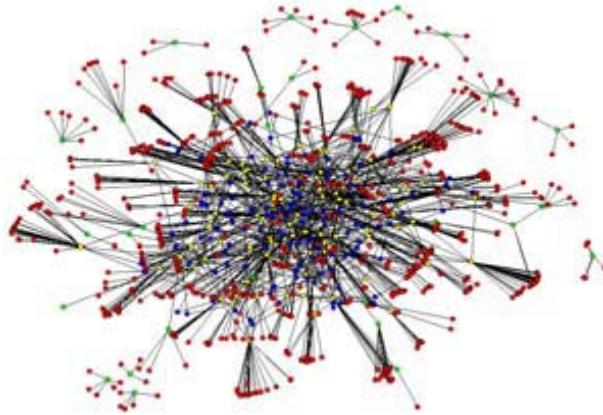# Human Sciences and Complexity
Four-Campus (Video-) and Conference Series

December 8: Friday, 10:25-1:00 **quarterly end-of-quarter conference at UCI**
Celebrating the Minor in Human Complex Systems proposal for 2007
With two conference presentations and discussions
Focusing on biological complexity, networks and evolution
UCI Social Science Tower 220A, followed by lunch at Chakra

10:25-11:20 Doug Wallace – UCI, MAMMAG: Founder of the ORU for Molecular and Mitochondrial Medicine and Genetics, which brings together basic scientists, clinical investigators, and patients within the UC system to determine the causes and to generate cures for the common metabolic and degenerative diseases, cancer, and aging. To achieve this ambitious goal, the Center applies a new biomedical paradigm which argues that age-related diseases are primarily caused by mitochondrial energy deficiency resulting from inherited partial energetic defects that are exacerbated by the age-related accumulation of somatic mtDNA mutations. This paradigm predicts that effective preventative therapeutics must emphasize the stabilization of mitochondrial function and that ameliorative therapies must focus on the replacement of cells lost due to cellular energy failure through use of stem cell technologies. MAMMAG's translational research has two main emphases: Mitochondrial and Molecular Medicine and Germ and Stem cell Biology.

"Molecular Anthropology: Application of Analysis of Mitochondrial Variation toward Understanding the Origins of Humans and Their Culture"

11:35-12:30 Natasa Przulj – UCI, Computer Science. Her research focuses on new tools for analyzing and modeling of complex networks in cellular biology.

"Protein-Protein Interaction Networks: Issues, Models, and Comparisons"

Abstract: One of the fundamental problems in computational biology is understanding the inner workings of a cell. Most cellular processes are carried out by protein-protein interactions (PPIs). Thus, analyzing and modeling of large PPI networks is an integral part of this process. Analogous to biological sequence comparison, comparing cellular networks is an important problem that provides insight into biological understanding and therapeutics. Although full-scale comparison of arbitrary networks is computationally intractable, heuristic measures are developed using a highly constraining network comparison metric based on local structural properties that are a direct generalization of the degree distribution.