

Curriculum Vitae

Yuji Zhang, Ph.D.

Associate Professor, Department of Epidemiology and Public Health
University of Maryland School of Medicine

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Contact Information

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Foreign Languages: Chinese (native)

Education

1996-2000 B.S., Biomedical Engineering, Southeast University, China
2000-2003 M.S., Bioinformatics, Southeast University, China
2005-2010 Ph.D., Computer Engineering, Virginia Polytechnic Institute and State University

Post Graduate Education and Training

2000-2003 Research Assistant, School of Biological Science & Medical Engineering,
Southeast University

2003-2004 Research Assistant, Department of Zoology, University of Oklahoma

2005-2010 Research Assistant (part time), Department of Oncology, Georgetown University
Medical Center

2005-2010 Research Assistant (part time), Department of Electrical and Computer
Engineering, Virginia Polytechnic Institute and State University

Employment History

Academic Appointments

2011-2014 Assistant Professor, Department of Health Sciences Research, Mayo Clinic
College of Medicine and Science

2014-2018 Assistant Professor, Department of Epidemiology and Public Health, UMSOM

2014-present Member, Hormone Response Cancers Program, UMGCCC, UMMC

2014-present Member, Population Science Program, UMGCCC, UMMC

2014-present Member, Program in Oncology, UMSOM

2015-present Member, Program for Personalized and Genomic Medicine, UMSOM

2016-present Affiliate Faculty Member, Institute of Global Health, UMSOM

- 2016-present Adjunct Faculty Member, School of Public Health, University of Maryland College Park
- 2016-present Affiliate Faculty Member, Center for Health-related Informatics and Bioimaging, University of Maryland College Park
- 2018-2020 Associate Professor, Department of Epidemiology and Public Health, UMSOM
- 2020-2023 Associate Professor (tenured), Department of Epidemiology and Public Health, UMSOM
- 2023-present Affiliate Faculty Member, Center for Research on Aging, UMSOM
- 2023-present Professor (tenured), Department of Epidemiology and Public Health, UMSOM

Professional Society Memberships

- 2005-2021 Member, Institute of Electrical and Electronics Engineers (IEEE)
- 2008-present Member, Society of Women Engineers
- 2009-present General Member, the Bioinformatics Organization
- 2010-2014 Member, Human Genome Organization
- 2010-present General Member, American Association for Cancer Research (AACR)
- 2010-present Member, International Society of Computational Biology (ISCB)
- 2010-present Member, Sigma Xi, The Scientific Research Society
- 2010-present Regular Member, The American Society of Human Genetics (ASHG)
- 2014-present Regular Member, American Medical Informatics Association (AMIA)
- 2021-present Senior Member, Institute of Electrical and Electronics Engineers (IEEE)

Honors And Awards

- 1996 First-class Prize, Jiangsu Physics Contest, China
- 2002 Excellent Student Fellowship, Southeast University, awarded for distinguished students university wide
- 2012 Travel Award, the 20th Annual International Conference on Intelligence Systems for Molecular Biology
- 2019 Merit Scholarship, Women in AMIA Leadership Program, American Medical Informatics Association
- 2020 Winner of WIA (Women in AMIA) Leadership 2020 Seed Grant, American Medical Informatics Association

Administrative Service

Institutional Service

- 2016-present Departmental Representative, UMSOM Faculty Council
- 2016-present Member of Admissions Committee, Epidemiology and Public Health Graduate Program, UMSOM
- 2016-present Member, Consulting Core Service of Biostatistics and Bioinformatics, UMSOM
- 2019-present Invited grant reviewer, the Institute for Clinical and Translational Research Accelerated Translational Incubator Pilot Grant Program, UMB
- 2019-present Faculty Judge, The Graduate Research Conference, UMB

- 2019-2020 Member, Cancer Genetic Epidemiology Faculty Search Committee, UMSOM
- 2020-present Faculty Judge, 43rd Annual Medical Student Research Day Celebration, UMSOM
- 2020-present Member, Selection Committee of STAR-PREP Science Training for Advancing Biomedical Research Postbaccalaureate Program, UMSOM
- 2020-present Interviewer, Admissions Committee of Medical Students, UMSOM
- 2020-present Member, Admissions Committee of the Cellular and Molecular Biomedical Science MS Program, UMSOM
- 2021 Member, Faculty Search Committee, Department of Neurology, UMSOM
- 2021-2022 Member, Cancer Genetic Epidemiology Faculty Search Committee, UMSOM
- 2022-present Member, Faculty Search Committee for Division of Endocrinology, Diabetes and Nutrition, Department of Medicine, UMSOM
- 2021-present Member, the General Management Working Group Advisory Committee, My Healthy Maryland Precision Medicine Research, UMSOM
- 2021-present Co-Chair, the Informatics Working Group, My Healthy Maryland Precision Medicine Research, UMSOM

