

# Informatics Today



UNIVERSITY OF PITTSBURGH

DEPARTMENT OF  
BIOMEDICAL INFORMATICS

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## The Biomedical Language Understanding Laboratory



The DBMI Biomedical Language Understanding (BLU) Laboratory, front row, left to right, Jeannie Irwin, Wendy Chapman, Henk Harkema; back row, left to right, Heather Piwowar, Lee Christensen, John Dowling, Danielle Mowery, Saeed Amizadeh.

The Biomedical Language Understanding (BLU) Laboratory at the University of Pittsburgh focuses on biomedical language processing. The BLU Lab is directed by Wendy W. Chapman, PhD, an assistant professor of biomedical informatics and intelligent systems in the Department of Biomedical Informatics (DBMI).

Natural language processing (NLP) is a branch of artificial intelligence that classifies, extracts, and encodes human natural language.

Chapman studied linguistics and Chinese language as an undergraduate student. After considering graduate studies in Chinese literature, Chapman serendipitously entered into the

world of computational linguistics and medical informatics. Her husband, Brian Chapman, PhD, had interviewed with Peter Haug, MD, professor of biomedical informatics at the University of Utah. At the time, Haug was applying computational linguistics techniques to extract and encode information within chest X-ray reports. "I thought the area was fascinating and convinced Peter to give me a try as a graduate student researcher with no background in science, medicine, or computers but with a degree in linguistics and a lot of energy," recalls Chapman. After several years of classes and experimentation with programming, Chapman soon found her niche in this specialized area, earning her doctoral degree in medical informatics in 2000 at the University of Utah. She came to Pittsburgh for a postdoctoral fellowship with Bruce Buchanan, PhD, and afterward stayed with DBMI as a faculty member.

The main focus of the BLU lab is to develop and evaluate computerized applications for understanding the clinical state of a patient from dictated reports. The initial step is to identify relevant concepts such as "shortness of breath" or "headache" in the text. The BLU lab is particularly interested in the next steps: understanding the context in which the concept is described.

Funded research areas of the BLU lab include the following:

**Identifying clinical conditions relevant to surveillance of disease outbreaks, funded by the National Library of Medicine:** The BLU Lab is developing a system, Topaz, for identifying acute onset of clinical conditions relevant to public health surveillance. Topaz processes emergency department reports to build a detailed understanding of why a patient presented to the emergency room.

**Automatically charting dental findings, funded by the National Institute of Dental and Craniofacial Research:** The BLU lab is extending the MPLUS system that was developed by Haug and colleagues at the University of Utah. This extension, MEDUSA (Medical Understanding and Semantic Analysis), will automatically chart the results of recorded dental examinations.

The following researchers work in the BLU lab with Chapman:

**Saeed Amizadeh**, a doctoral student in the Intelligent Systems Program, is applying machine learning methods to temporal modeling and clinical classification.

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## Training Program Update

The University of Pittsburgh Biomedical Informatics Training Program, funded in part by the National Library of Medicine, is in its 21st year of training individuals for research and development careers emphasizing the application of modern information technology to health care, basic biological and clinical research, and the education of health professionals.

Rebecca Crowley, MD, MSIS, is director of the program. Crowley is a graduate of the program, having earned her master's degree in information science (with a biomedical informatics concentration) at the University in 2001. Wendy Chapman, PhD, serves as associate director. Michael Becich, MD, PhD; Gregory Cooper, MD, PhD; and Titus Schleyer, DMD, PhD, serve as codirectors.

The training program annual retreat, coordinated by Schleyer, took place on August 22, 2008. The retreat was held for the second consecutive year at Seven Springs Mountain Resort in Seven Springs, Pa. Twenty-seven students and 16 training program faculty members enjoyed the rural setting of the Laurel Highlands.

The morning activities of the retreat consisted of an overview and state-of-the-program presentation by Crowley and Chapman and introductions of students and faculty. Afternoon activities consisted of student poster sessions, presentations of faculty research interests, and a biomedical informatics game show patterned after the popular quiz show *Jeopardy!* The game show was developed by the students and faculty at the University's Center for Dental Informatics.

## Master's and Doctoral Training Opportunities

The University of Pittsburgh Biomedical Informatics Training Program has openings for predoctoral and postdoctoral informatics traineeships beginning in the summer of 2009. The program has been offering training in informatics for more than 20 years.

For information about active research topics and areas of training concentration, please visit [www.dbmi.pitt.edu/trainingprogram](http://www.dbmi.pitt.edu/trainingprogram).

