

## Topological analysis of proteomic data

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Cells become cancerous because topological properties of their chemical state make it impossible for them not to become cancerous. 2-D PAGE gel electrophoresis protein assay data is embedded and analyzed within a topological computing framework. These data are produced using protocols that are standardized, established and widely used. They are also precise, specific and reliably calibrated alongside an internal reference standard and, importantly, they preserve local interactions. We will develop protein behavior models from longitudinal studies of changes in protein sample concentrations. We will show that continuous variations in behavior produce discontinuous phase shifts in protein concentrations and their interactive rates of change. Preliminary data indicate that a significant fraction of computer-generated surfaces reveal an explicit discontinuity of the protein behavior space for cancerous cells.

### Biography

D. Gnabasik is pursuing his Ph.D in Computer Science at the University of Colorado Denver (UCD). G. Alaghband is the Chair of the CS department at UCD, and is the co-author of Fundamentals of Parallel Processing (Prentice Hall, 2003), M. Duncan is in the Division of Endocrinology, Metabolism and Diabetes School of Medicine, University of Colorado Denver, and the Obesity Research Center, College of Medicine, King Saud University, Riyadh, Saudi Arabia.

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