

Zeyun Lu

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Summary	PhD Student in Biostatistics interested in developing statistical methods to better understand genetic architecture for complex diseases using summary-based data.	
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
Professional Experience	Graduate Research Assistant	08/2020 - Present
	Department of Population and Public Health Sciences Keck School of Medicine, USC	Los Angeles, CA
	Mentor: Dr. Nicholas Mancuso	
	<ul style="list-style-type: none">• Developed a Bayesian gene fine-mapping method for complex diseases using summary-based data and molecular data of multi-ethnic groups.• Developed a method to test post-transcriptional/translational regulatory mechanisms for complex diseases.• Constructed <i>cis</i>-protein Quantitative Loci reference panel using FUSION pipeline.	
Professional Experience	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	
Professional Experience	<ul style="list-style-type: none">• Participated as Biostatistician in study teams of several Alzheimer's Disease (AD) clinical trials and observational studies such as AD Neuroimaging Initiative 3 (ADNI3), Anti-Amyloid Treatment in Asymptomatic AD (A4), and Longitudinal Early-Onset AD Study (LEADS).• Designed and generated different study reports for ADNI3, A4, and LEADS. Reports include 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
Professional Experience	Mentor: Dr. Anthony C. Gamst	
	<ul style="list-style-type: none">• 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
Math Learning Center
Shoreline Community College
Mentor: Rosalie Tepper

01/2011 - 06/2012
Shoreline, WA

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

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.

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. **In Review**.
DOI: <https://doi.org/10.1101/2022.02.10.479993>
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

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, Ernstrom K, Jiang Y, **Lu Z**, Aisen P, Raman R. **Clinical Trials on Alzheimer's Disease**. Boston, MA. November, 2017.

* Equal Contribution

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

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	<p>3. FOCUS</p> <ul style="list-style-type: none"> • Python software to perform gene-trait fine-mapping from transcriptome-wide association studies in either single ethnic or multi-ethnic settings. • https://github.com/mancusolab/focus <p>2. ADNI3 and LEADS Dynamic Web Report</p> <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. <p>1. ADNI3, A4, and LEADS</p> <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	<p>Reviewer Services Reviewer for PLOS Computational Biology.</p> <p>Membership American Statistical Association.</p>
Skills	<p>R (Tidyverse, Shiny), Python, SAS, Stata, plink, gcta, bedtools, LDSC, Git, Latex, Linux, CDISC.</p>