GAVIN HA

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N.
Seattle, WA 98109
Tel: 206-667-2802
gha@fredhutch.org
GavinHaLab.org

RESEARCH SUMMARY

My laboratory is interested in studying the role of genomic alterations in cancer and expanding applications for precision medicine. We develop novel algorithms to identify genomic structural alterations in tumor and circulating cell-free DNA from patients with cancer. Our goals are to uncover the genetic and epigenetic mechanisms of treatment resistance, to identify blood-based genomic biomarkers, and to translate these findings and innovations to advance clinical research and precision medicine.

I have extensive experience in cancer genome analysis with expertise in developing probabilistic and statistical methods for studying genomic alterations in tumors and cell-free DNA. I have developed machine learning algorithms, such as the software APOLLOH, HMMcopy, TITAN, and ichorCNA, which are widely used within the cancer research community to analyze cancer genome sequencing data. Using these novel methods, I have made impactful contributions to the research in breast, ovarian and prostate cancers. Recently, I helped to discover the duplication of a novel enhancer leading to increased androgen receptor expression in prostate cancer, which has led to new insights into treatment resistance in this disease.

RESEARCH POSITIONS

Jul. 2018 – Present	**Assistant Member,** Fred Hutchinson Cancer Research Center, Seattle, WA Computational Biology Program, Public Health Sciences Division
Sep. 2014 – Jun. 2018	**Postdoctoral Research Fellow**, Dana-Farber Cancer Institute, Boston, MA and Broad Institute of Harvard and MIT, Cambridge, MA Principal Investigator and mentor: Dr. Matthew Meyerson Collaborators and mentors: Drs. Rameen Beroukhim, Gad Getz, J Chris Love
Sep. 2009 - Aug. 2014	**Graduate Student**, BC Cancer Agency, University of British Columbia, Canada Advisors: Drs. Sohrab P. Shah and Samuel Aparicio Thesis: Probabilistic approaches for profiling copy number aberrations and loss of heterozygosity landscapes in cancer genomes

EDUCATION

2014	**Ph.D., Bioinformatics** University of British Columbia, Vancouver, BC, Canada
2008	**B.Sc., Computer Science & Microbiology/Immunology** University of British Columbia, Vancouver, BC, Canada

HONORS, AWARDS, AND FUNDING

2015 – 2018	**Canadian Institutes of Health Research (CIHR) Postdoctoral Fellowship**
2012	**Lloyd Skarsgard Graduate Research Excellence Award**, BC Cancer Agency • Annual award to student with most outstanding Ph.D. research
2010 – 2013	**Natural Sciences and Engineering Research Council of Canada (NSERC) Postgraduate Scholarship**
2010 – 2014	**Four Year Fellowships (FYF)**, University of British Columbia
2008 – 2010	**Canadian Institutes of Health Research (CIHR) Graduate Scholarship**
2008 – 2010	**College for Interdisciplinary Studies Graduate Award**, University of British Columbia

PUBLICATIONS

PEER-REVIEWED ARTICLES

1. Viswanathan SR*, **Ha G***, Hoff AM*, Wala JA, Carrot-Zhang J, Whelan CW, Haradhvala NJ, Freeman SS, Reed SC, Rhoades J, Polak P, Cipicchio M, Wankowicz SA, Wong A, Kamath T, Zhang Z, Gydush G, Rotem D, International PCF/SU2C Prostate Cancer Dream Team, Love JC, Getz G, Gabriel S, Zhang C-Z, Dehm SM, Nelson PS, Van Allen EM, Choudhury AD, Adalsteinsson VA, Beroukhim R, Taplin M-E, Meyerson M. Structural alterations driving castration-resistant prostate cancer revealed by linked-read genome sequencing. ***Cell*** 2018 Jul 12;174(2):433-447.e19.
*equal contribution

2. Ben-David U, Siranosian B, **Ha G**, Tang H, Oren Y, Hinohara K, Strathdee C, Dempster J, Lyons NJ, Burns R, Nag A, Kugener G, Gimini B, Tsvetkov P, Maruvka Y, O'Rourke R, Garriti A, Tubelli AA, Feldman D, Bandopadhayay P, Tsherniak A, Vasquez F, Wong B, Birger C, Ghandi M, Thorner AR, Bittker J, Meyerson M, Getz G, Beroukhim R, Golub TR. Genetic and transcriptional evolution alters cancer cell line drug response. ***Nature*** 2018 Aug 15;560:325-330.

