**THE UNIVERSITY OF BRITISH COLUMBIA**

**Curriculum Vitae for Faculty Members**

**Date**: June 2017 **Initials**:SPS

**1.** **SURNAME**: Shah **FIRST** **NAME**: Sohrab

**MIDDLE NAME(S)**: Prakash

**2.** **DEPARTMENT/SCHOOL:** Pathology & Laboratory Medicine

**3.** **FACULTY**: Medicine

**4.** **PRESENT RANK**: Associate Professor (Grant Tenure Track) **SINCE**: Sep 1, 2010

**5.** **POST-SECONDARY EDUCATION**

Queen’s University, BSc (Hons) in Biology, 1996

University of British Columbia, BSc in Computer Science, 2001

University of British Columbia, MSc in Computer Science (Bioinformatics), 2005

* Title of Dissertation: “Detecting common secondary structure elements in RNA sequences”
* Research Supervisor: Dr. Anne Condon

University of British Columbia, PhD in Computer Science (Bioinformatics), 2008

* Title of Dissertation: “Model based approaches to array CGH data analysis”
* Research Supervisors: Drs. Raymond Ng and Kevin Murphy

**Special Professional Qualifications**

**6. EMPLOYMENT RECORD**

*(a) Prior to coming to UBC*

*(b) At UBC*

|  |  |  |
| --- | --- | --- |
| **University, Company or Organization** | **Rank or Title** | **Dates** |
| Centre for Molecular Medicine and Therapeutics | Bioinformatics Software Developer | 2000/05 - 2002/05 |
| UBC - High Throughput Bioinformatics | Chief | 2002/05 - 2004/08 |
| Canadian Bioinformatics Workshops Series, Canadian Genetic Diseases Network / Ontario Institute for Cancer Research | Instructor | 2002 - Present |
| UBC - Department of Computer Science | Research Assistant | 2005/05 - 2008/05 |
| UBC - Interprofessional Health and Human Services | Instructor | 2006/07 - 2009/08 |
| BC Cancer Agency | Postdoctoral Research Fellow (Advisors: Drs Sam Aparicio and David Huntsman) | 2008 - 2010 |
| BC Cancer Agency | Scientist | 2010 - Present |
| CIHR/MSFHR Bioinformatics Program | Faculty Member | 2010 - Present |
| UBC - Department of Computer Science | Associate Member | 2010 – Present |
| UBC - Genome Science and Technology Graduate Program | Faculty Member | 2013/03 – Present |
| Genome Sciences Centre | Associate Member | 2013/03 – Present |
| SFU - School of Computing Science | Adjunct Professor | 2013/06 – 2019/05 |
| UBC - Department of Pathology and Laboratory Medicine | Assistant Professor | 2010 - 2014 |
| UBC - Department of Pathology and Laboratory Medicine | Associate Professor | 2015 - Present |

*(c) Date of granting of tenure at U.B.C.:*

**7. LEAVES OF ABSENCE**

**8. TEACHING**

*(a) Areas of special interest and accomplishments*

As part of the steering committee for the development of a cross-disciplinary course in health informatics: IHHS302: “Topics in Health Informatics for Health/Life Science Students”, I helped to develop the curriculum and led the delivery of its content in 2007 and 2008. I have given lectures in the following UBC numbered courses: STAT 540, MEDG 421, STAT 547M. From 2001 until present I have been consistently involved in the development and delivery of content for the Canadian Bioinformatics Workshops (CBW) series (http://bioinformatics.ca) which has trained more than 1000 people since its inception in 2000. My role began as a teaching assistant, but I was recently the lead faculty in a new offering titled: “Clinical genomics and biomarker discovery”, which was offered in July 2009 and 2010 (teaching evaluation attached). This course was designed to fill an unmet need in bioinformatics training and had an initial cohort of 30 participants, including pathologists, graduate students and computer scientists. In summer of 2011, I was a core faculty member in another new course entitled Bioinformatics for Cancer Genomics where I introduced 2 new topics: “Copy number analysis using genotype microarrays” and “Somatic mutation detection in next generation sequencing data”. This course was offered to ~30 participants in Toronto in 2011, 2012 and is scheduled for May, 2013. Lastly, I am currently preparing a graduate course for the Dept of Pathology and Lab Medicine to cover the salient topics in cancer genome sequencing and bioinformatics analysis.

*(b) Courses Taught*

| **Year** | **Course #** | **Sched. Hrs** | **Class**  **Size** | **Contact**  **Hrs** | **Hours Taught** | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Lectures** | **Tutorials** | **Labs** | **Other** |
| 2005S (08/22/05-09/02/05) | IHHS  302 |  |  |  | 1.5 |  |  |  |
| 2006S (08/21/06-09/01/06) | IHHS  302 |  |  |  | 1.5 |  |  |  |
| 2007S (09/15/07) | IHHS  302 |  |  |  | 3 |  |  |  |
| 2009S  (08/26/09) | IHHS 302 |  |  |  | 1.5 |  |  |  |
| 2009W  (01/14/10) | STAT  547M |  |  |  | 1.5 |  |  |  |
| 2009W  (03/16/10) | MEDG421 |  |  |  | 1.5 |  |  |  |
| 2010W  (03/10/11) | MEDG421 |  |  |  | 1.5 |  |  |  |
| 2010W  (03/09/11) | STAT 540 |  |  |  | 1.5 |  |  |  |
| 2011W  (03/07/12) | STAT 540 |  |  |  | 1.5 |  |  |  |
| 2012W  (03/13/13- 03/18/13) | MBB 505 / BIOF 520 |  | 12 |  | 4 |  |  |  |
| 2012W  (03/27/13) | STAT 540 |  |  |  | 1.5 |  |  |  |
| 2013W  (10/16/13-11/08/13 | PRINb1 |  | 8 |  |  | 22 |  |  |
| 2013W  (01/29/14- 02/03/14) | MBB 505 / BIOF 520 |  |  |  | 4 |  |  |  |
| 2013W  (03/03/14-  03/10/14) | PATH 500B |  |  |  | 2.5 |  |  |  |
| 2013W (04/02/14) | STAT 540 |  |  |  | 1.5 |  |  |  |
| 2014W (01/19/15; 01/21/15; 01/23/15) | UBC Pathology Genomics Course |  |  |  | 3.5 |  |  |  |
| 2014W (02/23/15; 03/02/15) | PATH 502 |  |  |  | 2 |  |  |  |
| 2014W (04/01/15) | STAT540 |  |  |  | 1.5 |  |  |  |
| 2015W (01/26/16) | MEDG 421 |  |  |  | 1.5 |  |  |  |
| 2015W (02/22/16; 02/29/16) | PATH 502 |  | 19;4 |  | 2.5 |  |  |  |
| 2015W (03/09/16; 03/14/16) | BIOF 520 |  | 12 |  | 4.0 |  |  |  |
| 2015W  (04/04/16) | STAT 540 |  | 50 |  | 2.0 |  |  |  |
| 2016W  (02/20/17;02/27/17) | PATH 502 |  | 15 |  | 2.0 |  |  |  |
| 2016W (03/08/17; 03/13/17) | BIOF 520 |  | 11 |  | 4.0 |  |  |  |
| 2016W (03/04/17) | STAT 540 |  | 23 |  | 1.5 |  |  |  |

1  PBL Tutor

*(c) Other Teaching of Undergraduates, Graduates and Postgraduates*

|  |  |
| --- | --- |
|  | Lecturer, “Evolution in human cancer”; SFU MADD-GEN Workshop on Cancer Genomics, May 1, 2015. |
|  | Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Genomics Core Teaching. Jan 19-23, 2014 |
|  | Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Residency Training, Genomics Course for Pathology Trainees. Jan 6-10, 2014 (<http://pathology.ubc.ca/educational-programs/residency-training/new-genomics-course-for-pathology-trainees/>) |
|  | Panel Member, UBC Department of Pathology and Laboratory Medicine, Professional Advancement Learning Series. Dec 12, 2014 // “Interview Skills: How to be a truly hot commodity” |
|  | Panel Member, UBC Departments of Microbiology & Immunology and Computer Science (Combined Degree Career Panel). Jan 20, 2016 |

