{0}z_{ij}^{0}\\ x_{ij}^{0}y_{ij}^{0} & \left(y_{ij}^{0}\right)^{2} & y_{ij}^{0}z_{ij}^{0}\\ x_{ij}^{0}z_{ij}^{0} & y_{ij}^{0}z_{ij}^{0} & \left(z_{ij}^{0}\right)^{2}\end{bmatrix}$$

3N



Doruker et al. Proteins 40 (2000).
Atilgan et al. Biophys J 80 (2001).

Force constants

- Uniform within cutoff:

$$\gamma(\mathbf{r}_{ij}) = \begin{cases} \gamma & \left|\mathbf{r}_{ij}\right| < R_c \\ 0 & otherwise \end{cases}$$

Tirion, PRL 77 (1996).
Bahar et al. Folding & Des 2 (1997).
Doruker et al. Proteins 40 (2000).

- Exponential decay:

$$\gamma(\mathbf{r}_{ij}) = \gamma_0 \exp\left(-\frac{\left|\mathbf{r}_{ij}\right|^2}{r_0^2}\right)$$

Hinsen et al. Proteins 33 (1998).

- Power law decay:

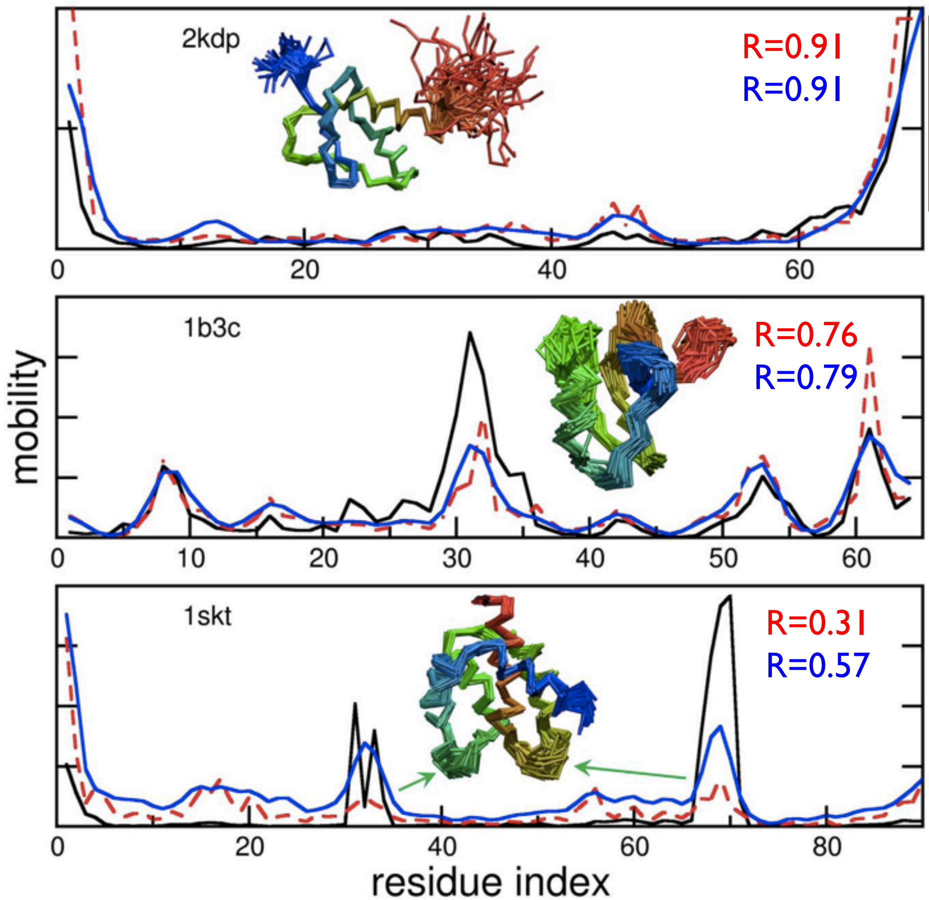
$$\gamma(\mathbf{r}_{ij}) = \begin{cases} c_0 + c_1\left|\mathbf{r}_{ij}\right| & \mathbf{r}_{ij} < R_0 \\ c_2\left|\mathbf{r}_{ij}\right|^{-6} & otherwise \end{cases}$$

Hinsen et al. Chem Phys 261 (2000).

$$\gamma(\mathbf{r}_{ij}) = \left|\mathbf{r}_{ij}\right|^{-2}$$

Yang et al. PNAS 106 (2009).

