

Stochastic multiscale modeling of spatially distributed biological systems

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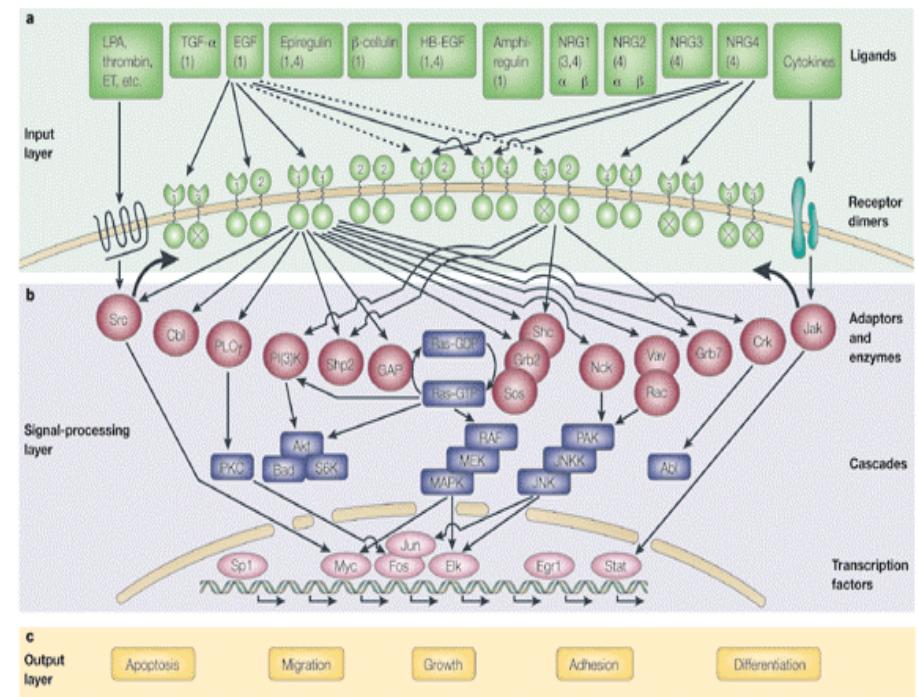
Supported by DOE (DE-FG02-05ER25702)

Outline

- Examples of multiple scales from cellular biology
 - Molecular scale and stochastic effects are crucial
- Multiscale mathematical and computational methods
 - Concepts
 - Mathematical tools
 - Numerical examples for model systems
- Comparison to real experimental data
- On-going and future work

EGF Receptor Signaling Network

- Important biological role
 - Trigger a rich network of signaling pathways and regulate functions such as proliferation, differentiation and migration.
 - Dysregulations in the signaling pathway lead to a variety of cancers: endometrial, breast, lung, prostate, colon, ovary, bladder, head and neck.
- Important as drug targets
 - EGFR is a target for anti-cancer drugs: ease of manipulation in the extracellular domain



Highly simplified signaling map of some of the proteins activated by the 4-member family of EGF receptors

EGFR pathway

- Adsorption and desorption of ligand
- Surface diffusion
- Surface dimerization

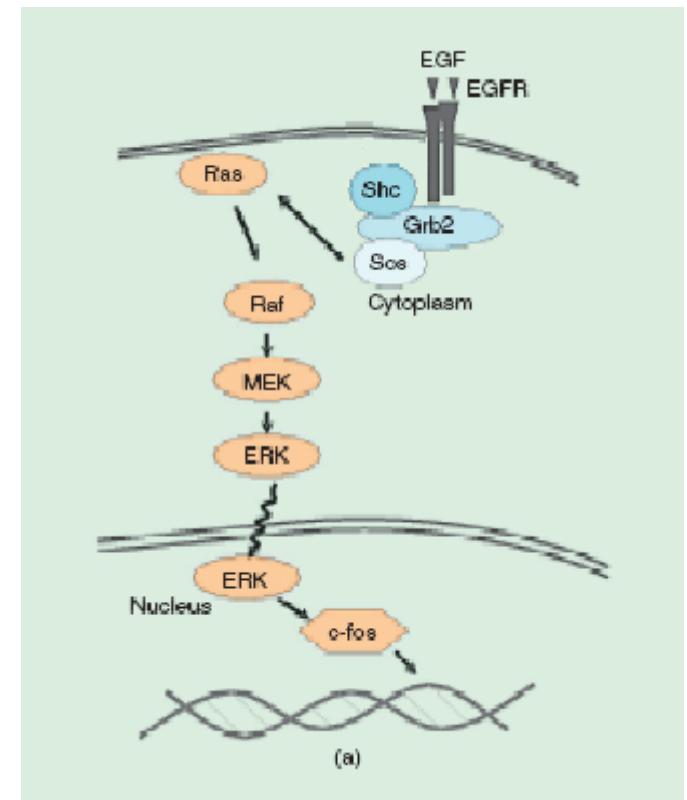
Dimerization Reactions



Ligand Binding Reactions

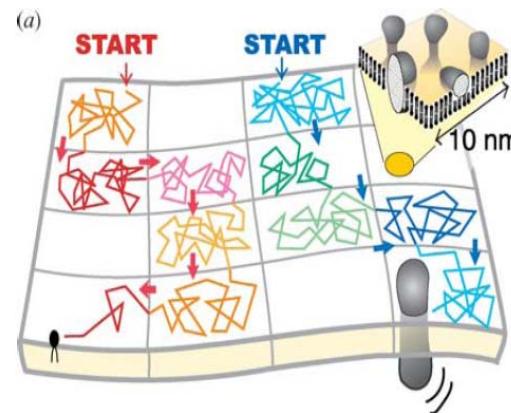
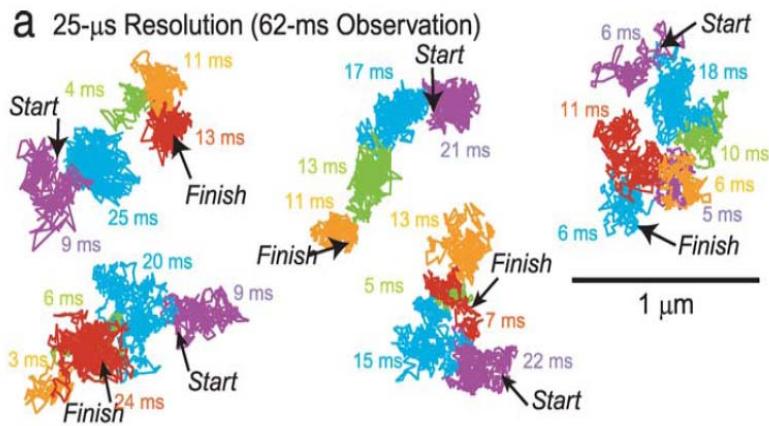


- Phosphorylation, internalization, etc.



J. Saez-Rodriguez, et al. (2004)

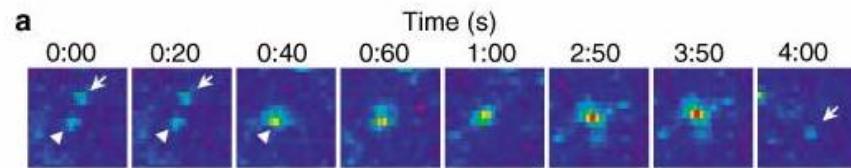
New Imaging Data at the Receptor Level



Single particle tracking (SPT) experiments track receptor movement at micro-second scale are indicating compartments in the plasma membrane

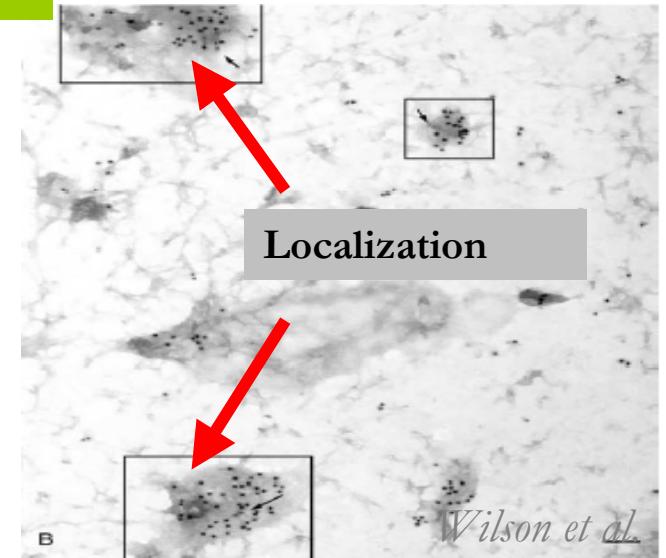
Kusumi et al.

