# Yan Dora Zhang

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## EDUCATION

2016	Ph.D. in Statistics, North Carolina State University, USA
	Thesis: Bayesian Methods for High-dimensional Data
	Advisor: Howard D. Bondell
2013	<b>M.S. in Statistics</b> , North Carolina State University, USA
2011	<b>B.S. in Statistics</b> , Nankai University, China

## **RESEARCH INTERESTS**

Statistical genetics, bioinformatics, Bayesian methods, big data, risk prediction **Application areas:** cancer genetics, psychology disease, public health/biomedical research

#### PROFESSIONAL EXPERIENCE

2019 -	Assistant Professor
	Department of Statistics & Actuarial Science
	Centre for Genomic Sciences
	The University of Hong Kong

- 2016–2019 **Postdoctoral Fellow** Department of Biostatistics, Bloomberg School of Public Health Johns Hopkins University Mentor: *Nilanjan Chatterjee*
- 2014–2015 **Research Assistant** Target Sciences Statistics, GlaxoSmithKline, *Durham, NC*
- 2014–2014 **Research Scientist Intern** Avaya Labs Research, Avaya, *Basking Ridge, NJ*
- 2013–2013 Research Assistant

Department of Civil Engineering, NCSU, Raleigh, NC

# PUBLICATIONS

## Peer-Reviewed

- Choudhury, P. P., Wilcox, A., Brook, M., Zhang, Y., Ahearn, T., Orr, N., ... Chatterjee, N., & García-Closas, M. (2019).Comparative validation of breast cancer risk prediction models and projections for future risk stratification. *JNCI: Journal of the National Cancer Institute*, djz113.
- Zhang, Y., Qi, G., Park, J. H., & Chatterjee, N. (2018). Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies across 32 complex traits. *Nature genetics*, 50(9), 1318-1326.
- 3. Zhang, Y., & Bondell, H. D. (2018). Variable selection via penalized credible regions with Dirichlet-Laplace global-local shrinkage priors. *Bayesian Analysis*, 13(3), 823-844.

## Under review or revision

- Zhang, Y., Wilcox, A. N., Zhang, H., Choudhury, P. P., Easton, D. F., Milne, R. L., ..., Chatterjee, N., & García-Closas, M. (2019+). Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers. *bioRxiv*, 723825. Under Review.
- 5. **Zhang, Y.**, Reich, B. J., & Bondell, H. D. (2019+). High-dimensional linear regression via the R2-D2 shrinkage priors. *Under revision*.
- Su, Y., Bhattacharya, A., Zhang, Y., Chatterjee, N., & Carroll, R. (2019+). Nonparametric Bayesian deconvolution of a symmetric unimodal density. Under revision.
- Hong, X., Fu, Z., Zhang, Y., ..., Wang, X. (2019+). Maternal metabolomic profile plus conventional risk factors help further distinguish preterm from term births in a sample of US urban, low income multi-ethnic population. Under revision.

# TEACHING

#### Lab Instructor

2013–2014 Experimental Statistics for Biological Sciences II

#### Teaching Assistant

2016	Applied Bayesian Statistics
2013	Applied Multivariate Statistical Analysis
2012	Experimental Statistics for Biological Sciences I
2012	Introduction to Mathematical Statistics I

2012 Experimental Statistics for Engineers II

2011 Introduction to Statistics

#### PRESENTATIONS

- 10/2018 **Poster presentation** on "Estimation of the polygenetic architecture of ten cancers and its implications for future discoveries", *ASHG*, *San Diego*, *CA*
- 09/2018 Invited talk on "Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies", School of Public Health, Peking University, Beijing, China
- 09/2018 Invited talk on "Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies", SJTU-YALE Joint Center of Biostatistics and Data Science, Shanghai, China
- 09/2018 Invited talk on "Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies", School of Statistics and Data Science, Nankai University, Tianjin, China
- 10/2017 **Poster presentation** on "Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies across 32 complex traits and implications for the future", *ASHG*, *Orlando*, *FL*
- 08/2017 **Invited talk** on "Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies", *JSM*, *Baltimore*, *MD*
- 08/2016 **Contributed talk** on "High-dimensional linear regression via the R2-D2 shrinkage priors", JSM, Chicago, Illinois
- 12/2015 **Invited talk** on "Bayesian penalized credible region variable selection and global-local shrinkage priors", *The Institute of Statistics, Nankai University, Tianjin, China*
- 08/2015 **Contributed talk** on "High-dimensional variable selection via penalized credible regions with global-local shrinkage priors", *JSM*, *Seattle*, *WA*
- 08/2014 **Contributed talk** on "Adaptive tensor regression with applications in neuroimaging data analysis", *JSM*, *Boston*, *MA*

#### MEMBERSHIP AND ACADEMIC SERVICES

- 2017– Member of American Society of Human Genetics (ASHG)
- 2017–2018 Committee Representative of Department of Biostatistics, School of Public Health, Johns Hopkins Postdoctoral Association
- 2016–2017 Member of International Chinese Statistical Association (ICSA) Community
- 2012–2016 Member of American Statistical Association (ASA) Community
- 2013–2014 Student Seminar Representative, Department of Statistics, NCSU
- 2013–2014 Executive of STATCOM NCSU Chapter, a student-run volunteer organization supported by ASA

#### SELECTED HONORS & AWARDS

2017 Honorable Mention for poster "Estimating effect-size distribution from summary-level statistics for large genome-wide association studies", Genetics Research Day, The Maryland Genetics, Epidemiology, and Medicine Training Program (MD-GEM)
2013 Nomination for the University Outstanding Teaching Assistant Award, NCSU
2013 Mu Sigma Rho Statistics Society Honor, NCSU
2011 Outstanding Graduates Honor, Nankai University, China
2010 Excellent Student Leader Honor, Nankai University, China
2009 National Scholarship, China

# SOFTWARE

• GENESIS: GENetic Effect-Size distribution Inference from Summary-level data

# PEER REVIEWER

- Bayesian Analysis
- Nature Communications