Diffusion-trapping models of protein receptor trafficking along spiny dendrites

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1D Discrete Model

1D Continuum Model

The amazing brain



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Neurons communicate at synapses



Kandel, Schwartz & Jessel (2000) (日) (四) (三) (三)

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Synapses can "learn"



Collingridge et al., Nat. Rev. Neurosci. (2004)

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Synapses "learn" by regulating receptor numbers



Scannevin & Huganir, Nat. Rev. Neurosci. (2000)

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Receptor trafficking at synapses



- constitutively recycled with intracellular stores
 - AMPA receptors turned over in 10-30 mins (or 16 hrs?)
- immobilized by scaffolding proteins in synapse
- diffuse laterally within membrane

Receptors diffuse laterally between synapses



Triller & Choquet, Nat. Rev. Neurosci. (2003)

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How are receptors transported to synapses?

Synapses located in dendritic spines



Kandel, Schwartz & Jessel (2000)





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Long-range transport of receptors along spiny dendrite



- motor transport along microtubules
- diffusion within dendritic membrane? (Adesnik et al., 2005)

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How should we model diffusion-trapping of receptors?

Treat dendritic membrane as cylinder with holes



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Diffusion equation on dendritic membrane

$$rac{\partial U}{\partial t} = D
abla^2 U$$
 on $\Omega_arepsilon$



- *U* = receptor concentration
- $\Omega_{arepsilon}$ is rectangle $(0,L) imes (-\pi l,\pi l)$ minus the holes

$$\Omega_j = \{ \mathbf{r} \in \Omega_0 \mid |\mathbf{r} - \mathbf{r}_j| \le \varepsilon \rho \}, \quad j = 1, \dots, N$$

Boundary conditions

- Periodic bcs at $y = \pm \pi I$
- No-flux bc at x = L, and at x = 0

$$-D\frac{\partial U}{\partial x} = J_{soma} = \frac{\sigma}{2\pi I}$$

bcs at the holes:

$$-\varepsilon D \frac{\partial U}{\partial \mathbf{n}}(\mathbf{r},t) = \frac{\mu_j}{2\pi\rho} (U(\mathbf{r},t) - R_j), \quad \mathbf{r} \in \partial \Omega_j$$

- $\mu_j = \text{spine neck hopping rate}$
- R_j = receptor concentration on surface of *j*th spine



Treat each spine as having 3 compartments



- P, Q: unbound, bound receptor concentrations in PSD
- R, U: free receptor concentrations in spine head, dendrite
- C: number of intracellular receptors
- k, GEXO: rates of endocytosis, exocytosis
- σDEG, δ: rates of degradation, intracellular delivery
- h, μ : hopping rates across boundary of PSD, spine neck
- α(Z-Q): rate of binding to scaffolding (Z = scaffolding concentration)
- β: rate of unbinding from scaffolding

Steady-state solution

 All steady-state concentrations at *j*th spine depend on the mean value of U on ∂Ω_j:

$$U_j = rac{1}{2\piarepsilon
ho} \int_{\partial\Omega_j} U(\mathbf{r}) d\mathbf{r}$$

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- U_j 's are determined by solving $\nabla^2 U = 0$ in Ω_{ε} with bcs
- But this is hard because of bcs at the holes!

$$-\varepsilon D \frac{\partial U}{\partial \mathbf{n}}(\mathbf{r}) = \frac{\mu_j}{2\pi\rho} (U(\mathbf{r}) - R_j), \quad \mathbf{r} \in \partial \Omega_j$$

Three steps for finding approximate steady-state solution

Solve assuming $U = U_j$ on the boundary of *j*th hole



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Three steps for finding approximate steady-state solution

() Solve assuming $U = U_j$ on the boundary of *j*th hole

• **Singular perturbation**: match logarithmic solutions in each inner region

$$|\mathbf{r} - \mathbf{r}_j| = \mathcal{O}(\varepsilon)$$

with Green's function singularities in outer region

$$|\mathbf{r} - \mathbf{r}_j| = \mathcal{O}(1)$$
 for all j

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Substitute this solution into N simplified bcs at holes

$$-\varepsilon D \frac{\partial U}{\partial \mathbf{n}}(\mathbf{r}) = \frac{\widehat{\mu}_j}{2\pi\rho} (U_j - \widehat{R}_j), \quad \mathbf{r} \in \partial \Omega_j$$

