

Tianyuan Lu, PhD  
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## Education

McGill University, Montreal, QC, Canada Sept. 2018 – May. 2022  
PhD in Quantitative Life Sciences, Statistical Genetics and Genetic Epidemiology Stream  
GPA: 4.0/4.0

Fudan University, Shanghai, China Sept. 2014 – Jun. 2018  
BSc in Biological Sciences, Biostatistics and Bioinformatics Stream  
GPA: 3.71/4.0

## Employment

University of Wisconsin-Madison, Madison, WI, United States of America Aug. 2024 - Present  
Assistant Professor  
Department of Population Health Sciences & Department of Biostatistics and Medical Informatics  
School of Medicine and Public Health

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

McGill University, Montreal, QC, Canada Sept. 2019 – Dec. 2019; Jan. 2020 – Apr. 2020; Sept 2020 – Dec. 2020  
Teaching Assistant

## Research Contributions

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.

Since 2018, I have contributed to **45** research articles published or accepted to be published in peer-reviewed journals, including Nature Genetics, Genome Medicine, Genetics in Medicine, Biological Psychiatry, JCEM, JBMR, Nature Metabolism, Nature Communications, Nature Aging, AJHG, Bioinformatics, Genetics, PLOS Genetics, Clinical Epigenetics, Cardiovascular Diabetology, Communications Biology, Cell Reports, Genetic Epidemiology, etc. These include **20** articles of which I am the senior/co-senior/first/co-first author. I have also led or contributed to multiple manuscripts under review or in preparation.

My research was supported by a **Schmidt AI in Science Postdoctoral Fellowship** (170,000 CAD), a **Vanier Canada Graduate Scholarship** (150,000 CAD), and an FRQS Doctoral Training Fellowship (84,000 CAD). In addition to these major fellowships, I have received 27 honors and awards, including international or institutional research fellowships, travel awards, presentation awards, and publication awards.

## Major Fellowships

3. Eric and Wendy Schmidt AI in Science Postdoctoral Fellowship (170,000 CAD, over two years), Schmidt Futures and University of Toronto, Canada, 2023

2. Vanier Canada Graduate Scholarship (150,000 CAD, over three years), Canadian Institutes of Health Research, Canada, 2021 <Terminated in 2022 upon graduation>
1. FRQS Doctoral Training Fellowship (84,000 CAD, over four years), Fonds de Recherche du Québec Santé, Québec, Canada, 2020 <Terminated in 2021 upon receiving funding from another source>

### **Other Honors and Awards (\*Competitive)**

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27. \*Early Career Researcher Travel Award (500 GBP), International Mendelian Randomization Conference, University of Bristol, 2024
26. \*James V. Neel Award (1,000 USD), International Genetic Epidemiology Society, 2023
25. Eric and Wendy Schmidt Conference Travel Award (travel reimbursement valued at 5,000 CAD), Schmidt Futures, 2023
24. \*Prix Relève Étoile Jacques-Genest Publication Award (1,500 CAD), Fonds de Recherche du Québec Santé, 2023
23. \*ECTS New Investigator Award (750 EUR), European Calcified Tissue Society, 2023
22. \*Annual McGill Biomedical Graduate Conference Outstanding Oral Presentation, Second Place Award (350 CAD), McGill University, 2022
21. \*CANSSI Ontario STAGE HostSeq Project Fellowship (10,000 CAD), Canadian Statistical Sciences Institute, 2022
20. \*Charles J. Epstein Trainee Awards Semifinalist (750 USD), American Society of Human Genetics, 2021
19. \*Young Investigator Travel Award (500 USD), American Society for Bone and Mineral Research, 2021 <Declined due to COVID-19 pandemic>
18. McGill Initiative in Computational Medicine Graduate Award (400 CAD), McGill University, 2021
17. Plan de Réussite Graduate Mobility Award (2,000 CAD), McGill University, 2021
16. \*McGill MedStar Publication Award / A. W. K. Akerley Award (500 CAD), Department of Medicine, McGill University, 2020
15. \*Faculty of Medicine Internal Studentship (12,000 CAD), Department of Medicine, McGill University, 2020 <Declined due to funding from another source>
14. Quantitative Life Sciences Travel Award (500 CAD), McGill University, 2019
13. \*Faculty of Medicine Internal Studentship / W. R. Lasha Research Fellowship (12,000 CAD), Department of Medicine, 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 (†Authors contributed equally †Corresponding author)

