

## ***Curriculum Vitae***

**NAME: HUA XU**

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### **EDUCATION**

<b>Ph.D. in Biomedical Informatics</b> Columbia University, New York, NY	<b>2008</b>
<b>M.A. in Biomedical Informatics</b> Columbia University, New York, NY	<b>2004</b>
<b>M.S. in Computer Science</b> New Jersey Institute of Technology, Newark, NJ	<b>2001</b>
<b>B.S. in Biochemistry</b> Nanjing University, Nanjing, P. R. China	<b>1998</b>

### **ACADEMIC APPOINTMENTS**

2015 - present	Professor School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX
2012 – present	Director, Center for Computational Biomedicine Robert H. Graham Professorship in Entrepreneurial Biomedical Informatics and engineering CPRIT Scholar in Cancer Research School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX
2012 – 2015	Associate Professor School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX
2008 – 2012	Assistant Professor Department of Biomedical Informatics, School of Medicine, Vanderbilt University, Nashville, TN

## PROFESSIONAL ORGANIZATIONS

- 2005 – Present American Medical Information Association (AMIA)  
 2005 – Present The Association for Computational Linguistics (ACL)

## PROFESSIONAL ACTIVITIES

### Intramural Committees:

- 2014 – present Interfaculty Council, The University of Texas Health Science Center at Houston  
 2014 - present Bylaw Committee, School of Biomedical Informatics, The University of Texas Health Science Center at Houston  
 2013 - present Faculty Promotion Committee, School of Biomedical Informatics, The University of Texas Health Science Center at Houston  
 2012 - present Faculty Search Committee, School of Biomedical Informatics, The University of Texas Health Science Center at Houston  
 2012 - present Executive Committee, Innovation for Cancer Prevention Research (ICPR) Training Program, The University of Texas School of Public Health  
 2012 BioVU (Vanderbilt's Biobank) Review Committee, Vanderbilt University  
 2010 - 2012 Academic Program Committee of Biomedical Informatics, Vanderbilt University

### Extramural Committees:

- Board of Scientific Counselors, Lister Hill Center, National Library of Medicine, NIH  
 2014 – present Board member

### AMIA Natural Language Processing (NLP) Working Group:

- 2013 – 2014 Chair  
 2012 Chair-Elect

### Conference Program Committee Chair/Track Chair:

- 2016 Medical Informatics Workshop, International Conference on Intelligent Biology and Medicine (ICIBM'16), Houston, TX, US  
 2014 The ACM Eighth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO'14), in conjunction with the ACM CIKM, Shanghai, China  
 2014 American Medical Informatics Association (AMIA) NLP Working Group pre-symposium – a doctoral consortium and a workshop on interoperability, Washington DC, US  
 2014 American Medical Informatics Association (AMIA) Translational Bioinformatics Summit, San Francisco, US, SPC Track-Chair  
 2013 The ACM Seventh International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO'13), in conjunction with the ACM CIKM, San Francisco, US

- 2013 American Medical Informatics Association (AMIA) NLP Working Group pre-symposium – a doctoral consortium and a workshop on open source clinical NLP systems, Washington DC, US
- 2012 International Conference on Intelligent Biology and Medicine (ICIBM), Nashville, Tennessee, US
- 2012 The ACM Sixth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO'12), in conjunction with the ACM CIKM, Hawaii, US
- 2012 American Medical Informatics Association (AMIA) NLP Working Group pre-symposium – a doctoral consortium and a data workshop, Washington DC, US

Conference Program Committee Member:

- 2016 The 5th International Conference on Health Information Science, Nanjing, China
- 2016 AMIA 2016 NLP WG Pre-symposium
- 2016 International Conference on Intelligent Biology and Medicine (ICIBM'16), Houston, TX, US
- 2016 IEEE International Conference on Healthcare Informatics (ICHI), Chicago, US
- 2015 Workshop on Data Management and Analytics for Medicine and Healthcare, Hawaii, US
- 2015 IEEE International Conference on Healthcare Informatics (ICHI), Dallas, US
- 2015 International Conference on Intelligent Biology and Medicine (ICIBM'15), Indianapolis, Indiana, US
- 2015 Biomedical Linked Annotation Hackathon (BLAH2015), Kashiwa-no-ha City, Japan
- 2015 American Medical Informatics Association (AMIA) Translational Bioinformatics Summit, San Francisco, US
- 2014 International Conference on Intelligent Biology and Medicine (ICIBM'14), San Antonio, Texas, US
- 2014 International Workshop on Biomedical and Health Informatics, IEEE BIBM, Belfast, UK
- 2014 IEEE International Conference on Healthcare Informatics (ICHI), Verona, Italy
- 2013 International Workshop on Biomedical and Health Informatics, IEEE BIBM, Beijing, China
- 2013 IEEE International Conference on Healthcare Informatics (ICHI), Philadelphia, PA, USA
- 2013 International Conference on Intelligent Computing (ICIC'13), Nanning, China
- 2013 International Conference on Intelligent Biology and Medicine (ICIBM'13), Nashville, Tennessee, US
- 2012 AMIA Annual Fall Symposium
- 2012 2<sup>nd</sup> ACM SIGHIT International Health Informatics Symposium, Miami, Florida, US
- 2012 IEEE Conference on Healthcare Informatics, Imaging, and System Biology (HISB), San Diego, US

- 2011 American Medical Informatics Association (AMIA) Translational Bioinformatics Summit, San Francisco, US
- 2011 IEEE Conference on Healthcare Informatics, Imaging, and System Biology (HISB), San Jose, US
- 2011 International Conference on Intelligent Computing (ICIC'12), Zhengzhou, China
- 2011 International Biomedical Informatics Summit at Peking University, Beijing, China
- 2011 International Workshop on Biomedical and Health Informatics, IEEE BIBM, Atlanta, Georgia, US

**Grant Reviewer:**

- 2016 VA Scientific Merit Review Meeting, HSR3 and HS3A
- 2014 The South African Medical Research Council
- 2014 Medical Research Council (MRC), UK
- 2014 Fragile X review, National Institute of Child Health and Human Development (NICHD), National Institutes of Health (NIH)
- 2013 Reviewer at Kentucky Science and Engineering Foundation
- 2013 Ad-hoc reviewer for GNOM-G Review Panel, National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH)
- 2012 Genomic Medicine Pilot Demonstration Projects, RFA-HG-12-006, National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH)
- 2012 Epidemiology and genetics of chronic diseases, PA-11-260, National Cancer Institute (NCI), National Institutes of Health (NIH)
- 2012 Mail reviewer, NIH Director's Early Independence Award (DP5), RFA-RM-11-007, National Institutes of Health (NIH)
- 2011 PFINDR: Phenotype Finder IN Data Resources: A Tool to Support Cross-study Data Discovery Among NHLBI Genomic Studies (UH2/UH3), RFA-HL-11-020, National Heart, Lung, and Blood Institute (NHLBI), National Institutes of Health (NIH)
- 2011 Conference Grant Applications (R13), PA-10-07, National Institute on Drug Abuse (NIDA), National Institutes of Health (NIH)

**Editorial Activities:**Editorial Board Member:

- 2013 – present Journal of American Medical Informatics Association (JAMIA)
- 2012 - present Journal of Biomedical Informatics (JBI)
- 2010 - present International Journal of Data Mining and Bioinformatics (IJDMB)

Guest Editor:

- 2012 BMC Systems Biology Supplement issue "Advances in Intelligent Biology and Medicine: Selected papers from 2012 ICIBM Conference". 6 (Suppl S2)
- 2012 BMC Genomics Supplement issue "Advances in Intelligent Biology and Medicine: Selected papers from 2012 ICIBM Conference". 13 (Suppl S7)

2012 International Journal of Computational Biology and Drug Design (IJCBD) special issue "Advances in Intelligent Biology and Medicine: Selected papers from 2012 ICIBM Conference". Volume 5, issue 4

Journal Reviewer:

Bioinformatics, Journal of American Medical Informatics Association, BMC Bioinformatics, BMC Medical Informatics and Decision Making, Journal of Biomedical Informatics, Journal of Biomedical Discovery and Collaboration, Methods of Information in Medicine, Transactions on Information Technology in BioMedicine, Journal of Medical Internet Research, PLoS ONE

Conference Reviewer:

2009 – 2014 AMIA TBI & CRI Summit  
 2007 - 2014 AMIA Fall Symposium  
 2012 2<sup>nd</sup> ACM SIGHIT International Health Informatics Symposium, Miami, Florida, US  
 2011 International Workshop on Biomedical and Health Informatics, IEEE BIBM, Atlanta, Georgia, US  
 2011 IEEE Conference on Healthcare Informatics, Imaging, and System Biology (HISB), San Jose, US  
 2011 International Conference on Intelligent Computing, Zhengzhou, China  
 2007 ACL BioNLP Workshop  
 2007 Symposium on Languages in Biology and Medicine (LBM)

**Honors/Awards:**

2014 **Elected Fellow of American College of Medical Informatics (ACMI)**  
 2014 Ranked #1, SemEval-2014 Task 7 – Analysis of Clinical Text  
 2013 **IBM Faculty Award**  
 2013 Top-scoring predictions for the NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge leaderboard  
 2013 Top ranked: Task 1a – 1<sup>st</sup>, Task 1b – 3<sup>rd</sup>, and Task 2 – 1<sup>st</sup>, at 2013 ShARe/CLEF eHealth Shared Tasks in Clinical NLP  
 2012 Frist in Temporal Relation Extraction tasks, 2012 i2b2 Clinical NLP challenge  
 2012 Best Paper of the Year by the International Medical Informatics Association, PMC3237759, 2012 Yearbook in Medical Informatics  
 2012 Finalist of best paper award, AMIA Translational Bioinformatics Summit  
 2011 Finalist of distinguished paper award, AMIA Fall Symposium  
 2011 Best Paper of the Year by the International Medical Informatics Association, PMC2815478, 2011 Yearbook in Medical Informatics  
 2010 2<sup>nd</sup> best system in Concept Extraction task, 2010 i2b2 Clinical NLP challenge  
 2009 **Homer R. Warner Award, AMIA Fall Symposium**  
 2009 Distinguished paper award (co-author), AMIA Fall Symposium  
 2009 2<sup>nd</sup> best system, 2009 i2b2 Clinical NLP challenge  
 2007-2008 National Library of Medicine Training Fellowship

