

Zeyun Lu

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Address: 2001 N Soto St, Los Angeles, CA 90033 Last Updated: 10/29/2022

Summary	PhD candidate in Biostatistics interested in developing causal inference methods on the genetic architecture of complex diseases.	
Education	Doctor of Philosophy in Biostatistics	08/2019 - Present
	University of Southern California	Los Angeles, CA
	Master of Science in Statistics	09/2015 - 12/2016
	University of California, San Diego	La Jolla, CA
Professional Experience	Bachelor of Science in Mathematics/Economics	09/2012 - 09/2014
	University of California, Los Angeles	Los Angeles, CA
	Associate in Arts	03/2010 - 06/2012
	Shoreline Community College	Shoreline, WA
	Graduate Research Assistant	08/2020 - Present
	Department of Population and Public Health Sciences	Los Angeles, CA
	Keck School of Medicine, USC	
	Mentor: Dr. Nicholas Mancuso	
	<ul style="list-style-type: none">Developed a Bayesian gene fine-mapping method (MA-FOCUS) for complex diseases leveraging GWAS and gene expression data from multiple ancestries.Developed a Bayesian stepwise selection approach (SuShiE) by modelling the covariance structures of SNPs' effect sizes across multiple ancestries to identify shared causal genetic variants of complex diseases.Developed an integrative approach (rPWAS) leveraging GWAS and protein abundance data to test post-transcriptional/translational regulatory mechanisms of complex diseases.	
	Research Internship	05/2022 - Present
	Dana-Farber Cancer Institute/Harvard Medical School	Online/Boston, MA
	Mentor: Dr. Alexander Gusev	
	<ul style="list-style-type: none">Developed a statistical framework to integrate experimental perturb-seq data for <i>trans</i> effects with GWAS and eQTL data for <i>cis</i> effects to identify "core" genes that are the <i>trans</i> targets of disease-relevant genomic variations.	
	Statistician	04/2017 - 06/2019
	Alzheimer's Therapeutic Research Institute (ATRI)	San Diego, CA
	Keck School of Medicine, USC	
	Mentor: Dr. Rema Raman and Dr. Michael Donohue	
	<ul style="list-style-type: none">Participated as Biostatistician in study teams of several Alzheimer's Disease clinical trials and observational studies such as ADNI3, A4, and LEADS by designing and generating different study reports including but not limited to performing data analysis with mixed models, investigating, data anomalies, and implementing patient randomization.Designed, built, and administered R Shiny projects that created dynamic online clinical data reporting system and risk-based monitoring system for ADNI3.	

- Mentored student intern in R Shiny, clinical trials, and statistical analysis.

Mathematics Graduate Research Internship 03/2016 - 06/2016
 Department of Mathematics 09/2016 - 12/2016
 University of California, San Diego La Jolla, CA
 Mentor: Dr. Anthony C. Gamst

- Analyzed several clinical trials data with visualization, tabulation, and statistical methods such as Linear Regression, Logistic Regression, and ANOVA etc.
- Investigated data errors and proposed fixing schemes.

Mathematics Tutor 01/2011 - 06/2012
 Math Learning Center Shoreline, WA
 Shoreline Community College
 Mentor: Rosalie Tepper

- Tutored students mathematics from basic algebra to calculus and statistics on a weekly basis.

Articles

2. *Multi-ancestry fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.* **Lu Z***, Gopalan S*, Yuan D, Conti D, Pasaniuc B, Gusev A, Mancuso N. **American Journal of Human Genetics.** August, 2022.
 DOI: <https://doi.org/10.1016/j.ajhg.2022.07.002>
1. *Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization.* Pathak GA*, Singh K*, Miller-Fleming TW, Wendt FR, Ehsan N, Hou K, Johnson R, **Lu Z**, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B, Polimanti R, Davis LK, Mancuso N. **Nature Communication.** July, 2021.
 DOI: <https://doi.org/10.1038/s41467-021-24824-z>

* Equal Contribution

Awards & Fellowship

4. **Third Place Winner**, KSOM Research Video Challenge 12/2021
 Video Competition for Keck School Of Medicine graduate students to showcase their research. Video Link: <https://youtu.be/Nc5SVhz7-aQ>
3. **Reviewers' Choice**, American Society of Human Genetics 2021 10/2021
 Abstract scored by reviewers in the top 10% of all poster abstracts.
2. **Outstanding Overall Performance**, Biostatistics Screening Exam 08/2020
 In recognition of the top two PhD students in the annual screening exams for theory and applied statistics.
1. **Keck School of Medicine/Graduate School Fellowship** 2019/2020
 In recognition of new PhD students' outstanding academic promise.

Posters & Abstracts

8. *Residual Proteome-wide Association Study Identifies Genes for Blood-Related Traits.* **Lu Z**, Jung J, Gazal S, Mancuso N. **American Society of Human Genetics.** October, 2021.
7. *Novel insight into the etiology of ischemic stroke gained by integrating human transcriptome-wide association study with rodent expression data.* Jung J, **Lu Z**, Mancuso N. **American Society of Human Genetics.** October, 2021.

