Tianyuan Lu, PhD
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Education

McGill University, Montreal, 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 Toronto, Toronto, Canada — Feb. 2023 – Present
Schmid AI in Science Postdoctoral Fellow

Five Prime Sciences, Montreal, Canada — Feb. 2023 – Sept. 2023
Senior Research Scientist (part-time)

Five Prime Sciences and Lady Davis Institute for Medical Research, Montreal, Canada — Jun. 2022 – Feb. 2023
Senior Research Scientist

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 **35** 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, AJHG, Genetics, PLOS Genetics, Clinical Epigenetics, Cardiovascular Diabetology, Communications Biology, Cell Reports, Genetic Epidemiology, etc. These include **18** articles of which I am the first or a co-first author. I have also led or contributed to multiple manuscripts under review or in preparation.
My research has been 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 24 honors and awards, including international or institutional research fellowships, travel awards, presentation awards, and publication awards.

Research Topics

Applied statistical genetics: genome-wide association study, polygenic risk prediction, Mendelian randomization, gene-by-environment interaction, dominance, rare variant association test, family history, natural selection
Statistics: penalized regression, nonlinearity, structural equation modelling
Complex traits: osteoporosis, diabetes, obesity, coronary artery disease, schizophrenia, bipolar disorder, major depressive disorder, Alzheimer's disease, breast cancer, colorectal cancer, short stature, systemic sclerosis
Multi-omics: genome-wide genotyping, whole-exome sequencing, whole-genome sequencing, proteomics, metabolomics, DNA methylation, histone modification, single-cell RNA sequencing

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

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 Scientific Departments (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*)

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

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.
https://asbmr.onlinelibrary.wiley.com/doi/10.1002/jbmr.4920
Topics: osteoporosis, rare variant association test, polygenic risk prediction

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
Topics: Mendelian randomization, diabetes, obesity, nonlinearity

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. 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
Topics: polygenic risk prediction, major depressive disorder, gene-by-environment interaction

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
Topics: polygenic risk prediction, gene-by-environment interaction, dominance, nonlinearity

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
Topics: penalized regression, polygenic risk prediction

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.
https://doi.org/10.1016/j.biopsych.2022.08.015
Topics: Mendelian randomization, proteomics, schizophrenia, bipolar disorder, major depressive disorder

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
Topics: polygenic risk prediction, family history, short stature, Alzheimer's disease, breast cancer, diabetes, coronary artery disease

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

Topics: osteoporosis, structural equation modelling

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
Topics: natural selection, whole-genome sequencing, DNA methylation

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
Topics: polygenic risk prediction, whole-exome sequencing, family history, breast cancer, colorectal cancer, diabetes, coronary artery disease

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.
https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22430
Topics: penalized regression, polygenic risk prediction

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
Topics: DNA methylation, diabetes, gene-by-environment interaction

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
Topics: polygenic risk prediction, short stature, penalized regression

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
Topics: polygenic risk prediction, osteoporosis

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
Topics: single-cell RNA sequencing

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
Topics: polygenic risk prediction, whole-exome sequencing, breast cancer, colorectal cancer, diabetes, coronary artery disease, osteoporosis

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
Topics: coronary artery disease, diabetes, polygenic risk prediction

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
Topics: systemic sclerosis, DNA methylation

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

17. Lei Sun¶, Zhong Wang, **Tianyuan Lu**, Teri A. Manolio, and Andrew 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

16. 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¶. Genomic atlas of the plasma metabolome prioritizes metabolites implicated in human diseases. ***Nature Genetics*** 2023.
https://doi.org/10.1038/s41588-022-01270-1

15. 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.
https://www.nature.com/articles/s42255-023-00742-w

14. 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

13. 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

12. 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

11. 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

10. 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¶, and Vahab D. Soleimani¶. Transcriptional reprogramming of skeletal muscle stem cells by the niche environment. ***Nature Communications*** 2023.
https://www.nature.com/articles/s41467-023-36265-x

9. Sahir Bhatnagar¶, **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 Rajaee, Rached Alkallas, **Tianyuan Lu**, Yasser Riazalhosseini, and Hamed S. Najafabadi¶. 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¶, and Nobuya Inagaki¶. 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¶. 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¶. 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†, Haifen Chen†, **Tianyuan Lu**, Cynthia Horth, Hamid Nikbakht, Brian Krug, Caterina Russo, Eric Bareke, Dylan M. Marchione, Mariel Coradin, Benjamin A. Garcia, Nada Jabado¶ and Jacek Majewski¶. 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¶, Yi Yang, **Tianyuan Lu**, Erwin Schurr, J.C. Loredo-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¶. 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¶. Indirect effect inference and application to GAW20 data. ***BMC Genetics*** 2018.
https://doi.org/10.1186/s12863-018-0638-3

- **Under Revision or Submitted**

11. **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. *Under review*.