Heterogeneity in receptor distribution: EM image suggesting localization of receptors

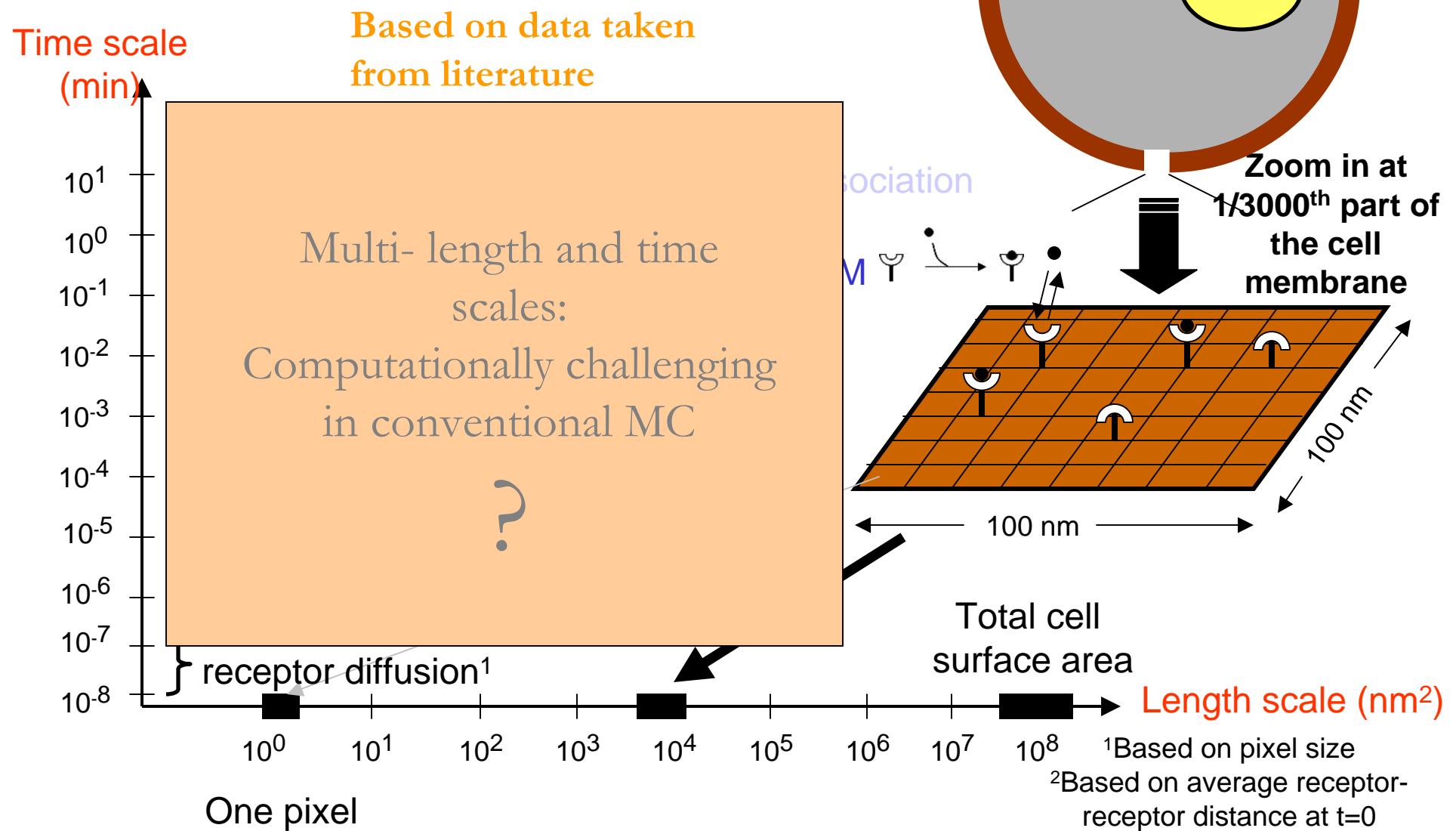


Sako et al.

SPT experiments tracking dimerization reaction events at the molecular level



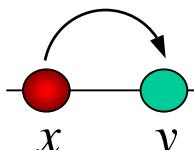
Time and Length Scales in Cell Surface Modeling of the EGFR



A hierarchy of coarse grained processes and KMC simulations

Microscopic Stochastic Process

Hamiltonian: $H(\sigma) = -\frac{1}{2} \sum_{x \in M} \sum_{y \neq x} J(x-y) \sigma(x) \sigma(y) + \sum_{x \in M} h \sigma(x)$



Microscopic processes/transition $v(x \rightarrow y, \sigma) = v_0 \sigma(x)(1 - \sigma(y)) \exp[-\beta(U_o + U(x))]$
probabilities, e.g., surface diffusion

Mesoscopic Stochastic Process

$$\eta_k = \sum_{y \in D_k} \sigma(y)$$

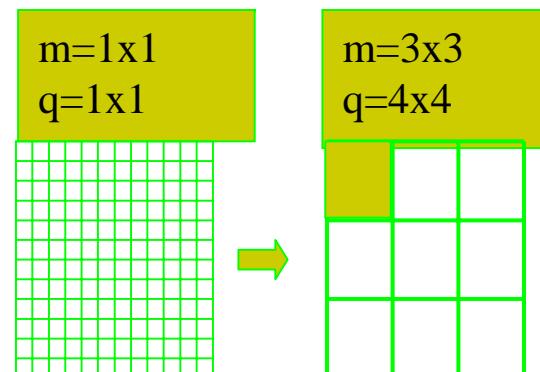
q =number of points in a coarse cell

$$\bar{U}_i = \sum_{k \in M_c} \bar{J}_{ik} \eta_k + \bar{J}_{00} (\eta_i - 1) - h$$

$$\bar{H}(\eta) = - \sum_{k \in M_c} \bar{U}_k \eta_k = -\frac{1}{2} \sum_{i \in M_c} \sum_{\substack{k \in M_c, \\ k \neq i}} \bar{J}_{ik} \eta_k \eta_i - \frac{\bar{J}_{00}}{2} \sum_{i \in M_c} \eta_i (\eta_i - 1) + \sum_{k \in M_c} h \eta_k$$

$$\bar{v}(k \rightarrow i, \eta) = v_0 \eta_k (q - \eta_i) \exp[-\beta(U_o + \bar{U}_k)]$$

Katsoulakis et al., PNAS 100, 782 (2003)
J. Comp. Phys. 186, 250 (2003)

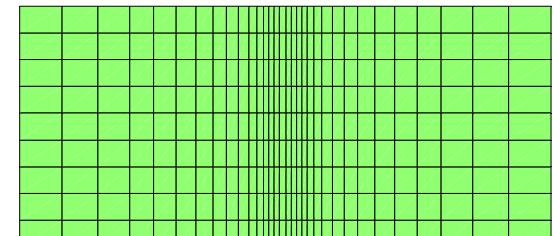


Features of coarse grained processes

- We never pass to any continuum limit
 - **Full hierarchy** from microscopic MC to global MF
- **Stochastic closure (local equil./LMF approximation)**
- **Detailed balance** is used as a **design tool** in deriving transition probabilities from the microscopics (self consistent fluctuations)
- **Haar wavelet basis** is used in estimating the coarse grained interactions
- Large Deviation Principles demonstrate proper **rare event** description
- **The method is exact when the potential length is infinite**
- Implementation is straightforward/**CPU savings: q^{2-4}**

Spatial acceleration methods

- Spatial adaptivity¹
 - Error estimates guide mesh refinement

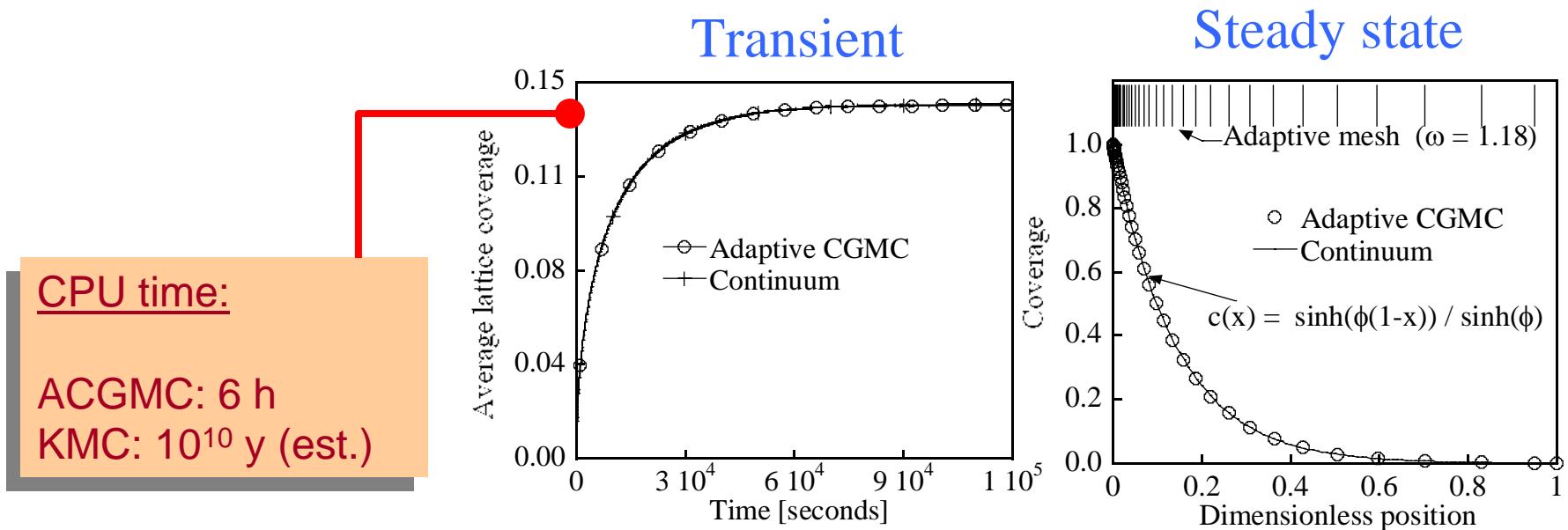


Non-uniform mesh

¹ Chatterjee et al., *JCP* **121**, 11420 (2004); *PRE* **71**, 0267021 (2005)

Example of diffusion-reaction in a 1 mm domain (pellet) using ACGMC

- Coarse-graining reduces computational intensity of ACGMC



- A posteriori error estimates are well-established in FEM.
How does one optimally adapt the mesh in MC?

