

Laurent Briollais, Ph.D

ACADEMIC DEGREES

1990	National School of Statistics	B.Sc.	Statistics/Economy
1994	University of Paris XI	M.Sc.	Biostatistics/Statistical Genetics
1998	University of Paris XI	Ph.D.	Biostatistics/Statistical Genetics

EMPLOYMENT

2016-	Assistant Professor (status-only) - Department of Statistical Sciences, University of Toronto, Toronto, Canada
2013-	Associate Professor (status-only) Dalla Lana School of Public Health Sciences (Biostatistics)
2000-2012	Assistant Professor (status-only) Dalla Lana School of Public Health Sciences (Biostatistics)
2007-present	Senior Scientist in Statistical Genetics/Biostatistics, Lunenfeld Tanenbaum Research Institute of Mount Sinai Hospital
2000-2006	Scientist in Statistical Genetics/ Biostatistics, Lunenfeld Tanenbaum Research Institute of Mount Sinai Hospital
1998-2000	Biostatistician, Hospital Clarac, Martinique, France
1993-1998	Research Assistant in Biostatistics, Hospital Saint Louis, Paris, France
1992-1992	Research Assistant, Research Institute for Exploitation of Sea, Martinique, France
1990-1991	Statistician, National Institute of Statistics, Martinique, France

PROFESSIONAL AFFILIATIONS

- Statistical Society of Canada (SSC)
- International Genetic Epidemiological Society (IGES)
- American Association of Human Genetics (ASHG)
- French Statistical Association (SFdS)
- Member of the Breast and Colon Family Cancer Registries (BCFR & CCFR)
- Member of PRACTICAL consortium (Prostate Cancer Association group to Investigate Cancer Associated Alterations in the Genome)

COMMITTEE MEMBERSHIPS

- CANSSI (Canadian Statistical Science Institute) Health Science Collaborating Centre for Statistical Omics steering committee
- STAGE (Strategic Training for Advanced Genetic Epidemiology) steering committee
- University of Toronto's Division of Biostatistics Curriculum committee
- University of Toronto's Division of Biostatistics MSc and PhD Admission committees
- University of Toronto's Division of Biostatistics PhD Activity Progress committee
- Family integrated care: data safety monitoring committee (Mount Sinai Hospital)
- Analytic Committee of the EARly Genetics and Lifecourse Epidemiology (EAGLE) consortium
- Publication committee of the International Genetic Epidemiological Society (IGES) in 2009
- Biostatistical mentor in Statistical Genetics, CIHR Strategic Training for Advanced Genetic Epidemiology (STAGE)
- Genetic Epidemiology group of the Western Australian Pregnancy Cohort (RAINE)

JOURNAL REVIEW ACTIVITIES

- Review editor in Frontiers in Statistical Genetics and Methodology since 2011
- Regular reviewer for Statistics in Medicine, Biometrics, PLoS One, American Journal of Human Genetics
- Also reviewed for Annals of Applied Statistics, Genetic Epidemiology, Biostatistics, Bioinformatics,

American Journal of Epidemiology, International Journal of Cancer, etc.

GRANT REVIEW ACTIVITIES

- CIHR genetic panel full member since March 2013
- CIHR STAGE fellowship application reviewer for 2014 round
- NSERC discovery grant reviewer (multiple applications since 2012)
- Medical Research Council (MRC) career award reviewer (Sept. 2014)
- MITACS Elevate postdoctoral fellowship application reviewer (2010 round)
- CBCF PhD and postdoctoral fellowship applications (Feb. 2008)

CURRENTLY FUNDED GRANTS

As PI:

- 2019-2023 CIHR project grant. Extending risk prediction models for hereditary breast ovarian cancer. Investigators: **Briollais L (PI)**, Choi YH, Andrulis I, Knight J. Requested: \$630,667
- 2019-2020 McLaughlin Centre Accelerating grant in Genomic Medicine. Team grant. A unified polygenic risk score analytics platform for risk prediction, causal inference and discovery. Gagnon F (NPI), Sun L (NPI), **Briollais (PI)**, Bull (PI), Strug L, Wang L, Goncalves V, Paterson A, Brooks J. \$375,000.
- 2019-2021 Statistical Methods for the Analysis of Genetic Data with Survival Outcomes. Lakhali-Chaieb L, **Briollais L**, Cook R. \$180,000
CANSSI Collaborative Research Team Project.
- 2015-2020 Development of Bayesian Graphical Models for Next-Generation Genetic Studies
Investigators: **Briollais L (PI)**
NSERC, Discovery grant competition
\$55,000

