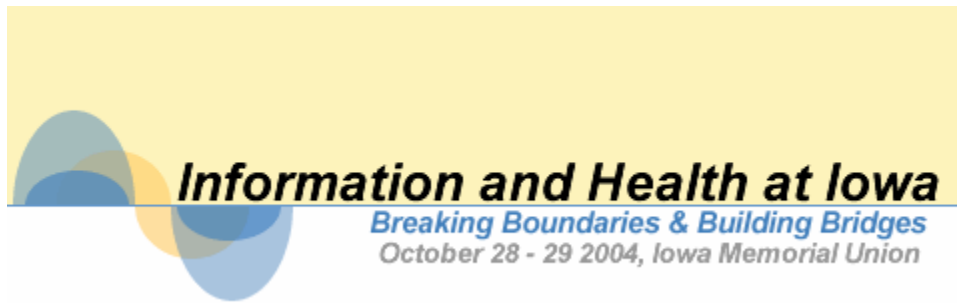


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- 2 Andreas Beyer  
Gene Expression Profiling Of Potential Ppar Target Genes In Mouse Aorta Under Different Physiological Conditions
- 3 Jared Bischof  
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## Poster Abstracts

### Students

#### 1. **Greg Alexander** MHA, RN

Department of Health Management and Informatics  
Sinclair School of Nursing  
University of Missouri, Columbia

Evaluating standardized assessment measures in Nursing Home Compare

Nursing homes have a long history of mandates from Congress to improve quality of care (Committee on Nursing Home Regulation, 1986). The Omnibus Reconciliation Act of 1987 (OBRA '87) included provisions to improve nursing home care. These provisions included developing The Minimum Data Set for Resident Assessment and Care Screening (MDS). Nursing Home Compare (NHC), a national database, is a tool available to researchers, consumers, and nursing home facilities at [www.medicare.gov](http://www.medicare.gov). This study evaluated nursing home facility QM scores, obtained from the NHC national database, in Missouri. Staffing measures, number of hours/resident/day, for RNs, LVNs, and CNAs were evaluated to determine differences in QMs associated with staffing levels.

Statistical measures in 3 QMs revealed differences in-group means: Two chronic, 1) residents who lose bowel control, 2) residents whose need for help with daily activities increased, and one post-acute, 3) short stay residents with moderate to severe pain, revealed differences in means of CNAs and RN/LPN groups, respectively. ANOVA results measuring low risk residents who lose bowel control indicated significant differences in CNA groups  $F(2, 318) = 3.94, p < .05$ . ANOVA for residents whose need for help with daily activities showed significant main effects in the RN and LPN groups,  $F(2, 374) = 3.48, p = .032$  and  $F(2, 374) = 3.45, p = .033$ , respectively. Finally, ANOVA for short stay residents with moderate to severe pain, indicated significant differences in LPN groups,  $F(2, 231) = 4.74, p = .01$ . ANOVA with the covariate, number/residents/facility, was investigated to determine if differences exist in-group means analyzed previously. The only significant interaction with number/residents/facility occurred in short stay residents who had moderate to severe pain ( $p = .001$ ).

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#### 2. **Andreas Beyer**

Graduate Student Genetic Ph.D. program

## Gene Expression Profiling Of Potential Ppar $\gamma$ Target Genes in Mouse Aorta under Different Physiological Conditions

Henry L. Keen<sup>1, 2</sup>, Michael J. Ryan<sup>1</sup>, Andreas Beyer<sup>1</sup>, Satya Mathur<sup>1</sup>, Carmen M. Halabi<sup>1</sup>, Todd E. Scheetz<sup>2</sup>, Barry D. Gackle<sup>2</sup>, Frank M. Faraci<sup>1</sup>, Thomas L. Casavant<sup>2</sup> and Curt D. Sigmund<sup>1</sup>

<sup>1</sup>Departments of Internal Medicine and Physiology & Biophysics and the <sup>2</sup>Center for Bioinformatics and Computational Biology University of Iowa College of Medicine Iowa City, IA 52242

Endothelial dysfunction, which develops in diabetic or chronically hypertensive patients, is thought to contribute to the progression of atherosclerosis, carotid artery disease, and stroke. Peroxisome proliferator activated gamma (PPAR $\gamma$ ) is a ligand activated transcription factor that has become an exciting research subject among many biological disciplines. PPAR $\gamma$  is particularly well studied with regard to its role in stimulating lipid metabolism and cancer. A group of drugs used to treat patients with non-insulin dependent diabetes mellitus (NIDDM), the Thiazolidinediones (TZDs) have been shown to bind to PPAR $\gamma$  with high affinity, thus demonstrating that PPAR $\gamma$  may play an important role in the pathophysiology of NIDDM.

Two separate dominant negative point mutations (P467L and V290M) in the human PPAR $\gamma$  are associated with an attenuation of PPAR $\gamma$  transcriptional activity. Patients with one of these mutations present severe insulin resistance and early onset hypertension. Interestingly, PPAR $\gamma$  is expressed in vascular endothelium and smooth muscle, suggesting a potentially important role for PPAR $\gamma$  in the regulation of vascular function and blood pressure. Additionally, activation of PPAR $\gamma$  by treatment with TZDs has been reported to lower blood pressure in patients with NIDDM. We recently demonstrated that treatment of hypertensive transgenic mice with TZDs show blood pressure improvement and impaired endothelial function. Additionally, PPAR $\gamma$  activation can inhibit the release of vasoconstrictors such as endothelin, stimulate the release of vasodilators such as c-natriuretic peptide, and nitric oxide (NO).

Since PPAR $\gamma$ 's role in the endothelium for the regulation of vascular function and blood pressure is not well understood, we generated three different mouse models expressing wt and the two dominant negative versions of PPAR $\gamma$  in the vascular endothelium to evaluate this mechanism and specifically dissect PPAR $\gamma$ 's significance in the endothelium from the vascular smooth muscle. Additional micro array studies are used to evaluate Novel target genes of PPAR $\gamma$  in the vasculature.

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**3. Jared Bischof**, Electrical Engineering, Computational Laboratory for Computational Genomics

Title:  
Identifying Pseudogenes Involved with Gene Conversion and Disease

Authors:  
Jared M. Bischof, Annie P. Chiang, Ed Stone, Val C. Sheffield, Thomas L. Casavant, Todd E. Scheetz, Terry A. Braun

**Abstract:**

Pseudogenes are remnants of gene duplication (unprocessed pseudogenes) and retrotransposition (processed pseudogenes) events. Recent studies have identified approximately 19,537 total pseudogenes in the human genome.

