# Informatics Today

### UNIVERSITY OF PITTSBURGH

### DEPARTMENT OF BIOMEDICAL INFORMATICS

#### Spring 2011

#### . . . . .

#### **Inside This Issue**

#### Page Two:

Training Program Curriculum Restructured: Integrating the Core

**Page Three:** Department Grant Support and Publications

Page Four:

Faculty Feature Xinghua Lu, MD, MS, PhD

#### **Page Five:**

Featured Alumni Q&A with Gerry Douglas (MSIS '99, PhD '09)

• • • • •

**Editors:** Lucy Cafeo Patricia Connell Charles Dizard

Informatics Today is a publication of the University of Pittsburgh Department of Biomedical Informatics.

The University of Pittsburgh is an affirmative action, equal opportunity institution. Published in cooperation with the Department of University Marketing Communications. UMC76198-0511

www.dbmi.pitt.edu

### Center for Advanced Study of Informatics in Public Health

The Center for Advanced Study of Informatics in Public Health (CASIPH) is developing a set of interrelated projects funded by the Centers for Disease Control and Prevention (CDC), the National Library of Medicine (NLM), and the Commonwealth of Pennsylvania. A five-year, \$5 million CDC grant awarded in September 2009 supports the operation of the center as one of four Centers of Excellence in Public Health Informatics and two research projects.

CASIPH is a collaboration with the University of Pittsburgh Graduate School of Public Health; the Allegheny County, Texas' Tarrant County, and Pennsylvania health departments; UPMC; and researchers at the Human-Computer Interaction Institute at Carnegie Mellon University. CASIPH's director, Michael Wagner, MD, PhD, explains that "the center's goal is not only to advance the state of the art in biosurveillance systems as far as possible during the five years of Center of Excellence funding but also to create a stateof-the-practice epidemiology unit in a health department, one that takes full advantage of the information in electronic medical records."

Under the direction of Rich Tsui, PhD, the first CDC-funded CASIPH research project is creating a Bayesian case detection system capable of



Allegheny County Health Department nurse investigators, epidemiologists, and University of Pittsburgh researchers. Back row, from left: Mike Wagner, Rich Tsui, Ron Voorhees, Greg Cooper. Front row, from left: Jim Lando, Megan Casey, Jeremy Espino, Sharon Silvestri

computing the posterior probability of notifiable diseases from information available in hospital information systems, including dictated reports. Gregory Cooper, MD, PhD, is leading the second CDC-funded research project, which is developing and validating a Bayesian outbreak detection and characterization system that takes as input the cases identified by the case detection system and other data and computes the posterior probability of outbreaks and their key characteristics, such as number infected.

Wagner also is the principal investigator of the NLM-funded Decision Making in Biosurveillance project, which has developed a decision-analytic application for epidemiologists called BioEcon. BioEcon automatically generates decision models for epidemiologists who are facing questions of which control measures to select in the setting of a suspected or ongoing outbreak. The BioEcon project spawned a second initiative, called Apollo, whose goal is to standardize the syntax and vocabulary used in epidemic models.

In September 2010, Shyam Visweswaran, MD, PhD, received NLM funding for a one-year project titled Optimization of Vaccine Strain Selection, which is using the BioEcon software to construct a model of the annual decision faced by the World Health Organization about which influenza strain to recommend for the annual influenza vaccine.

### Training Program Curriculum Restructured: Integrating the Core

The curriculum of the biomedical informatics (BMI) MS and PhD programs has undergone significant change over the past three years to better serve the mission of the training program. Rebecca Crowley, MD, MS, Department of Biomedical Informatics (DBMI) training program director, says "It's been a long process that has transformed the curriculum in a positive way. It's more in line with the model of a competency-based curriculum, with increased focus on methods and research. Early reports are that students enjoy it more."

The BMI training program offers MS and PhD degrees for students with interests in translational bioinformatics, clinical research informatics, health informatics, and public health informatics. The core curriculum of the University of Pittsburgh Biomedical Informatics Training Program provides a starting point for all candidates seeking an MS or PhD (including MD/ PhD) in biomedical informatics with research interests in any of the four basic areas as well as in the dental informatics track. The core courses are intended to do the following:

- Support a range of educational and professional backgrounds (Essentials series),
- Provide a broad overview of all four areas of biomedical informatics and statistics (Foundations series),
- Support the acquisition of quantitative and qualitative biomedical informatics research methods (Research Methods series), and
- Develop skills in critical reading of informatics literature, research design, project development, and scientific writing and speaking (Research Skills series).