Information theory in ACGMC

- Approach is completely different from finite elements
- Microscopic Gibbs measure $\mu_{\text{micro}} = Z_{\text{micro}}^{-1} e^{-H_{\text{micro}}/kT} P_{\text{micro}}(\underline{\sigma})$
- Coarse-graining results in loss of information (degrees of freedom)

0	1
1	1

1	1
0	1

1	1
1	0

1	0
1	1



MICROSCOPIC (4 states)

COARSE-GRAINED (1 state)

- Adaptive CG Gibbs measure $\mu_{\text{CG}} = Z_{\text{CG}}^{-1} e^{-H_{\text{CG}}/kT} P_{\text{CG}}(\underline{\eta})$

- Relative information entropy, R
- distance between the two distributions

$$R = \left\langle \log \frac{\mu_{\text{CG}}}{\mu_{\text{micro}}} \right\rangle$$

- Express in terms of difference of Hamiltonians

$$R = \langle \Delta H \rangle + \left\langle \log \sum_{\text{cell}} e^{-\Delta H/kT} \frac{P_{\text{CG}}(\underline{\eta})}{P_{\text{micro}}(\underline{\sigma})} \right\rangle$$

$$\Delta H = H_{\text{micro}} - H_{\text{CG}}$$

Information theory in ACGMC

- Microscopic solution is unknown! Estimate upper bounds

$$R = \langle \Delta H \rangle + \left\langle \log \frac{P_{CG}(\underline{\eta})}{\sum_{\text{cell}} e^{-\Delta H/kT} P_{\text{micro}}(\underline{\sigma})} \right\rangle \rightarrow R \leq c \langle \Lambda(\underline{\eta}) \rangle$$

$\Lambda(\underline{\eta}) = \text{Upper bound}(\Delta H)$

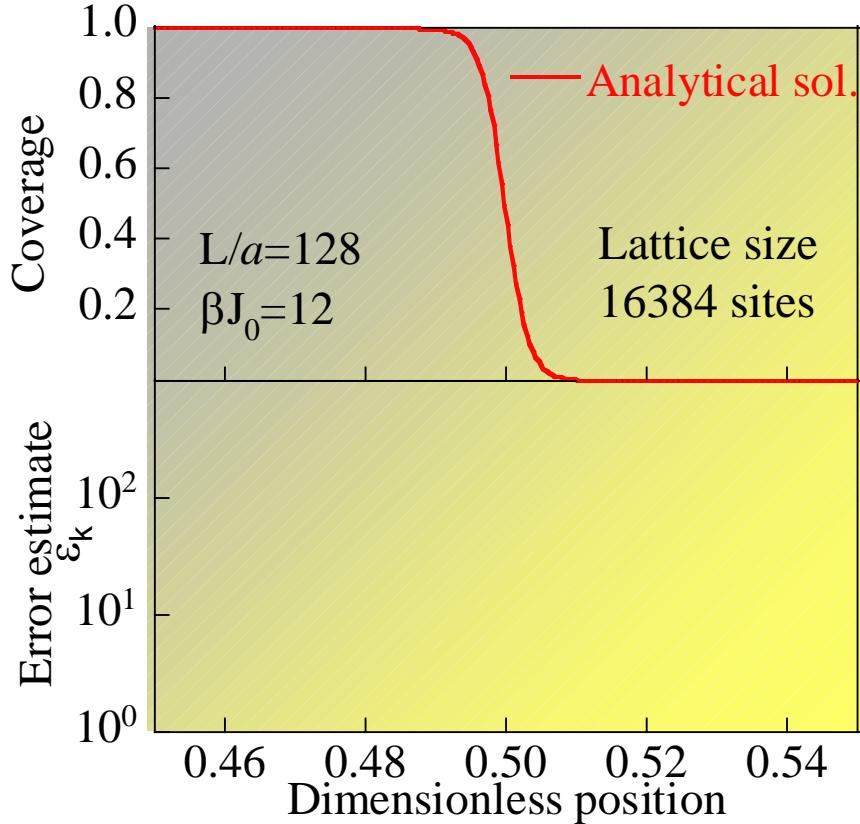
$$\langle \Lambda(\underline{\eta}) \rangle = 4 \sum_{\text{cells}, k} \left\{ \frac{j_{kk}}{q_k(q_k - 1)} \langle \eta_k(q_k - \eta_k) [\eta_k(\eta_k - 1) + (q_k - \eta_k)(q_k - \eta_k + 1)] \rangle + \right. \\ \left. \sum_{\text{interacting cells}, l} \frac{j_{kl}}{q_k q_l} \langle q_k^2 \eta_l (q_l - \eta_l) - 2 \eta_k \eta_l (q_k - \eta_k)(q_l - \eta_l) \rangle \right\}$$

- Overall:

$$\langle \Lambda(\underline{\eta}) \rangle = \sum_{\text{cells}, k} \langle \varepsilon_k \rangle$$

A *posteriori* error estimate based on the computed solution only!¹

Use error estimates for mesh adaptation



Standing wave in 1D

- Adsorption, desorption
- Strong long-ranged attractive potential
- Continuum (analytical) solution

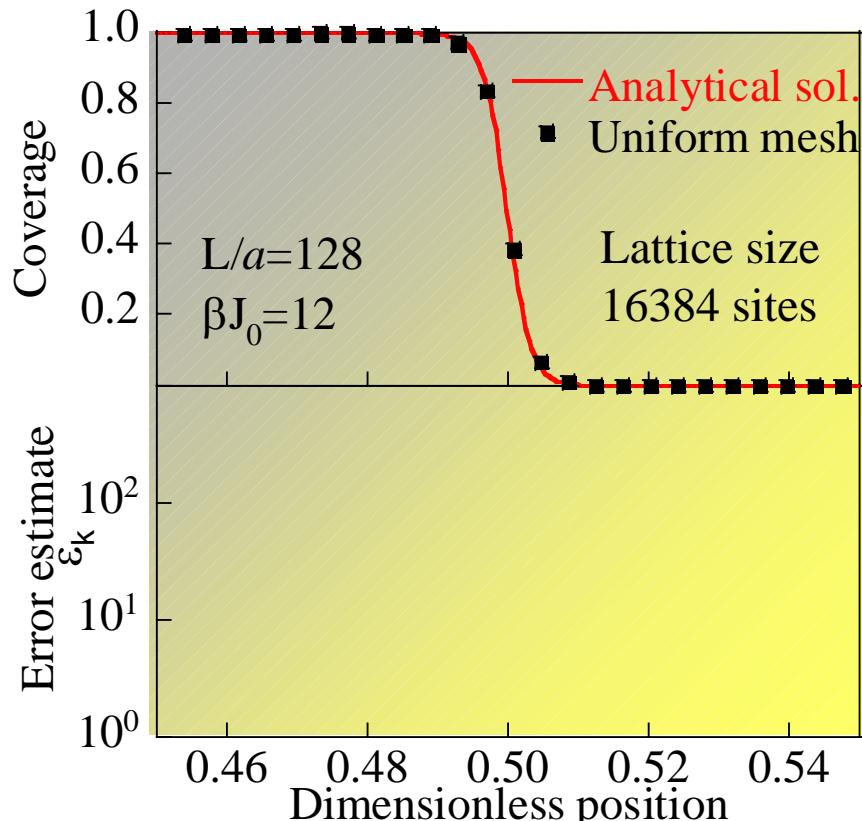
$$\theta(x) = \frac{1}{2} \left[(2\theta_+ - 1) \tanh(\beta J_0 (2\theta_+ - 1)x) + 1 \right]$$

θ_+ : Dense phase coverage

Mesh refinement

- Split offending coarse cells into two
- Equally distribute order parameters

Use error estimates for mesh adaptation



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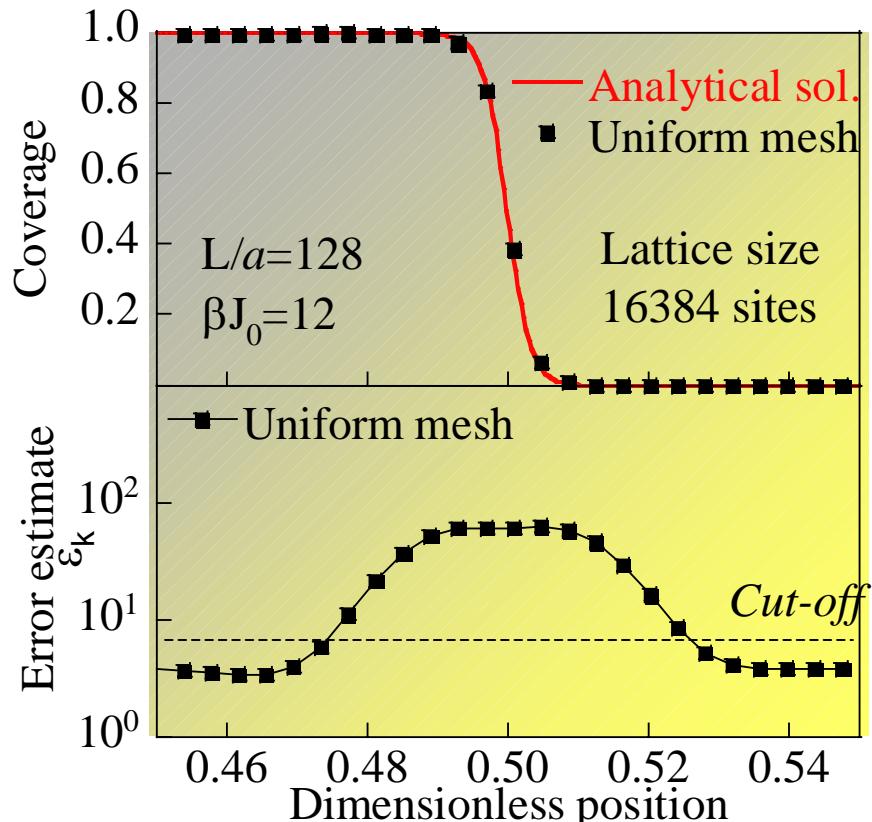
θ_+ : Dense phase concentration

Mesh refinement

- Split offending coarse cells into two
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||||| Uniform mesh, $q = 64$

