

YUCHAO JIANG

CONTACT INFORMATION

Mailing address 4115D McGavran-Greenberg Hall, 135 Dauer Drive
University of North Carolina at Chapel Hill
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PROFESSIONAL EXPERIENCE

Assistant Professor (tenure-track), Department of Biostatistics, Gillings School of Global Public Health 2017 – now
Assistant Professor (tenure-track), Department of Genetics, School of Medicine
Member, Lineberger Comprehensive Cancer Center
Core Faculty, Curriculum in Bioinformatics and Computational Biology, School of Medicine
University of North Carolina at Chapel Hill

EDUCATION

University of Pennsylvania

Ph.D. in Genomics and Computational Biology, Perelman School of Medicine 2017
M.A. in Statistics, The Wharton School 2014
Advisor: Dr. Nancy R. Zhang

Cornell University

B.S. (*magna cum laude*) in Biological Sciences (Computational Biology) 2012

HONORS & AWARDS

Maximizing Investigators' Research Award, National Institute of General Medical Sciences, 2020
Teaching Excellence and Innovation Award, Gillings School of Global Public Health, UNC Chapel Hill, 2020
Sigma Xi Scientific Research Honor Society Inductee, 2020
UNC Computational Medicine Program Pilot Award, 2019
UNC IBM Junior Faculty Developmental Award, 2019
UNC Lineberger Developmental Award, 2018
Saul Winegrad Award for Outstanding Dissertation, UPenn, 2017
President Gutmann Leadership Award, UPenn, 2016
Best Pre-Doc Poster, Symposium on Advances in Genomics, Epidemiology and Statistics (SAGES), 2015
Distinction in Research, Cornell University, 2012
National Scholarship, Ministry of Education of P.R. China, 2010

EDITORIAL SERVICE

Editorial Board Member, *BMC Genomics*

05/2021 – now

Review Editor, *Frontiers in Genetics*

05/2021 – now

PUBLICATIONS

† indicates (co-)corresponding author; * indicates advisee.

1. Harigaya Y*, Zhang Z, Zhang H, Zang C, Zhang NR†, **Jiang Y**†. Nonparametric interrogation of transcriptional regulation in single-cell RNA and chromatin accessibility multiomic data. *Submitted*, 2021. [Co-corresponding author]
2. Wang R*, Lin D†, **Jiang Y**†. EPIC: inferring relevant cell types for complex traits by integrating genome-wide association studies and single-cell RNA sequencing. *Submitted*, 2021. [Co-corresponding author]
3. Bi Z, **Jiang Y**, Yao B, Chen L. DeepChrInteract: A Python deep learning toolkit for predicting genome-wide chromatin interactions. *Submitted*, 2021.
4. Dong M, He Y, **Jiang Y**, Zou F. Joint gene network construction by single-cell RNA sequencing data. *Submitted*, 2021.
5. Wang R*, **Jiang Y**†. Copy number variation detection by single-cell DNA sequencing. *Submitted*, 2021. [Corresponding author]
6. Liu Z, Ruter DL, Quigley K, **Jiang Y**, Bautch VL. Single-cell RNA sequencing reveals endothelial cell gene expression heterogeneity under homeostatic shear stress. *Arteriosclerosis, Thrombosis, and Vascular Biology*, to appear, 2021. [Impact factor: 8.311]
7. Wang Y, **Jiang Y**, Yao B, Huang K, Liu Y, Wang Y, Qin X, Chen L. WEVar: a novel supervised learning framework for predicting functional noncoding variants. *Briefings in Bioinformatics*, bbab189, 2021. [Impact factor 11.62]
8. **Jiang Y**†, Li W, Lindsey-Boltz LA, Yang Y, Li Y, Sancar A†. Super hotspots and super coldspots in the repair of UV-induced DNA damage in the human genome. *Journal of Biological Chemistry*, 100581, 2021. [Co-first and co-corresponding author; impact factor 5.157]
9. Dong M*, Thennavan A, Urrutia E*, Li Y, Perou CM, Zou F†, **Jiang Y**†. SCDC: bulk gene expression deconvolution by single-cell RNA sequencing. *Briefings in Bioinformatics*, 22(1), 416-427, 2021. [Co-corresponding author; impact factor 11.62]
10. Wang Y, Bhattacharya T, **Jiang Y**, Qin X, Wang Y, Liu Y, Saykin AJ, Chen L. A novel deep learning method for predictive modeling of microbiome data. *Briefings in Bioinformatics*, 22(3), bbaa073, 2021. [Impact factor 11.62]
11. Mei W*, Jiang Z*, Chen L, Chen Y, Sancar A†, **Jiang Y**#. Genome-wide circadian rhythm detection methods: systematic evaluations and practical guidelines. *Briefings in Bioinformatics*, 22(3), bbaa135, 2021. [Co-corresponding author; impact factor 11.62]

