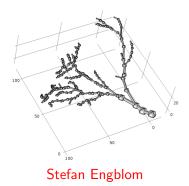
Mesoscopic Stochastic Modeling: Diffusion Operators, Multiphysics Couplings, and Convergence



Div of Scientific Computing, Dept of Information Technology, Uppsala University

BIRS Workshop, Banff, Alberta, Canada, November 10, 2014

Outline

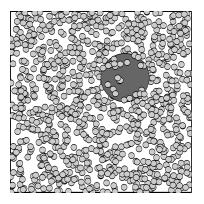
Session: Mesoscopic Methods and Modeling I

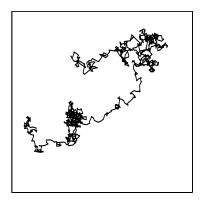
- 1A. Motivation and notation Simplicity & Accuracy Well-stirred kinetics Personal observations
- 1B. Spatial modeling Unstructured meshes: finite elements vs. volumes Convergence (of diffusion)
- 2. Multiphysics couplings

Summary

Brownian motion

Example: Particle in a fluid (Einstein 1905, & others...).





A stochastic model is simpler but depends on randomness.

Chemical reactions

Example: Bimolecular reaction $X + Y \rightarrow Z$.

-What is the probability $P(1X \text{ and } 1Y \text{ reacts in the interval } [0, \Delta t])$?



 $\implies P(X + Y \rightarrow Z \text{ in the interval } [0, \Delta t]) = \text{const} \cdot n_X n_Y \Delta t / V.$

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Let $\Delta t \rightarrow 0$. Then it so happens that this receipt describes a continuous-time Markov chain.

"Simpler, but random."

Multistability

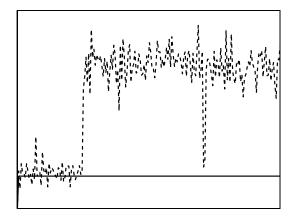


Figure: Solid: deterministic, dashed: stochastic.

Stochastic resonance

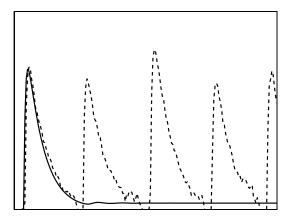


Figure: Solid: deterministic, dashed: stochastic.

Stochastic focusing

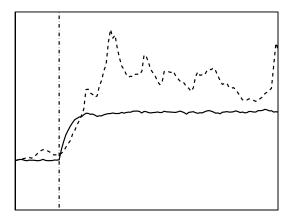


Figure: Nonlinear response to twofold signal increase; solid: partially deterministic, dashed: fully stochastic.

Well-stirred kinetics

Assuming a homogeneous probability of finding a molecule throughout the volume, and an energy which is independent on position.

-State $X \in \mathbf{Z}_{+}^{D}$, counting the number of molecules of each of D species. -Reactions are transitions between these states,

$$X \xrightarrow{w_r(X)} X - \mathbb{N}_r, \qquad \mathbb{N} \in \mathbf{Z}^{D \times R}$$
 (stoichiometric matrix)

where the propensity $w_r : \mathbf{Z}^D_+ \to \mathbf{R}_+$, r = 1...R, is the probability of reacting per unit of time.

 \implies Jump SDE formulation: $dX_t = -\mathbb{N}\mu(dt)$

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 \implies Jump SDE formulation: $dX_t = -\mathbb{N}\mu(dt) = -\mathbb{N}\mu(w(X_{t-}); dt)$ such that $E[\mu(w(X_{t-}); dt)] = w(X_{t-}) dt$.

More on notation

Where did the CME go?

Kolmogorov's forward differential system/Master equation, (Kolmogorov '31, Nordsieck/Lamb/Uhlenbeck '40), with p(x, t) := P(X(t) = x | X(0)).

$$\frac{\partial p(x,t)}{\partial t} = \sum_{r=1}^{R} w_r(x+\mathbb{N}_r)p(x+\mathbb{N}_r,t) - \sum_{r=1}^{R} w_r(x)p(x,t)$$
$$=: \mathcal{M}p.$$

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Jump SDE, *competing* counting measures:

$$dX_t = -\mathbb{N}\mu(w(X_{t-}); \ dt)$$
 ("First reaction method")

or, via a thinning of a single marked counting process,

$$dX_t = -\mathbb{N} \int_I \underbrace{\hat{w}(X_{t-}; z)}_{ ext{indicator functions}} \mu(dt imes dz)$$
 ("Direct method")

Some personal observations

Mesoscopic Methods and Modeling

-By now, many *methods*, many *acronyms*, a few good ideas, various trade-offs, combined modeling...