Pseudogenes have been identified to be involved in gene conversion events that lead to disease. The goal of my research is to identify additional pseudogenes involved in similar and related processes. Unprocessed pseudogenes that are derived from a gene duplication event are identified to evaluate their possible connection with disease. Identification of unprocessed pseudogenes involved with this mechanism is determined by searching for homology and proximity to the functional genes from which the pseudogene was copied. The locations of these gene/pseudogene pairs will then be compared to the loci of known disease genes and may be used to nominate disease genes.

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**4. Rong C. Guo**, Graduate Research Resident

Title: Computational Detection of Important Genetic Regulatory Sequences Using Comparative Analysis

**Acknowledgements:**

Thomas L. Casavant, Terry A. Braun, Henry L. Keen and Curt D. Sigmund.

**Abstract:**

Diminished activity of the transcription factor PPAR gamma (PPAR $\gamma$ ) has been suggested to play a role in hypertension and vascular dysfunction. The downstream actions of PPAR $\gamma$ , like other transcription factors, depend on binding to a specific DNA sequence and then activating/repressing transcription of target genes. We recently demonstrated using microarray analysis that chronic activation of a PPAR $\gamma$  agonist elicits changes in numerous pathways (181 genes) in mouse aorta. To prioritize this list of genes so that experimental efforts are directed toward the best candidates, we used a computational approach to screen the regions upstream of 142 of these genes for binding sites for PPAR $\gamma$  and for two transcription factors regulated by PPAR $\gamma$ , hypoxia-inducible factor 1 (HIF), and BHLHB2. All upstream sequences (5 kb) were downloaded from Ensembl. We found numerous binding sites for PPAR $\gamma$  (117), HIF (490), and BHLHB2 (105).

Because sequences that are highly conserved among different species are likely to be enriched for biological important sequences, we then obtained local alignments across human and mouse species. This allowed us to reduce the number of potential binding sites (and target genes) to less than 10 (PPRE=2, HIF=6, and BHLHB2=1). These high priority candidate PPAR $\gamma$  target genes include frizzled 4 (FZD4), BHLHB2, clusterin, and secreted frizzled related protein 2 (Sfrp2). Recent studies in human patients have provided evidence that lack of FZD4, a member of the Wnt-signaling pathway, impairs normal retinal vascularization. BHLHB2 is a basic helix-loop-helix (bHLH) transcription factor and has been suggested to be involved in the control of proliferation and/or differentiation of several cells including nerve cells, fibroblasts and chondrocytes. Clusterins are molecular chaperones that prevent the amorphous aggregation and precipitation of target proteins under stress conditions and may be involved in Alzheimer's, Creutzfeldt-Jakob and Parkinson's diseases. Sfrp2 has been reported to

induce cellular resistance to apoptosis, which in turn promotes tumorigenesis. Thus, by integrating computational approaches with comparative genomic techniques we were able, in a non-biased manner, to significantly narrow the list of potential PPAR $\gamma$  target genes. Experimental studies are currently underway to determine the physiological significance of these findings to vascular function.

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## 5. Kevin Jenner, Biomedical Engineering, The University of Iowa

Title: EST Processing Pipeline with Data Cataloging and Backup System

Mike Smith, Chris Moressi, Barry Gackle, Todd Scheetz, Ph.D., Brian O'Leary, Dylan Tack, Tom Casavant, Ph.D.

### Summary Abstract:

The EST Processing Pipeline is the primary data collection system for the Center for Bioinformatics and Computational Genomics at The University of Iowa. This pipeline provides the critical link for first-hand research data collection between the genomics laboratories at the Oakdale Research Campus and the research facility in Iowa City. Processing involves taking raw data files from ABI-sequencer machines generated by processing mRNA from selected tissues in selected species of organisms and converting that data into human-readable, statistically useful data for further genomic pattern analysis and gene-related disease research. Since this data is of critical importance to the lab, the EST Processing Pipeline also employs extensive data backup and long-term storage processes to preserve data and research integrity for decades to come.

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## 6. Krishna R. Kalari, Coordinated Laboratory for Computational Genomics

Krishna R. Kalari<sup>1</sup>, Todd E. Scheetz<sup>2,5</sup>, Terry A. Braun<sup>1,3,5</sup>, Thomas L. Casavant<sup>2,3,4</sup>

<sup>1</sup> Coordinated Laboratory for Computational Genomics, <sup>2</sup> Center for Bioinformatics and Computational Biology, <sup>3</sup> Department of Biomedical Engineering, <sup>4</sup> Department of Electrical and Computer Engineering,

<sup>5</sup> Department of Ophthalmology The University of Iowa, Iowa City, Iowa, USA. 52242.

Short Tandem Repeat Polymorphisms (STRPs), also known as micro satellites or simple sequence-length polymorphisms (SSLPs) are spread throughout mammalian genomes. The polymorphic nature of these repeats makes them powerful tools for mapping studies, disease diagnosis and other applications in understanding human disease. The presence of STRPs in coding and regulatory regions has been shown to alter transcriptional activity in some cases. We developed the Short Tandem Repeat data bank (STRPdb) as an integrated tool to provide STRP-related information to interested researchers. This information includes human-mouse-rat conservation, GC content, association with CpG islands, and the location of STRPs with respect to a number of other gene- and/or genome-related features (such as UTR, exon, intron or intergenic regions). The goal of this database is to provide an integrated STRP resource that may be used in identification and prioritization of candidate genes for mutation screening, and may also be helpful for evolutionary studies. This database was developed using a suite of computational

programs developed specifically for this project. It consists of all predicted dimer to hexamer repeats (501 distinct sequences) for different species. A web interface allows users to query all attributes of the STRP elements in different genomes.

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**7. Ling-Hua Lin**, Doctoral Student, College of Nursing, ling-hua-lin@uiowa.edu

Applying decision tree classification method to improve performance of screening scale: using the Geriatric Depression Scale as test case

Ling-Hua Lin, Doctoral Student, College of Nursing, ling-hua-lin@uiowa.edu  
Connie Delaney, Professor, College of Nursing, connie-delaney@uiowa.edu

The scale measurement method has been applied across specialties in both clinical practice and research. Traditionally, a cut-off point is used to differentiate cases and non-cases when applying a multi-item scale in screening a problem, for example geriatric depression. However, by using a total score, each individual item contributes equally to the screening performance even if certain items in the scale were more crucial. The purpose of this study was to apply a classification method of data mining, decision tree, to improve the performance of screening scales. The study was a secondary data analysis of depression screening data from cancer inpatients using Geriatric Depression Scale (GDS). The J48 pruned decision tree and analysis of Receiver Operating Characteristic (ROC) curve were proceeded by using the DSM-IV diagnosis as a golden standard. The validity of screening based on decision tree and different cut-off points was examined. Among 30 items of GDS, 14 were selected to build the decision tree with size 41 and 21 leaves. The accuracy of decision tree was 93.4% with a sensitivity of 85.7% and a specificity of 97.5%. The decision tree classification outperformed the cut-off point classification regardless of using the original cut-off point or the optimal cut-off point of ROC curve. The decision tree classification method seems to be useful in developing an optimal screening scale. It contributes to correct classification so that errors of judgment can be reduced and patient safety will be enhanced. Moreover, the possibility of applying the algorithms of decision tree analysis in computerized decision support systems within the Electronic Health Record (EHR) merits further investigation.

