

# YUCHAO JIANG

November 1, 2018

## CONTACT INFORMATION

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<b>Website</b>	<a href="https://yuchaojiang.github.io">https://yuchaojiang.github.io</a>	

## EMPLOYMENT

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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
<b>University of North Carolina, Chapel Hill</b>	

## EDUCATION

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### University of Pennsylvania

<b>Ph.D.</b> in Genomics and Computational Biology, Perelman School of Medicine	May 2017
<b>M.A.</b> in Statistics, The Wharton School	Aug 2014

### Cornell University

<b>B.S.</b> ( <i>magna cum laude</i> ) in Computational Biology	May 2012
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## PUBLICATIONS

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# 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. Revision under review, 2018.
- 3) 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. Under review, 2018.

- 4) **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.
- 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

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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

## **ADVISING**

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### PhD Dissertation Advisees

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

### 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**

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

BIOS 785, Statistical Methods for Gene Expression and Regulation  
Gillings School of Global Public Health, University of North Carolina, Chapel Hill (Spring 2019)

## HONORS & AWARDS

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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

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

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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

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### Service

Co-Chair, Seminar Committee, Department of Biostatistics, UNC-CH	07/2017 – now
Member, Computing Committee, Department of Biostatistics, UNC-CH	07/2017 – now
Member, Admission Committee, Biological and Biomedical Sciences Program, UNC-CH	11/2017 – 03/ 2018
Organizer, Single-Cell Omics Research Group, UNC-CH	02/2018 – now

### Referee

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

### Conference Program

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

Moderator, Single Cell Omics Technologies, ASHG 2017

### Invited Workshops & Consorsia

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

## **MEMBERSHIPS**

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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)