

# JUNYU CHEN

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## EDUCATION

**PhD, Epidemiology** 2020 - Present  
Rollins School of Public Health, Emory University Atlanta, GA  
Dissertation: “Investigating the genetic and epigenetic effects on kidney function among populations of African ancestry”, advised by Dr. Yan V Sun.

**MPH, Epidemiology** 2018  
Emory University Atlanta, GA

**BS, Biological Science, Concentration: Molecular biology** 2016  
Nanjing University Nanjing, China

## RESEARCH INTERESTS

Genetic Epidemiology, Statistical genetics, Kidney diseases, Multi-omics, Bioinformatics,

## PROFESSIONAL EXPERIENCE

**Center for Computational and Quantitative Genetics**  
**Department of Human Genetics, Emory University School of Medicine** Atlanta, GA  
**Research Specialist, Lead** 2018 - 2022  
Supervisor: Dr. Jingjing Yang

- ◆ Derived a scalable Bayesian tool to leverage quantitative annotation information to prioritize potential “causal” SNPs in GWAS ([https://github.com/jche453/BFGWAS\\_QUANT](https://github.com/jche453/BFGWAS_QUANT)).
- ◆ Developed and applied novel statistical methods to analyze high throughput sequence data.
- ◆ Built user-friendly pipelines for CHIP and RNA sequencing analyses.
- ◆ Evaluated polygenic risk scores using diverse machine learning algorithms.

**Coalition to Transform Advanced Care** Washington, D.C.  
**Public Health Analyst (Remote)** 2018 - 2020  
Supervisor: Dr. David Longnecker, William Hannon

- ◆ Collected and managed data related to measures of advanced illness care from diverse sources.
- ◆ Created an automatic index calculator (R) and a website ( [https://junyuchen.shinyapps.io/index\\_app/](https://junyuchen.shinyapps.io/index_app/) ) to monitor the quality of advanced illness care in the United States.

**Office of Public Health Genomics, Centers for Disease Control and Prevention** Atlanta, GA  
**Intern** May – August 2017

Supervisor: Dr. Marta Gwinn, Dr. Muin J. Khoury

- ◆ Managed CDC-authored publications data.
- ◆ Conducted a literature review and described trends in CDC-authored publications over time (Available at: <https://blogs.cdc.gov/genomics/2018/01/02/trends-in-cdc-publications/>).

## PUBLICATIONS

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### \* for equal contribution