Local and National Service

National Service

- 2010-present Peer review of over 200 scientific papers for 32 international journals (i.e., approximately 10 papers/5 journals per year), including but not limited to: *ACM-BCB 2018; Aids; AMIA 2019; BioData Mining; Bioinformatics; Biological Chemistry; Biomedical Engineering and Computational Biology; Biomedical Informatics Insights; BMC Bioinformatics; BMC Genomics; BMC Medical Genomics; BMC Supplements; Briefings in Bioinformatics; Canadian Journal of Cardiology; Cellular Physiology and Biochemistry; Computational and Structural Biotechnology Journal; Expert Review of Molecular Diagnostics; EURASIP Journal on Bioinformatics and Systems Biology; Gene; ICHI 2019; IEEE Signal Processing Letters; Integrative Bioinformatics; International Journal of Biomedical Science; JCO Clinical Cancer Informatics; Journal of Association for Information Science and Technology; Journal of Bioinformatics and Computational Biology; Journal of Biomedical Informatics; Journal of Biomedical Semantics; Journal of Integrative Bioinformatics; Mathematical Biosciences; Methods of Information in Medicine; Nature Communications; Onco Targets and Therapy; PLOS ONE; Systems and Synthetic Biology; Scientific Reports; SpringPlus; VDOS proceedings 2015-2022.*
- 2012 Member, Technical Program Committee, the 3rd International Conference on Biomedical Ontology, Graz, Austria.
- 2012 Member, Technical Program Committee, the 21st ACM International Conference on Information and Knowledge Management (CIKM 2012), Maui, Hawaii.
- 2012-present Abstract Reviewer, *AMIA Annual Symposium*
- 2012-present Abstract Reviewer, *AMIA Annual Informatics Summit*
- 2012-present Editorial Board Member, *Mutation & Cancer Studies*

- 2013-present Member, Technical Program Committee, International Workshop on Vaccine and Drug Ontology Studies, in conjunction with the International Conference on Biomedical Ontology (ICBO).
- 2014-present Editorial Board Member, *Annals of Hematology & Oncology*
- 2014 Program Co-Chair, the first workshop on Translational biomedical and clinical informatics, in conjunction with the 8th International Conference on Systems Biology and the 4th Translational Bioinformatics Conference (ISB/TBC 2014), Qingdao, China.
- 2014 Program Co-Chair, Workshop on Data Mining in Biomedical informatics and Healthcare, in conjunction with the 18th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD 2014), Taiwan.
- 2014 Local organizer and member, Technical Program Committee, International Symposium on Integrative Bioinformatics 2014, Newcastle University, UK.
- 2014-2015 Guest Editor, *Journal of BioData Mining*
- 2017 Program Co-Chair, the first workshop on Knowledge Discovery in Translational Biomedical Informatics, in conjunction with the IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2017, Kansas City, MO.
- 2018 Program Committee Member, The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Washington, DC.
- 2018 Session Chair of the Drug Discovery and Docking, The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Washington, DC.
- 2019 Reviewer, the Seventh IEEE International Conference on Healthcare Informatics (ICHI 2019), Xi'an, China.
- 2019 Member, Technical Program Committee, the 4th International Workshop on Semantics-Powered Data Mining and Analytics (SEPDA 2019), in conjunction with the 19th International Semantic Web Conference (ISWC 2019), Auckland, New Zealand.
- 2020 Member of External Advisory Committee, Kenley School, Abilene, TX, USA.
- 2020 Grant Reviewer of the Medical Research Council (MRC), United Kingdom.
- 2021 Member of the Awards Committee, Networks 2021: A Joint Sunbelt and NetSci conference, Washington, DC.
- 2021-present NSF Reviewer
- 2021 Panel Member, IEEE Senior Member Review Panel
- 2021-present Topic Editor, Editorial Board, *Genes*
- 2022-present Editorial Board Member and Academic Editor, *PLOS ONE*
- 2022-present Translational Bioinformatics/Precision Medicine Track Member, Scientific Program Committee, the AMIA 2023 Informatics Summit
- 2023 Session Chair, AMIA Summit 2023
- 2023 Secretary of Organizing Committee, IEEE WIE Forum USA East 2023

Local Service

- 2016-present Study Section Member, the UMB-UMCP Research & Innovation Seed Grant Program
- 2019-present Faculty Judge, Annual Public Health Research Day @ Maryland, UMCP

- 2020 Invited grant reviewer, COVID-19 response seed grant program, MPower Steering Council
- 2022-present Chair, Women in Engineering (WIE) Affinity Group in the Baltimore Section, IEEE
- 2022 Panelist, “Network, Career and Mentoring” Panel, Northern Virginia Women in Engineering Affinity Group, IEEE

