Andrew McPherson

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EMAIL: andrew.mcpherson@gmail.com
WEBSITE: http://amcpherson.github.io
BITBUCKET: http://bitbucket.org/dranew/
PROJECTS: deFuse, deStruct, ReMixT, citup, dollo, pypeliner

Research Interests

Cancer genomics, computational biology, phylogenomics, genome rearrangements, combinatorial algorithms, graph theory, probabilistic methods.

Education

Oct 2015 — **School of Computing Science, Simon Fraser University**
Ph.D. in Computing Science
Thesis: Characterization of Genome Rearrangements from Tumour Sequencing Data
Supervisors: S. Cenk Sahinalp and Sohrab P. Shah

Aug 2002 — **School of Engineering Science, Simon Fraser University**
B.A.Sc. in Engineering Science

Research Experience

May 2009 - — **Research Assistant, Shah Lab for Computational Cancer Biology**
Cancer genomics, high-throughput sequence analysis and computational method development. Lead researcher for a study of tumor evolution in High Grade Serous Ovarian Cancer.

Jan - Apr 2009 — **Research Assistant, SFU Brinkman Lab with Fiona Brinkman**
Proteomics analysis and pipeline development for novel drug discovery.

Sep - Dec 2008 — **BC Genome Science Centre with Marco Marra**
Analysis of microRNA sequencing from tumour samples.

May - Aug 2008 — **SFU Mathematics Department with Cedric Chauve**
Implemented combinatorial algorithms for comparative genomics.

Teaching Experience

May 2014 - — **Bioinformatics for Cancer Genomics Workshop, Toronto Canada**
Developed and teach the workshops Gene Fusion module, a 3 hour seminar and lab.

Work Experience

Apr 2005 - Sep 2007 — **Software Engineer, Electronic Arts, Vancouver Canada**
Lead PlayStation 2 Programmer for Need for Speed, one of EAs top selling franchises.

Oct 2002 - Nov 2004 — **Software Engineer, Argonaut Software Ltd, London UK**
Development of bespoke tools for game artists.

Funding and Awards

2015 Travel & Minor Research Award

2013 Travel & Minor Research Award
Graduate Prize in CMPT
DBMiner Graduate Scholarship in CMPT
Helmut and Hugo Eppich Family Graduate Scholarship

2012 **Alexander Graham Bell Canada Graduate Scholarship**
Graduate Fellowship
External Graduate Award
The ABC Recycling Ltd. Graduate Scholarship
The Clark Wilson Graduate Scholarship

2011 Michael & Grace Kreykenbohm Graduate Scholarship
Graduate Fellowship

2010 Faculty of Applied Sciences Graduate Fellowship
Hugo Eppich Graduate Scholarship

2008 **CIHR Bioinformatics Training Program Scholarship**
NSERC Undergraduate Student Research Award

Publications

2015 **Spatial genomic heterogeneity within localized, multifocal prostate cancer**
Boutros PC, Fraser M, Harding NJ, de Borja R, Trudel D, Lalonde E, Meng A, Hennings-Yeomans PH, ***McPherson A***, Sabelnykova VY, Zia A, Fox NS, Livingstone J, Shiah Y, Wang J, Beck TA, Have CL, Chong T, Sam M, Johns J, Timms L, Buchner N, Wong A, Watson JD, Simmons TT, P'ng C, Zafarana G, Nguyen F, Luo X, Chu KC, Prokopec SD, Sykes J, Dal Pra A, Berlin A, Brown A, Chan-Seng-Yue MA, Yousif F, Denroche RE, Chong LC, Chen GM, Jung E, Fung C, Starmans MHW, Chen H, Govind SK, Hawley J, D'Costa A, Pintilie M, Waggott D, Hach F, Lambin P, Muthuswamy LB, Cooper C, Eeles R, Neal D, Tetu B, Sahinalp C, Stein LD, Fleshner N, Shah SP, Collins CC, Hudson TJ, McPherson JD, van der Kwast T, Bristow RG
◇ Nat Genet, Jul 2015

