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Whole Genome Shotgun Assembly and other Adventures of a Computer Scientist Dabbling in Biology

Dr. Granger Sutton
The Venter Institute
Maryland, U.S.A.
Thursday, October 27, 2005
Walter Light Hall 212
2:30-3:30 p.m.

Visible Models for Interactive Pattern Recognition

Dr. George Nagy
DocLab, Rensselaer Polytechnic Institute,
Troy, NY
Thursday, December 8, 2005
Walter Light Hall 205
10:30-11:30 a.m.

A Baker's Dozen: 13 Grand Software Engineering Challenges

Dr. Jeffrey Voas
Director, Systems Assurance
Science Applications International Corporation
Thursday, January 19, 2006
Walter Light Hall 210
2:30-3:30 p.m.

Talk Preview (Powerpoint)

Even Accelerating Machines Are Not Universal

Dr. Selim Akl
School of Computing, Queen's University
Thursday, February 16, 2006
Miller Hall 201
3:00-4:00 p.m.

Analyzing Networks of Cellular Processes

Dr. Shoshana Wodak
Centre for Computational Biology,
The Hospital for Sick Children, Toronto
Dept. of Biochemistry, University of Toronto
Friday, March 17, 2006
Walter Light Hall 205
2:00-3:00 p.m.

Contextually-Aware Adaptive Visualizations for Software Tools

Dr. Margaret-Anne Storey
Department of Computer Science
University of Victoria
Thursday, April 27, 2006
Dupuis 215
2:30-3:30 p.m.

Programmable Pervasive Spaces

Dr. Sumi Helal
Department of Computer and
Information Science and Engineering
University of Florida
Monday, May 29, 2006
Dupuis Hall 215
11:00 a.m. - 12:00 p.m.

SCHOOL OF COMPUTING
DISTINGUISHED SEMINAR SERIES

Dr. Granger Sutton of
The Venter Institute
WLH212 2:30-3:30 pm
Thursday, October 27th, 2005

Whole Genome Shotgun Assembly and other Adventures of a Computer Scientist Dabbling in Biology

I will discuss my evolution from a computer scientist into a computational biologist emphasizing the joys and pitfalls along the way. A large part of this journey has involved my part in evolving the state of whole genome shotgun fragment assembly algorithms.

I will give a brief history of fragment assembly and highlight some of the interesting algorithmic advances. I will discuss the impact this has had on genome sequencing.

Finally, I will discuss fragment assembly challenges when dealing with environmental sequencing (DNA extracted from multiple unknown organisms in a given environment) and how this data can inform our knowledge of the protein universe.

BIO: Granger Sutton started his career as an electrical engineer. He received his B.S. in Electrical Engineering from the University of Maryland, followed by an M.S. in Computer Engineering from Stanford in 1983. After a few years as a member of the technical staff at AT&T Bell Laboratories, he went back to graduate school, earning a PhD in Computer Science from the University of Maryland in 1992.

As one of the pioneers in the young field of computational biology, he joined the then fledging Institute for Genomic Research (TIGR), and began working on new algorithms for the clustering and alignments of proteins and expressed sequence tags (ESTs).

The techniques he developed found new application in the assembly of whole genome shotgun data. In 1995, his software - the TIGR Assembler - was used to assemble the first complete whole genome of a free living organism, Haemophilus influenzae.

In 1998 he moved from TIGR to Celera Genomics, and along with Gene Myers led the team that developed a whole genome assembly pipeline for eukaryotic genomes, producing whole genome sequences for Drosophila melanogaster, human, mouse, rat, and mosquito.

In addition to genome assembly, as a director in the Informatics Research group, he led efforts at Celera in comparative genomics. Granger Sutton has recently joined the Bioinformatics Research team at the Venter Institute, where he is engaged in a variety of research efforts, including the comparative whole-community analysis of environmental samples.

Reading suggested by host, Hagit Shatkay: *The Genome War: How Craig Venter Tried to Capture the Code of Life and Save the World*, by James Shreeve.