**Invited Talks/Presentations:**Invited Talks:

- 2016 VA Nashville Field Meeting. "Improve transportability of clinical NLP systems using CLAMP"
- 2016 Zhongshang University, China. "Healthcare data analytics in US"
- 2015 Pennsylvania State University College of Medicine, "Studying drug outcomes using electronic health records and informatics approaches"
- 2015 University of Pittsburgh, Department of Biomedical Informatics, "Making sense of clinical text: methods, software, and applications"
- 2015 University of North Carolina, "Natural Language Processing: Methods, Software, and Applications in the Medical Domain"
- 2015 UTHealth Development Board Meeting, "Teaching an Old Drug New Tricks: using electronic health records and informatics"
- 2015 CHIMA annual conference, Xiamen, "Healthcare Analytics using EHR – Technologies and Applications"
- 2015 Xian Engineering University, Xian, "Informatics Approaches to Facilitating Secondary Use of EHRs for Drug Outcome Studies"
- 2015 Second Workshop of Translational Bioinformatics in China, Harbin, "Informatics Approaches to Facilitating Secondary Use of EHRs for Drug Outcome Studies"
- 2015 Annual Workshop of Translational Medical Informatics in China, Suzhou, "Healthcare Analytics using EHR – Technologies and Applications"
- 2014 JAMIA Journal Club, "*Validating drug repurposing signals using EHRs and informatics: a use case of metformin associated with reduced cancer mortality*"
- 2014 Wayne State University, Detroit, Department of Computer Science, "*Natural language processing in the medical domain: Methods and applications*"
- 2014 Suzhou University, China, Center for Systems Biology, "*An introduction to natural language processing in the medical domain*"
- 2014 Cancer Hospital, Shanghai, China, "*Cancer research using electronic health records.*"
- 2014 Harbin Institute of Technology, China, Department of Computer Science (Shenzhen), "*Methods and applications of natural language processing in the medical domain*"
- 2014 International Conference on Frontiers in Chronic Disease Research and Prevention, Shanghai, "*Electronic health records and informatics for epidemiological studies on chronic diseases*"
- 2013 The University of Texas Academia-Industry Partnership FreshAir Roundtable, "*The use of electronic health records for repurposing drugs for cancers*"
- 2013 The eMERGE consortium, "*MedEx-UIMA – an open source system for medication information extraction*".
- 2013 University of San Diego, Division of Biomedical Informatics, iDASH center, "*Medication information extraction from EHR – methods and applications.*"
- 2013 The Methodist Hospital Research Institute, Department of Systems Medicine and Bioengineering, "*Natural language processing: methods and applications in clinical research*"

- 2012 University of Wisconsin - Milwaukee, Center for Biomedical Data and Language Processing, *"Studying drug outcomes using electronic medical records and informatics approaches"*
- 2012 Pharmacogenomics Research Network (PGRN), Research-In-Progress Seminar, *"Pharmacogenomic discovery and replication using EHR, biobank, and informatics - the PGPop resource"*
- 2012 University of Michigan, Ann Arbor, Department of Computational Medicine and Bioinformatics, *"Studying drug outcomes using electronic medical records and informatics approaches"*
- 2012 The Ohio State University, Columbus, Department of Biomedical Informatics, *"Studying drug outcomes using electronic medical records, biobanks, and informatics"*
- 2012 Indiana University, School of Medicine, Center for Computational Biology and Bioinformatics, *"Pharmacogenomic studies using EHR, Biobank, and Informatics"*
- 2011 University of Alabama at Birmingham, Section on Statistical Genetics, *"Pharmacogenetic studies using electronic medical records, biobank, and informatics"*
- 2011 International Biomedical Informatics Summit at Peking University, Beijing, China, *"Linking EHR to DNA biobank for genomic research: an informatics perspective."*
- 2011 University of Texas Health Center at Houston, School of Biomedical Informatics, *"Pharmacogenomic discovery using electronic medical records, biobank, and informatics"*
- 2011 Vanderbilt University, Department of Medicine, "Dinner and Data" Seminars, *"Informatics approaches for EHR-based pharmacogenomics studies"*
- 2010 Peking University, China, Center of Medical Informatics, *"Research and Education in Medical Informatics at Vanderbilt University"*
- 2010 Shanghai Center for Bioinformation Technology, China, *"Research and Education in Medical Informatics at Vanderbilt University"*
- 2010 Medical University of South Carolina, Department of Biochemistry, *"Facilitating EMR-based Pharmacogenetic Studies using Informatics Methods"*
- 2010 George Town University, CTSA informatics division, *"Electronic Medical Records, Informatics, and Clinical Research"*
- 2009 eMERGE network meeting, *"Medication extraction from clinical text"*
- 2008 University of Kansas, Department of Electrical Engineering and Computer Science, *"Natural Language Processing in the Biomedical Domain"*
- 2008 Arizona State University, Department of Biomedical Informatics, *"A Framework for Handling Biomedical Abbreviations"*
- 2008 Ohio State University, Department of Biomedical Informatics, *"A Framework for Handling Biomedical Abbreviations"*
- Presentations:
- 2014 AMIA Fall Symposium, *"Mining electronic health records to detect drug repurposing signals for cancers"*
- 2014 AMIA Clinical Research Summit, *"Extracting and standardizing medication information in clinical text - the MedEx-UIMA system"*
- 2013 Medinfo. *"Analyzing differences between Chinese and English clinical"*

- text: a cross-institution comparison of discharge summaries in two languages*"
- 2013 ACM Sixth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO), "Clinical Entity Recognition using Structural Support Vector Machines with Rich Features"
- 2013 AMIA Annu Symp Proc. "Combining corpus-derived sense profiles with estimated frequency information to disambiguate clinical abbreviations"
- 2012 Pac Symp Biocomput, "Ranking gene-drug relationships in biomedical literature using latent dirichlet allocation"
- 2011 AMIA Translational Bioinformatics Summit, "Facilitating Electronic Health Records based Pharmacogenetic Studies using Natural Language Processing: a case study of warfarin."
- 2011 AMIA Clinical Research Informatics, "A Framework to Determine Patient Drug Exposure from EMR: an Application to warfarin."
- 2011 International Workshop on Biomedical and Health Informatics, IEEE Conference of Bioinformatics and Biomedicine (BIBM), "An Initial Study of Full Parsing of Clinical Text using the Stanford Parser."
- 2010 Workshop of i2b2 NLP Challenge, "Hybrid Approaches to Concept Extraction and Assertion Classification – Vanderbilt's systems for 2010 i2b2 NLP challenge"
- 2009 Workshop of i2b2 NLP Challenge, "Vanderbilt's System for Medication Extraction".
- 2009 AMIA Fall Symposium, "MedEx – A Medication Information Extraction System for Clinical Narratives"
- 2008 AMIA Fall Symposium, "Methods for Building Sense Inventories of Abbreviations in Clinical Notes"
- 2007 AMIA Fall Symposium, "A Study of Abbreviations in Clinical Notes"

#### Tutorials:

- 2013 MedInfo 2013, "Clinical Natural Language Processing"
- 2013 AMIA Annual Symposium, "Using Electronic Health Records to facilitate clinical, genomic, and pharmacogenomic research: Experiences from the eMERGE and PGRN Networks"
- 2012 AMIA Translational Bioinformatics Summit, "Reusing EHRs for Clinical, Genomic, and Pharmacogenomic Discovery at Vanderbilt and within the eMerge Network"
- 2011 AMIA Now, "NLP 101: Making sense of EMR text"

#### Panels:

- 2014 iDASH annual conference, San Diego, "Making biomedical data discoverable"
- 2013 AMIA Fall Symposium, "Informatics to enable routine personalized cancer therapy"
- 2012 Academy Health Annual Research Meeting, "Squeezing Blood from a Stone: Principles and Practice of Using Narrative Data in Health Services Research"
- 2012 NIH workshop on "Natural Language Processing: State of the Art, Future Directions and Applications for Enhancing Clinical Decision-Making", Session Chair of "Linguistics-based methods" panel.

- 2012 AMIA Clinical Research Informatics Summit, “*Natural Language Processing for Clinical and Translational Research*”
- 2012 Academy Health Annual Research Meeting, Health IT Interest Group, “*HIT Quality of Care and Reporting Panel*”
- 2011 AMIA Clinical Research Informatics Summit, “*Cross-Institutional Systems to Support Phenotyping in Biomedical Research – Experience from the emerge network*”

## TEACHING ACTIVITIES

### Courses:

- 2013 - present HI6330 Biomedical Natural Language Processing: Methods and Applications, instructor
- 2014 - present HI 6323 Data Mining in Biomedical Informatics, instructor
- 2010 - 2012 BMIF 300 Introduction to Biomedical Informatics, lecturer
- 2009 - 2012 BMIF-315 Methodological Foundations of Biomedical Informatics, lecturer
- 2009 BMIF-330 Machine Learning for Biomedicine, co-instructor

### Research Advisor:

#### Postdoctoral Fellow:

- 2014 – present Hee-jin Lee, Ph.D.
- 2014 – present Jun Xu, Ph.D.
- 2013 – 2015 Yaoyun Zhang, Ph.D.
- 2013 – 2015 Sungrim Moon, Ph.D.
- 2013 – 2015 Ergin Soysal, M.D., Ph.D.
- 2013 – 2014 Guocai Chen, Ph.D.
- 2011 - 2013 Buzhou Tang, Ph.D.
- 2010 - 2014 Yonghui Wu, Ph.D.
- 2009 - 2012 Mei Liu, Ph.D.
- 2010 - 2011 Samir AbdelRahman, Ph.D.
- 2009 - 2010 Son Doan, Ph.D.