As Co-Investigator:

- 2019-2024 Using MRI imaging to develop a personalized risk-based breast cancer screening strategy. Investigators: Martel A & Brooks J; Co-investigators: Astley S, **Briollais L**, Curpen B, Warner E.
CHIR project grant. \$925,650
- 2017-2022 Building Knowledge and a foundation for HeALthy lIfe trajectories: BUKHALI Trial. Investigators: Lye S, Matthews S, Norris S, Richter L (PIs), **Briollais L** et al. \$2,478,000
CIHR team grant: Healthy Life Trajectories Initiative (HeLTI) – South-Africa
- 2018-2019 Understanding early life origins of sex difference in insulin sensitivity
Luo ZC, **Briollais L**, Kingdom J, Lye S, Murphy K, Pausova Z. \$75,000.
CIHR Catalyst Grant: Sex as a Variable in Biomedical Research
- 2017-2020 Collaborating Centre for Statistical Omics
Investigators: Bull S (PI), **Briollais L** et al. \$50,000
CANSSI (Canadian Statistical Science Institute) Health Science

- 2017-2020 Novel germline mutation in the Kallikrein gene family and predisposition for aggressive prostate cancer.
Investigators: Zlotta A (PI), **Briollais L**, Fleshner N, Recker F, Kwiatkosvski M, Diamandis E.
Requested: \$1,489,000.
Prostate Cancer Canada – Movember translation acceleration grant.
- 2016-2020 Lipid signatures of plasma-derived exosomes as markers of health and disease in pregnancy
Investigators: Caniggia I (PI), **Briollais L**, Post M, Bocking A
Requested: \$1,305,000.
NIH – R01

GRANTS APPLIED FOR

- 2020-2024 CIHR project grant. Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Trajectories.
Investigators: **Briollais L (PI)**, Lye S, Matthews S, McGowan P, O'Connor D.
Requested: **\$1,600,000**
- 2020-2024 CIHR Team Grant: Canadian Microbiome Initiative. Programming the gut microbiome for child growth and development: a multi-national intervention study.
Investigators: **Comelli E (PI)**, Briollais L, O'Connor D, Connor K, Birken C, Lye S, Dennis CL, Matthews S, etc.

COMPLETED GRANTS (within past 5 years)

As PI or Co-PI:

- 2015-2018 Evaluation of Screening and Treatment Interventions Among Members of Breast Cancer BRCA1/2 Mutation Positive Families
Investigators: **Briollais L (PI)**, Andrulis I, Knight J, Terry MB, Choi Y.
Canadian Breast Cancer Foundation
\$449,139
- 2013-2016 Development, Application and Evaluation of Multistate Models for Risk Estimation and Screening Interventions in Lynch Syndrome Families and Familial Colorectal Cancer Type X Families
Investigators: **Briollais L (PI)**, Kopciuk K, Choi YH, McLaughlin J, Cotterchio M, Gallinger S, Parfrey P
Canadian Institutes of Health Research, Operating grant
\$273,334
- 2013-2016 Cancer risk factors and stability of telomere length during pregnancy; a pilot study to inform the use of telomere length as an intermediate outcome for cancer prevention studies
Investigators: Knight JA (PI), Anderson LN, **Briollais L**, Lye SJ
\$25,000
Cancer Care Ontario Population Studies Research Network
- 2012-2015 Exploring the Complexity of Pediatric Brain Tumors with Advanced Genomics and Novel Statistical Methods
Investigators: **Briollais L (PI)**, Hung R, McLaughlin J.
\$75,000
McLaughlin Centre of University of Toronto

- 2007-2014 Gene-environment interactions underlying the developmental origins of health and disease.
Investigators: Lye S (PI), **Briollais L**, Pennell CE, Palmer LJ, et al.
\$1,330,167
Canadian Institutes of Health Research
- 2012-2014 Early life gene-environment interactions and hypothalamic-pituitary-adrenal (HPA) axis function
Investigators: Anderson L (PI), **Briollais L** et al.
\$51,666
Canadian Institutes of Health Research, Postdoctoral fellowship