Individuals with interest in these training opportunities are invited to send e-mail to [dbmi@pitt.edu](mailto:dbmi@pitt.edu) or call 412-647-7176 for further information.

The retreat concluded with award presentations for Best Student Paper of the Year and Best Student Poster at the Annual Retreat. Both of these annual awards are determined by faculty judges and recognize the high quality of student research.

Christa Bartos, PhD, won the Best Student Paper of the Year award for her paper, "Negative CPOE Attitudes Correlate with Diminished Power in the Workplace." This winning paper was Bartos' second to be selected as an award finalist from a group of 21 entries. Other award finalists were papers written by Steven Handler, MD, MS; Heather Piwowar, MS; and Yanna Shen, MS. Bartos' winning paper recently has been accepted for publication in the Proceedings of the American Medical Informatics Association Annual (AIMA) Symposium.

Heather Piwowar, MS, won a blue ribbon for Best Student Poster at the Annual Retreat for her entry "Envisioning a Data Reuse Registry." This winning poster was selected from 19 entries.

After a volleyball game and a mountain barbecue dinner, students and faculty returned to the University, ready to begin the fall term and thinking ahead to the AMIA Annual Symposium.

Additional information about the training program is available at [www.dbmi.pitt.edu/trainingprogram](http://www.dbmi.pitt.edu/trainingprogram) or by calling 412-647-7176.

## DBMI External Advisory Board Holds Second Annual Meeting



The DBMI External Advisory Board, left to right: Marion Ball, Atul Butte, Christopher Chute, and Edward Shortliffe (Joyce Mitchell not pictured)

The DBMI External Advisory Board held its second annual meeting on September 23–24, 2008, in Pittsburgh. The board reviewed presentations on the department's research portfolio, training program, faculty demographics and recruitment, corporate-sponsored research, and finances.

## Department Grant Support, Direct and Indirect New Grants Since July 2008 • Total: \$5,165,298

Faculty	Grant Description	Program Start Date	Program End Date	TOTAL PERIOD		Total
				Direct	Indirect	
Michael Becich, MD, PhD	CDC: National Mesothelioma Virtual Bank for Translational Research	09/01/08	08/31/11	\$1,158,244	\$596,496	\$1,754,740
Michael Becich, MD, PhD	NIH: Administrative Supplement for CTSA Consortium Project	09/01/08	08/31/09	\$149,010	\$50,990	\$200,000
Michael Becich, MD, PhD	caBIG: DISC Work Group Participation	03/07/08	02/14/09	\$12,043	\$6,202	\$18,245
Michael Becich, MD, PhD	caBIG: ICR Work Group Participation	03/07/08	02/14/09	\$16,805	\$8,655	\$25,460
Michael Becich, MD, PhD	caBIG: VCDE Work Group Participation	03/07/08	02/14/09	\$28,604	\$14,731	\$43,335
Michael Becich, MD, PhD	SAIC-caBIG: Adoption of caTISSUE Suite	03/07/08	11/30/08	\$150,333	\$77,421	\$227,754
Roger Day, ScD	caBIG: ARCH Work Group Participation	03/07/08	02/14/09	\$37,290	\$19,204	\$56,494
Valerie Monaco, PhD, MHCI	caBIG: D & T Work Group Participation	03/07/08	02/14/09	\$13,277	\$6,838	\$20,115
Rich Tsui, PhD	Houston Department of Health: Biosurveillance Expansion Project	07/01/08	12/31/08	\$209,823	\$106,485	\$316,308
Rich Tsui, PhD	CDC: Building a Regional Biosurveillance Grid for Pennsylvania and Ohio	09/30/08	09/29/10	\$395,586	\$203,726	\$599,312
Michael Wagner, MD, PhD	NIH: Decision Making in Biosurveillance	09/30/08	09/29/12	\$1,264,589	\$638,946	\$1,903,535
<b>Total</b>				<b>\$3,435,604</b>	<b>\$1,729,694</b>	<b>\$5,165,298</b>

## DBMI Publications

April 1, 2008 – September 30, 2008

### Primary Faculty, Fellows, and Staff

Please see the online edition of *Informatics Today* for secondary appointment and adjunct faculty publications.