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**8. Christopher J. Moressi**, Graduate Research Assistant

Title: In Vitro Analysis of Feline Immunodeficiency Virus Vector Integration

Author name(s): Christopher J. Moressi, Yubin Kang, Litao Xie, Diane Thi Tran, Beverly L. Davidson, Todd E. Scheetz, Paul B. McCray Jr.

E-mail address: cmoressi@engineering.uiowa.edu

Abstract:

Currently, nothing is known regarding the integration preferences of non-primate lentiviral vectors derived from feline immunodeficiency virus (FIV) in human or murine cells. It was discovered in our study that FIV closely corresponded with the integration preferences of HIV. A total of 132 integration sites into the human genome were mapped in our study

and analyzed according to gene locality, go terms, and physics properties of flanking sequence. Approximately 68% of the FIV integrations events occurred within a RefSeq transcript and introns regions were preferred of exon regions. Of the 90 RefSeq genes targeted, 50 were represented on a publicly available HepG2 microarray data set. The median expression level for these 50 genes was ~6.3-fold higher than that of all the genes on the array, demonstrating that FIV integration favors actively transcribed genes. Furthermore FIV integrations occurred throughout the whole RefSeq transcript which is similar to the integration preference of HIV. These data suggest that while FIV integration preferences are more similar to HIV than to MLV, significant differences exist between FIV and HIV vectors.

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**9. Brian M O’Leary**, Masters Student in Electrical and Computer Engineering  
Graduate Research Assistant, [brian-oleary@uiowa.edu](mailto:brian-oleary@uiowa.edu)

Title:  
A Machine Learning Approach to Optimizing Annotation Parameters in the PAR Algorithm

Authors:  
Brian M O’Leary, Thomas L Casavant, Todd E Scheetz, Terry A Braun

Affiliation:

Abstract:  
The process of screening for disease-causing sequence mutations typically requires the examination of sub-regions of genes. Normally the entire coding region of a gene is examined from the first exon continuing until the entire gene has been screened. Previous work has shown that screening a prioritized sub-region of a gene is more efficient than exhaustively screening the entire gene. The gene attributes used to prioritize these sub-regions of genes, combined with parameters assigned to each attribute, are used in a calculation called Prioritization of Annotated Regions (PAR). While we have shown this approach to be more efficient than previous methods, it has not been optimized based on available attributes. This research aims to improve the PAR calculation and accelerate mutation identification by using known mutations with sequence-based annotation and machine learning algorithms to optimize the parameters assigned to each attribute. Our hypothesis is that there are optimal PAR parameter values that will increase the efficiency in using sequence attributes to find disease-related mutations.

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**10. Eun Jun Park**, Predoctoral Student  
College of Nursing  
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Internet Health Information and Health Behavior

Purpose: The purpose of this study was to understand current use of Internet health information and to examine its relationship to four health behaviors: smoking cessation, abstaining or restraining from drinking alcohol, weight control, and exercise.

Method: Two hundred and seventy-three university students were selected by a convenient sampling and surveyed in Korea in 2002. The questionnaire was developed for the purpose of this research.

Results: Approximately 67% of the respondents used Internet health information. Among these Internet health information users, 30% regarded Internet health information as a major source of health information. In order to access Internet health information, 53% used “search words” in general search engines.

Information on diet and nutrition, exercise and physical training, diseases, and sex were accessed by 25%, 23%, 16%, 14% of students respectively. Internet health information users on diet and nutrition were more likely to try to control their body weight than non-users of the related information ( $p < .001$ ). However, there is no evidence to support that Internet health information users, on smoking cessation, abstaining or restraining from drinking alcohol and exercises, used the related information to change their health behaviors.

Conclusion/ Discussion: Internet health information can replace or supplement the current function of health education considering a huge number of Internet users and technical development. However, this study shows that Internet health information does not influence effectively on our health behaviors. A cyber space through the Internet can be utilized in a various stages in order to deliver knowledge and to help people adopt a better health behavior. Nurses have played an important role as a health educator for a long time. Today, nurses need to learn current problems of Internet health information and develop effective strategies to improve utility of Internet health information.

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**11. Amit Paul**, Research Assistant, [akpaul@engineering.uiowa.edu](mailto:akpaul@engineering.uiowa.edu)

Authors

Amit Paul

Linda Boyle, PhD – Principle Investigator

[lnboyle@engineering.uiowa.edu](mailto:lnboyle@engineering.uiowa.edu)

Department

Human Factors and Statistical Modeling Lab (HFSM)

Department of Industrial Engineering, The University of Iowa

Title

Dimensions of Sleep and Driving Characteristics for Commercial Vehicle Drivers

Abstract

By 1990, motor vehicle crashes had become the third leading cause of death in the US and in 2000 alone, 41,800 people died and 3,219,000 were injured from vehicular crashes. To mitigate these high risks and enormous costs to society, it is important to discern which factors are crash risk predictors. Multivariate regression techniques were used to analyze factors related to driving, medical histories, sleeping habits, and drug and alcohol use for 406 commercial drivers. *Cluster Analysis* enabled the grouping of drivers with similar characteristics. Additional statistical analyses were then conducted among clusters to investigate the relationships of crashes to driver characteristics. The results

indicate a significant relationship of factors such as miles driven, driver age and drinking habits with crashes. The results of this study could be used in the formulation of traffic policies, and medical and educational interventions.

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**12. Xin Ying Qiu**, Graduate Student, Department of Management Sciences, University of Iowa, Email: xin-qiu@uiowa.edu

Title: Exploring Gene Cluster Coherence from a Text Perspective

Additional Authors:

Padmini Srinivasan, Associate Professor, School of Library and Information Science, University of Iowa, Email: padmini-srinivasan@uiowa.edu

Olivier Bodenreider, Staff Scientist, National Library of Medicine, Email: olivier@nlm.nih.gov

Kelly Zeng, Staff Scientist, National Library of Medicine, Email: zeng@nlm.nih.gov

Background and Purpose:

A typical strategy used in expression data analysis is to first identify clusters of genes that have similar expression patterns. Next one tries to describe each cluster's property using outside resources such as GO annotation and knowledge that resides in MEDLINE. In the second step, any approach that is used to generate descriptions of these expression clusters must be able to highlight the distinguishing "cohesive" characteristics of the clusters. Therefore, one way to compare the performance of alternative text-based approaches in describing gene clusters is to examine the extent to which the gene clusters are perceived "cohesive" from the text-based description approaches.

