

Tianyuan Lu, PhD

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E-mail: tianyuan.lu@wisc.eduLu Lab Website: <https://lulab.pophealth.wisc.edu/>Google Scholar Profile : <https://scholar.google.ca/citations?user=hBnK0YAAAAAJ&hl=en>**Education**

McGill University, Montreal, QC, Canada Sept. 2018 – May. 2022
 PhD in Quantitative Life Sciences, Statistical Genetics and Genetic Epidemiology Stream

Fudan University, Shanghai, China Sept. 2014 – Jun. 2018
 BSc in Biological Sciences, Biostatistics and Bioinformatics Stream

Employment

University of Wisconsin-Madison, Madison, WI, USA Aug. 2024 - Present
 Assistant Professor (Tenure-Track)
 Department of Population Health Sciences & Department of Biostatistics and Medical Informatics
 School of Medicine and Public Health

Five Prime Sciences Inc., Montreal, QC, Canada Dec. 2023 – Present
 Consultant

University of Toronto, Toronto, ON, Canada Feb. 2023 – Jul. 2024
 Schmid AI in Science Postdoctoral Fellow

Five Prime Sciences Inc., Montreal, QC, Canada Jun. 2022 – Sept. 2023
 Senior Research Scientist

Research Support

6. Eric and Wendy Schmidt AI in Science Postdoctoral Fellowship (Role: PI; 170,000 CAD, over two years), Schmidt Futures, 2023
5. CANSSI Ontario STAGE HostSeq Project Fellowship (Role: PI; 10,000 CAD, over one year), Canadian Statistical Sciences Institute, 2022
4. Vanier Canada Graduate Scholarship (Role: PI; 150,000 CAD, over three years), Canadian Institutes of Health Research, 2021
3. FRQS Doctoral Training Fellowship (Role: PI; 84,000 CAD, over four years), Fonds de Recherche du Québec Santé, 2020
2. Faculty of Medicine Fellowship (Role: PI; 12,000 CAD), Department of Medicine, McGill University, 2020
 <Declined due to funding from another source>
1. Faculty of Medicine Fellowship / W. R. Lasha Research Fellowship (Role: PI; 12,000 CAD, over one year), Department of Medicine, McGill University, 2019

Other Honors and Awards (**Competitive*)

24. *Early Career Researcher Travel Award (500 GBP), International Mendelian Randomization Conference, University of Bristol, 2024
23. *James V. Neel Award (1,000 USD), International Genetic Epidemiology Society, 2023
22. Eric and Wendy Schmidt Conference Travel Award (travel reimbursement valued at 5,000 CAD), Schmidt Futures, 2023
21. *Prix Relève Étoile Jacques-Genest Publication Award (1,500 CAD), Fonds de Recherche du Québec Santé, 2023
20. *ECTS New Investigator Award (750 EUR), European Calcified Tissue Society, 2023
19. *Annual McGill Biomedical Graduate Conference Outstanding Oral Presentation, Second Place Award (350 CAD), McGill University, 2022
18. *Charles J. Epstein Trainee Awards Semifinalist (750 USD), American Society of Human Genetics, 2021
17. *Young Investigator Travel Award (500 USD), American Society for Bone and Mineral Research, 2021
<Declined due to COVID-19 pandemic>
16. McGill Initiative in Computational Medicine Graduate Award (400 CAD), McGill University, 2021
15. Plan de Réussite Graduate Mobility Award (2,000 CAD), McGill University, 2021
14. *McGill MedStar Publication Award / A. W. K. Akerley Award (500 CAD), Department of Medicine, McGill University, 2020
13. Quantitative Life Sciences Travel Award (500 CAD), McGill University, 2019
12. Australian Institute of Bioengineering and Nanotechnology Research Fellowship (2,880 AUD), University of Queensland, 2018
11. *Excellent Graduate of Class 2018 (Top 5%), Fudan University, 2018
10. Visiting Student Research Fellowship (5,000 USD), King Abdullah University of Science and Technology, 2017
9. Scholarship of Summer Institute in Statistical Genetics (tuition exemption valued at 1,050 USD), Department of Biostatistics, University of Washington, 2017
8. *Fosun Pharma Scholarship, First Prize (Top 2%, 5,000 CNY), School of Life Sciences, Fudan University, 2017
7. *Fudan University Student Exchange Fellowship / Dong Fang Scholarship (29 recipients, 6,000 CNY), Fudan University, 2017
6. *Scholarship for Outstanding Students, First Prize/Arawana Scholarship (Top 5%, 10,000 CNY), Fudan University, 2016
5. *Jing Rong Life Sciences Scholarship, First Prize (Top 5%, 3,000 CNY), School of Life Sciences, Fudan University, 2016
4. *Outstanding Student Scholarship in Faculty of Science (Top 30%, 1,800 CNY), Fudan University, 2016
3. *Chinese College Students Math Competition, Third Prize, Chinese Mathematical Society, 2015
2. *Campbell's Scholarship, First Prize (Top 5%, 5,000 CNY), School of Life Sciences, Fudan University, 2015
1. *National Scholarship (Top 2%, 8,000 CNY), Ministry of Education of the People's Republic of China, 2015