(d) Students Supervised

**Undergraduate Students**

BSc Total = 8; 1 current; 7 completed

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Student Name** | **Program Type** | **Program Details** | **Year** | | **Supervisory Role** | **Current Position/**  **Awards** |
|  |  |  | **Start** | **Finish** |  |  |
| ***Directed Studies*** |  |  |  |  |  |  |
| Khushboo Chachcha | BSc | Computer Science | 2013/01 | 2013/04 | Primary Supervisor |  |
| Kenneth Wing Cheung Lui | BSc | Computer Science | 2011/09 | 2011/12 | Primary Supervisor | Chinese University of Hong Kong Graduate Program |
| ***Co-op*** |  |  |  |  |  |  |
| Minh (Alan) Le | BSc | Computer Science & Microbiology and Immunology | 2012/05 | 2012/12 | Primary Supervisor |  |
| Jeffrey Knaggs | BSc | Computational Linguistics (SFU) | 2012/05 | 2013/04 | Primary Supervisor |  |
| Kevin Wagner | BASc | Computer Engineering | 2014/01 | 2014/08 | Primary Supervisor |  |
| Yu Wang | Msc (co-op) | Mathematics and Statistics (UVIC) | 2014/09 | 2014/12 | Primary Supervisor |  |
| Boyang (Tom) Jin | BSc | Computer Science and Microbiology | 2014/09 | 2014/12 | Primary Supervisor |  |
| Lovedeep Malik | BSc | Computer Science | 2015/01 | 2015/08 | Primary Supervisor |  |
| Claire Barretto | BSc | Computer Science | 2015/05 | 2015/08 | Primary Supervisor |  |
| Jill (Yajie) Zhou | BSc | Computer Science (SFU) | 2015/05 | 2015/08 | Primary Supervisor |  |
| Jamie Xu | BSc | Computer Science (SFU) | 2016/01 | 2016/08 | Primary Supervisor |  |
| Curtis Huebner | BASc | Engineering Physics  (UBC) | 2017/05 | 2017/12 | Primary Supervisor |  |
| Jessica Ngo | BSc | Biotechnology | 2017/05 | 2017/12 | Primary Supervisor |  |

**Graduate Students Supervised**

MSc Total = 12; 1 current; 11 completed

PhD Total = 12; 5 current; 7 completed

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Student Name** | **Degree** | **Start** | **Finish** | **Supervisory Role** | **Program** | **Awards** |
| **MSc Students** |  |  |  |  |  |  |
| Rodrigo Goya | MSc (Thesis) | 2009/01 | 2009/05 | Co-supervisor with David Huntsman | CIHR Bioinformatics Program  2nd rotation |  |
| Andrew Roth | MSc (Thesis) | 2010/05 | 2010/08 | Primary Supervisor (SFU) | CIHR Bioinformatics Program  3rd rotation |  |
| Michael Peabody | MSc (Thesis) | 2011/01 | 2011/04 | Primary Supervisor (SFU) | CIHR Bioinformatics Program  2nd rotation |  |
| Ryan Giuliany | MSc (Thesis) | 2010/09 | 2012/08 | Primary Supervisor | CIHR Bioinformatics  Graduate Program |  |
| Calvin Lefebvre | MSc (Thesis) | 2012/05 | 2015/05 | Primary Supervisor | Graduate Program in Bioinformatics |  |
| Tyler Funnell | MSc  (Thesis) | 2012/09 | 2014/12 | Primary Supervisor | Graduate Program in Bioinformatics |  |
| Xin Ren | MSS (Thesis) | 2013/09 | 2013/12 | Primary Supervisor  (Co-op Student) | College for Interdisciplinary Studies  Software Systems |  |
| Diljot Singh Grewal | MSc  (Thesis) | 2014/01 | 2014/08 | Primary Supervisor (SFU; Co-op Student) | Computer Science |  |
| Emily Hindalong | MSc  (Thesis) | 2014/05 | 2015/08 | Primary Supervisor | CIHR Bioinformatics Program |  |
| Santina Lin | MSc (RotationStudent) | 2014/09 | 2014/12 | Primary Supervisor | CIHR Bioinformatics Program |  |
| Maia Smith | MSc (Thesis) | 2015/09 | 2016/09 | Primary Supervisor | Bioinformatics |  |
| Rebecca Asiimwe | MSc | 2016/09 |  | Primary Supervisor | Bioinformatics |  |
| **PhD. Students** |  |  |  |  |  |  |
| Andrew McPherson | PhD | 2008/09 | 2015/07 | Primary Supervisor  Co-supervisor: Cenk Sahinalp | SFU Graduate Program in Bioinformatics | NSERC CGS PhD scholarship |
| Jiarui Ding | PhD | 2009/09 | 2016/05 | Primary Supervisor | Graduate Program  Computer Science |  |
| Gavin Ha | PhD | 2009/09 | 2014/07 | Primary Supervisor  Co-supervisor: Sam Aparicio | Graduate Program in Bioinformatics | 2012 Lloyd Skarsgaard Research Excellence Prize (top graduating student at the BCCA)  2010 NSERC Postgraduate Scholarships-Doctoral |
| Andrew Roth | PhD | 2011/01 | 2015/11 | Primary Supervisor | Graduate Program in Bioinformatics | CIHR Doctoral Award-Frederick Banting & Charles Best Canada Graduate Scholarship |
| Fong Chun Chan | PhD | 2012/05 | 2017/03 | Co-supervisor with Christian Steidl | CIHR Bioinformatics  Graduate Program |  |
| Adi Steif | PhD | 2013/05 |  | Co-supervisor with Sam Aparicio | Genome Science and Technology Graduate Program | CIHR Doctoral Research Award: Vanier Canada Graduate Scholarship |
| Fatemeh Dorri | PhD | 2013/09 |  | Primary Supervisor | Graduate Program  Computer Science |  |
| Allen Zhang | MD/PhD | 2014/08 |  | Co-supervisor with Wyeth Wasserman | Bioinformatics | Frederick Banting and Charles Best Canada Graduate Scholarships Masters Award (CGS-M); CIHR Doctoral Research Award: Vanier Canada Graduate Scholarship |
| Alborz Mazloomian | PhD | 2014/10 | 2017/03 | Primary Supervisor | Bioinformatics |  |
| Tyler Funnell | PhD | 2015/01 |  | Primary Supervisor | Bioinformatics |  |
| Emily Hindalong | PhD | 2015/09 | 2016/04 (Transfered to Dr. Carenini’s lab in Comp Sci) | Primary Supervisor | Bioinformatics |  |
| Sohrab Salehi | PhD | 2016/01 |  | Co-supervisor (with Alex Bouchard Cote) | Bioinformatics |  |

**Graduate Student Supervisory Committees**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Ph. D. Students | **Program Type** | **Start** | **Finish** | **Supervisor** | **Department or Program** |
|  |  |  |  |  |  |
| Eloi Mercier | PhD | 2010 | Withdrawn  (2013/03) | Paul Pavlidis | CIHR/MSFHR Training Program in Bioinformatics |
| Melissa McConechy | PhD | 2010 | 2015/03/31 | David Huntsman | Pathology & Laboratory Medicine |
| Robert Kridel | PhD | 2010 | 2016/03/29 | Randy  Gascoyne | Pathology & Laboratory Medicine |
| Katayayoon Kasaian | PhD | 2010 | 2015/09/02 | Steven Jones | CIHR/MSFHR Training Program in Bioinformatics |
| Julie Chih-yu Chen | PhD | 2011 |  | Wyeth Wasserman | CIHR/MSFHR Training Program in Bioinformatics |
| Shing Hei Zhan | PhD | 2011 | Withdrawn (2016/03) | Steven Jones | CIHR/MSFHR Training Program in Bioinformatics |
| Alborz Mazloomian | PhD | 2011 | Transfer to Shah Lab (2014/10) | Irmtraud Meyer | CIHR/MSFHR Training Program in Bioinformatics |
| Casper Shyr | PhD | 2011 | 2016/04/21 | Wyeth Wasserman | CIHR/MSFHR Training Program in Bioinformatics |
| Wenqiang Shi | PhD | 2012 |  | Wyeth Wasserman | Graduate Program in Bioinformatics |
| Charles Soong | PhD | 2012 |  | Sam Aparicio | Pathology & Laboratory Medicine |
| Trace (Yue) Sun | PhD | 2012 |  | Martin Hirst | Bioinformatics |
| Rod Docking | PhD | 2013 |  | Aly Karsan | Experimental Medicine |
| Bruno Grande | PhD | 2013 |  | Ryan Morin | SFU Molecular Biology and Biochemistry |
| Josh Scurll | PhD | 2013 |  | Daniel Coombs | Mathematics |
| Jake Lever | PhD | 2013 |  | Steven Jones | Bioinformatics |
| Jasleen Grewal | PhD | 2015 |  | Steven Jones | Bioinformatics |
| **M.Sc. Students** |  | **Start** | **Finish** | **Supervisor** | **Program** |
| Fong Chun Chan | MSc | 2010 | 2011 (Moved to PhD program) | Randy Gascoyne | CIHR/MSFHR Training Program in Bioinformatics |
| Patrick Tan | MSc | 2010 | 2012 | Paul Pavlidis | Bioinformatics |
| Adrin Jalali | MSc | 2012 | Inactive | Ryan Brinkman | Bioinformatics |
| Raewyn Billings | MSc | 2012 | 2014 | Sam Aparicio | Medical Genetics |
| Thuy Nguyen | MSc | 2013 | 06/2016 | Art Poon | Bioinformatics |
| Sohrab Salehi | MSc | 2013 | 12/2015 | Alex Bouchard-Cote | Bioinformatics |
| Celia Siu | MSc | 2014 |  | Steven Jones | Bioinformatics |
| Emma Laks | MSc | 2015 |  | Sam Aparicio | Genome Science and Technology Graduate Program |
| Farhia Kabeer | MSc | 2015 |  | Sam Aparicio | Pathology and Lab Medicine |
| Michael Yuen | MSc | 2015 |  | Peter Lansdorp / Peter Stirling | Medical Genetics |