Methods and Results:

We first used two gold standard data sets where domain experts have already identified expression clusters of interest. We then examine the cohesiveness of each cluster as determined by the alternative text-based approaches. We defined the "cohesiveness" of a gene cluster as the intra-cluster similarity as perceived from free-text, Manjal, GO-basic, GO-expanded, and document-cooccurrence methods. Our findings suggest that GO-expanded method provides the view that brings out the most common features in the clusters.

Second, we assume that the gold standard gene clusters are not yet manually identified by domain experts. Instead, we will see if these text based approaches may be used to help identify interesting clusters. We used Eisen's gene sets and performed hierarchical clustering with different thresholds. We calculated Dunn's index (a measurement of clusters' compactness and separation) of each threshold for each of the text-based methods. This evaluation suggests free-text, Manjal, and GO-basic methods achieve similar pattern and higher Dunn's scores. These scores suggest that threshold 0.5 down to 0.1 are identified as better clustering results.

Finally, we wanted to know how the clustering results identified by the text-based approaches compare with the gold standard gene clusters. We calculated Rand's index for each threshold against Eisen's gold standard clusters. The results show that threshold

0.5 through 0.3 are the most similar to the gold standard, which is fairly consistent with the clustering results identified by the text-based methods.

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### **13. John Ritchison**, Student – Electrical and Computer Engineering

Title: Intrval: A Phenotype based genomic interval storage and viewing system

Authors: John Ritchison, Terry A. Braun, Thomas L. Casavant, Todd E. Scheetz

Email: [jritchis@engineering.uiowa.edu](mailto:jritchis@engineering.uiowa.edu)

#### Description:

Disease-oriented research often includes mapping of genome intervals that are associated or linked with a disease. This data is typically only accessible through thousands of journal articles in the scientific literature. Intrval is a resource to store, manage, and retrieve genetic interval related information. The goal of this project is to develop a database to store interval information for diseases along with corresponding phenotype information. The system is Java-based and allows the scientific community to upload and view data in the database. Each interval is associated with one or more publications. Basic operations (i.e. union, intersection) on intervals will allow researchers to refine intervals and genomic data interactively. Using the UCSC genome database, candidate gene lists for intervals (or sub-intervals) can be integrated. Extended analyses can be performed based upon multiple intervals with similar phenotypes, based upon the presence of similar genes (e.g., Paralogs, present in the same pathways, similar expression, etc).

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### **14. David F. Salazar**, Sophomore Industrial Engineering Student

Radiology Service Assistant at LaGrange Memorial Hospital for two years  
[david-salazar@uiowa.edu](mailto:david-salazar@uiowa.edu)

#### Digital Imaging for All Radiographic Studies

##### Purpose

Today, many radiology departments in hospitals all over the world are using the archaic method of developing radiographic films for performing radiology cases. For my poster proposal, I will explain the benefits of switching from the archaic method of developing radiographic films to a filmless radiology department and a picture archiving and communication system (PACS) (Goodman).

##### Poster Design

On my poster, I will be using the following items to display my ideas: an old, bent, and water damaged chest x-ray; new blank CDs for coping digital films; cost analysis of two systems; list of reason to switch (non- monetary reasons); pictures of old system including huge storage spaces needed to store films and pictures of new system.

##### Results

I am currently working with the Gerald T. Johnson, M.D.; the Suburban Radiologists; the Radiology Administration at LaGrange Memorial Hospital (LMH) in LaGrange, Illinois; Grant Square Imaging in Hinsdale, Illinois; and Glen Oaks Hospital in Glendale Heights, Illinois to collect my data and results. I will also be working with DuPage Radiologists and with Lutheran General Healthsystem in Park Ridge, Illinois.

#### Discussion and Conclusion

After my initial research, I have learned many reasons why switching from the archaic method of developing radiographic films to a filmless radiology department and a picture archiving and communication system is more beneficial for the following reasons:

- Avoid radiology retakes
- Less radiation exposure
- Radiographs can be read by a radiologist anywhere
- Increase in radiologist productivity
- Avoid delays due to radiology processor malfunction or low supply inventory
- Avoid delays due to the use of only one portable radiographic machine
- Save money from film storage, processor maintenance, films, developing fluid, cassettes to run films through the processor, and the film room staff.

#### References

Goodman, T.R. and McHugh, K.. Advances in radiology. Retrieved on from Archives of Disease in Childhood webpage October 4, 2004 from <http://adc.bmjournals.com/cgi/content/full/77/3/265>

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#### **15. Aditya Kumar Sehgal**

Student, The University of Iowa  
Dept. of Computer Science  
[sehgal@cs.uiowa.edu](mailto:sehgal@cs.uiowa.edu)

Title: Gene Terms with English Meanings: Facing the Retrieval Challenge

Padmini Srinivasan , Faculty, The University of Iowa  
School of Library and Information Science  
[padmini-srinivasan@uiowa.edu](mailto:padmini-srinivasan@uiowa.edu)

Introduction: Retrieving relevant documents for genes is a first step in many important applications such as information extraction and text mining. There are however many challenges associated with this task. One difficult aspect, which we address in this research, is negotiating ambiguity in gene nomenclature. In particular we focus on retrieval with gene terms that are also common English words. For example, TRAP, ART, ACT, are all gene symbols that also have English meanings. This kind of ambiguity makes retrieval of relevant information more difficult. We concentrate on ambiguous gene terms in the LocusLink database. LocusLink (<http://www.ncbi.nlm.nih.gov/projects/LocusLink/>) is a publicly available curated database, maintained by the National Center for Biotechnology Information (NCBI), that contains information, such as official name, aliases, products, etc., for over 200,000 genes related to different organisms.

Methods: In this paper we explore a variety of filtering methods that are applied to document sets retrieved by the ambiguous gene terms in LocusLink. Each filtering method is essentially a ranking strategy using a secondary ranking query to re-order the retrieved set. Our objective is to rank relevant documents higher than the non-relevant ones. We assess the quality of ranking using different IR measures. We also describe a process to automatically filter through relevant documents from the retrieved set for each gene.

