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Biocomputing in Cells and By Self-Assembly

Lila Kari
Canada Research Chair in Biocomputing
Department of Computer Science
University of Western Ontario
Thursday, September 23, 2004
Walter Light Hall 205
10:30-11:30 a.m.

The Role of Design in Software Product Development

Bill Buxton
Principal, Buxton Design
Friday, October 22, 2004
Walter Light Hall 205
2:30-3:30 p.m.

PatternHunter: Fast and Sensitive Homology Search

Ming Li
School of Computer Science
University of Waterloo
Friday, November 12, 2004
Dupuis 215
2:30-3:30 p.m.

Raising the Stakes

Jonathan Schaeffer
Department of Computer Science
University of Alberta
Friday, February 4, 2005
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Reflections on an Insecure Internet

Paul C. Van Oorschot
School of Computer Science
Carleton University
Friday, April 8, 2005
Dupuis 215
2:30-3:30 p.m.

Mirage, A Tool for Interactive Pattern Discovery, with Applications in the Virtual Observatory

Tin Kam Ho
Computing Sciences Research Center, Bell Laboratories
Thursday, May 5, 2005
Walter Light Hall 205
2:30-3:30 p.m.

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Distinguished Seminar Series

Biocomputing in cells and by self-assembly

Lila Kari

Department of Computer Science
University of Western Ontario
London, Ontario

Biomolecular (DNA) computing is an emergent field lying at the crossroads of mathematics, computer science and molecular biology. The main idea behind biomolecular computing is that data can be encoded in DNA strands, and molecular biology tools can be used to perform arithmetic and logic operations. The birth of this field was the 1994 breakthrough experiment of Len Adleman who solved a hard computational problem solely by manipulating DNA strands in test-tubes. Research into biomolecular computing could lead to new revolutionary ways of computing by using DNA, RNA or other biomolecules.

A complementary approach to understanding bioinformation is through biological computation, which studies the information processing capabilities of cellular organisms. Indeed, cells and nature ``compute'' all the time by reading and ``rewriting'' DNA through processes that modify DNA or RNA sequences. Research into the computational abilities of cellular organism has the potential to uncover the laws governing biological information and to enable us to harness the computational power of cells.

This talk will address two aspects of the DNA computing research: the computational power of unicellular organisms and the limits of computation by self-assembly (the process by which objects autonomously come together to form complex structures).

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Distinguished Seminar Series

The Role of Design in Software Product Development

Bill Buxton

Principal, Buxton Design
Toronto, Ontario

This talk could just as well be titled "What I have learned about software product design in 8 1/2 years of working with some of the best industrial designers and film makers in the world." The underlying premise is that filmmakers and industrial designers approach the design of new products in a fundamentally different way than the software industry. More often than not, software products are green-lighted, and then work begins. With films and product design, green-lighting comes at the end of a front-end process, not the beginning. Stated another way, software projects tend to go directly to development/engineering, leapfrogging over anything that an industrial designer, for example, would recognize as a design process. Our argument is that our industry's bypassing such an explicit and formal front-end design process (or in film terms, pre-production), lies at the root of many of our problems of quality, cost over-run, and late delivery. Furthermore, I would argue that the absence of this front-end process lies at the root of the software industry's abysmal track record in bringing out successful new (as opposed to n+1) products. To put my argument into perspective, I will briefly summarize the process followed in film and product design, and discuss how it can apply to software product design.

Bill Buxton is a leading interaction designer and researcher. He is Principal of the Toronto-based design and consulting firm, Buxton Design. He has had a long history with Xerox PARC, and the University of Toronto, where he is still an Associate Professor in the Department of Computer Science. He is also Chief Scientist of Bruce Mau Design in Toronto, and in the fall of 1994 is teaching a class in the Industrial Design Department of the

Ontario College of Art and Design. From 1994 until December 2002, he was Chief Scientist of Alias|Wavefront, and from 1995, its parent company SGI Inc. In 1995, Buxton became the third recipient of the Canadian Human-Computer Communications Society Award for contributions to research in computer graphics and human-computer interaction, and was given the New Media Visionary of the Year Award at the 2000 Canadian New Media Awards. In 2002, he was elected to the CHI Academy, and Time Magazine named him one of the top 5 designers in Canada. In 2001, The Hollywood Reporter named him one of the 10 most influential innovators in Hollywood.