#### PhD Student:

- 2016 – present Lingyi Tang, PhD student
- 2015 – present Xiao Dong, PhD student
- 2014 – present Qiang Wei, PhD student
- 2013 – present Lian Hu, PhD Candidate
- 2013 – present Jun Li, PhD Candidate
- 2012 - present, Min Jiang, PhD Candidate,
- 2011 - 2015 Yukun Chen, PhD
- 2012 – 2014 Jianbo Lei, PhD (Dissertation title: Named entity recognition in Chinese clinical text)

MS Student:

2014 – present	Michelle Scerbo, MS Candidate
2014 – present	Ginger Schirmer, MS Candidate
2014 – present	James Schlebus, MS Candidate
2013 – 2014	Anupama E. Gururaj, MS Candidate,
2013 – 2014	Ruiling Liu, MS Candidate
2013 – 2014	Heidi Jones, MS Candidate

Summer Intern:

2015 Summer	Manu Prakasam, High school student
2014 Summer	Kevin Zhu, BS
2013 Summer	Bonnie Nortz, Undergraduate student
2010 Summer	Oluwatoyin Arije, MPharm Candidate
2010 Summer	Kamilah McKinnon, MPharm Candidate

Visiting Student/Scholar:

2015-2016	Hui Chen, PhD
2014-2015	Yubo Zhou, PhD
2011-2012	Hongxin Cao, MS
2009-2010	Yanxin Lu, PhD Candidate

**Thesis/Dissertation Committee Member for:**

2014 - present	Qiang Wei, PhD student, University of Texas Health Science Center at Houston
2014 - present	Muhammad Amith, PhD student, University of Texas Health Science Center at Houston
2014 - present	Jun Li, PhD student, University of Texas Health Science Center at Houston
2013 - present	Melissa Resnick, PhD candidate, University of Texas Health Science Center at Houston
2013 - present	Frank Manion, PhD student, University of Texas Health Science Center at Houston
2013 - 2014	Safa Fathiamini, PhD student, University of Texas Health Science Center at Houston
2013 - 2014	Ning Shang, PhD, University of Texas Health Science Center at Houston
2012 - 2013	Sina Madani, PhD, University of Texas Health Science Center at Houston
2012 - 2013	Ravi V. Atreya, MS, Vanderbilt University
2011 - 2014	Robert Carroll, PhD candidate, Vanderbilt University
2009 - 2011	Firas Wehbe, PhD, Vanderbilt University
2010	Jerome Jourquin, MS, Vanderbilt University
2009	Xinxin Zhu, PhD, Columbia University

**RESEARCH PROGRAM**

**Current Grants:**Advancing Cancer Pharmacoepidemiology Research through EHRs and Informatics

NCI U24 CA194215 01A1 (MPI - Xu, Denny, Yang)

09/01/2016-08/31/2021

Total costs: \$3,125,128

Role: Contact PI

This project proposes to integrate and extend previously developed tools to build an informatics infrastructure for electronic health records (EHR) data extraction, interpretation, management, and analysis, to advance cancer pharmacoepidemiology research.

Partnership in Learning around Engagement, Data, Genomics, and Environment - Precision Medicine Initiative Data and Research Support Core

NIH U2C OD023196 01 (PI - Denny)

07/01/2016-06/30/2021

UTHealth subcontract total costs: \$893,322

Role: Site PI

This is the Data and Research Support Center (DRSC) for the Precision Medicine Initiative Cohort Program. The center will not only manage acquisition and organization of diverse datasets for the program but also provide research support and analysis tools for data mining.

Interactive machine learning methods for clinical natural language processing

NLM 2R01LM010681-05 (PI – Hua Xu)

09/29/2014 – 09/28/2018

Total direct costs: \$1,396,822

Role: PI

In this study, we propose to investigate interactive machine learning (IML) methods to address the challenges in clinical NLP about building annotated corpora and combining domain knowledge and statistical learning methods. We will conduct IML studies to three NLP related tasks including word sense disambiguation, named entity recognition, and clinical phenotyping.

Informatics Tools for Pharmacogenomic Discovery using Practice-based Data

NIGMS 1 R01 GM103859-01 (PI: Denny, Pathak, and Xu)

09/18/2014 – 5/31/2018

Total direct costs: \$1,588,692

Role: PI

In this study, we will develop natural language processing (NLP) and ontology tools to facilitate pharmacogenomics studies using EHR-linked biobanks.

BioCADDIE: Biomedical and healthCAre Data Discovery and Indexing Engine center

NIH 1U24HL126126-01 (PI – Lucila Ohno-Machado)

09/29/2014 – 09/38/2017

Total direct costs: \$6,000,000 (UTHealth \$1,025,558)

Role: Subcontract PI, co-investigator

BioCADDIE is a consortium of data producers, curators, publishers, and consumers who will work together to develop practical, sustainable solutions to the problem of biomedical and healthcare data discovery. This project is to develop an NIH BD2K Data Discovery Index Coordination Consortium.

Natural language processing for clinical and translational research

NIGMS 1R01GM102282 (MPI – Hongfang Liu, Serguel Pakhomov, and Hua Xu)

04/01/2013 – 03/31/2017

Total direct costs: \$1,345,476 (UTHealth \$524,560)

Role: PI

Natural Language Processing (NLP) has played a critical role in enabling secondary use of EHRs data for clinical and translational research. This study will facilitate efficient adoption of NLP to large-scale clinical studies by developing an open source framework that will enable semantic level interoperability among different NLP systems through defined standards and provide user-centric tools for clinical information extraction.

CPRIT Rising Stars Award - Repurposing Existing Drugs for Cancer Treatment using Electronic Health Records

Cancer Prevention & Research Institute of Texas, R1307 (PI – Hua Xu)

03/01/2013 – 02/28/2018

Total direct costs: \$2,806,000

Role: PI

This study is to develop novel informatics approaches to facilitate large-scale drug-repurposing studies for identifying potential cancer therapeutic agents by using Electronic Health Records (EHRs) data. The hypothesis is that EHRs can be used to detect new indications of existing drugs for cancer therapy in a very efficient way, with the help of advanced informatics methods.

Metadata applications on informed content to facilitate biorepository data regulation and sharing

NHGRI U01 HG009454 (PI - Cui Tao)

9/28 /2016-7/31/2019

Total Budget: \$1,359,655

Role – co-Investigator

This proposed study will focus on (1) developing a standard conforming metadata ontology to formally represent the informed consent domain; and (2) an automatic tool to semantically annotate informed consent documents to facilitate biorepository data regulation, sharing, and decision support.

Patient Medical History Representation, Extraction, and Inference from EHR Data

NLM 1R01LM011829 (PI – Cui Tao)

09/01/2014 – 08/31/2018

Total budget: \$1,358,868

Role: co-investigator

This proposed project fills in the current gaps among ontologies, Natural Language Processing (NLP), and EHR-based clinical research for temporal data representation, normalization, extractions, and reasoning. We propose to develop novel approaches for automatic temporal data representation, normalization and reasoning for large, diverse, and heterogeneous EHR data and prepare the integrated data for further analysis.

Learning from patient safety events: a case-based toolkit

AHRQ 1 R01 (PI: Yang Gong)

09/01/2014 – 8/31/2019

Total direct budget: \$ 1,246,715

Role: co-investigator

Timely reporting and effective learning from medical incidents is considered an effective way in developing strategies for reducing medical errors. Utilizing an innovative user-centered, learning-supportive, and ontological approach combining with case-based reasoning and natural language processing techniques, we propose to develop a knowledgebase and learning toolkit that can systematically collect and analyze incident reports, linking historical reports with WebM&M, the highest quality of voluntary reports and expert reviews on patient safety. We envision that the innovative approach will facilitate timely, quality reporting and learning from the incidents and ultimately cultivating a just and learning culture of patient safety.

**Completed Grants:**

An In-silico Method for Epidemiological Studies Using Electronic Medical Records

NCI R01CA141307 (PI – Hua Xu)

09/03/2009 – 07/31/2014

Total direct costs: \$762,738

Role: PI

The specific aim of this study is to develop an automated informatics approach to extract both fine-grained cancer findings and general clinical information from electronic medical records and use them to conduct cancer related epidemiological studies. It is an EUREKA award (Exceptional, Unconventional Research Enabling Knowledge Acceleration) funded by NCI.

Real-time Disambiguation of Abbreviations in Clinical Notes

NLM R01LM010681 (PI – Hua Xu)

05/31/2010 – 5/30/2014

Total direct costs: \$730,000

Role: PI

This project will develop, evaluate, and share a systematic approach to Clinical Abbreviation Recognition and Disambiguation (CARD), and in doing so substantially aims to improve existing NLP systems and computer-based documentation system by reducing ambiguities in electronic records in real-time.

An Informatics-based Approach to Pharmacogenetic Studies of Warfarin

NIH UL1 RR024975-KL2 Scholar Award (PI – Hua Xu)

07/01/2009 – 06/30/2010

Total direct costs: \$130,000

Role: PI (70%)

This project is to develop informatics approaches to extract phenotypic data for pharmacogenomics research from EHRs, using natural language processing and machine learning technologies. It was a three-year K Award, but terminated early due to the R01 award.

Using Biomedical Knowledge to Identify Plausible Signals for Pharmacovigilance

NLM 1R01LM011563 (PI - Trevor Cohen)

09/01/2013-08/31/2016

Total budget: \$611,718

Role: co-investigator

This project will develop novel informatics methods to mine electronic health records and biomedical literature to automatically identify adverse drug events, thus to provide a generalizable approach that can be used to apply knowledge derived from the biomedical literature to interpret clinical data.