Research Articles as First or Senior Author ([†]*Authors contributed equally* [¶]*Corresponding author*)

My research focuses on developing and implementing rigorous statistical genetics and genetic epidemiology methods to improve the prevention, diagnosis, and treatment of complex diseases, and translating research findings into new medical care approaches and therapies.

➤ Submitted

31. Yefeng Yang, Dandan Tan, Julia Carrasco-Zanini-Sanchez, Chen-Yang Su, Sirui Zhou, Satoshi Koyama, Pradeep Natarajan, Claudia Langenberg, **Tianyuan Lu[¶]**, and Satoshi Yoshiji[¶]. Plasma proteomics reveals coronary artery disease heterogeneity across discrete clusters and phenotypic continuum. *Under review.*

30. Jerome J. Choi, Noah Cohen Kalafut, Tim Gruenloh, Corinne D. Engelman, **Tianyuan Lu**[¶], and Daifeng Wang[¶]. COSIME: Cooperative multi-view integration and Scalable and Interpretable Model Explainer. *Under revision*.

29. Chen-Yang Su, Adriaan van der Graaf, Wenmin Zhang, Dong-Keun Jang, Susannah Selber-Hnatiw, Ta-Yu Yang, Guillaume Butler-Laporte, Kevin Y. H. Liang, Fumihiko Matsuda, Maria C. Costanzo, Noel P. Burt, Jason Flannick, Sirui Zhou, Vincent Mooser, **Tianyuan Lu**[¶], and Satoshi Yoshiji[¶]. Multi-ancestry proteome-phenome-wide Mendelian randomization offers a comprehensive protein-disease atlas and potential therapeutic targets. *Under revision*.

28. Wenmin Zhang[¶], Satoshi Yoshiji, Robert Sladek, Josée Dupuis[¶], and **Tianyuan Lu**[¶]. Benchmarking Bayesian colocalization methods in validating Mendelian randomization-based target discoveries from circulating proteins for cardiometabolic diseases. *Under revision*.

27. Nazim Rabouhi, Simon Guindon, Emilia Aisha Coleman, H. J. van Heesbeen, Celia M. T. Greenwood[¶], **Tianyuan Lu**[¶], and Philippe Campeau[¶]. Assessing in silico Tools for Accurate Pathogenicity Prediction in CHD Nucleosome Remodelers. *Submitted*.

26. **Tianyuan Lu**[¶], Lily N. Stalter, Kate V. Lauer, Bret M. Hanlon, Wenmin Zhang, and Luke M. Funk. A multi-ancestry polygenic risk score for body mass index predicts longitudinal weight change. *Under review*.

25. **Tianyuan Lu**[¶], David Stein, Wenmin Zhang, Yuval Itan, and Andrew D. Paterson. Development of polyphenotypic scores to prioritize detection of G6PD rs1050828-T carriers in African and African American populations. *Under review*.

➤ Published

24. **Tianyuan Lu**[¶], Wenmin Zhang, Fergus W. Hamilton, Guillaume Butler-Laporte, Nicholas J. Timpson, George Davey Smith, and J. Brent Richards[¶]. Challenges to the Independence Assumption in Mendelian Randomization due to Sample Selection and Complex Methods. *The Journal of Clinical Endocrinology & Metabolism* 2025.

<https://doi.org/10.1210/clinem/dgaf305>

23. **Tianyuan Lu**[¶] and Andrew D. Paterson[¶]. Estimating effects of serum vitamin B12 levels on psychiatric disorders and cognitive impairment: a Mendelian randomization study. *Communications Medicine* 2025.