- Who is the customer?
- What exactly are the customer's demands?
 - accuracy vs. speed trade-off
 - actual point of use

Some personal observations

Mesoscopic Methods and Modeling

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Who is the customer?

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-Sometimes the customer is another researcher (my only experience so far)

- results of simulations will be reported in a paper
- well characterized accuracy is highly desirable (eg. backward analysis: method solves exactly a certain perturbed problem)
- heuristics/unknown accuracy acceptable iff very serious speed-ups

Mesoscopic spatial kinetics

-The conditions for well-stirred kinetics are often violated, particularly so for reactions taking place inside living cells.

-Not well-stirred in the whole volume, but if the domain Ω is subdivided into smaller computational cells Ω_j such that their individual volume $|\Omega_j|$ is small, then diffusion suffices to make each cell well-stirred.

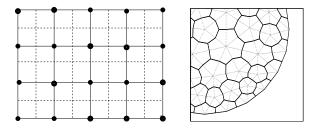


Figure: Primal mesh (solid), dual mesh (dashed). The nodal dofs are the # of molecules in each dual cell.

Mesoscopic spatial kinetics (cont)

- ► The state of the system is now an array X with D × K elements; D chemically active species X_{ij}, i = 1,..., D, counted separately in K cells, j = 1,..., K.
- ► This state is changed by chemical reactions occurring between the molecules in the same cell (vertically in X) and by diffusion/transport where molecules move to adjacent cells (horizontally in X).

Reactions

By assumption, each cell is well-stirred and consequently the jump SDE is valid as a description of *reactions*,

 $d\mathbb{X}_t = -\mathbb{N}\mu(dt),$

where μ is now *R*-by-*K*; $E[\mu_{rj}]dt^{-1} =$ propensity of the *r*th reaction in the *j*th cell.

Diffusion

A natural model of diffusion from one cell Ω_k to another cell Ω_i is

$$\mathbb{X}_{ik} \xrightarrow{q_{kj}\mathbb{X}_{ik}} \mathbb{X}_{ij},$$

where q_{kj} is non-zero only for connected cells.

-*Ideally*, q_{kj} should be taken as the inverse of the mean first exit time for a single molecule of species *i* from cell Ω_k to Ω_j . $\Longrightarrow q_{kj} \propto \sigma^2/h^2$, where $\sigma^2/2$ is the macroscopic diffusion, *h* the local length.

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Assuming that the diffusion constants are the same for all species,

$$d\mathbb{X}_t = \mathbb{E}(-\boldsymbol{\nu}^T + \boldsymbol{\nu})(dt),$$

where \mathbb{E} is *D*-by-*K* of all 1's, and ν is *K*-by-*K*; $E[\nu_{kj}] = q_{kj} \mathbb{X}_{ik} dt$.

The reaction-diffusion jump SDE "RDME"

Combining reactions with diffusions we arrive at

$$d\mathbb{X}_t = -\mathbb{N}\mu(dt) + \mathbb{E}(-\nu^T + \nu)(dt).$$

For example, ("Next Subvolume method")

$$egin{aligned} d\mathbb{X}_t &= -\mathbb{N}\int_I \hat{w}(\mathbb{X}_{t-};\ z)\otimesar{\mu}(dt imes dz)+\ && \mathbb{E}\int_I (-\hat{v}^{T}+\hat{v})(\mathbb{X}_{t-};\ z)\otimesar{
u}(dt imes dz). \end{aligned}$$

-An approximation, valid when

$$\rho^2 \ll h^2 \ll \sigma^2 \tau_\Delta,$$

 ρ the molecular radius, τ_{Δ} average molecular survival time.