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#### ➤ Published or Accepted (as senior- or co-senior author)

1. Wenmin Zhang, Chen-Yang Su, Satoshi Yoshiji, and **Tianyuan Lu**<sup>†</sup>. 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>

#### ➤ Published or Accepted (as first- or co-first author)

19. **Tianyuan Lu**<sup>†</sup>, Yiheng Chen, Satoshi Yoshiji, Yann Ilboudo, Vincenzo Forgetta, Sirui Zhou, and Celia M. T. Greenwood<sup>†</sup>. 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**<sup>†</sup>, Vincenzo Forgetta, Sirui Zhou, J Brent Richards, and Celia M. T. Greenwood<sup>†</sup>. 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**<sup>†</sup>, Tomoko Nakanishi, Satoshi Yoshiji, Guillaume Butler-Laporte, Celia M. T. Greenwood, and J. Brent Richards<sup>†</sup>. 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**<sup>†</sup>, Patrícia Pelufo Silveira, and Celia M. T. Greenwood<sup>†</sup>. Development of risk prediction models for depression combining genetic and early life risk factors. 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**<sup>†</sup>, Vincenzo Forgetta, J. Brent Richards, and Celia M. T. Greenwood<sup>†</sup>. Genetic determinants of polygenic prediction accuracy within a population. *Genetics* 2022.

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

14. Julian St. Pierre<sup>†</sup>, Xinyi Zhang<sup>†</sup>, **Tianyuan Lu**<sup>†</sup>, Lai Jiang<sup>†</sup>, Linbo Wang, Sahir Bhatnagar, Celia M. T. Greenwood<sup>†</sup>, 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<sup>†</sup>. 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**<sup>†</sup>, Vincenzo Forgetta, J. Brent Richards, and Celia M. T. Greenwood<sup>†</sup>. 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<sup>¶</sup>. 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<sup>†</sup>, **Tianyuan Lu**<sup>†</sup>, Ming-Rui Li, Ning Ding, Li-Zhen Lan, Xiang Gao, Ai-Sheng Xiong, Jian Zhang, and Lin-Feng Li<sup>¶</sup>. 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<sup>¶</sup>. 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 Escribete<sup>†</sup>, **Tianyuan Lu**<sup>†</sup>, Julyan Keller-Baruch, Vincenzo Forgetta, Bowei Xiao, J. Brent Richards, Sahir Bhatnagar, Karim Oualkacha and Celia M. T. Greenwood<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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**<sup>†</sup>, Vincenzo Forgetta<sup>†</sup>, 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<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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>

➤ **Published or Accepted (as co-author)**

25. Jiacheng Miao, Yixuan Wu, Zhongxuan Sun, Xinran Miao, **Tianyuan Lu**, Jiwei Zhao, and Qiongshi Lu<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>†</sup>, Maria Nethander<sup>†</sup>, Howard A. Fink<sup>†</sup>, Anna E. Törnqvist, Diana I. Jalal, Petra Buzkova, Joshua I. Barzilay, Laura Carbone, Maiken E. Gabrielsen, Louise Grahnmø, **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<sup>¶</sup>. A protein-based risk score improves hip fracture prediction. *Nature Aging* 2024.

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

21. Wenmin Zhang<sup>¶</sup>, **Tianyuan Lu**, Robert Sladek, Yue Li, Hamed S. Najafabadi, and Josée Dupuis<sup>¶</sup>. 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 Grahnmø, 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<sup>¶</sup>. 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<sup>¶</sup>, 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<sup>†</sup>, Sofia Movérare-Skrtic<sup>†</sup>, 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 Styrkarsdóttir, Outi Mäkitie, Kristian Hveem, J. Brent Richards, and Claes Ohlsson<sup>¶</sup>. 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<sup>¶</sup>, and Satya Dash<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>, Zhong Wang, **Tianyuan Lu**, Teri A. Manolio, and Andrew D. Paterson<sup>¶</sup>. 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<sup>¶</sup>. 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<sup>¶</sup>. Proteome-wide Mendelian randomization implicates nephronectin as an actionable mediator of the effect of obesity on COVID-19 severity. *Nature Metabolism* 2023.