12. Wang R*, Lin D, **Jiang Y**[†]. SCOPE: a normalization and copy number estimation method for single-cell DNA sequencing. *Cell Systems*, 10 (5), 445-452, 2020. [Corresponding author; impact factor 10.3]
13. Huh R, Yang Y, **Jiang Y**, Shen Y, Li Y. SAME-clustering: single-cell aggregated clustering via mixture model ensemble. *Nucleic Acids Research*, 48 (1), 86-95, 2020. [Impact factor 16.97]
14. Yimit A, Adebali O, Sancar A[†], **Jiang Y**[†]. Differential damage and repair of DNA-adducts induced by anti-cancer drug cisplatin across mouse organs. *Nature Communications*, 10 (1), 309, 2019. [Co-corresponding author; impact factor 14.92]
15. Yang Y, Hu J, Selby CP, Li W, Yimit A, **Jiang Y**[†], Sancar A[†]. Single nucleotide resolution analysis of nucleotide excision repair of ribosomal DNA in humans and mice. *Journal of Biological Chemistry*, 294 (1), 210-217, 2019. [Co-corresponding author; impact factor 5.157]
16. Urrutia E*, Chen L, Zhou H, **Jiang Y**[†]. Destin: toolkit for single-cell analysis of chromatin accessibility. *Bioinformatics*, 35 (19), 3818-3820, 2019. [Corresponding author; impact factor 6.937]
17. Li W, Liu W, Kakoki A, Wang R*, Adebali O, **Jiang Y**, Sancar A. Nucleotide excision repair capacity increases during differentiation of human embryonic carcinoma cells into neurons and muscle cells. *Journal of Biological Chemistry*, 294 (15), 5914-5922, 2019. [Impact factor 5.157]
18. Dong M*, **Jiang Y**[†]. Single-cell allele-specific gene expression analysis. *Methods in Molecular Biology*, 1935, 155-174, 2019. [Corresponding author]
19. **Jiang Y**[†], Wang R*, Urrutia E*, Anastopoulos IN, Nathanson KL, Zhang NR[†]. CODEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. *Genome Biology*, 19 (1), 202, 2018. [First and co-corresponding author; impact factor 10.81]
20. Urrutia E*, Chen H, Zhou Z, Zhang NR[†], **Jiang Y**[†]. Integrative pipeline for profiling DNA copy number and inferring tumor phylogeny. *Bioinformatics*, 34 (12), 2126-2128, 2018. [Co-corresponding author; impact factor 6.937]
21. **Jiang Y**, Zhang NR, Li M. SCALE: modeling allele-specific expression by single-cell RNA-sequencing. *Genome Biology*, 18 (1), 74, 2017. [First author; impact factor 10.81]
22. Chen H, **Jiang Y**, Maxwell KN, Nathanson KL, Zhang NR. Allele-specific copy number profiling using whole exome sequencing. *Annals of Applied Statistics*, 11 (2), 1169-1192, 2017.
23. Garman B, Anastopoulos IN, Krepler C, Brafford P, Sproesser K, **Jiang Y**, Wubbenhorst B, Amaravadi R, Bennett J, Beqiri M, Elder D, Flaherty KT, Frederick DT, Gangadhar TC, Guarino M, Hoon D, Karakousis G, Liu Q, Mitra N, Petrelli NJ, Schuchter L, Shannan B, Shields CL, Wargo J, Wenz B, Wilson MA, Xiao M, Xu W, Xu X, Yin X, Zhang NR, Davies MA, Herlyn M, Nathanson KL. Genetic and Genomic Characterization of 462 Melanoma Patient-Derived Xenografts, Tumor Biopsies, and Cell Lines. *Cell Reports*, 21 (7), 1936-1952, 2017. [Impact factor 9.423]
24. Maxwell KN, Wubbenhorst B, Wenz BM, Sloover DD, Pluta J, Emery L, Barrett A, Kraya A, Anastopoulos IN, Yu S, **Jiang Y**, Chen H, Zhang NR, Hackman N, D'Andrea K, Daber R, Morrissette JJD, Mitra N, Feldman M, Domchek SM, Nathanson KL. BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. *Nature Communications*, 8 (1), 319, 2017. [Impact factor 14.92]

