YUCHAO JIANG

November 24, 2018

CONTACT INFORMATION

Mailing address	Department of Biostatistics	Department of Genetics
	4115D McGavran-Greenberg Hall	5112 Genetic Medicine Building
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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

# indicates corresponding author; * indicates advisee.

1) Urrutia E*, Chen L, Zhou H, **Jiang Y#**. Destin: toolkit for single-cell analysis of chromatin accessibility. Submitted, 2018.

2) Yimit A, Adebali O, Sancar A#, **Jiang Y#**. Transcriptomic and epigenomic profiles explain differential damage and repair of DNA-adducts induced by anti-cancer drug cisplatin across mouse organs. *Nature Communications*, accepted, 2018.

3) **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*, accepted, 2018.

4) 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*, jbc-RA118, 2018.

5) 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.

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

7) 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

8) 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

9) 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

10) **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

11) **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

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*

ADVISING

Postdoctoral Research Fellow
Eugene Urrutia (Postdoc, Department of Biostatistics, joint with Dr. Haibo Zhou)   12/2017 – 10/2018

PhD Dissertation Advisee
Meichen Dong (PhD candidate, Department of Biostatistics, joint with Dr. Fei Zou)   12/2017 – now
Rujin Wang (PhD candidate, Department of Biostatistics, joint with Dr. Danyu Lin)   12/2017 – 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)
Yue Annie Shan (PhD candidate, Department of Biostatistics, advisor: Dr. Yun Li, Dr. Hongtu Zhu)
Bingxin Zhao (PhD candidate, Department of Biostatistics, advisor: Dr. Hongtu Zhao, Dr. Joe Ibrahim)

TEACHING

STAT101, Introductory Business Statistics, Summer 2016
Department of Statistics, The Wharton School, University of Pennsylvania

BIOS/BCB 785, Statistical Methods for Gene Expression Analysis, Spring 2019
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 2010

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

HONORS & AWARDS

Award, The Jayne Koskinas Ted Giovanis Foundation for Health and Policy, 2018

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

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

PRESENTATIONS

Department of Epidemiology & Biostatistics, University of South Carolina, Jan 2019

Department of Genetics, UNC Chapel Hill, Nov 2018

Invited talk, International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Oct 2018

Invited talk, Joint Statistical Meetings, Vancouver, Aug 2018

Bioinformatics and Computational Biology Colloquium, UNC Chapel Hill, Oct 2017

Highlight talk, 6th RECOMB Satellite Workshop on Computational Cancer Biology, Los Angeles, July 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

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

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

SERVICE & SYNERGISTIC ACTIVITIES

Service

Member, Computing Committee, Department of Biostatistics, UNC-CH	07/2017 – now
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

Nucleic Acids Research, PLOS Computational Biology, Statistical Methods in Medical Research, BMC Bioinformatics, Genetics in Medicine, GigaScience, Scientific Reports, PLOS One, PeerJ.

Conference Program

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.

Invited Workshops & Consortia

BD2K Data Science Innovation Lab (full travel and lodging support), Bend Oregon, June 2018.

MEMBERSHIPS

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