Clonality inference in multiple tumor samples using phylogeny
Malikic S, ***McPherson AW***, Donmez N, Sahinalp CS
◇ Bioinformatics, May 2015

Joint Inference of Genome Structure and Content in Heterogeneous Tumor Samples
McPherson A, Roth A, Chauve C, Sahinalp SC
◇ RECOMB 2015, Warsaw, Poland

Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution

Eirew P, Steif A, Khattra J, Ha G, Yap D, Farahani H, Gelmon K, Chia S, Mar C, Wan A, Laks E, Biele J, Shumansky K, Rosner J, ***McPherson A***, Nielsen C, Roth AJL, Lefebvre C, Bashashati A, de Souza C, Siu C, Aniba R, Brimhall J, Oloumi A, Osako T, Bruna A, Sandoval JL, Algara T, Greenwood W, Leung K, Cheng H, Xue H, Wang Y, Lin D, Mungall AJ, Moore R, Zhao Y, Lorette J, Nguyen L, Huntsman D, Eaves CJ, Hansen C, Marra MA, Caldas C, Shah SP, Aparicio S

◇ Nature, Feb 2015

2014 **TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data**

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

◇ Genome Res, Nov 2014

Heterogeneity in the inter-tumor transcriptome of high risk prostate cancer

Wyatt AW, Mo F, Wang K, McConeghy B, Brahmbhatt S, Jong L, Mitchell DM, Johnston RL, Haegert A, Li E, Liew J, Yeung J, Shrestha R, Lapuk AV, ***McPherson A***, Shukin R, Bell RH, Anderson S, Bishop J, Hurtado-Coll A, Xiao H, Chinnaiyan AM, Mehra R, Lin D, Wang Y, Fazli L, Gleave ME, Volik SV, Collins CC

◇ Genome Biol, Aug 2014

Genomic rearrangements involving programmed death ligands are recurrent in primary mediastinal large B-cell lymphoma

Twa DDW, Chan FC, Ben-Neriah S, Woolcock BW, Mottok A, Tan KL, Slack GW, Gunawardana J, Lim RS, ***McPherson AW***, Kridel R, Telenius A, Scott DW, Savage KJ, Shah SP, Gascoyne RD, Steidl C

◇ Blood, Mar 2014

2012 **Poly-gene fusion transcripts and chromothripsis in prostate cancer**

Wu C, Wyatt AW, ***McPherson A***, Lin D, McConeghy BJ, Mo F, Shukin R, Lapuk AV, Jones SJM, Zhao Y, Marra MA, Gleave ME, Volik SV, Wang Y, Sahinalp SC, Collins CC

◇ Genes Chromosomes Cancer, Dec 2012

nFuse: discovery of complex genomic rearrangements in cancer using high-throughput sequencing

McPherson A, Wu C, Wyatt AW, Shah S, Collins C, Sahinalp SC

◇ Genome Res, Nov 2012
◇ RECOMB 2012, Barcelona, Spain

From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer

Lapuk AV, Wu C, Wyatt AW, ***McPherson A***, McConeghy BJ, Brahmbhatt S, Mo F, Zoubeidi A, Anderson S, Bell RH, Haegert A, Shukin R, Wang Y, Fazli L, Hurtado-Coll A, Jones EC, Hach F, Hormozdiari F, Hajirasouliha I, Boutros PC, Bristow RG, Zhao Y, Marra MA, Fanjul A, Maher CA, Chinnaiyan AM, Rubin MA, Beltran H, Sahinalp SC, Gleave ME, Volik SV, Collins CC

◇ J Pathol, Jul 2012

The clonal and mutational evolution spectrum of primary triple-negative breast cancers

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 SG, Morin GB, Watson P, Gelmon K, Chia S, Chin S, 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

