

Yves A. Lussier, M.D.

Since 2006, Yves A. Lussier M.D. has been an Associate Professor in the Department of Medicine of The University of Chicago and Associate Director for Informatics of the Cancer Research Center. He is also the Director of the Center for Biomedical Informatics. He received a B. App. Sc. in Engineering from the University of Sherbrooke in 1985, an MD from the University of Sherbrooke in 1989, and completed a family medicine residency in 1992. From 1994 to 2000, he was an Adjunct Professor of Family Medicine at the University of Sherbrooke, and a postdoctoral research fellow in the Department of Biomedical Informatics at Columbia University from 1998 to 2001, under the mentorship of Dr. Carol Friedman and Dr. James J Cimino. From 2001-6, Yves A. Lussier has been an Assistant Professor in the Departments of Biomedical Informatics and Medicine of Columbia University where he has mentored or co-mentored 26 graduate students. During that tenure, he was also the Director of the Biomedical Informatics Core of the Northeast Research Center of Excellence in Emerging Infectious Diseases, and the Clinical Director of the Columbia Center for Advanced Technology.

His research group is currently conducting hypothesis-driven translational research in biomedical informatics that focuses on the high throughput use of clinical knowledge to accurately individualize the understanding, prediction and treatments of diseases. More specifically, he has developed computational methods to elucidate the molecular mechanism of diseases. These methods bring together ontologies, natural language processing (NLP), artificial intelligence and *heterogeneous data integration to analyze* an increasingly large and complex wealth of *textual and semi-structured phenotypic, clinical, genomic, and molecular database*. His research group has recently completed three significant projects in molecular medicine (manuscripts summarizing these findings are in preparation):

1. The design of an oligonucleotide microarray for the detection of all known vertebrate viruses [collaboration with Ian Lipkin PI, Columbia Un.]: this 9,366 probe array covers the entire 1,710 distinct species of vertebrate viruses and their 98,310 DNA sequence entries found in Genbank. This diagnostic technology is unprecedentedly comprehensive, rapid and affordable (Emerging Infectious Diseases, 2006 13(1):73-81).
2. He conducted the first genome scale comparative analysis of (i) the human phenome and (ii) of the prokaryotic phenome [collaborations: (i) Ada Hamosh, John Hopkins; (ii) Mark Gerstein, Yale Un.] He integrated clinical and molecular datasets, analyzed and validated these algorithms by recapitulating known associations between well characterized pathways and their phenotypes. More importantly, the analysis predicted new probable phenotypes for genes and pathways (PLoS Computational Biology, 2006 2(11): 1419-1435 - Editor's Pick).
3. He has developed the first system for analyzing, in large scale, relationships between phenotypes and genes, proteins, or bimolecular markers buried in biomedical narratives such as scientific publications or clinical records. The hybrid system is comprised of a knowledge understanding component (POS) and a NLP component, BioMedLEE [collaboration with Carol Friedman, Columbia Un.]. The system is undergoing evaluation over molecular pathology and oncology datasets (Bioinformatics, 2006 Oct 1;22(19):2421-9).

Teaching experience includes graduate courses of decision support tools, introduction to informatics and translational informatics offered in the Department of Biomedical Informatics and in the School of Physicians and Surgeons of Columbia University, as well as numerous tutorials on phenotypic ontologies in conferences (e.g. AMIA). He is actively involved with three major NIH-funded ontology groups: The National Research Center for Multiscale Analysis of Genomic and Cellular networks (MAGNET), the Systematized Nomenclature of Medicine (SNOMED), and the Phenotype Attribute Ontology Committee of the Gene Ontology Consortium. Furthermore, he also has served or is serving on more than a dozen boards (governance, scientific and editorial), including the Editorial Board of SNOMED from the College of American Pathologists. He cumulates over 170 publications, communications and invited lectures. In 2005, he was inducted fellow of the American College of Medical Informatics (ACMI).