

Curriculum Vitae and Bibliography

Zhifu Sun, MD, MS

Personal Information

Citizenship: United States of America
Work Address: Mayo Clinic Rochester
200 First St SW
Rochester, MN 55905-0001
507-266-1894
Email Address: Sun.Zhifu@mayo.edu

Present Academic Rank and Position

Assistant Professor of Epidemiology - Mayo Clinic College of Medicine and Science 05/2007 - Present
Associate Professor of Biomedical Informatics - Mayo Clinic College of Medicine and Science 03/2016 - Present
Consultant - Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota 11/2017 - Present

Education

College of Medicine, Qingdao University, Qingdao, China - MD 1979 - 1984
Shandong Provincial Qianfoshan Hospital, China - Resident, Anatomic Pathology 1984 - 1986
Hebei Medical University, China - MS, Pathology 1986 - 1989
Shandong Provincial Qianfoshan Hospital, China - Resident, Anatomic Pathology 1989 - 1991
University of Minnesota Medical School - MS, Health Informatics 1998 - 2000
Mayo Clinic Graduate School of Biomedical Sciences, Mayo Clinic College of Medicine and Science, Completed 10 classes for the Master Degree in Clinical Research 2002 - 2004

Certification

Board Certifications

Educational Commission for Foreign Medical Graduates (ECFMG)

ECFMG Certificate

United States Medical Licensing Examination (USMLE)

Step I

Step II Clinical Knowledge

Step II Clinical Skills

Honors and Awards

Research Assistantship - University of Minnesota 01/1998
Teaching Assistantship - University of Minnesota 01/1999

Previous Professional Positions and Major Appointments

Attending Pathologist - Shandong Provincial Qianfoshan Hospital, China, Shandong, China	07/1991 - 08/1997
Research Assistant/Database Developer - University of Minnesota Cancer Center, Minnesota	09/1998 - 08/1999
Research/Teaching Assistant - University of Minnesota Medical School, Minnesota	09/1999 - 05/2000
Intern Applications Programmer - Virtual Funds/Ensodex, St. Paul, Minnesota	06/2000 - 09/2001
Research Associate - Division of Epidemiology, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	06/2002 - 08/2007
Professional Associate in Research - Division of Epidemiology, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	08/2007 - 04/2008
Informatics Specialist II - Biomedical Statistics & Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	04/2008 - 06/2010
Assistant Professor in Biomedical Informatics - Mayo Clinic College of Medicine and Science	06/2010 - 02/2016
Research Associate - Biomedical Statistics & Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	06/2010 - 05/2012
Associate Consultant I-Research - Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	05/2012 - 05/2014
Senior Associate Consultant II-Research - Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota	05/2014 - 10/2017

Professional Memberships and Societies

Professional Memberships and Services

American Association for Cancer Research Member	2004 - Present
American Society for Human Genetics Member	2014 - Present
Chinese Society of Stereology & Computational Tissue Morphology Member	1989 - 1997
Epigenetics Society Member	2014 - Present
Human Genome Organisation (HUGO) Member	2012 - Present
International Association for the Study of Lung Cancer Member	2005 - Present
International Society of Computational Biology Member	2004 - Present
Sigma Xi, The Scientific Research Society Member	2005 - Present

Journal Responsibilities**Journal Editorial Responsibilities**

Dataset Papers in Medicine (Pulmonology Section) Editorial Board Member	2015 - Present
Epigenomics Editorial Board Member	2015 - Present
Frontiers in Genetics Guest Associate Editor	2017 - 2018
International Journal of Chronic Diseases Editorial Board Member	2012 - Present
Journal of Computational Biology and Bioinformatics (Austin) Editorial Board Member	2015 - Present
World Journal of Respiratory Associate Editor	2016 - 2018

Journal Other Responsibilities

BioData Mining Ad Hoc Manuscript Reviewer	09/2011
Bioinformatics Ad Hoc Manuscript Reviewer	03/2012
Ad Hoc Manuscript Reviewer	03/2013
Ad Hoc Manuscript Reviewer	05/2013
Ad Hoc Manuscript Reviewer	05/2013
Ad Hoc Manuscript Reviewer	07/2013
Ad Hoc Manuscript Reviewer	08/2014
Ad Hoc Manuscript Reviewer	11/2016