<https://www.nature.com/articles/s42255-023-00742-w>

11. Felicia Lazure, Rick Farouni, Korin Sahiyan, Darren M. Blackburn, Aldo Hernández-Corchado, Gabrielle Perron, **Tianyuan Lu**, Adrien Osakwe, Jiannis Ragoussis, Colin Crist, Theodore J. Perkins, Arezu Jahani-Asl, Hamed S. Najafabadi<sup>¶</sup>, and Vahab D. Soleimani<sup>¶</sup>. Transcriptional reprogramming of skeletal muscle stem cells by the niche environment. *Nature Communications* 2023.

<https://www.nature.com/articles/s41467-023-36265-x>

10. Yiheng Chen, **Tianyuan Lu**, Ulrika Pettersson-Kymmer, Isobel D. Stewart, Guillaume Butler-Laporte, Tomoko Nakanishi, Agustin Cerani, Kevin Y. H. Liang, Satoshi Yoshiji, Julian Daniel Sunday Willett, Chen-Yang Su, Parminder Raina, Celia M. T. Greenwood, Yossi Farjoun, Vincenzo Forgetta, Claudia Langenberg, Sirui Zhou, Claes Ohlsson, and J. Brent Richards<sup>¶</sup>. Genomic atlas of the plasma metabolome prioritizes metabolites implicated in human diseases. *Nature Genetics* 2023.

<https://doi.org/10.1038/s41588-022-01270-1>

9. Sahir Bhatnagar<sup>¶</sup>, **Tianyuan Lu**, Amanda Lovato, David L. Olds, Michael S. Kobor, Michael J. Meaney, Yi Yang and Celia M. T. Greenwood. A sparse additive model for high-dimensional interactions with an exposure variable. *Computational Statistics & Data Analysis* 2022.

<https://www.sciencedirect.com/science/article/abs/pii/S0167947322002043>

8. Gabrielle Perron, Pouria Jandaghi, Elham Moslemi, Tamiko Nishimura, Maryam Rajaei, Rached Alkallas, **Tianyuan Lu**, Yasser Riazalhosseini, and Hamed S. Najafabadi<sup>¶</sup>. Pan-cancer analysis of mRNA stability for decoding tumour post-transcriptional programs. *Communications Biology* 2022.

<https://www.nature.com/articles/s42003-022-03796-w>

7. Satoshi Yoshiji, Daisuke Tanaka, Hiroto Minamino, **Tianyuan Lu**, Guillaume Butler-Laporte, Takaaki Murakami, Yoshihito Fujita, J. Brent Richards<sup>¶</sup>, and Nobuya Inagaki<sup>¶</sup>. Causal associations between body fat accumulation and COVID-19 severity: A Mendelian randomization study. *Frontiers in Endocrinology* 2022.

<https://doi.org/10.3389/fendo.2022.899625>

6. Zhen-Hui Wang, Xin-Feng Wang, **Tianyuan Lu**, Ming-Rui Li, Peng Jiang, Jing Zhao, Si-Tong Liu, Xue-Qi Fu, Jonathan Wendel, Yves Van de Peer, and Lin-Feng Li<sup>¶</sup>. Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in *Panax*. *Nature Communications* 2022.

<https://www.nature.com/articles/s41467-022-29561-5>

5. Ming-Rui Li, Ning Ding, **Tianyuan Lu**, Zhen-Hui Wang, Peng Jiang, Bao Liu and Lin-Feng Li<sup>¶</sup>. Ancient and recent polyploidy drive genome evolution and speciation of the ginseng species complex. *Genome Biology and Evolution* 2021.

<https://doi.org/10.1093/gbe/evab051>

4. Ashot S. Harutyunyan<sup>‡</sup>, Haifen Chen<sup>‡</sup>, **Tianyuan Lu**, Cynthia Horth, Hamid Nikbakht, Brian Krug, Caterina Russo, Eric Bareke, Dylan M. Marchione, Mariel Coradin, Benjamin A. Garcia, Nada Jabado<sup>¶</sup> and Jacek Majewski<sup>¶</sup>. H3K27M in gliomas causes a one-step decrease in H3K27 methylation and reduced spreading within the constraints of H3K36 methylation. *Cell Reports* 2020.