Refreshments to follow in Goodwin 620

SCHOOL OF COMPUTING
DISTINGUISHED SEMINAR SERIES
DECEMBER 8TH 2005
WLH 205
10:30-11:30 AM

PROF. GEORGE NAGY
DOCLAB,
DEPARTMENT OF ELECTRICAL,
COMPUTER, AND SYSTEMS ENGINEERING
RENSSELAER POLYTECHNIC INSTITUTE,
TROY, NY

VISIBLE MODELS FOR INTERACTIVE PATTERN RECOGNITION

The bottleneck in interactive visual classification is the exchange of information between human and machine. We introduce the concept of the visible model, which is an abstraction of an object superimposed on its picture. For a narrow domain, like flowers or faces, it may be as simple as an outline of the entire object to be classified or a set of characteristic points. The visible model is not by itself sufficient for classification, because it contains no intensity, color or texture information. For every new object to be classified, the machine proposes a model. The model parameters are subject to constraints learned from a training set that help avoid implausible abstractions. Using features extracted from the picture based on the model, the classes are rank ordered according to the similarity of the unknown picture (in a hidden high-dimensional feature space) to the labeled reference pictures. If the rank ordering appears unsatisfactory, the operator may modify the model, resulting in the extraction of new features, and a new rank ordering. The interaction continues until the operator confirms a satisfactory match. The new object, with its model and label, is added to the reference database. Comprehensive experiments with several dozen naive subjects show that interactive recognition of flowers and faces is much more accurate than automated classification, much faster than unaided human classification, and that both machine and human performance improve with use.

BIOGRAPHY

George Nagy received the B.Eng. and M.Eng. degrees from McGill University, and the PhD in Electrical Engineering from Cornell University in 1962 (on neural networks). For the next ten years he studied pattern recognition at the IBM T.J. Watson Research Center in Yorktown Heights. From 1972 to 1985 he was Professor of Computer Science at the University of Nebraska - Lincoln (nine years as chair), and worked on geographic information systems, remote sensing applications, and human-computer computer interfaces. Since 1985 he has been Professor of Computer Engineering at Rensselaer Polytechnic Institute, where he established ECSE DocLab. In addition to document image analysis, OCR, geographic information systems and computational geometry, his students have engaged in solid modeling, finite-precision spatial computation, and interactive computer vision, often with a focus on systems that improve with use. He has benefited from visiting appointments at the Stanford Research Institute, Cornell, the University of Montreal, the National Scientific Research Institute of Quebec, the University of Genoa and the Italian National Research Council in Naples and Genoa, AT&T and Lucent Bell Laboratories, IBM Almaden, McGill University, the Institute for Information Science Research at the University of Nevada, and the Center for Image Analysis in Uppsala.

School of Computing

DISTINGUISHED SEMINAR SERIES

JEFFREY VOAS, PH.D.
DIRECTOR, SYSTEMS ASSURANCE
SCIENCE APPLICATIONS INTERNATIONAL CORPORATION
THURSDAY, JANUARY 19, 2006
WLH 210
2:30-3:30 P.M.

REFRESHMENTS TO FOLLOW IN GOODWIN 620

A Baker's Dozen:

13 Grand Software Engineering Challenges

This 1-hour talk will focus on 13 grand challenges facing the software engineering research and practitioner community. It will cover the key problems associated with these 13 topics: (1) what is software quality? (2) what is the ROI and economics behind existing software engineering techniques and methods?, (3) does process improvement matter?, (4) can you trust or even interpret software metrics and measurements?, (5) software engineering standards are too confusing and hard to implement and determine compliance thereof, (6) competing standards have no interoperability predictors, (7) how do you handle legacy software and decommissioning?, (8) where are the reasonable testing stoppage criteria that we must use?, (9) COTS software has little interoperability and little composability: why?, (10) reliability measurement and operational profiles are often viewed as suspicious, (11) designing in the "ilities" is wishful thinking and something we don't know how to handle technically or economically, (12) software certification is needed but we do not know how to do it or how to handle the liability issues, and (13) intelligence and autonomic computing sounds great but is it feasible?

