

Stephen B. Montgomery, last updated Feb 2014

## EDUCATION

### Doctorate of Philosophy, Genetics

*University of British Columbia, 2002-2006*

### Bachelor's of Applied Science, Engineering Physics

*University of British Columbia, 1997-2002*

## PROFESSIONAL EXPERIENCE

### Assistant Professor

July 2011 - present

*Stanford University School of Medicine, Stanford, California, USA*

Department of Pathology

Department of Genetics

Department of Computer Science, by courtesy

Director of Genome Informatics, Department of Pathology

### Senior Postdoctoral Researcher

September 2009 – Jun. 2011

*University of Geneva, Geneva, Switzerland*

### Postdoctoral Researcher

November 2006 – Aug. 2009

*Wellcome Trust Sanger Institute, Cambridge, United Kingdom*

### Ph.D. Graduate Student

September 2002 – Oct. 2006

*Canada's Michael Smith Genome Sciences Centre, Vancouver, Canada*

### Instructor

September 2002 – Oct. 2006

*Canadian Bioinformatics Workshops*

### Undergraduate Assistant

October 2001 – Apr. 2002

*PATSCAN – UBC Library Services, Vancouver, Canada*

### Undergraduate Assistant

September 2001 – Apr. 2002

*UBC Department of Forestry, Vancouver, Canada*

### Engineering Intern

May 2001 – Aug. 2001

*Department of National Defense, Ottawa, Canada*

### User Interface Session Management Engineering Intern

September 2001– Apr. 2001

*Raytheon Systems Canada Ltd., Richmond, Canada*

### Machines and Control Systems Research Assistant

May 2000 – Aug. 2000

*Laser Zentrum Hanover e.V., Hanover, Germany*

### Systems Integration and Test Engineering Intern

May 1999 – Apr. 2000

*Raytheon Systems Canada Ltd., Richmond, Canada*

### Software Configuration Management Engineering Intern

January 1999 – Apr. 1999

*Raytheon Systems Canada Ltd., Richmond, Canada*

## PUBLICATIONS

51. Nance, T., Smith, K.S., Anaya, V., Richardson, R. Ho, L., Pala, M., Mostafavi, S., Battle, A., Feghali-Bostwick, C., Rosen, G., Montgomery, S.B. (2014) **Transcriptome analysis reveals differential splicing events in IPF lung tissue**, *in press*
50. Miller, C.L., Assimes, T.L., Montgomery, S.B., Quertermous, T. (2014) **Investigation of causal genetic mechanisms for coronary heart disease genome-wide associations**, *in press*
49. Wu, E., Nance, T., Montgomery, S.B. (2014) **SplicePlot: a utility for visualizing splicing quantitative trait loci** *Bioinformatics*, epub Jan 12, 2014
48. Daneshjou, R.\* , Zappala, Z.\* , Kukurba, K., Boyle, S.M., Ormond, K.E., Klein, T.E., Snyder, M., Bustamante, C.D., Altman, R.B.@, Montgomery, S.B.@ (2014). **Path-scan: a reporting tool for identifying clinically actionable variants**. *Pac Symp Biocomput.* 2014;19:229-40. \*joint first-authors @joint corresponding authors