<https://www.sciencedirect.com/science/article/pii/S2211124720313796>

3. Sahir Bhatnagar<sup>¶</sup>, Yi Yang, **Tianyuan Lu**, Erwin Schurr, J.C. Loredó-Osti, Marie Forest, Karim Oualkacha and Celia M. T. Greenwood. Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. *PLOS Genetics* 2020.

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008766>

2. Ming-Rui Li, Hua-Ying Wang, Ning Ding, **Tianyuan Lu**, Ye-Chao Huang, Hong-Xing Xiao, Bao Liu and Lin-Feng Li<sup>¶</sup>. Rapid divergence followed by adaptation to contrasting ecological niches of two closely related columbine species *Aquilegia japonica* and *A. oxysepala*. *Genome Biology and Evolution* 2019.

<https://doi.org/10.1093/gbe/evz038>

1. Liming Li, Chan Wang, **Tianyuan Lu**, Shili Lin, and Yue-Qing Hu<sup>¶</sup>. Indirect effect inference and application to GAW20 data. *BMC Genetics* 2018.

<https://doi.org/10.1186/s12863-018-0638-3>

### ➤ Under Revision or Submitted

13. Wenmin Zhang<sup>¶</sup>, **Tianyuan Lu**, Robert Sladek, Josée Dupuis, and Guillaume Lettre<sup>¶</sup>. Robust fine-mapping in the presence of linkage disequilibrium mismatch. *Under review*.

12. 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. Constanzo, Noel P. Burt, Jason Flannick, Sirui Zhou, Vincent Mooser, **Tianyuan Lu**<sup>¶</sup>, and Satoshi Yoshiji<sup>¶</sup>. Multi-ancestry proteome-phenome-wide Mendelian randomization offers a comprehensive protein-disease atlas and potential therapeutic targets. *Under review*.

11. Wenmin Zhang<sup>¶</sup>, Satoshi Yoshiji, Robert Sladek, Josée Dupuis<sup>¶</sup>, and **Tianyuan Lu**<sup>¶</sup>. Benchmarking Bayesian colocalization methods in validating Mendelian randomization-based target discoveries from circulating proteins for cardiometabolic diseases. *Under review*.

10. **Tianyuan Lu**<sup>¶</sup>, Wenmin Zhang, Fergus W. Hamilton, Guillaume Butler-Laporte, Nicholas J. Timpson, George Davey Smith, and J. Brent Richards<sup>¶</sup>. Challenges to the Independence Assumption in Mendelian Randomization due to Sample Selection and Complex Methods. *Under revision*.

9. **Tianyuan Lu**<sup>¶</sup>, 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. *Under review*.

8. **Tianyuan Lu**<sup>¶</sup>, Despoina Manousaki, Lei Sun, and Andrew D. Paterson<sup>¶</sup>. Integrative proteogenomic analyses provide novel interpretations of type 1 diabetes risk loci through circulating proteins. *Under revision*.

7. **Tianyuan Lu**<sup>¶</sup> and Andrew D. Paterson<sup>¶</sup>. Estimating effects of serum vitamin B12 levels on psychiatric disorders and cognitive impairment: a Mendelian randomization study. *Under revision*.

6. 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, Vincenzo Forgetta, Yossi Farjoun, Hugo Zeberg, Sirui Zhou, Michael Hulström, Mitchell Machiela, Nicholas J. Wareham, Vincent Mooser, Nicholas J. Timpson, Claudia Langenberg, and J. Brent Richards<sup>¶</sup>. COL6A3-derived endotrophin mediates the effect of obesity on coronary artery disease: an integrative proteogenomics analysis. *Under revision*.