INFRASTRUCTURE FUNDING

- 2010-2015 A Clinical Phenotyping and Computational Facility for the Study of Complex Disease
Knight JA (PI), Bull SB, **Briollais L**, Logan A, Zinman B, Hung R, Lilge L
\$1,209,767
Canadian Foundation for Innovation Leading Edge Fund, Ontario Research Fund

PUBLICATIONS (since 2013)

1. Abarin T, Wu Y, Warrington N, Lye S, Pennell C, **Briollais L**. (2013) The impact of breastfeeding on FTO-related BMI growth trajectories. *International Journal of Epidemiology* 41(6):1650-60.
2. Parmar PG, Marsh JA, Taal HR, Kowgier M, Uitterlinden AG, Rivadeneira F, **Briollais L**, Newnham JP, Hofman A, Lye SJ, Steegers EAP, van Duijn CM, Palmer LJ, Jaddoe VWV, Pennell CE (2012) Polymorphisms in Genes within the IGF-axis Influence Antenatal and Postnatal Growth. *Journal of Developmental Origins of Health and Disease*. 2: S141-S.
3. Olkhov-Mitsel E, Van der Kwast T, Kron KJ, Ozcelik H, **Briollais L**, Massaey C, Recker F, Kwiatkowski M, Fleshner NE, Diamandis EP, Zlotta AR, Bapat B (2012) Quantitative DNA methylation analysis of genes coding for Kallikrein-related peptidases 6 and 10 as biomarkers for prostate cancer. *Epigenetics* 1;7(9).
4. Warrington NM, Wu Y, Pennell CE, Marsh JA, Beilin LJ, Palmer LJ, Lye SJ, **Briollais L**. (2013) Modelling BMI trajectories in children for genetic association studies. *PLoS One* 8(1):e53897
5. Agim S, Esendal M, **Briollais L**, Uyan O, Meschian M, Mendoza Martinez LA, Ding Y, Basak N, Ozcelik H. (2013) Discovery, validation and characterization of ERBB4 and NGR1 haplotypes using data from three genome-wide association studies of schizophrenia. *PLoS One* 8(1):e53042.
6. Kron K, Trudel D, Pethe VV, Briollais L, Fleshner NE, van der Kwast TH, Bapat B. Altered DNA methylation landscapes of polycomb-repressed loci are associated with Gleason score and ERG oncogene expression in prostate cancer. *Clin Cancer Res*. 2013; 19(13):3450-61.
7. Choi YH, **Briollais L**, Parfrey P, Green J, Kopciuk K. Estimating successive cancer risk in Lynch Syndrome families using a progressive three-state model. *Statistics in Medicine*, 2013; 33: 618-38. doi: 10.1002/sim.5938.
8. Warrington NM, Howe L, Wu YY, Timpson NJ, Tilling K, Pennell CE, Newnham J, Davey-Smith G, Palmer LJ, Beilin LJ, Lye S, Lawlor DA, **Briollais L**. Association of a Body Mass Index Genetic Risk Score with Growth throughout Childhood and Adolescence. *PLoS ONE* 2013; 8(11): e79547.
9. Howe LD, Parmar PG, Paternoster L, Warrington NM, Kemp JP, **Briollais L**, Newnham JP, Timpson NJ, Smith GD, Ring SM, Evans DM, Tilling K, Pennell CE, Beilin LJ, Palmer LJ, Lawlor DA. Genetic influences on trajectories of systolic blood pressure across childhood and adolescence. *Circ Cardiovasc Genet* 2013; 6(6): 608-14.
10. Abarin T, Li H, Wang L, **Briollais L** (2014) On Method of Moments Estimation in Linear Mixed Effects Models with Measurement Error on Covariates and Response with Application to Longitudinal studies of Gene-Environment Interaction. *Statistics in Biosciences* 6:1-18. doi:10.1007/s12561-012-9074-5.
11. Wu YY, **Briollais L**. Association of a Body Mass Index Genetic Risk Score with Growth throughout Childhood and Adolescence. *BMC proceedings* 2014; 8 (Suppl 1): S92.
12. **Briollais L**, Durrieu G. Application of Quantile Regression to Recent Genetic and -omic Studies. *Human Genetics* 2014; 133(8): 951-66.
13. Anderson LN, **Briollais L**, Atkinson HC, Marsh JA, Xu J, Connor KL, Matthews SG, Pennell CE, Lye SJ. Investigation of genetic variants, birthweight and hypothalamic-pituitary-adrenal (HPA) axis function suggests a genetic variant in the SERPINA6 gene is associated with corticosteroid binding globulin among adolescents in the Western Australia Pregnancy Cohort (Raine) Study. *PLoS One*. 2014; 9(4):e92957.