47. Zhang, R., Li, X., Ramaswami, G., Smith, K.S., Turecki, G., Montgomery, S.B.@, Li, J.B.@ (2014) **Quantifying RNA allelic ratios by multiplex PCR and sequencing** *Nature Methods*, Jan;11(1):51-4 @joint corresponding authors
46. Battle, A., Mostafavi, S., Zhu, X., Potash, J.B., Weismann, M.M., McCormick, C., Haudenschild, C.D., Beckman, K.B., Shi, J., Mei, R., Urban, A.E., Montgomery, S.B., Levinson, D.F., Koller, D. (2014) **Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals** *Genome Research*, Jan;24(1):14-24.
45. Karczewski, K.J., Montgomery, S.B. (2013) **The performance of genomic medicine** *Genome Biology*, 14:316
44. Morin, R. Montgomery, S.B. (2013) **Cancer Transcriptome Sequencing and Analysis (Chapter 5)** *Cancer Genomics: From Bench to Personalized Medicine*
43. Mostafavi, S., Battle, A., Zhu, X., Potash, J.B., Weissman, M.W., Shi, J., Beckman, K., Haudenschild, C., McCormick, C., Mei, R., Gamberoff, M.J., Gindes, H., Adams, P., Goes, F.S., Mondimore, F.M., MacKinnon, D., Notes, L., Schweizer, B., Furman, D., Montgomery, S.B., Urban, A.E., Koller, D., Levinson, D. (2013) **Type I interferon signaling genes in recurrent major depression: increased expression detected by whole-blood RNA sequencing**. *Molecular Psychiatry*, AOP Dec 3, 2013 [link](#)
42. Lappalainen, T., Sammeth, M., Freidlander, M.R., 't Hoen, P.A.C, Monlong, J., Ravis, M.A., Gonzalez-Porta, M., Kurbatova, N., Griebel, T., Ferreira, P.G., Barann, M., Wieland, T., Greger, L., van Iterson, M., Almlof, J., Ribeca, P., Pulyakhina, I., Esser, D., Giger, T., Tikhonov, A., Sultan, M., Bertier, G., MacArthur, D.G., Lek, M., Lizano, E., Buermans, H.P.J., Padioleau, I., Schwarzmayr, T., Karlberg, O., Ongen, H., Kilpinen, H., Beltran, S., Gut, M., Kahlem, K., Amstislavskiy, V., Stegle, O., Pirinen, M., Montgomery, S.B., Donnelly, P., McCarthy, M.I., Flicek, P., Strom, T.M., The Geuvadis Consortium, Lehrach, H., Schreiber, S., Sudbrak, R., Carracedo, A., Antonarakis, S.E., Hasler, R., Syvanen, A.C., van Ommen, G.J., Brazma, A., Meitinger, T., Rosentiel, P., Guigo, R., Gut, I.G., Estivill, X., Dermitzakis, E. T., (2013) **Transcriptome and genome sequencing uncovers functional variation in humans**. *Nature*, Advanced Online Access, September 15, 2013
41. Mostafavi, S., Battle, A., Zhu, X., Urban, A.E., Levinson, D., Montgomery, S.B., Koller, D. (2013) **Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge** *PLoS One*, July 8(7): e68141
40. Gutierrez-Arcelus, M., Lappalainen, T., Montgomery, S.B., Buil, A., Ongen, H., Yurovsky, A., Bryois, J., Giger, T., Romano, L., Planchon, A., Falconnet, E., Bielser, D., Gagnebin, M., Padioleau, I., Borel, C., Letourneau, A., Makrythanasis, O., Guipponi, M., Gehrig, C., Antonarakis, S.E., Dermitzakis, E.T. (2013) **Passive and active DNA methylation and the interplay with genetic variation in gene regulation** *eLIFE*, June, 4th

