

Biomedical and Health Informatics Series

Tuesday, October 31st, Room RR 134

Bob Cottingham

CTO and Co-Founder of vizXlabs

"Data Overload in Biomedical Research: Computational Imperatives in the Era of Super-exponential Data Growth"

That data repositories such as the GenBank sequence database are growing exponentially is commonly understood. There are now research tools that are generating data at much faster rates, well beyond Moore's Law. This is overwhelming most researchers ability to manage and analyze their experimental data. Traditional software and analytical approaches are not accessible for most researchers. Some of the newer, even more data-rich experimental tools such as exon arrays are being hampered by a lack of usable software solutions.

Biomedical research has relied to date primarily on standard commercially available computers and methods. New methods will be needed especially regarding data organization and management. For now, one approach is to provide very focused, ATM-like solutions instead of traditional software. However an ideal future would include systems that would more directly involve end user researchers in the development and use of not only the analytical process but also data models, integration and community data standards.

Bob Cottingham is one of the pioneers of bioinformatics, having begun his career in the field in the 1970s as a software developer on some of the first genetic analysis programs. Prior to co-founding VizX Labs, he was Vice President of Computing at Celltech Chiroscience, a UK biopharmaceutical company with a market capitalization of \$5 billion, developing drugs based on targets found through gene discovery. His previous positions include Assistant Professor and Operations Director of the Genome Database at Johns Hopkins University School of Medicine; Co-Director of the Informatics Core in the Baylor College of Medicine Human Genome Center, where he lead the development of software tools which made it possible to map increasingly large and complex data sets in genetic linkage analysis; and Directeur Informatique at Centre d'Etude du Polymorphisme Humain in Paris, France, where he was responsible for overseeing the CEPH family genotypes database, a resource used to construct some of the first maps of the human genome.

The Biomedical and Health Informatics lecture series covers current topics and developments in Biomedical and Health Informatics. Presenters include faculty, students, researchers and developers from the University of Washington, other academic institutions, government, and industry (locally and nationally). The intended audience is the broader University of Washington and Seattle area community with an interest in BHI as well as BHI faculty and students.

Series Website: <http://courses.washington.edu/mebi590/>