Zeyun Lu

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Address: 2001 N. Soto Street, Los Angeles, CA 90033

Education	University of Southern California Doctor of Philosophy in Biostatistics	09/2019 - Present
	University of California, San Diego Master of Science in Statistics	09/2015 - 12/2016
	University of California, Los Angeles Bachelor of Science in Mathematics/Economics	09/2012 - 09/2014

Professional Experience

Graduate Research Assistant — 08/2020 - Present
Department of Population and Public Health Science — Los Angeles, CA
Keck School of Medicine, USC
Mentor: Dr. Nicholas Mancuso

- Developed a gene fine-mapping method (ME-FOCUS) for complex traits using summary-based data and reference panels of multi-ethnic groups.
- Performed Proteome-Wide Association Studies (PWAS) to detect mRNA-free protein mediation genes for complex traits.
- Constructed *cis*-protein Quantitative Loci reference panel using FUSION pipeline.

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

- 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
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.

Awards and Fellowship

Keck School of Medicine/Graduate School Fellowship	2019/2020
Outstanding Overall Performance in Biostatistics Screening Exam	08/2020

Articles

1. *Integrative analyses identify susceptibility genes underlying COVID-19 hospitalization.* Pathak GA, Singh K, Miller-Fleming TW, Wendt FR, Ehsan N, Hou K, Johnson R, <u>Lu Z</u>, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B, Polimanti R, Davis LK, Mancuso N. **Nature Communication** (in Press). 2021.

Posters & **Abstracts**	3. *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, <u>Lu Z</u>, Gopalan S, Yang L, Mohammadi P, Pasaniuc B, Polimanti R, Davis L, Mancuso N. **Molecular Genetics and Metabolism**. April, 2021.
	2. *Brain Amyloid Burden, Sleep, and Circadian Rest/Activity Rhythms: Screening Findings from A4 and LEARN.* Rosenberg PB, Zipunnikov V, <u>Lu Z</u>, 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, <u>Lu Z</u>, Aisen P, Raman R. **Clinical Trials on Alzheimer's Disease (CTAD)**. Boston, MA. November 2017.

Talks	4. *Probabilistic fine-mapping of transcriptome-wide association studies.* <u>Lu Z</u>. **Seminar in Biostatistics and Epidemiology**. Department of Population and Public Health Science, Keck School of Medicine of USC. Online. September 2020.
	3. *Proteome-Wide Association Study Identifies Independent Protein QTLs for Blood-Related Traits.* <u>Lu Z</u>. **Seminar in Biostatistics and Epidemiology**. Department of Population and Public Health Science, Keck School of Medicine of USC. Online. September 2020.
	2. *A4 Actigraphy Study Pre-randomization Analysis.* <u>Lu Z</u>. **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, <u>Lu Z</u>. **ATRI Biostatistics Workshop**. Alzheimer's Therapeutic Research Institute, San Diego, CA. August 2018.

TAship **Experience**	**Analysis of Omics Data for Research Studies**	06/2021
	Multi-omics Boot Camp of SHARPP Training	
	Mailman School of Public Health, Columbia University	
	PM-522A: Introduction to the Theory of Statistics	Fall 2021 (Exp.)
	Department of Population and Public Health Science	
	Keck School of Medicine, University of Southern California	

Software

FOCUS
- 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

ADNI3 and LEADS Dynamic Web Report
- Two Shiny apps that transform static reports to interactive web pages for clinical trails investigators' monitoring on enrollment, primary outcomes, and safety.
- Interval apps that are not public accessible.

ADNI3, A4, and LEADS
- 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

Skills   R (Tidyverse, Shiny), Python, SAS, Stata, plink, gcta, bedtools, LDSC, Git, Latex, Linux, CDISC.