Peer Reviewer	07/2017
BioMed Research International	
Ad Hoc Manuscript Reviewer	11/2016
Biomedical Research International	
Ad Hoc Reviewer	11/2013
Ad Hoc Manuscript Reviewer	02/2014
BMC Bioinformatics	
Ad Hoc Manuscript Reviewer	05/2011
Ad Hoc Manuscript Reviewer	03/2013
Ad Hoc Manuscript Reviewer	08/2013
Ad Hoc Manuscript Reviewer	04/2014
Ad Hoc Manuscript Reviewer	03/2015
Ad Hoc Manuscript Reviewer	09/2015
BMC Biotechnology	
Peer Reviewer	05/2017
BMC Cancer	
Ad Hoc Manuscript Reviewer	07/2013
Ad Hoc Reviewer	05/2018
BMC Genomics	
Ad Hoc Manuscript Reviewer	11/2012
BMC Medical Genomics	
Ad Hoc Manuscript Reviewer	05/2014
Ad Hoc Manuscript Reviewer	06/2014
Ad Hoc Manuscript Reviewer	11/2014
Ad Hoc Manuscript Reviewer	03/2015
BMC Molecular Biology	
Ad Hoc Manuscript Reviewer	08/2011
Briefings in Bioinformatics	
Ad Hoc Manuscript Reviewer	05/2015
Ad Hoc Manuscript Reviewer	05/2016
Ad Hoc Manuscript Reviewer	09/2016
Reviewer	07/2017
Peer Reviewer	12/2017
AdHoc Journal Reviewer	02/2018
AdHoc Journal Reviewer	03/2018
AdHoc Journal Reviewer	09/2018
AdHoc Journal Reviewer	11/2018
AdHoc Journal Reviewer	12/2018
British Journal of Cancer	
Reviewer	02/2008
Cancer Epidemiology, Biomarkers and Prevention	
Reviewer	10/2005
Cancer Informatics	
Ad Hoc Manuscript Reviewer	07/2016

Cancer Letters	
Reviewer	09/2006
Reviewer of research articles	05/2008
Carcinogenesis	
Reviewer	10/2004
Cellular Physiology and Biochemistry	
AdHoc Journal Reviewer	12/2018
Chronic Diseases and Translational Medicine	
Ad Hoc Manuscript Reviewer	01/2016
Clinical and Applied Immunology Reviews	
Reviewer	11/2005
Clinical Cancer Research	
Reviewer	02/2004
Epigenomics	
Ad Hoc Manuscript Reviewer	02/2016
Editor/Reviewer	03/2016
Editor/Reviewer	06/2016
Invited Expert Reviewer	07/2016
Frontiers in Genetics	
Ad Hoc Journal Reviewer	08/2018
Frontiers in Physiology	
Ad Hoc Journal Reviewer	07/2018
Genes	
Peer Academic Reviewer	03/2017
Peer Academic Reviewer	04/2017
Ad Hoc Journal Reviewer	12/2018
Genome Biology	
Ad Hoc Journal Reviewer	06/2018
International Journal of Cancer	
Reviewer	12/2004
Reviewer	10/2005
Reviewer	01/2009
Reviewer	03/2011
International Journal of Environmental Research and Public Health	
Peer Reviewer	11/2017
International Journal of Molecular Sciences	
Ad Hoc Manuscript Reviewer	08/2016
Journal of Clinical Oncology	
Reviewer	02/2009
Journal of Pathology	
Reviewer	01/2006
Journal of the American Medical Association	
Reviewer	10/2005
Journal of Thoracic Oncology	

Ad Hoc Manuscript Reviewer	08/2015
Ad Hoc Manuscript Reviewer	06/2016
Peer Reviewer	09/2017
Ad Hoc Journal Reviewer	04/2018
Lung Cancer	
Reviewer	12/2004
Reviewer	07/2006
Reviewer of research articles	11/2008
Ad Hoc Manuscript Reviewer	02/2015
Molecular Cancer Therapeutics	
Reviewer	04/2008
Nature Communications	
Peer Reviewer	08/2017
Peer Reviewer	10/2017
Peer Reviewer	11/2017
Ad Hoc Journal Reviewer	08/2018
Oncology Letters	
Peer Academic Reviewer	04/2017
Oncology Reports	
Ad Hoc Journal Reviewer	09/2018
Oncotarget	
Ad Hoc Manuscript Reviewer	05/2015
OncoTarget	
Ad Hoc Manuscript Reviewer	03/2016
OncoTargets and Therapy	
Ad Hoc Manuscript Reviewer	02/2015
Ad Hoc Reviewer	04/2016
Ad Hoc Manuscript Reviewer	04/2016
Panminvera Medica	
Reviewer	06/2005
PeerJ	
Ad Hoc Manuscript Reviewer	09/2015
PLoS ONE	
Ad Hoc Manuscript Reviewer	06/2014
Ad Hoc Manuscript Reviewer	09/2015
PlosOne Journal	
Ad Hoc Manuscript Reviewer	06/2016
Science	
Ad Hoc Journal Reviewer	08/2018
Scientific Reports	
Peer Reviewer	03/2017
Peer Reviewer	09/2017
Peer Reviewer	10/2017
Peer Reviewer	11/2017