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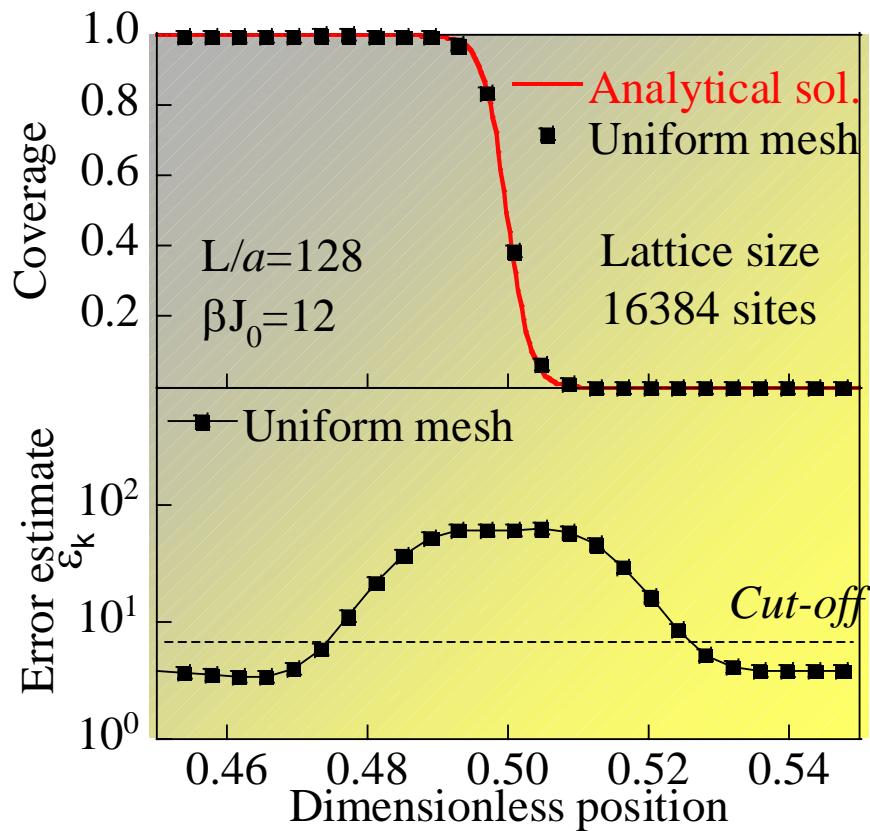
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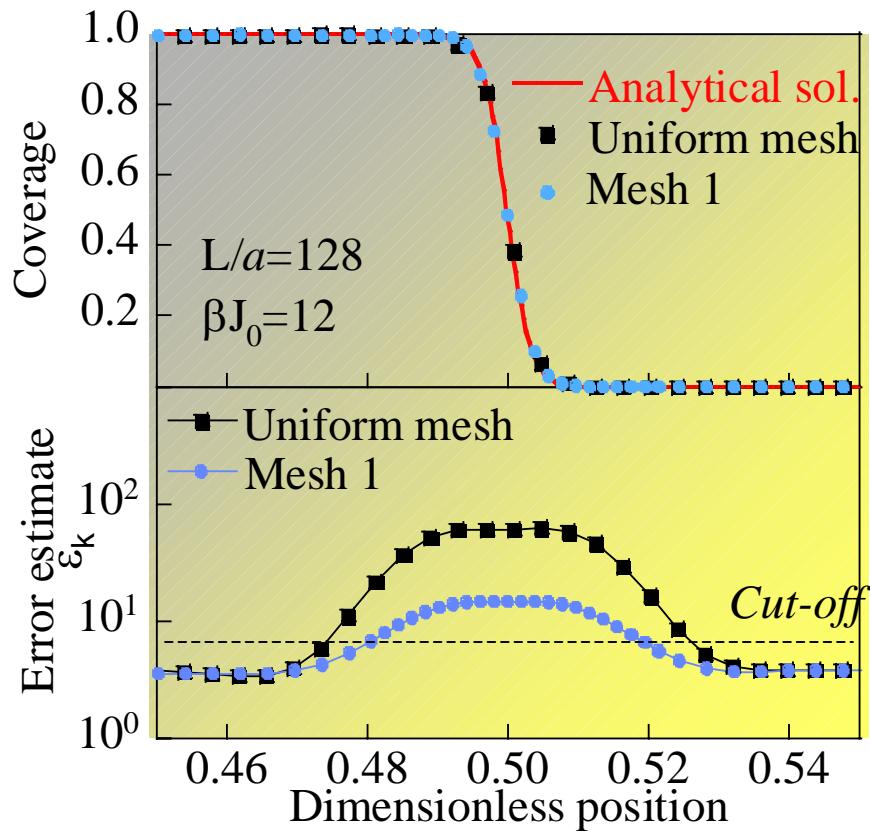
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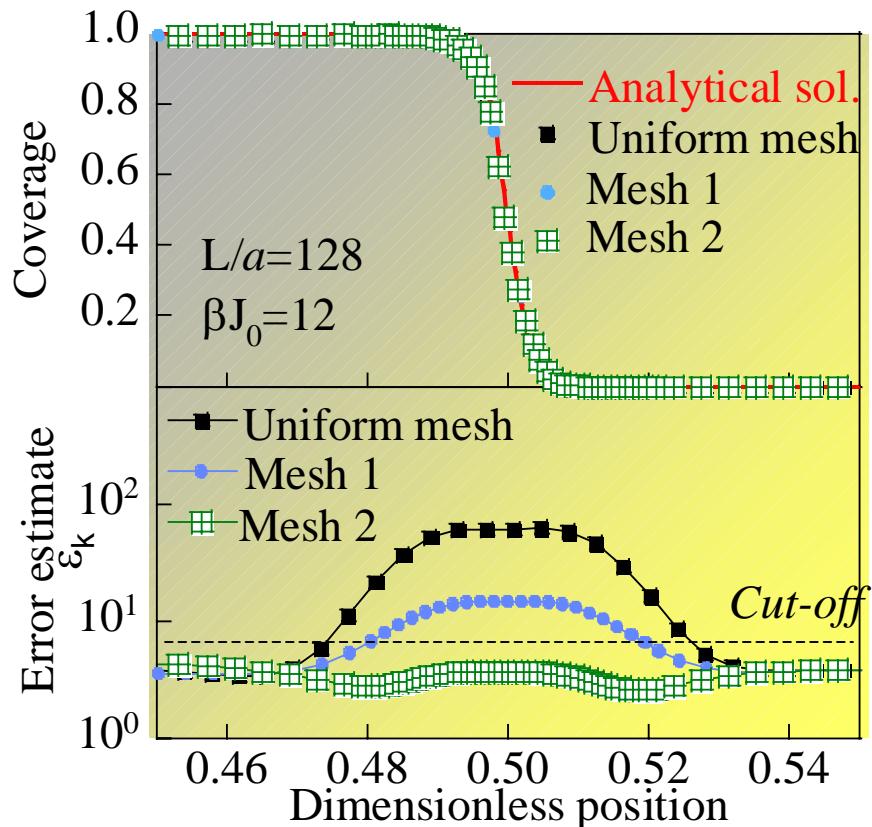
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||||| Uniform mesh, $q = 64$

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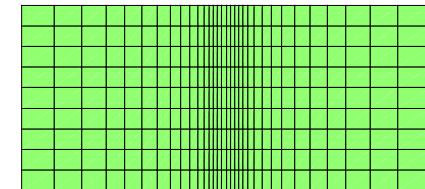
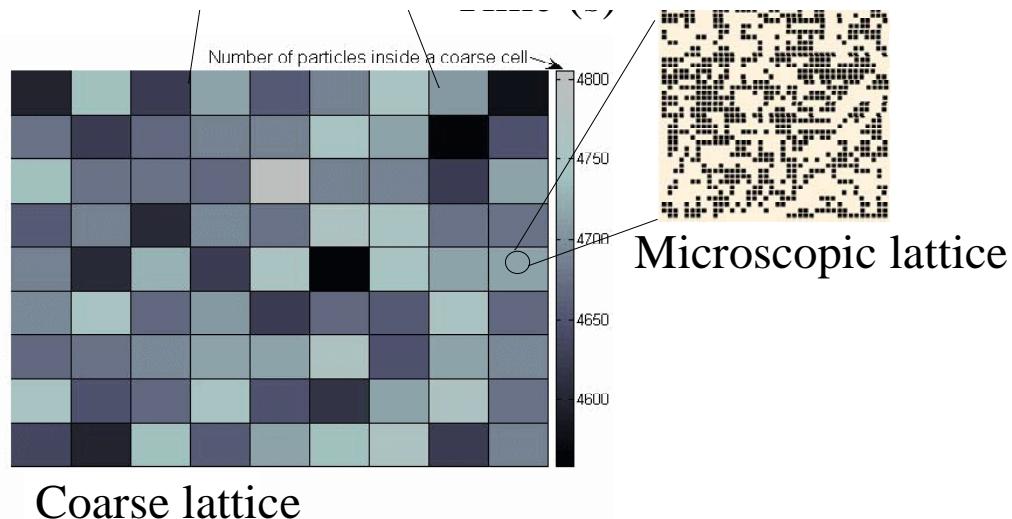
Uniform mesh, $q = 64$



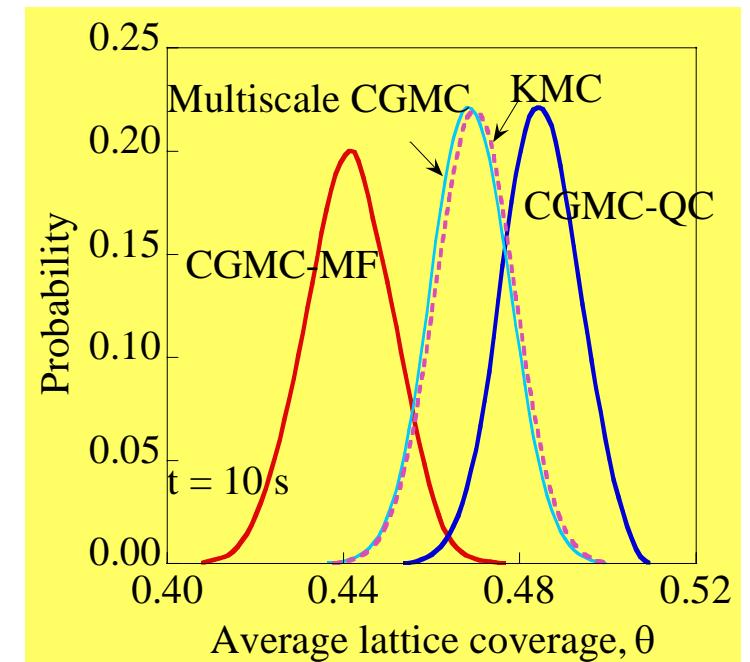
ACGMC: 30 minutes
KMC: 90 days (est.)