14. Warrington NM, Tilling K, Howe L, Paternoster L, Pennell CE, Wu YY, **Briollais L**. Robustness of the linear mixed effects model to distribution assumptions and consequences for genome-wide association studies. *Statistical Applications in Genetics and Molecular Biology* 2014; 13(5):567-87. (SA). IF 1.055
15. Kang S, Savas S, Liu J, Ozcelik H, **Briollais L**. Inferring Gene Network from Candidate SNP Association Studies using Bayesian Graphical Model: Application to a Breast Cancer Case-Control Study from Ontario. *Human Heredity*, 2014; 78(3):140-152.
16. Louise S, **Briollais L**, Mori TA, Mattes E, McCaskie PA, Pennell CE, Palmer LJ and Beilin LJ. Monoamine oxidase a gene polymorphisms common to blood pressure and depression scores in Caucasian children. *J Genet Stud.* 2014; 2:2.
17. Grant RC, Selander I, Connor AA, Selvarajah S, Borgida A, Briollais L, Petersen GM, Lerner-Ellis J, Holter S, Gallinger S. Prevalence of germline mutations in cancer predisposition genes in patients with pancreatic cancer. *Gastroenterology* 2015; 148(3):556-64.
18. NM Warrington, LD Howe, L Paternoster, M Kaakinen, S Herrala, V Huikari, Y Wu, JP Kemp, NJ Timpson, B St. Pourcain, G Davey-Smith, M-R Jarvelin, CE Pennell, DM Evans, DA Lawlor, **L Briollais**, LJ Palmer. A Genome-Wide Association Study of Body-Mass-Index across Early Life. *Int J Epidemiol.* 2015; 44(2): 700-12.
19. Wu YY, Wong A, Monette G and **Briollais L**. Evaluation of Third-order Method for the Test of Variance Component in Linear Mixed Models. *Open Journal of Statistics* 2015; 5: 233-244.
20. White SW, Marsh JA, Lye SJ, **Briollais L**, Newnham JP, Pennell CE. Improving customized fetal biometry by longitudinal modelling. *J Matern Fetal Neonatal Med.* 2015; 4:1-7.
21. **Briollais L**, Dobra A, Liu J, Friedlander M, Ozcelik H, Massam H. A Bayesian graphical model for genome-wide association studies (GWAS). *Annals of Applied Statistics* 2016; 10(2): 786-811.
22. P.G. Parmar, H.R. Taal, N.J. Timpson, E. Thiering T. Lehtimäki, M Marinelli, P.A. Lind, G. Verwoert, V. Aalto, A.G. Uitterlinden, **L. Briollais**, et al. International GWAS Consortium Identifies Novel Genes Associated with Blood Pressure in Children and Adolescents. *Circulation: Cardiovascular Genetics* 2016; 9: 266-78.
23. Heng YJ, Pennell CE, McDonald SW, Vinturache AE, Xu J, Lee M, **Briollais L**, Lyon AW, Slater DM, Bocking AD, Dolan SM, Tough SC, Lye SJ. Gene Expression in Maternal Whole Blood Predicts Spontaneous Preterm Birth in Asymptomatic Women as Early as 18 Weeks of Gestation. *PLoS One*, 2016; 11(6): e0155191.
24. Choi YH, **Briollais L**, Win AK, Hopper J, Buchanan D, Jenkins M, Lakhali-Chaieb L. Modelling of Successive Cancer Risks in Lynch Syndrome Families in the presence of competing risks using Copulas. *Biometrics* 2017; 73(1): 271-282. doi: 10.1111/biom.12561.
25. **L. Briollais**, H. Ozcelik, M. Kwiatkowski, J. Xu, S. Savas, F. Recker, C. Kuk, S. Hanna, N. Fleshner, T. Juvet, M. Friedlander, H. Li, K. Chadwick, J. Trachtenberg, A. Toi, T. van der Kwast, B. Bapat, E.P. Diamandis, P.C. Boutros, A.R. Zlotta. Fine-mapping of the *Kallikrein* Region supports a role for the *Kallikrein* 6 region in Genetic Predisposition for Aggressive Prostate Cancer: Results from a Canadian Cohort and the Swiss arm of the European Randomized Study for Prostate Cancer Screening. *J Natl Cancer Inst.* 2017 Apr 1;109(4). doi: 10.1093/jnci/djw258.
26. Wu YY, Lye S, **Briollais L**. The Role of Early-Life Growth Development, *FTO* gene and Exclusive Breastfeeding on Child BMI trajectories. *International Journal of Epidemiology* 2017 46(5):1512-1522.
27. Zhang J, Shynlova O, Sabra S, Bang A, **Briollais L**, Lye SJ. Immunophenotyping and activation status of maternal peripheral blood leukocytes during pregnancy and labour, both term and preterm. *J Cell Mol Med.* 2017;21(10):2386-2402.
28. **Briollais L**, Bristow R, Boutros P, the PRATICAL consortium, Zlotta A. Comment to Correspondence Re: Germline Mutations in the *Kallikrein* 6 region and Predisposition for Aggressive Prostate Cancer. Published online *J Natl Cancer Inst.* 2017, 109:12.
29. Choi YC, Lakhali-Chaieb L, Krol A, Yu B, Buchanan D, Ahnen D, Le Marchand L, Newcomb PA, Win AK, Jenkins M, Lindor NM, **Briollais L**. Risks of colorectal cancer and cancer-related mortality in Familial Colorectal Cancer Type X and Lynch Syndrome families. *J Natl Cancer Inst.* 2018. doi: 10.1093/jnci/djy159.
30. Dimitromanolakis A, Xu J, Krol A, **Briollais L**. sim1000G: a user-friendly genetic variant simulator in R for unrelated individuals and family-based designs. *BMC Bioinformatics.* 2019 Jan 15;20(1):26.
31. Choi YH, **Briollais L**, He W, Kopciuk K. FamEvent: An R Package for Generating and Modeling Time-to-Event Data in Family Designs. Accepted *Journal of Statistical Software*, Dec. 2019.
32. Xu J, Xu W, **Briollais L**. A Novel Bayesian Region-Based Analysis for Next Generation Sequencing Data. Accepted *Biometrics*, Apr. 2020.
33. Choi YH, Jacqmin-Gadda H, Król A, Parfrey P, **Briollais L**, Rondeau V. Joint nested frailty models for clustered recurrent and terminal events: An application to colonoscopy screening visits and colorectal