Informatics to support routine personalized cancer therapy

NCI 1U01CA180964-01(PI - Elmer Bernstam)

09/01/2013 – 8/31/2016

Total direct budget: \$622,500

Role: co-investigator

This project aims to develop an informatics framework to support personalized cancer therapy, which includes tools to 1) implement a bioinformatics pipeline for processing molecular data into actionable profiles, 2) create and maintain a database of therapeutic implications of common genomic aberrations using automated processing of publically-available sources, and 3) develop tools to summarize clinically-relevant genomic alterations encountered in a patient's tumor and genotype-relevant therapies.

Pharmacovigilance Methods: Leveraging Heterogeneous Adverse Drug Reaction Data

NLM R01 LM010016-05 (PI – Carol Friedman)

7/01/2013 – 6/30/2017

Total direct costs: \$1,158,496 (UTHealth subcontract \$138,000)

Role: Subcontract PI, co-investigator

This project will integrate heterogeneous sources including drug chemical structure, literature, and electronic health records (EHRs) to detect new adverse drug reactions.

Bridging Genomics and Medicine by Ontology Fingerprints

NLM 1R56LM010680 – 01A1 (PI – Jim Zheng)

09/01/2012 – 08/31/2014

Total direct costs: \$202,898

Role: Co-investigator

This study is to develop an ontology fingerprint - a set of ontology terms overrepresented in the PubMed abstracts linked to a gene or a disease along with the terms' corresponding enrichment p-value, to characterize genes and diseases. The ontology fingerprints are then used to quantify the relationship between a gene and a disease.

National Center for Cognitive Informatics and Decision Making in Healthcare SHARP

ONC 90TR000401 (PI – Jiajie Zhang)

04/10/10-03/31/2014

Total direct costs: \$15,000,000

Role: Co-investigator

SHARPC project 3 is to develop informatics methods to automatically create clinical summaries of patients.

Autonomic Cardiovascular Regulation

NHLBI P01HL056693 (PI - David Robertson)

05/01/2012 – 4/30/2017, Participated between 2012-2015

Total direct costs: \$5,907,583

Role: Co-investigator

This is a Program Project that is tightly coordinated testing of hypotheses addressing autonomic modulation of cardiovascular function in health and disease. We will use the EMR-linked DNA biobank to study associations between *ADRA2A* genetic variation and increased risk of stress-induced hyperglycemia in patients with myocardial infarction, as well as increased risk of gestational diabetes.

MOMENT (Monitoring for Outpatient Medication Effects and New Toxicities) in TIME

NLM R01 LM007995 (PI - Randy Miller)

02/01/2004 – 06/14/2010

Total direct costs: \$697,237

Role: Co-Investigator (10%)

The MOMENT project involves developing sophisticated text-mining and data extraction tools to examine adverse drug effects in patients presenting for emergency and hospital care.

VGER – Vanderbilt Genomic Electronic Medical Records (eMERGE-I)

NHGRI U01 HG004603 (PI - Dan Roden)

09/28/2007 – 07/31/2011

Total direct costs: \$6,466,499

Role: Co-Investigator (10%)

The VGER project promotes personalized medicine by conducting genome-phenome association studies using EMR data.

VESPA - Vanderbilt Electronic Systems for Pharmacogenomic Assessment

NIH RC2GM092618 (PI - Dan Masys & Dan Roden)

09/30/2009 – 08/31/2011

Total direct costs: \$6,406,203

Role: Co-Investigator (20%)

The VESPA project was a two-year GO grant, which aims to conduct pharmacogenomics studies using electronic health records and DNA biobank.

VGER – Vanderbilt Genomic Electronic Records Project (eMERGE-II)

NHGRI U01 HG006378 (PI - Dan Roden)

08/15/2011 – 07/31/2015

Total direct costs: \$4,237,100

Role: Co-investigator (5%), Participated between 2011-2012

The VGER-II project promotes personalized medicine by conducting genome-phenome association studies using EMR data and integrating genomic data into clinical settings.

Pharmacogenomics of Arrhythmia Therapy (PAT)

NHLBI U19HL065962 (PI - Dan Roden)

09/01/2010 – 06/30/2015

Total direct costs: \$13,986,828

Role: Co-investigator (30%), Participated between 2010-2012

PAT is one of the sites of Pharmacogenomics Research Network (PGRN). The aim of this project is to understand genetic associations for drugs in arrhythmia therapy. One of the particular projects is to investigate genetic variations associated with warfarin-caused bleedings by using electronic medical records (EMRs) and DNA biobank. We also support PGPop, a network resource for using EMRs and biobanks for pharmacogenomic research.

Evidence-based diagnostic tools for translational and clinical research (eTfor2)

NLM R01LM010828 (PI – Randy Miller)

9/30/2010-9/29/2013

Total direct costs: \$730,000

Role: Co-investigator (10%), Participated between 2010-2012

The eTfor2 project develops and evaluates open-source programs and knowledge representations to better characterize patients for translational and clinical research studies.

From GWAS to PheWAS: Scanning the EMR Phenome for Gene-Disease Associations

NLM R01LM010685 (PI - Josh Denny)

09/01/2011 – 8/31/2014

Total direct costs: \$652,500

Role: Co-investigator (5%), Participated between 2011-2012

The PheWAS project develops novel NLP and data analysis methods for gene-disease associations based on EMRs. For a given SNP, it scans hundreds of diseases to quickly identify possible associations.

## PUBLICATIONS

### Peer Reviewed Articles - Journal:

1. Sun J, Zhou Y, Wang J, Liu Q, **Xu H**. A systematic analysis of FDA-approved anticancer drugs. *BMC System Biology*. 2016 Accepted.
2. Chen H, Wu Y, Gong C, Pan Q, Zhang Y, Dong X, Zhang K, Wang S, Lei J, Xu H. Comorbidity in adult patients hospitalized with type 2 diabetes in Northeast China: an analysis of hospital discharge data from 2002 to 2013. *BioMed Research International*. 2016 Accepted.
3. Wu Y, Denny JC, Rosenbloom ST, Miller RA, Giuse DA, Wang L, Blanquicett C, Soysal E, Xu J, Xu H. A long journey to short abbreviations: developing an open-source framework for clinical abbreviation recognition and disambiguation (CARD)." *J Am Med Inform Assoc* (2016): ocw109.
4. Xu J, Lee L, Zeng J, Wu Y, Zhang Y, Huang L, Johnson A, Holla V, Bailey AM, Cohen T, Meric-Bernstam F, Bernstam EV, Hua Xu. Extracting Genetic Alteration Information for Personalized Cancer Therapy from ClinicalTrials.gov. *J Am Med Inform Assoc*. 2016;1–9. doi:10.1093/jamia/ocw009. 2016.
5. Xu J, Wu Y, Zhang Y, Wang J, Lee H, Xu H. CD-REST: A System for Extracting Chemical-induced Disease Relation in Literature. *Database*. 2016:1-9. doi:10.1093/database/baw036.
6. Zhang Y, Xu J, Chen H, Wang J, Wu Y, Manu P, Xu H. Chemical named entity recognition in patents by domain knowledge and unsupervised feature learning. *Database* 2016. doi: 10.1093/database/baw049.
7. Fathiamini S, Johnson AM, Zeng J, Araya A, Holla V, Bailey AM, Litzenburger BC, Sanchez NS, Khotkaya Y, Xu H, Meric-Bernstam F, Bernstam EV, Cohen T. Automated Identification of Molecular Effects of Drugs (AIMED). *J Am Med Inform Assoc*, 2016 23(4):758-65.
8. Chen Y, Lasko TA, Mei Q, Denny JC, **Xu H**. A study of active learning methods for named entity recognition in clinical text. *J Biomed Inform*, 2015 58:11-8
9. Stubbs A, Kotfila C, **Xu H**, Uzuner O. Identifying risk factors for heart disease over time: Overview of 2014 i2b2/UTHealth shared task Track 2. *J Biomed Inform*, In Press, 2015 Suppl:S67-77
10. Zheng K, Vydiswaran VG, Liu Y, Wang Y, Stubbs A, Uzuner O, Gururaj AE, Bayer S, Aberdeen J, Rumshisky A, Pakhomov S, Liu H, **Xu H**. Ease of adoption of clinical natural language processing software: An evaluation of five systems. *J Biomed Inform*, 2015 Suppl:S189-96
11. Zhang Y, Tang B, Jiang M, Wang J, **Xu H**. Domain adaptation for semantic role labeling of clinical text. *J Am Med Inform Assoc*. 2015 22(5):967-79.
12. Eduati F, Mangravite LM, Wang T, Tang H, ... **Xu H**, ... et al. Prediction of human population responses to toxic compounds by a collaborative competition. *Nature Biotechnology*, 2015, 33, 933–940.
13. Sun J, Zhao M, Jia P, Wang L, Wu Y, Iverson C, Zhou Y, Bowton E, Roden DM, Denny JC, Aldrich MC, **Xu H\***, Zhao Z\*. Deciphering Signaling Pathway Networks to Understand the Molecular Mechanisms of Metformin Action. *PLoS Computational Biology*. 2015;11(6):e1004202. (\* co-corresponding author)
14. Liu Z, Yefei Zhang Y, Franzin L, Cormier JN, Chan W, **Xu H**, Du XL. Trends and variations in breast and colorectal cancer incidence from 1995 to 2011: A comparative study between Texas Cancer Registry and National Cancer Institute's Surveillance, Epidemiology and End Results data. *International Journal of Oncology*. 2015, 1819-1826

