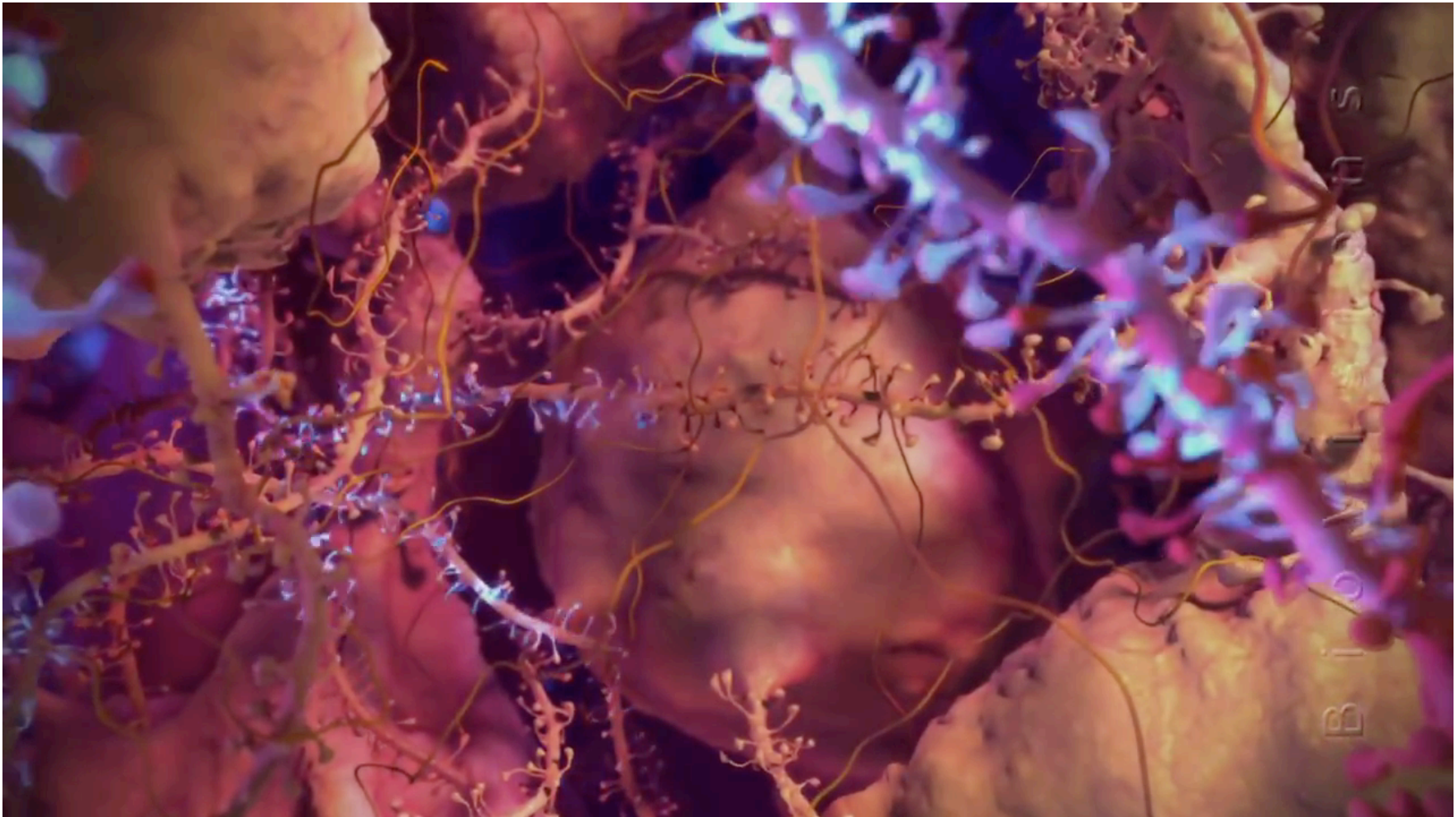


Introduction: Cellular-level simulation

CS/CME/Biophys/BMI 371

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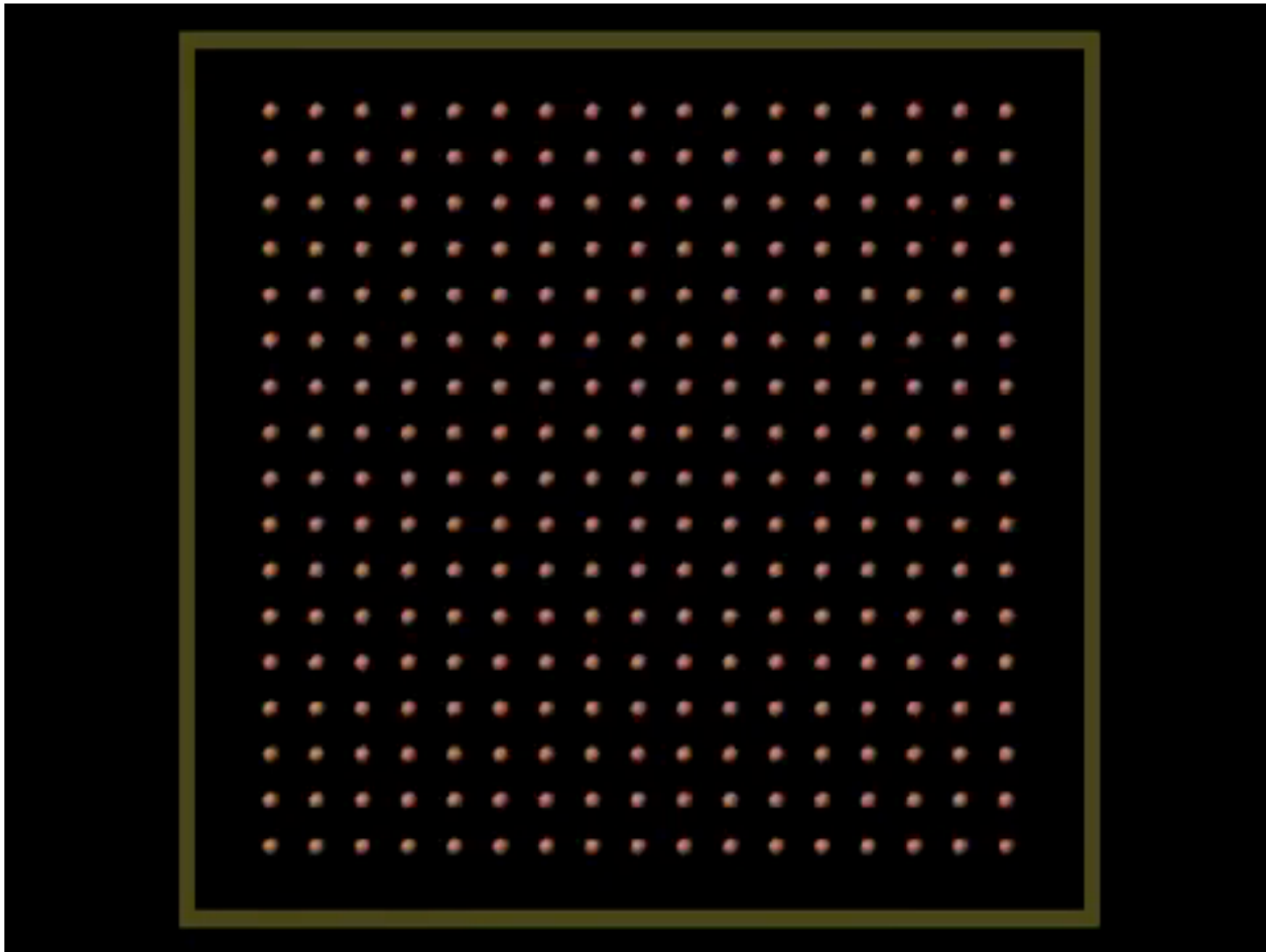
Ron Dror



From *Inner Life of the Cell* | *Protein Packing*, XVIVO and Biovisions @ Harvard

- The interior of the cell is crowded, and all the molecules jiggle about.
- Note that lots of molecules (e.g., water) aren't even shown in this movie. 2

Molecules jiggle about because other molecules keep bumping into them



Diffusion

- This “jiggling about” by lots of molecules leads to diffusion
- Individual molecules follow a random walk, due to collisions with surrounding molecules
- Diffusion = many random walks by many molecules
 - Substance goes from region of high concentration to region of lower concentration

Reaction-diffusion simulation

- A common way to model how molecules move within the cell involves *reaction-diffusion simulation*
- Basic rules:
 - Molecules move around by diffusion
 - When two molecules come close together, they have some probability of reacting to combine or modify one another
- Several implementation strategies:
 - Particle-based
 - Continuum models
 - In some (limited) cases, one can solve the partial differential equations analytically

Particle-based approach

- Represent molecules by particles, and track the motion of each one
- Example software: ReaDDy (topic of one paper)

Continuum approach

- Divide space into finite “voxels”
- Instead of tracking positions of molecules, track concentrations of each type of molecule in each voxel
- At each time step, update concentrations based on reactions of molecules within a voxel, and diffusion between neighboring voxels based on concentration differences
- Example software: Simmune (topic of one paper), Virtual Cell (used by another paper, which also presents some analytical solutions)

Background information

- Review paper (Models at the single cell level, 2010)
 - <http://onlinelibrary.wiley.com/doi/10.1002/wsbm.49/full>
- Slides from CS/CME/Biophys/BMI 279:
 - <http://web.stanford.edu/class/cs279/lectures/lecture10.pdf>