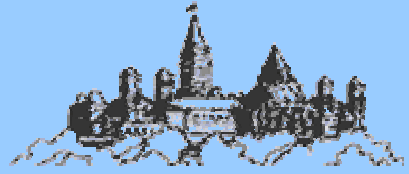




IEEE

**Ottawa
Section**



Dr. James Green

*Assistant Professor
Systems and Computer Engineering
Carleton University*

James Green received his B.A.Sc. in Systems Design Engineering from the University of Waterloo in 1998, and his M.Sc.(Eng.) degree from Queen's University in 2000 for research in the areas of genomics and proteomics. In 2000-2001, Dr. Green worked at Molecular Mining Corporation, a bioinformatics consulting firm in Kingston Ontario, where he helped to develop novel analysis methods for the interpretation of gene expression data which led to a patent pending. Dr. Green returned to Queen's University to pursue a PhD in Electrical and Computer Engineering under the supervision of Dr. Michael Korenberg which he received in 2005. Dr. Green joined the department of Systems and Computer Engineering at Carleton University as an Assistant Professor in September of 2005. His research interests include the application of nonlinear system identification techniques to pattern classification challenges in bioinformatics and medical informatics. His current emphasis is on the prediction of protein structure and function.



Discovering protein structure and function via nonlinear system identification

November 23, 2005

admission is free

5:30 – 7:00 pm

**Mackenzie Building 4359
Carleton University**

Predicting protein structure and function from sequence is of fundamental importance to biomedical research. An effective solution has the potential to accelerate the drug discovery process and may lead to an increased understanding of cancer and other disease processes. Unfortunately, experimental methods for elucidating a protein's structure are very costly and are not always applicable. Computational prediction techniques provide an attractive alternative; however, the accurate prediction of 3D tertiary protein structure directly from amino acid sequence data continues to elude researchers when homologous protein structures are not available or for longer domains. Even then, knowing a protein's tertiary structure may not be sufficient to fully understand its function: the majority of eukaryotic proteins are not functional in their original structure and must be activated through some form of post-translational modification (PTM).

In this talk, I will briefly introduce the biology of protein structure and function. I will then discuss our recent efforts in the area of protein secondary structure prediction where we have made use of Parallel Cascade Identification (PCI), a powerful method of nonlinear system identification, to form bioinformatics classifiers. While predicting secondary structure is a useful intermediate step, the ultimate goal of protein structure prediction is to predict the complete 3D structure of the active conformation(s) of a protein, including PTM information. I will conclude with a discussion of how PCI may be used to make significant contributions towards this and other important goals in biomedical informatics.



IEEE EMBS Ottawa Chapter

<http://ewh.ieee.org/r7/ottawa/embs/>

CU@EMBS

<http://www.embs.engsoc.org/>