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Solution Conservation condition gives (N + 1)th equation

$$\sigma = \sum \widehat{\mu}_j \left(U_j - \widehat{R}_j \right)$$

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Effect of ε on solution



- Dendrite $2\mu m$ long, circumference $1\mu m$
- One spine at $\mathbf{r} = (1, 0.5)$
- Numerical solutions look similar

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Comparison of dendritic receptor concentration



- Dendrite 100 μ m long, circumference 1 μ m, $\epsilon
 ho = 0.1 \mu$ m
- 100 identical spines spaced 1μ m apart, all in a row
- Solutions are almost identical!
- Similar results if spines are not identical, not in a row

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Can we make things simpler?

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2D model well-approximated by 1D model

When the aspect ratio $L/l \gg 1$, we can approximate 2D model by the following 1D model

$$\frac{\partial U}{\partial t} = D \frac{\partial^2 U}{\partial x^2} - \sum_{j=1}^N \delta(x - x_j) \mu_j (U_j - R_j)$$
$$-D \left. \frac{\partial U}{\partial x} \right|_{x=0} = J_{\text{soma}}, \quad \left. \frac{\partial U}{\partial x} \right|_{x=L} = 0.$$

Comparison of models



- 2D model as before
 - Dendrite 100 μ m long, circumference 1 μ m, $\epsilon
 ho = 0.1 \mu$ m
 - 100 identical spines spaced 1μ m apart, all in a row
- 1D model use same parameters when relevant
- Solutions are almost identical!

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Can we make things even simpler?

Treat spine population as continuous density

If spines are sufficiently dense, treat sum of delta functions as a density η

$$\frac{\partial U}{\partial t} = D \frac{\partial^2 U}{\partial x^2} - \eta(x)\mu(x)(U-R)$$
$$-D \left. \frac{\partial U}{\partial x} \right|_{x=0} = J_{\text{soma}}, \quad \left. \frac{\partial U}{\partial x} \right|_{x=L} = 0.$$

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Steady-state solution for identical spines: "cable" equation

• Assume all parameters are *x*-independent, then get "cable" equation for receptor trafficking

$$\frac{d^2 U}{dx^2} - \Lambda^2 U = -\Lambda^2 \widehat{R}$$

$$\Lambda = \sqrt{rac{\eta \widehat{\mu}}{D}}$$
 is length-scale of diffusive coupling

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Solve using Green's function methods

$$U(x) = \frac{J_{\text{soma}}}{D} \frac{\cosh(\Lambda(x-L))}{\Lambda \sinh(\Lambda L)} + \widehat{R}$$

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Steady-state receptor concentrations for identical spines



- Dendrite 1 mm long
- 1,000 identical spines spaced 1μ m apart
- Two sources of receptors
 - at soma
 - local intracellular delivery

Consequences of diffusive coupling



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Steady-state is nice... ...but what about time-dependent phenomena?

AMPA receptor recycling via thrombin cleavage



Passafaro et al., Nat. Neurosci. (2001)

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AMPA receptor recycling via photoinactivation



Adesnik et al., Neuron (2005)

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Fast or slow recycling of AMPA receptors?



Simulation of photoinactivation of AMPA receptors

- No intracellular delivery but source at soma
- In steady-state t < 0
- At t = 0 all surface AMPA receptors instantaneously "inactivated"



Simulation of photoinactivation of AMPA receptors

- No intracellular delivery but source at soma
- In steady-state t < 0
- At *t* = 0 all surface AMPA receptors instantaneously "inactivated"



• Rates of exo/endocytosis are **fast** (10-30 mins)

Rate of recycling depends on distance from soma



- Fast exo/endocytosis consistent with slow recycling
- There are many time scales!



Future directions

- Models with many kinds of receptors (AMPA, NMDA, kainate, etc.)
- Models with receptor function, electrophysiology
- Computational learning rules (e.g., STDP)
- Role of AMPA receptor trafficking in Alzheimer's disease

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Stochastic models

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Intrinsic vs. extrinsic noise of synaptic trafficking



- intrinsic noise: e.g., binding/unbinding
- extrinsic noise: e.g., fluctuating gate

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Time-course of variance during FRAP



- Is black: with binding
- gray: no binding

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Time-course of variance during Inverse FRAP



- black: with binding
- gray: no binding