Amin, W., A.V. Parwani, L. Schmandt, S.K. Mohanty, G. Farhat, A.K. Pople, S.B. Winters, N.B. Whelan, A.M. Schneider, J.T. Milnes, F.A. Valdivieso, M. Feldman, H.I. Pass, R. Dhir, J. Melamed, and M.J. Becich. "National Mesothelioma Virtual Bank: A Standard Based Biospecimen and Clinical Data Resource to Enhance Translational Research." *BMC Cancer* 8 (2008): 236.

Bain, K.T., H.M. Holmes, M.H. Beers, V. Maio, S.M. Handler, and S.G. Pauker. "Discontinuing Medications: A Novel Approach for Revising the Prescribing Stage of the Medication-Use Process." *J Am Geriatr Soc* (2008).

Chapman, B.E., E.S. Minalga, C. Brown, J.A. Roberts, and J.R. Hadley. "Reducing Morphological Variability of the Cervical Carotid Artery in Serial Magnetic Resonance Imaging Using a Head and Neck Immobilization Device." *J Magn Reson Imaging* 28, no. 1 (2008): 258-62.

Dara, J., J.N. Dowling, D. Travers, G.F. Cooper, and W.W. Chapman. "Evaluation of Preprocessing Techniques for Chief Complaint Classification." *J Biomed Inform* 41, no. 4 (2008): 613-23.

Grover, H., Lustgarten, J., Visweswaran, S., Gopalakrishnan, V. "Improving Peptide Identification via Validation with Intensity-based Modeling of Tandem Mass Spectra." In *Proceedings of the International Conference on Bioinformatics, Computational Biology, Genomics and Chemoinformatics* (BCBGC-08). (2008).pp. 56-63.

Handler, S.M., J.T. Hanlon, S. Perera, Y.F. Roumani, D.A. Nace, D.B. Fridsma, M.I. Saul, N.G. Castle, and S.A. Studenski. "Consensus List of Signals to Detect Potential Adverse Drug Reactions in Nursing Homes." *J Am Geriatr Soc* 56, no. 5 (2008): 808-15.

Handler, S.M., B.H. Shirts, S. Perera, M.J. Becich, N.G. Castle, and J.T. Hanlon. "Frequency of Laboratory Monitoring of Chronic Medications Administered to Nursing Facility Residents: Results of a National Internet-Based Study." *Consult Pharm* 23, no. 5 (2008): 387-95.

Hanlon, J.T., S. Aspinall, S.M. Handler, M. Rossi, L.F. Fried, S. Weisbord, C.B. Good, M. Fine, R. Stone, M. Pugh and T.P. Sema. "Consensus guidelines for dosing primarily renally cleared medications in older outpatients." *Journal of the American Geriatrics Society* 2008;56(4):S190-S190

Jiang, X., G. Wallstrom, G.F. Cooper, and M.M. Wagner. "Bayesian Prediction of an Epidemic Curve." *J Biomed Inform* (2008).

Jordan, R., S. Patel, H. Hu, and J. Lyons-Weiler. "Efficiency Analysis of Competing Tests for Finding Differentially Expressed Genes in Lung Adenocarcinoma." *Cancer Informatics*. 2008, 6, 389-421.

Kundel, H.L., C.F. Nodine, E.A. Krupinski, and C. Mello-Thoms. "Using Gaze-Tracking Data and Mixture Distribution Analysis to Support a Holistic Model for the Detection of Cancers on Mammograms." *Acad Radiol* 15, no. 7 (2008): 881-6.

Lustgarten, J.L., Grover, H., Visweswaran, S., Gopalakrishnan, V. "An Evaluation of Discretization Methods for Learning Rules from Biomedical Datasets." In *Proceedings of the 2008 International Conference on Bioinformatics and Computational Biology* (BIOCOMP'08). (2008). Editors Hamid R. Arabnia, Mary Qu Yang, Jack Y. Yang. pp. 527-532.

Mohanty, S.K., A.T. Mistry, W. Amin, A.V. Parwani, A.K. Pople, L. Schmandt, S.B. Winters, E. Milliken, P. Kim, N.B. Whelan, G. Farhat, J. Melamed, E. Taioli, R. Dhir, H.I. Pass, and M.J. Becich. "The Development and Deployment of Common Data Elements for Tissue Banks for Translational Research in Cancer - an Emerging Standard Based Approach for the Mesothelioma Virtual Tissue Bank." *BMC Cancer* 8 (2008): 91.