DBMI graduate students prepare for class in Shadyside Cancer Pavilion Training Room. Rear: Himanshu Grover, Seshan Ananthan. Front: Abid Shah, Vicky Chen, and Lujia Chen

Essentials series courses provide important background knowledge for students who enter our program from a wide variety of disciplines. They include Problem-Oriented Programming (BIOINF 2012), Mathematics for Biomedical Informatics (BIOINF 2015), and Introduction to Patient Care and Clinical Environments (BIOINF 2013).

Foundations series courses teach foundational knowledge in all four basic areas of biomedical informatics, as well as in probability and statistics. They include Foundations of Bioinformatics (BIOINF 2051), Foundations of Clinical and Public Health Informatics (BIOINF 2011), and Statistical Foundations of Biomedical Informatics (BIOINF 2118). Research Methods series courses provide in-depth methodological training, including formalisms, methods, techniques, and tools that apply broadly to all basic areas of biomedical informatics training. Each course includes a didactic component supplemented



Frank M. Ligons, DBMI doctoral fellow

with practice in the application of methods through supervised laboratory and homework assignments and group projects. The courses tightly integrate basic biomedical informatics methods and approaches with relevant application domains. Courses in this series include Artificial Intelligence Methods I (BIOINF 2119, Research Methods 1), Artificial Intelligence Methods II (BIOINF 2120, Research Methods 2), and Human Computer Interaction and Evaluation (BIOINF 2121, Research Methods 3).

Research Skills series courses provide a comprehensive and incremental approach toward learning skills of scientific inquiry in biomedical informatics. Courses in this series are taken in sequence and build on one other, culminating in a completed research manuscript and oral presentation midway through the second year. They include BIOINF 2032 Biomedical Informatics Journal Club, BIOINF 2014 Biomedical Informatics Project Course, and BIOINF 2134 Publication and Presentation in Biomedical Informatics.

With the new core curriculum in place, the faculty will increasingly turn to enhancing the electives offered in the department. Existing upper-level didactic courses will be turned into graduate seminars, providing students with more opportunities to develop their scholarly skills. Furthermore, new electives in areas such as translational bioinformatics, clinical research informatics, and global health informatics are planned.

DBMI students are finding the new curriculum to be challenging but well conceptualized. Frank M. Ligons, a second-year doctoral fellow, feels that although the core structure is more rigorous, "it is the responsible thing to do. As students, we need these foundational courses for a strong grounding in the field and to cultivate the professional well roundedness that students of an established biomedical informatics program should possess. Navigating these requirements opens up new vistas of interest, all pursuable through a growing array of elective courses."

Ligons suggests that "courses like Applied Medical Informatics encourage us to extend beyond the ivory tower to touch everyday folks outside of our research community. We experience both theoretical and applied training, allowing both types of trainees to thrive." He states in conclusion, "In this highly interdisciplinary program, DBMI graduates train as bridge builders, facilitating new synergies among a wide variety of stakeholders. The celebration of team science is embedded in the course work and the culture of DBMI."

#### Department Grant Support, Direct and Indirect

lew Grants Since May 2010 • Total New Funding: \$8,166,861

Faculty	Grant Description	Program Start Date	Program End Date	TOTAL PER Direct	IOD Indirect	Total Award
Michael Becich, MD, PhD	Core Oncology Informatics Services	08/01/10	07/31/15	\$986,855	\$508,230	\$1,495,085
Michael Becich, MD, PhD	Bioinformatics Core for the National Functional Genomics Center	07/16/10	08/15/11	\$198,020	\$101,980	\$300,000
Michael Becich, MD, PhD	Gynecologic Cancer Center at Walter Reed Medical Center	11/01/10	04/30/15	\$2,027,358	\$1,044,089	\$3,071,447
Steven Handler, MD, PhD	Enhancing the Detection and Management of Adverse Drug Events in the Nursing Home	05/01/10	04/30/14	\$1,426,895	\$565,719	\$1,992,614
Xia Jiang, PhD	Detecting Genome Wide Epistasis with Efficient Bayesian Network Learning	09/30/10	09/29/15	\$681,078	\$245,922	\$927,000
Shyam Visweswaran, MD, PhD	Recovery-Computational Thinking to Support Clinicians and Biomedical Scientists	09/27/10	09/26/11	\$255,631	\$125,084	\$380,715
			Total	\$5,575,837	\$2,591,024	\$8,166,861

#### DBMI Publications Primary Faculty, Fellows, and Staff (July–December 2010)

Becich MJ, Berman J, Kang HP. "The tissue microarray OWL Schema: An open source tool for sharing tissue microarray data." *Journal of Pathology Informatics*. 2010 Jul 14;1:9.