<https://doi.org/10.1038/s43856-025-01043-x>

22. **Tianyuan Lu**[¶], Wenmin Zhang, Cassiane Robinson-Cohen, Corinne D. Engelman, Qiongshi Lu, Ian H. de Boer, Lei Sun, and Andrew D. Paterson. Improved characterization of gene-environment interactions for vitamin D through variance quantitative trait loci. *American Journal of Clinical Nutrition* 2025.

<https://doi.org/10.1016/j.ajcnut.2025.01.021>

21. **Tianyuan Lu**[¶], Despoina Manousaki, Lei Sun, and Andrew D. Paterson[¶]. Integrative proteogenomic analyses provide novel interpretations of type 1 diabetes risk loci through circulating proteins. *Diabetes* 2025.

<https://doi.org/10.2337/db24-0380>

20. Wenmin Zhang, Chen-Yang Su, Satoshi Yoshiji, and **Tianyuan Lu**[¶]. MR Corge: Sensitivity analysis of Mendelian randomization based on the core gene hypothesis for polygenic exposures. *Bioinformatics* 2024.

<https://doi.org/10.1093/bioinformatics/btae666>

19. **Tianyuan Lu**[¶], Yiheng Chen, Satoshi Yoshiji, Yann Ilboudo, Vincenzo Forgetta, Sirui Zhou, and Celia M. T. Greenwood[¶]. Circulating metabolite abundances associated with risks of psychiatric disorders: a Mendelian randomization study. *Biological Psychiatry* 2024.

<https://doi.org/10.1016/j.biopsych.2024.04.016>

18. **Tianyuan Lu**[¶], Vincenzo Forgetta, Sirui Zhou, J Brent Richards, and Celia M. T. Greenwood[¶]. Identifying rare genetic determinants for improved polygenic risk prediction of bone mineral density and fracture risk. *Journal of Bone and Mineral Research* 2023. **Lady Davis Institute Paper of the Month** (December 2023)

<https://asbmr.onlinelibrary.wiley.com/doi/10.1002/jbmr.4920>

17. **Tianyuan Lu**[¶], Tomoko Nakanishi, Satoshi Yoshiji, Guillaume Butler-Laporte, Celia M. T. Greenwood, and J. Brent Richards[¶]. Dose-dependent association of alcohol consumption with obesity and type 2 diabetes: observational and Mendelian randomization analyses. *The Journal of Clinical Endocrinology & Metabolism* 2023.

<https://doi.org/10.1210/clinem/dgad324>

16. **Tianyuan Lu**[¶], Patrícia Pelufo Silveira, and Celia M. T. Greenwood[¶]. Development of risk prediction models for depression combining genetic and early life risk factors. *Frontiers in Neuroscience* 2023.

<https://www.frontiersin.org/articles/10.3389/fnins.2023.1143496/full>

15. **Tianyuan Lu**[¶], Vincenzo Forgetta, J. Brent Richards, and Celia M. T. Greenwood[¶]. Genetic determinants of polygenic prediction accuracy within a population. *Genetics* 2022.

<https://doi.org/10.1093/genetics/iyac158>

14. Julian St. Pierre[†], Xinyi Zhang[†], **Tianyuan Lu**[†], Lai Jiang[†], Linbo Wang, Sahir Bhatnagar, Celia M. T. Greenwood[¶], and CANSSI team on Improving Robust High-Dimensional Causal Inference and Prediction Modelling. Considering strategies for SNP selection in genetic and polygenic risk scores. *Frontiers in Genetics* 2022.

<https://www.frontiersin.org/articles/10.3389/fgene.2022.900595/full>

13. **Tianyuan Lu**, Vincenzo Forgetta, Celia M. T. Greenwood, Sirui Zhou, and J. Brent Richards[¶]. Circulating proteins influencing psychiatric disease: A Mendelian randomization study. *Biological Psychiatry* 2022. **Prix Relève Étoile Jacques-Genest / Best Student Publication Award of Québec** (March 2023)

<https://doi.org/10.1016/j.biopsych.2022.08.015>

12. **Tianyuan Lu**[¶], Vincenzo Forgetta, J. Brent Richards, and Celia M. T. Greenwood[¶]. Capturing additional genetic risk from family history for improved polygenic risk prediction. *Communications Biology* 2022.

