1046-65-1320 **Xinfeng Liu*** (`xliu1@math.uci.edu`), Department of Mathematics, Rowland Hall 340, Irvine, CA 92697, and **Nie Qing** and **Lee Bardwell**. *Mathematical modeling and numerical simulations of cell signaling pathways.*

A class of proteins referred to as scaffolds are thought to play many important roles during cell signaling. A model of generic, spatially localized scaffold protein has been developed, and the model indicated that a scaffold protein could boost signaling locally while simultaneously suppressing signaling at a distance. The mathematical equations for modeling cell signaling pathways or other complex biological systems are stiff reaction diffusion equations. We have developed a compact integration factor method to solve these equations. The part of the stability constraint due to diffusion can totally be removed if the linear diffusions are treated exactly using integration (IF) or exponential time differencing (ETD) methods. The storage and computations for such numerical approaches are usually prohibitive even for a moderate spatial size in two or three dimensions. In the novel approach of compact integration factor method, the required memory and computational cost are dramatically reduced for both IF and ETD methods, thus saving computational resources. This novel approach has been incorporated with adaptive mesh refinement and excellent performance has been observed. (Received September 15, 2008)