Scientific Reports, a Nature Journal Ad Hoc Manuscript Reviewer	08/2015
Transactions on Computational Biology and Bioinformatics Ad Hoc Manuscript Reviewer	10/2014
Tumor Biology Ad Hoc Manuscript Reviewer	06/2014
VirusDisease Ad Hoc Manuscript Reviewer	04/2014
World Journal of Clinical Oncology Ad Hoc Manuscript Reviewer	02/2014
World Journal of Surgery Reviewer	11/2005

Education Interests and Accomplishments

Curriculum and Course Development

CTSC5140 Mayo Graduate School & CCaTS Rochester, Minnesota	2012 - Present
BMB6660 Mayo Graduate School Rochester, Minnesota	2012 - Present
Introduction to Bioinformatics(BMI550) Teach remotely Arizona State University	2015 - Present

Teaching

Anatomic Pathology Shandong Medical University, School of Medicine Jinan, China	1996 - 1997
Pathophysiology Shandong Medical University, School of Medicine Jinan, China	1996 - 1997
Health Informatics System and Methods Graduate School, University of Minnesota Minneapolis, Minnesota	1999 - 2000
Epigenomics (BMB 8660) Mayo Graduate School Rochester, Minnesota	2012
microRNA: Function, Profiling and Clinical Applications Introduction to Bioinformatics (BMB 8350/6350) Mayo Graduate School Rochester, Minnesota	2012
Epigenetics & Epigenomics - Impact on Translational Research and Future Medical Practice (CTSC6140) --Bioinformatics Data Analysis for High Throughput Sequencing Data in Epigenomics Research CTSA Rochester, Minnesota	2013

microRNA: Function, Profiling and Clinical Applications Introduction to Bioinformatics (BMB 8350/6350) Mayo Graduate School Rochester, Minnesota	2013
CTSC5140:Epigenetics & Epigenomics: Impact on Translational Research and Future Medical Practice Bioinformatics Data Analysis for High Throughput Sequencing Data in Epigenomics Research Graduate School & CCaTS Rochester, Minnesota	2014
BMB6660:Transcription, Chromatin, and Epigenetics DNA Methylation and RNA-seq: Data Analyses and Representation Mayo Graduate School Rochester, Minnesota	2014
CTSC5140:Epigenetics & Epigenomics: Impact on Translational Research and Future Medical Practice Bioinformatics Data Analysis for High Throughput Sequencing Data in Epigenomics Research Graduate School & CCaTS Rochester, Minnesota	2015
Gene expression analysis(ASU BMI550) Arizona State University Phoenix, Arizona	2015
Bioinformatics: Analyses of Epigenomic Data – DNA Methylation CTSC5140 Rochester, Minnesota	2016
Correlative DNA methylation and RNA expression in Crohn's disease (a case study) CTSC5140 Rochester, Minnesota	2016
DNA Methylation and RNA-seq: Data Analyses and Representation BMB 6660 Rochester, Minnesota	2016
Bioinformatics: Analyses of Epigenomic Data – DNA Methylation (and gene expression by RNA-seq) CCaTS - CTSC5140 Rochester, Minnesota	2017
DNA Methylation Data and Analytics: Overview BSI Book Club Rochester, Minnesota	04/2018
DNA Methylation and RNA-seq: Data Analyses and Representation BMB 6660 Rochester, Minnesota	12/2018

Mentorship

Suginura, Hiroshi (Visiting Research Fellow) Description: Co-mentor Current Status: Chief Surgeon, Thoracic Surgery, Fujita Health University, Japan Outcome: Improved research skills; wrote a manuscript	01/2003 - 01/2005
Endo, Chiaki (Visiting Research Fellow) Description: Co-mentor Current Status: Chief Surgeon, Tohoko University, Japan Outcome: A first authored publication	01/2004 - 01/2005

