

## Zeyun Lu

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Education	<b>PhD in Biostatistics</b> University of Southern California (USC)	08/2019 - 12/2023 Los Angeles, CA
	<b>MS in Statistics</b> University of California, San Diego (UCSD)	09/2015 - 12/2016 La Jolla, CA
	<b>BS in Mathematics/Economics</b> University of California, Los Angeles (UCLA)	09/2012 - 09/2014 Los Angeles, CA
Academic Experience	<b>Research Fellow</b> Dana-Farber Cancer Institute Mentor: Dr. Alexander Gusev	07/2024 - Present Boston, MA
	<b>Research Fellow</b> Harvard Medical School Mentor: Dr. Alexander Gusev	07/2024 - Present Boston, MA
	<b>Postdoctoral Scholar</b> Keck School of Medicine of USC Mentor: Dr. Nicholas Mancuso	01/2024 - 06/2024 Los Angeles, CA
	<b>Graduate Research Assistant</b> Keck School of Medicine of USC Mentor: Dr. Nicholas Mancuso	08/2020 - 12/2023 Los Angeles, CA
	<b>Research Internship</b> Dana-Farber Cancer Institute Mentor: Dr. Alexander Gusev	05/2022 - 06/2024 Online/Boston, MA
Working Experience	<b>Statistician</b> Alzheimer's Therapeutic Research Institute (ATRI) Keck School of Medicine of USC Mentor: Dr. Rema Raman and Dr. Michael Donohue	04/2017 - 06/2019 San Diego, CA
	<ul style="list-style-type: none"><li>• 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.</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>	
Selected Publications	2. <b>Improved multi-ancestry fine-mapping identifies cis-regulatory variants underlying molecular traits and disease risk.</b> <b>Lu Z</b> , Wang X, Carr M, Kim A, Gazal S, Mohammadi P, Wu L, Gusev A, Pirruccello J, Kachuri L, Mancuso N.	

Under Review at Nature Genetics. April, 2024.  
DOI: <https://doi.org/10.1101/2024.04.15.24305836>

1. **Multi-ancestry fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.** Lu Z<sup>\*</sup>, Gopalan S<sup>\*</sup>, 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>

<sup>\*</sup> Equal Contribution

## Other Publications

6. **Inferring causal cell types of human diseases and risk variants from candidate regulatory elements.** Kim A, Zhang Z, Legros C, Lu Z, de Smith A, Moore J, Mancuso N, Gazal S. **Under Review at Nature Genetics**. May, 2024.  
DOI: <https://doi.org/10.1101/2024.05.17.24307556>
5. **Genes with differential expression across ancestries are cell-type-specific and enriched in ancestry-specific disease effects.** Wang J, Zhang Z, Lu Z, Mancuso N, Gazal S. **Under Review at Nature Communication**. October, 2023.  
DOI: <https://www.medrxiv.org/content/10.1101/2023.10.20.23297214v1>
4. **Characterizing prostate cancer risk through multi-ancestry genome-wide discovery of 187 novel risk variants.** Wang A, ..., Haiman C. **Nature Genetics**. November, 2023.  
DOI: <https://doi.org/10.1038/s41588-023-01534-4>
3. **Novel insight into the etiology of ischemic stroke gained by integrative transcriptome-wide association study.** Jung J, Lu Z, de Smith A, Mancuso N. **Human Molecular Genetics**. October, 2023.  
DOI: <https://doi.org/10.1093/hmg/ddad174>
2. **twas\_sim, a Python-based tool for simulation and power analysis of transcriptome-wide association analysis.** Wang X, Lu Z, Bhattacharya A, Pasaniuc B, Mancuso N. **Bioinformatics**. April, 2023.  
DOI: <https://doi.org/10.1093/bioinformatics/btad288>
1. **Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization.** Pathak GA<sup>\*</sup>, Singh K<sup>\*</sup>, Miller-Fleming TW, Wendt FR, Ehsan N, Hou K, Johnson R, Lu Z, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B<sup>§</sup>, Polimanti R<sup>§</sup>, Davis LK<sup>§</sup>, Mancuso N<sup>§</sup>. **Nature Communication**. July, 2021.  
DOI: <https://doi.org/10.1038/s41467-021-24824-z>

<sup>\*</sup> Equal Contribution

<sup>§</sup> Jointly Supervision

## Awards & Fellowship

4. **Commencement Student Speaker** 06/2024  
Keck School of Medicine of the University of Southern California (PhD, DNAP, MPH, MS) Commencement Ceremony.  
Video Link: <https://www.youtube.com/live/DGYKWieETKM?si=0lQT91KsJwd1GuUW&t=2825>
3. **Third Place Winner** 12/2021  
Video Competition for Keck School of Medicine of USC graduate students to showcase their research.  
Video Link: <https://youtu.be/Nc5SVhz7-aQ>