Force constants can be fine-tuned to improve agreement with data



- Distance-dependence
- 1st neighbors
- 2nd neighbors
- H bonds

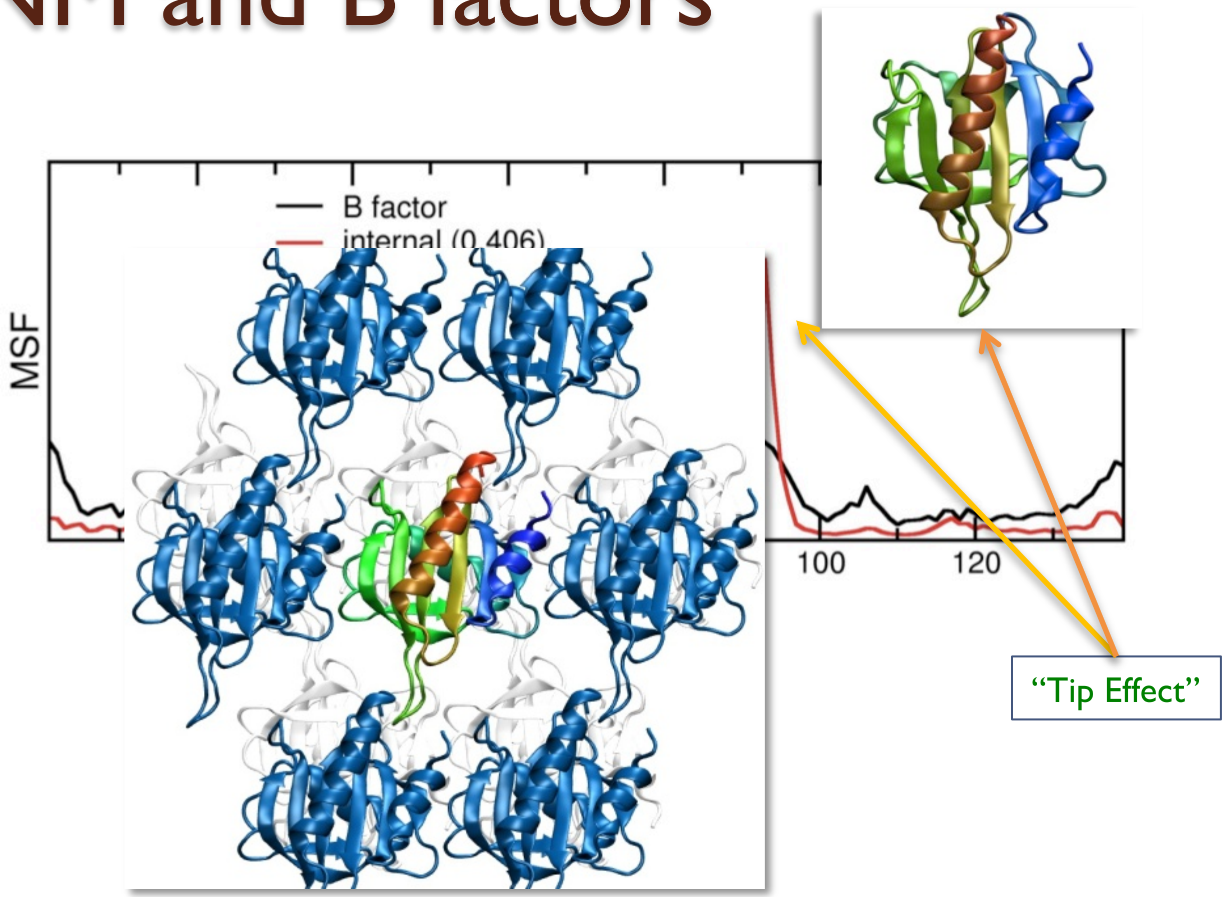
black: NMR
red: ENM
blue: modified ENM

GammaStructureBased()

ENM tutorial: Custom Gamma Functions

Lezon & Bahar. PLoS Comp Biol 6 (2010).