Teaching Service

Student Teaching

- 2012-2014 Lecturer, Introduction to Bioinformatics
Mayo Clinic College of Medicine and Science
Number of students: 20-28; hours of teaching: 1 hour/week; number of weeks: 12
- 2012-2014 Lecturer, Introduction to Bioinformatics,
Department of Computer Science, Winona State University
Number of students: 16-24; hours of teaching: 1 hour/week; number of weeks: 12
- 2014-present Attending Biostatistician, Journal Club of Epidemiology
Department of Epidemiology and Public Health, UMSOM
Number of students: 10-18; hours of teaching: 2 hours/semester
- 2015-2016 Lecturer, Statistics for Molecular Biology
Department of Epidemiology and Public Health, UMSOM
Number of students: 4-8; hours of teaching: 1 hour/week; number of weeks: 8
- 2018-present Lecturer, Molecular Toxicology
Department of Epidemiology and Public Health, UMSOM
Number of students: 8; hours of teaching: 4 hours/semester; number of weeks: 16
- 2018-present Lecturer, Molecular Epidemiology
Department of Epidemiology and Public Health, UMSOM
Number of students: 4; hours of teaching: 4 hours/semester; number of weeks: 12
- 2020-present Lecturer, Cancer Epidemiology
Department of Epidemiology and Public Health, UMSOM
Number of students: 12; hours of teaching: 4 hours/semester; number of weeks: 12
- 2021-present Lecturer, Introduction to Biocomputational Engineering
Department of Bioengineering, UMCP
Number of students: 10; hours of teaching: 2 hours/semester; number of weeks: 12

Mentoring

- 2001 Research Mentor
Qianru Yu, 4th year undergraduate student, 4 hours per week
- 2010-2014 Research supervisor
Asha Nair, Post-graduate, Bioinformatics, 4 hours per week
- 2012 Research mentor
Feichen Shen, Ph.D., Medical Informatics, 4 hours per week

2015-2018 Research Mentor
Lei Wang, post-graduate, Bioinformatics, 6 hours per week

2015-2018 Member of Ph.D. dissertation committee
Kara Moser, graduate student, Molecular Epidemiology, 10 hours per year

2016 Research Mentor
Haichen Zhang, graduate student, Human Genetics, 4 hours per week

2016-2020 Member of Ph.D. dissertation committee
Amol Carl Shetty, graduate student, Bioinformatics, 10 hours per year

2017-2020 Research Mentor
Junxiang Wang, graduate student, Computer Science, 2 hours per week

2018-2021 Research Mentor
Andrea Fava, Clinical Fellow, 2 hours per week

2018-2022 Member of Ph.D. dissertation committee
Emily Stucke, graduate student, Molecular Epidemiology, 10 hours per year

2018-2021 Member of Ph.D. dissertation committee
Haichen Zhang, graduate student, Molecular Epidemiology, 10 hours per year

2019 Research Mentor
Yi-Ju Chen, graduate student, Master Program, 4 hours per week

2020-2022 Member of Ph.D. dissertation committee
Elizabeth Humphries, graduate student, Molecular Epidemiology, 10 hours per year

2020-present Mentor, The Foundations of Research and Critical Thinking (FRCT), UMSOM

2020-2022 Research Mentor
Barry Bu, high school student, Wootton High School, 4 hours per week

2021 Rotation Research Mentor
Denisha Odie, graduate student, MS in Cellular & Molecular Biomedical Science (CMBS), Graduate Program in Life Sciences (GPILS), 4 hours per week

2021 Rotation Research Mentor
Victoria Baskerville, graduate student, MS in Cellular & Molecular Biomedical Science (CMBS), Graduate Program in Life Sciences (GPILS), 4 hours per week

2021-present Member of Ph.D. dissertation committee
Lydia He, graduate student, Molecular Epidemiology, 10 hours per year

2022-2023 Research Mentor
Kevin Liang, Undergraduate student, UMCP, 4 hours per week

Grant Support

Active Grants:

09/20/16 – 05/31/24 (Co-Inv 20%) PI: M. Terrin
“PCTC Administrative Coordinating Center”
 NHLBI/NIH, U24 HL134763
 Annual Direct Costs: \$1,131,510
 Total Direct Costs: \$7,920,570
Lead Bioinformatician and Biostatistician