◇ Nature, Jun 2012

Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer

Wu C, Wyatt AW, Lapuk AV, ***McPherson A***, McConeghy BJ, Bell RH, Anderson S, Haegert A, Brahmbhatt S, Shukin R, Mo F, Li E, Fazli L, Hurtado-Coll A, Jones EC, Butterfield YS, Hach F, Hormozdiari F, Hajirasouliha I, Boutros PC, Bristow RG, Jones SJ, Hirst M, Marra MA, Maher CA, Chinnaiyan AM, Sahinalp SC, Gleave ME, Volik SV, Collins CC

◇ J Pathol, May 2012

14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma

Lee C, Ou W, Mariño-Enriquez A, Zhu M, Mayeda M, Wang Y, Guo X, Brunner AL, Amant F, French CA, West RB, McAlpine JN, Gilks CB, Yaffe MB, Prentice LM, ***McPherson A***, Jones SJM, Marra MA, Shah SP, van de Rijn M, Huntsman DG, Dal Cin P, Debiec-Rychter M, Nucci MR, Fletcher JA

◇ Proc Natl Acad Sci U S A, Jan 2012

2011 **Simultaneous structural variation discovery among multiple paired-end sequenced genomes**

Hormozdiari F, Hajirasouliha I, ***McPherson A***, Eichler EE, Sahinalp SC

◇ Genome Res, Dec 2011
◇ RECOMB 2011, Vancouver, Canada

Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells

Kuchenbauer F, Mah SM, Heuser M, ***McPherson A***, Rüschmann J, Rouhi A, Berg T, Bullinger L, Argiropoulos B, Morin RD, Lai D, Starczynowski DT, Karsan A, Eaves CJ, Watahiki A, Wang Y, Aparicio SA, Ganser A, Krauter J, Döhner H, Döhner K, Marra MA, Camargo FD, Palmqvist L, Buske C, Humphries RK

◇ Blood, Sep 2011

Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data

McPherson A, Wu C, Hajirasouliha I, Hormozdiari F, Hach F, Lapuk A, Volik S, Shah S, Collins C, Sahinalp SC

◇ Bioinformatics, Jun 2011

deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data

McPherson A, Hormozdiari F, Zayed A, Giuliany R, Ha G, Sun MGF, Griffith M, Heravi Moussavi A, Senz J, Melnyk N, Pacheco M, Marra MA, Hirst M, Nielsen TO, Sahinalp SC, Huntsman D, Shah SP

◇ PLoS Comput Biol, May 2011

MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers

Steidl C, Shah SP, Woolcock BW, Rui L, Kawahara M, Farinha P, Johnson NA, Zhao Y, Telenius A, Neriah SB, ***McPherson A***, Meissner B, Okoye UC, Diepstra A, van den Berg A, Sun M, Leung G, Jones SJ, Connors JM, Huntsman DG, Savage KJ, Rimsza LM, Horsman DE, Staudt LM, Steidl U, Marra MA, Gascoyne RD

◇ Nature, Mar 2011

Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations

Starczynowski DT, Morin R, ***McPherson A***, Lam J, Chari R, Wegrzyn J, Kuchenbauer F, Hirst M, Tohyama K, Humphries RK, Lam WL, Marra M, Karsan A

◇ Blood, Jan 2011

2010 **ARID1A mutations in endometriosis-associated ovarian carcinomas**

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 SJM, Moore RA, Morin GB, Oloumi A, Boyd N, Aparicio SA, Shih I, Mes-Masson A, Bowtell DD, Hirst M, Gilks B, Marra MA, Huntsman DG

◇ N Engl J Med, Oct 2010

2009 **Prediction of contiguous regions in the amniote ancestral genome**

Ouangraoua A, Boyer F, ***Mcpherson A***, Tannier É, Chauve C

◇ ISBRA 2009, Ft. Lauderdale, Florida, USA