1. **Junyu Chen**, Evan Gatev, Todd M Everson, Karen N Conneely, Nastassja Koen, Michael P Epstein, Michael S Kobor, Heather J Zar, Dan J Stein, Anke Huels. Pruning and thresholding approach for methylation risk scores in multi-ancestry populations. 2022, Preprint, medRxiv (Submitted to Epigenetics).
2. **Junyu Chen**, Qin Hui, Zeyuan Wang, Francis P. Wilson, Kaku So-Armah, Matthew Freiberg, Amy C. Justice, Ke Xu, Wei Zhao, Farah Ammous, Jennifer A. Smith, Sharon L. R. Kadia, Marta Gwinn, Vincent C. Marconi, Yan V. Sun. Epigenome-wide meta-analysis reveals differential DNA methylation associated with estimated glomerular filtration rate among African American men with HIV. 2022, (Submitted to Kidney International Reports).
3. **Junyu Chen**, Qin Hui, Chang Liu, Jaysingh Brijkumar, Johnathan Alex Edwards, Claudia E Ordonez, Matthew R Dudgeon, Henry Sunpath, Selvan Pillay, Pravi Moodley, Daniel R Kuritzkes, Mohamed YS Moosa, Tooru Nemoto, Vincent C Marconi, Yan V Sun. Associations of inflammation-related proteome with demographic and clinical characteristics of people with HIV in South Africa. 2022, Preprint, medRxiv.
4. **Junyu Chen**, Lei Wang, Philip L De Jager, David A Bennett, Aron S Buchman, Jingjing Yang. A scalable Bayesian functional GWAS method accounting for multivariate quantitative functional annotations with applications for studying Alzheimer disease. 2022, Human Genetics and Genomics Advances.
5. Boghuma K Titanji, Mitch Lee, Zeyuan Wang, **Junyu Chen**, Qin Hui, Lo Re III, Kaku So-Armah, Amy Justice, Ke Xu, Matthew Freiberg, Marta Gwinn, Vincent C Marconi, Yan V Sun. Epigenome-wide association study of biomarkers of liver function identifies albumin-associated DNA methylation sites among male veterans with HIV. 2022, Frontiers in Genetics.
6. Sarina Abrishamcar, **Junyu Chen**, Dakotah Feil, Anna Kilanowski, Nastassja Koen, Aneesa Vanker, Catherine J Wedderburn, Kirsten A Donald, Heather J Zar, Dan J Stein, Anke Huels. DNA Methylation as a Potential Mediator of the Association Between Prenatal Tobacco and Alcohol Exposure and Child Neurodevelopment in a South African Birth Cohort. 2022, Translational Psychiatry.
7. Boghuma K Titanji, Zeyuan Wang, **Junyu Chen**, Qin Hui, Kaku So-Armah, Matthew Freiberg, Amy C Justice, Xu Ke, Vincent C Marconi, Yan V Sun. Soluble CD14-associated DNA methylation sites predict mortality among men with HIV infection. 2022, AIDS.
8. Grace M Christensen, Claire Rowcliffe, **Junyu Chen**, Aneesa Vanker, Nastassja Koen, Meaghan J Jones, Nicole Gladish, Nadia Hoffman, Kirsten A Donald, Catherine J Wedderburn, Michael S Kobor, Heather J Zar, Dan J Stein, Anke Hüls. 2022, Science of The Total Environment
9. Chang Liu, Zicheng Wang, Qin Hui, Yiyun Chiang, **Junyu Chen**, Jaysingh Brijkumar, Johnathan A Edwards, Claudia E Ordonez, Mathew R Dudgeon, Henry Sunpath, Selvan Pillay, Pravi Moodley, Daniel R Kuritzkes, Mohamed Moosa, Dean P Jones, Vincent C Marconi, Yan V Sun. Crosstalk between Host Genome and Metabolome among People with HIV in South Africa. 2022, Metabolites.
10. Anna Kilanowski, **Junyu Chen**, Todd Everson, Elisabeth Thiering, Rory Wilson, Nicole Gladish, Melanie Waldenberger, Hongmei Zhang, Juan C. Celedón, Esteban G. Burchard, Annette Peters, Marie Standl, Anke Hüls. Methylation risk scores for childhood aeroallergen sensitization: Results from the LISA birth cohort. 2022, Allergy.
11. Janise N Kuehner\*, **Junyu Chen\***, Emily C Bruggeman, Feng Wang, Yangping Li, Chongchong Xu, Zachary T McEachin, Ziyi Li, Li Chen, Chadwick M Hales, Zhexing Wen, Jingjing Yang, Bing Yao. 5-hydroxymethylcytosine is Dynamically Regulated During Forebrain Organoid Development and