**Postgraduate Students Supervised**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Student Name** | **Program Type** | **Program Details** | **Year** | | **Supervisory Role** | **Current Position/Awards** |
|  |  |  | **Start** | **Finish** |  |  |
| Gholamreza Haffari | Fellowship | Post-doc Fellow, PhD | 2010/04 | 2011/06 | Primary Supervisor | Lecturer, Monash University |
| Ali Bashashati | Fellowship | Post-doc Fellow, Research Assoc. | 2010/09 | 2013/09 | Primary Supervisor | Eli Lilly Fellowship, Staff Scientist |
| Yikan Wang | Fellowship | Post-doc Fellow | 2013/06 |  | Primary Supervisor | Michael Smith Foundation for Health Research /BC Cancer Foundation Post-Doctoral  Fellowship Award |
| Cydney Nielsen | Fellowship | Research Associate | 2013/07 |  | Primary Supervisor |  |
| Camila deSouza | Fellowship | Post-doc Fellow | 2013/10 | 2014/09 | Co-Supervisor with Jennifer Bryan and Nancy Heckman |  |
| Hossein Shahrabi Farahani | Fellowship | Post-doc Fellow | 2013/12 |  | Primary Supervisor |  |
| Yifei Huang | Fellowship | Post-doc Fellow | 2014/05 | 2015/05 | Primary Supervisor |  |
| Camila deSouza | Fellowship | Post-doc Fellow | 2014/10 |  | Primary Supervisor |  |
| Andrew McPherson | Fellowship | Post-doc Fellow | 2015/09 |  | Primary Supervisor |  |
| Andrew Roth | Fellowship | Post-doc Fellow | 2015/12 |  | Primary Supervisor |  |

*(e) Continuing Education Activities*

1. ***Activities as presenter/facilitator at CME Courses (UBC and non-UBC)***

|  |  |
| --- | --- |
|  | “Needles from Haystacks: Computational Biology and Distillation of Knowledge from Cancer Genomic Data”: Canadian Association of Pathologists, Vancouver, BC, June 4-6, 2011 |
|  | “Genomic architecture of novel breast cancer subtypes” 11th International Congress on the Future of Breast Cancer, Coronado CA, July 28, 2012 |
|  | “Interpreting the mutational landscapes of breast cancer through two in-silico lenses: models of evolution and gene expression impact” Triple Negative Breast Cancer Conference, London UK, Jun 26, 2013 |
|  | “Evolutionary dynamics of high-grade serous ovarian cancer genomes across anatomic space and time”. American Association of Cancer Research: Advances in Ovarian Cancer Research: From Concept to Clinic. Miami, Fl. Sep 20, 2013 |
|  | Lead Instructor, UBC Department of Pathology and Laboratory Medicine, Residency Training, Genomics Course for Pathology Trainees. Jan 6-10, 2014 (<http://pathology.ubc.ca/educational-programs/residency-training/new-genomics-course-for-pathology-trainees/>) |
|  | “Studying the evolution of ovarian cancers” Next Generation Sequencing Rounds, Child and Family Research Institute, BC Children’s Hospital, Vancouver, BC, May 16, 2014 |
|  | "Phylogenetic portraits of high grade serous ovarian cancers" Canadian Conference of Ovarian Cancer Research (CCOCR), Victoria BC, May 25-27, 2014 |
|  | "Phylogenetic portraits of high grade serous ovarian cancers" AACR Ovarian Cancer Research Symposium, Seattle WA, Sep 8-9, 2014 |
|  | “Advances in analytical mehods for clonal evolution inference at single-cell and bulk resolution” AACR Annual Meeting, Washington DC, April 1-5 2017 |

***2) CME activities as an attendee***

|  |  |
| --- | --- |
|  | Problem Based Learning Tutor Training Workshop, University of British Columbia, Faculty of Medicine, Vancouver, BC, Sep 24 and 26, 2013 |

*(f) Visiting Lecturer (indicate university/organization and dates)*

|  |  |
| --- | --- |
|  | “Measuring and modeling evolutionary dynamics in breast and ovarian cancer” MD Anderson Cancer Center, Houston TX; October 3, 2012 |
|  | “Computational Interpretation of Cancer Genomes”; Distinguished Speakers Lecture Series, Roswell Park Cancer Institute, Buffalo NY; Nov 14, 2012 |
|  | “Phylogenetic portraits of high grade serous cancers of the ovary” WIP Seminar, University of Pittsburgh,Pittsburgh, PA; Apr 3, 2014 |

*(g) Educational Leadership*

|  |  |
| --- | --- |
|  | UBC Department of Pathology and Laboratory Medicine, Genomics and Bioinformatics Program (for residents). Development and implementation/leadership. 2013 - present |

*(h) Curriculum Development & Innovation*

|  |  |
| --- | --- |
|  | Canadian Bioinformatics Workshops Series. Curriculum delivery and development. 2001 - present |
|  | IHHS302: “Topics in Health Informatics for Health/Life Science Students, Curriculum delivery and development. 2007, 2008 |

1. *Other Teaching & Learning Activities*

|  |  |
| --- | --- |
|  | Instructor: “Bioinformatics: Developing the Tools”, Canadian Bioinformatics Workshops Series, Montreal, PQ; 2005 |
|  | Instructor: “Introduction to Programming for Bioinformatics”, Canadian Bioinformatics Workshops Series, Vancouver, BC; February 18, 2005 |
|  | Instructor: “Analysis of array CGH data”, Canadian Bioinformatics Workshops Series. Vancouver, BC; July 2007 |
|  | Lead faculty: “Clinical genomics and biomarker discovery”. Canadian Bioinformatics Workshops Series. Toronto, ON; July 16-17, 2009. Developed and delivered curriculum. |
|  | Faculty: “Exploratory Data Analysis and Essential Statistics using R”. Canadian Bioinformatics Workshops Series. Vancouver, BC; May 2010 (www.bioinformatics.ca) |
|  | Lead faculty: “Clinical genomics and biomarker discovery”, Canadian Bioinformatics Workshops Series. Toronto, ON; September 2010 (www.bioinformatics.ca) |
|  | Lead faculty:”Bioinformatics for Cancer Genomics”, Canadian Bioinformatics Workshop (BiCG) Toronto, ON; August 2011 (www.bioinformatics.ca) |
|  | Core Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 29-30, 2012 |
|  | Invited Speaker: “Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time”, Department of Molecular Biology & Biochemistry, Simon Fraser University, Vancouver, BC; Nov 2, 2012 |
|  | Tutorial Lead and Speaker: “Overview of mutation discovery in cancer genome sequencing” in Tutorial Session 2 (Identifying and interpreting somatic mutations in cancer genomes), Asia Pacific Bioinformatics Conference (APBC), Vancouver, BC; Jan 20, 2013 |
|  | Invited Speaker: “Uncovering the impact of somatic mutations on transcriptional networks in cancer”, Invited Speaker, Canadian Institute for Advanced Research Genetic Networks workshop, Banff, AB; Apr 6, 2013 |
|  | Invited Speaker: “Towards identification of clonal populations in tumours through deep mutational profiling” Evolution of Cancer Symposium, Alpert Medical School, Brown University, Providence, RI; May 3, 2013 |
|  | Lead Faculty and Speaker: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 29, 2013 |
|  | Attendee: Problem based learning tutor training. UBC Division of Continuing Professional Development. Vancouver, BC; Sep 24-26, 2013 |
|  | “Studying the evolution of ovarian cancers” Next Generation Sequencing Rounds, Child and Family Research Institute, BC Children’s Hospital, Vancouver, BC; May 16, 2014 |
|  | Lead Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 26-30, 2014 |
|  | “Cancer as an example of where the field is headed”. Presentation at the Best Brains Exchange<<http://www.cihr-irsc.gc.ca/e/43978.html>> on “Canada as a Leader in the Development and Deployment of Precision/Personalized Medicine” being hosted in collaboration by the Canadian Institutes of Health Research (CIHR) and the Healthcare Innovation Secretariat to inform the work of the Advisory Panel on Healthcare Innovation<<http://www.hc-sc.gc.ca/hcs-sss/innovation/index-eng.php>>. Ottawa, ON; March 23, 2015 |
|  | Lead Faculty: Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, ON; May 26-28, 2015 |
|  | "Clonal dynamics in space and time: inference of evolutionary properties of cancer", AACR Annual Meeting Educational Session, New Orleans, LA, Apr 16, 2016 |
|  | Lead Faculty: Cancer Genomics - Canadian Bioinformatics Workshop, Ontario Institute of Cancer Research, Toronto, May 30-Jun 3, 2016 (teaching on Jun 1, 2016) |
|  | Invited Speaker: “Do clonal dynamics in human cancers reflect fitness properties? A spatio-temporal exploration.” The Institute of Cancer Research, and Barts Cancer Institute, London,UK; May 18-19, 2017 |

