

Signal Processing Seminar

Title: Computational Analysis for Live-cell FRET Imaging

Speaker: Shaoying (Kathy) Lu
University of Illinois
Department of Bioengineering

Date: Wednesday, November 12, 2008

Time: 4:00 - 5:00 pm

Where: 4269 Beckman Institute

Abstract: Genetically-encoded biosensors based on fluorescence resonance energy transfer (FRET) have been widely applied to visualize the molecular activity in live cells with high spatiotemporal resolution. Biological studies utilizing the FRET biosensor contributed significantly to our understanding of the organization of complex signaling networks in live cells, and therefore to the understanding and treatment of human disease. The vast amount of imaging data produced by FRET studies are in great need of automated and advanced image analysis methods and algorithms.

Using a Finite-Element-based diffusion model, we analyzed the diffusion kinetics of the FRET biosensor. Then the artifacts caused by biosensor diffusion were subtracted to enhance the spatial resolution of the FRET image. The result suggests that growth factor induced a Src activation at clustered regions proximal to cell periphery with well-coordinated spatiotemporal patterns.

The efficient and accurate quantification of the large amount of imaging data from these single-cell FRET measurements demands robust and automated data analysis. However, the nonlinear movement of live cells presents tremendous challenge for this task. Based on image registration of the single-cell movement and cluster analysis, we have developed automated image analysis methods to track and quantify the FRET signals within user-defined subcellular regions. The results revealed that the growth-factor-induced RhoA activity is polarized in the migratory cells, with the gradient of polarity oriented toward the opposite direction of cell migration.

Statistical analysis is important in live-cell studies because of the significant individual cell different during FRET assay. We have developed a uniform framework for analyzing the kinetics of molecular activation. The results were used to study the kinetics of chemically stimulated molecular activity in sub-microscopic domains (lipid rafts) in cellular membrane.

Our overall research goal is to design computational image analysis tools for studying the spatiotemporal activation pattern of signaling molecules, and to provide useful frameworks for high-throughput and systematic investigation of the molecular activities in live cells.

BIO: Dr. Shaoying Lu obtained her bachelor and master degrees in Applied Mathematics from Tsinghua University, Beijing, China, in 1995 and 1997, respectively. She worked with Dr. Randy Bank on parallel algorithms for solving large-scale linear systems and received her Ph.D. degree in Mathematics at UC San Diego in 2004. Later she continued working at UC San Diego as a LJIS postdoc fellow with Drs. Andrew McCulloch, Michael Holst and Randy Bank, on computational modeling of calcium dynamic in cardiac myocytes. Currently she is working in collaboration with Dr. Yingxiao Wang, as a research assistant professor in the Department of Bioengineering at UIUC. Dr. Lu's research is focused on elucidating the molecular mechanisms in cancer biology and mechano-biology, designing computational image analysis tools for studying the spatiotemporal activation characteristics of signaling molecules, and providing automated tools for high-throughput and systematic investigation of the molecular activities in live cells.