Curriculum Vitæ

Sahir Rai Bhatnagar

April 20, 2016

1 Identification

Name: Sahir Rai Bhatnagar

Designations: Associate of the Society of Actuaries (ASA)
Address: Lady Davis Institute for Medical Research

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Citizenship: Canadian

Languages: English, French, Hindi

2 Education

2013–present | Ph.D. (Biostatistics)

McGill University, Montreal QC, Canada

Passed Theoretical Comprehensive Exam, May 2014) Passed Applied Comprehensive Exam, May 2015) McGill Graduate Excellence Award \$18,000

2012–2013 | Master of Science (Biostatistics)

Queen's University, Kingston ON, Canada

MSc project title: Absolute risk estimation in a case cohort study of prostate cancer

MSc Queen's Graduate Studies Award \$20,000

(GPA 3.94/4.3)

2005–2008 Bachelor of Science (Actuarial Mathematics)

Concordia University, Montreal QC, Canada

3 Professional Examinations

2011 | Associate of the Society of Actuaries (ASA)

4 Experience

2015— Statistical Consultant

Research Assistant, McGill University
Working with Dr. Andrea Benedetti in the Respiratory Epidemiology and Clinical Research Unit at McGill, where our research is focused on methods for correlated data, as well as developing an R package for the clustering of DNA fingerprint data

2008–2012 Actuarial Analyst, Aon Hewitt
Preparation and verification of annual reports, financial reports, annual statements, valuation reports, budget projections, and pension costs for clients balance sheets. Responsible for translation of pension plan status to clients

5 Teaching

5.1 Teaching Assistant

2014 Teaching Assistant, McGill University
Inferential Statistics (EPIB 607)

2012–2013 Teaching Assistant, Queen's University
Tutorial leader in calculus (MATH 121)
Term and exam marker for numerical methods and actuarial mathematics

5.2 Short courses and Tutorials

Bhatnagar SR: Loops and Simulations in R. Department of Epidemiology, Biostatistics and Occupational Health, McGill University. Sponsored by Epidemiology, Biostatistics and Occupational Health Student Society (EBOSS).
Bhatnagar SR: Atelier sur le logiciel en R: Un introduction à la programmation en R. GERAD: Groupe d'études et de recherche en analyse, Université de Montréal. Sponsored by HEC Montréal.
Bhatnagar SR: Reproducible Research: An introduction to knitr. Department of Epidemiology, Biostatistics and Occupational Health, McGill University. Sponsored by the CRM Statistics Laboratory and the Montreal Biostatistics Seminar Series.
Bhatnagar SR: Introduction to LATEX. Queen's University, Department of Mathematics and Statistics.

6 Other Contributions

6.1 Administrative Responsibilities and Committees

2015 – International Genetic Epidemiology Society Communications Committee Member 2014–2015 – Post-Graduate Students' Society (PGSS) Councillor

6.2 Professional Associations

2011- Society of Actuaries
 2013- Statistical Society of Canada
 2016- International Genetic Epidemiology Society

6.3 Volunteer Service

2010-Present | Math Teacher, Aditya Youth Trust Fund

Teaching mathematics to a group of elementary and high school students who are financially under resourced. Motivate and inspire students to place a high value on education while promoting wholesome social involvement, and to encourage them to achieve their maximum potential

2011–2013 MAB - Mackay Rehabilitation Center

Working with elderly patients diagnosed with Retinitis Pigmentosa. Accompaniment to perform everyday tasks that would be difficult to do independently such as grocery shopping, banking transactions, and outdoor activities

7 Publications

7.1 Published/In Press

- 1. Wang Y, Murphy O, Turgeon M, Wang ZY, Bhatnagar SR, Schulz J, and Moodie EEM (2015) The perils of Quasi-likelihood Information Criteria. Stat. Feb 1;4(1):246-54.
- 2. Sun J., <u>Bhatnagar SR</u>, Oualkacha K, Ciampi A, Greenwood CMT (2015) Joint analysis of multiple blood pressure phenotypes in GAW19 data by using a multivariate rare-variant association test. Accepted in *BMC Genetics*.
- 3. Bhatnagar SR, Greenwood CMT, Labbe A (2015) Assessing transmission ratio distortion in extended families: a comparison of analysis methods. Accepted in *BMC Genetics*.
- 4. Bhatnagar SR, Atherton J, Benedetti A (2015). Comparing alternating logistic regressions to other approaches to modelling correlated binary data. *Journal of Statistical Computation and Simulation*. Jul 3;85(10):2059-71.

7.2 Submitted

1. Klein Oros K, Oualkacha K, Lafond M, <u>Bhatnagar SR</u>, Tonin PN, Greenwood CMT (2016). Gene coexpression analyses differentiate networks associated with diverse cancers harbouring TP53 missense or null mutations. Submitted (2016/04).