**9. SCHOLARLY AND PROFESSIONAL ACTIVITIES**

*(a) Areas of special interest and accomplishments*

**Cancer Genomics** My research program has driven discovery and computational model development in cancer genomics and tumour evolution with significant progress in breast, ovary and lymphoid cancers. This has led to recognition locally, nationally and internationally. My program of research focuses on evolutionary dynamics of cancers using a combination of genomics and statistical modeling of tumour progression. Since 2010, I have raised more than $8.4M (my portion) in competitive grant funding to support this work, and my papers have been cited 7469 times (Google Scholar, h-index: 35, i-index: 52). My work has produced 7 first/senior/corresponding author contributions in NEJM, Nature, and Nature Methods.

**Clonal Evolution in Solid Cancers** My research as resulted in several world firsts including the determination of tumour evolution demonstrated at nucleotide resolution in a lobular breast cancer (Shah et al., Nature 2009#), the first description of the mutational landscape and clonal evolution in a population of triple negative breast cancers (**Shah et al., Nature 2012#),** establishing reproducible patterns of clonal dynamics in patient derived xenografts (**Eirew et al., Nature 2014\*)** and quantifying the degree of clonal diversity in primary untreated HGS ovarian cancers (**Bashashati et al., J Path 2013\*).** My lab led the data analysis of the METABRIC project, leading to the most precise characterization of prognostically significant molecular subtypes of breast cancer, establishing a new standard in the field of breast cancer patient stratification (**Curtis et al., Nature 2012#**). Studying evolution in cancer has exploded in recent years in the field. The lobular breast cancer paper has been cited 718 times since 2009 and the triple negative breast cancer work has been cited 655 times since 2012.

**Discovery of New Cancer Genes** My work has identified 3 new cancer genes: FOXL2 (**Shah et al., NEJM 2009#**), ARID1A (**Wiegand et al., NEJM 2010**) and CIITA (**Steidl et al., Nature 2011#).** This series of papers describes discoveries of novel, somatic, recurrent alterations in ovarian cancers and lymphomas. These studies represent single gene discoveries associated with cancer subtypes that had not previously been implicated in disease progression. FOXL2 has led to new class of diagnostics for granulosa cells of the ovary, while ARID1A has opened up the study of chromatin remodeling as a disrupted process in cancer biology. Additional collaborative efforts with Drs. Marra, Gascoyne, Jones have led to the discovery of EZH2 mutations in follicular and diffuse large B cell lymphomas, and PTPN1 mutations in B cell lymphomas.

**Computational methods for cancer genome interpretation** My lab has developed several statistical and computational approaches for analysis and interpretation of cancer genomes. These include PyClone (**Roth et al., Nature Methods 2014\***) for inference of clonal population structures in tumours, TITAN (**Ha et al., Genome Research 2014\***) for identification of clonal diversity in the genome architecture of tumours, defuse (**McPherson et al., PLoS Computational Biology 2011\***) for identification of gene fusions from RNASeq and mutationSeq (**Ding et al., Bioinformatics 2012\***), SNVMix (**Goya et al., Bioinformatics 2011**), and JointSNVMix (**Roth et al., Bioinformatics 2012**) for point mutation detection**.**

We have also developed a conceptual advance in modeling the impact of somatic mutations on gene expression. This work has been published in Genome Biology (**Bashashati et al., 2012**). A very recent advance in this field will appear in Nature Communications (**Ding et al., 2015**) where we have determined a systematic landscape of mutations impacting gene expression across twelve major tumour types. In summary, our computational methods have been in continual application to NGS datasets in my and collaborator labs as described above, driving discovery. I have released numerous software tools that have been downloaded >4000 times and are in use in laboratories worldwide.

**Selected Publications (trainees underlined bold):**

***Clonal Evolution in Solid Cancers***

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 AJ, 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#.

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

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*(b) Research or equivalent grants (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC)).* ***BOLD = current funding***