03/15/19 – 02/28/24 (Collaborator 0%) PI: M. Levine

- “Active vaccination and passive antibody strategies to prevent disease caused by multidrug-resistant bacterial pathogens”
 NIAID/NIH, U19 AI142725
 Annual Direct Costs: \$1,654,708
 Total Direct Costs: \$8,273,540
Bioinformatician and Biostatistician
- 06/16/20 – 05/31/25 (Co-Inv 10%) PI: M. Terrin
 “CMCRC consortium-wide coordinating core”
 NIAID/NIH, U19 AI150574
 Annual Direct Costs: \$131,951
 Total Direct Costs: \$659,755
Lead Bioinformatician and Biostatistician
- 07/01/20 – 06/30/25 (Co-Inv 20%) PI: K. Cullen
 “Cigarette Restitution Fund Program”
 Maryland Department of Health and Mental Hygiene
 Annual Direct Costs: \$ 10,400,000
 Total Direct Costs: \$ 10,400,000
Lead Bioinformatician
- 07/24/20 – 04/30/24 (Site-PI 4%) PI: X. Xu
 “Discovering cardiomyopathy modifiers and therapies via zebrafish genetics”
 NHLBI/NIH, R01 HL107304
 Annual Direct Costs: \$328,617
 Total Direct Costs: \$1,314,468
Lead Bioinformatician and Biostatistician
- 04/01/21 – 03/31/26 (Co-Inv 2%) PI: H. Huang
 “Addressing Chemoresistance in Pancreatic and Ovarian Cancers: Photodynamic Priming and Repurposing of Tetracyclines using Targeted Photo-Activable Multi-Inhibitor Liposome”
 NIBIB/NIH, R01 CA260340
 Annual Direct Costs: \$548,466
 Total Direct Costs: \$2,742,330
Lead Bioinformatician and Biostatistician
- 06/01/21 – 05/31/26 (Co-Inv 20%) PI: S. Adebamowo
 “CARDiometabolic Disorders IN African-ancestry PopuLations (CARDINAL) Study Site”
 NCI/NIH, U01 HG011717
 Annual Direct Cost: \$790,000
 Total Direct Costs: \$3,950,000
Lead Bioinformatician and Biostatistician

07/01/21 – 06/30/26 (Co-Inv 4%) PI: H. Wang
“Novel noncanonical actions of CAR in human liver”
 NCI/NIH, R01 CA262084
 Annual Direct Cost: \$250,000
 Total Direct Costs: \$1,250,000
Lead Bioinformatician and Biostatistician

08/01/21 – 07/31/26 (Co-Inv 5%) PI: K. Cullen
“University of Maryland Comprehensive Cancer Center Support Grant”
 NCI/NIH, P30 CA134274
 Annual Direct Costs: \$1,500,000
 Total Direct Costs: \$7,500,000
Lead Bioinformatician

07/01/22 – 06/30/26 (Co-Inv 4%) PI: J. Lin
“Co-targeting IL-6 and CDK4/6 pathways as a novel approach of preventive therapy for triple-negative breast cancer”
 VA Merit Research Award
 Annual Direct Costs: \$150,000
 Total Direct Costs: \$600,000
Lead Bioinformatician and Biostatistician

07/01/22 – 06/30/26 (Site-PI 25%) PI: X. Xu
“Genetic Studies of Sarcomere-based Cardiac Diseases”
 NHLBI/NIH, R01 HL081753
 Annual Direct Costs: \$ 375,626
 Total Direct Costs: \$1,502,504
Lead Bioinformatician and Biostatistician

01/12/23 – 12/31/27 (Co-Inv 2%) PI: H. Huang
“Targeting Fluid Stress-induced Chemoresistance in a 3D Carcinomatosis Perfusion Model Using Mechanism-based Photo-immunoconjugate Nanoparticles”
 NIBIB/NIH, R01 CA256710
 Annual Direct Costs: \$450,191
 Total Direct Costs: \$2,250,955
Lead Bioinformatician and Biostatistician

Completed Grants:

09/01/10-06/30/14 (Co-Inv 20%) PI: R. Diasio
“Mayo comprehensive cancer center grant”
 National Cancer Institute, P30 CA15083
 Annual Direct Costs: \$5,115,009
 Total Direct Costs: \$20,460,036

Bioinformatician and Biostatistician

- 09/19/11-06/30/14 (Co-Inv 25%) PI: S. Thibodeau
“Prostate cancer susceptibility: the ICPCG study”
National Cancer Institute, U01 CA89600
Annual Direct Costs: \$1,272,612
Total Direct Costs: \$8,908,284
Bioinformatician and Biostatistician
- 09/19/11-06/30/14 (Co-Inv 10%) PI: S. Thibodeau
“Functional significance of prostate cancer risk-SNPs”
National Cancer Institute, R01 CA151254
Annual Direct Costs: \$228,217
Total Direct Costs: \$684,651
Bioinformatician and Biostatistician
- 09/31/12-06/30/14 (Site-PI 25%) PI: R. Rademakers
“GGGGCC hexanucleotide repeat expansions in neurodegenerative disease”
National Institute of Neurological Disorder and Stroke, R01 NS80882
Annual Direct Costs: \$361,947
Total Direct Costs: \$1,809,735
Bioinformatician and Biostatistician
- 01/01/13-07/31/14 (Co-Inv 5%) PI: J. Aaron
“Development of novel monocarboxylate transporter 1 inhibitors for the treatment of glioblastoma multiforme”
Minnesota Partnership for Biotechnology and Medical Genomics
Annual Direct Costs: \$116,393
Total Direct Costs: \$116,393
Bioinformatician and Biostatistician
- 03/20/13-06/30/14 (Co-Inv 5%) PI: M. J. Ackerman
“Cardiac channel mutations in SIDS”
Eunice Kennedy Shriver National Institute of Child Health and Human Development, R01 HD42569
Annual Direct Costs: \$352,194
Total Direct Costs: \$1,760,970
Bioinformatician and Biostatistician
- 07/01/13-06/30/14 (Co-Inv 15%) PI: T. Patel
“Extracellular non-coding RNA biomarkers of hepatocellular cancer”
National Institute of Health, UH2 TR000884
Annual Direct Costs: \$366,588
Total Direct Costs: \$366,588