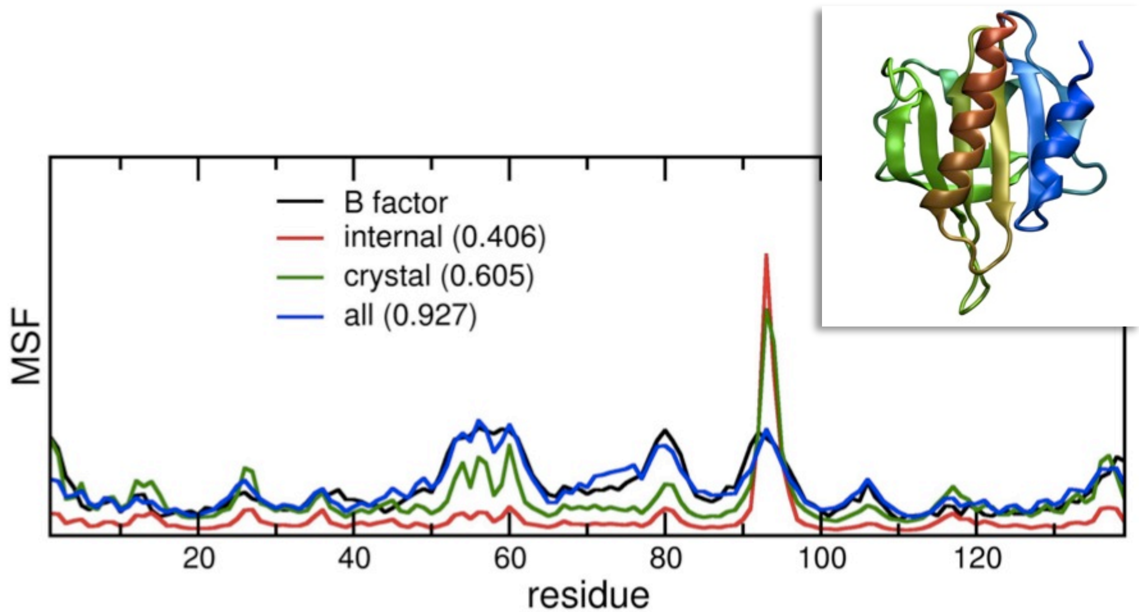
Improving correlation between ENM and B factors



Possible solution: Add crystal contacts

Lezon. Proteins 80 (2012).

Improving correlation between ENM and B factors

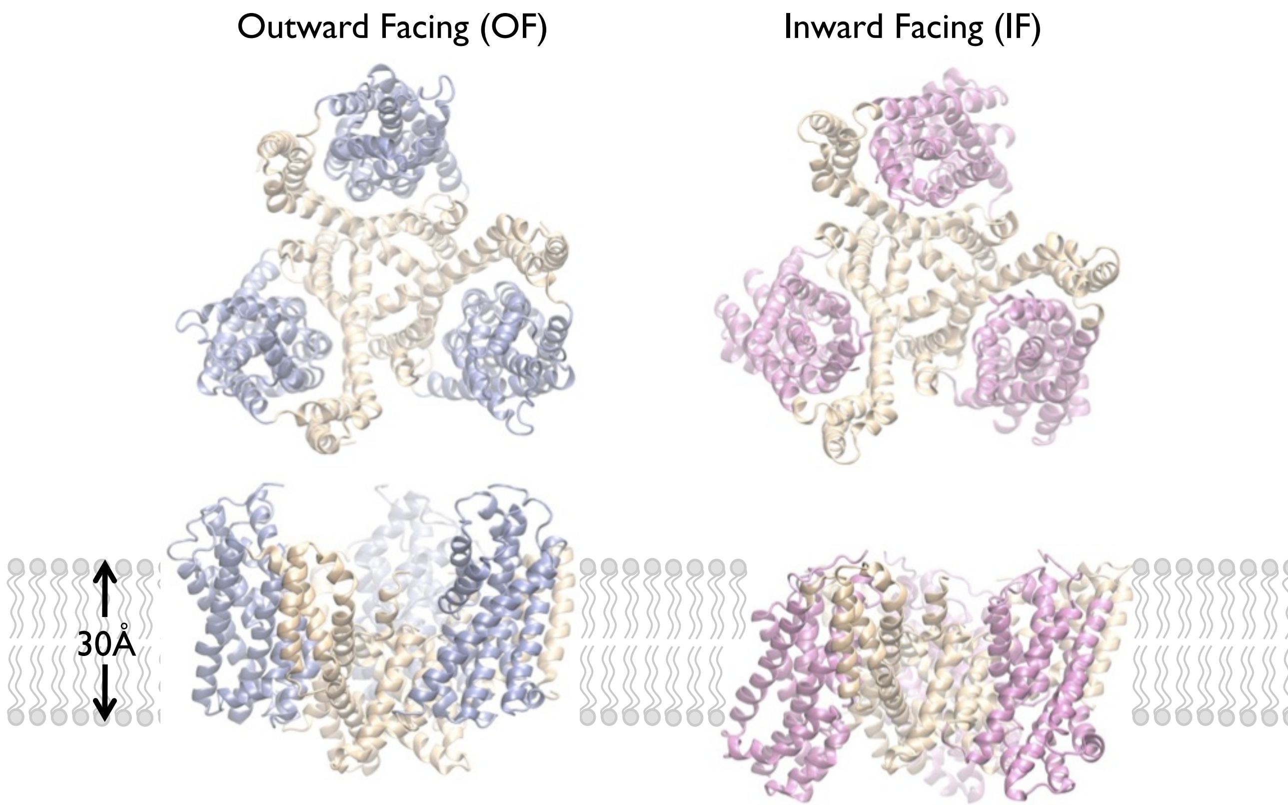


Crystal contacts help, but do not eliminate tip effect.
What about lattice vibrations?

reduceModel()