| **Granting**  **agency** | **Title** | **COMP**  **Or**  **Non-COMP** | **$ per year** | **Duration**  **mo/yy to mo/yy** | **Principal Investigator** | **Co-PI(s)** |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |
|  | **OPERATING GRANTS** |  |  |  |  |  |
| Canadian Institutes of Health Research  (CIHR) | Improving computational inference of single nucleotide variants from next generation sequencing of cancer genomes | C | $99,078 | Oct/09-Sept/10 | S Aparicio | **S Shah** |
| Canadian Institutes of Health Research  (CIHR) | Mutations in the SWI/SNF chromatin remodelling complex genes: an alternative mechanism for ovarian carcinogenesis | C | $135,410 | Oct/10-  Sept/14 | D Huntsman | **S Shah**, S Aparicio, |
| Canadian Breast Cancer Research Alliance | Genome heterogeneity in predictive models of drug action in triple negative breast cancer | C | $288,488 | Apr/11-Mar/15 | S Aparicio | S Shah, S Chia, K Gelmon, M Martin, T Mak, M Marra |
| Canadian Institutes of Health Research (CIHR) | Genomic disruption in high-grade serous ovarian carcinomas: Steady state or continuous drift? | C | $131,428 | Oct/11-Sept/15 | S Shah | J McAlpine, B Gilks, D Huntsman |
| Canadian Cancer Society Research Institute (CCSRI) | Finding driver mutations in cancer through integrative profiling of mutational landscapes and transcriptional networks | C | $99,803 | Apr/12-Mar/14 | S Shah |  |
| **Canadian Institutes of Health Research**  **(CIHR)** | **The Genetics of Hereditary Upper Gastrointestinal Cancers: Beyond CDH1 Germline Mutations** | **C** | **$186,467** | **Oct/12 – Sept/17** | **D Huntsman** | **D Schaeffer, G Zogopoulos, K Schrader, S Shah, S Gallinger** |
| Canadian Institutes of Health Research  (CIHR) | Prognostic markers and biology of relapsed Hodgkin lymphoma | C | $167,386 | Oct/12-Sept/15 | C Steidl | S Shah, R Gascoyne |
| TFRI | Are genomic instability and clonal diversity prognostic indicators of high grade serous ovarian cancer? | C | $149,834 | Nov/12-Nov/15 | S Shah |  |
| **Canadian Cancer Society Research Institute (CCSRI) / BC Cancer Foundation / VGH Foundation** | **Contextual Genomics: the Foundation for Subtype Specific Approaches to**  **Ovarian Cancer Control** | **C** | **$250,000 /**  **75,000 / 75,000** | **Feb/13-Jan/18** | **D Huntsman,**  **S Shah** | **B Gilks, M Anglesio, M Hirst, A Tone, J McAlpine** |
| **Canadian Cancer Society Research Institute (CCSRI)** | **Defining the role of clonal genomes in the evolution and treatment of cancers** | **C** | **$248,002** | **Feb/13-Jan/18** | **S Aparicio** | **S Shah, C Hansen** |
| **Canadian Institutes of**  **Health Research**  **(CIHR)** | **Linking clonal genomes to tumour evolution and therapeutics** | **C** | **$208,088** | **Apr/13-Mar/18** | **S Aparicio** | **S Shah, C Hansen** |
| Genome Canada | Measuring and modeling tumour evolution from next generation sequencing data: enabling clinical study of clonal diversity in cancer patients | C | $124,842 | Jul/13- Jun/15 | S Shah |  |
| Genome Canada | Computational interpretation of cancer genomes: defining mutational landscapes for translational genomics | C | $345,253 | Jul/13- Jun/16 | S Shah | R Morin,  P Boutros |
| Genome Canada | Applied Bioinformatics of Cis-regulation for Disease Exploration (ABC4DE) | C | $250,000 | Jul/13- Jul/16 | W Wasserman | S Shah, A Lehman, C Van Karnebeek |
| BC Cancer Foundation | Cancer Genomics Research Fund / High grade serous ovarian cancer genome sequencing | Non-COMP | $333,333 | Oct/13 – Sept/16 | S Shah |  |
| Canadian Cancer Society Research Institute (CCSRI) | Building a Bridge from the Cancer Genome to the Cancer Clinic with Visual Analytics | C | $99,831 | Feb/14 – Jan/16 | S Shah | S Aparicio,  D Huntsman, J Laskin, M Marra |
| Canadian Cancer Society Research Institute (CCSRI) | How does the immune system contend with intratumoral heterogeneity? | C | $99,969 | Feb/14 – Jan/16 | B Nelson | S Shah, R Holt |
| **Canadian Institutes of Health Research**  **(CIHR)** | **Integrating Quantitative Imaging Methods and Genomic Biomarkers to Assess the Therapeutic Response of Cancers** | **C** | **$398,605** | **Dec 2014 – Nov 2019 (5 y)** | **F Benard** | **Morin RD, Aparicio S, Celler A, Laskin J, Shah SP, Gelmon K, Connors J, Chia S, Hamarneh G** |
| **Canadian Cancer Society Research Institute (CCSRI)** | **REAL-PDX: Resistance modeling in EGFR and ALK Lung cancer Patient-derived xenografts for personalized post-progression therapy** | **C** | **$250,000** | **Feb/15 – Jan/20** | **G Liu (Toronto)** | **S Shah, Tsao M, Shepherd FA, Leighl N, Yasufuku K, Pintille M, Lupien M, Haibe-Kains B, Bradbury P,** |
| **Canadian Institutes of**  **Health Research**  **(CIHR) – Foundation Grant** | **The clonal dynamics of ovarian cancers: phylogenetic models of chemosensitivity and resistance** | **C** | **$182,126** | **July/15-June/20** | **S Shah** | **S Aparicio, P Hieter, J McAlpine, A Bouchard-Cote, D Huntsman, C Hansen, M Marra** |
| **CDMRP / US DOD** | **Mechanistic Investigation of Breast Cancer Synthetic Lethality Through Inhibition of CDK12** | **C** | **$1,032,242 USD TOTAL** | **May/2016-Apr/2019** | **G Morin, S Aparicio** | **S Shah** |
| **Genome Canada** | **Reimagining genome browsing for the era of single cell genomics – *Under Embargo*** | **C** | **$125,000** | **July/2016-Jun/2018** | **S Shah, C Nielsen** |  |
| **Canadian Cancer Society Research Institute (CCSRI)** | **Deciphering the cellular crosstalk in the tumour microenvironment of classical Hodgkin lymphoma** | **C** | **$98,000** | **Feb/17 - Jan/19** | **C Steidl, S Shah** | **A Weng, S Aparicio, K Savage** |
| **BC Cancer Foundation** | **Cancer Genomics Research** | **Non-Comp** | **$300,000** | **Apr/17-Mar/19** | **S Shah** |  |
| **CANARIE** | **Montage: a software platform to drive the revolution in single cell cancer genomics** | **C** | **$121,950** | **July/17-Sept/20** | **S Shah** |  |
|  | **TEAM GRANT** |  |  |  |  |  |
| Canadian Institutes of  Health Research  (CIHR) | CIHR Team in genomics of forme fruste tumours: new vistas on cancer biology and management. | C | $1,042,122 | Jul/10-Jun/13 | D Huntsman | S Shah, S Aparicio, C Hansen, P Sorensen |
| Canadian Institutes of  Health Research  (CIHR) | Forme fruste tumours Sub-project of the above. Sub-Project 1: Sequencing of Forme Fruste Tumours | C | $436,605 | Jul/10-Jun/13 | D Huntsman | S Shah |
| **Terry Fox Research Institute (TFRI)** | **The Terry Fox New Frontiers Program Project Grant, The Genomics of Forme Fruste tumours: New vistas on cancer biology and treatment** | **C** | **$1,500,000** | **Jul/13 – Jun/18** | **D Huntsman (Nominated PI)**  **S Aparicio, G Morin, R Morin, S Shah, C Hansen, M Hirst, C Lee, M Marra, T Nielsen, P Sorensen, TM Underhill, S Yip** |  |
| **Terry Fox Research Institute (TFRI)** | **Data Analysis Core. Sub-project of the above** | **C** | **$296,036** | **Jul/13 – Jun/18** | **S Shah** | **M Hirst, R Morin** |
| **Terry Fox Research Institute (TFRI)** | **Sub-project 2: Models for Clonal Diversity & Tumour Evolution in Forme Fruste Tumours. Sub-project of the above** | **C** | **$252,520** | **Jul/13 – Jun/18** | **S Aparicio** | **C Hansen, T Nielsen, S Shah** |
| Terry Fox Research Institute (TFRI) | The Terry Fox New Frontiers Program Project Grant, Molecular Correlates of Treatment Failure in Lymphoid Cancers | C | $1,295,209 | Jul/13 – Jun/16 | R Gascoyne (Nominated PI)  J Connors, M Marra, C Steidl, S Shah, S Jones |  |
| Terry Fox Research Institute (TFRI) | Sub-project 1: Evolutionary dynamics and driver mutations  underlying histological transformation and treatment resistance in  follicular lymphoma. Sub-project of the above | C | $210,261 | Jul/13 – Jun/16 | M Marra, S Shah |  |
| **Natural Sciences and Engineering Research Council of Canada (NSERC)** | **The Cancer Genome Collaboratory** | **C** | **$1,499,965** | **Mar/14 – Mar/18** | **L Stein** | **P Boutros, S Sahinalp, Ferretti, K EL Emam, BK Shoichet, BM Knoppers, BFFO Ouellette, G Bourque, GD Bader, S Shah, A Bouchard-Cote** |
| **Natural Sciences and Engineering Research Council of Canada (NSERC)** | **Research Module 3: Modeling tumour evolution. Sub-project of the above** | **C** | **$115,750** | **Mar/14 – Mar/18** | **S Shah** |  |
| **Terry Fox Research Institute (TFRI)** | **The Terry Fox New Frontiers Program Project Grant, Overcoming treatment failure in lymphoid cancers** | **C** | **$1,500,000** | **Jul/16 – Jun/21** | **J Connors (Nominated PI)**  **M Marra, C Steidl, S Shah, D Scott, A Weng, G Morin, A Mungall, G Slack** |  |
| **Terry Fox Research Institute (TFRI)** | **Sub-project 1: Co-evolution of malignant cell populations and infiltrating immune cells in B-cell lymphomas. Sub-project of the above** | **C** | **$255,760** | **Jul/16 – Jun/21** | **S Shah, A Weng** | **C Hansen** |
| **Cancer Research UK Grand Challenge** | **IMAXT, Imaging and Molecular Annotation of Xenografts and Tumours** | **C** | **$183,333 GBP** | **May/17 - Apr/23** | **G Hannon** | **S Aparicio, B Bodenmiller, E Boyden, J Joyce, X Zhuang** |
|  | **INFRASTRUCTURE GRANTS** |  |  |  |  |  |
| CFI Leaders Opportunity Fund /  BC Knowledge Development Funds (matching CFI funds) / Other eligible partners | 1Computational infrastructure for defining genomic landscapes and resolving the clinical impact of somatic mutations in cancer | C | $265,681 /  $265,680 /  $214,380  Total  $745,741 | Apr/13 – Mar/16 | S Shah |  |
| **CFI Leaders Opportunity Fund /**  **BC Knowledge Development Funds (matching CFI funds) / Other eligible partners** | **A surgical-genomic tissue bank for endometriosis** | **C** | **$125,000 / $125,000 / $62,500**  **Total**  **$312,500** | **May/14 – Apr/17** | **P Yong** | **S Shah** |
|  | **TRAINING**  **GRANTS** |  |  |  |  |  |
| **Natural Sciences and Engineering Research Council of Canada (NSERC)** | **Create Program for Computational Methods for the Analysis of the Diversity and Dynamics of Genomes** | **C** | **$300,000** | **Apr/13 – Mar/18** | **C Sahinalp** | **S Shah, F Brinkman, T Moller, C Chauve, P Unrau, J Chen, C Collins, M Ester, R Morin, A Shiraman** |
|  | **OTHER**  **GRANTS** |  |  |  |  |  |
| Department of  Defense (USA) *(Consortium Development Grant)* | Multidisciplinary Ovarian Cancer Outcomes Group | C | $328,625 | Jan/13-Jan/15 | M Pike | S Shah |
|  |  |  |  |  |  |  |