Bioinformatician and Biostatistician

- 07/14/14 – 07/31/16 (Co-Inv 5%) PI: K. Cullen
“University of Maryland Comprehensive Cancer Center Support Grant”
National Cancer Institute, P30 CA134274
Annual Direct Costs: \$1,000,000
Total Direct Costs: \$8,000,000
Bioinformatician and Biostatistician
- 09/30/14 – 09/29/15 (Co-Inv 5%) PI: T. MacVittie
“Medical countermeasures against radiological threats: product development support”
National Institute of Allergy and Infectious Disease,
272201000046C-14-0-1
Annual Direct Costs: \$1,334,877
Total Direct Costs: \$1,334,877
Bioinformatician and Biostatistician
- 07/01/15 – 06/30/19 (Co-Inv 10%) PI: R. Gartenhaus
“Lymphoma development in the elderly: Perturbed posttranscriptional regulation”
VA Merit Research Award
Annual Direct Costs: \$150,000
Total Direct Costs: \$600,000
Bioinformatician and Biostatistician
- 03/01/16 – 02/29/20 (Co-Inv 3%) PI: P. Yang
“Apoptotic mechanism of maternal diabetes-induced neural tube defects”
NIDDK/NIH, R01 DK083243
Annual Direct Costs: \$275,000
Total Direct Costs: \$1,375,000
Bioinformatician and Biostatistician
- 08/10/16 – 07/31/21 (Collaborator 0%) PI: J. Qi
“Role of histone demethylase JMJD1A in the DNA damage response of prostate cancer cells”
NCI/NIH, R01 CA207118
Annual Direct Costs: \$228,750
Total Direct Costs: \$1,143,750
Bioinformatician and Biostatistician
- 09/10/16 – 07/31/21 (Co-Inv 5%) PI: M. Petri
“Hopkins Lupus Cohort”
NIAMS/NIH, R01 AR069572

Annual Direct Costs: \$447,131
Total Direct Costs: \$2,235,655
Lead Bioinformatician

11/01/16 – 07/31/17 (Collaborator 0%) PI: K. Barry
“DNA methylation at chromosome 8q24 and the risk of aggressive prostate cancer”
UMGCCC
Annual Direct Costs: \$30,000
Total Direct Costs: \$30,000
Bioinformatician and Biostatistician

04/01/17 – 03/31/19 (Co-Inv 3%) PI: E. Davila
“Augmenting T cell activity to weak tumor antigens and reversing myeloid cell-mediated T cell inhibition”
National Cancer Institute, R01 CA207913
Annual Direct Costs: \$235,681
Total Direct Costs: \$1,178,405
Bioinformatician and Biostatistician

07/01/17 – 06/30/18 (Co-Inv 5%) PI: Y. Mei
“A blood test for the early detection of lung cancers based on newly-discovered sprRNAs”
The Maryland Innovation Initiative
Annual Direct Costs: \$115,000
Total Direct Costs: \$115,000
Bioinformatician and Biostatistician

07/01/17 – 04/30/21 (Co-Inv 2%) PI: P. Yang
“MicroRNA-suppressed mitochondrial fusion in mediating the teratogenicity of maternal diabetes leading to heart defects”
NHLBI/NIH, R01 HL134368
Annual Direct Costs: \$390,939
Total Direct Costs: \$1,563,756
Lead Bioinformatician and Biostatistician

04/01/18 – 03/31/21 (Co-Inv 5%) PI: J. Dorgan
“Early life exposures and breast density in young women”
NCI/NIH, R01 CA214783
Annual Direct Costs: \$204,482
Total Direct Costs: \$817,928
Lead Bioinformatician

08/01/18 – 05/31/19 (Co-Inv 2%) PI: X. Cao
“Novel method for enhancing cancer immunotherapy efficacy and minimizing toxicity”

TEDCO
Annual Direct Costs: \$2,888
Total Direct Costs: \$2,888
Bioinformatician and Biostatistician

05/01/21 – 04/30/22 (Co-Inv 5%) PI: J Magaziner
“University of Maryland Claude D. Pepper Older Americans Independence Center (UM-OAIC)”
NHLBI/NIA, P30 AG028747 15S2
Annual Direct Costs: \$249,898
Total Direct Costs: \$249,898
Bioinformatician and Biostatistician

