

James Lin Chen
Curriculum Vitae

Education / Training

UNIVERSITY OF CHICAGO (Chicago, IL), <i>Hematology/Oncology Fellowship</i>	6/2008 – 6/2012
5/2011 – 6/2012 <i>Instructor</i> , 10% time	
6/2008 – 6/2012 <i>Research Fellow</i> with focus on translational bioinformatics: computationally deriving oncological biomarkers for use in the clinic to better personalize patient care	
6/2008 – 5/2011 <i>Clinical Fellow</i>	
GEORGETOWN UNIVERSITY HOSPITAL (Washington, DC), <i>Internal Medicine Residency</i>	6/2005 – 6/2008
NEW JERSEY MEDICAL SCHOOL (Newark, NJ), <i>MD degree awarded</i>	8/2001 – 6/2005
HARVARD COLLEGE (Cambridge, MA), <i>Cum Laude, BA in Biochemistry and coursework in computer science</i>	9/1995 – 6/1999

Research / Technical Experience

THE OHIO STATE UNIVERSITY (Columbus, OH)	8/2012 – present
<i>Assistant Professor of Biomedical Informatics and of Internal Medicine in the Division of Medical Oncology</i>	
Duties: 10% Clinical, 90% Research; Dually appointed in two departments with a special focus in translational bioinformatics as applied to oncology. Expert in genitourinary malignancies and in genomic modeling.	
UNIVERSITY OF CHICAGO (Chicago, IL)	6/2008 – 6/2012
<i>Instructor and Fellow in Bioinformatics and Oncology</i>	
Mentors: Bioinformatics : Yves A. Lussier, MD; Clinical : Walter M. Stadler, MD	
-- Developed genome-level approaches to better understand clinical phenotypes and molecular pathways	
(1) Used protein-protein interaction level molecular pathway prioritization, identified JAK2/STAT as a potentially key oncogenic pathway in poor prognosis prostate cancer	
(2) Used pathway-level genomic signatures, identified homeobox developmental pathways that correspond to patients with more aggressive disease in prostate cancer	
-- Developed informatically and <i>in vitro</i> derived biomarkers for translation into the clinical setting	
(1) Identified blood-based microRNA expression clusters in advanced prostate cancer for treatment stratification	
(2) Identified a blood-based microRNA expression signature for response to mTOR inhibition in renal cancer	
COLUMBIA MEDICAL INFORMATICS (New York, NY)	8/2004 – 8/2007
<i>Visiting Student, PI: Yves A. Lussier, MD</i>	
-- Focused on disease to phenotype mining of public ontologies	
-- With clustering and information theoretic techniques, performed analysis organizing disease using clustering techniques	
<i>Visiting Student, PI: Justin Starren, MD</i>	6/2002 – 8/2002
-- Performed analysis of diabetes telemedicine project data using clustering and regression techniques	
INGENUITY SYSTEMS (Redwood City, CA)	8/1999 – 8/2001
<i>Head of Ontology Engineering</i>	
-- Co-Directed a division of eight persons building the knowledge-base underlying their core product Ingenuity System's Pathway Analysis (IPA) tool.	
-- Played a key role in the development of the schema of the central ontology and its underlying theories	
-- Developed novel automated methods for ensuring data coherence to scientific principles	
-- Significantly contributed to the architecture of how each unit of medical information was modeled and captured	
-- Developed high-throughput processes and designed tools for ontology building	
WHITEHEAD CENTER FOR GENOMIC RESEARCH (Cambridge, MA)	1998-1999
<i>Intern, Eric Lander Group, Supervisor: Pablo Tamayo, PhD</i>	
-- Developed programs clustering gene chip spots as a verification of integrity	
-- Wrote PERL scripts to help prototype high-throughput gene chip analysis	
BRISTOL-MYERS SQUIBB (Lawrenceville, NJ)	7/1997 – 10/1997
<i>Intern, High-Performance Computing/Bioinformatics</i>	
-- Architected the storage schema for the company-wide DNA sequencing center	
-- Administered and setup a SunBox	
<i>Intern, Worldwide Clinical Research and Development</i>	6/1996 – 8/1996
-- Developed PL/SQL and FoxPro programs to extract information from clinical trial databases (Oracle-based) and present them locally as web pages to facilitate access for clinical trial coordinators and investigators	
-- Streamlined existing clinical trial database programs; Learned four programming languages in the scope of two months	

