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CTL 02_4T–109: Application of the Control Volume Method to Mathematical Models of Cell Migration.

Dann Mallet, *Queensland University of Technology*.

Over the last few years, mathematical models of cell migration (and indeed, other models in mathematical biology) have become increasingly complex. These models have evolved from simple diffusion models to computationally troublesome reaction-diffusion-convection models. As such, the use of 'black box' numerical solvers has become less effective.

In this paper we discuss the application of the control volume technique for resolving complicated non-linear cell migration models. The non-linearity is treated using a full Newton solver and flux-limiting is used to ensure that the cell migration fronts are captured adequately. Two specific models are analysed. In the first model[1], we compare the numerical results of the proposed computational model developed in this research to previous results published by other researchers. The second model[2] is a new model of cell migration and results of this work will be compared with numerical output from a NAG routine. In both cases the finite volume computational model captures the physics of the processes with good accuracy using substantially reduced computational overheads.

[1] Perumpanani AJ, Sherratt JA, Norbury J, Byrne HM; *A two parameter family of travelling waves with a singular barrier arising from the modelling of extracellular matrix mediated cellular invasion*; Physica D, **126** 145–159, (1999).

[2] Mallet and Pettet; unpublished.

CTL 08_8T–076: A Computational Framework for the Efficient Simulation of Stochastic Chemical Kinetics.

Kevin Burrage, *University of Queensland*.

It is now universally recognised that stochasticity is an inherent property of cellular behaviour and regulation. In particular, in microscopic systems formed by living cells, the small numbers of reactant molecules can result in dynamical behavior that is discrete and stochastic rather than continuous and deterministic. One of the most important markers in this area was the development of the stochastic simulation algorithm (SSA) due to Gillespie. This is essentially an exact procedure for numerically simulating chemically reacting systems, where there may be relatively few molecules present of some key chemical species. Gillespie has recently proposed an approximation to the SSA called τ-leaping which offers a great potential for speeding up the computation in many situations of practical interest.

In this talk we will introduce a new class of numerical methods — which we call Poisson Runge–Kutta methods — which generalize and extend the τ-leaping idea, along with a theoretical framework for their analysis. A general formulation and theory for this class of Poisson Runge–Kutta methods will be given, and high order methods will be constructed. Numerical simulations will be presented to illustrate the performance of the new methods.

CTL 08_3T–066: Robustness of Biological System for Bistability Phenomena.

Tianhai Tian, *University of Queensland, Australia.*

Noise widely exists in biological systems. However, living systems are optimized to function in the presence of stochastic fluctuations. Such a property is known as robustness. We will discuss robustness of mathematical models for biological systems with bistability phenomena by parameter variation and stochastic simulation. The discussion will concentrate on a quantitative model with threshold values for bacteriophage Lambda. Numerical results suggested that this model has good stability property.

CTL 07_0T–011: Progressive Transmission of MR Images, through Energy-Ordering in S-Transform Space.

Alan Law, *University of Calgary, Canada.*

In medical imaging, evolving technologies combined with increasing user requirements are producing burgeoning amounts of data, for storage, transmission and analysis. For a network setting, progressive transmission of (medical) images is being actively investigated through various mathematical structures, including decorrelation techniques, wavelets and matrix splines[1].

If a 3D digital object consists of, say, a set of parallel 2D slices, these subsets may be transmitted one at a time, for progressive 3D renderings at the recipient node. The order in which the subsets should be selected for utilization poses an interesting question. The recent 2D Stockwell transform is a generalization of the Fourier transform that also includes both a time-frequency analysis capability and a multi-scaling feature. It is emerging[2] as a viable computational tool for Magnetic Resonance Imaging in which data frequency components may change over time or space - motion, respiratory/cardiac activity or blood flow; e.g., may cause temporal changes in spatial frequency within MRI data.

Background for progressive transmission of images will be reviewed, and a summary of mathematical features of the S-transform provided, along with computational aspects involving exploitation of the FFT in both a serial and distributed setting. An algorithm for ordering the constituent subsets of a digital object will be developed by employing arrangement, with respect to energy, of their S-transforms. Effectiveness of this scheme for progressive transmission will be illustrated with patient MRI data, and its performance evaluated.

[1] Defez *et al.*; *Matrix cubic splines for progressive transmission of images*; J. Imaging and Vision, Vol. 17 (2002), pp.41–53.

[2] Zhu *et al.*; *The Stockwell transform: a potentially powerful processing tool in MRI*, Proc. 10th Annual Meeting, Inter. Soc. for Magnetic Resonance in Medicine (ISMRM); Honolulu, May 18–24, 2002, No. 2449.

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Progressive Transmission of MR Images Through Energy Ordering in S-transform Space

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Outline

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