1 This equipment is high performance computing equipment to be used in various cancer genome sequencing projects and in the development of new computational methods for analysis.

*(c) Research or equivalent contracts, including funding for clinical trials (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC).* ***BOLD = current funding.***

*(d) Invited Presentations*

|  |  |
| --- | --- |
|  | “Pegasys: Workflow management for genome annotation.” Network Tools and Applications in Biology (NETTAB2005), Naples, Italy “Workflows management: new abilities for the biological information overflow”, Naples, Italy; Oct 7, 2005 |
|  | “Integrating copy number polymorphisms into array CGH analysis using a robust HMM.” International Conference on Intelligent Systems for Molecular Biology (ISMB) 2006, Fortaleza, Brazil; August 2006 |
|  | “Modeling recurrent DNA copy number alterations in array CGH data.” International Conference on Intelligent Systems for Molecular Biology (ISMB) 2007, Vienna, Austria; August 2007 |
|  | “Computational inference of copy number changes from next generation sequencing of cancer genomes.” AGBT 2009, Marco Island, USA; February 2009 |
|  | “Model-based clustering of array CGH data”. International Conference on Intelligent Systems for Molecular Biology (ISMB) 2009, Stockholm, Sweden; August 2009 |
|  | “Probabilistic models for detecting SNVs from next gen sequencing of tumours”. International Conference on Intelligent Systems for Molecular Biology (ISMB) 2009, Stockholm, Sweden; August 2009 |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models”. Centre for Cellular and Biomolecular Research, University of Toronto. Toronto, ON; Nov 3, 2009. Host: Michael Brudno. |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models”. Stanford University. Nov 13, 2009. Host: Matt van de Rijn. |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models”. Vancouver Bioinformatics Users Group Seminar Series, Vancouver, BC; Nov 26, 2009. |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models”. Memorial Sloan Kettering Cancer Center, New York, NY; Apr 2010 |
|  | Invited Speaker: “Integrative genomic and transcriptomic profiling of 1000 breast cancers”. 10th Annual McGill Workshop on Bioinformatics, Holetown, Barbados; January 2011 |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models”. The Hospital for Sick Children, Toronto, ON; May 2010 |
|  | “Beyond Sequencing”. San Francisco, CA; June 2010 |
|  | “Statistical models for inference of SNVs in cancer genomes”. Isaac Newton Institute, Cambridge, UK; July 2010 |
|  | “Defining mutational landscapes of tumors with sequencing and statistical models”. University of Washington COMBI Seminar series, Seattle, WA; Nov 2010 |
|  | “Defining mutational landscapes of tumors with sequencing and statistical models”. Aarhus University, Denmark; November 2010 |
|  | “Integrative genomic and transcriptomic profiling of 1000 breast cancers” 10th Annual McGill Workshop on Bioinformatics, Holetown, Barbados; January 2011 |
|  | “The cancer genome and probabilistic models” UBC Comp Science Faculty Lecture Series, Vancouver, BC; March 2011 |
|  | “The somatic mutational landscapes of breast cancer subtypes” 6th Annual Canadian Genetic Epidemiology & Statistical Genetics Meeting, King City, ON; May 2011 |
|  | "The mutational landscapes of breast cancer subtypes". Keynote address: Bioinformatics Training Program (BTP) and the Interdisciplinary Oncology Program (IOP), UBC. Vancouver, BC; May 27th, 2011 |
|  | “Mutation discovery in cancer using next generation sequencing and probabilistic models” University of Washington COMBI Seminar series, Seattle, WA; Nov 2011 |
|  | “Somatic mutation discovery in cancer with NGS sequencing: From allelic counts to biologic inference” Gene Technology Access Centre (GTAC), Walter and Eliza Hall Institute of Medical Research, Parkville Australia; December 5-7, 2011 |
|  | “Genome-wide mutational heterogeneity in breast and ovarian cancer” Peter McCallum Cancer Centre, Melbourne Australia; December 8, 2011 |
|  | “Measuring patterns of tumour evolution: Computational models and biological inference” Plenary Session on Computational Genomics. Canadian Human and Statistical Genetics Meeting, Niagara on the Lake, ON; May 2, 2012 |
|  | Keynote Speaker: Measuring Patterns of Tumour Evolution: computational models and biological inference, U of Toronto Genome Biology and Bioinformatics, Toronto, ON; May 23, 2012 |
|  | Measuring patterns of tumour evolution: Computational models and biological inference” Ontario Institute for Cancer Research Informatics and Bio-Computing (Canadian Bioinformatics Workshop), Toronto, ON; May 31, 2012 |
|  | “Measuring patterns of tumour evolution: Computational models and biological inference” Copenhagenomics, Kobenhavn, Copenhagen; June 14, 2012 |
|  | “Measuring patterns of tumour evolution: Computational models and biological inference” BioC 2012; Fred Hutchinson Cancer Centre, Seattle, WA; July 24, 2012 |
|  | “Computational Interpretation of Cancer Genomes” Takeda Shonan Research Centre Splicing Meeting, Shonan, Japan; Oct 18, 2012 |
|  | “Evolutionary Dynamics of High-Grade Serous Ovarian Cancer Genomes Across Anatomic Space and Time” New Principal Investigators Meeting, Mont-Gabriel, PQ; October 26-28, 2012 |
|  | “Modeling tumour evolution in breast and ovarian cancer”; University of British Columbia Department of Anesthesiology, Pharmacology and Therapeutics Seminar Series, Vancouver, BC; Nov 20, 2012 |
|  | “Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time”; BC Cancer Agency Annual Conference, Vancouver, BC; Nov 30, 2012 |
|  | “Measuring and modeling evolutionary dynamics of breast and ovarian cancer”, Princess Margaret Hospital, Ontario Cancer Institute, Toronto, ON; Dec 4, 2012 |
|  | “Evolutionary dynamics of high grade serous ovarian cancer genomes across anatomic space and time”, Pacific Symposium on Biocomputing (PSB) 2013, Big Island of Hawaii; January 5, 2013 |
|  | “Evolutionary dynamics in breast and ovarian cancer: implications for personalized therapy”, Invited Speaker, Ottawa Illumina Seminar 2013: The Age of Personalized Medicine, Ottawa, ON; Feb 19, 2013 |
|  | “Evolutionary dynamics of primary high-grade serous ovarian cancers revealed through spatial and temporal mutational profiling”, Invited Speaker, Quebec TFRI Node Research Day, Montreal, PQ; Apr 18, 2013 |
|  | “Forme Fruste Tumors”; Terry Fox Research Institute Annual Scientific Meeting, Ottawa, ON; May 10, 2013 |
|  | “Evolutionary dynamics of high-grade serous ovarian cancers: implications for personalized medicine”, Invited Speaker, Personalized Medicine and Individualized Drug Delivery Conference, 2013 Canadian Society for Pharmaceutical Sciences Annual Symposium. Vancouver, BC; Jun 12, 2013 |
|  | “Statistical models for evolutionary dynamics of tumour cell populations profiled with deep digital sequencing” Bertinoro Computational Biology Meeting 2013, Bertinoro, Italy; Sep 9, 2013 |
|  | “Are Genomic Instability and Clonal Diversity Prognostic Indicators of High Grade Serous Ovarian Cancer?”TFRI BC Node Research Day, Vancouver, BC; Oct 31, 2013 |
|  | “Modeling Tumour Evolution in the “Big Data” Era of Cancer Genome Sequencing” Plenary session at Canadian Cancer Research Conference, Toronto, ON; Nov 4, 2013 |
|  | “Modeling evolution of the structural genome in cancer cell populations” New York Bioinformatics Symposium, New York, NY; Nov 15, 2013 |