5. Fergus W. Hamilton, David A. Hughes, **Tianyuan Lu**, Apostolos Gkatzionis, Wes Spiller, Kate Tilling, Fernando Pires Hartwig, and George Davey Smith<sup>¶</sup>. Non-linear Mendelian randomization: evaluation of effect modification in the residual and doubly-ranked methods. *Submitted*.
4. Thomas M. Zheng, Yann Ilboudo, **Tianyuan Lu**, Guillaume Butler-Laporte, Tomoko Nakanishi, David Morrison, Darin Adra, and J. Brent Richards. Differential circulating proteomic responses associated with ancestry during severe COVID-19 infection. *Submitted*.
3. 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*.
2. Tsegaselassie Workalemahu<sup>¶</sup>, 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*.
1. 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<sup>¶</sup>. Aquaporin 3 genotype modulates the risk of death conferred by plasma osmolality in COVID-19. *Submitted*.

## Scientific Presentations

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### ➤ Oral Presentations

22. International Genetic Epidemiology Society, November 4, 2023 “Improved characterization of gene-environment interactions for vitamin D through variance quantitative trait loci” (15 minutes plenary oral presentation). Denver, CO, USA
21. BIRS Workshop, July 25, 2024 “Challenges in causal interpretation of Mendelian Randomization with large biobank data” (20 minutes oral presentation). Banff International Research Station, Banff, AB, Canada
20. Mendelian Randomization Conference, June 19, 2024 “Core gene assumption-based Mendelian randomization sensitivity analysis for complex exposures” (15 minutes platform oral presentation). Bristol, UK
19. International Genetic Epidemiology Society, November 6, 2023 “Integrative proteogenomic analyses identify circulating protein abundances associated with type 1 diabetes risk” (15 minutes plenary oral presentation). Nashville, TN, USA
18. Endocrine Society Annual Conference, June 15, 2023 “Polygenic risk scores for osteoporosis” (30 minutes platform oral presentation). Chicago, IL, USA
17. CHARGE Consortium Semi-annual Meeting, May 10, 2023 “New opportunities for fracture risk management through improved characterization of genetic architecture underlying hip and spine bone mineral density” (10 minutes platform oral presentation). Boston, MA, USA

16. Department of Population Health Sciences Research Seminar, May 2, 2023 “Genetic epidemiology for better population health: From associations to actions” (60 minutes oral presentation). University of Wisconsin-Madison, Madison, WI, USA
15. European Calcified Tissue Society Congress 2023, April 17, 2023 “New opportunities for fracture risk management through improved characterization of genetic architecture underlying hip and spine bone mineral density” (10 minutes plenary oral presentation). Liverpool, UK
14. Data Science Methods in Population Health & Health Systems Research Seminar, February 14, 2023 “Leveraging human genetics for improving population health and health management of complex diseases: Advances and challenges” (45 minutes oral presentation). Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada
13. Statistical Methods for Genetics & Genomics (SMGG) Research Seminar and Journal Club, January 27, 2023 “Identifying molecular therapeutic targets in circulation using Mendelian randomization” (60 minutes oral presentation). University of Toronto, Toronto, ON, Canada
12. Montreal Clinical Research Institute Early-Career Scientist Symposium, May 5, 2022 “Genetic risk scores for complex diseases: new opportunities for clinical use” (30 minutes oral presentation). Institut de Recherches Cliniques de Montréal (IRCM), Montreal, QC, Canada
11. Annual McGill Biomedical Graduate Conference 2022, March 22, 2022 “Circulating proteins influencing psychiatric disease: A Mendelian randomization study” (10 minutes plenary oral presentation). Event held online
10. American Society of Human Genetics Conference 2021, October 19, 2021 “Modelling hidden genetic risk from family history for improved polygenic risk prediction” (15 minutes platform oral presentation). Event held online
9. International Genetic Epidemiology Society Conference 2021, October 13, 2021 “Modelling hidden genetic risk from family history for improved polygenic risk prediction” (5 minutes plenary lightning talk and poster presentation). Event held online
8. American Society for Bone and Mineral Research Conference 2021, October 3, 2021 “Identifying causes of fracture independent of bone density: evidence from human genetics” (15 minutes platform oral presentation). Event held online
7. Manitoba Machine Learning Seminar, September 17, 2020 “Machine learning in state-of-the-art methods for developing polygenic risk scores” (20 minutes oral presentation). Event held online
6. International Genetic Epidemiology Society Conference 2020, July 3, 2020 “Individuals with common diseases, but with a low polygenic risk score could be prioritized for rare variant screening” (3 minutes plenary lightning talk and poster presentation). Event held online
5. Ludmer Centre Special Symposium, November 20, 2019 “State-of-the-art methods for developing a polygenic risk score” (10 minutes oral presentation). Montreal Neurological Hospital, Montreal, QC, Canada