03/01/18 – 02/28/23 (Co-Inv 5%) PI: V. Njar
“Development of next generation galeterone analogs for prostate cancer therapy”
NCI/NIH, R01 CA224696
Annual Direct Costs: \$ 290,238
Total Direct Costs: \$1,451,190
Lead Bioinformatician and Biostatistician

07/01/20 – 03/31/23 (Co-Inv 1%) PI: H. Huang
“Photodynamic priming for bidirectional modulation of drug transport across the blood-brain tumor barrier”
NIBIB/NIH, R21 EB028508
Annual Direct Costs: \$135,907
Total Direct Costs: \$407,721
Lead Bioinformatician and Biostatistician

Patents

1. Kohli M, Oberg AL, Mahoney DW, Zenka RM, **Zhang Y**, Zhang S. Predicting responses to androgen deprivation therapy and methods for treating prostate cancer. Publication number: WO2013116742.

Publications

Peer-reviewed journal articles

1. **Zhang Y**, Zhu J, Sun X, Lu Z. A method of oligonucleotide synthesis optimization. *Biotechnology*. 2002;12(4):26-28.
2. Resson HW, **Zhang Y***, Xuan J, Wang Y, Clarke R. Inferring network interactions using recurrent neural networks and swarm intelligence. *Proceedings of the 28th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*. 2006 Aug 30;4241-4244. (*primary author to design the experiment, perform the analysis, and write the manuscript*)

3. Resson HW, **Zhang Y***, Xuan J, Wang Y, Clarke R. Inference of gene regulatory networks from time course gene expression data using neural networks and swarm intelligence. Proceedings of 2006 IEEE Symposium on Computational Intelligence and Bioinformatics and Computational Biology. 2006 Sep 28;435-442. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
4. Resson HW, **Zhang Y***, Xuan J, Wang Y, Clarke R. Integrating multi-source biological data for transcriptional regulatory module discovery. Proceedings of IEEE/NIH Life Science Systems and Applications Workshop 2007. 2007 Nov 8;184-187. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
5. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Resson HW. Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. BMC Bioinformatics. 2008;9(1):203.
6. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Resson HW. Reverse engineering module networks by PSO-RNN hybrid modeling. Proceedings of the 2008 International Conference on Bioinformatics and Computational Biology. 2008; 401–407.
7. **Zhang Y**, Xuan J, de Los Reyes BG, Clarke R, Resson HW. Network motif-based identification of breast cancer susceptibility genes. Proceedings of the 30th Annual International Conference of the IEEE Engineering in Medicine and Biology Society. 2008 Aug 20;5696-5699.
8. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Resson HW. Reverse engineering module networks by PSO-RNN hybrid modeling. BMC Genomics. 2009 Jul 7;10(1):S15.
9. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Resson HW. Reconstruction of gene regulatory modules in cancer cell cycle by multi-source data integration. PLOS ONE. 2010;5(4):e10268.
10. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Resson HW. Module-based biomarker discovery for breast cancer. Proceedings of 2010 IEEE International Conference on Bioinformatics & Biomedicine. 2010;352-356.
11. Sun Z, Baheti S, Middha S, Kanwar R, **Zhang Y**, Li X, Beutler AS, Klee E, Asmann YW, Thompson EA, Kocher JP. SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. Bioinformatics. 2012; 28(16): 2180-2181. *(participated in determining analytic method, running analyses, and providing statistical interpretation)*
12. Asmann YW, Middha S, Hossain A, Baheti S, Li Y, Chai HS, Sun Z, Duffy PH, Hadad AA, Nair A, Liu X, **Zhang Y**, Klee EW, Kalari KR, Kocher JP. TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. Bioinformatics. 2012; 28(2):277-278. *(determined analytic method, ran analyses, provided statistical interpretation)*
13. Wang J, **Zhang Y***, Marian C, Resson HW. Identification of aberrant pathways and network activities from high-throughput data. Briefings in Bioinformatics. 2012;13(4):406-419. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
14. Craig TA, **Zhang Y***, McNulty MS, Middha S, Ketha H, Singh RJ, Magis AT, Funk C, Price ND, Ekker SC, Kumar R. Research resource: whole transcriptome RNA sequencing detects multiple 1alpha, 25-dihydroxyvitamin D(3)-sensitive metabolic pathways in developing zebrafish. Molecular Endocrinology. 2012;26(9):1630-1642. *(primary author to design the experiment, perform the analysis, and write the manuscript)*