Monzon, F.A., J.M. Hagenkord, M.A. Lyons-Weiler, J.P. Balani, A.V. Parwani, C.M. Sciuilli, J. Li, U.R. Chandran, S.I. Bastacky, and R. Dhir. "Whole Genome Snp Arrays as a Potential Diagnostic Tool for the Detection of Characteristic Chromosomal Aberrations in Renal Epithelial Tumors." *Mod Pathol* 21, no. 5 (2008): 599-608.

Piwowar, H.A., M. J. Becich, H. Bilofsky, and R.S. Crowley. "Towards a Data Sharing Culture: Recommendations for Leadership from Academic Health Centers." *PLoS Med* 5, no. 9 (2008): e183.

Scotch, M., B. Parmanto, and V. Monaco. "Evaluation of Sovat: An Olap-Gis Decision Support System for Community Health Assessment Data Analysis." *BMC Med Inform Decis Mak* 8 (2008): 22.

Shen, Y., C. Adamou, J.N. Dowling, and G.F. Cooper. "Estimating the Joint Disease Outbreak-Detection Time When an Automated Biosurveillance System Is Augmenting Traditional Clinical Case Finding." *J Biomed Inform* 41, no. 2 (2008): 224-31.

Wallstrom, G., J. Liebner and R.E. Kass. "An implementation of Bayesian adaptive regression splines (BARS) in C with S and R wrappers." *Journal of Statistical Software* 2008;26(1).

Wilson, R.R., Silowash, R., Anthony, L., Cecil, R.A. and Eller, Andrew. "Telemedicine Process Used to Implement an Effective and Functional Screening Program for Diabetic Retinopathy." *Journal of Diabetes Science and Technology* 2:5, 785-791.

Yudelson, M.V., O.P. Medvedeva and R.S. Crowley. "A multifactor approach to student model evaluation." *User Modeling and User-Adapted Interaction* 2008;18(4):349-382

Zheng, B., C. Mello-Thoms, X.H. Wang, G.S. Abrams, J. H.Sumkin, D.M. Chough, M.A. Ganott, A. Lu, and D. Gur. "Interactive Computer-Aided Diagnosis of Breast Masses: Computerized Selection of Visually Similar Image Sets from a Reference Library." *Acad Radiol* 14, no. 8 (2007): 917-27.

## The Clinical Research Informatics Service

Posters from the Clinical and Translational Sciences Institute (CTSI) on display throughout the University of Pittsburgh describe a common research problem: “We need extensive de-identified clinical data from the electronic health records on patients ... for an outcomes study.” Health sciences researchers have successfully solved this problem by using the Clinical Research Informatics Service (CRIS), directed by Melissa Saul, MS, who also is an adjunct assistant professor of health information management in the School of Health and Rehabilitation Sciences.

CRIS was established in 2001 by Charles Friedman, PhD, director of the Center for Biomedical Informatics from 1996 to 2003, and Clifford Schold Jr, MD, associate vice chancellor for clinical research from 2001 to 2005. Randall Smith, PhD, senior associate dean of the School of Pharmacy, also was instrumental in developing the business model. CRIS currently is sponsored by the University’s Department of Biomedical Informatics (DBMI) and CTSI.

Saul, the founding director of CRIS, has more than 20 years of experience working with health information systems. Saul was an early developer of the Medical Archival Retrieval System (MARS), the UPMC data repository for clinical and financial data. MARS currently contains more than 190 million reports and is indexed on every word in every report, enabling researchers to search millions of reports based on a clinical term or phrase.

“CRIS taps UPMC’s enormous data sources and makes the data available to clinicians and health sciences faculty in an integrated and timely fashion,” says Saul. “We make this data available in accordance with institutional and governmental regulations.”

The University’s Institutional Review Board (IRB) has certified CRIS as an “honest broker” of electronic medical record data. An honest broker serves as a disinterested intermediary between the researcher and the patients whose data are being studied. The use of an honest broker ensures that the investigator neither interacts with patients, nor records any identifiable patient information. However, the added value that CRIS provides is the use of De-ID™, a software application that removes patient-identifying information from clinical reports. Using an automated tool to remove patient identifiers and assign pseudoidentifiers enables CRIS to process thousands of records from multiple sources into one data set for the clinical researcher. This service makes CRIS unique in its product offerings.

CRIS provides health sciences researchers with an extensive range of services, including:

**Data Identification:** CRIS identifies data sources supporting the researcher’s request, examines the limitations of the data, identifies variables of interest, and refines the scope of the project as needed.

**Data Collection:** CRIS develops extraction methodologies using MARS and other data sources to acquire the data and complete quality assurance testing.