Honors

- 1999 Graduated Cum Laude, Harvard College
2003 Summer scholarship for HIV curriculum development, NJ Medical School
2005 Gold Humanism Society Inductee, NJ Medical School
2005 Alumni Scholarship Recipient, NJ Medical School
2007 ACP Regional Meeting 1st Place Podium Presentation, Fulminant Granulomatous Meningoencephalitis in a Patient Treated with Alemtuzumab
2008 String of Pearls Teaching Award Nominee, Georgetown University Hospital
2008 William P. Argy Memorial Teaching Award, Georgetown University Hospital
2009 AACR Molecular Biology in Clinical Oncology participant, Aspen, CO
2010 NIH Loan Repayment Program Recipient
2010 Outstanding Paper Award from the American Medical Informatics Association: Stromal Microenvironment Processes Unveiled by Biological Component Analysis of Gene Expression in Xenograft Tumor Models. (BMC Bioinformatics. 2010. 11(Suppl 9):S11)
2011 ECCO-AACR-EORTC-ESMO Methods in Clinical Cancer Research participant, FLIMS, Switzerland
2011 AMIA 2011 Annual Symposium Attendee Survey Award: Complex Disease Networks of Trait-associated SNPs Unveiled by Information Theory (Li H, Lee Y, Li J, **Chen JL** et al)
2011 JAMIA Editor's Choice Award for article: Protein-Network Modeling of Prostate Cancer Gene Signatures Reveals Essential Pathways in Disease Recurrence. (**Chen JL et al.** J Am Med Inform Assoc 18:392-402, 2011)
2012 ASCO Genitourinary Cancers Symposium Merit Award Recipient
2012 The Molecular and Translational Oncology Workshop selected participant (May 18-22), Fort Myers, FL
2012 ASCO Annual Meeting Merit Award Recipient

Peer-Reviewed Journal Articles

1. **Chen JL**, Liu Y, Sam LT, Li J, Lussier YA. Evaluation of High-Throughput Functional Categorization of Human Disease Genes. (BMC Bioinformatics 2007, 8, Suppl 3:S7)
2. Yang X, Huang Y, **Chen JL**, Xie J, Sun X, Lussier YA. Mechanism-Anchored Profiling Derived from Epigenetic Networks Predicts Outcome in Acute Lymphoblastic Leukemia. (BMC Bioinformatics. 2009 Sep 17;10 Suppl 9:S6)
3. Yang X, Lee Y, Huang Y, **Chen JL**, Xing HR, Lussier YA. Stromal Microenvironment Processes Unveiled by Biological Component Analysis of Gene Expression in Xenograft Tumor Models. (BMC Bioinformatics. 2010. 11(Suppl 9):S11)
4. **Chen JL**, Sam L, Huang Y, Lee Y, Li J, Liu Y, Xing HR, Lussier YA. Protein Interaction Network Underpins Concordant Prognosis among Heterogeneous Breast Cancer Signatures. (J Biomedical Informatics. 2010 Jun;43(3):385-96)
5. **Chen JL**, Li J, Stadler W, Lussier YA. Protein-Network Modeling of Prostate Cancer Gene Signatures Reveals Essential Pathways in Disease Recurrence. (J Am Med Inform Assoc 18:392-402, 2011) – Editor's Choice Award
6. Ferreira CM, **Chen JL**, Li J, Shimomura K, Yang X, Lussier YA, Pinto LH, Solway J. Genetic interactions between loci on chromosomes 11 and 18 contribute to native airway constrictor hyperresponsiveness in A/J vs C57Bl/6 mice (PLoS One. 2012;7(1):e29579. Epub 2012 Jan 10).
7. Li H, Lee Y, Li J, **Chen JL**, Rebman E, Lussier YA. Complex Disease Networks of Trait-Associated SNPs Unveiled by Information Theory. J Am Med Inform Assoc (J Am Med Inform Assoc doi:10.1136/amiainl-2011-000482)
8. **Chen JL**, Li J, Kirlik K, Rosen A, Paner G, Antic T, Lussier YA, Vander Griend D. Dereglulation of a Hox Protein Regulatory Network Spanning Prostate Cancer Initiation and Progression (Clin Cancer Res. 2012 Aug 15;18(16):4291-302. Epub 2012 Jun 21)

Perspectives / Book Chapters

1. **Chen JL**, Lussier YA, "Clinical Ontologies," Encyclopedia of Database Systems, Editors-in-chief: Özsu, M. Tamer; Liu, Ling, Springer, 2009. (print and online)
2. Lussier YA, **Chen JL**, The Emergence of Genome-Based Drug Repositioning. (Sci. Transl. Med. 3, 96ps35, 2011)
3. Lussier YA, Stadler WM, **Chen JL**. Advantages of Genomic Complexity: Bioinformatic Opportunities in MicroRNA Cancer Signatures. (J Am Med Inform Assoc. 2011 Nov 18. 9)

