Interdisciplinary Faculty Seminar in Bioinformatics

sponsored by Fordham College at Rose Hill Dean’s Office

Department of Computer & Information Science presents:

“Next Generation High-Throughput DNA Sequencing for Biomedical Research”

Talk by Dr. Stuart Brown
Center for Health Informatics and Bioinformatics
NYU School of Medicine

Wednesday, April 6, 2011

5:00 – 5:50 pm

McGinley Center, Room 235

Reception to follow in McGinley Center, Music Room

Rose Hill Campus, Fordham University
For more information please contact Danielle Aprea at Aprea@Fordham.edu or 718-817-4480.

“Next Generation High-Throughput DNA Sequencing for Biomedical Research”

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**Abstract:** This talk will address the challenges of optimizing computational methods to process data for the next-generation sequencing technique known as ChIP-seq. ChIP-seq is a new research method that is potentially useful for all aspects of the study of the regulation of gene transcription as well as DNA structure and epigenetics. ChIP-seq provides comprehensive genome-wide empirical data on the actual binding of regulatory proteins to transcription factor binding sites on the chromosome, which can be used for the reverse engineering of regulatory pathways. However, a ChIP-seq experiment produces millions of short sequence reads for each sample, which must be mapped to a reference genome, and then processed to identify enriched regions. This presents a significant data analysis challenge.

ChIP-seq is used to study transcription factors as regulators of gene expression and histone modifications as mediators of epigenetic information. There are many other applications of ChIP-seq, including: DNase hypersensitivity, DNA methylation, RNA polymerase II interactions with DNA. While ChIP-seq is not currently used for diagnostic or clinical medicine, the understanding of gene expression and epigenetics are important to cancer biology and relevant to most other branches of biology, medicine and agriculture.

**Biography:** Dr. Stuart Brown is Associate Professor in the Center for Health Informatics and Bioinformatics at NYU School of Medicine and Director of the NYU Bioinformatics Consulting Core. Dr. Brown completed a BS degree in Botany at the University of Michigan, and completed his Ph.D. in Molecular Biology at Cornell University in 1992. He conducted postdoctoral fellowships at the University of Manitoba and the USDA ARS Genetic Resources Unit in Griffin, GA. Dr. Brown is the author of textbooks on Bioinformatics and Medical Genomics and a reviewer for NIH and NSF bioinformatics study sections. He is a frequent speaker at Next nexpression, evolutionary biology, and pattern detection.