15. Wu Y, Denny JC, Rosenbloom ST, Miller RA, Giuse DA, Song M, **Xu H**. A Preliminary Study of Clinical Abbreviation Disambiguation in Real Time. *Appl Clin Inform* 6.2 (2015): 364-374.
16. Chen G, Zhao J, Cohen T, Tao C, Sun J, **Xu H**, Bernstam E, Zeng J, Johnson A, Holla, Ann Balley V, Meric-Bernstam F and Zheng WJ, Standardized Pharmacological Class Profile in the Web Ontology Language (OWL). *Database* (Oxford), 2015: bav034. doi: 10.1093/database/bav034
17. Tao C, Sun J, Zheng W, Chen J, **Xu H**, Drug target prediction for colorectal cancer by combining ontology and network approaches. *Database* (Oxford), 2015:bav015. doi: 10.1093/database/bav015
18. Jiang M, Huang Y, Fan JW, Tang B, Denny J, **Xu H**. Parsing clinical text: how good are the state-of-the-art parsers? *BMC Medical Informatics and Decision Making*. 2015, 15(Suppl 1):S2
19. **Xu H**, Aldrich MC, Chen Q, Liu H, Peterson NB, Dai Q, Levy M, Shah A, Han X, Ruan X, Jiang M, Li Y, Julien JS, Warner J, Friedman C, Roden DM, Denny JC. Validating drug repurposing signals using electronic health records: a case study of metformin associated with reduced cancer mortality. *J Am Med Inform Assoc*. 2015, 22(1): 179-91. [PMID: 25053577]
20. Huang LC, Soysal E, Zheng W, Zhao Z, **Xu H**<sup>\*</sup>, Sun J<sup>\*</sup>. A weighted and integrated drug-target interactome: drug repurposing for schizophrenia as a use case. *BMC Systems Biology*, 2015.9 (Suppl 4), S2. (\* co-corresponding author)
21. Tang B, Feng, Y, Wang X, Wu Y, Zhang Y, Jiang M, Wang J, **Xu H**. A comparison of conditional random fields and structured support vector machines for chemical entity recognition in biomedical literature. *Journal of Cheminformatics*. 2015 7(Suppl 1):S8 [PMCID: PMC4331698]
22. Krallinger M, Rabal O, Leitner F, Vazquez M, Salgado D, Lu Z, ...**Xu H**, ... Valencia, A. The CHEMDNER corpus of chemicals and drugs and its annotation principles. *Journal of Cheminformatics*, 2015, 7(Suppl 1), S2. [PMCID: PMC4331692]
23. Zhu K, Liu Q, Zhou Y, Tao C, Zhao Z, **Xu H**<sup>\*</sup>, Sun J<sup>\*</sup>. Oncogenes and tumor suppressor genes: comparative genomics and network perspectives. *BMC Genomics*, 2015. 16 (Suppl 7), S8. (\* co-corresponding author)
24. Chen Y, Sun, J, Huang LC, **Xu H**<sup>\*</sup>, Zhao Z<sup>\*</sup>. Classification of primary cancer sites using machine learning and somatic mutations. *BioMed Research International*, 2015. (\* co-corresponding author)
25. Niadoo D, Wu AC, Brilliant MH, Denny JC, Ingram C, Kitchner TE, Linneman JG, McGeachie MJ, Roden DM, Shaffer CM, Shah A, Weeke P, Weiss ST, **Xu H**, Medina MW. A polymorphism in HLA-G modifiers statin benefit in asthma. *The Pharmacogenomics Journal*. 2015, 15(3):272-7. [PMCID PMC4379135]
26. Kawai VK, Cunningham A, Vear SI, Van Driest SL, Oginni A, **Xu H**, Jiang M, Li C, Denny JC, Shaffer C, Bowton E, Gage BF, Ray WA, Roden DM, Stein CM. Genotype and risk of major bleeding after the warfarin initiation phase. *Pharmacogenomics*, 2014. 15(16):1973-83. [PMCID: PMC4304738]
27. Shang N, **Xu H**, Rindflesch TC, Cohen T. Identifying plausible adverse drug reactions using knowledge extracted from the literature. *J Biomed Inform*. 2014. 52:293-310. [PMCID PMC4261011]
28. Gobbel GT, Garvin J, Reeves R, Cronin RM, Heavirland J, Williams J, Weaver A, Jayaramaraja S, Giuse D, Speroff T, Brown SH, **Xu H**, Matheny ME. Assisted annotation of medical free text using RapTAT. *J Am Med Inform Assoc*. 2014, 21(5): 833-41. [PMCID PMC4147611]

29. Sun J, Huang L, **Xu H**, Zhao Z. Network-assisted prediction of potential drugs for addiction. *BioMed Research International*. 2014, doi:10.1155/2014/258784. [PMCID pending]
30. Tang B, Cao H, Wang X, Chen Q, **Xu H**. Evaluating word representation features in biomedical named entity recognition tasks. *BioMed Research International*. 2014, doi:10.1155/2014/240403. [PMCID PMC5932722]
31. Liu M, Cai R, Hu Y, Matheny ME, Sun J, Hu J, **Xu H**. Determining molecular predictors of adverse drug reactions with causality analysis based on structure learning. *J Am Med Inform Assoc*. 2014, 21(2):245-51. [PMCID: PMC3932464]
32. Doan S, Lin KW, Conway M, Ohno-Machado L, Hsieh A, Feupeo SF, Garland A, Ross MK, Jiang X, Farzaneh S, Walker R, Alipanah N, Zhang J, **Xu H**, Kim HE. PhenDisco: phenotype discovery system for the database of genotypes and phenotypes. *J Am Med Inform Assoc*. 2014, 21(1):31-6. [PMCID: PMC3912702]
33. Denny JC, Bastarache L, Ritchie MD, Carroll RJ, Zink R, Mosley JD, Field JR, Pulley JM, Ramirez AH, Bowton E, Basford MA, Carrell DS, Peissig PL, Kho AN, Pacheco JA, Rasmussen LV, Crosslin DR, Crane PK, Pathak J, Bielinski SJ, Pendergrass SA, **Xu H**, Hindorff LA, Li R, Manolio TA, Chute CG, Chisholm RL, Larson EB, Jarvik GP, Brilliant MH, McCarty CA, Kullo IJ, Haines JL, Crawford DC, Masys DR, Roden DM. Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. *Nature Biotechnology*. 2013 31(12):1102-10. [PMCID PMC3969265]
34. Zheng H, Wang H, **Xu H**, Wu Y, Zhao Z, Azuaje F. Linking biochemical pathways and networks to adverse drug reactions. *IEEE Trans Nanobioscience*. 2013: 131-137.
35. Wei WQ, Feng Q, Jiang L, Waitara MS, Iwuchukwu OF, Roden DM, Jiang M, **Xu H**, Krauss RM, Rotter JI, Nickerson DA, Davis RL, Berg RL, Peissig PL, McCarty CA, Wilke RA, Denny JC. Characterization of Statin Dose Response in Electronic Medical Records. *Clin Pharmacol Ther*. 2013, 95(3):331-8. [PMCID PMC3944214]
36. Lei J, Tang B, Lu X, Gao K, Jiang M, **Xu H**. A comprehensive study of named entity recognition in Chinese clinical text. *J Am Med Inform Assoc*. 2014, 21(5):808-14. [PMCID PMC4147609]
37. Van Driest SL, Shah A, Marshall MD, **Xu H**, Smith AH, McGregor TL, Kannankeril PJ. Opioid use after cardiac surgery in children with Down syndrome. *Pediatr Crit Care Med*. 2013, 14(9):862-8. [PMCID: PMC3830692]
38. Fan JW, Yang EW, Jiang M, Prasad R, Loomis RM, Zisook DS, Denny JC, **Xu H**, and Huang Yang\*. Syntactic parsing of clinical text: guideline and corpus development with handling ill-formed sentences. *J Am Med Inform Assoc*. 2013, 20(6):1168-77 [PMCID:PMC3822122]. (\* Co-corresponding Authors)
39. Chen Y, Carroll RJ, Shah A, Eyley AE, Denny JC, **Xu H**. Applying active learning to high-throughput phenotyping algorithms for electronic health records data. *J Am Med Inform Assoc*. 2013, 20(e2):e253-9. [PMCID: PMC3861916]
40. Tang B, Wu Y, Jiang M, Chen Y, Denny JC, **Xu H**. A hybrid system for temporal information extraction from clinical text. *J Am Med Inform Assoc*. 2013, 20(5):828-35. [PMCID: PMC3756274]
41. McCoy AB, Wright A, Eysenbach G, Malin BA, Patterson ES, **Xu H**, Sittig DF. State of the art in clinical informatics: evidence and examples. *IMIA Yearbook of Medical Informatics*. 2013, 8(1):13-9. [PMID:23974543]
42. Mani S, Chen Y, Li X, Arlinghaus L, Chakravarthy AB, Abramson V, Bhave SR, Levy MA, **Xu H**, Yankeelov TE. Machine learning for predicting the response of breast cancer to neoadjuvant chemotherapy. *J Am Med Inform Assoc*. 2013, 20(4):688-95. [PMCID: PMC3721158]