|  | “Inferring clonal population structure in human cancer” SFU MADD-GEN/DiDy Annual Joint Workshop, Burnaby, BC; Mar 5, 2014 |
|  | "Phylogenetic portraits of high grade serous ovarian cancers" Genome Sciences Centre All Staff Meeting, Vancouver, BC; Mar 14, 2014 |
|  | "Phylogenetic portraits of high grade serous ovarian cancers" Defeating Ovarian Cancer, Long Island, NY; Apr 21-23, 2014 |
|  | “The evolutionary dynamics of follicular lymphoma revealed through whole genome sequencing” TFRI Conference, Montreal, PQ; May 8, 2014 |
|  | “Clonal dynamics in space and time in human cancer” Evolution of Drug Resistance, the Kavli Institute for Theoretical Physics – University of California, Santa Barbara, CA; Sept 18, 2014 |
|  | “DNA and the hidden faces of cancer” Interface 2014, Vancouver, BC; Sept 29, 2014 |
|  | “Genomics + cancer + big data = Startup” Interface 2014, Vancouver, BC; Sept 30, 2014 |
|  | “Clonal Dynamics of Human Cancers Measured in Space and Time at Single Cell Resolution” CIFAR Genetic Networks Workshop, University of Washington, Seattle, WA; Nov 9, 2014 |
|  | “Clonal dynamics in space and time in human cancers” 12th Annual Symposium of the Dept. of Genome Sciences, University of Washington, Seattle, WA; Nov 10, 2014 |
|  | “Comparing the genomic landscapes of poor responders and long-term survivors of high grade serous ovarian cancer” Seventh AACR Conference on the Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved, San Antonio, TX; Nov 11, 2014 |
|  | “Clonal dynamics in space and time in human cancers”, Precursors to breast cancer and tumor evolution, 14th Annual BCI-McGill Workshop, Bellairs Research Institute, Holetown, Barbados; January 24, 2015 |
|  | “Characterization of Cancer Genomes”, Cambridge Healthtech Institute’s Third Annual Clinical Sequencing - Translating NGS to Practice; part of the 22nd Annual Molecular Medicine Tri-Conference, San Francisco, CA; Feb 18, 2015 |
|  | “Cancer as an example of where the field is headed”. Presentation at the Best Brains Exchange <http://www.cihr-irsc.gc.ca/e/43978.html> on “Canada as a Leader in the Development and Deployment of Precision/Personalized Medicine” being hosted in collaboration by the Canadian Institutes of Health Research (CIHR) and the Healthcare Innovation Secretariat to inform the work of the Advisory Panel on Healthcare Innovation <http://www.hc-sc.gc.ca/hcs-sss/innovation/index-eng.php>. Ottawa, ON; March 23, 2015 |
|  | “Evolution in human cancer”, SFU MADD-GEN Workshop on Cancer Genomics, Burnaby, BC; May 1, 2015 |
|  | “Clonal dynamics in human cancers measured across time and space”, Canadian Cancer Immunotherapy Conference Genomics, Vancouver, BC; May 20, 2015 |
|  | “Comprehensive approaches to mutation interpretation: tumour evolution and gene expression integration.” Genetics and Genomics for the Practicing Clinician, Session 1: Overview of Available Technologies and Pathology, ASCO Pre-annual meeting seminar, Chicago, IL; May 28, 2015 |
|  | “Tracking clonal dynamics in human cancers across space and time.” Oxford University. London, UK; June 10, 2015 |
|  | “Tracking clonal dynamics in human cancers in space and time at single cell resolution”. BACR/CRUK Evolution and Intratumoural Heterogeneity Meeting. Royal Society of Medicine. London, UK; June 11, 2015 |
|  | “Tracking clonal dynamics in human cancers in space and time at single cell resolution”. Plenary Session 2: Molecular Genomics. BCCA Translational Retreat, Vancouver, BC; June 19, 2015. Plenary speaker and session chair. |
|  | “Tracking clonal dynamics in human cancers in space and time at single cell resolution”. Forecasting Evolution, Lisbon, Portugal; July 6, 2015 |
|  | “Somatic mutations in two cancer contexts: evolutionary dynamics and gene expression impact”. Statistical and Computational Challenges In Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics meeting (15w5142), Banff, AB; August 7, 2015 |
|  | “Tracking Clonal Dynamics in Human Cancers". 2015 Gordon Research Conference (GRC) on Hormone-Dependent Cancers: mechanisms to tailored therapeutics. Sunday River Resort, Newry, ME, USA; August 17, 2015 |
|  | “Somatic Mutations in Context: Toward Modeling Cancer Ecosystems”. Workshop “Systems Genetics of Cancer 2015”- Lucy Cavendish College, Cambridge, UK; Sept 21, 2015 |
|  | “Inferring fitness landscapes in cancers”. International Workshop on Computational Precision Medicine, Montpelier, FR; Sept 24, 2015 |
|  | “Somatic mutations in two cancer contexts: evolutionary dynamics and gene expression impact”. Stanford Cancer Systems Biology Symposium, Stanford, CA; Oct 22, 2015 |
|  | “Towards modeling clonal fitness in human cancers”, Invited Seminar, Ontario Institute for Cancer Research, Toronto, ON; Oct 26, 2015 |
|  | “Phylogenetic analysis reveals divergent modes of clonal spread and intraperitoneal mixing in high grade serous ovarian cancer”. NCRI Cancer Conference 2015, Liverpool UK; Nov 3, 2015 |
|  | “Towards modelling fitness in human cancers”, Genomics Seminar Series, Imperial College Hammersmith, London, UK; Nov 4, 2015 |
|  | “Towards modelling fitness in human cancers”, The Institute of Cancer Research, London, UK; Nov 5, 2015 |
|  | “Tumour Complexity – Overview of Tumour Heterogeneity”, 41st Annual D.A. Boyes Society Meeting & Obstetrics and Gynaecology Clinical Review, Vancouver, BC; Nov 6, 2015 |
|  | “Towards modeling fitness of clonal populations in human cancers”, Mayo Clinic, Rochester, MN; Nov 19, 2015[Delete](http://td.pathology.ubc.ca/f16/templates/delete/2665/9908) |
|  | “Towards inference of fitness landscapes in human cancer”, University of Toronto, Toronto, ON; Jan 18, 2016 |
|  | “Towards inference of fitness landscapes in human cancer”, Simons Institute Computational Cancer Biology Workshop, Berkeley, CA, Feb 1-5, 2016 |
|  | “Towards inference of evolutionary fitness landscapes in human cancer”, Tucson Symposium, Tucson, AZ, Mar 8, 2016 |
|  | "Clonal dynamics in space and time: inference of evolutionary properties of cancer", AACR Annual Meeting Educational Session, New Orleans, LA, Apr 16, 2016 |
|  | “Clonal evolution in high grade serous ovarian cancer: implications for intraperitoneal spread”, National Invited Speaker: Canadian Conference on Ovarian Cancer Research, Niagara Falls, ON, May 15, 2016 |
|  | "Clonal dynamics in space and time: inference of evolutionary properties of cancer", Latsis Symposium on “Personalized Medicine – Challenges and Opportunities”, Zurich, Switzerland, Jun 28, 2016 |
|  | “Evolutionary dynamics of cancer: a spatio-temporal analysis”. Keynote speaker, 14th RECOMB Comparative Genomics Satellite Workshop. Montréal, Canada, October 11-14, 2016. |
|  | “Cancer Evolution Using Bulk and Single Cell Analysis”, American Association for Cancer Research Annual Meeting 2017. Washington, DC, Apr 1-5, 2017. |
|  | “Machine learning for cancer evolution”, Microsoft Research, Redmond, USA, May 15, 2017 |
|  | “Clonal fitness in human cancers: a spatio-temporal exploration”, Institute for Cancer Research, Royal Marsden Hospital, London UK, May 18, 2017 |
|  | “Clonal fitness in human cancers: a spatio-temporal exploration”, Barts Cancer Institute, London UK, May 18, 2017 |
|  | “Cancer evolution: a spatio-temporal exploration”, Arnie Charbonneau Cancer Institute, Calgary, Canada, Jun 10, 2017 |
|  | “Machine learning for cancer evolution”, Google Research, MountainView, CA, Jun 20, 2017 (scheduled) |
|  | “Cancer evolution: a spatio-temporal exploration”, Memorial Sloan Kettering Cancer Center, NY, USA, Aug 23, 2017 (scheduled) |