39. Karczewski, K.J., Dudley, J.T., Kukurba, K.R., Chen, R., Butte, A.J., Montgomery, S.B., Snyder, M (2013) **Systematic functional regulatory assessment of disease-associated variants** PNAS, (epub) May 20
38. Sweeney, R.T., Zhang, B., Zhu, S.X., Varma, S., Smith, K.S., Montgomery, S.B., van de Rijn, M., Zehnder, J., West, R.B. (2013) **Desktop transcriptome sequencing from archival tissue to identify clinically relevant translocations.** American Journal of Surgical Pathology, (epub) Apr 16
37. Li, X., Montgomery, S.B. (2013) **Detection and impact of rare regulatory variants in human disease** Frontiers in Statistical Genetics and Methodology
36. Montgomery, S.B.\*@, Goode, D.\*, Kvikstad, E.\*, Albers, C.A., Zhang, Z., Xinmeng, J.M., Ananda, G., Howie, B., Karczewski, K.J., Smith, K.S., Anaya, V., Richardson, R., Davis, J., The 1000 Genomes Pilot Project Consortium, MacArthur, D.G., Sidow, A., Duret, L., Gerstein, M., Makova, K.D., Marchini, J., McVean, G., Lunter, G.@ (2013) **The origin, evolution and impact of short insertion-deletion variants identified in 179 human genomes** Genome Research, online Advanced Access, 2013 Mar 11 \*joint first-authors @joint corresponding-authors
35. Conde, L., Bracci, P.M., Richardson, R., Montgomery, S.B.@, Skibola, C.F.@ (2013) **Integrating GWAS and expression data for functional characterization of disease-associated SNPs: an application to follicular lymphoma** American Journal of Human Genetics Jan 10;92(1):126-30. @joint corresponding authors
34. Granel, R., Henderson, A.J., Timpson, N., St Pourcain, B., Kemp, J.P., Ring, S.M., Ho, K., Montgomery, S.B., Dermitzakis, E.T., Evans, D.M., Sterne, J.A. (2013) **Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes** J Allergy Clin Immunology Mar;131(3):685-94
33. Dimas, A.S., Nica, A., Montgomery, S.B., Stranger, B.E., Raj, T., Buil, A., Giger, T., Lappalainen, T., Gutierrez-Arcelus, M., McCarthy, M., Dermitzakis, E.T. (2012) **Sex-biased genetic effects on gene regulation in humans** Genome Research December; 22(12): 2368–2375
32. Grundberg, E., Small, K.S., Hedman, A.K., Nica, A.C., Buil, A., Keildson, S., Bell, J.T., Yang, T.P., Meduri, E., Barrett, A., Nisbett, J., Sekowska, M., Wilk, A., Shin, S.Y., Glass, D., Travers, M., Min, J.L., Ring, S., Ho, K., Thorleifsson, G., Kong, A., Thorsteindottir, U., Ainali, C., Dimas, A.S., Hassanali, N., Ingle, C., Knowles, D., Krestyaninova, M., Lowe, C.E., Di Meglio, P., Montgomery, S.B., Parts, L., Potter, S., Surdulescu, G., Tsaprouni, L., Tsoka, S., Bataille, V., Durbin, R., Nestle, F.O., O'Rahilly, S., Soranzo, N., Lindgren, C.M., Zondervan, K.T., Ahmadi, K.R., Schadt, E.E., Stefansson, K., Smith, G.D., McCarthy, M.I., Deloukas, P., Dermitzakis, E.T., Spector, T.D.; The Multiple Tissue Human Expression Resource (MuTHER) Consortium. (2012) **Mapping cis- and trans-regulatory effects across multiple tissues in twins.** Nature Genetics Sep 2;44(10):1084-1089
31. Lefebvre, J.F., Vello, E., Ge, B., Montgomery, S.B., Dermitzakis, E.T., Pastinen, T., Labuda, D. (2012) **Genotype-Based Test in Mapping Cis-Regulatory Variants from Allele-Specific Expression Data** PLoS One 7(6): e38667
30. Stranger, B.E.\*, Montgomery, S.B.\*, Dimas, A.S.\*, Parts, L., Stegle, O., Ingle, C.E., Sekowska, M., Davey Smith, G., Evans, D., Gutierrez-Arcelus, M., Price, A., Raj, T., Nisbett, J., Nica, A.C., Beazley, C., Durbin, R., Deloukas, P., Dermitzakis, E.T. (2012) **Patterns of Cis Regulatory Variation in Diverse Human Populations.** PLoS Genetics. 8(4): e1002639 \*joint first authors.
29. MacArthur, D.G., Balasubramanian, S., Frankish, A., Huang, N., Morris, J., Walter, K., Jostins, L., Habegger, L., Pickrell, J.K., Montgomery, S.B., Albers, C.A., Zhang, Z., Conrad, D.F., Lunter, G., Zheng, H., Ayub, Q., DePristo, M.A., Banks, E., Hu, M., Handsaker, R.E., Rosenfeld, J., Fromer, M., Jin, M., Mu, X.K., Khurana, E., Ye, K., Kay, M., Saunders, G.I., Suner, M., Hunt, T., Barnes, I., Amid, C., Carvalho-Silva, D.R., Bignell, A.H., Snow, C., Yngvadottir, B., Bumpstead, S., Cooper, D.N., Xue, Y., Romero, I.G., 1000 Genomes Project Consortium, Wang, J., Li, Y., Gibbs, R.A., McCarroll, S.A., Dermitzakis, E.T., Pritchard, J.K., Barrett, J.C., Harrow, J., Hurler, M.E., Gerstein, M.B., Tyler-Smith, C. (2012) **A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes.** Science. 335 (6070), 823-828

