Mesoscale Modeling of Cell Membrane-Mediated Trafficking*

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Minimal Models for Intracellular Trafficking based on Coarse-Coarse Graining from Direct Experimental Data

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Length, Time

Complexity Simplicity



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Acknowledgements

Mark





Boris



Raj

Dave



Vlad

Ayya

Funding

- NSF CBET-0730955, 0853539, 0853389
- NIH/NIBIB-1R01EB006818, NHLBI-1R01HL087036
- NPACI-MCB060006



Computational Biology Group Members





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Modeling at Multiple Simulation Scales and Connection with Experiment





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Mesoscale Elastic Model for Membranes

Helfrich Free Energy Nelson, Piran, Weinberg, 1987

$$f_{\rm c} = \frac{1}{2}k(H - H_0)^2 + \bar{k}K.$$

H₀:Intrinsic curvature k: Bending Modulus k: Gaussian Curvature Modulus



$$E = \int_{A} \frac{\kappa}{2} (H - H_0)^2 dA + \sigma (A - A_{\text{flat}})^2$$

Elastic free energy including frame tension on a membrane patch

 $\begin{array}{l} H \Rightarrow 1/2[1/R_1 + 1/R_2] \\ K \Rightarrow 1/R_1 \times 1/R_2 \end{array}$

Plane: H=0. K=0



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Mesoscale Linearized Elastic Model for Membrane (small deformation limit)



Time-Dependent Ginzburg Landau Eq.



Langevin Equation (TDGL) Hohenberg and Halperin, 1977 Helfrich Free Energy

$$f_{\rm c} = \frac{1}{2}k(H - H_0)^2 + \bar{k}K.$$

Cartesian (Monge) notation: z=h(x,y)

$$H = \frac{(1+h_x^2)h_{yy} + (1+h_y^2)h_{xx} - 2h_x h_y h_{xy}}{2[(1+h_x^2+h_y^2)]^{3/2}},$$

$$K = \frac{h_{xx}h_{yy} - h_{xy}^2}{(1+h_x^2+h_y^2)^2}.$$

$$E = \int \int_{A} \frac{\kappa}{2} \left(\nabla^{2} z - H_{0} \right)^{2} + \left(\frac{\kappa}{4} H_{0}^{2} + \frac{\sigma}{2} \right) \left(\nabla z \right)^{2} + \overline{\kappa} \left(z_{xx} z_{yy} - z_{xy}^{2} \right) dx dy$$

$$F_{z} = -\frac{\delta E}{\delta z} = 2H_{0}\kappa\left(z_{x}H_{0,x} + z_{y}H_{0,y}\right) + \left(\frac{\kappa}{2}H_{0}^{2} + \sigma\right)\left(\nabla^{2}z\right) - \kappa\nabla^{4}z + \kappa\nabla^{2}H_{0} + \xi$$



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Coarse-Grained Representation of Protein-Membrane Interaction



Integral Membrane Proteins

Membrane is attached to the protein at a fixed contact angle Goulian M, Bruinsma R, Pincus P (1993) Lubensky T (1997) Kim KS, Neu J, Oster G (1998)

LOCAL CURVATURE INDUCER MODEL

McMahon, 2003, 2005

Tubule diameter=20 nm; $\Delta E_{binding}$ = -14 k_BT





Seifert, et. al. 2006; Weinstein, Radhakrishnan, 2006; Agrawal, Weinstein, Radhakrishnan, 2008 $C_0=0.1 \text{ nm}^{-1}$; b=8 nm; $\kappa=20 \text{ k}_B\text{T}$ b nm



$$H_0 = C_0 e^{-s^2/b^2}$$



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Multiscale Integration: Protein-Mediated Membrane Fluctuations



Proteins perform a random walk on membrane surface with a membrane mediated force field





State Diagram: Protein-Mediated Membrane Fluctuations

- ρ*, Surface Density 1-100 per μm²
- R=b/2, Range 10-50 nm
- C_0 or H_0 , Intrinsic Curvature 0-40 μ m⁻¹
- Radial Distribution, Orientational Correlation
- Membrane Height Autocorrelation
 - J. Weinstein, R. Radhakrishnan, 2006 N. J. Agrawal, J. Weinstein, R. Radhakrishnan, 2008.





How does the protein induced curvature affect the equilibrium properties and conformations of the membrane ?