4. Quantitative Life Sciences Research Day, October 3, 2019 “Polygenic risk for coronary heart disease acts through atherosclerosis in type 2 diabetes” (15 minutes oral presentation). McGill University, Montreal, QC, Canada

3. Advances and Thoughts at the Genome Centre (ATGC Meeting), September 19, 2019 “Single-cell RNA sequencing uncovers cellular heterogeneity in clear cell renal cell carcinoma” (60 minutes oral presentation). McGill University and Génome Québec Innovation Center, Montreal, QC, Canada

2. Advances and Thoughts at the Genome Centre (ATGC Meeting), January 17, 2019 “Modelling deposition dynamics of H3K27 methylation” (60 minutes oral presentation). McGill University and Génome Québec Innovation Center, Montreal, QC, Canada

1. OncoHistone Group Semi-annual Meeting, December 6, 2018: “How are H3K27 methylation patterns inherited and stabilized” (30 minutes oral presentation). The Rockefeller University, New York, NY, USA

### ➤ **Poster Presentations**

8. Combining polygenic and monogenic causes for improved osteoporotic fracture risk prediction. American Society of Human Genetics Conference 2022, Los Angeles, CA, USA (Poster)

7. Combining polygenic and monogenic causes for improved osteoporotic fracture risk prediction. International Genetic Epidemiology Society Conference 2022, Paris, France (Poster)

6. Polygenic risk score as a possible tool for identifying familial monogenic causes of complex diseases. American College of Medical Genetics and Genomics Conference 2022, held online (Poster)

5. Individuals with common diseases, but with a low polygenic risk score could be prioritized for rare variant screening. American Society of Human Genetics Conference 2020, held online (Poster)

4. Improved prediction of fracture risk leveraging a genome-wide polygenic risk score. American Society for Bone and Mineral Research Conference 2020, held online (Poster)

3. Capitalizing purity estimates for better profiling transcriptomic signatures of tumour. 28<sup>th</sup> Conference on Intelligent Systems for Molecular Biology (ISMB) 2020, held online (Poster)

2. Whole-genome bisulfite sequencing in systemic sclerosis provides novel targets to understand disease pathogenesis. International Genetic Epidemiology Society Conference 2019, Houston, TX, USA (Poster)

1. Genetic influences on coronary heart disease act on atherosclerosis in type 2 diabetes. American Society of Human Genetics Conference 2019, Houston, TX, USA (Poster)

### **Teaching**

Department of Population Health Sciences, University of Wisconsin-Madison	Fall 2024
POPHLTH 805 Advanced Epidemiology: Causal Inference in Epidemiological Studies	
Lecturer (x2 lectures on causal directed acyclic graphs)	

International Genetic Epidemiology Society Annual Conference Workshop	Sept. 2022
Epidemiology and architecture of large genetic biobanks: hands-on illustrations	
Workshop Lecturer	

McGill Initiative in Computational Medicine, McGill University Polygenic risk scores - Theory, Development and Evaluation Workshop Lecturer	Apr. 2021
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

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American Society of Human Genetics Annual Conference <b>Conference abstract reviewer</b> “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 <b>Conference abstract reviewer</b> “Omics Approaches for Musculoskeletal Biology, Diseases and Treatments”	Jun. 2024
American Society of Human Genetics Annual Conference <b>Platform session co-chair</b> “Novel tools and data resources for genetic data analysis”	Nov. 2023
American Society of Human Genetics Annual Conference <b>Platform session co-chair</b> “Genetic impacts on the epigenome and beyond”	Oct. 2022
International Genetic Epidemiology Society Annual Conference <b>Platform session co-chair</b> “Biobanks and polygenic risk scores”	Sept. 2022
International Genetic Epidemiology Society Annual Conference <b>Poster session co-chair</b>	Oct. 2021
Quantitative Life Sciences Program, McGill University <b>Steering committee member</b> for seminar series in Quantitative Life Sciences and Medicine	Jun. 2021