28. Paternoster, L. et al. (2011) **Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis**. *Nature Genetics* doi:10.1038/ng.1017
27. Lappalainen, T., Montgomery, S.B., Nica, A., Dermitzakis, E.T. (2011) **Epistatic Selection between Coding and Regulatory Variation in Human Evolution and Disease**. *American Journal of Human Genetics*. Volume 89, Issue 3, 459-463, 9
26. Sharp, A.J., Stathaki, E., Migliavacca, E., Brahmachary M., Montgomery, S.B., Dupre, Y., Antonarakis, S.E. (2011) **DNA methylation profiles of human active and inactive X chromosomes**. *Genome Research*. Published in Advance August 23, 2011
25. Montgomery, S.B., Lappalainen, T., Gutierrez-Arcelus, M., Dermitzakis, E.T. (2011) **Rare and Common Regulatory Variation in Population-Scale Sequenced Human Genomes**. *PLoS Genetics* 7(7): e1002144.
24. Montgomery, S.B., Dermitzakis, E.T. (2011) **From Expression QTLs to Personalized Transcriptomics**. *Nature Reviews Genetics* March 9 (AOP)
23. Spurdle, A.B, Thompson, D.J., Ahmed, S., Ferguson, K., Healey, C.S., O'Mara, T., Walker, L.C., Montgomery, S.B., Dermitzakis, E.T., The Australian National Endometrial Cancer Study Group, Fahey, P., Montgomery, G.W., Webb, P.M., Fasching, P.A., Beckmann, M.W., Ekici, A.B., Hein, A., Lambrechts, D., Coenegrachts, L., Vergote, I., Amant, F., Salvesen, H.B., Trovik, J., Njolstad, T.S., Helland, H., Scott, R.J., Ashton, K., Proietto, T., Otton, G., National Study of Endometrial Cancer Genetics Group, Tomlinson, I., Gorman, M., Howarth, K., Hodgson, S., Garcia-Closas, M., Wentzensen, N., Yang, H., Chanock, S., Hall, P., Czene, K., Liu, J., Li, J., Shu, X.O., Zheng, W., Long, J., Xiang, Y.B., Shah, M., Morrison, J., Michailidou, K., Pharoah, P.D., Dunning, A.M., Easton, D.F. (2011) **Genome-wide association study identifies a common variant associated with risk of endometrial cancer**. *Nature Genetics* May;43(5):451-454
22. Nica, A.C., Parts, L., Glass, D., Nisbett, J., Barrett, A., Sekowska, M., Travers, M., Potter, S., Grundberg, E., Small, K., Hedma, A., Bataille, V., Bell, J.T., Surdulescu, G., Dimas, A.S., Ingle, C., Nestle, F.O., di Meglio, P., Min, J.L, Wilk, A., Hammond, C.J., Hassanali, N., Yang, T., Montgomery, S.B., O'Rahilly, S., Lindgren, C.M., Zondervan, K.T., Soranzo, N., Barroso, I., Durbin, R., Ahmadi, K., Deloukas, P., Dermitzakis, E.T., Spector, T.D. (2011) **The Architecture of Gene Regulatory Variation across Multiple Human Tissues: the MuTHER Study**. *PLoS Genetics* 7(2): e1002003
21. Borel, C., Deutsch, S., Letourneau, A., Migliavacca, E., Montgomery, S.B., Dimas, A.S., Vejnar, C.E., Attar, H., Gagnebin, M., Gehrig, C., Falconnet, E., Dupré, Y., Dermitzakis, E.T. and Antonarakis, S.E. (2011) **Identification of cis- and trans- regulatory variation modulating microRNA expression levels in human fibroblasts** *Genome Research* 21(1):68-73
20. 1000 Genomes Project Consortium, Durbin, R.M., Abecasis, G.R., Altshuler, D.L., Auton, A., Brooks, L.D., Durbin, R.M., Gibbs, R.A., Hurles, M.E., McVean, G.A. (2010) **A map of human genome variation from population-scale sequencing** *Nature* 467(7319):1061-73.
19. The International HapMap 3 Consortium (2010) **Integrating common and rare genetic variation in diverse human populations**. *Nature* 467(7311):52-58.
18. Yang, T.P., Beazley, C., Montgomery, S.B., Dimas, A.S., Gutierrez-Arcelus, M., Stranger, B.E., Deloukas, P., Dermitzakis, E.T., (2010) **Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies**. *Bioinformatics* 26(19):2474-6
17. Nica, A.C., Montgomery, S.B., Dimas, A.S., Stranger, B.E., Beazley, C., Barroso, I., Dermitzakis, E.T., (2010) **Candidate causal regulatory effects by integration of expression QTLs with complex trait genetic associations**. *PLoS Genetics* 6(4): e1000895. doi:10.1371/journal.pgen.1000895
16. Ning, Z., Montgomery, S.B., (2010) **Out of the sequencer and into the wiki as we face new challenges in genome informatics**. *Genome Biology* 11:308