3. Klega K, Imamovic-Tuco A, **Ha G**, Clapp AN, Meyer S, Ward A, Clinton C, Nag A, Van Allen E, Mullen E, DuBois SG, Janeway K, Meyerson M, Thorner AR, Crompton BD. Detection of Somatic Structural Variants Enables Quantification and Characterization of Circulating Tumor DNA in Children With Solid Tumors. ***JCO Precision Oncology*** 2018 Jul 5 Epub.

4. Taylor AM, Shih J, **Ha G**, Gao GF, Zhang X, Berger AC, Schumacher SE, Wang C, Hu H, Liu J, Lazar AJ; Cancer Genome Atlas Research Network., Cherniack AD, Beroukhim R, Meyerson M. Genomic and Functional Approaches to Understanding Cancer Aneuploidy. ***Cancer Cell*** 2018 Apr 9;33(4):676-689.e3.

5. Guo G, Raje NS, Seifer C, Kloeber J, Isenhart R, **Ha G**, Yee AJ, O'Donnell EK, Tai YT, Richardson PG, Bianchi G, Laubach JP, Warren D, Gemme E, Voisine J, Frede J, Kokkalis A, Yun H, Dimitrova V, Vijaykumar T, Meyerson M, Munshi NC, Anderson KC, Knoechel B, Lohr JG. Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. ***Leukemia*** 2018 Mar 27.

6. Stover DG*, Parsons HA*, **Ha G***, Freeman S, Barry WT, Guo H, Choudhury AD, Gydush G, Reed SC, Rhoades J, Rotem D, Hughes ME, Dillon DA, Partridge AH, Wagle N, Krop IE, Getz G, Golub TR, Love JC, Winer EP, Tolaney SM, Lin NU, Adalsteinsson VA. Association of cell-free DNA tumor fraction and somatic copy number alterations with survival in metastatic triple-negative breast cancer. ***Journal of Clinical Oncology*** 2018 Jan 3:JCO2017760033. *equal contribution

7. Radovich M, Pickering CR, Felau I, **Ha G**, Zhang H, Jo H, Hoadley KA, Anur P, Zhang J, McLellan M, Bowlby R, Matthew T, Danilova L, Hegde AM, Kim J, Leiserson MDM, Sethi G, Lu C, Ryan M, Su X, Cherniack AD, Robertson G, Akbani R, Spellman P, Weinstein JN, Hayes DN, Raphael B, Lichtenberg T, Leraas K, Zenklusen JC, The Cancer Genome Atlas Network, Fujimoto J, Scapulatempo-Neto C, Moreira AL, Hwang D, Huang J, Marino M, Korst R, Giaccone G, Gokmen-Polar Y, Badve S, Rajan A, Ströbel P, Girard N, Tsao MS, Marx A, Tsao AS, Loehrer PJ. The integrated genomic landscape of thymic epithelial tumors. ***Cancer Cell*** 2018 Feb 12;33(2):244-258.

8. Adalsteinsson, VA *, **Ha G***, Freeman SS*, Choudhury AD, Stover DG, Parsons HA, Gydush G, Reed SC, Rotem D, Rhoades J, Loginov D, Livitz D, Rosebrock D, Leshchiner I, Kim J, Stewart C, Rosenberg M, Francis JM, Zhang CZ, Cohen O, Oh C, Ding H, Polak Paz, Lloyd M, Mahmud S, Helvie S, Merrill MS, Santiago RA, O'Connor EP, Jeong SH, Leeson R, Barry RM, Kramkowski JF, Zhang Z, Polacek L, Lohr J, Schleicher M, Lipscomb E, Saltzman A, Oliver NM, Marini L, Waks AG, Harshman LC, Tolaney SM, Van Allen EM, Winer EP, Lin NU, Nakabayashi M, Taplin ME, Johannessen CM, Garraway LA, Golub RE, Boehm JS, Wagle N, Getz G*, Love JC*, Meyerson M*. Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. ***Nature Communications*** 2017 8:1324. *equal contribution

9. Ben-David U, **Ha G**, Tseng YY, Greenwald NF, Oh C, Shih J, McFarland JM, Wong B, Boehm JS, Beroukhim R, Golub TR. Patient-derived xenografts undergo mouse-specific tumor evolution. ***Nature Genetics*** 2017 Nov;49(11):1567-1575