Wilson RA, Chapman WW, DeFries SJ, Becich MJ, Chapman BE. "Automated ancillary cancer history classification for mesothelioma patients from free-text clinical reports." *J Pathol Inform.* 2010;1:24.

Landis Lewis Z, Douglas G, Monaco V, Crowley RS. "Touchscreen Task Efficiency and Learnability in an Electronic Medical Record at the Point-of-Care." 13th World Congress on Medical and Health Informatics Medinfo 2010, Cape Town, South Africa, September 12–15, 2010 *Stud Health Technol Inform.* 2010;160:101-5 (Second Place, Best Student Paper, Sep. 2010).

Crowley RS, Gryzbicki D, Legowski E, Wagner L, Castine M, Medvedeva O, Tseytlin E, Jukic D, Raab S. "Use of a Medical ITS Improves Reporting Performance among Community Pathologists." 10th International Conference on Intelligent Tutoring Systems: Bridges to Learning (ITS 2010), Carnegie Mellon University, Pittsburgh, PA, June 14-18, 2010 *Computer Science Intelligent Tutoring Systems Lecture Notes in Computer Science, 2010*, Volume 6094/2010, 338-348 [PubMed in process].

Lui K, Hogan WR, Crowley RS. "Natural Language Processing Methods and Systems for Biomedical Ontology Learning." *J Biomed Inform*. 2010 Jul 17. [Epub ahead of print] PMID: 20647054 [PubMed in process].

Liu K, Chapman WC, Savova G, Chute C, Sioutos N, Crowley RS. "Effectiveness of Lexico-Syntactic Pattern Matching for Ontology Enrichment with Clinical Documents." In press: *Methods of Information in Medicine*, Oct 2010.

Bigbee W, Zeng X, Hood BL, Sun M, Conrads T, Day RS, Weissfeld JL, Siegfried JM. "Lung Cancer Serum Biomarker Discovery Using Glycoprotein Capture and Liquid Chromatography Mass Spectrometry," *J Proteome Res.* Oct 8, 2010. [Epub ahead of print] PMID: 20931982 [PubMed in process].

Hochheiser H, Borromeo C, Schmandt LM, Desai KV, Stefanko M, Becich MJ, Murray J, Marazita ML. "The FaceBase Management and Coordination Hub: Development and Design Principles for a Translational BioInformatics Data Portal." 2011 AMIA Summit on Translational Bioinformatics; Mar 7–9, 2011; San Francisco, CA.

Wentz B, Hochheiser H, Lazar J. "Email usability for blind users." Designing Inclusive Interactions (Proceedings of the 2010 Cambridge Workshop on Universal Access and Assistive Technology); London: Springer-Verlag; 2010. p.197-206 (in press).

Sauer G, Holman J, Lazar J, Hochheiser H, Feng J. "Accessible Privacy and Security: A Universally Usable Human-Interaction Proof." *Universal Access in Information Society* epub Mar 2010 doi:10.1007/s10209-009-0171-2. 2010; 9 (3):239-248.

Desai KV, Borromeo C, Stefanko M, Schmandt LM, Pople A, Becich MJ, Murray J, Marazita ML, Hochheiser H. "FaceBase: Using the Drupal Content Management Software (CMS) as a framework for OMICS/Imaging-based collaboration." Poster session presented at: 2010 Pathology Informatics Sep 19–22, 2010. Boston, MA.

Aspinall SL, Zhao X, Handler SM, Stone RA, Kosmoski JC, Libby EA, Francis SD, Goodman DA, Roman RD, Bieber HL, Voisine JM, Jeffery SM, Hepfinger CA, Hagen DG, Martin MM, Hanlon JT. "The quality of Warfarin prescribing and monitoring in Veterans Affairs nursing homes." *Journal of the American Geriatrics Society.* 2010;58:1475-1480. PMID: 20662956. PMCID:PMC2955176.