	2. <b>Outstanding Overall Performance</b>	08/2020
	In recognition of top PhD students in the annual screening exams.	
	1. <b>Graduate School Fellowship</b>	2019/2020
	In recognition of new PhD students' outstanding academic promise at Keck School of Medicine of USC.	
Invited Talks	4. Zhou Lab Journal Club	03/2024
	Department of Biostatistics Journal Club	Online
	University of Michigan, Ann Arbor	
	3. Platform Talk	11/2023
	American Society of Human Genetics (ASHG)	Washington, DC
	2. Invited Talk	10/2023
	Program in Quantitative Genomics (PQG) Conference	Boston, MA
	Harvard University	
	1. Division of Epidemiology Journal Club	01/2023
	Vanderbilt University Medical Center	Online
Posters & Abstracts	9. <b>An integrative approach with Perturb-seq, eQTL, and GWAS data identifies mediating genes in regulatory networks of complex traits.</b>	
	• Conferences: ASHG 2023	
	• Awards: Platform Talk	
	8. <b>Multi-ancestry fine-mapping of gene expression data identifies more <i>cis</i>-regulatory mechanisms.</b>	
	• Conferences: ASHG 2023, PQG 2023, ProbGen 2023, BoG 2024.	
	• Awards: Stellar Abstract Award, Invited Speaker (PQG)	
	7. <b>Residual Proteome-wide Association Study Identifies Genes for Blood-Related Traits</b>	
	• Conferences: ASHG 2021	
	• Awards: Reviewers' Choice	
	6. <b>Novel insight into the etiology of ischemic stroke gained by integrating human transcriptome-wide association study with rodent expression data.</b>	
	• Conferences: ASHG 2021.	
	5. <b>Multi-ethnic fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.</b>	
	• Conferences: ProbGen 2021, ASHG 2020.	
	4. <b>Integrative analyses identify genes and their functional consequences underlying COVID-19 hospitalization.</b>	
	• Conferences: ACMG Annual Clinical Genetics Meeting 2021.	
	• Publications: Molecular Genetics and Metabolism 04/2021.	

3. **Integrative analyses with large-scale COVID-19 GWAS identifies susceptibility genes underlying hospitalized outcomes.**
  - Conferences: ASHG 2020.
2. **Brain Amyloid Burden, Sleep, and Circadian Rest/Activity Rhythms: Screening Findings from A4 and LEARN.**
  - Conferences: AAIC 2017.
  - Publications: Alzheimer's & Dementia. 11/2018.
1. **An Open-source Implementation of Data Standards for Alzheimer's Disease Clinical Trials.**
  - Conferences: CTAD. 2017.

## **TAship**

2. **Multi-omics Boot Camp of SHARPP Training**
  - Online course at Mailman School of Public Health, Columbia University.
  - Time: 06/2023, 01/2023, 06/2022, 06/2021.
1. **PM-522A: Introduction to the Theory of Statistics**
  - Graduate level course at KSOM, USC.
  - Time: Fall 2021.

## **Developed Software**

6. **Mr. PEG**
  - A command-line Python software to perform Mendelian Randomization integrating Perturb-seq, eQTL, and GWAS summary data with high-speed inference by leveraging JAX JIT compilation.
5. **SuShiE**
  - A command-line Python software to perform SNP fine-mapping on molecular QTL data with high-speed inference by leveraging JAX Just In Time compilation.
  - <https://github.com/mancusolab/sushie>
4. **TWAS Simulator**
  - A Python software to perform Transcriptome-wide Association Studies (TWAS) simulations.
  - [https://github.com/mancusolab/twas\\_sim](https://github.com/mancusolab/twas_sim)
3. **MA-FOCUS**
  - A command-line 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**
  - 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"> <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>Reviewership</b>	Nature Genetics, Nature Communication, American Journal of Human Genetics, Molecular Psychiatry, Genome Biology, Genetics, BMC Cancer, BMC Genomics, BMC Urology, BMC Pulmonary Medicine, Scientific Reports.
<b>Membership</b>	American Statistical Association. American Society of Human Genetics.
<b>Skills</b>	R (Tidyverse, Shiny), Python, Linux, plink, gcta, bedtools, LDSC, Git, Latex, CDISC, SAS, Stata.
<b>Reference</b>	<ul style="list-style-type: none"> <li>• <b>Alexander Gusev, PhD</b>  Title: Associate Professor  Affiliation: Dana-Farber Cancer Institute/Harvard Medical School  Email: alexander.gusev@dfci.harvard.edu  Relationship: Postdoc Advisor</li> <li>• <b>Nicholas Mancuso, PhD</b>  Title: Associate Professor  Affiliation: University of Southern California  Email: nmancuso@usc.edu  Relationship: PhD Advisor</li> <li>• <b>Steven Gazal, PhD</b>  Title: Assistant Professor  Affiliation: University of Southern California  Email: gazal@usc.edu  Relationship: PhD Dissertation Committee Member</li> </ul>