43. Wei W, Cronin RM, **Xu H**, Lasko TA, Bastarache L, Denny JC. Development and evaluation of an ensemble resource linking medications to their indications. *J Am Med Inform Assoc.* 2013, 20(5):954-61. [PMCID: PMC3756263]
44. Tang B, Cao H, Wu Y, Jiang M, **Xu H**. Recognizing clinical entities in hospital discharge summaries using Structural Support Vector Machines with word representation features. *BMC Medical Informatics and Decision Making* 2013, 13(Suppl 1):S1. [PMCID: PMC3618243]
45. Chen Y, Cao H, Mei Q, Zheng K, **Xu H**. Applying Active Learning to Supervised Word Sense Disambiguation in MEDLINE. *J Am Med Inform Assoc.* 2013, 20(5):1001-6. [PMCID: PMC3756255]
46. Wiley LK, Shah A, **Xu H**, Bush WS. ICD-9 Tobacco Use Codes are Effective Identifiers of Smoking Status. *J Am Med Inform Assoc.* 2013, 20(4):652-8. [PMCID: PMC3721171]
47. Liu M, McPeck Hinz ER, Matheny ME, Denny JC, Schildcrout JS, Miller RA, **Xu H**. Comparative Analysis of Pharmacovigilance Methods in Detection of Adverse Drug Reactions from Electronic Medical Records. *J Am Med Inform Assoc.* 2013, 20(3):420-6. [PMCID: PMC3628053]
48. **Xu H**, Wu Y, Elhadad N, Stetson PD, Friedman C. A new clustering method for detecting rare sense of abbreviations in clinical notes. *J Biomed Inform.* 2012, 45(6):1075-83. [PMID: 22742938]
49. Liu M, Wu Y, Chen Y, Sun J, Zhao Z, Chen X, and **Xu H**. Large-scale prediction of adverse drug reaction by integrating chemical, biological, and phenotypic properties of drugs. *J Am Med Inform Assoc.* 2012. 19(e1): e28-e35. [PMCID:PMC3392844]
50. Denny JC, Schildcrout JS, Bowton EA, Gregg W, Pulley JM, Basford MA, Cowan J, **Xu H**, Ramirez AH, Crawford DC, Ritchie MD, Peterson JF, Masys DR, Wilke RA, Roden DM. Optimizing drug outcomes through pharmacogenetics: A case for preemptive genotyping. *Clin Pharmacol Ther.* 2012. 92(2):235-42. [PMID: 22739144]
51. Wu Y, Levy MA, Micheel CM, Yeh P, Tang B, Cantrell MJ, Cooreman SM, **Xu H**. Identifying the status of genetic lesions in cancer clinical trial documents using machine learning. *BMC Genomics.* 2012, 13 Suppl 8:S21 [PMCID: PMC3535695]
52. Han B, Chen XW, Talebizadeh Z, **Xu H**. Genetic studies of complex human diseases: characterizing SNP-disease associations using Bayesian networks. *BMC Syst Biol.* 2012. 6 Suppl 3: S14 [PMCID: PMC3524021]
53. Lu Y, **Xu H**, Peterson NB, Dai Q, Jiang M, Denny JC, Liu M. Extracting epidemiological exposure and outcome terms from literature using machine learning approaches. *Int J Data Min Bioinform.* 2012; 6(4):447-59. [PMID: 23155773]
54. Roden DM, **Xu H**, Denny JC, Wilke RA. Electronic Medical Records as a Tool in Clinical Pharmacology: Opportunities and Challenges. *Clin Pharmacol Ther.* 2012, Apr 25. [PMID:22534870]
55. Delaney JT, Ramirez AH, Bowton EA, Pulley JM, Basford MA, Schildcrout JS, Shi Y, Zink R, Oetjens M, **Xu H**, Cleator JH, Jahangir E, Ritchie MD, Masys DR, Roden DM, Crawford DC, Denny JC. Predicting clopidogrel response using DNA samples linked to an electronic health record. *Clin Pharmacol Ther.* 2012 Feb;91(2):257-63. [PMID: 22190063]
56. Birdwell KA, Grady B, Choi L, **Xu H**, Bian A, Denny JC, Jiang M, Vranic G, Basford M, Cowan JD, Richardson DM, Robinson MP, Ikizler TA, Ritchie MD, Stein CM, Haas DW. The use of a DNA biobank linked to electronic medical records to characterize pharmacogenomic predictors of tacrolimus dose requirement in kidney transplant recipients. *Pharmacogenet Genomics.* 2012 22(1):32-42. [PMCID: PMC3237759]

57. Ramirez AH, Shi Y, Schildcrout JS, Delaney JT, **Xu H**, Oetjens MT, Zuvich RL, Basford MA, Bowton EA, Jiang M, Speltz P, Zink R, Cowan J, Pulley JM, Ritchie MD, Masys DR, Roden DM, Crawford DC, Denny JC. Predicting warfarin dosage in European and African Americans using DNA samples linked to an electronic health record. *Pharmacogenomics*. 2012, 13(4):407-18. [PMCID: PMC3361510]
58. Sun J, **Xu H**, Zhao Z Network-assisted investigation of antipsychotic drugs and their targets. *Chem Biodivers*. 2012, 9(5): 900-10. [PMID:22589091]
59. Sun J, Wu Y, **Xu H**, Zhao Z. DTome: a web-based tool for drug-target interactome construction, *BMC Bioinformatics*. 2012, 13(Suppl 9): 57.
60. Carroll RJ, Thompson WK, Eyster AE, Mandelin AM, Cai T, Zink RM, Pacheco JA, Boomershine CS, Lasko TA, **Xu H**, Karlson EW, Perez RG, Gainer VS, Murphy SN, Ruderman EM, Pope RM, Plenge RM, Kho AN, Liao KP, Denny JC. Portability of an algorithm to identify rheumatoid arthritis in electronic health records. *J Am Med Inform Assoc*. 2012, 19(e1):e162-9. [PMCID: PMC3392871]
61. Doan S, Collier N, **Xu H**, Pham HD, and Tu MP. Recognition of medication information from discharge summaries using ensembles of classifiers. *BMC Medical Informatics and Decision Making*. 2012, 12(1):36. [PMID: 22564405]
62. Chen Y, Mani S, **Xu H**. Applying active learning to assertion classification of concepts in clinical text. *J Biomed Inform* 2012, 45(2): 265-272. [PMCID: PMC3306548]
63. Wilke RA, **Xu H**, Denny JC, Roden DM, Krauss RM, McCarty CA, Davis RL, Skaar T, Lamba J, and Savova G. The emerging role of electronic medical records in pharmacogenomics. *Clin Pharmacol Ther*. 2011, 89(3): 379-86. [PMCID: PMC3204342]
64. Rosenbloom ST, Denny JC, **Xu H**, Lorenzi N, Stead WW, Johnson KB. Data from clinical notes: a perspective on the tension between structure and flexible documentation. *J Am Med Inform Assoc*. 2011, 18(2):181-6. [PMCID: PMC3116264]
65. Jiang M, Chen Y, Liu M, Rosenbloom ST, Mani S, Denny JC, **Xu H**. A study of machine-learning-based approaches to extract clinical entities and their assertions from discharge summaries. *J Am Med Inform Assoc*. 2011, 18(5):601-6. [PMCID: PMC3168315]
66. **Xu H**, Jiang M, Oetjens M, Bowton EA, Ramirez AH, Jeff JM, Basford MA, Pulley JM, Cowan JD, Wang X, Ritchie MD, Masys DR, Roden DM, Crawford DC, Denny JC. Facilitating pharmacogenetic studies using electronic health records and natural language processing: a case study of warfarin. *J Am Med Inform Assoc*. 2011; 18(4): 387-91. [PMCID: PMC3128409]
67. **Xu H**, AbdelRahman S, Lu Y, Denny JC, Doan S. Applying semantic-based probabilistic context free grammar to medical language processing – a preliminary study on parsing medication sentences. *J Biomed Inform* 2011, 44(6): 1068-75. [PMCID: PMC3226929]
68. **Xu H**, Stenner SP, Doan S, Johnson KB, Waitman LR, Denny JC. MedEx – A Medication Information Extraction System for Clinical Narratives. *J Am Med Inform Assoc*. 2010; 17(1):19-24. [PMCID: PMC2995636]
69. Denny JC, Peterson JF, Choma NN, **Xu H**, Miller RA, Bastarache L, Peterson NB. Development of a Natural Language Processing System to Identify Timing and Status of Colonoscopy Testing in Electronic Medical Records. *J Am Med Inform Assoc*. 2010; 17(4): 393-8. [PMCID: PMC2815478]
70. Doan S, Bastarache L, Klimkowski S, Denny JC, **Xu H**. Integrating Existing NLP Tools for Medication Extraction from Discharge Summaries. *J Am Med Inform Assoc*. 2010, 17:528-31. [PMCID: PMC2995674]

71. **Xu H**, Stetson P, Friedman C. Methods for Building Sense Inventories of Abbreviations in Clinical Notes. *J Am Med Inform Assoc*. 2009 16(1):103-108. [PMCID: PMC2605589]
72. Chen ES, Hripcsak G, **Xu H**, Markatou M, Friedman C. Automated Acquisition of Disease-Drug Knowledge from Biomedical and Clinical Documents. *J Am Med Inform Assoc*. 2008, 15(1):87-98. [PMCID: PMC2274872]
73. Tulipano KP, Tao Y, Millar WS, Zanzonico P, Kolbert K, **Xu H**, Yu H, Chen L, Lussier YA, Friedman C. Natural language processing and visualization in the molecular imaging domain. *J Biomed Inform*. 2007; 40:3, 270-281. [PMID: 17084109]
74. Fan JW, **Xu H**, Friedman C. Using Contextual and lexical features to restructure and validate the classification of biomedical concepts. *BMC Bioinformatics*. 2007; 8: 264. [PMCID: PMC2014782]
75. **Xu H**, Fan JW, Hripcsak G, Mendonça EA, Markatou M, Friedman C. Gene symbol disambiguation using knowledge-based profiles. *Bioinformatics*, 2007 23(8):1015-1022. [PMID: 17314123]
76. **Xu H**, Markatou M, Dimova R, Liu H, Friedman C. Machine learning and word sense disambiguation in the biomedical domain: design and evaluation issues. *BMC Bioinformatics*. 2006; 7:334. [PMCID: PMC1550263]
77. Lee HT, Krichevsky IE, **Xu H**, Ota-Setlik A, D'Agati VD, Emala CW. Local anesthetics worsen renal function after ischemia-reperfusion injury in rats. *Am J Physiol Renal Physiol*. 2004; 286(1):F111-9. [PMID: 14519592]
78. Lee HT, **Xu H**, Nasr SH, Schnermann J, Emala CW. A1 adenosine receptor knockout mice exhibit increased renal injury following ischemia and reperfusion. *Am J Physiol Renal Physiol*. 2004; 286(2):F298-306. [PMID: 14600029]
79. Lee HT, **Xu H**, Ota-Setlik A, Emala CW. Oxidant preconditioning protects human proximal tubular cells against lethal oxidant injury via p38 MAPK and heme oxygenase-1. *Am J Nephrol*. 2003; 23(5):324-33. [PMID: 12915776]
80. Lee HT, Ota-Setlik A, **Xu H**, D'Agati VD, Jacobson MA, Emala CW. A3 adenosine receptor knockout mice are protected against ischemia- and myoglobinuria-induced renal failure. *Am J Physiol Renal Physiol*. 2003; 284(2):F267-73. [PMID: 12388399]
81. Lee HT, **Xu H**, Siegel CD, Krichevsky IE. Local anesthetics induce human renal cell apoptosis. *Am J Nephrol*. 2003; 23(3):129-39. [PMID: 12586958]