- Prematurely Altered in Forebrain Organoids of Alzheimer's Disease. 2021, Cell Reports.
12. Justin M Luningham, **Junyu Chen**, Shizhen Tang, Philip L De Jager, David A Bennett, Aron S Buchman, Jingjing Yang. Bayesian Genome-wide TWAS Method to Leverage both cis- and trans-eQTL Information through Summary Statistics. 2020, The American Journal of Human Genetics.
  13. Yanyan Xing, **Junyu Chen**, Henry Hilley, Haley Steele, Jingjing Yang, and Liang Han. Molecular signature of pruriceptive MrgprA3. 2020, Journal of Investigative Dermatology.
  14. **Junyu Chen**, Yunfeng Huang, Qin Hui, Raina Mathur, Marta Gwinn, Kaku So-Armah, Matthew S Freiberg, Amy C Justice, Ke Xu, Vincent C Marconi, Yan V Sun. Epigenetic Associations with Estimated Glomerular Filtration Rate Among Men With Human Immunodeficiency Virus Infection. 2020, Clinical Infectious Diseases
  15. Anne C. Spaulding, **Junyu Chen**, Carolyn A. Mackey, Madeline Adee, Chava J. Bowden, W. David Selvage, Karla A. Thornton. 2019. Assessment and Comparison of Hepatitis C Viremia in the Prison Systems of New Mexico and Georgia. 2019, JAMA Network Open.
  16. Anne C. Spaulding, Gloria D. Eldridge, Cynthia E. Chico, Nancy Morisseau, Ana Drobeniuc, Rebecca Fils-Aime, Carolyn Day, Robyn Hopkins, Xingzhong Jin, **Junyu Chen**, and Kate A. Dolan. Smoking in Correctional Settings Worldwide: Prevalence, Bans, and Interventions. 2018, Epidemiologic reviews.

### **Abstract Presentation**

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1. **Junyu Chen**, Michael P. Epstein, Joellen M. Schildkraut, Siddhartha P. Kar. Cross-disorder genetic analysis identifies auto-immune disease loci inversely associated with diverse cancer types (Poster). American Society of Human Genetics, Oct 2022.
2. Sarina Abrishamcar, **Junyu Chen**, Aneesha Vanker, Kirsten Donald, Heather Zar, Dan Stein, Anke Huels. 2021. Exploring the Mediation of Maternal Substance Use and Neurodevelopmental Outcomes in Toddlers by DNA Methylation: A Methylation Risk Score Approach (Oral). Epigenomics of Common Diseases Conference, Nov 2021.
3. Anna Kilanowski, **Junyu Chen**, Todd Everson, Elisabeth Thiering, Rory Wilson, Nicole Gladish, Melanie Waldenberger, Hongmei Zhang, Juan C. Celedón, Esteban G. Burchard, Annette Peters, Marie Standl, Anke Hüls. Methylation risk scores for childhood aeroallergen sensitization: Results from the LISA birth cohort (Poster). Epigenomics of Common Diseases Conference, Nov 2021.
4. **Junyu Chen**, Evan Gatev, Karen N. Conneely, Nastassja Koen, Michael P. Epstein, Michael S. Kobor, Heather J. Zar, Dan J. Stein, Anke Huels. Methylation risk score usage and performance in populations of multi-ethnic ancestry (Poster). Society of Epidemiologic Research 2021 Virtual Meeting.
5. J. Yang, **J. Chen**, P. L. De Jager, D. A. Bennett, A. S. Buchman. A scalable Bayesian approach to leverage quantitative and overlapping functional annotations in GWAS of complex traits. 4<sup>th</sup> International Conference on Econometrics and Statistics 2021 Meeting.
6. Claire Rowcliffe, **Junyu Chen**, Aneesha Vanker, Nastassja Koen, Meaghan J Jones, Nicole Gladish, Kirsten A. Donald, Catherine J Wedderburn, Michael S Kobor, Heather J Zar, Dan J Stein, Anke Huels. In-utero exposure to indoor air pollution or tobacco smoke and cognitive development in a South African birth cohort study (Poster). International Society for Environmental Epidemiology 2021 Virtual Meeting.
7. Claire Rowcliffe, **Junyu Chen**, Aneesha Vanker, Nastassja Koen, Meaghan J Jones, Nicole Gladish, Kirsten A. Donald, Catherine J Wedderburn, Michael S Kobor, Heather J Zar, Dan J Stein, Anke Huels. In-utero exposure to indoor air pollution or tobacco smoke and cognitive development in a South African birth cohort study. SERdigital 2020.
8. **J. Chen**, P. L. De Jager, D. A. Bennett, A. S. Buchman, J. Yang. A scalable Bayesian approach to leverage quantitative and overlapping functional annotations in GWAS of complex traits (poster).

American Society of Human Genetics Oct 2020 Virtual Meeting.