State Diagram

RU: Repressed Undulations; No N: No nucleation **NVOO:** Nucleation via orientational ordering **NVA:** Nucleation via diffusional association



NVA



NVOO



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State Diagram

RU: Repressed Undulations; No N: No nucleation NVOO: Nucleation via orientational ordering NVA: Nucleation via diffusional association





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Free Energy Calculations via Thermodynamic Integration



Free energy change with spatial extent of the curvature function





Entropy change is small (<5% of the Energy change) but is of order k_BT

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Agrawal, Radhakrishnan, 2009

$$\left(\frac{\partial F}{\partial \lambda}\right)_{N,V,T} = -\frac{1}{\beta} \frac{\partial}{\partial \lambda} \ln Q = \left\langle \frac{\partial E}{\partial \lambda} \right\rangle_{\lambda}$$

By choosing $\lambda = C_0$,

$$\frac{\partial F}{\partial C_0} = \left\langle \Gamma(r_0) \kappa \sum_{N} \left[-\left(\nabla^2 z_i - \lambda \Gamma(r_0) \right) + \frac{\lambda}{2} \left(\nabla z_i \right)^2 \right] \left(\Delta r_i \right)^2 \right\rangle$$

$$\Delta F = F(C_0) - F(0) = \int_0^{C_0} \frac{\partial F}{\partial C_0} dC_0$$

Nucleation via Hexatic Orientational Ordering: NVOO



Sustained orientational correlations beyond nearestneighbors drives nucleation



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Clathrin-Mediated Endocytosis: Inference-Based Model



Recent Experimental Observations

- HeLa Cells: In absence of clathrin, AP-2 and accessory proteins form curvature lacking sub-domain. Hinrichsen, PNAS 2006.
- HeLa Cells: Knockdown of AP-2 significantly reduces the number of clathrin coated pits (CCP) at the plasma membrane. Hinrichsen, J. Biol. Chem. 2003.
- Neurons: epsin antibodies change the morphology of CCP. Jakobsson, PNAS, 2008.
- Effect of accessory proteins is receptor (cargo) dependent.



Surface Evolution

- Exact minimization of Helfrich energy possible for any (axisymmetric) membrane deformation.
- Energy is minimized instead of Free Energy
- **Δ** Membrane parameterized by arc length, s and angle ψ .



Surface evolution provides a route to compute the profiles and energetics associated with minimum energy conformations of membranes subject to extreme curvature



Seifert, 1995

Bond-Orientational Patterning of Epsin on Clathrin Lattice Leads to a Mature Vesicle Formation



Agrawal, Radhakrishnan, Submitted



Effect of Clathrin-Coat Size on Membrane Vesiculation



Critical size of a growing clathrin coat leads to membrane invagination

Agrawal, Radhakrishnan, Submitted



Energy Considerations in Clathrin Induced Membrane Vesiculation



For κ =20k_BT, E_C ~ 500 k_BT

Agrawal, Radhakrishnan, Submitted



Energy Considerations in Clathrin Induced Membrane Vesiculation

Calculated

Experimental







Jakobsson, J.; PNAS 2008, 6445.

Our results highlight the unique and central role played by epsin in the process of vesicle nucleation during endocytosis



Minimal Model for Clathrin Coat Nucleation



Point defects serve the role of disclinations in a hexagonal lattice and enable the coat to adaptively assume a curvilinear scaffold



Minimal Model for Clathrin Coat Nucleation





Effect of Interaction Energy Variation on Number of Point Defects Autocorrelation and Persistence Time



Effect of Bending Rigidity on Membrane Vesiculation

Diameter of the budding vesicle depends strongly on membrane bending rigidity





Due to cell-cell variability, diameter of clathrin-coated vesicles range from 50-100 nm



Neuronal Cells d=50 nm

Epithelial Cells d=100 nm



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Integrated Molecular-Systems Model for ErbB Signaling, Trafficking

Clathrin adaptor	Cargo motif recognized	Ubiquitin binding	Membrane component bound	Activation of downstream effectors of cellular response is specific to the molecular context
AP2 complex	ΦxxYxxΦ [DE]xxxL[LI]	Yes	PtdIns(4,5)P ₂	 ErbB1-4 internalize at different rates FYRALM recognition motif
AP1 complex	ΦxxYxxΦ [DE]xxxL[LI]	Yes	PtdIns4P	 Receptor:AP-2 in 2:2 is optimal Some ErbB1 mutants internalize
GGA	DxxLL	Yes	ArfGTP	 Link to altered downstream
Epsin		Yes	PtdIns(4,5)P ₂	signaling: Erk vs. Akt vs. STAT5
HRS/Vps27		Yes	PtdIns3P	 Akt activation is optimal in membrane-bound receptor
DAB2/ARH	[FY]xNPxY	Yes	PtdIns(4,5)P ₂	Erk signaling occurs for internalized as well as membrane-bound
Arrestin	GPCRs	Yes	PtdIns(4,5)P ₂	
AP180/CALM		Yes	PtdIns(4,5)P ₂	STAT5 activation could be mutually
Amphiphysin	TOFMS	Yes	Acidic phospholipid including PtdIns(4,5)P ₂	exclusive of internalization