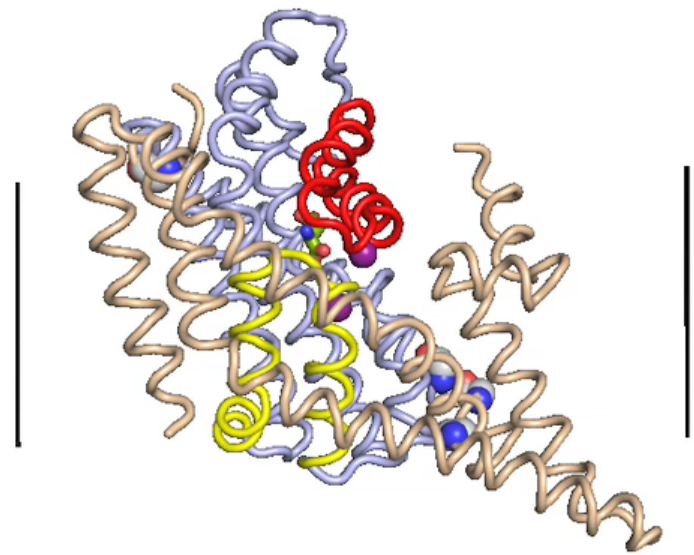
Lezon. Proteins 80 (2012).

Exploring structural transitions: Glutamate transporter



Exploring structural transitions: Glutamate transporter

Single subunit showing the transport domain moving across the membrane

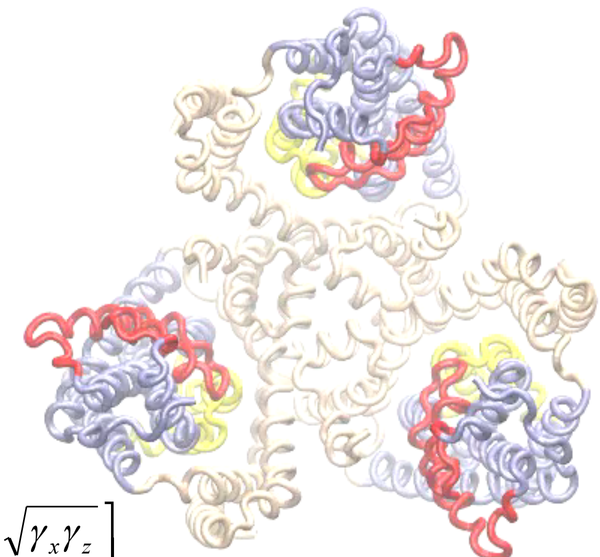


Reyes *et al.* Nature 462 (2009).

Exploring structural transitions: Glutamate transporter

ANM predicts large radial motions of the trimer. Can we invent a better model?

$$\mathbf{H_{ij}} = -\frac{\gamma}{\left(R_{ij}^0\right)^2}\begin{bmatrix} \left(x_{ij}^0\right)^2 & x_{ij}^0 y_{ij}^0 & x_{ij}^0 z_{ij}^0 \\ x_{ij}^0 y_{ij}^0 & \left(y_{ij}^0\right)^2 & y_{ij}^0 z_{ij}^0 \\ x_{ij}^0 z_{ij}^0 & y_{ij}^0 z_{ij}^0 & \left(z_{ij}^0\right)^2 \end{bmatrix}$$

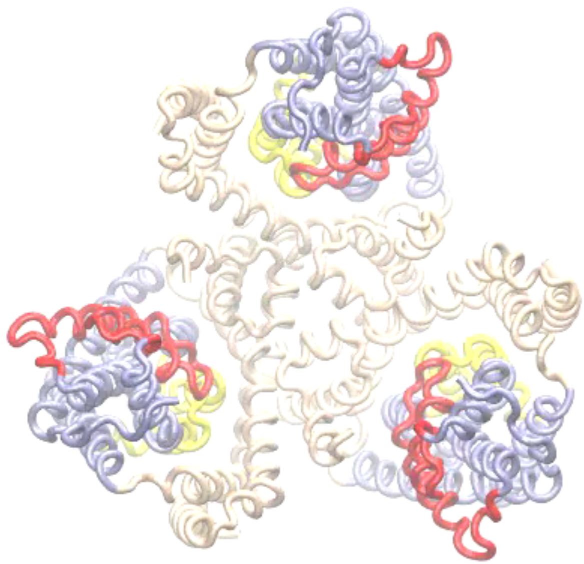


Altered radial force constants:

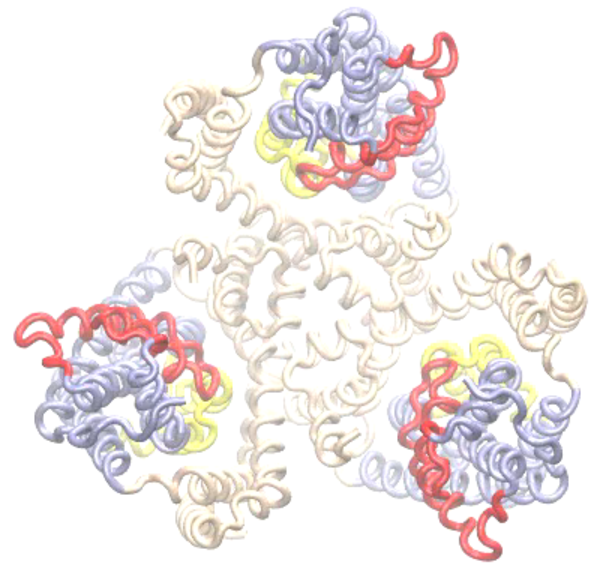
$$\mathbf{H_{ij}} = -\left(R_{ij}^0\right)^{-2}\begin{bmatrix} \left(x_{ij}^0\sqrt{\gamma_x}\right)^2 & x_{ij}^0 y_{ij}^0\sqrt{\gamma_x\gamma_y} & x_{ij}^0 z_{ij}^0\sqrt{\gamma_x\gamma_z} \\ x_{ij}^0 y_{ij}^0\sqrt{\gamma_x\gamma_y} & \left(y_{ij}^0\sqrt{\gamma_y}\right)^2 & y_{ij}^0 z_{ij}^0\sqrt{\gamma_y\gamma_z} \\ x_{ij}^0 z_{ij}^0\sqrt{\gamma_x\gamma_z} & y_{ij}^0 z_{ij}^0\sqrt{\gamma_y\gamma_z} & \left(z_{ij}^0\sqrt{\gamma_z}\right)^2 \end{bmatrix}$$

Lezon & Bahar. Biophys J 102 (2012).

Exploring structural transitions: Glutamate transporter



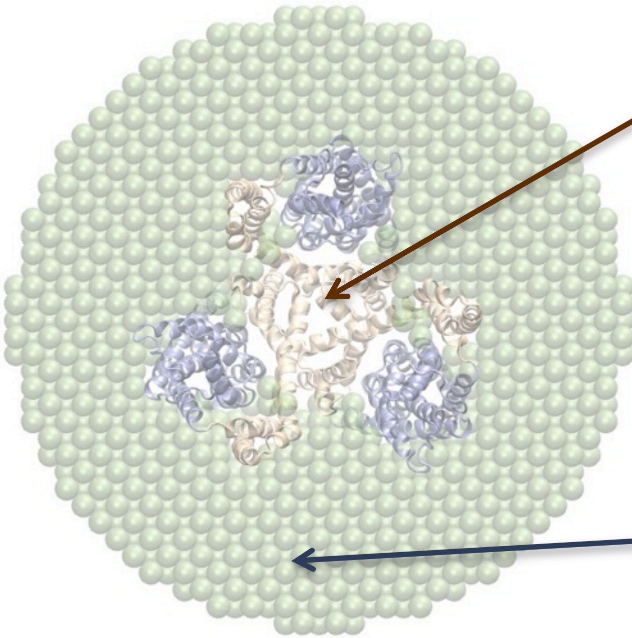
ANM: Large radial motions

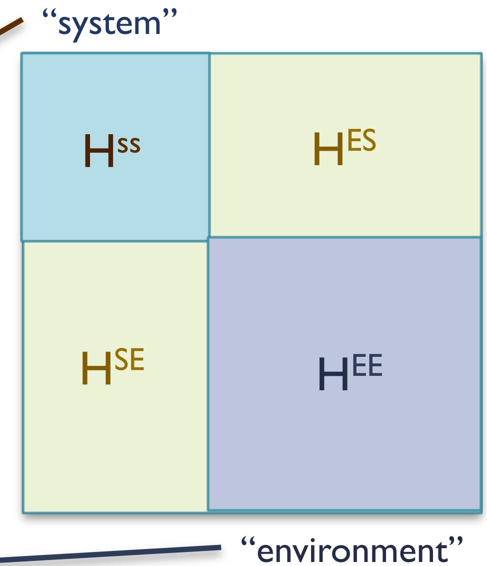


imANM

Lezon & Bahar. Biophys J 102 (2012).