<https://www.nature.com/articles/s42003-022-03532-4>

11. **Tianyuan Lu**, Vincenzo Forgetta, Celia M. T. Greenwood, and J. Brent Richards[¶]. Identifying causes of fracture beyond bone mineral density: Evidence from human genetics. *Journal of Bone and Mineral Research* 2022.

<https://asbmr.onlinelibrary.wiley.com/doi/10.1002/jbmr.4632>

10. Zhen-Hui Wang[†], **Tianyuan Lu**[†], Ming-Rui Li, Ning Ding, Li-Zhen Lan, Xiang Gao, Ai-Sheng Xiong, Jian Zhang, and Lin-Feng Li[¶]. Genetic and epigenetic associated with the divergence of *Aquilegia* species. *Genes* 2022.

<https://www.mdpi.com/2073-4425/13/5/793>

9. **Tianyuan Lu**, Vincenzo Forgetta, J. Brent Richards, and Celia M. T. Greenwood[¶]. Polygenic risk score as a possible tool for identifying familial monogenic causes of complex diseases. *Genetics in Medicine* 2022.

[https://www.gimjournal.org/article/S1098-3600\(22\)00717-1/fulltext](https://www.gimjournal.org/article/S1098-3600(22)00717-1/fulltext)

8. Célia Escribe[†], **Tianyuan Lu**[†], Julyan Keller-Baruch, Vincenzo Forgetta, Bowei Xiao, J. Brent Richards, Sahir Bhatnagar, Karim Oualkacha and Celia M. T. Greenwood[¶]. Block coordinate descent algorithm improves variable selection and estimation in error-in-variables regression. *Genetic Epidemiology* 2021. **Highlight of Issue** (December 2021)

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22430>

7. **Tianyuan Lu**, Andres Cardenas, Patrice Perron, Marie-France Hivert, Luigi Bouchard, and Celia M. T. Greenwood[¶]. Detecting cord blood cell type-specific epigenetic associations with gestational diabetes mellitus and early childhood growth. *Clinical Epigenetics* 2021.

<https://clinicalepigeneticsjournal.biomedcentral.com/articles/10.1186/s13148-021-01114-5>

6. **Tianyuan Lu**, Vincenzo Forgetta, Haoyu Wu, John R. B. Perry, Ken K. Ong, Celia M. T. Greenwood, Nicholas J. Timpson, Despoina Manousaki, and J. Brent Richards[¶]. A polygenic risk score to predict future adult short stature among children. *The Journal of Clinical Endocrinology & Metabolism* 2021.

<https://doi.org/10.1210/clinem/dgab215>

5. **Tianyuan Lu**[†], Vincenzo Forgetta[†], Julyan Keller-Baruch, Maria Nethander, Derrick Bennett, Marie Forest, Sahir Bhatnagar, Robin G. Walters, Kuang Lin, Zhengming Chen, Liming Li, Magnus Karlsson, Dan Mellström, Eric Orwoll, Eugene V. McCloskey, John A. Kanis, William D. Leslie, Robert J. Clarke, Claes Ohlsson, Celia M. T. Greenwood, and J. Brent Richards[¶]. Improved prediction of fracture risk leveraging a genome-wide polygenic risk score. *Genome Medicine* 2021.

<https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-021-00838-6>

4. **Tianyuan Lu** and Jessica C. Mar[¶]. Investigating transcriptome-wide sex dimorphism by multi-level analysis of single-cell RNA sequencing data in ten mouse cell types. *Biology of Sex Differences* 2020.

<https://link.springer.com/article/10.1186/s13293-020-00335-2>

3. **Tianyuan Lu**, Sirui Zhou, Haoyu Wu, Vincenzo Forgetta, Celia M. T. Greenwood, J. Brent Richards[¶]. Individuals with common diseases, but with a low polygenic risk score could be prioritized for rare variant screening. *Genetics in Medicine* 2020. **Editor's Featured Article** (March 2021)

<https://www.nature.com/articles/s41436-020-01007-7>

2. **Tianyuan Lu**, Vincenzo Forgetta, Oriana H. Y. Yu, Lauren Mokry, Madeline Gregory, George Thanassoulis, Celia M. T. Greenwood and J. Brent Richards[¶]. Genetic influences on coronary heart disease act on atherosclerosis in type 2 diabetes. *Cardiovascular Diabetology* 2020.

