YUCHAO JIANG

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CONTACT INFORMATION

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EMPLOYMENT

Assistant Professor, Department of Biostatistics, Gillings School of Global Public Health — Sept 2017 – now
Assistant Professor, Department of Genetics, School of Medicine — Sept 2017 – now
Member, Lineberger Comprehensive Cancer Center — Nov 2017 – now
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

Cornell University
B.S. (*magna cum laude*) in Computational Biology — May 2012

PUBLICATIONS

# denotes corresponding author, *denotes advisee

1) Yimit A, Adebali O, Sancar A, **Jiang Y#**. Tissue-specific transcriptomic and epigenomic profiles explain differential damage and repair of anti-cancer drug cisplatin induced DNA-adducts across mouse organs. *Nature Communications*, under review, 2018.

2) **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*, revision under review, 2018.

3) Urrutia E*, Chen H, Zhou Z, Zhang NR, **Jiang Y#**. Integrative pipeline for profiling DNA copy number and inferring tumor phylogeny. *Bioinformatics*, bty057, 2018.

4) **Jiang Y**, Zhang NR, Li M. SCALE: modeling allele-specific expression by single-cell RNA-sequencing. *Genome Biology*, 18 (1), 74, 2017. PMCID: PMC5407026

5) 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. PMCID: PMC5627665

6) 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. PMCID: PMC5709812

7) Maxwell KN, Wubbenhorst B, Wenz BM, Sloover DD, Pluta J, Emery L, Barrett A, Kraya A, Anastopoulos IN, Yu S, **Jiang, Y**, et al. BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. *Nature Communications*, 8 (1), 319, 2017. PMCID: PMC5567274

8) **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. PMCID: PMC5027458

9) **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. PMCID: PMC4381046

ACTIVE GRANT SUPPORT

5 P01 CA142538-08 (Kosorok) 4/1/15 3/31/20 10% effort
National Cancer Institute 377,715.00
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 inter-individual 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*

5 R35 GM118102-02 (Sancar) 4/1/16 3/31/21 20% effort
National Institute of General Medical Sciences 644,830.00
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*

2017T109 (Jiang) 1/1/18 12/31/18
UNC Lineberger Comprehensive Cancer Center 50,000.00
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*

Award (Hicks, Hormoz, Jiang) 9/1/18 8/31/19
The Jayne Koskinas Ted Giovanis Foundation 30,000.00
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* (multi-PI with Stephanie Hicks, Sahand Hormoz)

PENDING GRANT SUPPORT

1 DP5 OD026419-01 (Jiang) 9/1/18 8/31/23
Office of the Director, National Institutes of Health 250,000.00
Tumor heterogeneity from bulk tissue to single cells
This research addresses statistical challenges in assessing tumor heterogeneity by high-throughput bulk DNA and single-cell RNA sequencing, which will facilitate our understanding of tumor progression, metastasis, and how they are related to diagnosis and prognosis.
Role: *Principal Investigator*

1 U2C CA233226-01 (Troester) 10/1/18 9/30/23 10% effort
National Cancer Institute 200,765.00
An Atlas to Advance Risk Stratification of Pre-Cancerous Breast - Unit 003 Data Analysis Unit
The UNC-PCA Data Analysis Unit provides the pipelines, resources, and expertise in biostatistics, genomics, and informatics. This Research Unit will work closely with the Characterization Unit to accept raw sequencing data and processed image data from stained tissue sections and mammography. The Research Unit provides biostatistical support to all Research Units from project design and power calculations to integrated analysis and support for final publications and atlas construction.
Role: *Co-Investigator*

ADVISING

PhD Dissertation Advisees

Meichen Dong (PhD candidate, Department of Biostatistics, joint with Dr. Fei Zou) Dec 2017 – now
Rujin Wang (PhD candidate, Department of Biostatistics, joint with Dr. Danyu Lin) Dec 2017 – now
Gene Urrutia (Postdoc, Department of Biostatistics, joint with Dr. Haibo Zhou) Dec 2017 – now

PhD Dissertation Committee

Chong Jin (PhD candidate, Department of Biostatistics, advisor: Dr. Wei Sun, Dr. Danyu Lin)
Ruth Huh (PhD candidate, Department of Biostatistics, advisor: Dr. Yun Li)

TEACHING

STAT101, Introductory Business Statistics, University of Pennsylvania (Summer 2016)

HONORS & AWARDS

Award, The Jayne Koskinas Ted Giovanis Foundation for Health and Policy, 2018
Finalist, NIH Director's Early Independence Award (impact score 20, award pending), 2018
UNC Lineberger Developmental Award, 2018
Saul Winegrad Award for Outstanding Dissertation, UPenn, 2017
President Gutmann Leadership Award, UPenn, 2016
Certificate in College and University Teaching, Penn Center for Teaching and Learning, 2016
Best Pre-Doc Poster, Symposium on Advances in Genomics, Epidemiology and Statistics (SAGES), 2015
Biomedical Graduate Studies Fellowship, Perelman School of Medicine, UPenn, 2012 – 2014
Distinction in Research, Cornell University, 2012
Summer Research Scholarship, Shoals Marine Lab, Cornell University and University of New Hampshire, 2011
National Scholarship, Ministry of Education of P.R. China, 2010

SERVICE & SYNERGISTIC ACTIVITIES

Service

Co-Chair, Seminar Committee, Department of Biostatistics, UNC-CH	July 2017 – now
Member, Computing Committee, Department of Biostatistics, UNC-CH	July 2017 – now
Member, Admission Committee, Biological and Biomedical Sciences Program, UNC-CH	Nov 2017 – now
Organizer, Single-Cell Omics Research Group, UNC-CH	Feb 2018 – now

Referee

- Nucleic Acids Research (2)
- PLOS Computational Biology (2)
- BMC Bioinformatics (2)
- Genetics in Medicine (1)
- GigaScience (1)
- Scientific Reports (2)
- PLOS One (3)
- PeerJ (1)

Conference Program

- Organizer, Statistical methods in single-cell genomics, ENAR 2018
- Moderator, Single Cell Omics Technologies, ASHG 2017

PRESENTATIONS

Invited talk, International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Oct 2018
Invited talk, Joint Statistical Meetings, Vancouver, Aug 2018
Bioinformatics & Computational Biology Colloquium, UNC, Chapel Hill, Oct 2017
ENAR, Washington DC, Mar 2017
Department of Human Genetics, Emory University, Feb 2017
Department of Biostatistics & Department of Genetics, UNC Chapel Hill, Jan 2017
Department of Biostatistics and Medical Informatics, Univ. of Wisconsin Madison, Jan 2017
Department of Computational Medicine and Bioinformatics, Univ. of Michigan, Jan 2017
Invited talk, ICSA International Conference, Shanghai China, Dec 2016
Joint Statistical Meetings, Chicago, Aug 2016
ENAR, Austin, Mar 2016

INVITED WORKSHOPS & CONSORSIA

BD2K Data Science Innovation Lab (full travel and lodging support), Bend Oregon, June 2018
Highlight talk, 6th RECOMB Satellite Workshop on Computational Cancer Biology, Los Angeles, July 2017

MEMBERSHIPS

American Statistical Association (ASA)
International Chinese Statistical Association (ICSA)
International Biometric Society Eastern North American Region (ENAR)
American Association for Cancer Research (AACR)
American Society of Human Genetics (ASHG)

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

CERTIFICATES

Neural Networks and Deep Learning (deeplearning.ai)
Improving Deep Neural Networks: Hyperparameter Tuning, Regularization, and Optimization (deeplearning.ai)