**Data De-Identification:** De-ID software—developed at the University by Saul and Greg Cooper, MD, PhD, an associate professor of biomedical informatics, computer science, and intelligent systems—allows researchers to use protected health information collected for patient care purposes for studies.

**Data Analysis:** Data analysis is available for post-processing output for summary statistics and other customized reports.

The CRIS team consists of many collaborators from the University and UPMC. Within DBMI, software developer Lena Gemmer provides programming support for the data de-identification tools and other data management projects. Andrew Pople, a senior software architect at DBMI, provides oversight on the software development process for De-ID software.

The Cancer Text Information Extraction System (CATies) group—Rebecca Crowley, MD, MSIS, Girish Chaven, and Kevin Mitchell—work with CRIS to identify new functionality that could be added to the De-ID system.

Steven Handler, MD, MS and Shyam Visweswaran, MD, PhD, both assistant professors of biomedical informatics, collaborate with CRIS in their research into adverse event detection in the nursing home setting.

From the School of Pharmacy, Kim Coley, PharmD, FCCP, director of the Center for Pharmcoinformatics and Outcomes, and Robert Weber, MS, FASHP, chairman of the Department of Pharmacy and Therapeutics, work with CRIS to engage new researchers at the University, as well as pharmaceutical corporations.

CRIS is working closely with the CTSI informatics group to further develop the Clinical and Research Data Informatics Foundation Framework (CARDIFF.) One goal of this project is to provide clinical researchers the ability to come to CRIS for de-identified clinical data and have the data integrated into an existing data model so that the researcher can begin data analysis. This would allow the researcher to use the data sets obtained from CRIS in a more streamlined manner, as well as promote data sharing. In this framework, data that already have been collected and stored within a CARDIFF database are able to be reused for a future research project. The data de-identification process would also be a component of CARDIFF.

For more information about CRIS, visit [www.dbmi.pitt.edu/cris](http://www.dbmi.pitt.edu/cris) and [www.ctsi.pitt.edu](http://www.ctsi.pitt.edu).

## Denver Dash, PhD

2003, Post Doctoral Research Fellow  
Research Scientist, Intel Research Pittsburgh

**Q: What have you been doing since completing your postdoctoral fellowship at Pitt?**

A: I did a brief fellowship with Greg Cooper at the Center for Biomedical Informatics before joining Intel Research in Santa Clara, Calif. as a research scientist in late 2003. I moved to the Intel Research Pittsburgh lab on the campus of Carnegie Mellon University in 2006. At Intel, I've been applying graphical models to detecting intrusion detections in networks, and lately I've been working on improving computer perception by incorporating many diverse sensors and multiple perspectives into the problem and on parallelizing machine learning algorithms.

**Q: What are your most memorable experiences from your days at Pitt?**

A: I enjoyed summers at Lake Arthur, spelunking, Latin dancing at Rosebud on Thursdays, playing ultimate Frisbee, teaching a semester in Poland, and meeting and courting my amazing wife.

**Q: How did your training and education benefit your career?**

A: My advisor, Marek Druzdzal, did a great job preparing me for my career. He gave me a solid foundation in Bayesian networks with his decision support systems class. He exposed me to excellent programmers who taught me a lot about first-class development, and he encouraged me to teach a course in Poland which forced me to polish my knowledge of machine learning well enough to teach it to others. Greg Cooper's reading courses in bioinformatics gave me a great broad-based background in that field that has been invaluable as well. Kirk Pruhs' algorithms class from the Pitt computer science department has been one of those classes that I am grateful for every day.

**Q: What are your research interests?**

A: I have been pretty active in disease outbreak detection research, much of which can be applied to intrusion detection as well. Recently, I have been working on cluster onset detection, a method for real-time unsupervised clustering to detect the onset of possibly diseased clusters in a population. I'm also very interested in taking a lot of these machine learning and detection algorithms and understanding how to implement them efficiently in a cluster-computing environment. A lot of people don't realize that Moore's law on a single processor is basically over. If we want our algorithms

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Denver Dash and Dagny



Weng-Keen Wong

## Q & A with Weng-Keen Wong, PhD

2005, Post Doctoral Research Fellow  
Assistant Professor of Computer Science, Oregon State University

**Q: What have you been doing since completing your postdoctoral fellowship at Pitt?**

A: After completing my fellowship at Pitt, I started as an assistant professor in the School of Electrical Engineering and Computer Science at Oregon State University.

