ABSTRACTS: AMSI-ANZIAM LECTURER 2008 - DR LINDA PETZOLD

Abstract 1
Computational Methods for Phase Response Analysis of Circadian Clocks

Circadian clocks govern daily behaviors of organisms in all kingdoms of life. In mammals, the master clock resides in the suprachiasmatic nucleus (SCN) of the hypothalamus. It is composed of thousands of neurons, each of which contains a sloppy oscillator – a molecular clock governed by a transcriptional feedback network. Via intercellular signaling, the cell population synchronizes spontaneously, forming a coherent oscillation. This multi-oscillator is then entrained to its environment by the daily light/dark cycle.

Both at the cellular and tissular levels, the most important feature of the clock is its ability not simply to keep time, but to adjust its time, or phase, to signals. We present the parametric impulse phase response curve (pIPRC), an analytical analog to the phase response curve (PRC) used experimentally. We use the pIPRC to understand both the consequences of intercellular signaling and the light entrainment process. Further, we determine which model components determine the phase response behavior of a single oscillator by using a novel model reduction technique. We reduce the number of model components while preserving the pIPRC and then incorporate the resultant model into a couple SCN tissue model. Emergent properties, including the ability of the population to synchronize spontaneously are preserved in the reduction. Finally, we present some mathematical tools for the study of synchronization in a network of coupled, noisy oscillators.

Abstract 2
Multiscale Simulation of Copper Electrodeposition

Copper electrodeposition is the process whereby solid copper is deposited onto a surface immersed in a chemical solution containing copper ions and various additives. This technique is widely used to fill on-chip interconnects and vias in the fabrication of computer processors. We make use of a 3D mass transport model to describe the bulk electrolyte, which is stiffly coupled to an active surface where reactions and deposition occur. The active surface is modeled in two ways, depending on the length scales involved. A continuous differential equation model is used for larger length scales, while a stochastic kinetic Monte-Carlo model is used for the smaller length scales, comparable to surface roughness. Simulation of this model is both challenging and very computationally intensive, due to the structure of the electrolyte mass transport model, the need for resolution at the smallest scales, and the difficulty in coupling the electrolyte and surface simulations. Here, we have developed a breakthrough numerical algorithm that performs much faster than previous methods, scales well with grid refinement and is naturally parallelizable. The new algorithm is being used in close collaboration with experimental efforts in the development of effective strategies for 3D infill optimization and copper nucleation and growth.

Abstract 3 (Anziam)
Multiscale Simulation of Biochemical Systems

In microscopic systems formed by living cells, the small numbers of some reactant molecules can result in dynamical behavior that is discrete and stochastic rather than continuous and deterministic. An analysis tool that respects these dynamical characteristics is the stochastic simulation algorithm

(SSA). Despite recent improvements, as a procedure that simulates every reaction event, the SSA is necessarily inefficient for most realistic problems. There are two main reasons for this, both arising from the multiscale nature of the underlying problem: (1) the presence of multiple timescales (both fast and slow reactions); and (2) the need to include in the simulation both chemical species that are present in relatively small quantities and should be modeled by a discrete stochastic process, and species that are present in larger quantities and are more efficiently modeled by a deterministic differential equation. We will describe several recently developed techniques for multiscale simulation of biochemical systems, and outline some of the future challenges.