#### Peer Reviewed Articles - Conference:

82. Zhang Y, Jiang M, Wang J, Xu H, Semantic Role Labeling of Clinical Text: Comparing Syntactic Parsers and Features, AMIA 2016, accepted
83. Lee H, Zhang Y, Xu J, Moon S, Wang J, Wu Y, and Xu H, UTHealth at SemEval-2016 Task 12: an End-to-End System for Temporal Information Extraction from Clinical Notes, Proceedings of the 10th International Workshop on Semantic Evaluation (SemEval-2016), 1292-1297, San Diego, California, June, 2016.
84. Tang B, Wang X, Wu Y, Zhang Y, Liu B, Fan Y, Xu H. Recognizing disjoint clinical concepts: challenges and solutions. *AMIA Annu Symp Proc*, 2015. 1184–1193 [PMCID: PMC4765674]
85. Xu J, Zhang Y, Wu Y, Wang J, Dong X, **Xu H**. Citation Sentiment Analysis in Clinical Trial Papers. *AMIA Annu Symp Proc*, 2015. 1334–1341 [PMCID: PMC4765697]
86. Wu Y, Xu J, Jiang M, Zhang Y, **Xu H**. A Study of Neural Word Embeddings for Named Entity Recognition in Clinical Text. *AMIA Annu Symp Proc*, 2015. 1326–1333. [PMCID: PMC4765694]
87. Xu J, Zhang Y, Wang J, Wu Y, Jiang M, Soysal E, and **Xu H**. UTH-CCB: The Participation of the SemEval 2015 Challenge – Task 14. Proceedings of the 9th

- International Workshop on Semantic Evaluation (SemEval 2015), pages 311–314, Denver, Colorado, June 4-5, 2015.
88. Wu Y, Jiang M, Lei J, **Xu H**. Named Entity Recognition in Chinese Clinical Text Using Deep Neural Network. *Medinfo 2015, Stud Health Technol Inform.* 2015;216:624-8
  89. Wu Y, Xu J, Zhang Y, **Xu H**. Clinical Abbreviation Disambiguation Using Neural Word Embeddings. *Proceedings of the 2015 Workshop on Biomedical Natural Language Processing (BioNLP 2015)*, 171–176
  90. Zhang Y, Soysal E, Moon S, Wang J, Tao C, **Xu H**. Integrating Multiple On-line Knowledge Bases for Disease-Lab Test Relation Extraction - *AMIA Summits on Translational Science Proceedings*, 2015, 204-210
  91. Chen Y, Wrenn J, **Xu H**, Spickard A, Habermann R, Powers J, Denny JC, Automated Assessment of Medical Students' Clinical Exposures according to AAMC Geriatric Competencies, *AMIA Annu Symp Proc* 2014, 375-84.
  92. Madani S, Aley R, Sittig DF, **Xu H**. Information extraction from clinical narratives: assessing ontology components. *International Conference on Biomedical Ontologies (ICBO)* 2014.
  93. Jiang M, Wu Y, Shah A, Priyanka P, Denny JC, **Xu H**. Extracting and standardizing medication information in clinical text – the MedEx-UIMA system. *AMIA Clinical Research Informatics Summit*, 2014.
  94. Zeng J, Wu Y, Balley, A, Johnson A, Halla V, Bernstam EV, **Xu H**, Meric-Bernstam F. Adapting a natural language processing tool to facilitate clinical trial curation for personalized cancer therapy. *AMIA Translational Bioinformatics Summit*, 2014.
  95. Tang B, Wang X, Wu Y, Jiang M, Wang J, **Xu H**. Recognizing Chemical Entities in Biomedical Literature using Conditional Random Fields and Structured Support Vector Machines. *BioCreative Challenge Evaluation Workshop* 2013 vol. 2, 70
  96. Wu Y, Tang B, Jiang M, Moon S, Denny JC, **Xu H**. Clinical Acronym/Abbreviation Normalization using a Hybrid Approach. 2013. *Proceedings of CLEF 2013 Evaluation Labs and Workshop*.
  97. Wu Y, Denny JC, Rosenbloom ST, Miller RA, Giuse D, Song M, **Xu H**. A Prototype Application for Real-time Recognition and Disambiguation of Clinical Abbreviations. *ACM Seventh International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO)*, 2013, San Francisco, USA.
  98. Tang B, Wu Y, Jiang M, and **Xu H**. A Machine Learning based System for Disorder Concept Extraction. 2013. *Proceedings of CLEF 2013 Evaluation Labs and Workshop*.
  99. Moon S, Berster BT, **Xu H**, Cohen T. Word sense disambiguation of clinical abbreviations with hyperdimensional computing. *AMIA Annu Symp Proc.* 2013. 16;1007-16. [PMCID: PMC3900125]
  100. Wu Y, Lei J, Wei W, Tang B, Denny JC, Rosenbloom ST, Miller RA, Giuse DA, Zhang K, **Xu H**. Analyzing differences between Chinese and English clinical text: a cross-institution comparison of discharge summaries in two languages. *Stud Health Technol Inform*, 2013, 192:662-6. [PMID: 23920639]
  101. Sun S., Zhou X., Denny JC, Rosenbloom CT, **Xu H**. Messaging to Your Doctors: Understanding Patient-Provider Communications via a Portal System. *Proceedings of ACM Conference on Human Factors in Computing Systems (SIG'CHI)*, 2013, Paris, France. 1739-48.
  102. Tang B, Can H, Wu Y, Jiang M, **Xu H**. Clinical Entity Recognition using Structural Support Vector Machines with Rich Features. *ACM Sixth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO)*, 2012, 13-20.

103. **Xu H**, Stetson PD, Friedman C. Combining corpus-derived sense profiles with estimated frequency information to disambiguate clinical abbreviations. *AMIA Annu Symp Proc.* 2012. 1004-13. [PMCID PMC3540457]
104. Wu Y, Denny JC, Rosenbloom ST, Miller RA, Giuse DA, **Xu H**. A comparative study of current clinical natural language processing systems on handling abbreviations in discharge summaries. *AMIA Annu Symp Proc.* 2012. 997-1003.
105. Liu M, Shah A, Min J, Peterson NB, Dai Q, Aldrich MC, Chen Q, Bowton EA, Liu H, Denny JC, **Xu H**. A study of transportability of an existing smoking status detection module across institutions. *AMIA Annu Symp Proc.* 2012. 577-86.
106. Jiang M, Denny JC, Tang B, Cao H, **Xu H**. Extracting semantic lexicons from discharge summaries using machine learning and c-value method. *AMIA Annu Symp Proc.* 2012. 409-16.
107. Wu Y, Liu M, Zheng W, Zhao Z, **Xu H**. Ranking gene-drug relationships in biomedical literature using latent dirichlet allocation. *Pac Symp Biocomput.* 2012: 422-33. [PMID: 22174297]
108. **Xu H**, Fu Z, Shah A, Chen Y, Peterson NB, Chen Q, Mani S, Levy MA, Dai Q, Denny JC. Extracting and integrating data from entire electronic health records for detecting colorectal cancer cases. *AMIA Annu Symp Proc.* 2011, 1564-72. [PMCID: PMC3244156]
109. Liu M, Kawai VK, Stein CM, Denny JC, Roden DM, **Xu H**. Modeling drug exposure data in electronic medical records: an application to warfarin. *AMIA Annu Symp Proc.* 2011, 815-23. [PMCID: PMC3243123]
110. Wu Y, Rosenbloom ST, Denny JC, Miller RA, Mani S, Giuse DA, **Xu H**. Detecting abbreviations in discharge summaries using machine learning methods. *AMIA Annu Symp Proc.* 2011, 1541-9. [PMCID: PMC3243185]
111. **Xu H**, AbdelRahman S, Jiang M, Fan JW, Huang Y. An Initial Study of Full Parsing of Clinical Text using the Stanford Parser. *International Workshop on Biomedical and Health Informatics, IEEE Conference of Bioinformatics and Biomedicine (BIBM)*, 2011.
112. **Xu H**, Doan S, Birdwell KA, Cowan JD, Vincz AJ, Haas DW, Basford MA, Denny JC. An automated approach to calculating the daily dose of tacrolimus in electronic health records. *AMIA Summits Transl Sci Proc.* 2010:71-5. [PMCID: PMC3041548]
113. Denny JC, Speltz P, Maddox R, Stein G, **Xu H**, Spickard A. Comparing Content Coverage in Medical Curriculum to Trainee-Authored Clinical Notes. *AMIA Annu Symp Proc.* 2010, 157-161. [PMCID: PMC3041398]
114. Doan S and **Xu H**. Recognizing Medication related Entities in Hospital Discharge Summaries using Support Vector Machine. *COLING 2010*, the 23<sup>rd</sup> International Conference on Computational Linguistics, 259-266.
115. **Xu H**, Lu Y, Jiang M, Liu M, Denny JC, Dai Q, Peterson NB. Mining Biomedical Literature for Terms related to Epidemiologic Exposures. *AMIA Annu Symp Proc.* 2010, 897-901. [PMCID: PMC3041399]
116. Fan JW, **Xu H**, Friedman C. Using Distributional Analysis to Semantically Classify UMLS Concepts. *In Proceedings of Medinfo.* 2007; 519-23. [PMID: 17911771]
117. **Xu H**, Fan JW, Friedman C. Combine multiple evidence for gene symbol disambiguation. *ACL 2007, BioNLP Workshop*, p41-48.
118. **Xu H**, Stetson P, Friedman C. A Study of Abbreviations in Clinical Notes. *AMIA Annu Symp Proc.* 2007; 821-5.
119. **Xu H**, Anderson, K, Grann, V, Friedman, C. Facilitating Cancer Research using Natural Language Processing of Pathology Reports. *In Proceedings of Medinfo.* 2004; 565-72. [PMID: 15360876]