6. *Multi-ethnic fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.* Gopalan S*, **Lu Z***, Jiang L, Conti DV, Gusev A, Pasaniuc P, Mancuso N. **Probabilistic Modeling In Genomics**. April, 2021.
5. *Integrative analyses identify genes and their functional consequences underlying COVID-19 hospitalization.* Singh K, Pathak G, Miller-Fleming T, Wendt F, Ehsan N, Hou K, Johnson R, **Lu Z**, Gopalan S, Yang L, Mohammadi P, Pasaniuc B, Polimanti R, Davis L, Mancuso N. **Molecular Genetics and Metabolism**. April, 2021.
4. *Integrative analyses with large-scale COVID-19 GWAS identifies susceptibility genes underlying hospitalized outcomes.* Pathak G*, Singh K*, Ehsan N, Hou K, Johnson R, **Lu Z**, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B, Polimanti R, Davis LK, Mancuso N, COVID-19 Host Genetics Initiative. **American Society of Human Genetics**. October, 2020.
3. *Multi-ethnic fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.* Gopalan S, **Lu Z**, Conti DV, Gusev A, Pasaniuc B, Mancuso, N. **American Society of Human Genetics**. October, 2020.
2. *Brain Amyloid Burden, Sleep, and Circadian Rest/Activity Rhythms: Screening Findings from A4 and LEARN.* Rosenberg PB, Zipunnikov V, **Lu Z**, Raman R, Carlsson CM, Mintzer JE, Marshall GA, Porsteinsson AP, Yaari R, Wanigatunga SK, Romano C, Wu MN, Aisen PS, Sperling RA, Spira AP. **Alzheimer's & Dementia**. November, 2018.
1. *An Open-source Implementation of Data Standards for Alzheimer's Disease Clinical Trials.* Sun CK, Donohue M, Ernststrom K, Jiang Y, **Lu Z**, Aisen P, Raman R. **Clinical Trials on Alzheimer's Disease**. Boston, MA. November, 2017.

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Talks

6. *Residual Proteome-wide Association Study Identifies Genes for Blood-Related Traits.* **Lu Z. Seminar in Biostatistics and Epidemiology.** Department of Population and Public Health Sciences, Keck School of Medicine of USC. Los Angeles, CA. October, 2021.
5. *Multi-ethnic fine-mapping in transcriptome-wide association studies.* **Lu Z. Seminar in Biostatistics and Epidemiology.** Department of Population and Public Health Sciences, Keck School of Medicine of USC. Los Angeles, CA. September, 2021.
4. *Probabilistic fine-mapping of transcriptome-wide association studies.* **Lu Z. Seminar in Biostatistics and Epidemiology.** Department of Population and Public Health Sciences, Keck School of Medicine of USC. Online. September, 2020.
3. *Proteome-Wide Association Study Identifies Independent Protein QTLs for Blood-Related Traits.* **Lu Z. Seminar in Biostatistics and Epidemiology.** Department of Population and Public Health Sciences, Keck School of Medicine of USC. Online. September, 2020.
2. *A4 Actigraphy Study Pre-randomization Analysis.* **Lu Z. ATRI Biostatistics Workshop.** Alzheimer's Therapeutic Research Institute, San Diego, CA. November, 2018.
1. *Dynamic Reporting Web Framework for Clinical Trials Using R Shiny.* Jain S, **Lu Z. ATRI Biostatistics Workshop.** Alzheimer's Therapeutic Research Institute, San Diego, CA. August, 2018.

TAship	3. Analysis of Omics Data for Research Studies 06/2022 Multi-omics Boot Camp of SHARPP Training Mailman School of Public Health, Columbia University
	2. PM-522A: Introduction to the Theory of Statistics 08/2021 - 12/2021 Department of Population and Public Health Sciences Keck School of Medicine, University of Southern California
	1. Analysis of Omics Data for Research Studies 06/2021 Multi-omics Boot Camp of SHARPP Training Mailman School of Public Health, Columbia University
Software	4. TWAS Simulator <ul style="list-style-type: none"> • A Python software to perform Transcriptome-wide Association Studies (TWAS) simulations. Users can choose different prediction methods to fit eQTL model, such as LASSO, ENET, and GBLUP. • https://github.com/mancusolab/twas_sim 3. MA-FOCUS <ul style="list-style-type: none"> • A Python software to perform gene-trait fine-mapping from TWAS in either single ancestry or multi-ancestry settings. • https://github.com/mancusolab/ma-focus 2. ADNI3 and LEADS Dynamic Web Report <ul style="list-style-type: none"> • Two Shiny apps that transform static reports to interactive web pages for clinical trials investigators' monitoring on enrollment, primary outcomes, and safety. • Interval apps that are not public accessible. 1. ADNI3, A4, and LEADS <ul style="list-style-type: none"> • Three R packages that crawl EDC API, transform data into CDISC format, and automatically build several reports (enrollment, safety etc) for clinical research. • Interval packages that are not public accessible.
Other Contributions	Reviewer Services Reviewer for PLOS Computational Biology.
Membership	American Statistical Association. American Society of Human Genetics.
Skills	R (Tidyverse, Shiny), Python, SAS, Stata, plink, gcta, bedtools, LDSC, Git, Latex, Linux, CDISC.