<https://link.springer.com/article/10.1186/s12933-020-0988-9>

1. **Tianyuan Lu**, Kathleen Oros Klein, Inés Colmegna, Maximilien Lora, Celia M. T. Greenwood and Marie Hudson[¶]. Whole-genome bisulfite sequencing in systemic sclerosis provides novel targets to understand disease pathogenesis. *BMC Medical Genomics* 2019.
<https://doi.org/10.1186/s12920-019-0602-8>

Research Articles as Co-Author ([†]*Authors contributed equally* [¶]*Corresponding author*)

➤ Submitted

36. Dandan Tan, Akhil Garg, Keely Hammond, Zahra Sohani, **Tianyuan Lu**, Fergus W. Hamilton, Takayoshi Sasako, J. Brent Richards, Lisa Iannattone, Michael Fein, Todd C Lee, and Guillaume Butler-Laporte. Common helping rare: biobank genomics guiding treatment of a rare disease. *Submitted*.

35. Basile Jumentier, HuiQi Qu, **Tianyuan Lu**, Kai Liu, Erica Kleinbrink, Kathleen Klein, Wiame Belbellaj, Isabel Gamache, Lauric Ferrat, Guillaume Butler-Laporte, Yangxi Li, Hakon Hakonarson, Wei Wu, Constantin Polychronakos, Celia M. T. Greenwood, and Despoina Manousaki. Development and validation of a Trans-Ancestry polygenic risk score for Type 1 Diabetes. *Submitted*.

34. Takayoshi Sasako[¶], Yann Ilboudo, Kevin Y. H. Liang, Yiheng Chen, Dandan Tan, **Tianyuan Lu**, Guillaume Butler-Laporte, and J. Brent Richards. The Receptor Trap in Proteogenomic MR: How Receptor-Ligand Feedback Loops Can Give Incorrect and Opposite Directions of Effect. *Under review*.

33. Guillaume Butler-Laporte[¶], **Tianyuan Lu**, Sam Morris, Wenmin Zhang, Gavin Band, Fergus W. Hamilton, Amanda Chong, Kuang Lin, Ruth Nanjala, J. Brent Richards, Mei-Hsuan Lee, Ling Yang, Pang Yao, Liming Li, Zhengming Chen, Yang Luo, Iona Y. Milwood, Robin G. Walters, and Alexander J. Mentzer[¶]. An accurate genetic colocalization method for the HLA locus. *Under revision*.

32. Wenmin Zhang[¶], **Tianyuan Lu**, Robert Sladek, Josée Dupuis, and Guillaume Lettre[¶]. Robust fine-mapping in the presence of linkage disequilibrium mismatch. *Under revision*.

31. Yiheng Chen, Satoshi Yoshiji, **Tianyuan Lu**, Yann Ilboudo, Guillaume Butler-Laporte, Kevin Liang, Isobel Stewart, Julian Willett, Takayoshi Sasako, Vincenzo Forgetta, Fossi Farjoun, Parminder Raina, Claudia Langenberg, Nicholas Wareham, Celia M. T. Greenwood, Sirui Zhou, and J. Brent Richards. The untreated metabolomic burden of hypothyroidism: A multi-omics approach. *Under review*.

30. Tsegaselassie Workalemahu[¶], Jian Ying, Berhanu G. Gebremeskel, **Tianyuan Lu**, April Mohanty, Tali Elfassy, Fasil Tekola-Ayele, Timothy A. Thornton, Cohen Jordana, Marguerite R. Irvin, Robert M. Silver, Michael W. Varner, Kristine Yaffe, Myriam Fornage, Donald M. Lloyd-Jones, Mario Sims, Daichi Shimbo, Yuichiro Yano, Paul Muntner, and Adam Bress. Associations of cardiometabolic polygenic risk scores with cardiovascular disease in African Americans. *Submitted*.

➤ Published

29. Thomas M. Zheng, Yann Ilboudo, **Tianyuan Lu**, Guillaume Butler-Laporte, Tomoko Nakanishi, David Morrison, Darin Adra, Lena Cuddeback, and J. Brent Richards[¶]. Differential circulating proteomic responses associated with ancestry during severe COVID-19 infection. *Journal of Proteome Research* 2025.
<https://pubs.acs.org/doi/abs/10.1021/acs.jproteome.4c00956>

28. Fergus W. Hamilton[¶], David A. Hughes, **Tianyuan Lu**, Zoltán Kutalik, Apostolos Gkatzionis, Kate Tilling, Fernando Pires Hartwig, and George Davey Smith. Non-linear Mendelian randomization: evaluation of effect modification in the residual and doubly-ranked methods. *European Journal of Epidemiology* 2025.