Baheti, Saurabh (Allied Health Staff)	01/2010 - Present
Description: Scientific and technical mentor as a faculty lead	
Current Status: Lead Informatics Specialist	
Outcome: Wrote first authored papers and currently a Lead Informatics Specialist	
Li, Yafei (Postdoctoral Research Fellow)	01/2010 - 01/2012
Description: Co-mentor	
Current Status: Professor, Department of Epidemiology, Military Medical University	
Outcome: First authored publications; continued collaborations; and currently the Director of the Department of Epidemiology	
Nair, Asha (Allied Health Staff)	01/2011 - Present
Description: Scientific and technical mentor as a faculty lead	
Current Status: Lead Informatics Specialist	
Outcome: Promoted to Lead Informatics Specialist; A more independent thinker for scientific research; Co-first authored publications	
Evans, Jared (Allied Health Staff)	01/2012 - Present
Description: Scientific and technical mentor as a faculty lead	
Current Status: Lead Informatics Specialist	
Outcome: Mentored miRNA workflow development and manuscript writing; currently a Lead Informatics Specialist at Mayo	
Bo, Deng (Postdoctoral Research Fellow)	01/2012 - 01/2013
Description: Co-mentor	
Current Status: Associate Chief Surgeon and Associate Professor, Daping Hospital, Third Military Medical University	
Outcome: Mentored publications and enhanced research skills	
Bhagwate, Aditya (Allied Health Staff)	01/2013 - Present
Description: Scientific and technical mentor as a faculty lead	
Current Status: Informatics Specialist II	
Outcome: The mentee has become more independent and knowledgeable in biological and bioinformatics aspects; promoted to IS II	
Wang, Chen (Associate Consultant)	01/2014 - Present
Description: Co-mentor as mentoring committee	
Current Status: Senior Associate Consultant I and Associate Professor	
Outcome: Senior Associate Consultant I and Associate Professor	
Li, Ying (Visiting Scientist)	12/2014 - 05/2016
Description: Primary mentor	
Current Status: Associate Professor and Chief Physician, Peoples' Hospital of Zhengzhou University	
Outcome: First authored publication and continued collaboration in research	
Yan, Huihuang (Mayo Clinic Staff)	01/2016 - Present
Description: Co-mentor as mentoring committee	
Current Status: Senior Associate Consultant I and Associate Professor	
Outcome: Mentored publications; More familiar with Mayo research environment	
Zhang, Yun (Intern)	05/2016 - 07/2016
Description: Primary mentor	
Current Status: Research Scientist at The J. Craig Venter Institute	
Outcome: The mentee published a first authored paper in a high impact bioinformatics journal	

Rong, Huang (Intern) Description: Primary mentor Current Status: PhD candidate Outcome: Contributed a manuscript; successfully added to PhD program from MS program	07/2016 - 09/2016
Yu, Gu (Summer Intern) Description: Primary mentor Current Status: PhD Candidate Outcome: Developed statistical method for single cell analyses and contributed to a manuscript	06/2017 - 08/2017
He, Yanqi (Postdoctoral Research Fellow) Description: Co-mentor Current Status: Visiting Research Fellow at Mayo Attending Physician at Huanxi Medical University Outcome: Ongoing with manuscripts	05/2018 - Present
Tian, Long (Summer Intern) Description: Primary mentor Current Status: PhD Candidate Outcome: A web-based application and meeting presentation	05/2018 - 08/2018
Haijing, Liu (Visiting Research Fellow) Description: Primary mentor and sponsor Current Status: Visiting research fellow (ongoing) Outcome:	09/2018 - Present
Zhao, Hao (Oncology Fellow) Description: As a mentor for bioinformatics and data mining in personalized medicine Current Status: Clinical Oncology Fellow Outcome: Ongoing	01/2019 - Present

Academic Career Development

Presentation Skills workshop Office of Leadership and Organization Development Rochester, Minnesota	06/2015
The Leadership Effect Office of Leadership and Organization Development Rochester, Minnesota	07/2015
New Physician & Scientist - Professionalism II 251001LEDR000215 Office of Leadership and Organization Development Rochester, Minnesota	02/2016
New Physician & Scientist - Leading with Emotional Intelligence Course 251101EMPL001015 Office of Leadership and Organization Development Rochester, Minnesota	02/2016
New Physician & Scientist - Professionalism III Course 251101LEDR001915 Office of Leadership and Organization Development Rochester, Minnesota	06/2016

Educational Activities

Bioinformatics; Epigenetics and Epigenomics; Molecular Epidemiology

Institutional/Departmental Administrative Responsibilities, Committee Memberships and Other Activities

Mayo Clinic

Department of Health Sciences Research

Member, Division of Biomedical Statistics and Informatics, Bioinformatics Core, Recruiting Committee	2010 - Present
Member, Division of Biomedical Statistics and Informatics, Biostatistics Job Evaluation Committee	2010 - 2014
Group Leader, Division of Biomedical Statistics and Informatics, Bioinformatics Core, Methyl-Seq workgroup	2011 - Present
Group Leader, Division of Biomedical Statistics and Informatics, Bioinformatics Core, miRNA-Seq Workgroup	2012 - Present
Associate Director, Division of Biomedical Statistics and Informatics, Bioinformatics Core	2015 - Present

Mayo Clinic Center for Individualized Medicine

Committee Member, Epigenomics Program	2010 - Present
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Activities at Other Institutions