### Academic Services as Editorial Board Member

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BMC Medicine

## Academic Services as Ad Hoc Reviewer

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2024 Nature Communications (2 Research Articles reviewed)  
 2024 Nature Human Behaviour (1 Research Article reviewed)  
 2024 Biological Psychiatry (1 Research Article reviewed)  
 2024 Cell Discovery (1 Research Article reviewed)  
 2024 BMC Medicine (1 Research Article reviewed)  
 2024 Communications Biology (1 Research Article reviewed)  
 2024 Journal of Clinical Endocrinology & Metabolism (4 Research Articles reviewed)  
 2024 Genomics, Proteomics & Bioinformatics (1 Research Article reviewed)  
 2024 Osteoporosis International (1 Research Article reviewed)  
 2024 Human Genetics (1 Review Article reviewed)  
 2024 JMIR Bioinformatics and Biotechnology (1 Research Article reviewed)  
 2024 Scientific Reports (1 Research Article reviewed)  
 2024 Lipids in Health and Disease (1 Research Article reviewed)  
 2024 BMC Musculoskeletal Disorders (1 Research Article reviewed)  
 2023 Nature Communications (1 Research Article reviewed)  
 2023 BMC Medicine (1 Research Article reviewed)  
 2023 Journal of Bone and Mineral Research (2 Research Articles reviewed)  
 2023 Journal of Clinical Endocrinology & Metabolism (3 Research Articles reviewed)  
 2023 npj Genomic Medicine (1 Research Article reviewed)  
 2023 Nutrition Journal (1 Research Article reviewed)  
 2023 Lipids in Health and Disease (4 Research Articles reviewed)  
 2023 Progress in Neuropsychopharmacology & Biological Psychiatry (1 Research Article reviewed)  
 2023 Frontiers in Psychology (1 Research Article reviewed)  
 2023 BMC Genomics (1 Research Article reviewed)  
 2023 BMC Medical Genomics (2 Research Articles reviewed)  
 2023 BMC Research Notes (1 Research Article reviewed)  
 2023 Cell Genomics (1 Research Article co-reviewed with Dr. Celia MT Greenwood)  
 2023 Scientific Reports (2 Research Articles reviewed)  
 2023 Clinical and Translational Discovery (1 Review Article reviewed)  
 2022 Diabetes Care (1 Research Article reviewed)  
 2022 Journal of Clinical Endocrinology & Metabolism (3 Research Articles reviewed)  
 2022 Journal of the American College of Cardiology (1 Research Article co-reviewed with Dr. J Brent Richards)  
 2022 Frontiers in Endocrinology (1 Research Article reviewed)  
 2022 Frontiers in Psychiatry (1 Research Article reviewed)  
 2022 Frontiers in Genetics (8 Research Articles reviewed)  
 2022 BMC Cancer (1 Research Article reviewed)  
 2022 BMC Cardiovascular Disorders (1 Research Article reviewed)  
 2022 Annals of Human Biology (1 Review Article reviewed)  
 2022 Genes (1 Research Article co-reviewed with Dr. J Brent Richards)  
 2022 Scientific Reports (2 Research Articles reviewed)  
 2022 Pharmacogenomics and Personalized Medicine (1 Research Article reviewed)  
 2022 STAR Protocols (2 Research Protocols reviewed)  
 2021 BMC Genomics (1 Research Article reviewed)  
 2021 Scientific Reports (1 Research Article reviewed)  
 2021 Montreal AI Symposium (2 Abstracts reviewed)  
 2021 STAR Protocols (1 Research Protocol reviewed)  
 2020 eLife (1 Research Article reviewed)



2020 Biostatistics (1 Research Article reviewed)

2020 STAR Protocols (1 Research Protocol reviewed)

2020 Osteoporosis International (1 Research Article co-reviewed with Dr. J Brent Richards)

2020 Montreal AI Symposium (2 Abstracts reviewed)

### **Programming, Computational Software and Language Skills**

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Extremely familiar with R, Python, Unix-based operating systems, and Cloud Computing; Highly experienced in developing and implementing computational tools in statistical genetics and bioinformatics; Capable of Perl, SPSS, Minitab, STATA and MATLAB; Mandarin Chinese (native); English (proficient); French (intermediate)