

YUCHAO JIANG

CONTACT INFORMATION

Mailing address 4115D McGavran-Greenberg Hall, 135 Dauer Drive
University of North Carolina at Chapel Hill
Chapel Hill, NC 27599-7420

Email yuchaoj@email.unc.edu

Office phone (919) 843-3656

Fax (919) 966-3804

Website <https://yuchaojiang.github.io>

EMPLOYMENT

Assistant Professor (tenure-track) Jun 2017 – now
Department of Biostatistics, Gillings School of Global Public Health (75%)
Department of Genetics, School of Medicine (25%)
Lineberger Comprehensive Cancer Center
University of North Carolina, Chapel Hill

EDUCATION

University of Pennsylvania

Ph.D. in Genomics and Computational Biology, Perelman School of Medicine May 2017

M.A. in Statistics, The Wharton School Aug 2014

Advisor: Dr. Nancy R. Zhang

Cornell University

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

HONORS & AWARDS

Teaching Innovation Award, Gillings School of Global Public Health, UNC Chapel Hill, 2020

UNC Computational Medicine Program Pilot Award, 2019

IBM Junior Faculty Developmental Award, 2019

Finalist, NIH Director's Early Independence Award (impact score 20), 2018

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

PUBLICATIONS

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

1. **Jiang Y#**, Li W, Lindsey-Boltz LA, Yang Y, Li Y, Sancar A#. Nucleotide excision repair hotspots of UV-induced DNA damage in the human genome. *Under review*, 2020. [**Co-first and co-corresponding author**]
2. Mei W*, Jiang Z*, Chen L, Chen Y, Sancar A#, **Jiang Y#**. Genome-wide circadian rhythm detection methods: systematic evaluations and practical guidelines. *Revision under review*, 2020. [**Co-corresponding author**]
3. 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**]
4. 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*, bbaa073, 2020.
5. 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*, bbz166, 2020. [**Co-corresponding author**]
6. 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.
7. 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**]
8. 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**]
9. 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**]
10. 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.
11. Dong M*, **Jiang Y#**. Single-cell allele-specific gene expression analysis. *Methods in Molecular Biology*, 1935, 155-174, 2019. [**Invited book chapter; corresponding author**]
12. **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**]
13. 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**]
14. **Jiang Y**, Zhang NR, Li M. SCALE: modeling allele-specific expression by single-cell RNA-sequencing. *Genome Biology*, 18 (1), 74, 2017. [**First author**]

15. 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.
16. 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.
17. 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, Morrisette 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.
18. **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**]
19. **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**]

GRANT SUPPORT

Active

P01 CA142538 (Kosorok) 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

This research intends to develop novel and high-impact statistical and computational tools for discovering genetic variants associated with interindividual differences in the efficacy and toxicity of cancer medications and for optimizing drug therapy on the basis of each patient's genetic constitution.

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

The goal of this research is to understand the molecular mechanisms of excision repair, DNA damage checkpoints, and the circadian clock and to apply this information for cancer prevention and treatment.

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)

The North Carolina Translational and Clinical Sciences Institute (TraCS) is the integrated hub of the NIH Clinical and Translational Science Awards (CTSA) program at the University of North Carolina at Chapel Hill (UNC). Over the next five years, we will apply our expertise and infrastructure to support clinical and translational research, to advance health care for North Carolinians and the national goals of NCATS.

Role: *Biostatistician*

Not assigned (Jiang, Zhang) 02/01/19 01/31/21

UNC Computational Medicine Program Pilot Award (\$50,000)

Single-Cell Omics Analyses for Assessing Genomic, Transcriptomic and Epigenomic Heterogeneity in Cancer

Research objectives are to develop new statistical methods and computational algorithms for single-cell omics analyses to assess genomic, transcriptomic, and epigenomic heterogeneity in tumors. Their goal is to use the methods developed as part of this pilot award to facilitate our understanding of tumor progression and metastasis, aid biomarker discovery for diagnosis, and tailor personalized treatment.

Role: *Principal Investigator*

Completed

Not assigned (Hicks, Hormoz, Jiang) 09/01/18 08/31/19

The Jayne Koskinas Ted Giovanis Foundation (\$30,000)

Single-Cell Dynamics for Precision Medicine in Cancer

This research proposes a novel experimental and computational framework to understand the manifestation of Philadelphia chromosome-negative chronic myeloid leukemia using multimodal single-cell omics data collected from the same patient.

Role: *Principal Investigator*

Not assigned (Jiang) 01/01/18 06/01/19

UNC Lineberger Comprehensive Cancer Center Developmental Award (\$50,000)

Cross-Technology Inference of Tumor Phylogeny

This research addresses key analytical challenges in assessing tumor heterogeneity and profiling cancer evolution by both bulk DNA sequencing and single-cell RNA sequencing.