2017 International Conference on Bioinformatics Research and Applications Session Moderator	12/09/2017
2018 6th International Conference on Bioinformatics and Computational Biology Conference Program Committee Member	03/12/2018 - 03/14/2018
2018 International Conference on Digital Medicine and Image Processing Conference Program Committee Chair/Track Chair	11/12/2018 - 11/14/2018
2019 IEEE 7th International Conference on Bioinformatics and Computational Biology (ICBCB 2019) Committee Member	03/21/2019 - 03/23/2019
2019 International Conference on Bioinformatics Research and Applications Scientific Committee	06/19/2019 - 06/21/2019
Genome USA 2018 Conference Program Committee Member	01/29/2018 - 01/31/2018
International Conference on Bioinformatics Research and Applications Scientific Committee	12/27/2018 - 12/29/2018
International Conference on Intelligent Biology and Medicine 2018 Session Moderator	06/10/2018 - 06/12/2018

Presentations Extramural

National or International

Invited

SnowShoes -- a comprehensive analytical workflow for mRNA-Seq at Mayo Clinic Distinguished faculty Next-Gen Sequencing Congress 2011 Boston, Massachusetts	04/2011
Next generation sequencing in modern medical research: bioinformatics analysis and clinical applications Third Military Medical University Chongqing, China	10/2014

Pathway deregulation and clinical implications of somatic mutations in DNA and RNA of lung adenocarcinoma World DNA and Genome Day (2015) Nanjing, China	04/2015
Detect and characterize actionable mutations and deregulated pathways in lung adenocarcinoma for personalized medicine from NGS data Joint Meeting - World Congress on Advances in Oncology & International Symposium on Molecular Medicine Athens, Greece	10/2015
Characteristic DNA methylation shift in CD4+ lymphocytes of Crohn's disease and its impact on gene expression revealed by high throughput sequencing International Conference on Computational Genomics and Proteomics Panama City, Panama	08/2017
UCIncr: Ultrafast and Comprehensive long non-coding RNA detection from RNA-seq Organizing committee member International Conference on Bioinformatics Research and Applications (ICBRA 2017) Barcelona, Spain	12/2017
Methylome changes in CD4+ lymphocytes of Crohn's disease and its association with gene expression Genome USA 2018 Las Vegas, Nevada	01/2018
Indel sensitive and comprehensive variant/mutation detection from RNA-seq for precision medicine Organizing committee member ICBCB2018 Chengdu, China	03/2018
Mine big methylome data for cancer early diagnosis and drug response signatures Invited keynote speaker and program chair DMIP2018 Okinawa, Japan	11/2018
Oral Chromosome X genomic abnormalities in breast cancer cells revealed by RNA, DNA, and methylation sequencing Bioinformatics of Human and Animal Genomes Cold Spring Harbor Asia Conference 2011 Suzhou, China	11/2011
Whole-genome DNA methylation analysis in HSAN1E patients with DNMT1 mutation Epigenetics 2013 Shoal Bay, NSW, Australia	12/2013
Indel sensitive and comprehensive variant/mutation detection from RNA sequencing data for precision medicine Translational Bioinformatics in Precision Medicine - TBC 2017 Los Angeles, California	09/2017

Poster

Histologic Grade of Differentiation Is an Independent Prognostic Factor for Non-Small Cell Lung Cancer. Sun Z, Aubry MC, Marks RS, Deschamps C, Okuno SH, Williams BA, Sugimura H, Pankratz VS, Yang P. American Association for Cancer Research (AACR) Annual Meeting Anaheim, California	01/2005
Multivariate Approach to Select Genes Associated With Clinical Outcomes of Lung Adenocarcinoma from DNA Microarray. Sun Z and Yang P. American Association for Cancer Research (AACR) Annual Meeting Washington, District of Columbia	04/2006
Genetic Abnormality, Tobacco Smoke, Lung Disease, and Lung Cancer Risk. Sun Z, de Andrade M, Krowka MJ, Aubry MC, Scanlon PD, Bamlet WR, Wampfler JA, Thibodeau SN, Katzmman JA, Allen MS, Midthun DE, Marks RS, Yang P. International Genetic Epidemiology Society Conference Tampa, Florida	11/2006
Deep sequence analysis of the relationship between gene expression, CpG island methylation, and gene copy number in breast cancer cells Zhifu Sun, Yan W Asmann, Krishna R Kalari, Brian Bot, Jeanette E Eckel-Passow, Tiffany R. Baker, Jennifer M. Carr, Irina Khrebtukova, Shujun Luo, Lu Zhang, Gary P. Schroth, Edith A. Perez, E. Aubrey Thompson. American Association for Cancer Research (AACR) Annual Meeting Orlando, Florida	04/2011
SAAP-RRBS: Streamlined Analysis and Annotation Pipeline for Reduced Representation Bisulfite Sequencing Intelligent Systems for Molecular Biology Long Beach, California	07/2012
CPAP-miRseq: a comprehensive pre-processing and analytical pipeline for deep miRNA sequencing Center for Individualized Medicine Rochester, Minnesota	10/2012
SAAP-BS: Streamlined Analysis and Annotation Pipeline for Bisulfite Sequencing Pacific Symposium on Biocomputing 2013 Big Island, Hawaii	01/2013
Impact of library preparation on downstream analysis and interpretation of RNA-seq data: comparison between Illumina PolyA and NuGEN Ovation protocol Joint Conference of the Human Genome Meeting and 21st International Congress of Genetics Singapore, Singapore	04/2013
Whole-genome DNA methylation analysis in HSN1E patients with DNMT1 mutation Individualizing Medicine 2013: From Promise to Practice Rochester, Minnesota	10/2013
Chromosome X genomic abnormalities of breast and other women's cancers and their clinical implications Cancer Epigenetics, Keystone Symposia (2014) Santa Fe, New Mexico	02/2014
Illumina 450K microarray vs. RRBS in genome-wide methylation study: which one to choose? Midwest Chromatin and Epigenetics Meeting Madison, Wisconsin	05/2014