25. **Jiang Y**, Qiu Y, Minn AJ, Zhang NR. Assessing intratumor heterogeneity and tracking longitudinal and spatial clonal evolution by next-generation sequencing. *Proceedings of the National Academy of Sciences*, 113 (37), E5528-E5537, 2016. [First author; impact factor 11.2]
26. **Jiang Y**, Oldridge DA, Diskin SJ, Zhang NR. CODEX: a normalization and copy number variation detection method for whole exome sequencing. *Nucleic Acids Research*, 43 (6), e39-e39, 2015. [First author; impact factor 16.97]

GRANT SUPPORT

Active

R35 GM138342 (Jiang) 09/05/20 07/31/25

National Institute of General Medical Sciences (\$1,877,086.00)

Statistical Methods for Bulk-Tissue and Single-Cell Multi-Omics Integration

Role: Principal Investigator

U01 TR003715 (Hingtgen, Baldwin, Flores, Floyd) 07/01/21 04/30/25

National Center for Advancing Translational Sciences

A consortium effort to translate therapies for neurological diseases via an ex vivo organotypic platform

Role: Co-Investigator

R61 DA053599 (Browne) 07/01/21 05/31/24

National Institute on Drug Abuse

Defining the impact of cannabinoids on the latent HIV reservoir through multi-omic analysis

Role: Co-Investigator

UL1 TR002489 (Buse) 03/30/18 02/28/23

National Center for Advancing Translational Sciences

North Carolina Translational and Clinical Science Institute (NC TraCS) - Biostatistics, Epidemiology, and Research Design (BERD)

Role: Biostatistician

Completed

Not assigned (Alexander) 08/01/20 07/31/21

Pediatric Oncology Research (UNC HemOnc Trust Fund)

Single-Cell Transcriptomic and Epigenomic Profiles of Leukemia Cells from Diagnosis to Residual Disease

Role: Collaborator

P01 CA142538 (Kosorok, Davidian, Owzar) 04/01/15 03/31/21

National Cancer Institute

Statistical Methods for Cancer Clinical Trials - Project 3: Statistical/Computational Methods for Pharmacogenomics and Individualized Therapy

Role: Co-Investigator

R35 GM118102	(Sancar)	04/01/16	03/31/21
National Institute of General Medical Sciences			
Molecular Mechanism of Mammalian DNA Excision Repair, DNA Damage Checkpoints, and the Circadian Clock			
Role: <i>Co-Investigator</i>			
Not assigned	(Jiang, Zhang)	02/01/19	01/31/21
UNC Computational Medicine Program Pilot Award (\$50,000.00)			
Single-Cell Omics Analyses for Assessing Genomic, Transcriptomic and Epigenomic Heterogeneity in Cancer			
Role: <i>Principal Investigator</i>			
Not assigned	(Hicks, Hormoz, Jiang)	09/01/18	08/31/19
The Jayne Koskinas Ted Giovanis Foundation (\$30,000.00)			
Single-Cell Dynamics for Precision Medicine in Cancer			
Role: <i>Principal Investigator</i>			
Not assigned	(Jiang)	01/01/18	06/01/19
UNC Lineberger Comprehensive Cancer Center Developmental Award (\$50,000.00)			
Cross-Technology Inference of Tumor Phylogeny			
Role: <i>Principal Investigator</i>			

MENTORING

As postdoc mentor

Eugene Urrutia (Postdoc, Department of Biostatistics, joint with Dr. Haibo Zhou) 2017 – 2018
(Joint Hill-Rom as senior data scientist)

As doctoral thesis advisor

Wenwen Mei (PhD candidate, Department of Biostatistics) 2021 – now
Ann Marie Weideman (PhD candidate, Department of Biostatistics, joint with Dr. Joe Ibrahim) 2021 – now
Yuriko Harigaya (PhD candidate, Bioinformatics and Computational Biology) 2020 – now
Rujin Wang (PhD candidate, Department of Biostatistics, joint with Dr. Danyu Lin) 2017 – 2021
(joint Regeneron Pharmaceuticals as senior statistical geneticist)