10. Pectasides E, Stachler MD, Derks S, Liu Y, Maron S, Islam M, Alpert L, Kwak H, Kindler H, Polite B, Sharma MR, Allen K, O'Day E, Lomnicki S, Maranto M, Kanteti R, Fitzpatrick C, Weber C, Setia N, Xiao SY, Hart J, Nagy R, Kim KM, Choi MG, Min BH, Nason KS, O'Keefe L, Watanabe M, Baba H, Lanman R, Agoston AT, Oh DJ,

Dunford A, Thorner AR, Ducar MD, Wollison BM, Coleman HA, Ji Y, Posner MC, Roggin KK, Turaga K, Chang P, Hogarth K, Siddiqui U, Gelrud A, **Ha G**, Freeman SS, Rhoades J, Reed S, Gydush G, Rotem D, Davison J, Imamura Y, Adalsteinsson V, Lee J, Bass AJ, Catenacci DV. Genomic Heterogeneity as a Barrier to Precision Medicine in Gastroesophageal Adenocarcinoma. ***Cancer Discovery*** 2018 Jan;8(1):37-48.

11. Zhang X, Choi PS, Francis JM, Gao GF, Campbell JD, Ramachandran A, Mitsuishi Y, **Ha G**, Shih J, Vazquez F, Tsherniak A, Taylor AM, Zhou J, Wu Z, Berger AC, Giannakis M, Hahn WC, Cherniack AD, Meyerson M. Somatic super-enhancer duplications and hotspot mutations lead to oncogenic activation of the KLF5 transcription factor. ***Cancer Discovery*** 2017 Jan;8(1):108-125.

12. McPherson AW, Roth A, **Ha G**, Chauve C, Steif A, de Souza CPE, Eirew P, Bouchard-Côté A, Aparicio S, Sahinalp SC, Shah SP. ReMixT: clone-specific genomic structure estimation in cancer. ***Genome Biology*** 2017 Jul 27;18(1):140.

13. Wang YK, Bashashati A, Anglesio MS, Cochrane DR, Grewal DS, **Ha G**, McPherson A, Horlings HM, Senz J, Prentice LM, Karnezis AN, Lai D, Aniba MR, Zhang AW, Shumansky K, Siu C, Wan A, McConechy MK, Li-Chang H, Tone A, Provencher D, de Ladurantaye M, Fleury H, Okamoto A, Yanagida S, Yanaihara N, Saito M, Mungall AJ, Moore R, Marra MA, Gilks CB, Mes-Masson AM, McAlpine JN, Aparicio S, Huntsman DG, Shah SP. Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. ***Nature Genetics*** 2017 Jun;49(6):856-865

14. Mishima Y, Paiva B, Shi J, Park J, Manier S, Takagi S, Massoud M, Perilla-Glen A, Aljawai Y, Huynh D, Roccaro AM, Sacco A, Capelletti M, Detappe A, Alignani D, Anderson KC, Munshi NC, Prosper F, Lohr JG, **Ha G**, Freeman SS, Van Allen EM, Adalsteinsson VA, Michor F, San Miguel JF, Ghobrial IM. The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. ***Cell Reports*** 2017 Apr 4;19(1):218-224.

15. Lohr JG, Kim S, Gould J, Knoechel B, Drier Y, Cotton MJ, Gray D, Birrer N, Wong B, **Ha G**, Zhang CZ, Guo G, Meyerson M, Yee AJ, Boehm JS, Raje N, Golub TR. Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. ***Science Translational Medicine*** 2016 Nov 2;8(363):363ra147.

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17. Ben-David U, **Ha G**, Khadka P, Jin X, Wong B, Franke L, Golub TR. The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. ***Nature Communications*** 2016 Jul 4;7:12160.

18. McPherson A, Roth A, Laks E, Masud T, Bashashati A, Zhang AW, **Ha G**, Biele J, Yap D, Wan A, Prentice LM, Khattra J, Smith MA, Nielsen CB, Mullaly SC, Kalloger S, Karnezis A, Shumansky K, Siu C, Rosner J, Chan HL, Ho J, Melnyk N, Senz J, Yang W, Moore R, Mungall AJ, Marra MA, Bouchard-Côté A, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, Shah SP. Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. ***Nature Genetics*** 2016 Jul;48(7):758-67.

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20. Anglesio MS, Bashashati A, Wang YK, Senz J, **Ha G**, Yang W, Lefebvre C, Aniba MR, Prentice LM, Chang HL, Kazernis A, Sharabi-Farahani H, Hirst M, Marra MA, Shah SP, Huntsman DG. Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. ***The Journal of Pathology*** 2015 Jun;236(2):201-9.

