

YUCHAO JIANG

March 9, 2018

CONTACT INFORMATION

Mailing address	Department of Biostatistics 4115D McGavran-Greenberg Hall 135 Dauer Drive Chapel Hill, NC 27599-7420	Department of Genetics 5112 Genetic Medicine Building 120 Mason Farm Road Chapel Hill, NC 27599-7264
Email	yuchaoj@email.unc.edu	
Office phone	(919) 843-3656	
Fax	(919) 966-3804	
Website	https://yuchaojiang.github.io/	

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. (<i>magna cum laude</i>) in Computational Biology	May 2012
---	----------

PUBLICATIONS

denotes corresponding author, *denotes advisee

- 1) Urrutia E*, Chen H, Zhou Z, Zhang NR, **Jiang Y**#. Integrative pipeline for profiling DNA copy number and inferring tumor phylogeny. *Bioinformatics*, bty057, 2018
- 2) **Jiang Y**, Zhang NR, Li M. SCALE: modeling allele-specific expression by single-cell RNA-sequencing. *Genome Biology*, 18 (1), 74, 2017. PMCID: [PMC5407026](https://pubmed.ncbi.nlm.nih.gov/27400000/)
- 3) 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](https://pubmed.ncbi.nlm.nih.gov/27400000/)
- 4) 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](#)

- 5) 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](#)
- 6) **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](#)
- 7) **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](#)

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

Internal	(Jiang)	1/1/18	12/31/18
UNC Lineberger Developmental Award		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

ADVISING

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

TEACHING

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

HONORS & AWARDS

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

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

Referee

- Nucleic Acids Research (2)
- PLOS Computational Biology (2)
- BMC Bioinformatics (1)
- Genetics in Medicine (1)
- Scientific Reports (1)
- PLOS One (1)
- 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
Highlight talk, 6th RECOMB Satellite Workshop on Computational Cancer Biology, Los Angeles, July 2017
Contributed talk, ENAR, Washington DC, Mar 2017
Invited talk, Department of Human Genetics, Emory University, Feb 2017
Invited talk, Department of Biostatistics & Department of Genetics, UNC Chapel Hill, Jan 2017
Invited talk, Department of Biostatistics and Medical Informatics, Univ. of Wisconsin Madison, Jan 2017
Invited talk, Department of Computational Medicine and Bioinformatics, Univ. of Michigan, Jan 2017
Invited talk, ICSA International Conference, Shanghai China, Dec 2016
Contributed talk, Joint Statistical Meetings, Chicago, Aug 2016
Contributed talk, ENAR, Austin, Mar 2016

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/>