15. Montgomery, S.B., Sammeth, M., Gutierrez-Arcelus, M., Lach, R.P., Ingle, C., Nisbett, J., Guigo, R., Dermitzakis, E.T. (2010) **Transcriptome genetics using second generation sequencing in a Caucasian population.** Nature 464(7289):773-7
14. Montgomery, S.B., Kasaian, K., Jones, S.J.M., Griffith, O.L. (2010) **Annotating the Regulatory Genome (Chapter 20).** Computational Biology of Transcription Factor Binding. Methods Mol Biol. 2010;674:313-49.
13. Southam, L., Soranzo, N., Montgomery, S.B., Frayling, T.M., McCarthy, M.I., Barroso, I., Zeggini, E. (2009) **Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants?** Diabetologia. 52(9) :1846-51
12. Dimas, A.S.\* , Deutsch, S.\* , Stranger, B.E.\* , Montgomery, S.B.\* , Borel, C., Attar-Cohen, H., Ingle, C., Beazley, C., Gutierrez-Arcelus, M., Sekowska, M., Gagnebin, M., Nisbett, J., Deloukas, P., Dermitzakis, E.T., Antonarakis, S.E. (2009) **Common regulatory variation impacts gene expression in a tissue-dependent manner.** Science 325(5945) :1246-50 \*joint first authors.
11. Montgomery, S.B., Dermitzakis, E.T. (2009) **The resolution of the genetics of gene expression.** Human Molecular Genetics R(2):R211-5
10. Montgomery S.B. (2009) **Current computational methods for prioritizing candidate regulatory polymorphisms.** Methods in Molecular Medicine. Humana Press. 569 :89-114
9. Aerts, S., Haeussler, M., van Vooren, S., Griffith, O.L., Hulpiau, P., Jones, S.J.M., Montgomery, S.B., Bergman, C.M., The Open Regulatory Annotation Consortium (2008) **Text-mining assisted regulatory annotation.** Genome Biology. 9:R31
8. Griffith, O.L.\* , Montgomery, S.B.\* , Bernier, B., Chu, B., Aerts, S., Sleumer, M.C., Bilenky, M., Haeussler, M., Griffith, M., Gallo, S.M., Giardine, B., Mahony, S., Hooghe, S., Van Loo, P., Blanco, E., Ticoll, A., Lithwick, S., Portales-Casamar, E., Donaldson, I.J., Robertson, A.G., Wadelius, C., De Bleser, P., Vlieghe, D., Halfon, M.S., Wasserman, W.W., Hardison, R., Bergman, C.M., Jones, S.J.M. The Open Regulatory Annotation Consortium (2008) **OREgAnno: an open-access community-driven resource for regulatory annotation.** Nucleic Acids Research. Nov. 15th \*joint first authors.
7. Stranger, B.E., Nica, A.C., Forrest, M.S., Dimas, A., Bird, C.P., Beazley, C., Ingle, C.E., Dunning, M., Flicek, P., Koller, D., Montgomery, S.B., Tavare, S., Deloukas, P. and Dermitzakis, E.T. (2007) **Population genomics of human gene expression.** Nature Genetics. 39(10):1217-24
6. Montgomery, S.B., Griffith, O.L., Scheutz, J.M., Brooks-Wilson, A., Jones, S.J. (2007) **A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms.** PLoS Computational Biology 8;3(6):e106
5. Montgomery, S.B.\* , Griffith, O.L.\* , Sleumer, M.C., Bergman, C.M., Bilenky, M., Pleasance, E.D., Prychyna, Y., Zhang, X., Jones, S.J. (2006) **OREgAnno: an open access database and curation system for literature-derived promoters, transcription factor binding sites and regulatory variation.** Bioinformatics 1;22(5):637-50 \*joint first authors
4. Robertson, A.G., Bilenky, M., Lin, K., He, A., Yuen, W., Dagginar, M., Varhol, R., Teague, K., Griffith, O.L., Zhang, X., Pan, Y., Hassel, M., Sleumer, M.C., Pan, W., Pleasance, E.D., Chuang, M., Hao H., Li, Y.Y., Robertson, N., Fjell, C., Li, B., Montgomery, S.B., Astakhova, T., Zhou, J., Sander, J., Siddiqui, A.S. and Jones, S.J. (2006) **cisRED: A database system for genome scale computational discovery of regulatory elements.** Nucleic Acids Research 1;34 (Database issue):D68-73.
3. Montgomery, S.B., Fu, T., Guan, J., Lin, K., Jones, S.J.M., (2005) **An application of peer-to-peer technology to the discovery, use and assessment of bioinformatics programs.** Nature Methods 2(8):563

