

Tianyuan Lu, PhD
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Education

McGill University, Montreal, Canada PhD in Quantitative Life Sciences	Sept. 2018 – May. 2022
Fudan University, Shanghai, China BSc in Biological Sciences	Sept. 2014 – Jun. 2018

Employment

Five Prime Sciences, Montreal, Canada Senior Research Scientist	Jun. 2022 – Present
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Research Contributions

My research focuses on developing and implementing rigorous statistical genetics 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 published **25** research articles in peer-reviewed journals, and have led or contributed to multiple manuscripts under review or in preparation. These include **15** articles of which I am the first or a co-first author that have been published in field-leading journals, such as Genome Medicine, Genetics in Medicine, Biological Psychiatry, JCEM, JBMR, Genetics, Clinical Epigenetics, and Genetic Epidemiology.

My research has been supported by a **Vanier Canada Graduate Scholarship**, an FRQS Doctoral Training Fellowship, and multiple international or institutional fellowships, travel grants, 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, 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

2. Vanier Canada Graduate Scholarship (50,000 CAD per annum, for three years), Canadian Institutes of Health Research, Canada, 2021 <Terminated in 2022 upon graduation> CA

1. FRQS Doctoral Training Fellowship (21,000 CAD per annum, for four years), Fonds de Recherche du Québec Santé, Québec, Canada, 2020 <Terminated in 2021 upon receiving funding from another source> CA

Other Honors and Awards

22. Annual McGill Biomedical Graduate Conference Outstanding Oral Presentation, Second Place Award (350 CAD), 2022 **CA**
21. CANSSI Ontario STAGE HostSeq Project Fellowship (10,000 CAD), Canadian Statistical Sciences Institute, 2022 **CA**
20. Charles J. Epstein Trainee Awards Semifinalist (750 USD), American Society of Human Genetics, 2021 **us**
19. Young Investigator Travel Award (500 USD), American Society for Bone and Mineral Research, 2021
<Declined due to COVID-19 pandemic> **us**
18. McGill Initiative in Computational Medicine Graduate Award (400 CAD), McGill University, 2021 **CA**
17. Plan de Réussite Graduate Mobility Award (2,000 CAD), McGill University, 2021 **CA**
16. McGill MedStar Publication Award / A. W. K. Akerley Award (500 CAD), Department of Medicine, McGill University, 2020 **CA**
15. Faculty of Medicine Internal Studentship (12,000 CAD), Department of Medicine, McGill University, 2020
<Declined due to funding from another source> **CA**
14. Quantitative Life Sciences Travel Award (500 CAD), McGill University, 2019 **CA**
13. Faculty of Medicine Internal Studentship / W. R. Lasha Research Fellowship (12,000 CAD), Department of Medicine, McGill University, 2019 **CA**
12. Australian Institute of Bioengineering and Nanotechnology Research Fellowship (2,880 AUD), University of Queensland, 2018 **AU**
11. Excellent Graduate of Class 2018 (Top 5%), Fudan University, 2018 **CN**
10. Visiting Student Research Fellowship (5,000 USD), King Abdullah University of Science and Technology, 2017 **SA**
9. Scholarship of Summer Institute in Statistical Genetics (tuition exemption valued at 1,050 USD), Department of Biostatistics, University of Washington, 2017 **us**
8. Fosun Pharma Scholarship, First Prize (Top 2%, 5,000 CNY), School of Life Sciences, Fudan University, 2017 **CN**
7. Fudan University Student Exchange Fellowship / Dong Fang Scholarship (29 recipients, 6,000 CNY), Fudan University, 2017 **CN**
6. Scholarship for Outstanding Students, First Prize/Arawana Scholarship (Top 5%, 10,000 CNY), Fudan University, 2016 **CN**
5. Jing Rong Life Sciences Scholarship, First Prize (Top 5%, 3,000 CNY), School of Life Sciences, Fudan University, 2016 **CN**
4. Outstanding Student Scholarship in Scientific Departments (Top 30%, 1,800 CNY), Fudan University, 2016 **CN**
3. Chinese College Students Math Competition, Third Prize, Chinese Mathematical Society, 2015 **CN**
2. Campbell's Scholarship, First Prize (Top 5%, 5,000 CNY), School of Life Sciences, Fudan University, 2015 **CN**
1. National Scholarship (Top 2%, 8,000 CNY), Ministry of Education of the People's Republic of China, 2015 **CN**

Research Articles (†Authors contributed equally)

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

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](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 Escribete†, **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)

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. Genomic atlas of the plasma metabolome prioritizes metabolites implicated in human diseases: An analysis of the Canadian Longitudinal Study on Aging (CLSA). *Accepted, Nature Genetics*.

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 Rajaei, 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. Loredó-Ostí, 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

5. **Tianyuan Lu**, Tomoko Nakanishi, Satoshi Yoshiji, Guillaume Butler-Laporte, Celia M. T. Greenwood, and J. Brent Richards (brent.richards@mcgill.ca). Dose-dependent association of alcohol consumption with obesity and type 2 diabetes: observational and Mendelian randomization analyses. *Submitted*.

