

Zeyun Lu

Cell: (858)207-8318 **Email:** zeyunlu@usc.edu zeyunlu@usc.edu **Web:** zeyunlu.github.io
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 Department of Population and Public Health Science Keck School of Medicine, USC Mentor: Dr. Nicholas Mancuso | 08/2020 - Present Los Angeles, CA |
| | <ul style="list-style-type: none">• 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 <i>cis</i>-protein Quantitative Loci reference panel using FUSION pipeline. | |
| | Statistician Alzheimer's Therapeutic Research Institute (ATRI) Keck School of Medicine, USC Mentor: Dr. Rema Raman and Dr. Michael Donohue | 04/2017 - 06/2019 San Diego, CA |
| | <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 Department of Mathematics University of California, San Diego Mentor: Dr. Anthony C. Gamst | 03/2016 - 06/2016 09/2016 - 12/2016 La Jolla, CA |
| | <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. | |
| Awards and Fellowship | Keck School of Medicine/Graduate School Fellowship | 2019/2020 |
| | Outstanding Overall Performance in Biostatistics Screening Exam | 08/2020 |
| Publications | 3. <i>Integrative analyses identify genes and their functional consequences underlying COVID-19 hospitalization.</i> 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. | |

| | |
|---------------------------|---|
| | <ol style="list-style-type: none"> 2. <i>Integrative analyses identify susceptibility genes underlying COVID-19 hospitalization</i>. 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. In Submission. 2020. 1. <i>Brain Amyloid Burden, Sleep, and Circadian Rest/Activity Rhythms: Screening Findings from A4 and LEARN</i>. 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. |
| Posters and Presentations | <ol style="list-style-type: none"> 5. <i>Probabilistic fine-mapping of transcriptome-wide association studies</i>. <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. 4. <i>Proteome-Wide Association Study Identifies Independent Protein QTLs for Blood-Related Traits</i>. <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. <i>A4 Actigraphy Study Pre-randomization Analysis</i>. <u>Lu Z</u>. ATRI Biostatistics Workshop. Alzheimer's Therapeutic Research Institute, San Diego, CA. November 2018. 2. <i>Dynamic Reporting Web Framework for Clinical Trials Using R Shiny</i>. Jain S, <u>Lu Z</u>. ATRI Biostatistics Workshop. Alzheimer's Therapeutic Research Institute, San Diego, CA. August 2018. 1. <i>An Open-source Implementation of Data Standards for Alzheimer's Disease Clinical Trials</i>. Sun CK, Donohue M, Ernststrom K, Jiang Y, <u>Lu Z</u>, Aisen P, Raman R. Clinical Trials on Alzheimer's Disease (CTAD). Boston, MA. November 2017. |
| TA-ship Experience | <p>Analysis of Omics Data for Research Studies 06/2021 Multi-omics Boot Camp of SHARPP Training Mailman School of Public Health, Columbia University</p> <p>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</p> |
| Software | <p>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>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>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> |

Skills

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