Statistical Models in Differentially Methylated CpG detection for Bisulfite Sequencing Data: the simple beats the complex Individualizing Medicine 2014 Rochester, Minnesota	10/2014
Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing American Society of Human Genetics (ASHG) Annual Meeting San Diego, California	10/2014
TRACE-RRBS: Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing Quantitative Biology: from Genes, Cells to Networks Cold Spring Harbor Suzhou, China	10/2014
Accurate strategies to detect clinical important long indels from RNA-seq data: EGFR as example World Conference on Lung Cancer Denver, Colorado	09/2015
Challenges and strategies to detect clinical important long indels from RNA-seq data Center for Individualized Medicine Rochester, Minnesota	09/2015
UClincR: Ultrafast and comprehensive lincRNA detection pipeline from RNA-seq Zhifu Sun, Asha Nair, Xianfeng Chen, Naresh Prodduturi, and Jean-Pierre Kocher Keystone Symposia: Noncoding RNAs in Health and Disease (Q5) Santa Fe, New Mexico	02/2016
Accurate detection of mutations from RNA-seq in lung adenocarcinoma for clinical translation of precision medicine Zhifu Sun, Naresh Prodduturi, Aditya Bhagwate, Ping Yang, and Jean-Pierre A. Kocher International Congress of Human Genetics Kyoto, Japan	04/2016
eSNVIndel: Fast and light-weight RNA-seq pipeline to detect actionable mutations from RNA-seq Naresh Prodduturi, Aditya Bhagwate, Jean-Pierre A. Kocher, Zhifu Sun Center for Individualized Medicine Rochester, Minnesota	10/2016
Adipose tissue DNA methylome changes in development of new onset diabetes after kidney transplantation American Society of Human Genetics (ASHG) Annual Meeting Vancouver, British Columbia, Canada	10/2016
RNA-seq as primary source for comprehensive mutation detection in tumor precision medicine Genomic Variation in Precision Medicine 2017 Guangzhou, China	05/2017
Regional Invited	
Bioinformatics Analysis of Epigenome Data: A primer and essence Epigenomics Interest Group Seminar Rochester, Minnesota	09/2014

Mining large epigenomic data to facilitate research and biomarker discovery Epigenomics Interest Group Seminar Rochester, Minnesota	10/2018
Oral	
Developing Networked Palm Computing Applications for Medical Education. Speedie S and Sun Z. Health Informatics Seminar, University of Minnesota Rochester, Minnesota	01/2000
Can Gene Expression Profiling Predict Survival for Patients With Squamous Cell Carcinoma of The Lung? Microarray Interest Group Rochester, Minnesota	02/2005
Tissue Microarray in Epidemiologic Biomarker Study Genetic Epidemiology Journal Club Rochester, Minnesota	02/2005
Gene-expression Profiling in Predicting Lung Cancer Outcome - An Update: What's New Out There and Inside Here? Microarray Interest Group Rochester, Minnesota	02/2007
Gene Expression Profiling in Clinical Outcome Research of Lung Cancer: Is It Better Than Conventional Predictors? Health Sciences Research Seminar Rochester, Minnesota	12/2007
Whole genome methylation data processing and analysis BSI Computational Genomics Seminar Rochester, Minnesota	03/2010
RNASeq Data Analysis for Differentially Expressed Genes-available methods, issues, and solutions BSI Computational Genomics Seminar Rochester, Minnesota	07/2010
Dealing with batch effect of Illumina Infinium methylation data BSI Computational Genomics Seminar Rochester, Minnesota	12/2010
Understanding Lung Cancer - _from Etiology to Patient Outcome: Contributions and Challenges from Genomic Analyses Genomics Interest Group Seminar Rochester, Minnesota	02/2011
Genome-Wide Methylation Sequencing BSI Computational Genomics Seminar Rochester, Minnesota	05/2011
Whole Genome HumanMethylation27 Data QC and Analysis - an update BSI Computational Genomics Seminar Rochester, Minnesota	05/2011
Whole Genome Methylation Profiling - from microarray to deep sequencing Genetic Epidemiology and Risk Assessment Program Meeting Rochester, Minnesota	06/2011
Base resolution methylome research: technologies, data preprocessing, and analysis Genomics Interest Group Seminar Rochester, Minnesota	05/2012