4. 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, J. Brent Richards (brent.richards@mcgill.ca). Proteome-wide Mendelian randomization implicates nephronectin as an actionable mediator of the effect of obesity on COVID-19 severity. *Under revision*.

3. Julian Daniel Sunday Willett, **Tianyuan Lu**, Tomoko Nakanishi, Satoshi Yoshiji, Guillaume Butler-Laporte, Vincent Mooser, Sirui Zhou, Yossi Farjoun, and J. Brent Richards (brent.richards@mcgill.ca). Colocalization of expression transcripts with COVID-19 outcomes is dependent on cell type and cell state. *Submitted*.

2. 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. *Submitted*.

1. Felicia Lazure, Rick Farouni, Korin Sahiyan, Darren M. Blackburn, Aldo Hernández-Corchado, Gabrielle Perron, **Tianyuan Lu**, Jiannis Ragoussis, Colin Crist, Theodore J. Perkins, Arezu Jahani-Asl, Hamed S. Najafabadi, and Vahab D. Soleimani (vahab.soleimani@mcgill.ca). Transcriptional reprogramming of skeletal muscle stem cells by the niche environment. *Under revision*.

Scientific Presentations

➤ Oral Presentations

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, 110 Pine Ave, Montreal, 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, 3801 Rue University, Montreal, 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, 3506 Rue University, Montreal, 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, 740 Dr Penfield Ave, Montreal, 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, 740 Dr Penfield Ave, Montreal, 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, 1230 York Ave, New York, USA

➤ Poster Presentations

8. Combining polygenic and monogenic causes for improved osteoporotic fracture risk prediction. American Society of Human Genetics Conference 2022, Los Angeles, 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 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, USA (Poster)
1. Genetic influences on coronary heart disease act on atherosclerosis in type 2 diabetes. American Society of Human Genetics Conference 2019, Houston, USA (Poster)

Academic Services as Ad Hoc Reviewer

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- 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 (6 Research Articles reviewed)
 - 2022 BMC Cancer (1 Research Article reviewed)
 - 2022 BMC Cardiovascular Disorders (1 Research 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 Montreal AI Symposium (2 Abstracts reviewed)
 - 2021 BMC Genomics (1 Research Article reviewed)
 - 2021 STAR Protocols (1 Research Protocol reviewed)

2021 Scientific Reports (1 Research Article reviewed)
 2020 Montreal AI Symposium (2 Abstracts 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)

Other Academic Services

American Society of Human Genetics Annual Conference Platform session chair “Genetic impacts on the epigenome and beyond”	Oct. 2022
International Genetic Epidemiology Society Annual Conference Platform session chair “Biobanks and polygenic risk scores”	Sept. 2022
International Genetic Epidemiology Society Annual Conference Poster session chair	Oct. 2021
Quantitative Life Sciences Program, McGill University Steering committee member for seminar series in Quantitative Life Sciences and Medicine	Jun. 2021

Teaching

International Genetic Epidemiology Society Annual Conference 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	Sept. 2022
Workshop Lecturer, McGill Initiative in Computational Medicine, McGill University 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	Apr. 2021
Workshop Lecturer, Department of Human Genetics, McGill University Co-organized and lectured a three-hour statistics workshop for graduate students in the Human Genetics department Designed workshop materials	Nov. 2020
Teaching Assistant, Department of Biology, McGill University 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	Sept. 2020 – Dec. 2020
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

Research Experience

McGill University, Canada

Sept. 2019 – Jun. 2022

Lady Davis Institute

Supervisors: Dr. J Brent Richards and Dr. Celia MT Greenwood (PhD thesis)

McGill University, Canada

May. 2018 – Aug. 2019

Department of Human Genetics

Supervisors: Dr. Hamed S Najafabadi (PhD rotation)

McGill University, Canada

Jan. 2019 – Apr. 2019

Lady Davis Institute

Supervisors: Dr. Celia MT Greenwood (PhD rotation)

McGill University, Canada

Sept. 2018 - Dec. 2018

Department of Human Genetics

Supervisor: Dr. Jacek Majewski (PhD rotation)

University of Queensland, Australia

Jul. 2018 – Sept. 2018

Australian Institute for Bioengineering and Nanotechnology

Supervisor: Dr. Jessica C Mar (Research internship)

Fudan University, China

Mar. 2018 – Aug. 2018

Department of Evolutionary Biology, School of Life Sciences

Supervisor: Dr. Lin-Feng Li (Research assistantship)

King Abdullah University of Science and Technology, Saudi Arabia

Oct. 2017 – Mar. 2018

Red Sea Research Center

Supervisor: Dr. Manuel Aranda (Research internship)

Fudan University, China

Sept. 2016 – Sept. 2017

Department of Biostatistics and Computational Biology, School of Life Sciences
Supervisor: Dr. Yue-Qing Hu (Research assistantship)

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)