



Hosted by the Rat Genome Database and the Clinical & Translational Science Institute

"Hypothesis-driven Translational Bioinformatics Acceleration *in silico, in vitro, in vivo,* and in Clinical Trial"

presented by

Yves A. Lussier, MD.
The University of Chicago

- * Associate Director for Informatics, U of C Cancer Research Center
- * Co-director, CTSA Biomedical Informatics Core
- * Director, Center for Biomedical Informatics
- * Associate Professor of Medicine, Section of Genetic Medicine
- * Fellow, Computation Institute
- * Fellow, Institute for Genomic and Systems Biology
- * Member, Center for Metastasis Research

Tuesday, November 3rd
11:00 AM – 12:00 PM
HMGC Conference Room (5th Floor, HRC)

Questions?

Contact Laura Schuman 456-7351

lschuman@mcw.edu



Dr. Lussier is the Associate Director for Informatics at the University of Chicago and Co-director of the CTSA Biomedical Informatics Core at U of C. His research group focuses on the development and use of high throughput phenotyping technologies to integrate and analyze genomes with phenotypes and to accurately individualize the prediction and the treatment of diseases. More specifically, he has developed automated computational methods that bring together the fields of molecular bioinformatics, ontologies, and natural language processing in order to code, integrate, structure and mine the escalating wealth of complex and heterogeneous phenotypes. Contributing to the emerging field of “systems medicine”, these methods bridge the “phenotype gap”, as phenotypes are amassed in diverse and insufficiently related clinical, post-genomic and model organism databases.