

## Zeyun Lu

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| <b>Education</b>               | University of Southern California<br>Doctor of Philosophy in Biostatistics  | 09/2019 - Present                                      |
|                                | University of California, San Diego<br>Master of Science in Statistics  | 09/2015 - 12/2016                                      |
|                                | University of California, Los Angeles<br>Bachelor of Science in Mathematics/Economics   | 09/2012 - 09/2014                                      |
| <b>Professional Experience</b> | <b>Graduate Research Assistant</b><br>Department of Population and Public Health Sciences<br>Keck School of Medicine, USC<br>Mentor: Dr. Nicholas Mancuso   | 08/2020 - Present<br>Los Angeles, CA                   |
|                                | <ul style="list-style-type: none"><li>• Developed a gene fine-mapping method (ME-FOCUS) for complex traits using summary-based data and reference panels of multi-ethnic groups.</li><li>• Performed Proteome-Wide Association Studies (PWAS) to detect mRNA-free protein mediation genes for complex traits.</li><li>• Constructed <i>cis</i>-protein Quantitative Loci reference panel using FUSION pipeline.</li></ul>   |  |
|                                | <b>Statistician</b><br>Alzheimer's Therapeutic Research Institute (ATRI)<br>Keck School of Medicine, USC<br>Mentor: Dr. Rema Raman and Dr. Michael Donohue  | 04/2017 - 06/2019<br>San Diego, CA                     |
|                                | <ul style="list-style-type: none"><li>• 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).</li><li>• 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.</li><li>• Designed, built, and administered R Shiny projects that created dynamic online clinical data reporting system and risk-based monitoring system for ADNI3.</li><li>• Mentored student intern in R Shiny, clinical trials, and statistical analysis.</li></ul> |  |
|                                | <b>Mathematics Graduate Research Internship</b><br>Department of Mathematics<br>University of California, San Diego<br>Mentor: Dr. Anthony C. Gamst   | 03/2016 - 06/2016<br>09/2016 - 12/2016<br>La Jolla, CA |
|                                | <ul style="list-style-type: none"><li>• Analyzed several clinical trials data with visualization, tabulation, and statistical methods such as Linear Regression, Logistic Regression, and ANOVA etc.</li><li>• Investigated data errors and proposed fixing schemes.</li></ul>  |  |
| <b>Awards and Fellowship</b>   | Keck School of Medicine/Graduate School Fellowship  | 2019/2020  |
|                                | Outstanding Overall Performance in Biostatistics Screening Exam   | 08/2020  |
| <b>Articles</b>                | 1. <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. <b>Nature Communication</b> (in Press). 2021.   |  |

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| <b>Posters &amp; Abstracts</b> | <ol style="list-style-type: none"> <li>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. <b>Molecular Genetics and Metabolism.</b> April, 2021.</li> <li>2. <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. <b>Alzheimer's &amp; Dementia.</b> November 2018.</li> <li>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. <b>Clinical Trials on Alzheimer's Disease (CTAD).</b> Boston, MA. November 2017.</li> </ol> |
| <b>Talks</b>                   | <ol style="list-style-type: none"> <li>4. <i>Probabilistic fine-mapping of transcriptome-wide association studies.</i> <u>Lu Z</u>. <b>Seminar in Biostatistics and Epidemiology.</b> Department of Population and Public Health Sciences, Keck School of Medicine of USC. Online. September 2020.</li> <li>3. <i>Proteome-Wide Association Study Identifies Independent Protein QTLs for Blood-Related Traits.</i> <u>Lu Z</u>. <b>Seminar in Biostatistics and Epidemiology.</b> Department of Population and Public Health Sciences, Keck School of Medicine of USC. Online. September 2020.</li> <li>2. <i>A4 Actigraphy Study Pre-randomization Analysis.</i> <u>Lu Z</u>. <b>ATRI Biostatistics Workshop.</b> Alzheimer's Therapeutic Research Institute, San Diego, CA. November 2018.</li> <li>1. <i>Dynamic Reporting Web Framework for Clinical Trials Using R Shiny.</i> Jain S, <u>Lu Z</u>. <b>ATRI Biostatistics Workshop.</b> Alzheimer's Therapeutic Research Institute, San Diego, CA. August 2018.</li> </ol>         |
| <b>TAship Experience</b>       | <p><b>Analysis of Omics Data for Research Studies</b> 06/2021<br/> Multi-omics Boot Camp of SHARPP Training<br/> Mailman School of Public Health, Columbia University</p> <p><b>PM-522A: Introduction to the Theory of Statistics</b> Fall 2021 (Exp.)<br/> Department of Population and Public Health Sciences<br/> Keck School of Medicine, University of Southern California</p>   |
| <b>Software</b>                | <p><b>FOCUS</b></p> <ul style="list-style-type: none"> <li>• Python software to perform gene-trait fine-mapping from transcriptome-wide association studies in either single ethnic or multi-ethnic settings.</li> <li>• <a href="https://github.com/mancusolab/focus">https://github.com/mancusolab/focus</a></li> </ul> <p><b>ADNI3 and LEADS Dynamic Web Report</b></p> <ul style="list-style-type: none"> <li>• Two Shiny apps that transform static reports to interactive web pages for clinical trials investigators' monitoring on enrollment, primary outcomes, and safety.</li> <li>• Interval apps that are not public accessible.</li> </ul> <p><b>ADNI3, A4, and LEADS</b></p> <ul style="list-style-type: none"> <li>• Three R packages that crawl EDC API, transform data into CDISC format, and automatically build several reports (enrollment, safety etc) for clinical research.</li> <li>• Interval packages that are not public accessible.</li> </ul>   |
| <b>Other Contributions</b>     | <p><b>Reviewer Services</b><br/> Reviewer for PLOS Computational Biology</p>  |

**Skills**

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