J.M. Voas

Jeffrey Voas is Director of Systems Assurance Technologies at SAIC is an SAIC Technical Fellow. Before joining SAIC, Voas was the Chief Scientist at Cigital (www.cigital.com). Voas has been highly active in the software engineering research community for over 15 years. He has served on numerous journal and magazine editorial boards. He is currently the 2005 IEEE Reliability Society President, and has been nominated to be Director of IEEE's Division VI for 2006-07. Dr. Voas has co-authored two John Wiley books, and has two additional Wiley books slated for publication in 2006-2007. Dr. Voas is currently an Associate Editor-In-Chief of IEEE's IT Professional magazine, and serves on the Advisory Board of IEEE's Software magazine. Dr. Voas is the U.S. voting member of NATO's Task Force on Dual Use of High Assurance Technologies (RTG-020), and is an adjunct professor at West Virginia University. In addition, Dr. Voas has given numerous keynote lectures, and has performed many program chair, general chair, and program committee roles for IEEE and other non-profit professional societies. He holds one U.S. patent (#6,862,696) in "how to certify software, and has published over 125 refereed publications. Voas's interests are in various aspects of software quality, including software testing, reliability, safety, standards, and fault tolerance and certification.

Finally, Dr. Voas has spent much of the last 15 years in business development and mentoring, and co-founded a small company, Cigital, that was listed in the Inc. 500 for two years in a row as one of the fastest growing small companies in the U.S. Voas received his undergraduate degree in computer engineering from Tulane University in 1985, and received his Ph.D. in computer science from the College of William and Mary in 1990. Voas also performed a two-year post-doc for the National Research Council between 1990 and 1992 at NASA's Langley Research Center in Hampton, Virginia.

School of Computing

DISTINGUISHED SEMINAR SERIES

DR. SELIM AKL
SCHOOL OF COMPUTING
QUEEN'S UNIVERSITY

THURSDAY, FEBRUARY 16TH, 2006
3:00-4:00 PM
MILLER HALL 201

REFRESHMENTS TO FOLLOW IN GOODWIN 620

Even Accelerating Machines Are Not Universal *

Abstract:

The year 2006 marks two important anniversaries, the publication 75 and 70 years ago, respectively, of Gödel's proof of the incompleteness of formal systems of arithmetic, and of Turing's proof of the undecidability of first-order predicate calculus. This talk will briefly review these landmark results and their impact on Mathematics, Computer Science, and Philosophy. I will then show how these results, as well as Heisenberg's 80-year-old uncertainty principle in Physics, inspired some of my recent work on the principle of simulation and the universality thesis in Computer Science. The principal actors in this story will be featured here: David Hilbert, Kurt Gödel, Alan Turing, John von Neumann, and many others. As well, there will be appearances by unexpected characters, including (the ubiquitous) Bertrand Russell, Ludwig Wittgenstein, Jorge Luis Borges, and Alexandra Kosteniuk.

Here's a small homework (obvious answers are not necessarily correct):

1) Who were the two mathematicians to first fully appreciate Gödel's result?
2) Why was the computer invented?
3) Who first stated the Halting Problem, named it, and proved its undecidability?
4) How do you convince a mathematician (that what you do is Math)?

Brief Biography: Selim G. Akl is a Professor of Computing at Queen's University, Kingston, Ontario, Canada. His research interests are in parallel computation. He is author of *Parallel Sorting Algorithms* (Academic Press, 1985), *The Design and Analysis of Parallel Algorithms* (Prentice Hall, 1989), and *Parallel Computation: Models and Methods* (Prentice Hall, 1997). He is also a co-author (with K. Lyons) of *Parallel Computational Geometry* (Prentice Hall, 1992). His books were translated to Spanish, Italian and Japanese. Dr. Akl is former editor of the *Journal of Cryptology*, *Information Processing Letters*, and *Parallel Algorithms and Applications*. Presently, he serves on the editorial boards of *Computational Geometry*, *Communications in Applied Geometry*, *Parallel Processing Letters*, and the *International Journal of Parallel, Emergent, and Distributed Systems*, and is a founding editorial board member of the *International Journal of High Performance Computing and Networking.*

Dr. Akl received the Howard Staveley Excellence in Teaching Award in 2004, and is the winner of the Queen's University Prize for Excellence in Research in 2005.