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22. Chan FC, Telenius A, Healy S, Ben-Neriah S, Mottok A, Lim R, Drake M, Hu S, Ding J, **Ha G**, Scott DW, Kridel R, Bashashati A, Rogic S, Johnson N, Morin RD, Rimsza LM, Sehn L, Connors JM, Marra MA, Gascoyne RD, Shah SP, Steidl C. An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. ***Blood*** 2015; 125(6):959-66.

23. **Ha G**, Roth A, Khattra J, Ho J, Yap D, Prentice LM, Melnyk N, McPherson A, Bashashati A, Laks E, Biele J, Ding J, Le A, Rosner J, Shumansky K, Marra MA, Gilks CB, Huntsman DG, McAlpine JN, Aparicio S, Shah SP. TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. ***Genome Research*** 2014; 24(11):1881-93.

24. Roth A, Khattra J, Yap D, Wan A, Laks E, Biele J, **Ha G**, Aparicio S, Bouchard-Côté A, Shah SP. PyClone: statistical inference of clonal population structure in cancer. ***Nature Methods*** 2014; 11(4):396-8.

25. Bashashati A*, **Ha G***, Tone A*, Ding J, Prentice LM, Roth A, Rosner J, Shumansky K, Kalloger S, Senz J, Yang W, McConechy M, Melnyk N, Anglesio M, Luk MT, Tse K, Zeng T, Moore R, Zhao Y, Marra MA, Gilks B, Yip S, Huntsman DG, McAlpine JN, Shah SP. Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. ***The Journal of Pathology*** 2013; 231(1):21-34. * equal contribution

26. Bashashati A*, Haffari G*, Ding J*, **Ha G**, Lui K, Rosner J, Huntsman DG, Caldas C, Aparicio SA, Shah SP. DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. ***Genome Biology*** 2012; 13(12):R124. *equal contribution

27. **Ha G**, Roth A, Lai D, Bashashati A, Ding J, Goya R, Giuliany R, Rosner J, Oloumi A, Shumansky K, Chin SF, Turashvili G, Hirst M, Caldas C, Marra MA, Aparicio S, Shah SP. Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. ***Genome Research*** 2012; 22(10):1995-2007.

28. Curtis C, Shah SP, Chin SF, Turashvili G, Rueda OM, Dunning MJ, Speed D, Lynch AG, Samarajiwa S, Yuan Y, Gräf S, **Ha G**, Haffari G, Bashashati A, Russell R, McKinney S; METABRIC Group, Langerød A, Green A, Provenzano E, Wishart G, Pinder S, Watson P, Markowetz F, Murphy L, Ellis I, Purushotham A, Børresen-Dale AL, Brenton JD, Tavaré S, Caldas C, Aparicio S. The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. ***Nature*** 2012; 486(7403):346-52.

29. Shah SP, Roth A*, Goya R*, Oloumi A*, **Ha G***, Zhao Y*, Turashvili G*, Ding J*, Tse K*, Haffari G*, Bashashati A*, Prentice LM, Khattra J, Burleigh A, Yap D, Bernard V, McPherson A, Shumansky K, Crisan A, Giuliany R, Heravi-Moussavi A, Rosner J, Lai D, Birol I, Varhol R, Tam A, Dhalla N, Zeng T, Ma K, Chan SK, Griffith M, Moradian A, Cheng SW, Morin GB, Watson P, Gelmon K, Chia S, Chin SF, Curtis C, Rueda OM, Pharoah PD, Damaraju S, Mackey J, Hoon K, Harkins T, Tadigotla V, Sigaroudinia M, Gascard P, Tlsty T, Costello JF, Meyer IM, Eaves CJ, Wasserman WW, Jones S, Huntsman D, Hirst M, Caldas C, Marra MA, Aparicio S. The clonal and mutational evolution spectrum of primary triple-negative breast cancers. ***Nature*** 2012; 486(7403):395-9. *equal contribution

30. Roth A, Ding J, Morin R, Crisan A, **Ha G**, Giuliany R, Bashashati A, Hirst M, Turashvili G, Oloumi A, Marra MA, Aparicio S, Shah SP. JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. ***Bioinformatics*** 2012; 28(7):907-13.