9. J. Yang, J. M. Luningham, **J. Chen**, S. Tang, P. L. De Jager, D. A. Bennett, A. S. Buchman. Novel Bayesian Genome-Wide TWAS method to leverage both cis- and trans- eQTL information through summary statistics (poster). American Society of Human Genetics Oct 2020 Virtual Meeting.
10. J. Kuehner, **J. Chen**, E. Bruggeman, F. Wang, C. Xu, Z. Wen, J. Yang and B. Yao. Genome-wide 5hmC dynamics during human organoid development and its dysregulation in Alzheimer's disease (poster). American Society of Human Genetics, Oct 2019.
11. F. Wang, L. Chen, **J.Y. Chen**, E.C. Bruggeman, J.K. Kuehner, B. Yao. Global alteration of circRNA landscape in Alzheimer's disease (poster). American Society of Human Genetics, Oct 2019.

## **RESEARCH EXPERIENCE**

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**Department of Epidemiology, Rollins School of Public Health**

Atlanta, GA

**Graduate research assistant**

2017 - 2018, 2020 - Present

Supervisor: Dr. Yan V Sun

- ◆ Evaluate the performance of polygenic scores derived from European ancestry in African descendants.
- ◆ Conduct cell-type specific epigenome-wide association studies (EWAS) of IL-6.
- ◆ Conducted EWAS of multiple phenotypes including Apolipoprotein L1 high-risk genotypes for kidney disease, eGFR, CD4 count, liver functions and inflammatory markers.
- ◆ Performed data preprocessing, quality control and variant calling for whole exome sequence data.
- ◆ Examined the associations of proteomics and mosaic chromosomal alterations with demographic, clinical characteristics and comorbidities in people living with HIV.

**Department of Epidemiology, Rollins School of Public Health**

Atlanta, GA

**Graduate research assistant**

2021 - Present

Supervisor: Dr. Anke Huels

- ◆ Propose to develop a DNA methylation risk score (MRS) tailored for mediation analysis.
- ◆ Derived a pruning and thresholding (P+T) MRS and evaluated its performance across diverse ancestries through simulation studies and real data analyses.
- ◆ Developed a user-friendly analytic pipeline for P+T MRS (<https://github.com/jche453/Pruning-Thresholding-MRS>).

**Department of Epidemiology, Rollins School of Public Health**

Atlanta, GA

**Graduate research assistant**

2021 - Present

Supervisors: Drs. Siddhartha Kar, Joellen Schildkraut and Michael Epstein

- ◆ Conducted a literature review on statistical methods for pleiotropy in human complex traits.
- ◆ Performed cross-disorder GWAS to identify pleiotropic alleles that have opposite effects on major autoimmune diseases and common cancers.
- ◆ Investigated the function of pleiotropic alleles by SNP-based annotation pipelines such as FUMA and gene-based approaches such as TWAS.

**Center for the Health of Incarcerated Persons, Emory University**

Atlanta, GA

**Research Assistant**

2017 -2018

Supervisor: Dr. Anne Spaulding

- ◆ Performed quantitative analysis on longitudinal healthcare data in correctional facilities.
- ◆ Supported the principal investigator with protocols development, grant and manuscripts writing, and progress track throughout the submission process.

## **TEACHING EXPERIENCE**

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<b>Rollins School of Public Health, Emory University</b>	Atlanta, GA
<b>Teaching Assistant</b> , EPI 550 Epidemiological method III (Modelling)	2022
<b>Teaching Assistant</b> , EPI 540 Epidemiological method II	2020-2021
<b>Teaching Assistant</b> , EPI 550 Epidemiological method III (Modelling)	2020
<b>Teaching Assistant</b> , EPI 517 Case Studies in Infectious Disease Epidemiology	2017 -2018

## **SKILLS & TRAINING**

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- ◆ Programming: R, SAS, Python, C++; Linux/Unix, AWS.
- ◆ Methods: Bayesian statistics, statistical genetics and genomics, epidemiology methods, machine learning.
- ◆ Language: fluent in Mandarin, Cantonese, and English; Limited working experience in Japanese.