Hanlon JT, Handler SM, Aspinall SL. "Program to improve prescribing of primarily renally cleared oral medications in older Veteran Community Living Center patients." *Federal Practitioner*. 2010;27(10):34-36.

Jiang X, Cooper GF. "A Bayesian spatio-temporal method for disease outbreak detection." *Journal of the American Medical Informatics Association*; Jul-Aug; 17(4):462-71 (2010). PMCID: 20595315.

Visweswaran S, Angus DC, Hsieh M, Weissfeld L, Yealy D, Cooper GF. "Learning patient-specific predictive models from clinical data." *Journal* of Biomedical Informatics, Oct; 43(5):669-85 (2010). PMCID: 20450985.

Visweswaran S, Cooper GF. "Learning Instance-Specific Predictive Models." *Journal of Machine Learning Research* (to appear).

Cooper GF, Hennings-Yeomans P, Visweswaran S, Barmada M. "An efficient Bayesian method for predicting clinical outcomes from genome-wide data." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Visweswaran S, Mezger J, Clermont G, Hauskrecht M, Cooper GF. "Identifying Deviations from Usual Medical Care using a Statistical Approach." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Hauskrecht M, Valko M, Batal I, Clermont G, Visweswaran S, Cooper GF. "Conditional Outlier Detection for Clinical Alerting." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Jiang X, Barmada M, Visweswaran S, Cooper GF. "A Fast Algorithm for Learning Epistatic Genomic Relationships." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Visweswaran S, Angus DC, Hsieh M, Weissfeld L, Yealy D, Cooper GF. "Learning patient-specific predictive models from clinical data." *Journal of Biomedical Informatics*; Oct 2010; 43(5):669-85. PMCID: 20450985.

Visweswaran S, Cooper GF. "Learning Instance-Specific Predictive Models." *Journal of Machine Learning Research* (to appear).

Visweswaran S, Mezger J, Clermont G, Hauskrecht M, Cooper GF. "Identifying deviations from usual medical care using a statistical approach." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Wang J, Day R, Visweswaran S, Hogan W. "The use of semantic distance metrics to support ontology." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Jiang X, Neapolitan RE, Barmada MM, Visweswaran S, Cooper GF. "A fast algorithm for learning epistatic genomic relationships." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Cooper GF, Hennings-Yeomans P, Visweswaran S, Barmada MM. "An efficient Bayesian method for predicting clinical outcomes from genome-wide data." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

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

Hauskrecht M, Valko M, Batal I, Clermont G, Visweswaran S, Cooper GF. "Conditional outlier detection for clinical alerting." *Proceedings of the Fall Symposium of the American Medical Informatics Association* (Nov 2010).

Boyce R, Harkema H, Conway M. "Leveraging the Semantic Web and Natural Language Processing to Enhance Drug-mechanism Knowledge in Drug Product Labels." *Proceedings of the 2010 ACM International Health Informatics Symposium*. Arlington, VA. Nov 2010.

Salangsang JA, Harrison LH, Brooks MM, Shutt KA, Saul MI, Muto CA. "Patient-associated risk factors for acquisition of methicillin-resistant Staphylococcus aureus in a tertiary care hospital." *Infection Control Hospital Epidemiology*. Nov 2010;31(11):1139-47. PubMed PMID: 20923281.

Regueiro M, Rodemann J, Kip KE, Saul M, Swoger J, Baidoo L, Schwartz M, Barrie A, Binion D. "Physician assessment of ulcerative colitis activity correlates poorly with endoscopic disease activity." *Inflammatory Bowel Disease*. Sep 1, 2010. [Epub ahead of print] PubMed PMID: 20812333.

Lavsa SM, Fabian TJ, Saul MI, Corman SL, Coley KC. "Influence of medications and diagnoses on fall risk in psychiatric inpatients." *Am J Health System Pharmacy.* Aug 2010;67(15):1274-80. PubMed PMID: 20651318.

Eisenberg DP, Wey J, Bao PQ, Saul M, Watson AR, Schraut WH, Lee KK, James Moser A, Hughes SJ. "Short- and long-term costs of laparoscopic colectomy are significantly less than open colectomy." *Surgical Endoscopy.* Sep 2010;24(9):2128-34. PubMed PMID: 20174941.