**Q: What are your most memorable experiences from your days at Pitt?**

A: My most memorable experiences were interacting with the graduate students, staff, and faculty at the Center for Biomedical Informatics. I particularly enjoyed working with Greg Cooper, who was my postdoctoral advisor.

**Q: How did your training and education benefit your career?**

A: Under Greg Cooper, I learned a great deal about applying Bayesian networks and Bayesian statistics to problems in disease outbreak detection. I am now using these same concepts to help solve ecological problems such as species distribution mapping.

**Q: What is your role on the faculty of Oregon State University?**

A: Apart from teaching courses, I am also involved in research. Generally speaking, my research interests are in machine learning and data mining. Currently, I am investigating the following research areas:

- 1) Enduser debugging of machine learning programs: How can end users, who know nothing about machine learning, correct machine learning programs such as spam filters and intelligent desktop assistants that adapt themselves to the end user's behavior?
- 2) Species distribution mapping: Can we develop accurate predictive models for the presence of a species in a geographic location? How does climate change affect species distributions?
- 3) Learning from demonstration: Can a machine learning algorithm learn a complex task by watching a rich, informative demonstration from an expert?

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**Lee Christensen**, codeveloper of MPLUS, is the software architect for MEDUSA.

**John Dowling**, MD, MS, is a retired physician with a degree in biomedical informatics. He provides domain expertise and supervises annotation efforts.

**Henk Harkema**, PhD, a postdoctoral research associate at DBMI, collaborates on MEDUSA and Topaz, is developing a part-of-speech tagger for clinical text, and is helping to develop an annotation schema for temporality and discourse structure in reports.

**Jeannie Irwin**, MS, a doctoral student in the Biomedical Informatics Training Program, is working on developing and evaluating the semantic component in MEDUSA, along with evaluating speech recognition performance on dental charts.

**Danielle Mowery**, a doctoral student in the Biomedical Informatics Training Program, is developing a richer temporal model for the information described in clinical reports.

**Heather Piwowar**, MS, a doctoral student in the Biomedical Informatics Training Program, is participating in Topaz development and is applying NLP techniques to the biomedical literature to determine whether a research article shared microarray data.

**Tyler Thornblade**, a computer science graduate student, is working on an algorithm that examines the contextual features of natural language.

The Biomedical NLP Lab is collaborating with other researchers from both inside and outside the University.

Within the University, the Biomedical NLP Lab is collaborating with Rebecca Crowley, MD, MSIS, assistant professor of biomedical informatics, intelligent systems, and pathology, in developing a system that can be used for information extraction and for automated enrichment of ontologies. The BLU lab also is collaborating on Topaz with Jan Wiebe, PhD, professor and director of the Intelligent Systems Program, and Rebecca Hwa, PhD, an assistant professor of computer science.

Outside Pitt, the Biomedical NLP Lab is collaborating on current projects with Haug, MultiModal Technologies, and Guergana Savova, PhD, from the Mayo Clinic. The lab also is collaborating with researchers from the VA hospitals who are developing NLP applications for clinical text (Matt Samore, MD; Brett South, and Adi Gundlapalli, PhD).

For more information, please visit [www.dbmi.pitt.edu](http://www.dbmi.pitt.edu).

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## Q & A with Denver Dash, PhD continued from page 5

to continue to exploit the benefits of microprocessor advances, the only way forward is to look at parallel and distributed computing methods.

### *Q: What advice would you give to current fellows in the training program?*

A: If you expect to be doing any programming, I would strongly recommend taking Pruhs' algorithms class in the computer science department. It has a lot of broad applicability, and I have personally found it invaluable in my career. I would also recommend looking around at other departments and taking advantage of the strong interdisciplinary atmosphere that being at Pitt provides. I would include in that some of the great offerings available via cross-registration at Carnegie Mellon University.

### *Q: Anything about your personal life you would like to share?*

A: A few months ago, my wife gave birth to our first child, Dagny Dash. Even in such a short time I have been amazed and inspired by how human beings are able to perceive the world around them and become self-aware, not to mention store nearly an entire lifetime's worth of experience and memories in such a compact form-factor.

## Q & A with Weng-Kenn-Wong, PhD continued from page 5

### *Q: What advice would you give to current fellows in the training program?*

A: Don't forget to get out of the lab once in a while.

### *Q: Anything about your personal life you would like to share?*

A: I'm a big fan of the Pittsburgh Penguins. Let's go Pens!



# University of Pittsburgh

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