Spatial acceleration methods

- Spatial adaptivity¹
 - Error estimates guide mesh refinement
- Multiscale MC methods for high accuracy
 - Higher order closures²
 - Multigrid/Relaxation criteria²
 - Rigorous cluster expansions³



Non-uniform mesh



¹ Chatterjee et al., *JCP* **121**, 11420 (2004); *PRE* **71**, 0267021 (2005)

² Chatterjee and Vlachos, *JCP* **124**, 0641101 (2006)

³ Katsoulakis, Plechac, et al., *ESAIM, Math Model. Num. Anal.*, to appear

Higher-order coarse-grained MC: Rigorous cluster expansions

- Corrections around \bar{H}^o from prior work of Katsoulakis and Vlachos: Renormalization Group Map

$$H^c(\eta) = \bar{H}^o(\eta) - \frac{1}{\beta} \log E[e^{-\beta(H_N - \bar{H}^o)} |_{\eta}]$$

- Heuristics (expansion of exp and log)
$$= E[\Delta H |_{\eta}] + E[(\Delta H)^2 |_{\eta}] - E[\Delta H |_{\eta}]^2 + O((\Delta H)^3)$$
 - Formal calculations inadequate since: $\Delta H = H_N - \bar{H}^o = N \cdot O(\varepsilon)$
 - Rigorous analysis: Cluster expansion **around** \bar{H}^o

³ Katsoulakis, Plechac, Rey-Bellet, Tsagkarogiannis, ESAIM, Math Model. Num. Anal., to appear

Higher-order coarse-grained MC: Rigorous cluster expansions – Cont.

- Corrections to the Hamiltonian – **many body** terms

$$H^c(\eta) = \bar{H}^0(\eta) + \bar{H}^1(\eta) + \dots$$

$$\bar{H}^1(\eta) = \beta \sum_{k_1} \sum_{k_2 > k_1} \sum_{k_3 > k_2} [j^2_{k_1 k_2 k_3} (-E_1(k_1) E_2(k_2) E_1(k_3) + \dots)]$$

$$E_r(k) = E_r(\eta(k)) = (2\eta(k)/q - 1)^r + O_q(1)$$

- **Moments** of the potential

$$j^2_{k_1 k_2 k_3} = \sum_{x \in C_{k_1}} \sum_{y \in C_{k_2}} \sum_{z \in C_{k_3}} [(J(x - y) - \bar{J}(k_1, k_2))(J(y - z) - \bar{J}(k_2, k_3))]$$

- **Clusters expansions give**

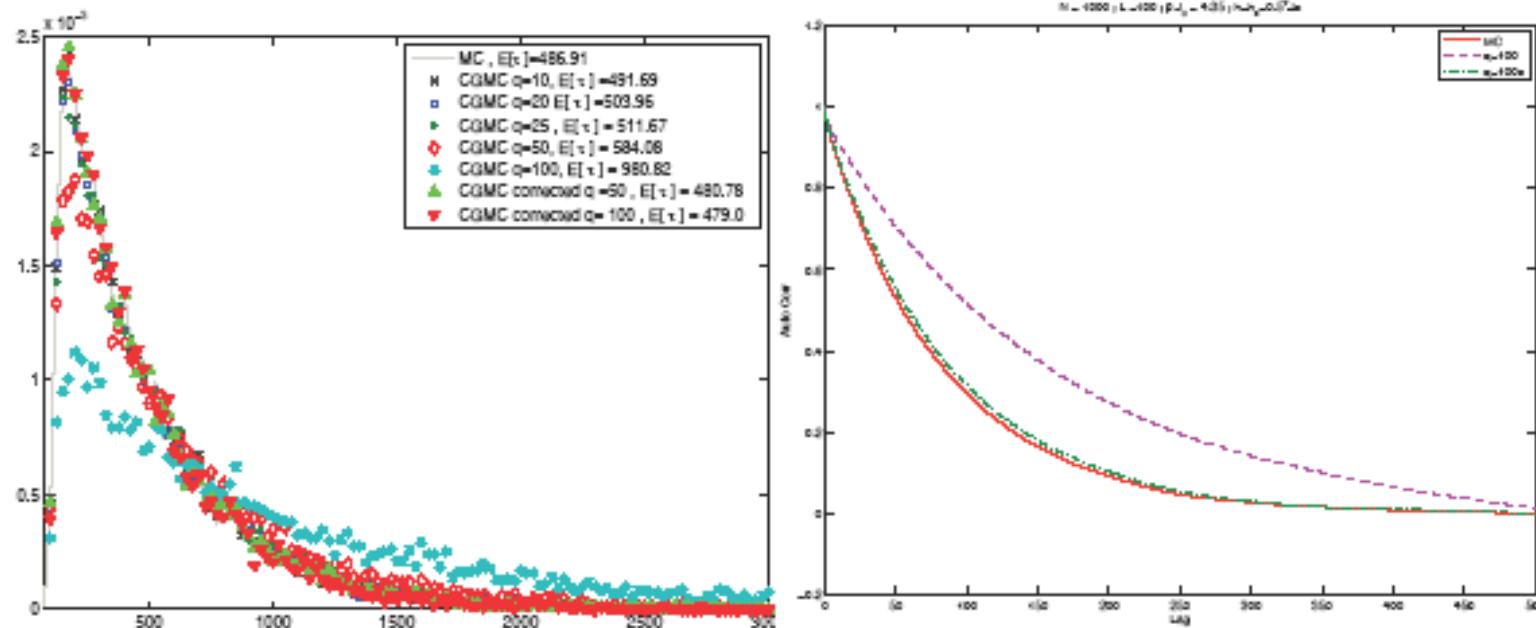
- Sharp a posteriori error estimates/Adaptivity
- Higher-order CGMC schemes

A numerical example

- Phase transitions between two states: PDF of switching times

Demonstration: Metastability for CG Arrhenius dynamics

Switching Time PDFs/Autocorr.: with and w/o corrections



Joint work with Sasanka Are (UMass)

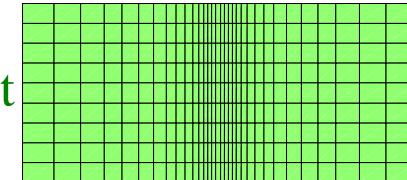
Error quantification in CG schemes

- **Theorem:** *A priori* error estimate
 - Define a small parameter: $\varepsilon \equiv C\beta \frac{q}{L} \| J' \|_1$
 - Then, specific relative entropy: $R(\mu_{M,q,\beta} || \mu_{N,\beta^o} T^{-1}) = O(\varepsilon^{\alpha+2})$
 α =order of truncation in cluster expansion
 - $T\sigma$ =projection on coarse variables = $\sum_{y \in D_k} \sigma(y)$
- Error estimates for observables – ‘**quantity of interest**’⁴
 - Difficulty in dynamics: $T\sigma$ is not a Markov process
- **Reverse CG map** – Microscopic reconstruction possible⁴
 - Reverse the CG via the conditional prior
 - Numerical error estimate for the reconstruction

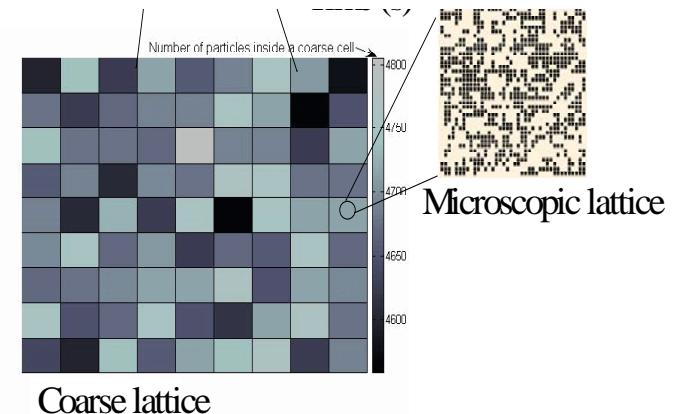
⁴ Katsoulakis, Plechac, Sopasakis, SIAM Num. Anal. (2006)

Spatial acceleration methods

- Spatial adaptivity¹
 - A posteriori error estimates guide mesh refinement and generation of phase diagrams
- Multiscale MC methods for high accuracy
 - Higher order closures²
 - Multigrid/Relaxation criteria²
 - Rigorous cluster expansions/Theory^{3,4}
- Multicomponent interacting systems⁵
- Time scale acceleration



Non-uniform mesh



¹ Chatterjee et al., *JCP* **121**, 11420 (2004); *PRE* **71**, 0267021 (2005); Katsoulakis, Plechac, et al., *J. Non Newtonian Fluid Mech.* (2007)

² Chatterjee and Vlachos, *JCP* **124**, 0641101 (2006)