Results and Conclusions: We find that using gene summary descriptions and product information available in the LocusLink records in addition to the gene term performs the best in terms of re-ranking the retrieved documents. Interestingly, a close competitor is derived from the product field alone. Using our filtering technique we find significant improvements in precision and F-score (a standard measure for such problems) for almost all gene terms we consider.

Implications: We now have an approach that may be used to counter the ambiguity in gene terms with English meanings during retrieval. The approach is also likely to be useful in other types of ambiguities such as homonymy and synonymy. We will test this in future research.

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**16. Michael F. Smith**, Email: [msmith@engineering.uiowa.edu](mailto:msmith@engineering.uiowa.edu)  
Department: Electrical & Computer Engineering, student

Co-authors: T.A. Braun, T.L. Casavant, T.E. Scheetz

Title: PrimerManager: An Oligonucleotide Primer Ordering and Management Interface

Abstract:

DNA primers are a key component to *in vitro* genetic experiments. The quantity of genetic regions of interest lends itself to the necessity of a large abundance of primer sequences to amplify DNA for experimental validation of functional genes. The sheer number of potentially useful primers prohibits maintaining a comprehensive collection of all possible primers. Instead, oligonucleotide primers are ordered as needed. Ordering and managing such a large and complex set of primers exceeds a simple 'pen and paper' book-keeping process for a researcher or lab technician. PrimerManager is a Java™ based application that is part of a disease gene screening system (the TrAPSS software suite) that allows users to optimally design, electronically order, and track primer reagents; beginning with the optimal sequence selection and design, and tracking each primer through the order being placed, received, used in experiments and eventually exhausted. This allows for a 'central hub' of information for each primer order in the TrAPSS system; circumventing extraneous materials and saving time by making the process a more automated task.

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**17. Gufeng Wang**, Graduate student, Chemistry department

Two-Dimensional Correlation for Peak Identification in DNA Analysis

Lei Geng\*

\*: Contact person, professor of Chemistry Department, University of Iowa. Email: lei-geng@uiowa.edu

The analysis of DNA sequence involves identification of peaks and subsequent assignment of the entire sequence. This project is to apply recently developed two-dimensional correlation techniques in DNA sequencing to increase the base-calling quality and reduce the sequencing cost. Two approaches are currently being investigated. Instrumentally, dynamic two-dimensional correlation electrophoresis collects the fluorescence signals with a sinusoidal perturbation in the excitation. Only one detection channel is required and the bases are differentiated based on the fluorescence lifetimes of the tagged dyes. The sensitivity of detection is enhanced and the cross-talk between channels is minimized. Plain, reliable identification of a sequence of 39 peaks has been demonstrated. Simplicity of two-dimensional cross-correlation results in peak identification that is easier to automate.

For sequencing data collected in conventional four-color detection, the low resolution and high noise in the end region of a trace restrict the yield of current base-callers. A new algorithm based on statistical two-dimensional correlation analysis is proposed to replace the current peak-location based callers. The trace is broken down into short segments representing different bases. The bases are then called based on the assumption that the physical existence of each oligonucleotide fragment is locally uniform. The number of bases is better estimated in the less-resolved region because all the data points within a peak are being examined. Noises are suppressed by considering all four channels of information in calculating the cross correlation. Preliminary result shows that the new algorithm has a comparable and even better accuracy than current top-of-the-line callers.

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**18. Phil Wynn**, M2, Phillip-wynn@uiowa.edu  
Carver College of Medicine at the University of Iowa

Simulation of Hemodynamic Parameters Following Aortic Unclamping With and Without Phenylephrine Support  
Franklin Scamman, MD,  
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Professor, Department of Anesthesia, University of Iowa Hospital & Clinics

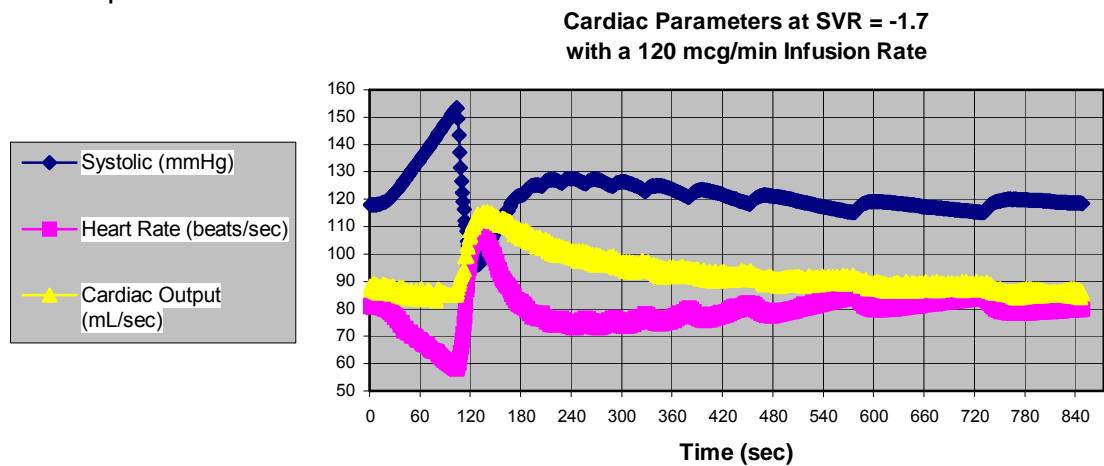
**Introduction:** The traditional approach to handling hypotension during abdominal aortic aneurysm surgery has been to infuse additional fluids in anticipation of hypotension as the aortic clamp is released. Unfortunately, this method leads to a hypervolemic condition after the period of hypotension and requires the use of diuretics for treatment. In this study, we anticipate the resulting hypotension from the release of the aortic clamp by starting a drip of phenylephrine, a vasoconstrictor, before the clamp is removed.

**Methods:** We modeled the hypotensive event of an abdominal aortic aneurysm surgery using a high, fidelity patient simulator from MedSim. Phenylephrine was chosen because of its action on the  $\alpha_1$  adrenergic receptors in the peripheral vasculature. Four levels of phenylephrine infusion were used –0 mcg/min, 80, 100, and 120. We used the default pharmacodynamic and pharmacokinetic parameters in the simulator's drug database.

The simulator uses normalized values for systemic vascular resistance (SVR). The values may range from  $-2.0$  to  $+2.0$ . We used values of  $-1.5$ ,  $-1.6$ , and  $-1.7$  to simulate a range of a 50% fall in SVR. We assumed that SVR would return to normal exponentially over a 12-minute period following unclamping, this was accomplished by changing the values manually on the simulator by monitoring a stopwatch for timing. The clamp was removed following the start of the infusion when the systolic BP reached 152 mmHg. The infusion was stopped when the SBP recovered 3 mmHg after its nadir. Data were captured using a modified debugging program native to MedSim.