As master thesis advisor

Lihao Wang (MS student, Department of Biostatistics) 2020 – 2021
(joint Jiangsu Hengrui Medicine as SAS programmer)

Zhiwen Jiang (MS student, Department of Biostatistics) 2019 – 2021
(joint UNC Biostatistics PhD program)

As undergraduate honor thesis advisor

Bella Qian (BSPH student, Department of Biostatistics, joint with Dr. Qian Li) 2021 – now

As GRA/rotation advisor

Andy Lee (rotation student, Bioinformatics and Computational Biology) 2021 – now

Jess Byun (rotation, Bioinformatics and Computational Biology, joint with Edward Browne) 2021 – now

Xiaofei Wei (MS student, Department of Biostatistics) 2021 – now

John Lin (rotation student, Bioinformatics and Computational Biology, joint with Thomas Alexander) 2021

Manas Tiwari (BSPH student, Department of Biostatistics) 2021

Matthew Regner (rotation student, Bioinformatics and Computational Biology) 2020

Meichen Dong (graduate research assistant, Department of Biostatistics, joint with Dr. Fei Zou) 2017 – 2019

As thesis committee member

Logan Whitehouse (PhD candidate, Bioinformatics and Computational Biology) ongoing

Matthew Regner (PhD candidate, Bioinformatics and Computational Biology) ongoing

Jamshaid Shahir (PhD candidate, Bioinformatics and Computational Biology) ongoing

Meichen Dong (PhD, Department of Biostatistics) 2021

Yue Shan (PhD, Department of Biostatistics) 2021

Cheyenna Anne Crowley (DrPh, Department of Biostatistics) 2021

Eric Van Buren (PhD, Department of Biostatistics) 2020

Chong Jin (PhD, Department of Biostatistics) 2020

Bingxin Zhao (PhD, Department of Biostatistics) 2020

Daniel Shiloh Malawsky (BSPH, Department of Biostatistics) 2020

Ruth Huh (PhD, Department of Biostatistics) 2019

PRESENTATIONS

Invited conference talks / departmental seminars

ICSA International Conference, Hong Kong 12/2022

Joint Statistical Meeting, Washington DC 08/2022

ENAR Spring Meeting, Houston 03/2022

Department of Computational Medicine and Bioinformatics, University of Michigan 12/2021

ICSA Applied Statistics Symposium, virtual	09/2021
Genetics Colloquium, UNC Chapel Hill	05/2021
Computational Genomics Forum, Mayo Clinic	04/2021
ENAR Spring Meeting, virtual	03/2021
ENAR Spring Meeting, virtual	03/2020
Grand Rounds, Holden Comprehensive Cancer Center, University of Iowa	01/2020
Computational Medicine Program, UNC Chapel Hill	12/2019
ICSA International Conference, Hangzhou, China	12/2019
ICSA Applied Statistics Symposium, Raleigh	06/2019
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences	03/2019
Michigan Center for Single-Cell Genomic Data Analytics, University of Michigan	02/2019
Department of Epidemiology & Biostatistics, University of South Carolina	01/2019
Genetics Colloquium, UNC Chapel Hill	11/2018
International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Greensboro	10/2018
Joint Statistical Meetings, Vancouver Canada	08/2018
Bioinformatics and Computational Biology Colloquium, UNC Chapel Hill	10/2017
Department of Human Genetics, Emory University	02/2017
Department of Biostatistics, UNC Chapel Hill	01/2017
Department of Biostatistics and Medical Informatics, University of Wisconsin Madison	01/2017
Department of Computational Medicine and Bioinformatics, University of Michigan	01/2017
ICSA International Conference, Shanghai China	12/2016

Invited/selected workshops & consortia

Young Scholars Forum on Statistics and Biostatistics, Beijing China	12/2019
Young Bioinformatics PI Workshop, Beijing China	08/2019
Tutorial, Conference on Intelligent Systems for Molecular Biology, Basel Switzerland	07/2019
BD2K Data Science Innovation Lab, Bend Oregon	06/2018
Highlight talk, 6 th RECOMB Satellite Workshop on Computational Cancer Biology, Los Angeles	07/2017

TEACHING

STAT101, Introductory Business Statistics, Summer 2016 ([Evaluation](#))