Explicit membrane models



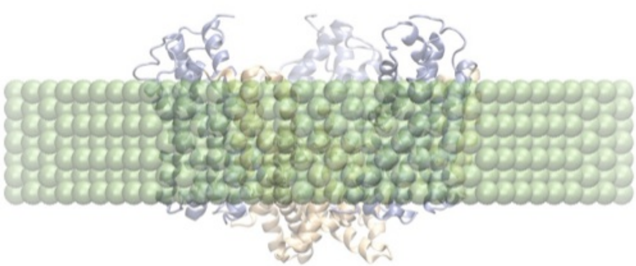


As the *environment* fluctuates randomly, the effective motion of the *system* is given by

$$V_{eff}\left(\mathbf{s}\right) = \tfrac{1}{2}\Delta\mathbf{s}^T\left(\mathbf{H}^{ss\,\prime}\right)\Delta\mathbf{s}$$

$$\mathbf{H}^{ss\,\prime} = \mathbf{H}^{ss} - \mathbf{H}^{SE}\left(\mathbf{H}^{EE}\right)^{-1}\mathbf{H}^{ES}$$

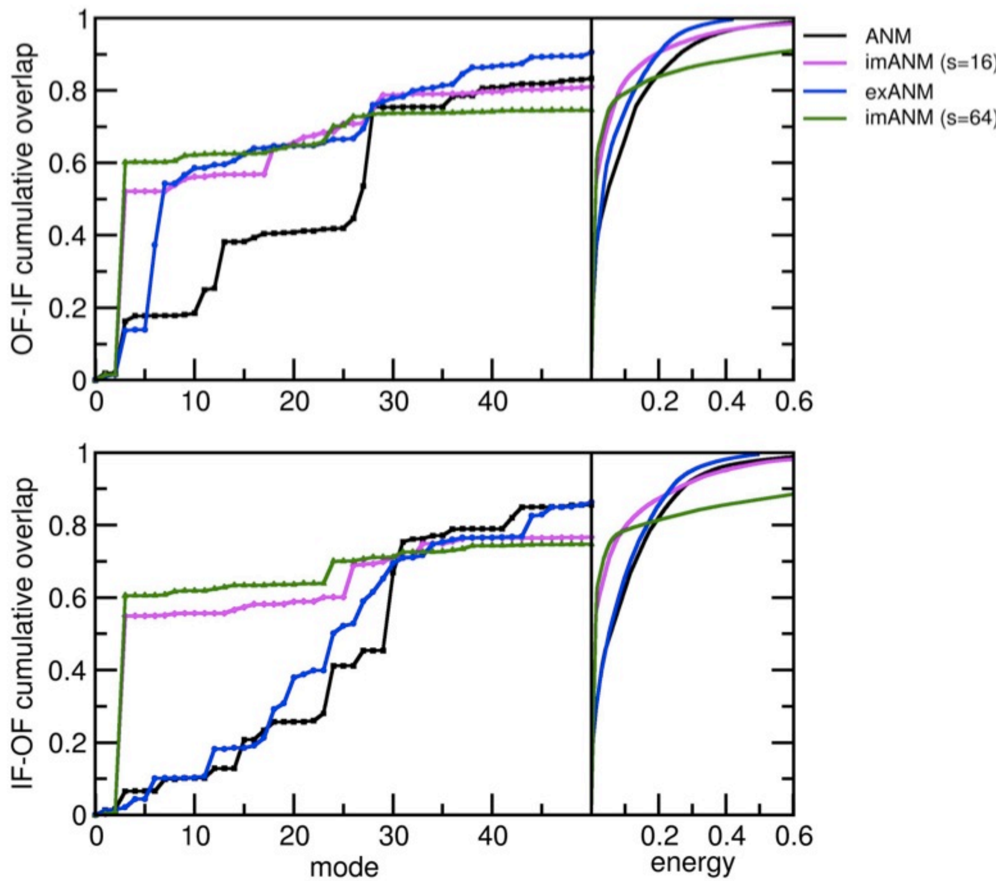
reduceModel()



Lezon & Bahar. Biophys J 102 (2012).

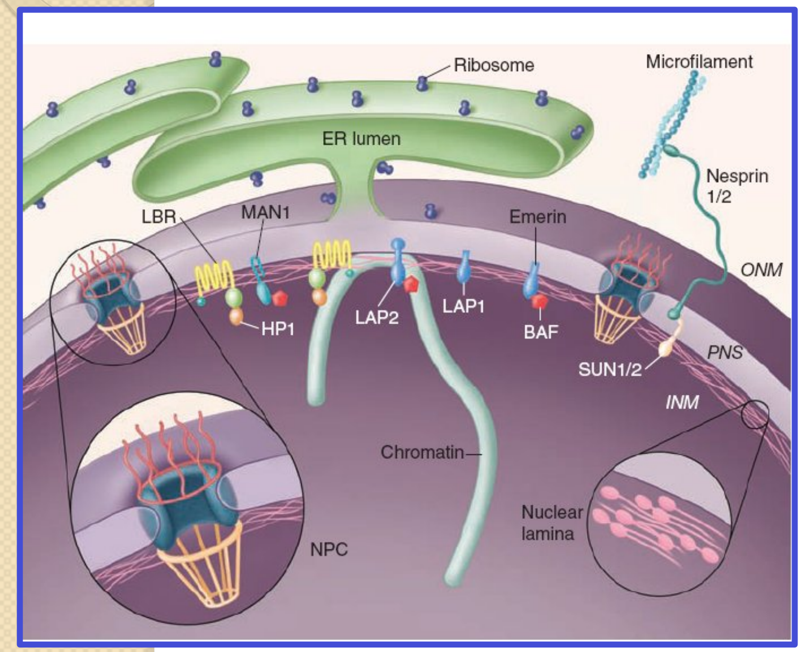
Ming & Wall. PRL 95 (2005).
Zheng & Brooks. Biophys J 89 (2005).