SAAP-BS: A streamlined analysis and annotation pipeline for bisulfite sequencing BSI Computational Genomics Seminar Rochester, Minnesota	03/2013
Profound impacts of library preparation and RNA source in RNA-seq data pre-processing, analysis and interpretation Bioinformatics Program Technical Meeting Rochester, Minnesota	04/2013
Conserved mutations in RNA are likely drivers and dictate tumor phenotypes in lung adenocarcinoma of never-smokers Center for Individualized Medicine Rochester, Minnesota	08/2013
Fusion gene detection from FFPE RNA-seq data: challenges and opportunities? NextGen Seq Working Group Seminar Rochester, Minnesota	10/2013
Better understand a disease and improve health through genomics and epigenomics Health Sciences Research Seminar Rochester, Minnesota	10/2013
Genotype 5th and 6th base of DNA - new sequencing technologies at your doorstep and their applications Bioinformatics Program Technical Meeting Rochester, Minnesota	11/2013
Somatic mutations from paired DNA vs. RNA - a biological reality or technical limitations in view of a few overlaps? Bioinformatics Core Technical Meeting Rochester, Minnesota	06/2014
Somatic mutations from paired DNA vs. RNA - what's next? Lung Cancer Group Meeting	09/2014
Tackle the challenging and clinical relevant issues in NGS data for Precision Medicine Health Sciences Research Seminar Rochester, Minnesota	02/2015
Integrated epigenome profiling of SL1 patients (lymphoma and MDS) for potential epi-drug therapy BSI Computational Genomics Seminar Rochester, Minnesota	06/2016
Mine 'gold' from the waste of RNA-seq: updates and experience from the indel and lincRNA projects BIC Technical meeting Rochester, Minnesota	06/2016
An overview and useful tools of ENCODE project BSI Computational Genomics Seminar Rochester, Minnesota	08/2016
Updates on the recent ASHG Meeting BSI Computational Genomics Seminar Rochester, Minnesota	11/2016
UCIncr: Ultrafast and Comprehensive long non-coding RNA detection from RNA-seq BSI Computational Genomics Seminar Rochester, Minnesota	03/2017

UCInCR: Ultrafast and Comprehensive long non-coding RNA detection from RNA-seq BSI Computational Genomics Seminar Rochester, Minnesota	03/2017 - 03/2018
Noncoding variant annotation and Prioritization – what are the options? BIC Technical Meeting Rochester, Minnesota	03/2017
GTEX data – what can we benefit from it? Computational Genomics Forum Rochester, Minnesota	03/2018
Poster Statistical method evaluation for differentially methylated CpGs in base resolution next generation DNA sequencing data CS Scientific Session	02/2017
Unclassified	
Oral Gene Expression Profiling in Clinical Outcome Research of Lung Cancer Microarray Interest Group Rochester, Minnesota	12/2005
SAAP-RRBS: Streamlined Analysis and Annotation Pipeline for Reduced Representation Bisulfite Sequencing NextGen Seq Working Group Seminar Rochester, Minnesota	03/2012

Visiting Professorship

Visiting Professorships

Qingdao Medical College Qingdao, China	10/2014
Applications of next generation sequencing to modern medical research and clinical practice Qingdao University Qingdao, China	10/2014
Lung Cancer Transcriptome and Precision Medicine Henan Provincial People's Hospital, Zhengzhou Henan Henan Sheng, China	05/2017
Epigenomics in human disease and personalized medicine South China Institute of Stem Cell & Regenerative Medicine Guangzhou, China	05/2017
lncRNA analysis from RNA-seq and its applications to biomedical discovery Chongqing Third Medical University Chongqing, China	03/2018

