

YUCHAO JIANG

December 4, 2017

CONTACT INFORMATION

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EMPLOYMENT

Assistant Professor, Department of Biostatistics, Gillings School of Global Public Health	July 2017 – now
Assistant Professor, Department of Genetics, School of Medicine	July 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
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PUBLICATIONS

• Methods

- 1) **Jiang Y**, Zhang NR, Li M. SCALE: modeling allele-specific expression by single-cell RNA-sequencing. *Genome Biology*, 18 (1), 74, 2017. PMCID: [PMC5407026](#)
- 2) 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](#)
- 3) **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](#)

- 4) **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](#)

- **Collaborations**

- 1) 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](#)
- 2) 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](#)

GRANT SUPPORT

5 P01 CA142538-08	(Kosorok)	4/1/10 – 3/31/20	10% effort
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 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

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

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
Moderator, American Society of Human Genetics 2017 Annual Meeting, Orlando, FL	Oct 2017

Referee

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

PRESENTATIONS

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
 Poster, ASHG Annual Meeting, Vancouver, Oct 2016
 Invited talk, Single-Cell Omics Working Group, Perelman School of Medicine, UPenn, Oct 2016
 Contributed talk, Joint Statistical Meetings, Chicago, Aug 2016
 Invited talk, Institute for Biomedical Informatics/Genomics and Comp. Bio retreat, Philadelphia, June 2016
 Poster, American Association for Cancer Research Annual Meeting, New Orleans, April 2016
 Contributed talk, ENAR, Austin, Mar 2016
 Poster, EMBL Cancer Genomics, Heidelberg Germany, Nov 2015
 Poster, Symposium on Advances in Genomics, Epidemiology and Statistics, Philadelphia, May 2015
 Student Seminar, Department of Statistics, The Wharton School, University of Pennsylvania, May 2015
 Poster, American Association for Cancer Research Annual Meeting, Philadelphia, April 2015
 Chalk talk, Genomics and Computational Biology, Perelman School of Medicine, UPenn, Apr 2014

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>