# Biology Seminar

Dr. Marc Turcotte
Department of Pharmacology, UT Southwestern Medical Center

Hybrid Computational and Experimental Approaches to Signaling Regulation at Many Scales

More and more, following successes in other sciences, a theoretically-based approach has begun to define a role in biology. Thus, much beyond application of ever more sophisticated analysis techniques to understand data, systems biology begins to offer a uniquely powerful global model-based strategy to understand overwhelmingly unintuitive aspects of biological phenomena that are rooted in the inescapable facts of the nonlinearity and stochasticity of many complex biological systems. In this talk, I will show how using a mathematically grounded computational approach anchored in experimental data –a hybrid approach- leads to otherwise unattainable insight into detailed signaling regulation, at multiple resolution scales. I will show examples from detailed G protein signaling regulation, from the subtle intricacies of signaling pathway interactions in mammalian cells, from the signaling underlying cancer onset and maintenance and from stochastic regulation of gene expression in bacteria underlying the phenomenon of competence. I will discuss this last topic more describing a new ongoing project that relies on a math-based computational approach, to recapitulate evolutionary choices in archetypical gene regulation network topologies. I will discuss how this is expected to feedback into the laboratory. The ultimate goals of this research always are to understand biological phenomena better but the upshot of unequivocally bringing math-based modeling supported by massive computational resources right from the start, is to begin on the path of expanding the range of questions we have traditionally asked in biology from "how" living systems work, towards more of the "why" type of questions, thus paralleling the successful history from other quantitative sciences.
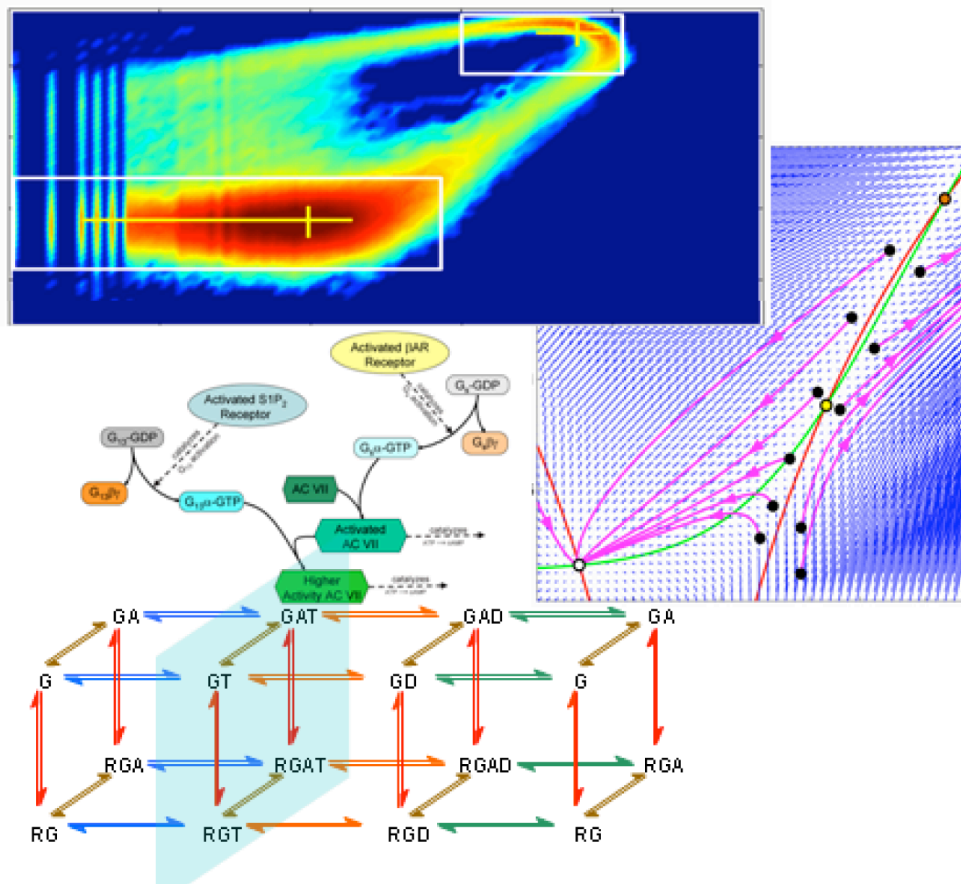
Friday Sept 4, 2009   **2:00 PM**   **ENV125 (EESAT)**