1077-00-512 **Kanadpriya Basu*** (basuk@mailbox.sc.edu), 1523 Greene Street, Leconte College, Dept. of Mathematics, Columbia, SC 29208, and **Dr. Xinfeng Liu**. *Multisite phosphorylation with substrate sequestration can robustly generate bistability.* Preliminary report.

The mitogen-activated protein kinase (MAPK) cascades that are evolutionally conserved from yeast to mammals play a pivotal role in many aspects of cellular functions.The mating decision in yeast is a switch-like or bistability response that allows cells to filter out weak pheromone signals or avoiding improper mating when a mate is sufficiently close. In many cases, scaffold proteins are thought to play a key role during this process. The molecular mechanisms that control the bistability decision is not yet fully understood. Here we show that bistability mechanism can arise from multisite phosphorylation system with substrate sequestration when phosphorylation and dephosphorylation occurs at different locations. This scaffold binding in a multisite phosphorylation system can robustly result in multiple steady states. We argue that the scaffold protein plays an important role in creating bistability by the generic mathematical models, and by treating parameters symbolically, we also thereby reduce the complexity of calculating steady states from simulating differential equations to finding the roots of polynomials, of which the degree depends on the number of phosphorylation sites N.In addition we present some results considering the complex spatio-temporal case. (Received September 06, 2011)