Exploring structural transitions: Glutamate transporter

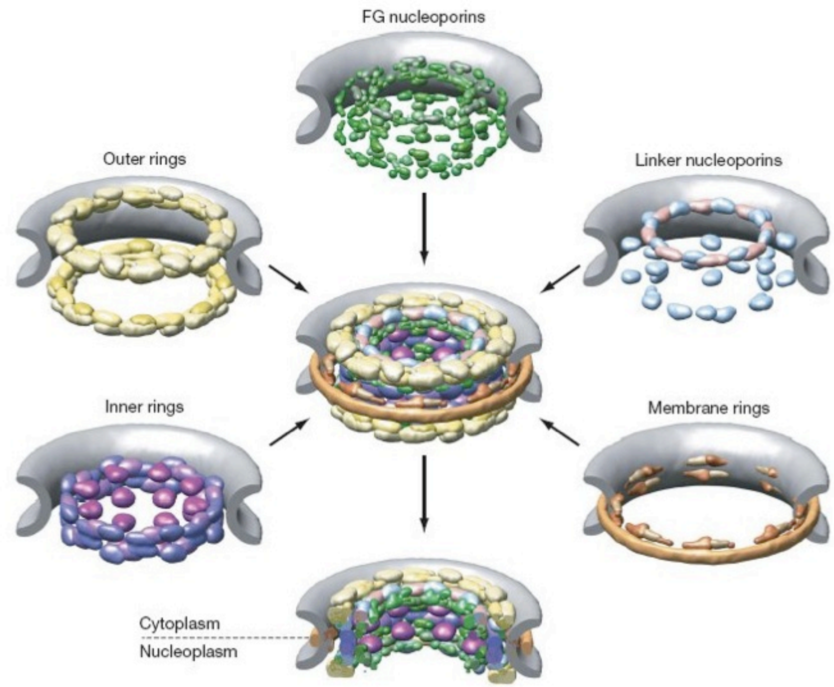


Lezon & Bahar. Biophys J 102 (2012).

Thinking bigger: The yeast nuclear pore complex



Stewart *et al.* Science 318 (2007).



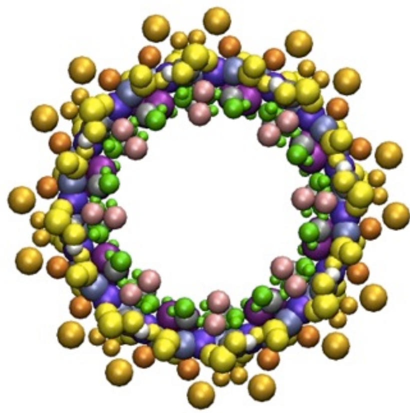
Alber *et al.* Nature 450 (2007).

