

## **Laurent Briollais, Ph.D**

### **ACADEMIC DEGREES**

1990	National School of Statistics and Economic Administration (ENSAE), France	B.Sc.	Statistics/Economy
1994	University of Paris X1	M.Sc.	Biostatistics/Statistical Genetics
1998	University of Paris X1	Ph.D.	Biostatistics/Statistical Genetics

### **EMPLOYMENT**

2009-	Associate Professor (status-only) Dalla Lana School of Public Health Sciences (Biostatistics)
2000-2008	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)
- Collaborator to the Breast and Colon Family Cancer Registries (CCFR)

### **COMMITTEE MEMBERSHIPS**

- 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:

- 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
- 2015-2020 Development of Bayesian Graphical Models for Next-Generation Genetic Studies  
Investigators: **Briollais L** (PI)  
NSERC, Discovery grant competition  
\$55,000
- 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
- 20012-2015 Exploring the Complexity of Pediatric Brain Tumors with Advanced Genomics and Novel Statistical Methods  
Investigators: **Briollais L** (PI),  
\$75,000  
McLaughlin Centre of University of Toronto

### As Co-Investigator:

- 2016-2021 Lipidomics: A Novel Tool to Define Human Placental Development and Function Across Pregnancy  
Role: Co-Applicant (PI: I. Caniggia)  
National Institute of Health  
RFA-HD-16-036 Using Omics to Define Human Placental Development and Function Across Pregnancy (R01) grant  
Awarded
- 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
- 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

#### **COMPLETED GRANTS (within past 5 years)**

##### **As PI or Co-PI:**

2010-2013 Semen Proteomics to Identify Novel Prostate Cancer Biomarkers.  
Jarvis (PI), **Briollais L** et al.  
\$413,853  
Canadian Cancer Society Research Institute

2011-2012 Proof of Principle: Novel semen biomarkers to identify sperm production in men with infertility: A non-invasive method to characterize men with azoospermia or no sperm in the semen, into those with and without testicular sperm production  
Jarvis (PI), **Briollais L** et al.  
\$152,499  
CIHR

2009-2013 A Graphical Modelling Framework to Study Complex Dependence Patterns in High-Dimensional Biological.  
**Briollais L** (PI), Massam H, Dobra A, Bader G, Ozcelik H.  
\$110,000  
MITACS

2009-2013 Genetic, Epigenetic and Proteomic Analysis of the Kallikrein Family in Search for Novel Diagnostic, Prognostic and Risk Susceptibility Algorithms for Prostate Cancer  
Diamandis (PI), **Briollais L**, Bapat B, Zlotta A, Ozcelik H, Van der Kwast T  
\$599,728  
Canadian Institutes of Health Research

2009-2013 A proteomic and genetic biomarker panel for improving Prostate Specific Antigen performance and identify individuals at risk of prostate cancer using a unique patient population accrued in the European Randomized Study for Prostate Cancer Screening.  
Zlotta A (PI), **Briollais L**, Bapat B, Diamandis D, Ozcelik H, Van der Kwast T  
\$631,232  
OICR

2007-2012 Determinants of Inflammatory Arthritis.  
Dr. Siminovitch (PI), **Briollais L** et al.  
Canadian Institutes of Health Research  
\$1,100,000

- 2006-2011 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
- 2008-2011 SNP-profiles of DNA repair genes discriminate breast cancer risk in the population  
Investigators: Ozcelik H (PI), Briollais L.  
\$447,953  
Canadian Breast Cancer Foundation-Ontario Chapter
- 2006-2011 Interdisciplinary research on the determinants and impact of colorectal cancer: molecular-genetic factors, risk modifiers and population health  
Investigators: McLaughlin J (PI), Briollais L et al.  
\$340,000 (for the statistical component)  
CIHR team grant

### GRANTS APPLIED FOR

- 2016-2018 Examining selection for resistant clones following neo-adjuvant chemotherapy in high-grade serous ovarian cancers.  
Applicants: May T (PI), Briollais L, Brown T, Amit O, Tone A, Virtanen C  
Requested: \$99,996.  
DOD Ovarian Cancer Research Program Pilot Award (W81XWH-16-OCRP-PA)
- 2016-2017 Genetic Determinism of Interval Prostate Cancers.  
Applicants: Briollais L (PI), Zlotta A, Boutros P, Bristow R.  
Collaborators: Kwiatkowski M, Rekker F.  
Requested: \$200,000.  
CCSRI Innovation grant.

