



## UMass Lowell Computer Science Colloquium Announcement

**Speaker:** Howard Goodell, INRIA  
**Date & Time:** Wednesday, Dec. 13, 2006, 3:00pm--4:00pm  
**Place:** Olsen 311, Refreshments are served at 2:30pm

---

### **100,000 Nodes and 6,000,000 Edges: Making sense of large, dense graphs with Adjacency Matrix representations and matrix reordering techniques**

“Quantity has a quality all its own.”

-- Attributed to Joseph Stalin [http://en.wikiquote.org/wiki/Joseph\\_Stalin](http://en.wikiquote.org/wiki/Joseph_Stalin)

Many fields such as bioinformatics and social network analysis produce huge, dense graphs. In our Microbiogenomics project <http://microbiogenomics.u-psud.fr/> we are analyzing a graph of gene relationships in 400 microbial species that has 100,000 nodes connected by an average of 60 edges apiece -- and next year, it will expand to 1400 species. Social-network projects such as mapping contributions to the French Wikipedia (401,000 articles -- the English version has 1,508,000) add the complication of power-law edge distribution, with key nodes having many thousands of edges. Standard Node-Link diagrams are extremely difficult to draw or read at these scales. This talk describes our work with a different and complementary approach -- Adjacency Matrix graph representations combined with matrix reordering algorithms -- that can provide useful insights where standard techniques fail.

#### *Bio:*

Howard Goodell received his doctorate in Computer Science at U. Mass. Lowell in Spring, 2006. He is currently working as a post-doctoral researcher for INRIA Futurs at the University of Paris 11 in Orsay, France. His primary research interest is interactive information visualization and analysis of biological data. Before receiving his doctorate, he earned BS and MS degrees in Analytical Chemistry from Northeastern University and developed a wide variety of scientific, industrial, and personal electronics software.