Results: Without phenylephrine, the SBP reached dangerously low levels in the 30 mmHg range for about 1 minute. With phenylephrine, SBP remains above 80 mmHg in all cases. At the highest rate, SBP drops no more than 20% and overshoots no more than 10% of the baseline SBP (figure). Heart rate changes were blunted using phenylephrine.

Conclusion: Phenylephrine demonstrates promise in the prevention of hypotension during an abdominal aortic aneurysm surgery. The use of a high fidelity patient simulator illustrates benefits both as a teaching tool for trainees as well as a prototyping tool for current practitioners.



**19. Ye Xu**, Ph.D student, Dept. of Computer Science

3-D Tissue Classification of MDCT Images for Characterization of Regional Emphysema

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<sup>4</sup>Asso. Research Scientist, Dept. of Radiology, Univ. of Iowa

Purpose

Lung parenchyma evaluation via multidetector-row CT (MDCT) has significantly altered clinical practice, especially for evaluation of interstitial lung diseases including emphysema. We extended our feature from 2D to 3D on Adaptive Multiple Feature

Method (AMFM) by generating volumetric data with isotropic voxels. Our goal is to help physicians in the diagnosis, treatment and follow-up for patient with emphysema at the beginning stage of the disease.

#### Methods

We performed MDCT (120kV, 25-100 mAs and a pitch of 1.5 with 0.7 mm slice thickness), on 34 human volunteers: 9 smokers w/ emphysema in severe COPD (EC), 10 smokers w/ emphysema in mild COPD (MC) or normal appearing lung in COPD (NC), 8 non-smokers w/ normal lung function (NN) and 7 smokers with normal function (NS). Using the Iowa PASS software, cubic regions of interest (ROI) were marked (31x31 in plane pixels) by experts: EC 404 samples; MC 305 samples; NC 343 samples, NN 433 samples and NS 365 samples. We calculated 25 features for each ROI; excluded the airway and vessel region and Bayesian rules were used for discrimination. Leave one out and half-half methods were used for testing.

#### Results

Sensitivity, Specificity and Accuracy were calculated. The accuracy of the leave-one-out method is provided here for the four class classification in the form of 3D/2D is: EC: 84.9%/70.7%, MC: 89.8%/82.7%; NC: 87.5.0%/49.6%; NN: 100.0%/60.0%  
The overall accuracy of the half-half testing for four class classification in the form of 3D/2D is: 94.1%/70.1%. The accuracy of the leave-one-out method for the two-class classification in the form of 3D/2D is: NN: 99.3%/71.6%; NS: 99.7%/74.5%.

#### Conclusion

We conclude that 3D AMFM analysis of the lung parenchyma improves discrimination of early pathologic processes compared to 2D analysis of the same images. Additionally, the normal appearing lung from non-smokers and normal-smokers are different structurally based upon differentiation by the 3D AMFM.

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**20. Ding Yuan** (ding-yuan@uiowa.edu) PhD Candidate Management Sciences Dept.

A New Machine Learning Technique for Identifying  
Response-Specific Subpopulation

Ding Yuan, PhD Candidate Management Sciences Dept.

Nick Street (nick-street@uiowa.edu) Associate Professor Management Sciences Dept.

Phyllis Cullen (phyllis-cullen@uiowa.edu) Assistant Professor College of Nursing

In some knowledge discovery in databases (KDD) tasks, we wish to find subgroups of a large population that behave alike. Further, the characteristics defining the groups may be different from those affecting the behaviors of the individuals. For example, in health care, sub-populations defined by demographics (such as age and marital status) might respond differently to standard interventions (such as treatments).

Specifically, in this study we wish to find sub-populations among the elderly that react differently to nursing interventions. We propose a novel method combining supervised and unsupervised learning that achieves the dual objectives of accuracy and interpretability. We extend the traditional clustering method of mixture models optimized

with Expectation Maximization (EM), by adding a logistic classifier. Other more flexible classifiers are also applicable to this approach in general.

This method utilizes an integrated two-level modeling process. At first, the features are divided into two sets, one set to divide the data into groups and the other set to build a classifier for each particular group. The method is integrated because the performance of the classifier affects the construction of clusters. Thus, we are trying to not only segment the data, but also to segment them into more easily classified and more easily explained subgroups.

The accuracy of the our method is comparable to using Logistic alone, while at the same time, the proposed method provides better understanding of each subgroup by providing individualized response models.

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**21. Ding Yuan** (ding-yuan@uiowa.edu) PhD Candidate Management Sciences Dept.

An Applied Machine Learning Technique for Bio-Entity Classification

Padmini Srinivasan (padmini-srinivasan@uiowa.edu) Associate Professor School of Library & Information Science & Department of Management Sciences

In order to study the relationships between DNA, RNA, protein and cells from MEDLINE abstracts, we need to correctly identify and categorize the entity names. Sometimes, the same entity can be either a DNA or a protein depending on its context, thus we need to distinguish the different cases.

In this study, we combined traditional text retrieval techniques and machine learning techniques to do text categorization automatically. In the name identification step, we use a combination of dictionary-based and rule-based method to mark the fragments of bio-medical names. After phrases are identified, we choose the feature set to build the classifier. We define the feature set to be the last five words in each phrase, together with the left and right two words around the phrase. Altogether, there are nine features for each phase. Thus, we consider the phrase context as an important classification factor. The Naïve Bayes classifier is used to classify the phrases. We tried two ways to build the classifier, one considering the position of each word, and the other one without the word position information.

Under the condition of correct phrase fragmentation, the results show that if the word position information is not used, the accuracy of the classifier will increase 45.06%, from 58.52% to 84.89%. When our phrase fragmentation is used, the accuracy of the classifier without word position information changed to 70.83%, which means that the imprecise fragmentation affects the classifier's performance.

Our method can automatically identify phrases in natural language text and then effectively classify those phrases. Other name identification techniques and classifiers can be tried to increase precision in future work.

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**22. Fei Zhao**, Graduate Research Assistant

## Predicting Vascular Disease Status from Genetic and Clinical Data.

Fei Zhao<sup>1</sup>, Trudy Burns<sup>1</sup>, David Iovannisci<sup>2</sup>, Edward Lammer<sup>2</sup>, Ronald Lauer<sup>1</sup>, Milan Sonka<sup>1</sup>

<sup>1</sup>The University of Iowa, <sup>2</sup>Children's Hospital of Oakland Research Institute

Assessment of cardiovascular disease and prediction of its future course is of utmost importance for timely prevention. The objective of our project is to use patients' genetic and clinical information to predict future vascular disease status.