<https://link.springer.com/article/10.1007/s10654-025-01208-x>

27. Amanda M. Marks, Guillaume Butler-Laporte, Satoshi Yoshiji, **Tianyuan Lu**, Dave R. Morrison, Tomoko Nakanishi, Yiheng Chen, Vincenzo Forgetta, Yossi Farjoun, Robert Frithiof, Miklós Lipcsey, Hugo Zeberg, J. Brent Richards, and Michael Hultström[¶]. Aquaporin 3 genotype modulates the risk of death conferred by plasma osmolality in COVID-19. *Physiological Genomics* 2025.

<https://journals.physiology.org/doi/full/10.1152/physiolgenomics.00174.2024>

26. Satoshi Yoshiji[¶], **Tianyuan Lu**, Guillaume Butler-Laporte, Julia Carrasco-Zanini-Sanchez, Yiheng Chen, Kevin Liang, Julian D. S. Willett, Chen-Yang Su, Shidong Wang, Darin Adra, Yann Ilboudo, Takayoshi Sasako, Satoshi Koyama, Tetsushi Nakao, Vincenzo Forgetta, Yossi Farjoun, Hugo Zeberg, Sirui Zhou, Michael Hultström, Mitchell Machiela, Rama Kaalia, Hesam Dashti, Melina Claussnitzer, Jason Flanick, Nicholas J. Wareham, Vincent Mooser, Nicholas J. Timpson, Claudia Langenberg, and J. Brent Richards[¶]. Integrative proteogenomic analysis identifies COL6A3-derived endotrophin as a mediator of the effect of obesity on coronary artery disease. *Nature Genetics* 2025.

<https://www.nature.com/articles/s41588-024-02052-7>

25. Jiacheng Miao, Yixuan Wu, Zhongxuan Sun, Xinran Miao, **Tianyuan Lu**, Jiwei Zhao, and Qiongshi Lu[¶]. Valid inference for machine learning-assisted GWAS. *Nature Genetics* 2024.

<https://www.nature.com/articles/s41588-024-01934-0>

24. Ariel Madrigal, **Tianyuan Lu**, Larisa M. Soto, and Hamed S. Najafabadi[¶]. A unified model for interpretable latent embedding of multi-sample, multi-condition single-cell data. *Nature Communications* 2024.

<https://www.nature.com/articles/s41467-024-50963-0>

23. Yann Ilboudo, Satoshi Yoshiji, **Tianyuan Lu**, Guillaume Butler-Laporte, Sirui Zhou, and J. Brent Richards[¶]. Vitamin D, Cognition, and Alzheimer's Disease: Observational and Two-Sample Mendelian Randomization Studies. *Journal of Alzheimer's Disease* 2024.

<http://dx.doi.org/10.3233/JAD-221223>

22. Thomas R. Austin[†], Maria Nethander[†], Howard A. Fink[†], Anna E. Törnqvist, Diana I. Jalal, Petra Buzkova, Joshua I. Barzilay, Laura Carbone, Maiken E. Gabrielsen, Louise Grahnemo, **Tianyuan Lu**, Kristian Hveem, Christian Jonasson, Jorge R. Kizer, Arnulf Langhammer, Kenneth J. Mukamal, Robert E. Gerszten, Bruce M. Psaty, John A. Robbins, Yan V. Sun, Anne Heidi Skogholt, John A. Kanis, Helena Johansson, Bjørn Olav Åsvold, Rodrigo J. Valderrabano, Jie Zheng, J. Brent Richards, Eivind Coward, and Claes Ohlsson[¶]. A protein-based risk score improves hip fracture prediction. *Nature Aging* 2024.

<https://doi.org/10.1038/s43587-024-00639-7>

21. Wenmin Zhang[¶], **Tianyuan Lu**, Robert Sladek, Yue Li, Hamed S. Najafabadi, and Josée Dupuis[¶]. SharePro: an accurate and efficient genetic colocalization method accounting for multiple causal signals. *Bioinformatics* 2024.