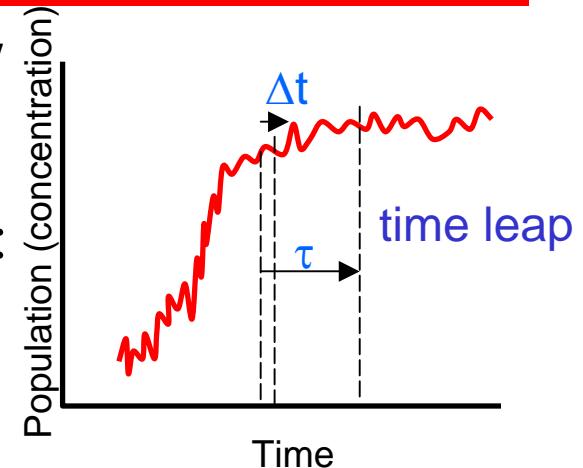
³ Katsoulakis, Plechac, et al., *ESAIM, Math Model. Num. Anal.*, to appear

⁴ Katsoulakis, Plechac, Sopasakis, *SIAM Num. Anal.* (2006)

⁵ Chatterjee and Vlachos, *JCP*, accepted

Time scales acceleration methods

- Binomial τ -leap method: fire multiple events^{6,7}
 - Time step increment based on stability
- Stochastic low dimensional manifold (SLDM): overcome stiffness
 - Computational singular perturbation (CSP) assisted partitioning⁸
 - Statistical criteria for convergence to the LDM^{8,9}
- Hybrid multiscale Monte Carlo method⁹
 - Deal with simultaneous separation of time scales and populations
- *Incorporate these algorithms in spatial MC¹⁰*



⁶ Chatterjee et al., *J. Chem. Phys.* **122**, 024112 (2005)

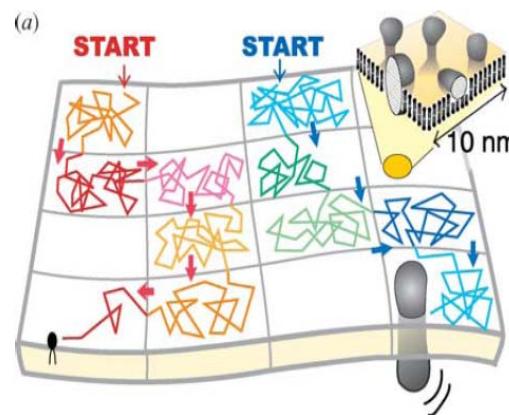
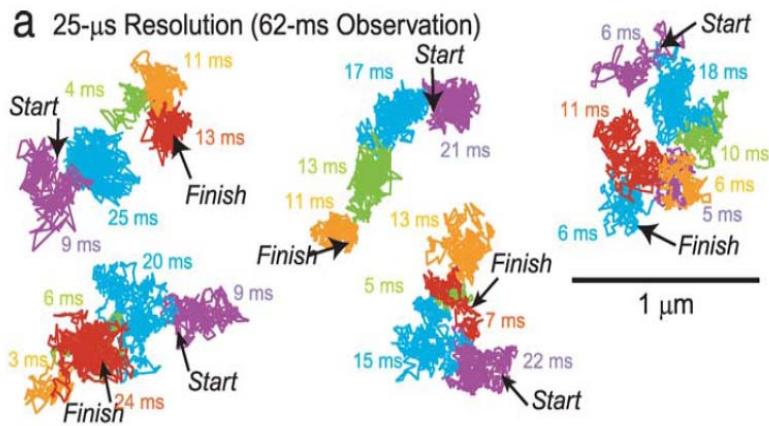
⁷ Chatterjee et al., *Bioinformatics* **21**(9), 2136 (2005)

⁸ Samant and Vlachos, *J. Chem. Phys.* **123**, 144114 (2005)

⁹ Samant et al. BCM Bioinformatics, accepted

¹⁰ Chatterjee and Vlachos, *J. Comp. Phys.* **211**, 596 (2006)

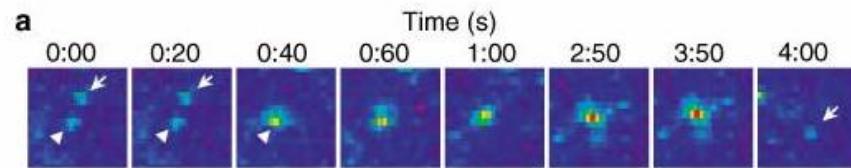
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Single particle tracking (SPT) experiments track receptor movement at micro-second scale are indicating compartments in the plasma membrane

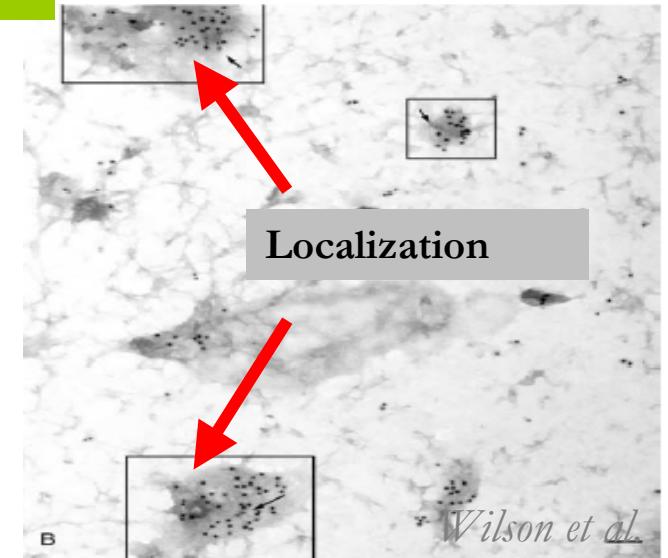
Kusumi et al.

Heterogeneity in receptor distribution: EM image suggesting localization of receptors



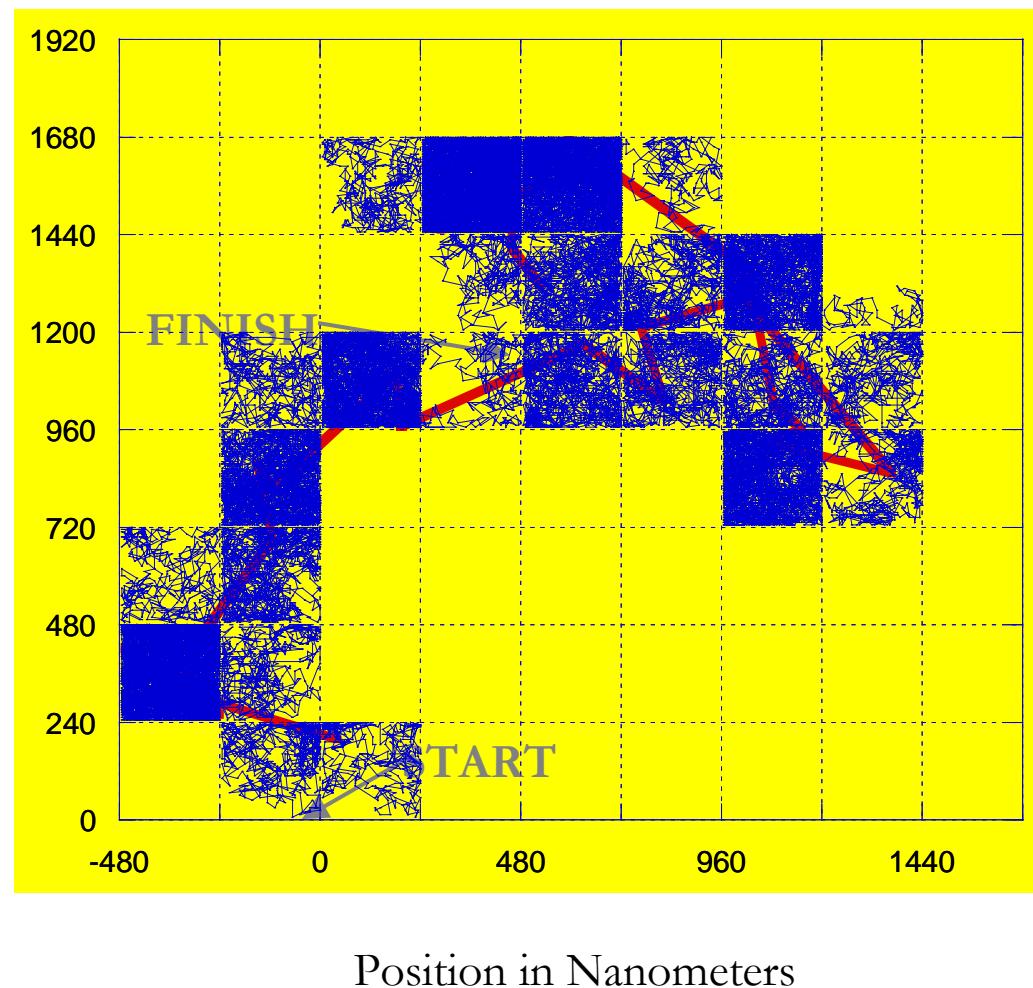
Sako et al.