Abstract(s) / Oral Presentations

1. **Chen JL**, Fulminant Granulomatous Meningoencephalitis in a Patient Treated with Alemtuzumab, (2007 ACP Regional Meeting, Bethesda, MA)
2. **Chen JL**, Context-Constrained Molecular Interaction Networks Uncover Shared Biological Pathways Among Breast Cancer Signatures. Podium Presentation. (AMIA 2010 Summit on Translational Bioinformatics, San Francisco, CA March 10, 2010)
3. **Chen JL**, Li J, Stadler YM, Lussier YA. Use of Protein-Network Modeling of Prostate Cancer Gene Signatures to Investigate Essential Pathways in Disease Recurrence. Poster presentation (2011 ASCO Genitourinary Cancers Symposium, Orlando, FL, Feb 17-19, 2011)
4. **Chen JL**, Appelbaum DE, Kocherginsky M, Rathmell WK, McDermott DF, Stadler WM. FDG-PET as a Predictive Marker for Therapy With Everolimus in Metastatic Renal Cell Cancer (mRCC). (J Clin Oncol 29: 2011 (suppl; abstr e15047))
5. **Chen JL**, Otto K, Vander Griend D. Homeobox Pathway Underlies Differences in Seminal Vesicle and Prostate Epithelium and May be Critical to Prostate Carcinogenesis. (2012 ASCO Genitourinary Cancers Symposium, San Francisco, CA, February 2-4, 2012)
6. **Chen JL**, Rathmell WK, McDermott DF, Stadler WM. Circulating Mir-21 and Mir-378 are Predictive of Progression Free Survival (PFS) in Patients Treated with Everolimus in Metastatic Renal Cell Cancer (mRCC). (2012 ASCO Annual Meeting, Chicago, IL June 1-5)
7. **Chen JL**, Hsu A, Yang Y, Li J, Parinandi G, Lussier YA. Curation-Free Biomodule Mechanisms in Prostate Cancer Predict Recurrent Disease (2012 TBC Conference, Jeju Island, Korea).
8. Lee Y, Li H, Li J, Rebman E, Regan K, Gamazon ER, **Chen JL**, Yang X, Cox NJ, Lussier YA. Network Models of GWAS Uncover the Topical Centrality of Protein Interactions in Complex Disease Traits (2012 TBC Conference, Jeju Island, Korea)

Manuscripts Under Review / In Preparation

1. **Chen JL**, Appelbaum DE, Kocherginsky M, Rathmell WK, McDermott DF, Stadler WM., FDG-PET as a Predictive Biomarker for Therapy With Everolimus in Metastatic Renal Cell Cancer (mRCC) (under review, Clinical Cancer Research)
2. **Chen JL**, Song SS, Khodarev NN, Kregel S, Weichselbaum RR, Vander Griend D, Stadler WM., Jak2 Activation is a Critical Prosurvival Pathway in Advanced Prostate Cancer (manuscript under preparation)

Invited Talks / Presentations

ACP Regional Meeting, Bethesda, Maryland 2007
University of Chicago Cancer Center, Chicago, IL, February 11, 2011
American Medical Informatics Association Webinar Series, online at www.amia.org, August 5, 2011
Northwestern/University of Chicago Prostate Cancer SPORE, Northwestern University, August 17, 2011

Review Panel

Invited Reviewer: Journal of the American Medical Informatics Association, Molecular Cancer Therapeutics, PLoS ONE, Bioinformatics

Research Support / Grants

COMPLETED

- UL1 RR024999, CTSA/ITM Fellow Short-Term Pilot Study Award, \$2,074	<i>1/28/2010 – 5/12/2010</i>
- T32 CA09566 (Olopade), NIH/NCI, \$341,424	<i>7/1/09-6/30/12</i>
- UL1 RR024999, CTSA/ITM Pilot, \$40,000	<i>10/15/2011 – 10/15/2012</i>

Professional Memberships

American College of Physicians	American Society of Clinical Oncology
American Society of Hematology	American Association for Cancer Research
American Medical Informatics Association	

Teaching Experience

UNIVERSITY OF CHICAGO (Chicago, IL) <i>Module Instructor</i> , “Introduction to Clinical Ontologies”, (BIOS 27100, CCTS 42100) <i>Curriculum Organizer (medical student didactics), Ad hoc lecturer</i>	<i>11/15/2010</i> <i>9/2009-12/2009</i>
GEORGETOWN UNIVERSITY HOSPITAL (Washington, DC) <i>Argy (Teaching) Resident</i> : Organized medical student didactics and lectured three days a week	<i>4/2005</i>
NEW JERSEY MEDICAL SCHOOL: STUDENTS TEACHING AIDS TO STUDENTS (Newark, NJ) <i>Director (2003)</i>	<i>9/2001 – 6/2003</i>

Community Service

NEW JERSEY MEDICAL SCHOOL: STUDENT FAMILY HEALTH CARE CENTER (Newark, NJ) <i>Director (6/2003- 6/2005)</i>	<i>9/2001 – 6/2005</i>
SAN FRANCISCO AIDS FOUNDATION (San Francisco, CA) <i>HIV Counselor</i>	<i>12/1999 – 8/2001</i>

Skills

Computer: PERL, Python, R/Bioconductor, SQL, ASK, PL/SQL, C, HTML, Java Script, Ingenuity IPA, Spotfire, Cytoscape, BRB-Tools
Languages: English (native speaker), Taiwanese (verbal), basic Spanish and French (verbal and written), basic Mandarin (verbal)

Personal

Hobbies: international travel, triathlons, making pastries