Role: *Principal Investigator*

PRESENTATIONS

Departmental seminars

Grand Rounds, Holden Comprehensive Cancer Center, University of Iowa	01/2020
Computational Medicine Program, UNC Chapel Hill	12/2019
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
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

Invited conference talks

ICSA Applied Statistics Symposium, Houston	12/2020
ENAR Spring Meeting, Nashville/virtual	03/2020
ICSA International Conference, Hangzhou China	12/2019
ICSA Applied Statistics Symposium, Raleigh	06/2019
International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Greensboro	10/2018
Joint Statistical Meetings, Vancouver Canada	08/2018
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, 6th RECOMB Satellite Workshop on Computational Cancer Biology, Los Angeles	07/2017

MENTORING

As postdoc mentor

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

Rujin Wang (PhD candidate, Department of Biostatistics, joint with Dr. Danyu Lin)	2017 – now
Wenwen Mei (PhD student, Department of Biostatistics)	2019 – now
Zhiwen Jiang (MS student, Department of Biostatistics)	2019 – now
Yuriko Harigaya (PhD student, Bioinformatics and Computational Biology)	2020 – now
Matthew Regner (PhD student, Bioinformatics and Computational Biology, rotation) (Joint Hector Franco Lab)	2020
Meichen Dong (PhD candidate, Department of Biostatistics, joint with Dr. Fei Zou) (Joint Fei Zou Lab)	2017 – 2019

As thesis committee member

Chong Jin (PhD candidate, Department of Biostatistics; advisor: Drs. Wei Sun, Danyu Lin)	ongoing
Yue Annie Shan (PhD candidate, Department of Biostatistics; advisor: Drs. Yun Li, Hongtu Zhu)	ongoing
Eric Van Buren (PhD candidate, Department of Biostatistics; advisor: Drs. Yun Li, Di Wu)	ongoing
Cheyanna Anne Crowley (DrPh candidate, Department of Biostatistics; advisor: Dr. Yun Li)	ongoing

Jamshaid Shahir (PhD candidate, Bioinformatics and Computational Biology; advisor: Dr. Jeremy Purvis)	ongoing
Bingxin Zhao (PhD, Department of Biostatistics; advisor: Drs. Hongtu Zhu, Joe Ibrahim)	2020
Daniel Shiloh Malawsky (BSPH, Department of Biostatistics; advisor: Timothy Gershon)	2020
Ruth Huh (PhD, Department of Biostatistics; advisor: Dr. Yun Li)	2019

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](#))
 Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill

BIOS/BCB 785, Statistical Methods for Gene Expression Analysis, Fall 2020
 Department of Biostatistics, Gillings School of Global Public Health, UNC Chapel Hill
 Curriculum in Bioinformatics and Computational Biology, School of Medicine, UNC Chapel Hill

SERVICE & SYNERGISTIC ACTIVITIES

Service

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, Breast Cancer Now, UK	09/2019 – 10/2019
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
Member, Admission Committee, Biological and Biomedical Sciences Program, UNC-CH	11/2017 – 03/2018

Referee

Genome Biology (2)
 Genome Research (1)
 Nature Communications (3)
 Nucleic Acids Research (4)
 PLOS Computational Biology (6)
 Briefings in Bioinformatics (2)
 Bioinformatics (2)
 Biometrics (1)
 Statistical Methods in Medical Research (1)
 Genetics in Medicine (2)

Nature Machine Intelligence (2)
GigaScience (3)
European Journal of Human Genetics (1)
BMC Bioinformatics (2)
Genomics, Proteomics & Bioinformatics (1)
Scientific Reports (5)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (1)
PLOS One (8)
PeerJ (2)

Conference program

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

CODEX R package (Bioconductor): <http://bioconductor.org/packages/CODEX>
Canopy R package (CRAN): <https://CRAN.R-project.org/package=Canopy>
SCALE R package (GitHub): <https://github.com/yuchaojiang/SCALE>
Falcon-X R package (CRAN): <https://CRAN.R-project.org/package=falconx>
CODEX2 R package (GitHub): <https://github.com/yuchaojiang/CODEX2>
MARATHON R package (GitHub): <https://github.com/yuchaojiang/MARATHON>
Destin R package (GitHub): <https://github.com/urrutiag/destin>
SCOPE R package (GitHub): <https://github.com/rujinwang/SCOPE>
SCDC R package (GitHub): <https://meichendong.github.io/SCDC>
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)