Clinical Practice, Interests, and Accomplishments

Molecular Pathology

Research Interests and Accomplishments

As a physician converted research scientist, my research is mostly patient centric and focuses on application of bioinformatics to clinical research and practice, which falls into following five main areas: (1) Lung cancer etiology, precision therapy and outcome. Although lung cancer is mostly cigarette smoking related, a growing number of non-smokers develops lung cancer, particularly in women, and genetics or other environmental factors play a significant role. Through several large scale studies we identified several new genetic variants contributed to lung cancer development in non-smokers. In addition to cancer risk, we also found genomic variants in drug metabolic pathways such as glutathione pathway were related to treatment response and survivals. Lung cancer is the most common cancer but is also one of a few cancers with multiple targeted therapy options. EGFR mutations, ALK-AML4 fusion, and high mutation load are all indicative of precision therapy with specific drugs. Accurate identification of these mutations through more sensitive sequencing technologies and moving the technologies to clinic is also my strong interest and focus. We demonstrated that RNA-seq could detect all of them in a single experiment vs. multiple clinical assays. (2) Early cancer detection and diagnosis through DNA methylation markers. Unlike somatic mutations with a low recurrent frequency in most cancers, DNA methylation changes occur in almost all tumors universally and these cancer hallmarks can be detected through tumor released DNA in blood circulation (cfDNA). Through mining pan-cancer datasets with tens of thousands of samples, we identified sets of both universal and site specific cancer markers with very high sensitivity and specificity that were also validated in independent datasets. Moving these into early cancer detection through cfDNA clinical testing is our ongoing work. (3) Translational epigenomics: Epigenomics is a new and fascinating field in exploring disease mechanisms, identifying new treatment targets and predicting treatment response. Collaborating with clinician investigators, I am investigating the roles of abnormal epigenetic regulation in autoimmune diseases of primary biliary cholangitis, primary sclerosing cholangitis and Crohn's disease. Genome-wide DNA methylation, open chromatin accessibility through ATAC sequencing or histone modifications by Chip-sequencing are being used to untangle the complex interplay of different regulations. We found that TH17 T cells were critical in Crohn's disease and potential new targets are being evaluated. (4) Large genomics data integration and system biology. In current research environment, multiple different types of genomic data are frequently generated from next-generation sequencing technologies for the same set of samples and integrated analysis of these are needed which requires novel algorithm and method developments. I am actively working on this area and have published several highly cited papers. (5) Bioinformatics workflow and method developments. Next generation sequencing data are huge and complex. They need efficient algorithms and seamless workflows so that a large number of samples can be processed quickly and accurately. I have led a team and developed workflows for DNA methylation sequencing, miRNA sequencing, long non-coding RNA sequencing and RNA sequencing. These tools are used routinely not only internally but also externally around the world. My influential research and work has been recognized by the research communities nationally and internally as demonstrated by multiple journal editorial roles (Editorial Board of the Epigenomics, 2014-present; the Associate Editor of World Journal of Respiratory, 2016-2018; and Guest Associate Editor of Frontier in Genetics, 2017-2018), frequent invites for talks and presentations, and frequent requests for manuscript review for top journals.

Research Grants Awarded

Active Grants

Federal

- | | | |
|-----------------|--|-------------------|
| Co-Investigator | Palliating EGFR Inhibitor Rash in African American and Other Cancer Patients. Funded by National Cancer Institute. (R01 CA 207183) | 04/2017 - 03/2022 |
| Co-Investigator | Dissecting the pathogenesis and outcomes of PSC using multi-omics by studying the exposome and genome. Funded by National Institute of Diabetes and Digestive and Kidney Diseases. (RC2 DK 118619) | 09/2018 - 07/2023 |

Federal sub award

- | | | |
|-----------------|--|-------------------|
| Co-Investigator | Integrative translational discovery of vascular risk factors in aging and dementia. Funded by National Institute on Aging. (AG 51504-S2) | 09/2018 - 08/2020 |
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Completed Grants**Federal**

Co-Investigator Genetic Determinants of Lung Cancer Survival. Funded by National Cancer Institute. (R01 CA 84354) 02/2007 - 01/2014

Federal sub award

Program Fusion gene mutations as biomarkers of pancreatic cancer lymph node metastases. Funded by National Cancer Institute. (CA 151160) 07/2010 - 06/2012
Director /

Principal
Investigator

Co-Investigator Breast Cancer Translational Genomics. Funded by Donna Foundation 01/2012 - 12/2012

Foundation

Co-Investigator Jen - Tumor Heterogeneity and Lung Adenocarcinoma Prognosis through Next Generation Sequencing. Funded by American Cancer Society, inc.. (IRG-09-060-01) 01/2009 - 11/2012

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* Indicates that the primary author was a mentee of this author.