10. 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. *Submitted*.

9. 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¶. COL6A3-derived endotrophin mediates the effect of obesity on coronary artery disease: an integrative proteogenomics analysis. *Under review*.

8. 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. *Under revision.*

7. 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. *Submitted*.

6. 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*.

5. 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. *Under revision*.

4. 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. *Submitted*.

3. Maria Nethander†, Sofia Movérare-Skrtic†, Anders Kämpe, Eivind Coward, Ene Reimann, Louise Grahnemo, Éva Borbély, Zsuzsanna Helyes, 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. *Under revision*.

2. 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. *Under revision.*

1. Yann Ilboudo, Satoshi Yoshiji, **Tianyuan Lu**, Guillaume Butler-Laporte, Sirui Zhou, and J. Brent Richards¶. Vitamin D and the preclinical Alzheimer cognitive composite cognition (PACC) score: a two-sample Mendelian randomization study. *Under revision*.

Scientific Presentations

- **Oral Presentations**

18. Endocrine Society Annual Conference, June 15, 2023 "Polygenic risk scores for osteoporosis" (30 minutes 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 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. 28th Conference on Intelligent Systmes 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

International Genetic Epidemiology Society Annual Conference Sept. 2022
Workshop host
Developed and hosted an educational workshop titled "Epidemiology and architecture of large genetic biobanks: hands-on illustrations"
Designed workshop materials, including hands-on tutorials

Workshop Lecturer, McGill Initiative in Computational Medicine, McGill University Apr. 2021
Organized and lectured a four-hour workshop on developing and using polygenic risk scores in genetic studies for students from diverse fields of medical sciences
Designed workshop materials, including hands-on tutorials

Workshop Lecturer, Department of Human Genetics, McGill University Nov. 2020
Co-organized and lectured a three-hour statistics workshop for graduate students in the Human Genetics department
Designed workshop materials

Teaching Assistant, Department of Biology, McGill University Sept. 2020 – Dec. 2020
Served as Teaching Assistant for BIOL 324 Ecological Genetics, lectured by Dr. Daniel Schoen (dan.schoen@mcgill.ca)
Designed materials and lectured one class (one hour) on complex trait genetics and genome-wide association studies, in supplementary to other lectures with a strong theoretical focus

Monitored online lectures and provided feedback on in-class group discussions
Held online weekly office hours answering students' questions about course materials and practice problems

Teaching Assistant, Department of Biology, McGill University Jan. 2020 – Apr. 2020
Served as Teaching Assistant for BIOL 202 Basic Genetics, lectured by Drs. Tamara Western (tamara.western@mcgill.ca), Daniel Schoen (dan.schoen@mcgill.ca), Laura Nilson (laura.nilson@mcgill.ca) and Nam-Sung Moon (nam.moon@mcgill.ca)
Led 22 semi-weekly conferences (one hour each) on revision, reflection and extension of course content, using materials prepared with joint efforts of other four teaching assistants
Held six in-person weekly office hours and three online weekly office hours answering students' questions about course materials and practice problems
Graded exam and provided feedback

Teaching Assistant, Department of Biology, McGill University Sept. 2019 – Dec. 2019
Served as Teaching Assistant for BIOL 324 Ecological Genetics, lectured by Dr. Daniel Schoen (dan.schoen@mcgill.ca)
Designed materials and lectured one class (one hour) on real data analysis in genetics and genomics, in supplementary to other lectures with a strong theoretical focus
Held in-person and online weekly office hours answering students' questions about course materials and practice problems
Graded exam and assignments, and provided feedback

Academic Services as Ad Hoc Reviewer

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 (1 Research Article reviewed)
2023 npj Genomic Medicine (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)

Other Academic Services

American Society of Human Genetics Annual Conference — Oct. 2022
Platform session chair "Genetic impacts on the epigenome and beyond"

International Genetic Epidemiology Society Annual Conference — Sept. 2022
Platform session chair "Biobanks and polygenic risk scores"

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

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

Society Membership

American Society of Human Genetics
International Genetic Epidemiology Society
American College of Medical Genetics and Genomics

Programming, Computational Software and Language Skills

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)