- cancer risks in Lynch Syndrome families. *Stat Methods Med Res.*, Dec. 2019.
34. Rustand D, Briollais L, Tournigang C, Rondeau V. Two-part joint model for a longitudinal semicontinuous marker and a terminal event with application to metastatic colorectal cancer data. Accepted in *Biostatistics*, Feb 2020.
 35. Choi YH, Jung H, Tounkara F, Buys S, Daly M, John E, Hopper J, Andrulis I, Terry MB, Briollais L. A Competing Risks Model with Time Varying Covariates for Estimation of Breast Cancer Risks in BRCA1 Families. Submitted to *Biostatistics*, Jan 2020.
 36. Wang N, Massam H, Briollais L. The Birth-Death MCMC algorithm for mixed graphical model learning with application to genomic data integration. Submitted to *Annals of Applied Statistics*, Apr. 2020.
 37. Wu Y, Dennis CL, Lye S, Briollais L. Exclusive breastfeeding can attenuate body-mass-index increase among genetically susceptible children: a longitudinal study from the ALSPAC cohort. In revision for *PLoS Genetics*.

PUBLICATIONS (Submitted)

1. Nazeri Rad N, Choi YH, Kopciuk K, Green J, Parfrey P, Lawless J, and **Briollais L**. Multistate Models for Colorectal Cancer Screening Evaluation in Lynch Syndrome Families. Submitted to *Stat. Methods in Medical Research*, 2018.
2. Rustand D, Wu YY, Govinda Rajan S, Lye S, McGowan P, Matthews S, **Briollais L**. Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Trajectories. Submitted to *PNAS*, September 2018.
3. Krol A, Romanescu R, Bull SB, Gos G, Andrulis A, Rondeau A, Choi YH, Briollais L. Correlated frailty model for analysis of genetic association in family studies