Chang G, Xu S, Dhir R, Chandran U, O'Keefe D, Greenberg NM and Gingrich JR. "Hypoexpression and epigenetic regulation of candidate tumor suppressor gene CADM-2 in human prostate cancer." 2010, *Clin Cancer Res*.16:5390-5401.

Boyce R, Harkema H, Conway M. "Leveraging the Semantic Web and Natural Language Processing to Enhance Drug-mechanism Knowledge in Product Labels." *Proceedings of the 1st ACM International Health Informatics Symposium*. Arlington, VA. 2010.

Harkema H, Chapman WW, Mehrotra A. "Natural Language Processing for Evaluating the Quality of Colonoscopy Procedures." *Proceedings of the American Medical Informatics Association (AMIA) Annual Symposium 2010.* Washington, DC. 2010.

Mowery DL, Harkema H, Chapman BE, Hwa R, Wiebe J, Chapman WW. "An Automated SOAP Classifier for Emergency Department Reports." *Proceedings of the American Medical Informatics Association (AMIA) Annual Symposium 2010*. Washington, DC. 2010.

Mowery D, Schleyer T, Harkema H, Chapman W. "Developing a Discourse Model for Charting Dictated Dental Exams." American Association for Dental Research Annual Meeting 2010. San Diego, CA. 2010. Submitted.

Chapman W, Conway M, Dowling J, Tsui R, Li Q, Christensen L, Harkema H, Sriburadej T, Espino JU. "Challenges in Adapting an NLP System for Real-time Surveillance." 9th Annual Conference of the International Society for Disease Surveillance. Park City, UT. 2010.

### FACULTY FEATURE

### Xinghua Lu, MD, MS, PhD

(Lu) calls his biomedical informatics training "a career-changing experience, because without it, I wouldn't be able to embark on what I'm doing now. My two years at DBMI were some of the best years of my professional life to date."



Translational Systems Biology Group (left to right): Hatice Osmanbeyoglu, Xinghua Lu, Vicky Chen, Lujia Chen, and Songjian Lu.

Xinghua Lu, MD, MS, PhD, has returned to the University of Pittsburgh Department of Biomedical Informatics (DBMI) as a visiting associate professor. Lu received his MD and MS in clinical research in the 1980s in China, where he worked in the Shandong Provincial Hospital academic medical center for nine years. While there, he received a grant for evaluation of thrombolytic therapy for unstable angina from the Shandong Province Health Department.

Lu began his research career in basic biomedical sciences at the University of Connecticut Health Center, where he was awarded a PhD in pharmacology in 1998. He then worked as a postdoctoral research associate in the University of Pittsburgh Department of Pharmacology and Chemical Biology. His research output included eight journal articles in cellular signal transduction systems and biophysics.

An interest in studying disease mechanisms and developing drug treatments using systems biology approaches led Lu to become a National Library of Medicine postdoctoral fellow from 2001 to 2003 in what was then the Center for Biomedical Informatics at the University of Pittsburgh. His research interests included bioinformatics, artificial intelligence, and machine learning. He calls his biomedical informatics training "a careerchanging experience, because without it, I wouldn't be able to embark on what I'm doing now. My two years at DBMI were some of the best years of my professional life to date, especially working with Drs. Vanathi Gopalakrishnan, Gregory Cooper, Milos Hauskrecht, Roger Day, and Bruce Buchanan." He also remembers the collaborative aspect of the training program with Carnegie Mellon University as an advantage.

Lu then moved on to become a faculty member in what is now the Division of Biostatistics and Epidemiology at the Medical University of South Carolina. He was an associate professor in the Department of Biochemistry and Molecular Biology and served as director of the bioinformatics research and education programs for four years. Lu's research focuses on developing computational methodologies for automatically mining and discovering biomedical knowledge from large volumes of biomedical literature and data in order to provide systematic perspectives for understanding physiological and pathological processes. Examples include statistical text mining for protein annotation and systems biology statistical models in signal transduction systems.

Lu hopes to utilize his cross-disciplinary expertise in DBMI to further research in translational bioinformatics because "highthroughput technology requires bioinformatic techniques to assist data usage in clinical disease outcomes research and biomarker identification." He says it is exciting to see the active research in this area currently in the department, and that level of productivity in translational bioinformatics is one of the main reasons he has decided to return to DBMI.

To Lu, translational bioinformatics approaches such as "nextgenerational sequencing will be huge for studying individual genome variations in personalized medicine as well as to studying disease mechanisms" at the systems level. He also hopes to teach courses in machine learning, bioinformatics, and systems biology.