2. Montgomery, S.B., Astakhova, T., Bilenky, M., Birney, E., Fu, T., Hassel, M., Melsopp, C., Rak, M., Robertson, A.G., Sleumer, M.C., Siddiqui, A.S., and Jones, S.J. (2004) **Sockeye: A 3D Environment for Comparative Genomics**. *Genome Research* 14:956-962 (Sockeye featured on the cover of Linux Journal)

1. Marra, M.A., Jones, S.J., Astell, C.R., Holt, R.A., Brooks-Wilson, A., Butterfield, Y.S., Khattra, J., Asano, J.K., Barber, S.A., Chan, S.Y., Cloutier, A., Coughlin, S.M., Freeman, D., Girn, N., Griffith, O.L., Leach, S.R., Mayo, M., McDonald, H., Montgomery, S.B., Pandoh, P.K., Petrescu, A.S., Robertson, A.G., Schein, J.E., Siddiqui, A.S., Smailus, D.E., Stott, J.M., Yang, G.S., Plummer, F., Andonov, A., Artsob, H., Bastien, N., Bernard, K., Booth, T.F., Bowness, D., Czub, M., Drebot, M., Fernando, L., Flick, R., Garbutt, M., Gray, M., Grolla, A., Jones, S., Feldmann, H., Meyers, A., Kabani, A., Li, Y., Normand, S., Stroher, U., Tipples, G.A., Tyler, S., Vogrig, R., Ward, D., Watson, B., Brunham, R.C., Krajden, M., Petric, M., Skowronski, D.M., Upton, C., Roper, R.L. (2003) **The Genome sequence of the SARS associated coronavirus**. *Science* 300(5624):1399-404

## AWARDS AND SPECIAL RECOGNITION

- 2011 Genome Technology Magazine Rising PI (December 2011 issue)
- 2010 A-Star New Investigator Award (not accepted)
- NSERC (Natural Sciences and Engineering Research Council) postdoctoral fellowship.
- NSERC UK Millennium Research Award.
- EMBO (European Molecular Biology Organization) Long-term postdoctoral fellowship.
- Co-PI on Genome BC funding for "The Regcreative Workshop" in Ghent, Belgium.
- Co-PI on Genome Canada funding for "The Regcreative Workshop" in Ghent, Belgium.
- BC Cancer Agency Lloyd Skarsgard Research Excellence Prize (awarded annually to single BC Cancer Agency graduate student)
- NSERC PGS-Doctoral Scholarship.
- Invited to attend "Encoding Information in DNA Sequences" conference in Okinawa, Japan (40 students of 400 selected)
- BCNET Best Overall winner for Chinook project.
- MSFHR (Michael Smith Foundation for Health Research) Senior Studentship Award.
- UBC PhD Tuition Fee Award.
- EBI Travel Grant for EnSEMBL Developers Day.