Department of Statistics, The Wharton School, University of Pennsylvania

BIOS/BCB 785, Statistical Methods for Gene Expression Analysis, Spring 2019 ([Website](#), [Evaluation](#))

Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill

Curriculum in Bioinformatics and Computational Biology, School of Medicine, UNC Chapel Hill

BIOS 635, Introduction to Machine Learning, Spring 2020 ([Website](#), [Evaluation](#))

Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill

BIOS/BCB 785, Statistical Methods for Gene Expression Analysis, Fall 2020 ([Website](#), [Evaluation](#))

Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill
Curriculum in Bioinformatics and Computational Biology, School of Medicine, UNC Chapel Hill

BIOS 635, Introduction to Machine Learning, Spring 2022

Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill

SERVICE & SYNERGISTIC ACTIVITIES

Referee

Nature Methods (2)

Genome Biology (3)

Nature Communications (6)

Genome Research (1)

Nucleic Acids Research (7)

PLOS Computational Biology (8)

Bioinformatics (4)

Biometrics (1)

PLOS Genetics (1)

Briefings in Bioinformatics (6)

Statistical Methods in Medical Research (1)

Communications Biology (2)

Genetics in Medicine (2)

Nature Machine Intelligence (2)

GigaScience (3)

Frontiers in Genetics (1)

Computational and Structural Biotechnology Journal (1)

BMC Bioinformatics (2)

European Journal of Human Genetics (1)

Genomics, Proteomics & Bioinformatics (1)

IEEE/ACM Transactions on Computational Biology and Bioinformatics (1)

Scientific Reports (5)

PeerJ (2)

PLOS One (8)

Committee

Member, MPH Data Science Committee, Gillings School of Global Public Health, UNC-CH	06/2019 – now
Member, Computing Committee, Department of Biostatistics, UNC-CH	07/2017 – now
Grant Reviewer, New Jersey Alliance for Clinical and Translational Research	05/2021
Grant Reviewer, Breast Cancer Now, UK	09/2019
Member, Greenberg Award Committee, Gillings School of Global Public Health, UNC-CH	02/2019 – 03/2019
Co-Chair, Seminar Committee, Department of Biostatistics, UNC-CH	07/2017 – 12/2018

Conference program

Organizer, Statistical methods in the era of next-generation sequencing, ICSA International Conference, 2022

Organizer, Statistical mechanics meets single-cell biology, JSM 2022.

Organizer, Statistical methods for single-cell sequencing data, ENAR 2022.

Organizer, Recent advances in statistical methods for single-cell omics analysis, ENAR 2020.

Organizer, Recent advances in statistical methods for single-cell analysis, ICSA International Conference 2019.

Organizer, From bulk tissue to single cells: advances in statistical genetics and genomics, ICSA Symposium 2019.

Organizer, Statistical methods in single-cell genomics, ENAR 2018.

Moderator, Single Cell Omics Technologies, ASHG 2017.

AUTHORED SOFTWARE

Copy number variation detection

CODEX R package (Bioconductor): <http://bioconductor.org/packages/CODEX>

CODEX2 R package (GitHub): <https://github.com/yuchaojiang/CODEX2>

Falcon-X R package (CRAN): <https://CRAN.R-project.org/package=falconx>

Cancer genomics

Canopy R package (CRAN): <https://CRAN.R-project.org/package=Canopy>

MARATHON R package (GitHub): <https://github.com/yuchaojiang/MARATHON>

Single-cell omics

SCALE R package (GitHub): <https://github.com/yuchaojiang/SCALE>

Destin R package (GitHub): <https://github.com/urrutiag/destin>

SCOPE R package (Bioconductor): <https://bioconductor.org/packages/SCOPE>

SCDC R package (GitHub): <https://meichendong.github.io/SCDC>

EPIC R package (GitHub): <https://github.com/rujinwang/EPIC>

TRIPOD R package (GitHub): <https://github.com/yharigaya/TRIPOD>

DNA damage, repair, and circadian rhythm

DNA Damage and Repair (GitHub): https://github.com/yuchaojiang/damage_repair

Circadian Rhythm Detection (GitHub): https://github.com/wenwenm183/Circadian_Genes_Benchmark

MEMBERSHIPS

American Statistical Association (ASA)

International Biometric Society Eastern North American Region (ENAR)

International Chinese Statistical Association (ICSA)

American Society of Human Genetics (ASHG)

American Association for Cancer Research (AACR)