Radial basis artificial neural networks (ANNS) were employed to construct a discrimination model. To select the most discriminative features with respect to the classification outcome from a large number of available genotyping and clinical indices, genetic algorithms were employed to gain the best prediction result in the classification step. To assess the performance of the developed method, presence of coronary calcium as identified on a recent CT scan was predicted from genetic and clinical data acquired during the previous 20 years.

Data from 630 subjects (493 normal, 137 diseased, mean age 35 years) were available. Each data set consisted of 109 genetic features associated with atherosclerosis and 26 clinical features. The employed clinical features did not include coronary calcium indices. Thus, 135 features were available for each subject out of which the 64 most discriminative features were used for classifier training and performance evaluation. During the classifier training process, the discriminative features were used on the input while the coronary artery calcium presence was the binary prediction output (normal/abnormal). To facilitate complete separation of training and testing data and to obtain the most representative result, a leave-1-out validation method was used to evaluate the predictive classifier performance. Performance was assessed in terms of the overall classification correctness and expressed in %.

The method reached the predicted coronary calcium classification correctness of 76.8%. When the same prediction problem was attempted with genotyping information (clinical information) only, comparable classification correctness of 78.9% (78.7%) was achieved.

Our method demonstrates the feasibility of predicting presence of coronary calcium from genetic and clinical information. Formal validation studies are ongoing.

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**23. Li Zhou**, Graduate Research Assistant, Interdisciplinary Studies in Health Informatics

Concept Space Comparison: The Case of Autism

Li Zhou<sup>1,3</sup> (student), Padmini Srinivasan<sup>1,2</sup> (faculty)

<sup>1</sup>School of Library and Information Science

<sup>2</sup>Department of Management Sciences

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## INTRODUCTION

An Internet phenomenon that has a growing impact on health care is that of patient-initiated dialog in chat rooms, message boards and blogs. These occur parallel to the more established dialog in health care research via publications. Our goal is to explore automatic methods for comparing patient and professional communications and examine the degree to which they are similar.

## METHODS

We illustrate our methods in the area of autism. We collect four document sets on autism from PubMed. One is a general autism collection; the others are on diagnosis, etiology and therapy. We also collect a document set from autism message boards\*. We weed out the irrelevant documents. We then use MetaMap\*\* to extract UMLS concepts from each data set which we use to represent its concept space. The relative importance of the extracted concepts is determined. We also represent concept links by their co-occurrences in documents. We make quantitative and qualitative comparisons of concept space pairs at different granularities; using cosine similarity to measure similarity in concepts and topological measures to estimate structural similarity. Finally, we compare the central topics in each space.

## RESULTS AND CONCLUSION

We find for example a concept similarity of 41%, a symmetric topological similarity of only 9% between the general autism and message board documents. There are also interesting differences in central topics such as the relative emphasis on *Mercury*. The measures are consistent across sub-space pairs.

## APPLICABILITY

Contrast lay-peoples' and professionals' views of hot topics. Use these to provide guidance for consumer health education and public health promotion.

\* <http://www.autismchannel.net/cgi-bin/autboard.pl?b=1>  
<http://www.healthboards.com/boards/archive/index.php/f-17>

\*\* A NLP tool available at <http://skr.nlm.nih.gov/batch-mode/index.shtml>

## Poster Abstracts

### Non-Students

#### 24. Shannon Bradshaw, Department of Management Sciences

Title: Carving Out and Maintaining Paths to Knowledge in Bioscience Literature

Marc Light, Linguistics Department and SLIS

Debashish Bhattacharya, Department of Biological Sciences

David Eichmann, SLIS and CS Dept.

Brian Almquist, Department of Management Sciences

Robert Arens, Department of Computer Science

## Abstract:

Ideally, up-to-date review articles would exist for every information need a biologist could have. Unfortunately, this is not the case. In the biosciences, a simple keyword search usually turns up hundreds if not thousands of relevant articles. The major problem is assembling the relevant fragments of information within those articles.

Regardless of the information need, many individuals search the literature to acquire the same knowledge in roughly the same way, each individual duplicating the efforts of the others. Our hypothesis is that available tools for document processing, text mining algorithms, and common client-server architectures can be interleaved and extended to help biologists create review-like information on the fly.

We are developing a tool called Machete that will reuse the efforts of individuals to help others make sense of the literature. In Machete, investigators view PDF files and web pages, selecting fragments of information that help satisfy a particular knowledge need. These fragments may be passages, figures, or tables from articles, gene sequences, animations, etc. from web pages. To aid the investigator in finding such fragments Machete incorporates human language technologies.

For example, Machete finds passages of a particular type (e.g., descriptive of a gene's function). Machete also compiles tables of facts (e.g., protein interactions). These items can then be used to browse the articles to answer questions such as, "In what context is this protein interaction mentioned?"

With a simple mouse action users may save a passage, a figure, or some structured piece of information extracted by the system. Machete then assembles all fragments for a particular line of inquiry into a "knowledge artifact" for later review. Knowledge artifacts provide a wealth of personal information management benefits.

Artifacts are also portable and the information they contain may be shared at the organization (laboratory), research community, or public levels. The creator of an artifact may email the information to other researchers who can view the artifact in their own Machete clients.

Search engines indexing knowledge artifacts will support information sharing with varying freedom of accessibility.

This is work in progress. Our poster will describe both the current state and the future on the project.

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**25. Denise H. Britigan**, MA, Information Services Librarian

Title: *"The BioMedical Informatics Experience at Woods Hole!"*

Purpose:

The purpose of this poster is to share with others my experiences as a participant in the

BioMedical Informatics I Course at the Marine Biological Laboratory in Woods Hole, Massachusetts during the week of May 30 - June 6, 2004. This course for health professionals is a combination of lectures and hands-on computer exercises to introduce participants to the conceptual and technical components of medical informatics.<sup>1</sup>

**Background:**

"This is a National Library of Medicine fellowship program directed at medical educators, medical librarians, medical administrators, and young faculty who are not currently knowledgeable but can become agents of change in their institutions."<sup>1</sup>

Although the timing of my Medical Informatics I Course fell between my previous employment at the University of Iowa's Hardin Library for the Health Sciences and my current employment at the University of Cincinnati's Medical Center Academic Information Technology and Libraries, I believe that sharing my Woods Hole experience may allow me to be an agent of change by promoting this gem of an opportunity to health professionals at both institutions.