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Queen's University

School of Computing

Distinguished Seminar Series

PatternHunter: Fast and Sensitive Homology Search

Ming Li

School of Computer Science
University of Waterloo

Homology search is the most fundamental task in bioinformatics, consuming a nontrivial fraction of world's supercomputing time.

Three decades ago, the dynamic programming technique was adopted to solve this problem (edit distance in CS) "efficiently", for a short while, but it was quickly overwhelmed by the sea of molecular sequences being generated.

Two decades ago, heuristics represented by FASTA and BLAST were introduced, trading sensitivity for speed. Today, they are not only lacking sensitivity, but also too slow, for example, taking years to compare two mammalian genomes on a modern computer.

This talk will bring you a new fundamental idea and a new software.

We are no longer interested in trading sensitivity with speed; we will improve both simultaneously with the novel idea of optimized spaced seeds. Equipped with the optimal spaced seeds, PatternHunter approches Smith-Waterman's sensitivity while being thousands of times faster; at the same sensitivity level it runs many times faster than BLASTn. This finally brings homology search technology back to a full circle.

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Queen's University

School of Computing

Distinguished Seminar Series

Raising the Stakes

Jonathan Schaeffer

Department of Computing Science
University of Alberta

Poker is a challenging problem for AI research: multiple agents (up to 10), stochastic element (cards being dealt), imperfect information (don't know the opponent's cards), user modelling (identifying player patterns), and risk management (betting decisions). For over 10 years the University of Alberta Computer Poker Group has been been working on building a high-performance poker program. This work has led us through four distinct phases of program design:

1. knowledge-based system,
2. simulations,
3. game theory, and
4. tree searching with learning.

The prospects of a program successfully challenging the best human players in the near future is excellent. In this talk we will motivate the research, compare the different program designs, and discuss future directions.

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Queen's University

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Reflections on an Insecure Internet

Paul C. Van Oorschot

School of Computer Science
Carleton University

How is it possible, that despite the continuous introduction and use of powerful Internet security technologies - firewalls, anti-virus software, cryptographic algorithms, public-key infrastructure, intrusion detection systems, email filters, and others - the Internet has become more complex, and yet arguably, less secure than ever? In this talk, we explore this question, reflecting upon the speaker's personal experiences in academic research, in industry, and in real life.

Paul Van Oorschot (Ph.D. Waterloo, 1988) is Canada Research Chair in Network and Software Security, a Professor in the School of Computer Science at Carleton University, and founding director of Carleton's Digital Security Group. His industrial experience has involved research, development, and senior management including positions at Bell-Northern Research and Entrust Technologies. He regularly serves on program committees for international security and cryptography conferences, and is co-author of the standard reference Handbook of Applied Cryptography.

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Mirage, A Tool for Interactive Pattern Discovery, with Applications in the Virtual Observatory

Tin Kam Ho

Bell Labs
Lucent Technologies

The Virtual Observatory provides rich infrastructure for sharing diverse and massive observational data sets among astronomical researchers, enabling both targeted pursuits and open-ended exploration into many directions. To maximize its advantages, flexible and effective data analysis tools that can handle large data volumes, diverse data types, a wide range of objectives, and highly variable demands on speed are in critical need. We discuss our experiences with Mirage, a prototypical software for interactive pattern discovery, and its applications in the Virtual Observatory. We focus on how to organize the analysis tool to lay a solid foundation for meeting these requirements and enabling continuous growth. We identify several key challenges in data analysis that need to be addressed in addition to core demands for data visualization and pattern recognition algorithms.

Tin Kam Ho is a Member of Technical Staff in the Computing Sciences Research Center of Bell Laboratories. Her interests are in pattern recognition, data mining, and computational modeling and simulation. She received a Ph.D. in Computer Science from SUNY at Buffalo in 1992. She is Editor-in-chief of the journal Pattern Recognition Letters, and has served on the editorial board of several other journals. In 1999 she received the ICDAR Young Scientist Award for her contributions to document image analysis and recognition. She is a Fellow of IAPR, and has received 6 U.S. patents for her work in pattern recognition and image analysis.

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