* Note: The seminar by Prof. Akl will feature a new talk not previously delivered. It is not the same as the one presented at the Excellence in Research public lecture, or in the Mathematics & Statistics Departmental Colloquium.

School of Computing

DISTINGUISHED SEMINAR SERIES

Shoshana J. Wodak
Structural Biology and Biochemistry
Hospital for Sick Children
Toronto

Friday, March 17th, 2006
Walter Light Hall 205
2:00-3:00 pm
Refreshments to follow, Goodwin 620

Analyzing Networks of Cellular Processes

The focus of biology has shifted from the investigation of individual genes and proteins, to the study of large complex networks featuring interactions between tens of thousands of molecular and cellular components. Information on these networks is obtained from genome-scale experimental and theoretical analyses, which yield valuable but noisy data, on biological processes that are still poorly understood. A very active and inspiring area of activity has been the development of new bioinformatics and computational approaches for the interpretation of this large body of data in terms of biological knowledge. Two examples taken from our own work will be used to illustrate such approaches. One deals with analyzing the networks of metabolic reactions and compounds, and has applications in the area of inferring metabolic pathways from the knowledge of enzyme-coding genes. The second deals with the interpretation of data on protein-protein interactions and protein complexes, derived using high throughput affinity purification techniques. As these examples will illustrate, building biologically meaningful networks is a challenging problem with no simple solutions. But it is the basis on which any further interpretation must rest.

Croes D, Couche F, Wodak SJ, van Helden J.
Inferring meaningful pathways in weighted metabolic networks.
J Mol Biol. (2006) 356:222-36

Simonis N. Gonze D. Orsi C. van Helden J. and Wodak SJ.
Modularity of the transcriptional response of protein complexes,
J. Mol. Biol. in Press

Shoshana J. Wodak

Dr. Shoshana J. Wodak is the Scientific Director of the Center for Computational Biology and a Senior Scientist in the Structural Biology Program at the Hospital for Sick Children. She is a Professor at the Departments of Biochemistry and of Medical Genetics and Microbiology, at the University of Toronto. She was formerly a Professor, as well as a co-founder and co-director of the Centre for Structural Biology and Bioinformatics at the Free University of Brussels.

Dr. Wodak has gained worldwide recognition for her pioneering work on computational methods for protein-protein docking, domain assignment in proteins from their atomic coordinates, and protein 3D structure prediction. She has introduced automatic procedures for structure alignment and for the classification of local protein structure motifs, and has been at the origins of many of the software tools, now routinely used in protein modeling and simulation. More recently Dr. Wodak has turned her attention to the representation and analysis of cellular processes. Together with her colleagues, she has been developing advanced database tools for the representation and the analysis of biochemical networks and pathways. Much of her recent work has also been devoted to elucidating the mechanism of transcriptional regulation of multi-protein complexes in yeast, and to understanding how the biological function of genes and proteins are determined by their structural and chemical properties as well as by their interactions.

Dr. Wodak has authored more than 170 papers in international scientific journals, including – among many others - Nature, PNAS, J. Mol. Biol., and Nucleic Acid Research. She is on the Editorial Board of the Journal Proteins Structure Function and Bioinformatics and of BMC Bioinformatics. Dr. Wodak was elected as a member of the EMBO (European Molecular Biology Organization) in 1990. She has consulted for several pharmaceutical companies, and served as an advisor for government organizations and research institutes throughout Europe. She was a recipient of a CIHR Canada Establishment Grant in 2004, and was awarded a Tier 1 Canada Research Chair in Computational Biology and Bioinformatics in June 2005.

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School of Computing

DISTINGUISHED SEMINAR SERIES

DR. MARGARET-ANNE STOREY
DEPARTMENT OF COMPUTER SCIENCE
UNIVERSITY OF VICTORIA

THURSDAY, APRIL 27, 2006
2:30-3:30 PM
Dupuis Hall 215

Refreshments to follow in Goodwin 620

Title: Contextually-Aware Adaptive Visualizations for Software Tools

Abstract:

Software systems are becoming more complex and are being combined in many different ways to achieve the seamless integration of services required in the world today. Modern software development environments must adapt if they are to keep pace with this increasing complexity. The goal of our research projects is to improve software development tools through features that will help programmers better manage this complexity. To address comprehension, navigation and collaboration challenges during development, we combine and integrate techniques from information visualization, adaptive user interfaces, computer-supported collaborative work and web-based learning tools. During this talk, I will first provide some background on the research area of program comprehension. Next, I will present several technologies that we are designing to improve software tools for novices, experts and teams of developers.