31. Heravi-Moussavi A, Anglesio MS, Cheng SW, Senz J, Yang W, Prentice L, Fejes AP, Chow C, Tone A, Kalloger SE, Hamel N, Roth A, **Ha G**, Wan AN, Maines-Bandiera S, Salamanca C, Pasini B, Clarke BA, Lee AF, Lee CH, Zhao C, Young RH, Aparicio SA, Sorensen PH, Woo MM, Boyd N, Jones SJ, Hirst M, Marra MA, Gilks B, Shah SP, Foulkes WD, Morin GB, Huntsman DG. Recurrent somatic DICER1 mutations in nonepithelial ovarian cancers. ***The New England Journal of Medicine*** 2012; 366(3):234-42.

32. Crisan A, Goya R, **Ha G**, Ding J, Prentice LM, Oloumi A, Senz J, Zeng T, Tse K, Delaney A, Marra MA, Huntsman DG, Hirst M, Aparicio S, Shah S. Mutation discovery in regions of segmental cancer genome amplifications with CoNAn-SNV: a mixture model for next generation sequencing of tumors. ***PLoS One*** 2012; 7(8):e41551.

33. Schrader KA, Heravi-Moussavi A, Waters PJ, Senz J, Whelan J, **Ha G**, Eydoux P, Nielsen T, Gallagher B, Oloumi A, Boyd N, Fernandez BA, Young TL, Jones SJ, Hirst M, Shah SP, Marra MA, Green J, Huntsman DG. Using next-generation sequencing for the diagnosis of rare disorders: a family with retinitis pigmentosa and skeletal abnormalities. ***The Journal of Pathology*** 2011; 225(1):12-8.

34. McPherson A, Hormozdiari F, Zayed A, Giuliany R, **Ha G**, Sun MG, Griffith M, Heravi Moussavi A, Senz J, Melnyk N, Pacheco M, Marra MA, Hirst M, Nielsen TO, Sahinalp SC, Huntsman D, Shah SP. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. ***PLoS Computational Biology*** 2011; 7(5):e1001138.

35. Kortmann U, McAlpine JN, Xue H, Guan J, **Ha G**, Tully S, Shafait S, Lau A, Cranston AN, O'Connor MJ, Huntsman DG, Wang Y, Gilks CB. Tumor growth inhibition by olaparib in BRCA2 germline-mutated patient-derived ovarian cancer tissue xenografts. ***Clinical Cancer Research*** 2011; 17(4):783-91.

36. Wiegand KC, Shah SP, Al-Agha OM, Zhao Y, Tse K, Zeng T, Senz J, McConechy MK, Anglesio MS, Kalloger SE, Yang W, Heravi-Moussavi A, Giuliany R, Chow C, Fee J, Zayed A, Prentice L, Melnyk N, Turashvili G, Delaney AD, Madore J, Yip S, McPherson AW, **Ha G**, Bell L, Fereday S, Tam A, Galletta L, Tonin PN, Provencher D, Miller D, Jones SJ, Moore RA, Morin GB, Oloumi A, Boyd N, Aparicio SA, Shih IeM, Mes-Masson AM, Bowtell DD, Hirst M, Gilks B, Marra MA, Huntsman DG. ARID1A mutations in endometriosis-associated ovarian carcinomas. ***The New England Journal of Medicine*** 2010; 363(16):1532-43.

37. Goya R, Sun MG, Morin RD, Leung G, **Ha G**, Wiegand KC, Senz J, Crisan A, Marra MA, Hirst M, Huntsman D, Murphy KP, Aparicio S, Shah SP. SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. ***Bioinformatics*** 2010; 26(6):730-6.

BOOK CHAPTERS

1. **G. Ha**, S. P. Shah, Distinguishing Somatic and Germline Copy Number Events in Cancer Patient DNA Hybridized to Whole-Genome SNP Genotyping Arrays, Vol. 973 of *Array Comparative Genomic Hybridization: Protocols and Applications*, *Methods in Molecular Biology*, D. Banerjee, S. P. Shah (Eds.), Springer Science and Business Media, LLC, 2013, chapter 22, pg 355-372. (PMID: 23412801)