## PROFESSIONAL AND VOLUNTEER SERVICE

Journal Reviewer – Nature Genetics	2013
Journal Reviewer – Science	2013
NIH NIAID Study Section reviewer on Immunity in the Elderly	2013
NIH Study Section reviewer on Investigator initiated program projects	2013
NSERC Discovery Grant reviewer	2013
Genetics Graduate Student Admission committee	2012
Department Senator – Stanford School of Medicine	2011-2014
Genome Quebec – Grant reviewer	2012
Genetics Graduate Student Admission committee	2011
Associate Editor – BMC Genomics	2011
Journal reviewer – Human Molecular Genetics	2011
Journal reviewer – Human Mutation	2011
Journal reviewer – Human Genetics	2011
Journal reviewer – Database	2011
Journal reviewer – Molecular Systems Biology	2011
Journal reviewer – American Journal of Human Genetics	2010
Faculty of 1000 – Associate Member	2010
Journal reviewer – PLoS One	2010
Guest Editor – PLoS Genetics	2010
Journal reviewer – Genome Research	2010
Education outreach – STIMULUS Cambridge	2009
Journal reviewer – Genome Biology and Evolution	2009
Journal reviewer – PLoS Genetics	2008
Grant reviewer – Ministry of Health, Singapore	2007
Journal reviewer – Bioinformatics	2007
Journal reviewer – Nucleic Acids Research	2007

Group memberships – NESCENT cisevol working group, 1000 Genomes Project, Hapmap 3 Consortium, GEUVADIS project, MuTHER project and Alspac analysis group.  
Conference organizer – The Regcreative Jamboree, Ghent Belgium 2006  
Education outreach – UBC Let's Talk Science Partnership Program 2003  
Conference organizer – Vancouver Bioinformatics User Group ([www.vanbug.org](http://www.vanbug.org)). 2002  
Education outreach – Java and bioinformatics article series for O'Reilly and Associates. 2002  
“Java for Bioinformatics” and “Java APIs for Bioinformatics” appeared on OnJava ([www.onjava.com](http://www.onjava.com)).

## COPYRIGHTS AND PATENTS

**Montgomery, S.B.** (2002) BindingSite Application. Computer Application and Code used for Comparing Multiple Strands of DNA. Canadian Intellectual Property Office Copyright. File No. 418724

## RECENT PRESENTATIONS/INVITED MEETINGS

Tricon Molecular Medicine (2014), CSHL Precision Medicine (2013), ASHG(2013), IGES (2013), Sardinia Summer School in Genomics (2013), CIFAR(2013), BIRS(2013), Sardinia Summer School in Genomics (2012), International Conference on Systems Biology (2012), Capita Select in Complex Disease Analysis (2012), Personalized Medicine World Congress (2012), Swedish Medical Genetics Society (2011), International Society for Systems Biology (2011), Sardinia Summer School in Genomics (2011), European Society of Human Genetics (2011), Gordon Conference on Quantitative Genetics and Genomics (2011)

## GRANTS

NIH/NHGRI U01 for RFA-HG-12-016 # U01 HG007436 (PI: Bustamante and Plon)  
6/1/2013 - 5/31/2017 5% effort (**Co-Investigator**)

### **Clinically Relevant Genome Variation Database**

NIH/NHGRI (RFA-RM-12-019) # R01MH101814 (PI: Dermitzakis/McCarthy/Bustamante/Guigo)  
08/01/2013-07/31/2016 7% effort (**Co-Investigator**)

### **Methods for high-resolution analysis of genetic effects on gene expression**

This project is for the second phase of statistical analyses as part of the GTEx project.

Edward Mallinckrodt Junior Research Grant  
10/1/2012 – 9/30/2014 4% effort

### **Expression response to environment in coronary artery smooth muscle cells.**

This project is to investigate transcriptome responses to serum-starvation in human coronary artery smooth muscle cells using RNA-sequencing data. (In collaboration with Tom Quertermous)

## ADVANCED TRAINING

- CITI Human Subjects Research Protections Curriculum # 8919278
- NIH Protecting Human Research Participants certificate # 422835 (2010)
- UBC Advanced Molecular Biology Laboratories “Molecular Biology Techniques Workshop” (2005)
- UBC Professional Training Workshop “Leadership and Management Workshop” (2004)