Unstructured meshes

-Mean first exit time only known for very simple geometries (e.g. circles). -How to handle complicated geometries? Attempt to converge in expectation to the macroscopic diffusion equation. A numerical method applied to $u_t = \sigma^2/2 \Delta u$ yields the *discretized* form

$$\frac{d\mathbf{u}}{dt} = \frac{\sigma^2}{2} D\mathbf{u}.$$

-Define $\varphi_{ij} = E[\Omega_i^{-1} X_{ij}]$. By linearity of the diffusion intensities,

$$egin{aligned} rac{darphi_{ij}}{dt} &= \sum_{k=1}^{K} rac{|\Omega_k|}{|\Omega_j|} q_{kj} arphi_{ik} - \left(\sum_{k=1}^{K} q_{jk}
ight) arphi_{ij}, \ &\Longleftrightarrow rac{darphi_{i\cdot}^T}{dt} = \mathcal{Q} arphi_{i\cdot}^T. \end{aligned}$$

FEM vs. FVM

An insane summary

Consider the strong formulation $u_t = \Delta u$ in Ω ,

- 1. Variational form (Green's theorem): find $u \in V$ s.t. $(v, u_t) = -(\nabla v, \nabla u)$ for $\forall v \in V$, where $(f, g) \equiv \int_{\Omega} fg \, dx$.
- 2. A FEM is obtained by approximating $V \approx V_h = \operatorname{span}_i \varphi_i \subset V.$ 2. With $\varphi_i = \nabla \varphi_i$ (t) a vec
- 3. With $u_h = \sum_i \mathbf{u}_i(t)\varphi_i$ we get $M\mathbf{u}_t = -A\mathbf{u}; M_{ij} = (\varphi_i, \varphi_j),$ $A_{ij} = (\nabla \varphi_i, \nabla \varphi_j).$

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- 1. Integrating over the *j*th finite volume and invoking the divergence theorem we get $\int_{\omega_j} u_t \, dx = \int_{\partial \omega_j} \mathbf{n} \cdot \nabla u \, da.$
- 2. Approximating ∇ with a difference and defining \mathbf{u}_j as a volume average gives $|\omega_j|d/dt \mathbf{u}_j = \sum_k |\partial \omega_{jk}||e_{jk}|^{-1}(\mathbf{u}_k \mathbf{u}_j), e_{jk}$ the distance between nodes j and k.

Weak convergence

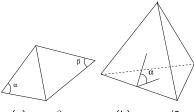
Key observation: by linearity, the diffusion CTMC on the unstructured grid has an expected value which coincides with the exact solution to the deterministic numerical method.

FEM convergence

 $M\mathbf{u}_t = -A\mathbf{u} \text{ or } \mathbf{u}_t = -M^{-1}A\mathbf{u} \approx -\tilde{M}^{-1}A\mathbf{u} =: D\mathbf{u}.$

1) Converges in L^2 , $||u_h - u|| = O(h^2)$ as $h \to 0$, under very mild assumptions on the mesh.

2) Under stringent conditions on the mesh, the maximum principle holds.



(a) $\alpha + \beta < \pi$ (b) $\alpha < \pi/2$

These conditions are needed to ensure that

$$D_{jk} \ge 0, \ D_{jj} < 0, \ \sum_{k=1}^{K} D_{jk} = 0.$$

FVM convergence

$$|\omega_j|d/dt \,\mathbf{u}_j = \sum_k |\partial \omega_{jk}||e_{jk}|^{-1}(\mathbf{u}_k - \mathbf{u}_j)$$

1) The maximum principle always holds.

2) If the mesh is a Delaunay triangulation, the method converges as $||u_h - u|| = O(h^2)$. Unfortunately (in 3D) such meshes have a very poor quality except for very simple geometries. Then the "C" in $O(h^2)$ is very large.

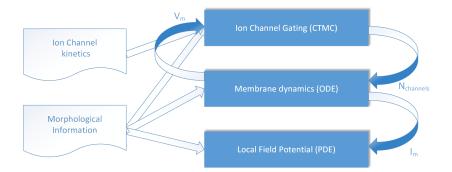
On balance...

-With a (very) good mesh both methods converge as $h \rightarrow 0$ and satisfy the maximum principle. With an "average" mesh, (truncated) FEM seems to have an accuracy edge to FVM.