<https://doi.org/10.1093/bioinformatics/btae295>

20. Thomas R. Austin, Howard A. Fink, Diana I. Jalal, Anna E. Törnqvist, Petra Buzkova, Joshua I. Barzilay, **Tianyuan Lu**, Laura Carbone, Maiken E. Gabrielsen, Louise Grahnemo, Kristian Hveem, Christian Jonasson, Jorge R. Kizer, Arnulf Langhammer, Kenneth J. Mukamal, Robert E. Gerszten, Maria Nethander, Bruce M. Psaty, John A. Robbins, Yan V. Sun, Anne Heidi Skogholt, Bjørn Olav Åsvold, Rodrigo J. Valderrabano, Jie Zheng, J. Brent Richards, Eivind Coward, and Claes Ohlsson[¶]. Large-scale Circulating Proteome Association Study (CPAS)

meta-analysis identifies circulating proteins and pathways predicting incident hip fractures. *Journal of Bone and Mineral Research* 2024.

<https://doi.org/10.1093/jbmr/zjad011>

19. Guillaume Butler-Laporte[¶], Joseph Farjoun, Tomoko Nakanishi, **Tianyuan Lu**, Erik Abner, Yiheng Chen, Michael Hulström, Andres Metspalu, Lili Milani, Reedik Mägi, Mari Nelis, Georgi Hudjashov, Estonian Biobank Research Team, Satoshi Yoshiji, Yann Ilboudo, Kevin Y. H. Liang, Chen-Yang Su, Julian D. S. Willett, Tõnu Esko, Sirui Zhou, Vincenzo Forgetta, Daniel Taliun, and J. Brent Richards. HLA allele-calling using whole-exome sequencing identifies 129 novel associations in 11 autoimmune diseases: a multi-ancestry analysis in the UK Biobank. *Communications Biology* 2023.

<https://www.nature.com/articles/s42003-023-05496-5>

18. Maria Nethander[†], Sofia Movérare-Skrtic[†], Anders Kämpe, Eivind Coward, Ene Reimann, Louise Grahnemo, Éva Borbély, Zsuzsanna Helyes, Thomas Funck-Brentano, Martine Cohen-Solal, Juha Tuukkanen, Antti Koskela, Jianyao Wu, Lei Li, **Tianyuan Lu**, Maiken E. Gabrielsen, Estonian Biobank Research Team, Reedik Mägi, Mari Hoff, Ulf H. Lerner, Petra Henning, Henrik Ullum, Christian Erikstrup, Søren Brunak, DBDS Genomic Consortium, Arnulf Langhammer, Tiinamaija Tuomi, Asmundur Oddsson, Kari Stefansson, Ulrika Pettersson-Kymmer, Sisse Rye Ostrowski, Ole Birger Vesterager Pedersen, Unnur Styrkarsdottir, Outi Mäkitie, Kristian Hveem, J. Brent Richards, and Claes Ohlsson[¶]. An atlas of genetic determinants of forearm fracture. *Nature Genetics* 2023.

<https://www.nature.com/articles/s41588-023-01527-3>

17. Delnaz Roshandel, **Tianyuan Lu**, Andrew D. Paterson[¶], and Satya Dash[¶]. Beyond apples and pears: Sex-specific genetics of body fat percentage. *Frontiers in Endocrinology* 2023.

<https://www.frontiersin.org/articles/10.3389/fendo.2023.1274791/full>

16. Julian Daniel Sunday Willett, **Tianyuan Lu**, Tomoko Nakanishi, Satoshi Yoshiji, Guillaume Butler-Laporte, Vincent Mooser, Sirui Zhou, Yossi Farjoun, and J. Brent Richards[¶]. Colocalization of expression transcripts with COVID-19 outcomes is dependent on cell type and cell state. *Human Genetics* 2023.

<https://link.springer.com/article/10.1007/s00439-023-02590-w>

15. Jeffrey C. Y. Yu, Yixiao Zeng, Kaiqiong Zhao, **Tianyuan Lu**, Kathleen Oros Klein, Inés Colmegna, Maximilien Lora, Sahir Bhatnagar, Andrew Leask, Celia M. T. Greenwood, and Marie Hudson[¶]. Novel insights into systemic sclerosis using a sensitive computational method to analyze whole-genome bisulfite sequencing data. *Clinical Epigenetics* 2023.

<https://clinicalepigeneticsjournal.biomedcentral.com/articles/10.1186/s13148-023-01513-w>

14. Lei Sun[¶], Zhong Wang, **Tianyuan Lu**, Teri A. Manolio, and Andrew D. Paterson[¶]. eXclusionarY: Ten years later, where are the sex chromosomes in GWAS? *American Journal of Human Genetics* 2023.