Biography:

Dr. Margaret-Anne Storey is an associate professor of computer science at the University of Victoria, a Visiting Scientist at the IBM Centre for Advanced Studies in Toronto and a Canada Research Chair in Human Computer Interaction for Software Engineering. Her research goal is to understand how technology can help people explore, understand and share complex information and knowledge. She applies and evaluates techniques from knowledge engineering and visual interface design to applications such as reverse engineering of legacy software, medical ontology development, digital image management and learning in web-based environments. She is also an educator and enjoys the challenges of teaching programming to novice programmers.

School of Computing

DISTINGUISHED SEMINAR SERIES

DR. SUMI HELAL
DEPARTMENT OF COMPUTER AND INFORMATION SCIENCE AND ENGINEERING
UNIVERSITY OF FLORIDA

MONDAY, MAY 29, 2006
11:00am-12:00pm
DUPUIS HALL 215

REFRESHMENTS AT 10:15 in GOODWIN 620

Programmable Pervasive Spaces

ABSTRACT: Pervasive computing environments have recently been explored trough a series of university and industry research prototypes. Many of them emphasized the "calmness" requirement of the technology and the "predictability" of the environment behavior and interaction. By carefully integrating sensors, computers, devices and networks, it was possible to craft the first generation of pervasive environments, also referred to by the research community as "integrated environments".

In this talk I will describe our efforts in middleware design that aim at shifting the pervasive computing paradigm from "integrated environments" to "programmable spaces". I will present "Matilda Smart House", a pervasive environment to achieve successful aging and independence that we have developed following the integrated environment approach. I will then present the programmable space approach and middleware based on a simple sensors-actuators-contexts model. I will revisit "Matilda Smart House" that we recently remodeled as a highly programmable space. Finally, I will address the main issues and enablers necessary to take pervasive computing and its applications from the confines of research laboratories to a multi-billion dollar mainstream industry.

The research I will present is currently being funded by the National Science Foundation, National Institute on Disabilities and Rehabilitation Research (NIDRR), the Veteran Administration, and Intel Corporation.

ABOUT THE SPEAKER:

Dr. Sumi Helal is a Professor at the Computer and Information Science and Engineering Department (CISE) at the University of Florida. His research interests span the areas of Pervasive Computing, Mobile Computing and networking and Internet Computing. He directs the Mobile and Pervasive Computing Laboratory and leads the technology development of the NIDRR-funded Rehabilitation Engineering Research Center on Successful Aging (RERC). He is cofounder and Director of the Gator Tech Smart House, an experimental home for applied pervasive computing research in the domain of elder care. Additionally, he is founder, President and CEO of Phoneomena, Inc., a mobile application and middleware company, and President of Pervasa, Inc., a University of Florida start-up focused on platform and middleware products for sensor networks.

Outside of his teaching and research, Dr. Helal is a co-founder and an editorial board member of the IEEE Pervasive Computing magazine. He is the Editor of the magazine's column on Standards, Tools and Emerging Technologies. He is also an Associate Editor of the IEEE Transaction on Mobile Computing. He has published over 200 books, book chapters, journal articles, and conference or workshop papers. He is a Senior member of the Institute of Electrical and Electronics Engineers (IEEE), and a member of the Association for Computing Machinery (ACM) and the USENIX Association.

Born in Suez, Egypt, Dr. Helal earned his B.E. and M.E. degrees in Computer Science and Engineering from Alexandria University, Egypt, in 1982 and 1985 respectively. He earned his Ph.D. in Computer Sciences from Purdue University in 1991. Before joining the University of Florida, he held academic and industrial research positions at MCC, Purdue University and the University of Texas at Arlington.