15. Tao C, **Zhang Y***, Jiang G, Bouamrane MM, Chute CG. Optimizing semantic MEDLINE for translational science studies using semantic web technologies. Proceedings of the 2nd international workshop on Managing interoperability and complexity in health systems. 2012 Oct 29;53-58. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
16. **Zhang Y**, Li D, Tao C, Shen F, Liu H. An integrative computational approach to identify disease-specific networks from PubMed literature information. Proceedings of IEEE International Conference on Bioinformatics and Biomedicine 2013. 2013 Dec 18;72-75.
17. Leonard B, Hart SN, Burns MB, Carpenter MA, Temiz NA, Rathore A, Isaksson Vogel R, Nikas JB, Law EK, Brown WL, Li Y, **Zhang Y**, Maurer MJ, Oberg AL, Cunningham JM, Shridhar V, Bell DA, April C, Bently D, Bibikova M, Cheetham RK, Fan JB, Grocock R, Humphray S, Kingsbury Z, Peden J, Chien J, Swisher EM, Hartmann LC, Kalli KR, Goode EL, Sicotte H, Kaufmann SH, Harris RS. APOBEC3B upregulation and genomic mutation patterns in serous ovarian carcinoma. Cancer Research. 2013;73(24):7222-7231. *(determined analytic method, ran analyses, provided statistical interpretation)*
18. Hart SN, Therneau TM, **Zhang Y**, Poland GA, Kocher JP. Calculating sample size estimates for RNA sequencing data. Journal of Computational Biology. 2013;20(12):970-978. *(determined analytic method, ran analyses, provided statistical interpretation)*
19. **Zhang Y**, Tao C, He Y, Kanjamala P, Liu H. Network-based analysis of vaccine-related associations reveals consistent knowledge with the vaccine ontology. Journal of Biomedical Semantics. 2013;4(1):33.
20. Sun Z, Asmann YW, Nair A, **Zhang Y**, Wang L, Kalari KR, Bhagwate AV, Baker TR, Carr, JM, Kocher JP, Perez EA, Thompson EA. Impact of library preparation on downstream analysis and interpretation of RNA-Seq data: comparison between Illumina PolyA and NuGEN Ovation protocol. PLOS ONE. 2013;8(8):e71745. *(determined analytic method, ran analyses, provided statistical interpretation)*
21. Pugazhenth S, **Zhang Y***, Bouchard R, & Mahaffey G. Induction of an inflammatory loop by interleukin-1 beta and tumor necrosis factor-alpha involves NF- kappa B and STAT-1 in differentiated human neuroprogenitor cells. PLOS ONE. 2013;8(7): e69585. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
22. **Zhang Y**, Tao C, He Y, Kanjamala P, Liu H. Analysis of vaccine-related networks using Semantic MEDLINE and the vaccine ontology. CEUR Workshop Proceedings, 2013; 1061:1-6.
23. **Zhang Y**, Xuan J, Clarke R, Ransom HW. Module-based breast cancer classification. International Journal of Data Mining and Bioinformatics. 2013;7(3):284-302.
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78. DiCarlo AL, Cassatt DR, Rios CI, Satyamitra MM, **Zhang Y**, Golden TG, Taliaferro LP. Making Connections: The Scientific Impact and Mentoring Legacy of Dr. John E. Moulder. *International Journal of Radiation Biology*. 2023;15:1-7. (*Cover Story; Oversaw computational design, analyses, and results interpretation*)

Book Chapters

1. **Zhang Y**, Resson HW, Kocher JPA: Reverse engineering gene regulatory networks by integrating multi-source biological data, *Reverse Engineering - Recent Advances and Applications*. Edited by Telea AC, InTech Press, 2012.
2. **Zhang Y**: Gene regulatory networks: real data sources and their analysis, *Evolutionary Computation in Gene Regulatory Network Research*. Edited by Iba H, Noman N, Wiley Press, 2016.

Major Invited Speeches

Local

1. **Zhang Y**, Network-based approaches in systems medicine: current applications and future directions, Hormone Response Program, UMGCCC, UMSOM, Baltimore, MD, USA, Nov 14, 2014.
2. **Zhang Y**, Integrative informatics approaches and their applications in “Big Data” medicine era, Institute of Genome Sciences, UMSOM, Baltimore, MD, USA, Aug 17, 2015.

3. **Zhang Y**, From big data to precision medicine: a data science perspective, IEEE R2 Women in Engineering (WIE) 2022 Kick-off Meeting, Feb 28, 2022.
4. **Zhang Y**, Advancing Precision Medicine Using Data Science and Big Data, Guest Lecture of Introduction to Biocomputational Engineering, UMCP, Mar 8, 2022.

National and International

5. **Zhang Y**, Systematic computational approaches in precision medicine era, School of Biological Science & Medical Engineering, Southeast University, Nanjing, China, Sep 16, 2014.
6. **Zhang Y**, Identification of association patterns in public literature using network-based computational approaches: case studies in vaccine research, CBIL Seminar, Department of Electrical and Computer Engineering, Virginia Tech, Arlington, VA, USA, Nov 19, 2014.
7. **Zhang Y**, Subnetwork association pattern identification in drug-disease-gene networks, Department of Computer Science, Virginia Tech, Arlington, VA, USA, Apr 14, 2015.
8. **Zhang Y**, From big data to precision medicine: a data science perspective, Hillman Cancer Center, University of Pittsburgh (Virtual), Jan 31, 2022.