<https://doi.org/10.1016/j.ajhg.2023.04.009>

13. Kevin Y. H. Liang, Yossi Farjoun, Vincenzo Forgetta, Yiheng Chen, Satoshi Yoshiji, **Tianyuan Lu**, and J. Brent Richards[¶]. Predicting ExWAS findings from GWAS data: A shorter path to causal genes. *Human Genetics* 2023.

<https://link.springer.com/article/10.1007/s00439-023-02548-y>

12. Satoshi Yoshiji, Guillaume Butler-Laporte, **Tianyuan Lu**, Julian Daniel Sunday Willett, Chen-Yang Su, Tomoko Nakanishi, David Morrison, Yiheng Chen, Kevin Y. H. Liang, Michael Hultström, Yann Ilboudo, Zaman

Afrasiabi, Shanshan Lan, Naomi Duggan, Chantal DeLuca, Mitra Vaezi, Chris Tselios, Xiaoqing Xue, Meriem Bouab, Fangyi Shi, Laetitia Laurent, Hans Markus Münter, Marc Afilalo, Jonathan Afilalo, Vincent Mooser, Nicholas J. Timpson, Hugo Zeberg, Sirui Zhou, Vincenzo Forgetta, Yossi Farjoun, and J. Brent Richards[¶]. Proteome-wide Mendelian randomization implicates nephronectin as an actionable mediator of the effect of obesity on COVID-19 severity. *Nature Metabolism* 2023.

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Mentoring

➤ Graduate Student Mentees

Jerome J. Choi (co-mentored with Corinne D. Engelman and Daifeng Wang); PhD in Epidemiology; Graduated in May 2025; Now Senior Scientist at AbbVie

Jovana Jovanovska (co-mentored with Corinne D. Engelman); MSc in Epidemiology; Graduated in Jul. 2025

➤ Undergraduate Student Mentees

Xinyuan Hong (Sept. 2024 – Present)

Yifei Wu (Feb. 2025 – Present)

Teaching

Department of Population Health Sciences, University of Wisconsin-Madison POPHLTH 551 Introduction to Biostatistics for Population Health Principal Instructor	Fall 2025
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Department of Population Health Sciences, University of Wisconsin-Madison POPHLTH 805 Advanced Epidemiology: Causal Inference in Epidemiological Studies Guest Lecturer	Fall 2024
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International Genetic Epidemiology Society Annual Conference Workshop Epidemiology and architecture of large genetic biobanks: hands-on illustrations Workshop Lecturer	Sept. 2022
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McGill Initiative in Computational Medicine, McGill University Polygenic risk scores - Theory, Development and Evaluation Workshop Lecturer	Apr. 2021
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Department of Human Genetics, McGill University
Statistics 101
Workshop Lecturer
Nov. 2020

Department of Biology, McGill University
BIOL 324 Ecological Genetics
Teaching Assistant
Fall 2020

Department of Biology, McGill University
BIOL 202 Basic Genetics
Teaching Assistant
Winter 2020

Department of Biology, McGill University
BIOL 324 Ecological Genetics
Teaching Assistant
Fall 2019

Academic Services

Population Health Sciences PhD and MS Admission Committee
Committee member
Dec. 2024

American Society of Human Genetics Annual Conference
Platform session co-chair “Long-read sequencing offering new insights into neurological disease”
Nov. 2024

American Society of Human Genetics Annual Conference
Conference abstract reviewer “Complex Traits and Polygenic Disorders II: Diabetes, obesity, metabolic syndromes, diseases of internal organs and of the endocrine system”
Jun. 2024

American Society for Bone and Mineral Research Conference
Conference abstract reviewer “Omics Approaches for Musculoskeletal Biology, Diseases and Treatments”
Jun. 2024

American Society of Human Genetics Annual Conference
Platform session co-chair “Novel tools and data resources for genetic data analysis”
Nov. 2023

American Society of Human Genetics Annual Conference
Platform session co-chair “Genetic impacts on the epigenome and beyond”
Oct. 2022

International Genetic Epidemiology Society Annual Conference
Platform session co-chair “Biobanks and polygenic risk scores”
Sept. 2022

International Genetic Epidemiology Society Annual Conference
Poster session co-chair
Oct. 2021

Quantitative Life Sciences Program, McGill University
Steering committee member for seminar series in Quantitative Life Sciences and Medicine
Jun. 2021

Academic Services as Editorial Board Member

BMC Medicine