BIOINFORMATICS SOFTWARE

ichorCNA	Homepage: https://github.com/broadinstitute/ichorCNA/ Description: Cell-free DNA analysis tool for estimating the tumor fraction and predicting large-scale copy number alterations in ultra-low-pass whole genome sequencing (0.1x coverage) from metastatic cancer patients (Adalsteinsson, Ha, Freeman, et al. *Nature Commun.* 2017)
TitanCNA	Homepage: https://github.com/gavinha/TitanCNA/ Bioconductor: http://www.bioconductor.org/packages/release/bioc/html/TitanCNA.html Description: Cancer genomics software for inferring clonal structure and detecting subclonal copy number alterations and loss of heterozygosity from genome sequencing data of tumors (Ha et al. *Genome Res.* 2014)
HMMcopy	Homepage: http://shahlab.ca/projects/hmmcopy_utils/ Bioconductor: http://bioconductor.org/packages/release/bioc/html/HMMcopy.html Description: Copy number prediction with correction for GC and mappability bias for HTS data (Ha et al. *Genome Res.* 2012) Co-authors: Daniel Lai and Sohrab Shah
APOLLOH	Homepage: http://shahlab.ca/projects/apolloh/ Description: Cancer genomics software for detecting loss of heterozygosity from whole genome sequencing data of tumors (Ha et al. *Genome Res*. 2012)
HMM-Dosage	Homepage: http://compbio.bccrc.ca/software/hmm-dosage/ Description: Prediction of both somatic and germline copy number changes in SNP-genotyping data of tumours (Ha et al. *Methods Mol Biol.* 2013)

PRESENTATIONS

Apr. 16-20, 2016	**AACR Annual Meeting,** New Orleans, Louisiana Poster Title: "High concordance of whole-exome sequencing of cell-free DNA and matched biopsies enables genomic discovery in metastatic cancer" (Abstact LB-136)
Jan. 27, 2014	**Seminars in Quantitative Biology**, Cancer Research UK, Cambridge, UK

Title: “Profiling the Subclonal Copy Number Architecture from Whole Genome Sequencing of Heterogeneous Tumours” (**Invited**)

Jul. 20, 2013 — **21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Berlin, Germany
Title: “Probabilistic inference of subclonal copy number alterations and LOH in whole genome sequencing of tumours”

Feb. 25, 2013 — **Research Seminar Series**, BC Cancer Research Centre, Vancouver
Title: “Profiling copy number aberrations and loss of heterozygosity mutational landscapes in cancer genomes”
- **Invited** as recipient of the Lloyd Skarsgard Graduate Research Excellence Award

Jul. 16, 2011 — **19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB),** High Throughput Sequencing Analysis and Algorithms (HiTSeq) Special Interest Group, Vienna, Austria
Title: “APOLLOH: copy number aware approach to detect loss of heterozygosity in tumour genome sequence data”.

MENTORSHIP

Mar 2018-Present — **Mentor** to Kar-Tong Tan, graduate student, Biological and Biomedical Sciences, Harvard Medical School

Sept 2017-Present — **Mentor and Supervisor** to Christopher Lo, computational biologist, Broad Institute of Harvard & MIT
- Supervising analysis and development of tools to analyze methylation patterns in cell-free DNA

Jan 2017-Present — **Mentor and Supervisor** to Justin Rhoades, MSc., Broad Institute of Harvard & MIT
- Supervising analysis and development of tools and their applications to cell-free DNA genome sequencing data

Apr 2015-Present — **Mentor** to Samuel Freeman, graduate student, Bioinformatics and Integrated Genomics, Harvard Medical School
- Supervising the development of a probabilistic approach to detect somatic mutations in cell-free DNA and single-cell genome sequencing data

Jan-Apr 2015 — **Mentor** to Jacqueline Xu, sophomore, Massachusetts Institute of Technology
- Supervising project on mutation analysis in single-cell sequencing data of cancer

May-Aug 2011 — **Mentor** to Daniel Lai, junior graduate student, University of British Columbia
- Supervised and oversaw project to design a method for correcting biases in genome sequencing, leading to development of R/Bioconductor package, HMMcopy

TEACHING

May 2017, May 2018 — **Broad Institute Cancer Program BootCamp,** Cambridge, MA
Lecturer: Introduction to data analysis of cell-free DNA and applications for studying metastatic cancer.

Jan.-Feb. 2016 — **Broad Cancer Program BootCamp,** Cambridge, MA
Coach: Teaching, mentoring, supervising 3 experimental biologists (postdocs) on a cancer genomics project.

Jan. 21, 2013 — **11th Annual Asia Pacific Bioinformatics Conference (APBC)**, Vancouver, Canada
Tutorial: “Profiling genome architecture for copy number alterations and loss of heterozygosity”

May 30, 2012 **Canadian Bioinformatics Workshop**, Cancer Genomics, Toronto, Canada
Lecturer: Copy number alterations in cancer (Module 4) and Somatic mutations in cancer (Module 5)
Teaching assistant: All 9 modules

Jan.-Apr. 2007 **Teaching Assistant**, Computer Science Dept., University of British Columbia
Introduction to Software Development (CPSC211)