SPT experiments tracking dimerization reaction events at the molecular level



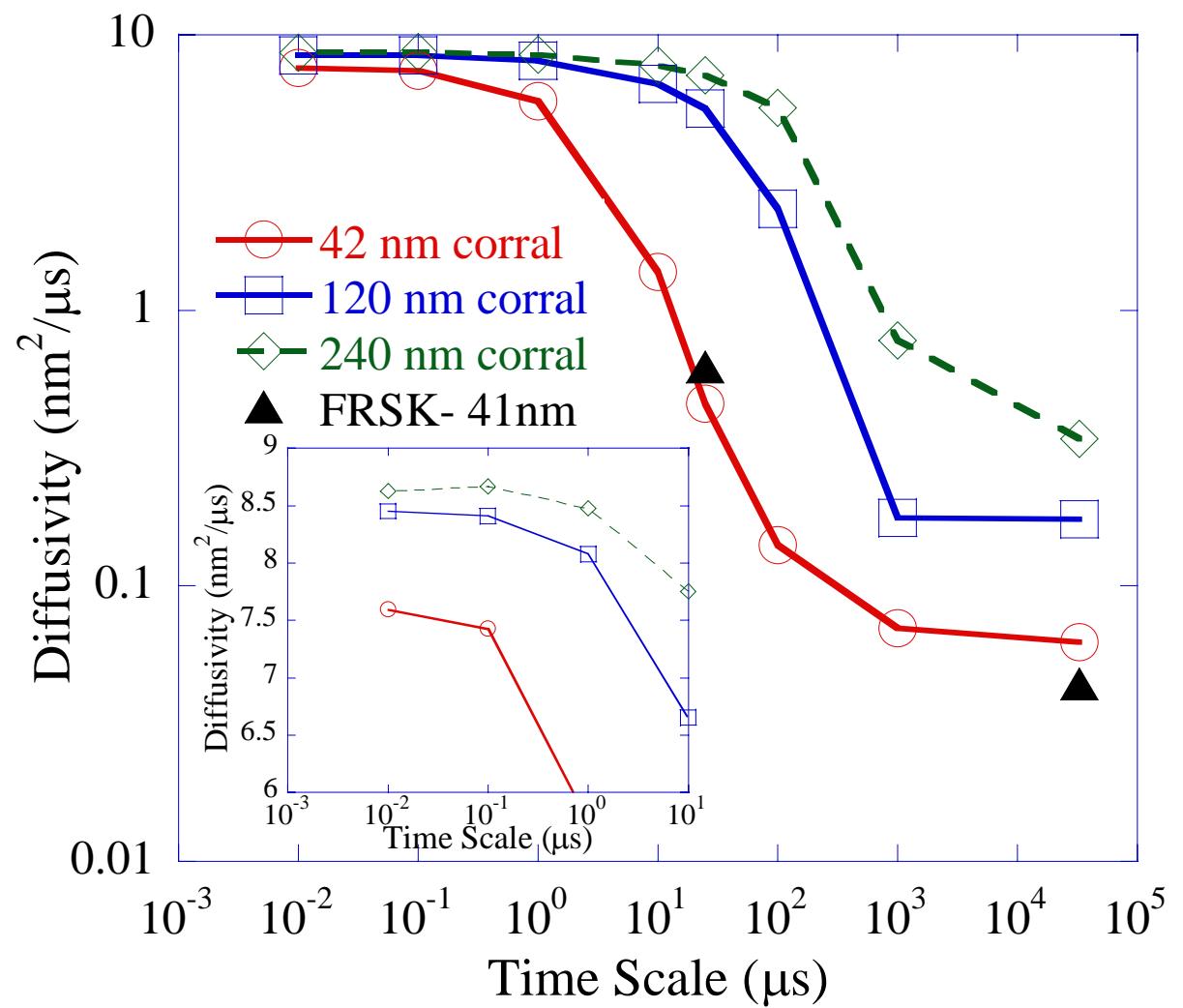
Single Particle Simulation Reveals Hop Diffusion

- At a low frame rate (33 ms), simple Brownian Motion.
- At a high frame rate (25 μ s), corrals trapping receptors.

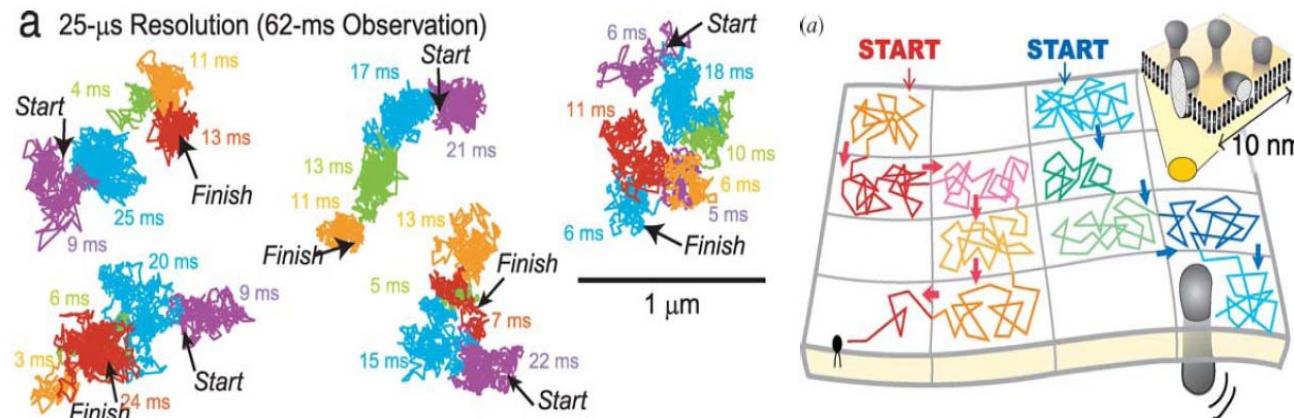


Effect of Sampling Time

- D depends on time resolution of data collection
- Good agreement with data
- Kusumi's data give macro D and a transition D
- At short times, receptors are unaffected by observation time but affected slightly by corral size
 - D can be lower than the intrinsic value!



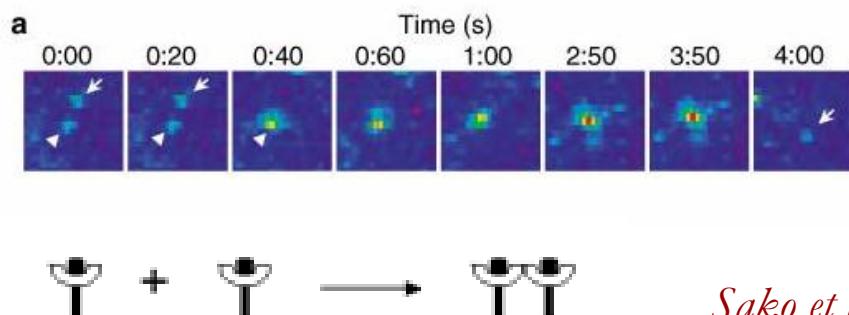
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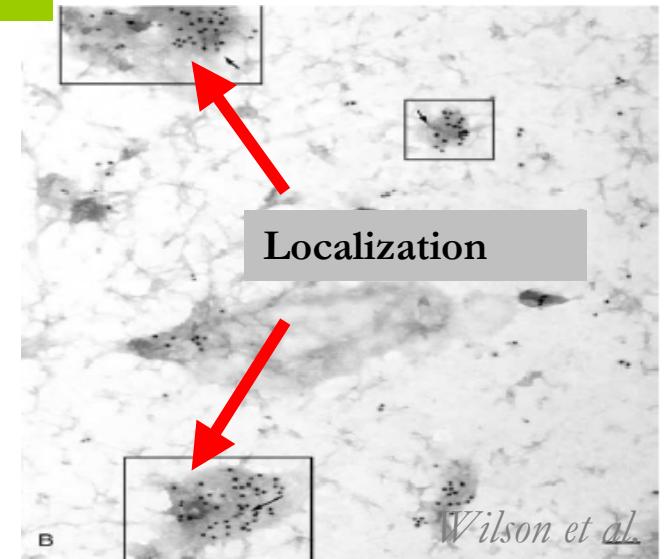
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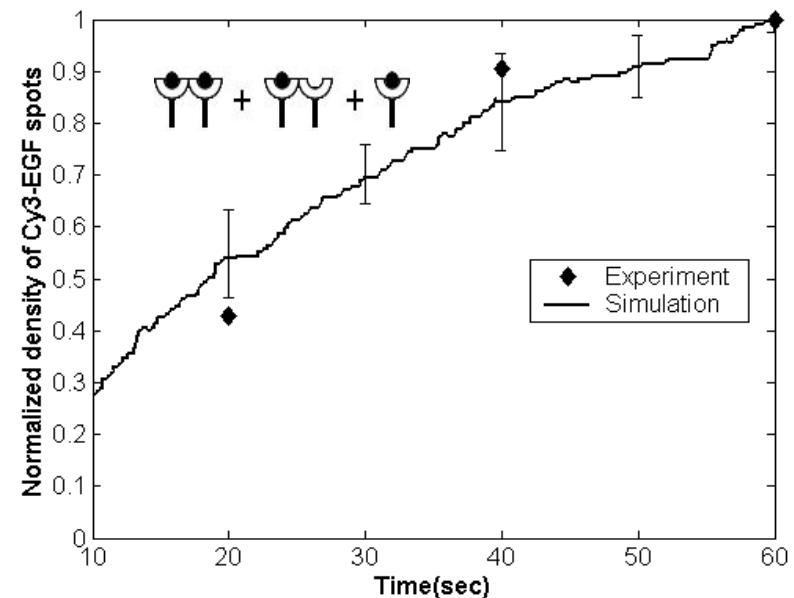
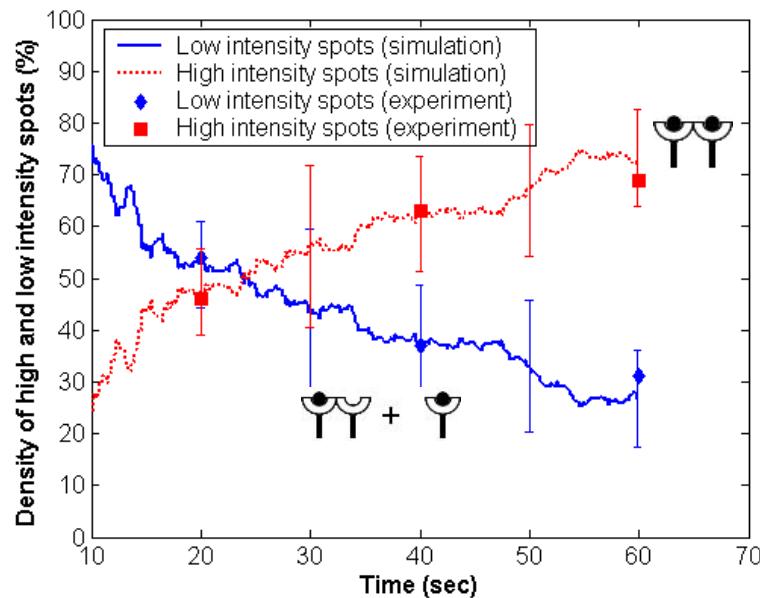


Sako et al.