8 Presentations

8.1 Invited conference presentations

2016/07/10	Bhatnagar SR*, Yang Y, Blanchette M, Greenwood CMT: Strong Heredity Models in High Dimensional Data. 28th International Biometrics Conference, Victoria, Canada.
2016/04/18	Bhatnagar SR*, Yang Y, Blanchette M, Greenwood CMT: A Model for Interpretable High-Dimensional Interactions. 5th Annual Canadian Human and Statistical Genetics Meeting, Halifax, Canada.
2015/04/19	Bhatnagar SR*, Houde A, Voisin G, Bouchard L, Blanchette M, Greenwood CMT: DNA methylation and Expression to predict childhood obesity. 4th Annual Canadian Human and Statistical Genetics Meeting, Vancouver, Canada.

^{*} indicates the person that gave the presentation

8.2 Poster Presentations

2016/05/12	Hull M*, Bhatnagar SR, Moodie EEM, Klein M: Trends in causes of mortality in the Canadian Co-infection cohort (CCC) 2005 2015. 25th Annual Canadian Conference on HIV/AIDS Research, Winnipeg, Canada.
2016/04/17	Bhatnagar SR*, Yang Y, Blanchette M, Greenwood CMT: A Model for Interpretable High Dimensional Interactions. 5th Annual Canadian Human and Statistical Genetics Meeting, Halifax, Canada.
2015/04/19	Bhatnagar SR*, Houde A, Voisin G, Bouchard L, Blanchette M, Greenwood CMT: Integrating DNA Methylation and Gene Expression data in Placenta Tissue to Predict Childhood Obesity. 4th Annual Canadian Human and Statistical Genetics Meeting, Vancouver, Canada. \$1,000 Award for Best Poster
2014/08/24	Bhatnagar SR*, Greenwood CMT, Labbe A: Transmission Ratio Distorition in Extended Families. Genetic Analysis Workshop 19, Vienna, Austria.
2014/08/25	Sun J, Bhatnagar SR*, Oualkacha K, Ciampi A, Greenwood CMT: Joint analysis of multiple blood pressure phenotypes in GAW19 data by using a multivariate rare-variant association test. Genetic Analysis Workshop 19, Vienna, Austria.
2014/05/26	Bhatnagar SR*, McGregor K*, Turgeon M*: Effect of economy on TV time use. 42nd Annual Meeting of the Statistical Society of Canada, Toronto, Ontario.

8.3 Seminar Presentations

2015/08/12	Bhatnagar SR: Introduction to knitr and R Markdown. Montréal UseR Group, Notman House, Montréal.
2015/03/12	Bhatnagar SR: Imputing the Epigenome. Lady Davis Institute, Montreal Jewish General Hospital.
2015/03/05	Bhatnagar SR: Making sense of Methylation & Expression data in Cordblood and Placenta Tissues. Lady Davis Institute, Montreal Jewish General Hospital.
2014/04/07	Bhatnagar SR: Estimation and Accuracy after Model Selection by Bradley Efron. Department of Mathematics and Statistics, McGill University.
2014/01/23	Bhatnagar SR: Reproducible Research and Biostatistics. Biostatistics Reading Group, McGill University.
2014/08/07	Bhatnagar SR*, Greenwood CMT, Labbe A: Transmission Ratio Distortion in Extended Families. Lady Davis Institute, Montreal Jewish General Hospital.
2013/08/30	Bhatnagar SR: Absolute Risk Estimation in a Case Cohort Study of Prostate Cancer. Department of Mathematics and Statistics, Queen's University.
2013/03/06	Bhatnagar SR: Colorectal Cancer Screening in Visible Minorities in Canada. Department of Public Health Sciences, Queen's University.
2012/11/27	Bhatnagar SR: Computational Methods for the Case-Cohort Design. Department of Public Health Sciences, Queen's University.

9 Software

9.1 R Packages

acm4r | http://cran.r-project.org/web/packages/acm4r/index.html

Fragment lengths or molecular weights from pairs of lanes are compared, and a number of matching bands are calculated using the Align-and-Count Method.

eclust http://sahirbhatnagar.com/eclust/

A Statistical Software Tool for the Analysis of High-Dimensional Interactions. It's main functionality is to fit statistical models for analyzing interactions between a high dimensional dataset (e.g. genomics, brain imaging), the environment and a response.

casebase http://sahirbhatnagar.com/casebase/

A statistical software tool to fit smooth-in-time parametric hazard functions using case-base sampling. This approach allows the explicit inclusion of the time variable into the model, which enables the user to fit a wide class of parametric hazard functions. For example, including time linearly recovers the Gompertz hazard, whereas including time logarithmically recovers the Weibull hazard; not including time at all corresponds to the exponential hazard. This is joint work with Maxime Turgeon, Olli Saarela and James Hanley.

10 Technical Skills

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SAS

IATEX

Microsoft Office suite

Unix/Linux operating system, Bash Shell Script

Git, GitHub

Jekyll, HTML