### PUBLICATIONS (LAST 5 YEARS)

1. Hasan T, Choi Y, Briollais L (2011) A Sequential Approach for Clustered Survival Data in Family Studies Based on a Weighted Log-Rank Statistic. *Journal of Applied Statistical Science* 18: 1-16.
2. Choi YH, Briollais L (2011) An EM Composite likelihood for multistage sampling of family data. *Statistica Sinica* 21: 231-253.
3. Sow M, Durrieu G, Briollais L, Ciret P, Massabuau JC (2011) Modeling high-frequency serial valvometry data: A kernel-regression approach. *Environmental Monitoring and Assessment* 182(1-4):155-70.
4. Liu L, Kron KJ, Pethe VV, Demetrashvili N, Nesbitt ME, Trachtenberg J, Ozcelik H, Fleshner NE, Briollais L, van der Kwast TH, Bapat B (2011) Association of tissue promoter methylation levels of APC, TGFb2, HOXD3, and RASSF1A with prostate cancer progression. *Int J Cancer* 129(10): 2454-62.
5. Sovio U, Mook-Kanamori DO, Warrington NM, Lawrence R, Briollais L, Palmer CN, Cecil J, Sandling JK, SyvŁnen AC, Kaakinen M, Beilin LJ, Millwood IY, Bennett AJ, Laitinen J, Pouta A, Molitor J, Davey Smith G, Ben-Shlomo Y, Jaddoe VW, Palmer LJ, Pennell CE, Cole TJ, McCarthy MI, JŁrvelin MR, Timpson NJ; Early Growth Genetics Consortium (2011) Association between common variation at FTO locus and changes in body mass index from birth to adolescence: Longitudinal analysis of over 19,000 children of European ancestry. *PLOS Genetics* 7(2):e1001307.
6. Savas S, Azorsa DO, Jarjanazi H, Ibrahim-Zada I, Gonzales IM, Arora S, Henderson MC, Choi YH, Briollais L, Ozcelik H, Tuzmen S (2011) NCI60 cancer cell line panel data and RNAi analysis help identify EAF2 as a modulator of simvastatin and lovastatin response in HCT-116 cells. *PLoS One*

- 6(4):e18306.
7. Tram E, Ibrahim-Zada I, Briollais L, Knight JA, Andrulis IL, Ozcelik H (2011) Identification of germline alterations of the mad homology 2 domain of SMAD3 and SMAD4 from the Ontario site of the breast cancer family registry (CFR). *Breast Cancer Res.* 11; 13(4):R77.
  8. Islam M, Chowdhury R, Briollais L. (2012) A bivariate binary model for testing dependence in outcomes. *Bulletin of the Malaysian Mathematical Society* 35(4) (2012), 845-858.
  9. R. Chowdhury, M. Islam, S. Huda and L. Briollais (2012) Parameter Estimation in Logistic Regression for Transition, Reverse Transition and Repeated Transition from Repeated Outcomes. *J Applied Mathematics*, Vol. 3 No. 11A, 2012, pp. 1739-1749. doi: 10.4236/am.2012.331240.
  10. Louise S, Warrington NM, McCaskie PA, Oddy WH, Zubrick SR, Hands B, Mori TA, Briollais L, Silburn S, Palmer LJ, Mattes E, Beilin LJ. (2012) Associations between aggressive behaviour scores and cardiovascular risk factors in childhood. *Pediatr Obes.* 7(4):319-28.
  11. Fehringer G, Liu G, Briollais L, Brennan P, Amos C, Spitz M, Bickeb ller H, Wichmann HE, Risch A, Hung R (2012) Comparison of pathway analysis approaches using lung cancer GWAS data sets. *PLoS One*, 7(2): e31816.
  12. Louise S, Warrington NM, McCaskie PA, Oddy WH, Zubrick SR, Hands B, Mori TA, Briollais L, Silburn S, Palmer LJ, Mattes E, Beilin LJ (2012) Associations between anxious-depressed symptoms and cardiovascular risk factors in a longitudinal childhood study. *Prev. Med.* 54(5):345-50.
  13. Marsh JA, Pennell CE, Warrington NM, Mook-Kanamori D, Briollais L, Lye SJ, Beilin LJ, Steegers E, Hofman A, Jaddoe VWV, Newnham JP and Palmer LJ (2012). Fat mass and obesity-associated obesity-risk genotype is associated with lower foetal growth: an effect that is reversed in the offspring of smoking mother. *Journal of Developmental Origins of Health and Disease* 3:10-20.
  14. 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. (SA). IF 9.197
  15. 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.
  16. 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).
  17. 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.
  18. 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.
  19. 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.
  20. 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.
  21. 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.
  22. 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.
  23. 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.
  24. 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.
25. Briollais L, Durrieu G. Application of Quantile Regression to Recent Genetic and -omic Studies. *Human Genetics* 2014; 133(8): 951-66.
  26. 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.
  27. 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
  28. 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.
  29. Wu YY, Briollais L. Mixed-effects models for joint modeling of sequence data in longitudinal studies. *BMC Proc.* 2014 Jun 17;8(Suppl 1):S92.
  30. 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.
  31. Grant RC, Selander I, Connor AA, Selvarajah S, Borgida A, Briollais L, Petersen GM, Lerner-Ellis J, Holter S, Gallinger S. Germline mutations in 13 genes in pancreatic cancer. *Gastroenterology*. 2015 Mar;148(3):556-64.
  32. 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.
  33. 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.
  34. 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.
  35. 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
  36. 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(3): 266-78.
  37. 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*, *PLoS One*. 2016; 11(6): 0155191.
  38. Choi YH, Briollais L, Lakhal-Chaieb L. Modelling of Successive Cancer Risks in Lynch Syndrome Families in the presence of competing risks using Copulas. *Biometrics* 2016. doi: 10.1111/biom.12561.
  39. 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. Accepted in *JNCI*, Oct. 2016.