**Design/Methods:**

This poster will be a visual presentation of information from the week-long course which includes a list of nationally-recognized faculty, the topics of the various presentations, and the class schedule. I will have a laptop computer set up to provide an on-going slide show of almost 200 digital photographs, taken both in and out of the classroom, during the week in Woods Hole.

**Results/Discussion/Conclusion:**

First-hand experience is priceless. I would be happy to answer any questions that the conference participants may have regarding the MBL-NLM BioMedical Informatics course and/or the application process involved. This "*Information and Health at Iowa*" conference seems to be the perfect venue to expose health professionals to this opportunity and to encourage them to apply for this fellowship.

<sup>1</sup> BioMedical Informatics homepage. Marine Biological Laboratory -National Library of Medicine, <http://courses.mbl.edu/mi/index.html>

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**26. Bartley J. Brown**, Coordinate Laboratory for Computational Genomics

**MICROARRAY PROBE SELECTION AND ANNOTATION**

The current large-scale sequence-based gene discovery program at the University of Iowa provides a unique opportunity for microarray expression profiling.

In order to select cDNA probes to be printed on microarray slides one must identify a reasonably sized subset of clones from a much larger initial set and from a variety of sources. In this selection process the annotation of clones is a sine qua non. The type and extent of annotation required is different for each potential probe set. The annotation may include "primary" sequencing information such as library, library tag, tissue, cluster size, rearray verification, polyA signal, and double banding. So-called "secondary" annotation may also be important in the probe selection process. This includes Unigene cluster, accession number, go-terms, best NT hit, etc.

In order to store this wide variety of information we have adapted our database schema so that it utilizes tables with generic fields. Instead of “number in cluster”, or “accession number” our fields are “id”, “type”, and “value”. With this table structure and our especially designed web application we can quickly and easily make sequence annotation available for a wide variety of projects.

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**27. Beth Houlahan** RN, MSN

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**ELECTRONIC GENERATION OF BRIEF PATIENT HISTORY FORMS**

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The intake process for the nursing staff in busy ambulatory clinics can be lengthy and arduous. Patients may be on multiple medications and frequently don't remember the names of the medications or whether they need to be renewed. Some patients don't remember past allergies. Other patients aren't even sure why they have an appointment that day. Nursing staff must take the time to navigate through these issues, thereby extending the intake process, causing delays for the physician and other patients, and creating a sea of dissatisfaction.

The need to improve and expedite the intake process by enhancing communication between the patient and nurse was identified as a priority in the General Internal Medicine clinic at University of Iowa Hospitals and Clinics. The clinical director met with a team from the IT department to discuss the feasibility of creating a standardized form that would allow patients to review and confirm data about their health history extracted from their own electronic record.

These discussions led to the development of a new form called the “Brief Patient History” (BPH), which is automatically printed and given to a patient upon check-in to the clinic. Extracting data from the patient's electronic medical record, the BPH lists the patient's current medications, denotes a need for renewal, known allergies, and space for the patient to list the top two reasons for the visit and to screen for pain. The patient is able to make use of the time spent in the waiting room by reviewing, updating and completing the information on the BPH and by giving thought to the purpose of the day's visit.

The pilot of the BPH forms was conducted in the General Internal Medicine clinic and received high marks from the nursing staff. The success of the pilot was shared with the Ambulatory Nurse Manager Council in May 2004. Three clinics have subsequently implemented the BPH form and five others are scheduled for implementation. Nursing staff and patient satisfaction surveys were developed and conducted in the General Internal Medicine clinic to measure the benefits of the BPH. The findings were favorable from both perspectives with 100% of the staff perceiving the form improves the intake process and 65% of patients finding the form helpful in discussing their health history.

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**28. Bonnie Wakefield**, PhD, RN, Research Scientist  
Center for Research in the Implementation of Innovative Strategies in Practice (CRIISP)  
Associate Chief, Nursing Research VA Medical Center

A Comparison of Nurse-Patient Communication Between Telephone and Interactive Video in Home Care

Carma Bylund, John Holman, Annette Ray, Jane Morse, Anna Broulik, Lindsay Griffieon, Michael Kienzle

#### Objectives

Although use of telehealth in health care is growing, almost no research has been conducted on the effect of these technologies on the patient-provider interaction. The objective of this study is to compare communication behaviors of nurses and patients during telephone and videophone interactions conducted during a larger clinical trial of home telehealth in veterans with heart failure.

#### Methods

The sample includes 41 audiotaped interactions (26 telephone and 15 videophone) conducted during the 12-week telehealth intervention. Data were collected at Weeks 1, 6, and 12. Data were analyzed using the Roter Interaction Analysis System (RIAS). The RIAS focuses on two important components of the medical interview: instrumental (Task Oriented) and affective (Socioemotional) behavior. The unit of analysis is an "utterance", defined as the smallest discriminable speech segment to which a classification may be assigned. Interrater reliability for three coders, trained in the RIAS, averaged  $r=0.88$  (range .72-.95).

#### Results

Videophone calls lasted significantly longer than telephone calls (44.3 minutes vs. 32.5 respectively;  $t=-2.69$ ,  $p<0.01$ ). Nurses had a significantly higher mean number of utterances in the Socioemotional category relative to patients (142.7 vs. 72.6;  $t=5.11$ ,  $p<0.001$ ). Patients had a significantly higher mean number of utterances in the Task Oriented category (157.7 vs. 110.7;  $t=-3.14$ ,  $p<0.002$ ), primarily due to more Information Giving. Relative to telephone, videophone calls had a greater number of Task Oriented utterances (266.2 telephone vs. 272.1 video) and telephone calls had a greater number of Socioemotional utterances (230.2 telephone vs. 186.6 video) although these differences were not statistically significant. Over the 12 weeks, there were differences between Task Oriented utterances for patients, but not nurses. For patients, Task Oriented showed a U-shaped curve with a greater number of utterances in Week 1 and Week 12,

relative to Week 6. For both nurses and patients, Socioemotional talk declined over the 12-week intervention.

#### Conclusion

Video calls may be longer because of transmission delays due to slow connection speeds, noise interference, or the face-to-face nature of the interaction. Nurses provided more Socioemotional talk relative to patients, probably due to time spent encouraging patients to follow the treatment regimen and providing social support. Not surprisingly, Socioemotional talk declined over time for both nurses and patients. The U-shaped curve for patients in Task Orientation may reflect the patient's need for information at different points during the intervention time period, i.e., beginning and end. There may be more relationship building (Socioemotional) on the telephone due to the lack of face-to-face interaction.

#### Impact

Given the widespread use of telemedicine in the VA, the aging population, and the significance of the provider-patient relationship on important patient outcomes, these results will contribute knowledge about how to best utilize technology to improve care for chronically ill veterans.