**Editorials and Invited Articles:**

120. Ruan J, Jin V, Huang Y, **Xu H**, Edwards JS, Chen Y, Zhao Z. Education, collaboration, and innovation: intelligent biology and medicine in the era of big data *BMC Genomics* 2015, 16(Suppl 7):S1
121. Zhao Z, Zhang B, Huang Y, **Xu H**, McDermott JE. Computational methods for biomedical big data. *International Journal of Computational Biology and Drug Design (IJCBD)*. 2014, 7(2-3):97-101
122. McDermott JE, Huang Y, Zhang B, **Xu H**, Zhao Z. Integrative genomics and computational systems medicine. *BioMed Research International*. 2014, Article ID: 945253
123. Zhao Z, Zhang B, Huang Y, **Xu H**, McDermott JE. Computational methods for biomedical big data. *International Journal of Computational Biology and Drug Design (IJCBD)*. 2014, 7(2-3):97-101
124. McDermott JE, Huang Y, Zhang B, **Xu H**, Zhao Z. Integrative genomics and computational systems medicine. *BioMed Research International*. 2014, Article ID: 945253
125. Zhao Z, **Xu H**, Zhang B, Huang Y. Advances in intelligent biology and medicine. *International Journal of Computational Biology and Drug Design (IJCBD)*, 2013, 6(1-2):1-4
126. Zhang B, Huang Y, McDermott JE, Posey RH, **Xu H**, Zhao Z. Interdisciplinary dialogue for education, collaboration, and innovation: Intelligent biology and medicine in and beyond 2013. *BMC Genomics*, 2013, 14 (Suppl S8):S1
127. Liu M, Matheny ME, Hu Y, **Xu H**. Data mining methodologies for pharmacovigilance. *ACM SIGKDD Explorations Newsletter*. 2012; 14(1), 35-42.
128. Huang Y, Zhao Z, **Xu H**, Shyr Y, Zhang B. Advances in systems biology: Computational algorithms and applications. *BMC Systems Biology*, 2012, 6 (Suppl S3):S1
129. Zhao Z, Zhang B, Shyr Y, Huang Y, **Xu H**. Genomics in 2012: challenges and opportunities in the next generation sequencing era. *BMC Genomics*, 2012, 13 (Suppl S8):S1

**Book Chapters:**

1. Liu M, Hu Y, Matheny ME, and **Xu H**. Artificial Intelligence Approaches for Drug Safety Surveillance and Analysis. *Medical Applications of Artificial Intelligence*, Taylor & Francis Group, 2013.
2. Denny JC and **Xu H**. Linking genomic and clinical data for discovery and personalized care. *Methods in Biomedical Informatics: A Pragmatic Approach*. Academic Press, 2013
3. **Xu H** and Denny JC. Unlocking Information in Electronic Health Records Using Natural Language Processing: A Case Study in Medication Information Extraction. *Text Mining of Web-based Medical Content*, De Gruyter, 2014

**Abstracts/Posters:**

1. Chen G, Zhao J, Cohen T, Tao C, Sun J, **Xu H**, Bernstam E, Zeng J, Johnson A, Holla, Ann Balley V, Meric-Bernstam F and Zheng WJ, Standardized Pharmacological Class Profile in the Web Ontology Language (OWL), *International Conference on Biomedical Ontologies (ICBO)* 2014

2. Tao C, Sun J, Zheng W, Chen J, **Xu H**, Drug target prediction for colorectal cancer by combining ontology and network approaches, *International Conference on Biomedical Ontologies (ICBO) 2014*
3. Jiang M, Huang Y, Fan JW, Tang B, Denny J, **Xu H**. Parsing clinical text: how good are the state-of-the-art parsers? *ACM Eighth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO)*, 2014, Shanghai, China.
4. Chen Y, Zhang Y, Mei Q, Lasko T, Denny JC, **Xu H**. A preliminary study of coupling transfer learning with active learning for clinical named entity recognition between two institutions. *AMIA Annu Symp Proc*, 2014, Washington DC, US.
5. Moon S, Cohen T, **Xu H**. A study of synonym extraction from clinical texts using semantic vector models. *AMIA Annu Symp Proc*, 2014, Washington DC, US.
6. Sun J, Cui T, Zhu KW, Zheng J, Chen J, **Xu H**. an integrative framework for drug target prediction and repurposing. *AMIA Annu Symp Proc*, 2014, Washington DC, US.
7. Wu Y, Wright A, **Xu H**, McCoy AB, Sittig DF. Development of a unified computable problem-medication knowledge base. *AMIA Annu Symp Proc*, 2014, Washington DC, US.
8. Jiang M, Huang Y, Fan JW, Yang EW, **Xu H**. Building a Treebank of hospital discharge summaries. *AMIA Annu Symp Proc*, 2014, Washington DC, US.
9. **Xu H**, Aldrich MC, Chen Q, Peterson NB, Dai Q, Levy M, Shah A, Xue H, Li Y, Friedman C, Liu H, Denny JC. Electronic health record data suggests metformin improves cancer survival: A new model for drug repurposing studies. *AMIA Annu Symp Proc*, 2012, Chicago, IL.
10. Sun S, Zhou X, Denny JC, Rosenbloom CT, **Xu H**. (2012). Understanding Patient-Provider Communication Entered Via a Patient Portal System. *ASIS&T 2012*, Baltimore, Maryland.
11. Sun S, Zhou X, Denny JC, Rosenbloom CT, **Xu H**. Understanding Patient-Provider Communication via a Patient Portal. *AMIA Annu Symp Proc*, 2012, Chicago, IL.
12. Tang B, Wu Y, Jiang M, **Xu H**. Clinical Entity Recognition using Structural Support Vector Machines. *AMIA Annu Symp Proc*, 2012, Chicago, IL.
13. Shah A, Jiang M, Wu Y, Denny JC, **Xu H**. MedEx-UIMA – An Open-Source System for Medication Information Extraction from Clinical Text. *AMIA Annu Symp Proc*, 2012, Chicago, IL.
14. Ramirez AH, Shi Y, Schildcrout, Delaney JT, **Xu H**, Oetjens MT, Zuvich RL, Basford MA, Bowton E, Jiang M, Zink R, Cowan J, Pulley JM, Ritchie MD, Peterson JF, Masys DM, Roden DM, Crawford DC, Denny JC. Predicting warfarin dosage in European and African Americans using DNA samples linked to an electronic health record. *International Congress of Human Genetics*, 2011.
15. Liu M, McPeck Hinz ER, Denny JC, Mani S, Chen Y, Schildcrout JS, Miller RA, **Xu H**. A Feasibility Study in Detection of Adverse Drug Effects using Inpatient Laboratory Test Results. *International Biomedical Informatics Summit at Peking University*, Beijing, China, 2011
16. Birdwell KA, Grady B, Choi L, **Xu H**, Denny JC, Jiang M, Ritchie MD, Vranic G, Cowan JD, Basford BA, Stein CM, Ikizler TA, Haas DW. Use of a Novel Genomics/Informatics Resource to Identify Predictors of Tacrolimus Blood Concentrations in Kidney Transplant Recipients. *American Transplant Congress*, Philadelphia, PA, 2011.
17. Schildcrout JS, Denny JC, Bowton E, Gregg W, Pulley JM, Basford MA, Cowan J, **Xu H**, Ramirez AH, Crawford DC, Ritchie MD, Peterson JF, Masys DR, Wilke RA, Roden DM. Optimizing drug outcomes through pharmacogenetics: A case for preemptive genotyping. *International Congress of Human Genetics*, 2011.

18. Denny JC, Bastarache L, Ritchie MD, Basford MA, Pulley JM, Zuvich RL, Peissig PL, Carrell D, Pathak P, Rasmussen L, Pacheco J, Kho A, Weston N, Pendergrass S, **Xu H**, Li R, Manolio TA, Kullo IJ, Chute CG, Chisolm RL, Larson EB, McCarty CA, Masys DR, Roden DM, Crawford DC. A phenome-wide analysis of SNPs in the National Human Genome Research Institute genome-wide association catalog. *International Congress of Human Genetics*, 2011.
19. **Xu H**, Cunningham AJ, Roden DM, Stein CM. Facilitating Pharmacogenetic studies of warfarin outcomes using informatics methods. *ACRT 2010*
20. Liu M, Denny JC, Mani S, Chen Y, Hu Y, **Xu H**. Identifying potential drugs that induce QT prolongation using electronic medical records. *UT-ORNL-KBRIN Bioinformatics Summit 2010*.
21. Jiang M and **Xu H**. Fine-grained semantic analysis of numbers in clinical text. *AMIA Annu Symp Proc*, 2010.
22. Ramirez AH, **Xu H**, Oetjens M, Jeff JM, Zuvich R, Basford MA, Bowton E, Pulley JM, Ritchie MD, Crawford DC, Masys DR, Roden DM, Denny JC. Identifying genotype-phenotype relations in electronic medical record systems: application to warfarin pharmacogenomics. *American Heart Association*, 2010.
23. **Xu H**, Krupke D, Blake J, Friedman C. A Natural Language Processing (NLP) Tool to Assist in the Curation of the Laboratory Mouse Tumor Biology Database. *AMIA Annu Symp Proc*. 2006:1150.
24. **Xu H**, Friedman C. Facilitating Research in Pathology using Natural Language Processing. *AMIA Annu Symp Proc*. 2003:1057.
25. Lee HT, **Xu H**, Emala CW. Sevoflurane Protects Against Renal Ischemic Reperfusion Injury in Rats. *ASA Meeting 2002*.