## **PUBLICATIONS (Submitted)**

40. 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*.

41. 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 *Statistics in Medicine*.

## BOOK CHAPTERS

- Dobra, A., Briollais, L., Jarnazi H, Ozcelik H, Massam H. Applications of the mode oriented stochastic search (MOSS) algorithm for discrete multi-way data to genomewide studies. In Bayesian Modeling in Bioinformatics Taylor & Francis, D. Dey, S. Ghosh and B. Mallick (eds.), 2011, pages 63-94.
- Briollais L and Durrieu G. Quantile regression for genetic and genomic applications. In Handbook of quantile regression. Taylor & Francis, Koenker, Chernozhukov, He and Peng (eds.), 2016, In preparation.

## PROCEEDINGS

- Choi YH, Briollais L. Impact of competing risks on the risk estimation of multiple cancers in family studies. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Boston, Aug 2-7, 2014.
- Briollais L, Dobra A, Massam H. Detection of gene by gene and gene by environment interactions in genome-wide association studies (GWAS) through Bayesian graphical models. Proceeding of the Société Française de Statistique, 6p. Rennes, June 2-6, 2014.
- Briollais L, Choi YH. An EM Composite Likelihood Approach based on Frailty Model for Family Studies of Unknown Genetic Factors with Incomplete Genetic Data. Proceeding of the Société Française de Statistique, 6p. Toulouse, May 27-31, 2013.
- Briollais L, Choi YH, Yildaz Y. Multistate models for the evaluation of screening interventions in family designs. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Montreal, Aug 3-8, 2013.
- Choi Y-H, Briollais L. A frailty-model-based approach to estimating the age-dependent penetrance function of a gene mutation using family-based study designs. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Vancouver, Jul 31-Aug 5, 2010.
- M Sow, G Durrieu, L Briollais. A robust statistical framework for eQTL analysis. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Vancouver, Jul 31-Aug 5, 2010.
- Liu J, Briollais L, Dobra A, Massam H. Impact of informative prior in discrete Bayesian graphical models: application to genome-wide association studies. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Washington D.C., Aug 1-8, 2009.

## SOFTWARES

- R package GenMOSS implementing Bayesian graphical models for GWAS analysis.
- R package GenMOSSplus implementing Bayesian graphical models for GWAS analysis and various preprocessing steps for GWAS.
- R package FamEvent to generate family data for diseases with variable age at onset.

## PRESENTATIONS (last 5 years)

**(I=International; N=National; L=Local)**

*Note: Only my own presentations are included here. Students' and collaborators' presentations where I was involved are not given.*

### **Invited**

- Quantile regression for genetic and genomic applications. International workshop on quantile regressions. Cambridge, December 2015. **(I)**
- Bayesian graphical models for gene network analysis in large-scale problems. Canadian Statistical Association Annual Meeting, Halifax, Canada, June 2015 **(N)**
- Evaluation of screening efficiency with colonoscopy in Lynch Syndrome families. Colon CFR. Complex disease epidemiology discussion group. Toronto, Canada, April 2015. **(L)**
- Modeling health trajectories and impact on prevention programs. Big Data for Health Workshop. Toronto, July 2014. **(L)**
- Detection of gene by gene and gene by environment interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Banff International workshop, July 2014. **(I)**
- Statistical challenges in modeling time-to-event data in family studies. Lessons learned from the analysis of Lynch syndrome and breast cancer families. Statistical Society of Canada annual meeting, Toronto, June 2014. **(N)**
- Modeling health trajectories and impact on prevention programs. LTRI annual retreat. Orillia, Canada, May 2014. **(L)**
- Detection of SNP by SNP interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Journée de Statistiques, Société Française de Statistiques, Rennes, France, June 2014. **(I)**
- Predicting prostate cancer progression through gene network analysis of methylation data. Second Annual Canadian Human and Statistical Genetic meeting, Esterel, Quebec, April 2013. **(N)**
- Detection of SNP by SNP interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Dept. of Mathematics & Statistics, Laval University, Oct 2013. **(N)**
- Graphical Models in Genetic Association Studies. Dept. of Mathematics & Statistics, University of South Brittany, France (December 2013) **(I)**
- An EM Composite likelihood approach for family studies with incomplete genetic data. Workshop on Composite Likelihood Methods, Banff, Canada, April 2012. **(I)**
- A Bayesian Graphical Model for Genome-wide Association Studies (GWAS). Biostatistics Dept., McGill University. September 2011. **(N)**
- A General Statistical Framework for Genome-wide Association Studies (GWAS) Based on Bayesian Graphical Modeling. Statistics Dept., York University, Toronto, July 2011. **(L)**