-Importantly, truncated FEM is amenable to backward analysis: the solution satisfies exactly a perturbed equation $u_t = \nabla \cdot (\tilde{\sigma}^2(x)/2 \times \nabla u)$ where $\tilde{\sigma}$ can be explicitly obtained, and where $\|\tilde{\sigma} - \sigma\|$ is small and localized.

-Key challenges: (i) convergence in distribution — retrieving the correct Brownian motion, (ii) convergence with reactions, (iii) getting to grip of when it actually matters...

Application: multiscale neuronal model



Joint work with Pavol Bauer and Emil Berwald.

Bottom level

lon channel gating

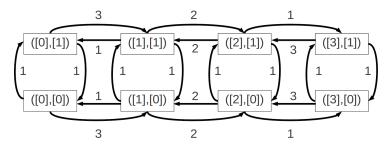


Figure: Gating process: sodium channels.

Bottom level lon channel gating

The gating process of ion channels can be mesoscopically described as

$$N_0 \underset{\beta_m(\mathbf{V}_m)N_1}{\overset{3\alpha_m(\mathbf{V}_m)N_0}{\rightleftharpoons}} N_1 \underset{2\beta_m(\mathbf{V}_m)N_2}{\overset{2\alpha_m(\mathbf{V}_m)N_1}{\rightleftharpoons}} N_2 \underset{3\beta_m(\mathbf{V}_m)N_3}{\overset{\alpha_m(\mathbf{V}_m)N_2}{\rightleftharpoons}} N_3,$$

again a *continuous-time Markov chain. Output:* N_3 , the number of open gates.

For efficient model coupling we freeze the voltage dependency for a short time-step τ ("Euler method/1st order Strang split"):

$$X_{t+\tau} = X_t - \int_t^{t+\tau} \mathbb{N}\mu(\underline{V}_m(t), w(X_{s-}); ds).$$

Middle level

Membrane dynamics

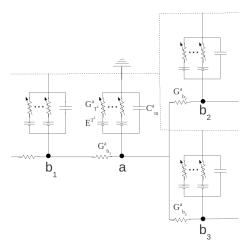
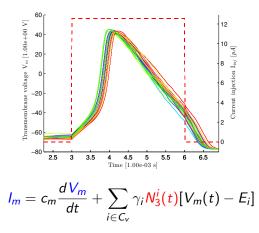


Figure: Cable equation circuit.

Middle level

Membrane dynamics





- Morphological information extracted using the *Trees toolbox*
- System of current-balance and cable equations is solved for each time step τ

Top level Maxwell's equations, potential form

Electric field intensity E in terms of the electric scalar potential V,

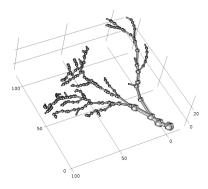
$$\mathsf{E} = -\nabla V.$$

Trans-membrane current l_m is scaled with the compartement surface area and coupled as a current source,

$$-\nabla\cdot\left(\sigma\nabla V+\varepsilon_{0}\varepsilon_{r}\frac{\partial}{\partial t}\nabla V\right)=\frac{1}{\Omega_{c}}I_{m},$$

with conductivity σ and permittivity ε . Finally, the time dependent potential V is solved via finite element methods.

Top level Geometry coupling



- Bottom and middle level: compartments (cylindrical volumes)
- Coupling with PDE requires a mesh
- Approximation with curves much more efficient than volumetric elements



Coupled solution

Summary

- Simplicity and Accuracy: Who is the customer?
- Accurately capturing a stochastic nonlinear phenomenon is a very hard constraint for method's development!
- Spatially inhomogeneous case, consistency with macroscopic equations, FEM vs. FV
- The numerical method's convergence to the macroscopic equation implies weak convergence of the corresponding stochastic model, backward analysis
- Sample multiscale neuronal application solved in URDME (www.urdme.org): coupling different types of models

Summary

In case somebody asks: more on notation Compare with ODEs...

For states $x \in \mathbf{R}^D$; either one may consider

$$\frac{\partial}{\partial t} p(t,x) = -\Delta \cdot (f(x)p(t,x)),$$

or,

$$x'(t)=f(x).$$

-In method's development and modeling, " $f \rightarrow f_h$ ", one almost exclusively deals with the latter representation.