Proffered Communications

1. **Zhang Y**, Wang H. Comparative analysis of circadian clock genes in Zebrafish, Fugu and Tetraodon. The 6th International Meeting on Zebrafish Development and Genetics, Madison, Wisconsin, Jul 2004.
2. **Zhang Y**, Xuan J, Wang Y, Resson HW. Inferring gene regulatory networks from time-series gene expression data using recurrent neural networks and swarm intelligence. Fifth Asia Pacific Bioinformatics Conference (APBC 2007), Hongkong, China, Jan 14-17, 2007.
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4. **Zhang Y**, Xuan J, Wang Y, Clarke R, Resson HW. Identification of network motifs in transcriptional regulators by integrating multi-source biological data. Pacific Symposium on Biocomputing 2008 (PSB 2008), Big Island, HI, Jan 4-8, 2008.
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6. Sicotte H, Therneau T, **Zhang Y**, Prodduturi N, Wang C, Kocher JP. Integrative survival analysis of TCGA tumors using cross-validated cox models. TCGA 1st Annual Scientific Symposium: Research Through TCGA, National Harbor, MD, Nov 17-18, 2011.
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8. **Zhang Y**, Wang C, Sun Z, Middha S, Kumar R, Kocher JP. Dynamic network analysis reveals stage-specific changes in early zebrafish embryo development. The 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach CA. Jul 15-17, 2012.

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14. **Zhang Y**, Nair A, Middha S, Wang L, Sun Z, Asmann YW, Kocher JPA. A novel bioinformatics pipeline for identification and characterization of long non-coding RNAs in whole transcriptome sequencing data. The 14th annual Advances in Genome Biology and Technology meeting, Marco Island, FL, Feb 20-23, 2013.
15. **Zhang Y**, Tao C, Jiang G, Nair A, Su J, Liu H. Network-based analysis reveals distinct association patterns in a semantic MEDLINE-based drug-disease-gene network. Summit on Translational Bioinformatics, San Francisco, CA, Mar 18-22, 2013.
16. **Zhang Y**, Craig TA, Middha S, Ekker SC, Kumar R, Kocher JPA. Network-based analysis of time series gene expression data by integrating the interactome and Gene Ontology information. Individualizing Medicine 2013: From Promise to Practice, Rochester, MN, Sep 30-Oct 2, 2013.
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20. **Zhang Y**, French AJ, Nair A, McDonnell S, Middha S, Riska S, Fogarty Z, Schaid D, Thibodeau SN. Identification of tissue-specific long intergenic non-coding RNAs in normal prostate tissue. The American Society of Human Genetics Annual Meeting 2013, Boston, MA, Oct 22-26 2013.

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22. **Zhang Y**. ICQ-lincRNA: A bioinformatics tool for Identification, characterization and quantification of long intergenic non-coding RNAs in RNA-Seq data. Systems Biology of Gene Regulation and Genome Editing Conference, Cold Spring Harbor Asia, Suzhou, China, Sep 9-12, 2014.
23. **Zhang Y**, Yu P, & Tao, C. Network Analysis Identifies sex-associated patterns in VAERS RDF graph. The Workshop of Vaccine and Drug Ontology Studies (VDOS 2014), in conjunction with the International Conference on Biomedical Ontologies (ICBO), Houston, TX, Oct 6-9, 2014.
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29. **Zhang Y**. Regulation of the immune response by long non-coding RNAs in healthy subjects and stage IV melanoma patients. 2016 Advances in Genome Biology and Technology (AGBT) Meeting, Marco Island, FL, Feb 10-13, 2016.
30. Felts S, **Zhang Y**, Pease L. Transcriptomic fingerprints reveal an immune phenotype shared by melanoma patients and a subset of healthy people. FOCIS 2016 Annual Meeting, Boston, MA, June 22-25, 2016.
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36. Fava A, **Zhang Y**, Hacoheh N, Arazi A, Berthier C, Rao D, Brenner M, Wofsy D, Davidson A, Kretzler M, Hildeman D, Woodle S, Diamond B, Petri M. Single cell RNA expression in lupus nephritis comparing African American and Caucasian patients identifies differential expression of Type I Interferon pathway. The 13th International Lupus Conference (Lupus 2019), San Francisco, CA, Apr 5-8, 2019.
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38. Fava A, **Zhang Y**, Hacoheh N, Arazi A, Berthier C, Rao D, Brenner M, Wofsy D, Davidson A, Kretzler M, Hildeman D, Woodle S, Diamond B, Petri M. Renal single cell genomics links Type II Interferon and lupus nephritis in African Americans. The 2019 ACR/ARP Annual Meeting, Atlanta, GA, November 8–13, 2019.
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