### **Contributed**

- Evaluation of screening efficiency with colonoscopy and risk estimation of second cancers in Lynch Syndrome families. Colon CFR Steering Committee. Honolulu, Hawaii, June 2015. **(I)**
- Evaluation of screening efficiency with colonoscopy in Lynch Syndrome families. Colon CFR Steering Committee. Kauai, Hawaii, Oct 2014. **(I)**
- French Statistical Society, Toulouse, France, June 2013. **(I)**
- Multistate models for the evaluation of screening interventions in family designs. Joint Statistical Meeting, Montreal, Canada, August 2013. **(I)**
- Composite likelihood estimation in family studies with incomplete genetic data. International Symposium in Statistics (ISS) on Longitudinal Data Analysis Subject to Outliers, Measurement Errors, and/or Missing Values. St. John's, Canada, July 2012. **(N)**
- A General Statistical Framework for Genome-wide Association Studies (GWAS) Based on Bayesian Graphical Modeling. International Biometric Society, Bordeaux, France, April 2011. **(N)**
- Bayesian Graphical Models (BGMs) for Genetic Association Studies. Annual meeting of the Statistical Society of Canada (SSC), Acadia University, Wolfville, Canada, June 2011. **(I)**



## **Student Supervision Activities**

### ***Actual Students***

- Narges Nazeri Rad: 2<sup>nd</sup> year Postdoc; Development of multistate models for screening evaluation in Cancer families)
- Jingxiong Xu: 3<sup>rd</sup> year PhD student. Bayesian approaches for the analysis of complex genetic data
- Jingchun Pei (MSc practicum): Application of multistate models for PSA screening evaluation

### ***Past Students***

#### **Postdoc fellows**

- Yan Yan Wu (2011-2014). Currently Assistant Professor in the Department of Public Health Studies, University of Hawaii, USA.
- Taraneh Abarin (2009-2011). Currently Assistant Professor in the Department of Mathematics and Statistics at Memorial University, NL, Canada
- Jinnan Liu (2007-2009). Currently statistician in a private company (USA).
- Sohee Kang (2006-2008). Currently Assistant Professor in the Department of Statistics, University of Toronto Scarborough, ON, Canada.
- Yun-Hee Choi (2005-2008). Currently Associate Professor in the Department of Epidemiology and Biostatistics, Western Ontario, ON, Canada.
- Tariq Hasan (2005-2006). Currently Associate Professor in the Department of Mathematics and Statistics, University of New Brunswick, NB, Canada
- Wenqing He (2004). Currently Associate Professor in the Department of Statistical and Actuarial Science, Western University, ON, Canada
- Marcia Wang (2003-2005). Currently statistician in a pharmaceutical company (USA).

#### **PhD students**

- Nicole Warrington (2011-2014). University of Western Australia (Co-supervisor). Currently postdoctoral student at the University of Queensland Diamantina Institute.
- Priya Parmar (2012-2015). University of Western Australia (Co-supervisor). Currently lecturer at Auckland University of Technology.
- Mohamedou Sow (2007-2011). University Bordeaux 1 (Co-supervisor). Currently research associate at CNRS, Bordeaux, France.

#### **MSc and undergraduate students**

- Yuan Sun (2015). Undergraduate student, University of Toronto (Statistics). Supervised research project.
- Rosita Bajari (2014). MSc student, Ryerson University (Computer Science). Supervised research project.
- Ely Fish (2013). Undergraduate student, University of Toronto. Supervised research project.
- Razvan Romanescu (2012) MSc student, University of Toronto (Statistics). Supervised research project.
- Vanessa Lestang (2011) MSc student, University Bordeaux 2 (ISPED). Supervised Master I project.
- Mathieu Raimbault (2010). MSc student, University Bordeaux 2 (ISPED). Supervised Master I project.
- Nino Demetrashvili (2008-2009). MSc student, University of Toronto (Biostatistics). Supervised research project.
- Aditya Sagar (2008). Undergraduate student, Indian Institute of Technology. Supervised research project.
- Elena Parkhomenko (2004). MSc student, University of Toronto (Biostatistics). Supervised lab course.
- Yana Tcharaktchiev (2003). Undergraduate student, University of Waterloo (Computer Science). Supervised research project.