SPT experiments tracking dimerization reaction events at the molecular level

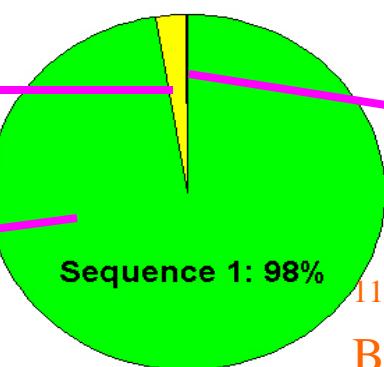
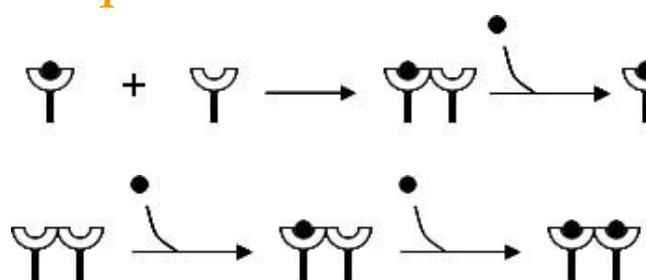


Comparison of MC with Single Particle Tracking Experiment Data



Points: Experimental data
 Curves and error bars: Simulation results

Sequence 2: 0-4.9%



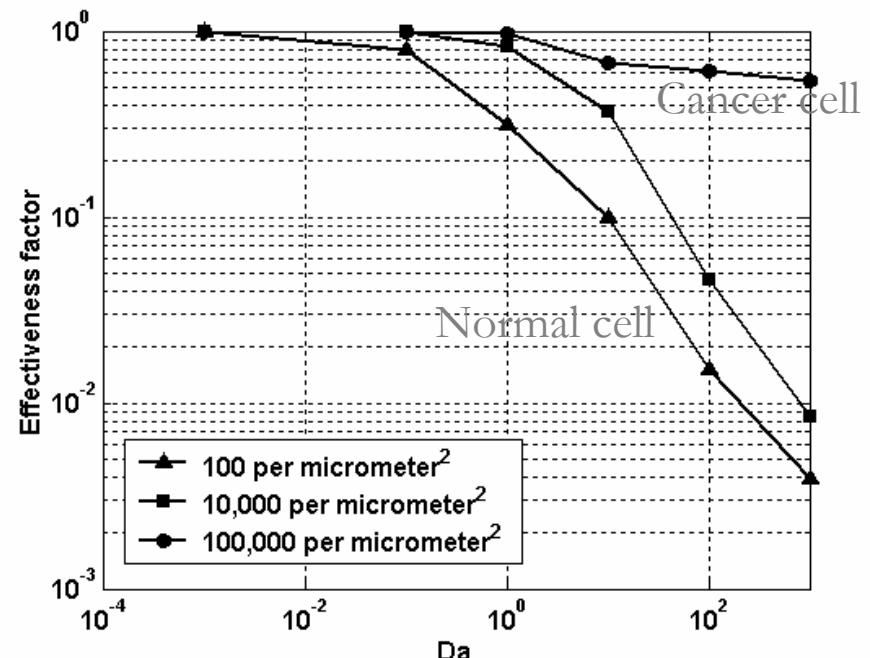
Sequence 1: 95-100%

¹¹ Mayawala et al.,
 BMC Cell Biology 6: No. 41 (2005)

Effect of Localization on EGFR Dimerization Rate

- EGFR Diffusivity: 10^{-9} - 10^{-11} cm²/s.
Range is likely due to presence of membrane microdomains (lipid rafts).
- Localization is unlikely to cause a significant increase in EGFR dimerization rates in normal cells.
- in cancer cells, localization leads to 1-2 orders of magnitude increase in rate!

¹² Mayawala et al., *Biophys. Chem.* **121**, 194–208 (2006)

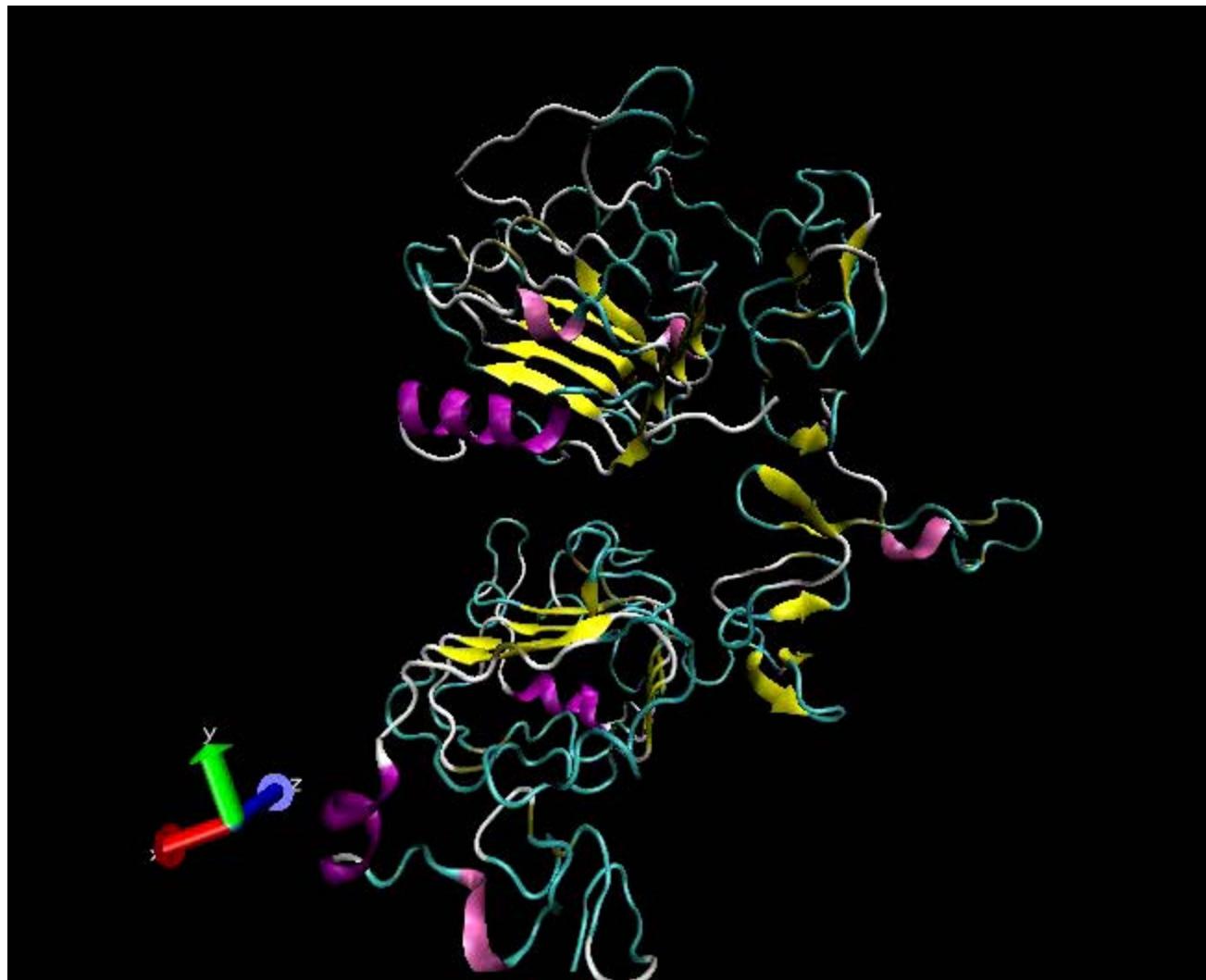


Y-axis Effectiveness factor: Measure of reduction in dimerization rate due to diffusion limitation.

X-axis Damköhler number, Da: Ratio of time scales of diffusion and reaction.

100 EGFR/ μm^2 : Avg. density in normal cells
10,000 EGFR/ μm^2 : Avg. density in cancer cells
or Localization in normal cells
100,000 EGFR/ μm^2 : Localization in cancer cells

Molecular dynamics of extra-cellular part of EGFR



Summary of accomplishments

- Develop a multiscale stochastic framework for spatiotemporal dynamics
 - Adaptivity
 - *A posteriori* error estimates
 - Cluster expansion-based corrections
 - Multigriding
 - Temporal acceleration
- Modeled real biological systems
 - Good agreement with experimental data
 - Plasma membrane heterogeneity and localization can lead to substantial increase in dimerization rates in cancer cells
- The framework applies to many other areas
 - Growth of nanomaterials
 - Separations (e.g., hydrogen production)
 - Distributed and portable energy production (e.g., alternative fuels, biofuels)

Acknowledgements

- Collaborators
 - Petr Plechac (UTN/ORNL)
 - Luc Rey-Bellet (UMass)
 - Andy Majda (Courant)
 - Dimitri Tsagkarogiannis (Max Planck)
 - Jose Trashorras (Paris IX)
 - Anders Szepessy (KTH/Sweden)
- Students and postdocs (UD, UMass, UNM)
 - Kapil Mayawala
 - Anne-Marie Niehaus
 - Abhijit Chatterjee
 - Alex Sopasakis
 - Altaf Karim
 - Michelle Costa
 - Sasanka Are