In addition to his teaching and research interests, Lu's professional activities include being a standing panel member of the Biomedical Library Information and Research Committee study section of the National Institutes of Health and an editorial board member of the journal *Open Systems Biology*.

### Q&A with Gerry Douglas (MSIS '99, PhD '09)

#### Q: How did you get started in biomedical informatics?

A: My first exposure to working with medical information was as a volunteer in Malawi in 1996. I worked with the Ministry of Health and provided technical assistance in producing an annual report describing the state of the health of the nation compiled from data submitted from roughly 700 health facilities across the country. After leaving Malawi, I moved to Pittsburgh to be with my then fiancée, Thuy, and learned about what was then called the Center for Biomedical Informatics at the University of Pittsburgh. I started my training in biomedical informatics in 1998 under the umbrella of a master's degree in information science with an area of concentration in medical informatics. In 2000, Thuy and I created Baobab Health, a not-for-profit organization aimed at improving health care in Malawi through medical informatics. Through Baobab, I applied lessons learned in my training to conceptualize the Baobab touch screen system.

### Q: What have you been doing since completing your PhD in the Department of Biomedical Informatics (DBMI)?

A: Since completing my PhD in April 2009, I've been occupied with both technical and governance issues within Baobab. On the technical side, I've been researching ways to make our system more off the shelf so that others can replicate our work should they choose to do so. On the governance side, I've been focusing on learning how to be an effective trustee, something with which I have little experience. In November 2010, I officially joined the Department of Biomedical Informatics as an assistant professor and took up the position of director of the Center for Health Informatics for the Underserved, a newly established center addressing the challenges of delivering health care in low-resource settings, both within the United States and internationally.



Sister Elise Mambala talks with Gerry Douglas about changes in pediatric workflow at Kamuzu Central Hospital.

### Q: What do you see as the difference between biomedical informatics and information technology?

A: A biomedical informatics system has to add value; it can't just be a system reporting information.

"...the most influential part of



my education at DBMI was gaining an understanding and appreciation for Charles Y. Friedman's proposed fundamental theorem of informatics (doctor + computer > doctor alone) ... This has greatly influenced my work in building point-of-care systems in Malawi."

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

A: I think the most influential part of my education at DBMI was gaining an understanding and appreciation for Charles Y. Friedman's proposed fundamental theorem of informatics (doctor + computer > doctor alone) at an early stage, then framing subsequent classes in that context. This has greatly influenced my work in building point-of-care systems in Malawi.

### Q: What are some of your more memorable moments from your time at DBMI?

A: From my early days in the training program, there are two things that I think I will always remember. I recall sitting in my first class (Evaluation Methods in Medical Informatics, with Charles Y. Friedman, now chief scientific officer for the Office of the National Coordinator for Health Information Technology in the U.S. Department of Health and Human Services) and feeling like I was the only one who didn't get it. I was surrounded by students with backgrounds in medicine who seemed to have no trouble dealing with the medical terminology and who managed to summarize weekly reviewed journal papers in a matter of minutes when it typically took me four to six hours. I wondered at the time if I had made a poor decision in pursuing medical informatics. Fortunately, I didn't give up. In a subsequent class (Probabilistic Methods for Computer-based Decision Support, with Greg Cooper) I remember successfully completing a complex programming assignment that took me roughly 40 hours, during which I taught myself a new programming language. I recall many students struggled to complete the assignment and I realized that my background in computer science would serve me well in a career in medical informatics.



## University of Pittsburgh

School of Medicine Department of Biomedical Informatics Parkvale Building, M-183 200 Meyran Avenue Pittsburgh, PA 15260





### Q&A with Gerry Douglas continued from page 5



### Douglas discusses challenges in using the patient registration system with clerks Winstone Mabunya and Mercy Phambala at Kamuzu Central Hospital.

### Q: What advice would you give to current PhD students in the training program?

A: In terms of advice, I can certainly echo some advice I was given as a PhD student, which went something like this: Take whatever dissertation topic you are considering and make it 10 times smaller. Then divide it in half and pick the easier half. If you do this, you might finish in four years.

#### Q: What are your continuing research interests?

A: My current research interests relate to abstracting the work we have done in Malawi to the point that we can apply it more generally to low-resource settings not specifically limited to the developing world.

www.dbmi.pitt.edu