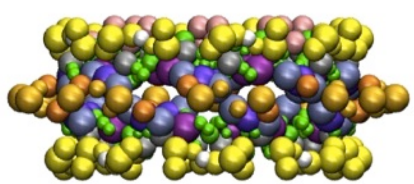
ENM of NPC

R_c = { 12nm protein-protein; 8nm NE-NE; 10nm protein-NE }

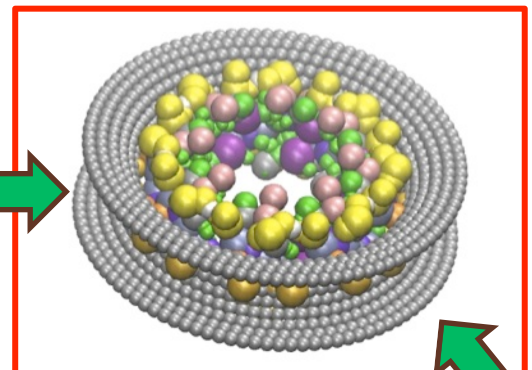
γ = { 1.0 protein-protein; 10 NE-NE }

NPC Model





456 proteins:
57 proteins/spoke
30 unique proteins



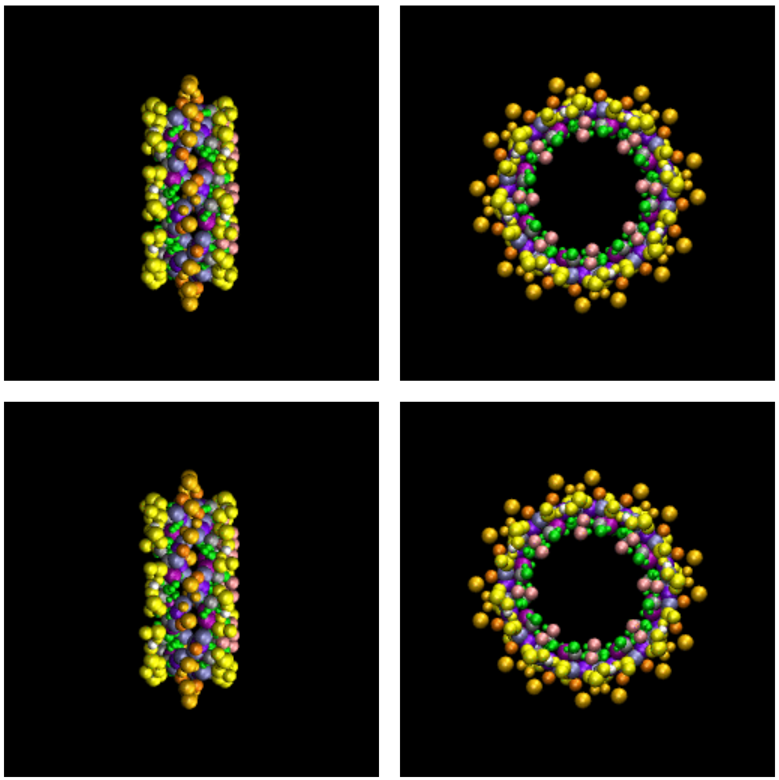
NE:
2070 discrete points

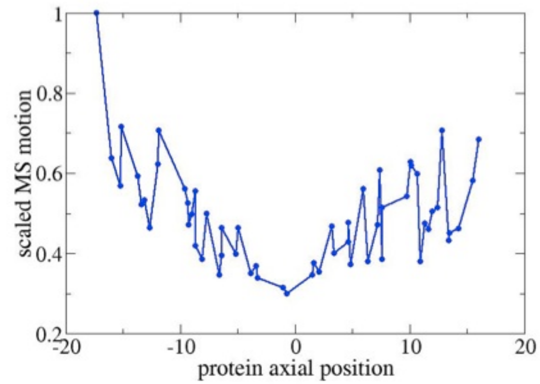
Lezon *et al.* PLoS Comp Biol 5 (2009).

NPC slow modes

Mode 1

Mode 2

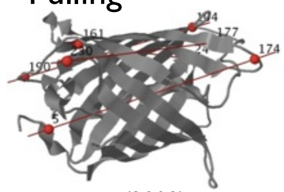




Lezon *et al.* PLoS Comp Biol 5 (2009).

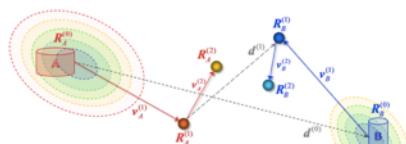
Other ENM applications

Pulling



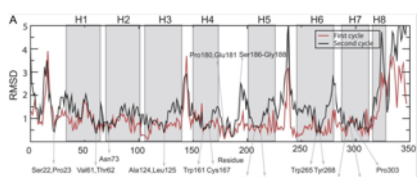
Eyal & Bahar (2008) *Biophys J* **94**:3424.

Transitions



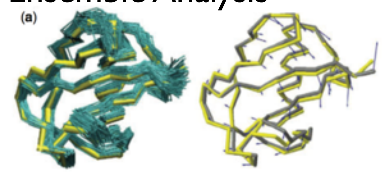
Z Yang et al. (2009) *PLoS Comput Biol* **5**:e1000360.

Steered MD



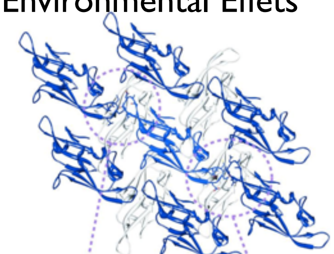
Isin et al. (2008) *Biophysical J* **95**:789.

Ensemble Analysis



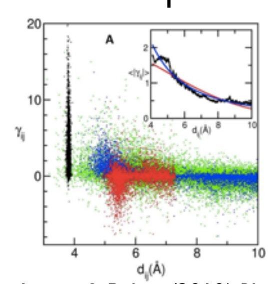
L-W Yang et al. (2009) *Bioinformatics* **25**: 606.
Bakan & Bahar (2009) *Proc Natl Acad Sci USA* **106**:14349.

Environmental Effets



Eyal et al. (2007) *Bioinformatics* **23**:i175.
L Liu et al. (2009) *Proteins* **77**:927.

Model Optimization



Lezon & Bahar (2010) *PLoS Comput Biol* **6**:e1000816.