*(e) Invited Participation*

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|  | Peter Wall Theme Development Workshop on “Public engagement around a new model for access to research resources”, Vancouver, BC, May 25, 2016 |

*(f) Conference Participation (Organizer, Chair, Moderator, etc.)*

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| --- | --- |
| 1. | Scientific committee for the Network Tools and Applications in Biology (NETTAB2005) workshop entitled: “Workflows management: new abilities for the biological information overflow”, Naples, Italy Subject: workflows in bioinformatics. Oct 5-7, 2005 |
|  | Chair, International Conference on Research in Computational Molecular Biology (RECOMB) Satellite Workshop on Computational Cancer Biology (RECOMB-CCB), Vancouver, BC, March 2011 |
|  | Organizer, Speaker, Bioinformatics in Cancer Genomics (BiCG), Toronto, ON, August 28 - September 2, 2011 |
|  | Program Committee Member: International Conference on Intelligent Systems for Molecular Biology (ISMB) 2012 Satellite Meeting on High Throughput Sequencing (HitSeq), Los Angeles, CA, July 2012 |
|  | Organizing Committee Member: International Conference on Intelligent Systems for Molecular Biology (ISMB) 2013 Satellite Meeting on High Throughput Sequencing, Berlin, Germany, July 2013 |
|  | Organizing Committee Member and Plenary One Chair: 2014 Terry Fox Research Institute Annual Scientific Meeting, Montreal, PQ, May 8-10, 2014 |
|  | Plenary speaker and Session Chair. Plenary Session 2: Molecular Genomics. BCCA Translational Retreat, Vancouver, BC, June 19, 2015. |
|  | Co-organizer / Plenary Session Chair, 2016 Keystone Symposium, The Cancer Genome. Banff, AB. Feb 7-12, 2016 |
|  | Committee Member, AACR Scientific Program Committee, Apr 16-20, 2016 |
|  | Scientific Committee Member, The European Society for Medical Oncology (ESMO)  Congress in partnership with EACR, Madrid, Spain. Sept 8-12, 2017 |

*(g) Other Presentations*

|  |  |
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|  | Invited Speaker: “Molecular investigations of breast cancer: What’s in the genome?” Canadian Breast Cancer Foundation Speaker Series , West Vancouver Community Centre, March, 2011. |

*(h) Other Scholarship of Education Activities*

*(i) Other Professional Contributions*

**10. SERVICE TO THE UNIVERSITY**

*(a) Areas of special interest and accomplishments*

|  |  |
| --- | --- |
|  | Associate member: Peter Wall Institute of Advanced Studies. 2012-2013 |
|  | Ad hoc data sciences working group. UBC Faculty of Medicine. 2015- |
|  | FoM IT Governance Committee. UBC Faculty of Medicine. Jan/2016-Dec/2018 |

*(b) Memberships on committees, including offices held and dates*

|  |  |
| --- | --- |
|  | ***Department of Pathology and Laboratory Medicine Committees*** |
|  | Committee Member, Tier 2 Canada Research Chair (CRC) Search Committee, Dec 2012 – present. |

*(c) Faculty mentoring*

*(d) Other service, including dates*

**11. SERVICE TO THE HEALTH PROFESSIONS/HEALTH AUTHORITIES**

*(a) Areas of special interest and accomplishments*

*(b) Memberships on committees, including offices held and dates*

*(c) Other service, including dates*

**12. SERVICE TO THE COMMUNITY**

*(a) Areas of special interest and accomplishments*

*(b) Memberships on scholarly societies, including offices held and dates*

*(c) Memberships on other societies, including offices held and dates*

*(d) Memberships on scholarly committees, including offices held and dates*

|  |  |
| --- | --- |
|  | Scientific officer and reviewer. Canadian Cancer Society Research Institute, Panel J2 competition, 2009 – 2011 |
|  | Member, CIHR Doctoral Awards A Committee, 2011 - |
|  | Reviewer, Aarhus University Interdisciplinary Research Centre competition, 2011 |
|  | Reviewer, Strategic Grants competition of Quebec Breast Cancer Foundation, 2011 |
|  | Committee Member, Michael Smith Foundation for Health Research. Research Advisory Council, Jun 2011 - present |
|  | Scientific Reviewer, National Grants Competition, Canadian Breast Cancer Foundation, 2012 - |
|  | Reviewer. Canadian Cancer Society Research Institute, Innovation Grants Panel Biomarkers and Genomics (Panel I1a), 2012 – present (2012, 2013, 2014) |
| 1. 2 | Referee, Health Innovation Challenge Fund, Wellcome Trust, Jan – Feb 2013 |
|  | Committee Member, TFRI COEUR Study Committee, Jul 2013 - present |
|  | Member, Canadian Institute for Advanced Research (CIFAR) Genetic Networks Program, Jul 2013 - present |
|  | Committee Member, TFRI PPG Competition Peer Review Committee, 2014 |
|  | Reviewer, NSERC Discovery Grant, 2014 |
|  | Committee Member, NSERC-Create Steering Committee, 2015 |
|  | Reviewer, CIHR GMX Peer Review Committee, 2015 |
|  | Reviewer, CFI John R Evans Fund, 2015 |
|  | Reviewer, Prostate Cancer Canada Movember Discovery Grant Competition (**Panel B –** Early Detection and Biomarkers), 2016 |
|  | Reviewer. CIHR Foundation Scheme (Stage 2), 2016 |
|  | Steering Committee Member. High Dimensional Bioinformatics (NSERC CREATE grant), 2015- |
|  | Reviewer, Canada Research Chairs Program 2016 |

*(e) Memberships on other committees, including offices held and dates*

*(f) Editorships (list journal and dates)*

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| 1. 1 | Associate Editor, BMC Cancer, Jan 2010 - present |

*(g) Reviewer (journal, agency, etc. including dates)*

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|  | Ad hoc Evaluation of Articles. Referee for Biometrika, Bioinformatics (3 manuscripts Aug 23, 2013) NAR, Pacific Symposium on Biocomputing, Journal of Statistical Methodology, BMC Bioinformatics, BMC Genomics, PLoS Computational Biology, Genome Research, Genome Biology, Molecular Cancer Research, Nature Communications, Nature Biotechnology, Nature, BioMedCentral Cancer, Journal of Pathology, Nature Genetics |

*(h) External examiner (indicate universities and dates)*

|  |  |
| --- | --- |
|  | University of British Columbia, Department of Pathology and Laboratory Medicine; Vincent Montoya, M.Sc., Thesis title “A Metagenomic Analysis of Female Genital Tract Diseases”, Apr 9, 2013 |
|  | University of Toronto, Institute of Medical Science; Zaheer S Kanji, M.Sc., Thesis title “Somatic Copy Number Aberrations In Familial Pancreatic Cancer: Integrative Genomics And Gene Discovery”, Sep 11, 2013 |
|  | Chair. University of British Columbia, Department of Bioinformatics; Adriana Sedeno, Oct 9, 2014 |
|  | Research Proficiency Evaluation (RPE) Committee. University of British Columbia, Department of Computer Science. Mohamed Ahmed, April 15, 2015 |
|  | University of Toronto, Dept of Molecular Genetics; Gavin Wilson, Thesis title “Accurate identification of adenosine deamination with RNA-seq”, Jan 18, 2016 |
|  | University of British Columbia, Department of Pathology and Laboratory Medicine;  Robert Kridel, PhD., Thesis Title “The genetic basis of transformation and progression in follicular lymphoma”, Mar 29, 2016 |
|  | University of British Columbia, Department of Computer Science; Jiarui Ding, PhD, Thesis Title “Computational methods for systems biology data of cancer”, May 4, 2016 |
|  | University of British Columbia, Department of Bioinformatics; Thuy Nguyen, M.Sc., Thesis Title “Overcoming missing data in phylogenetic analysis of shotgun sequencing to detect HIV adaptation to immune response”, June 6, 2016 |
|  | University of British Columbia, Department of Bioinformatics; Maia A. Smith, M.Sc., Thesis Title “E-scape: interactive visualization of single cell phylogenetics and spatio-temporal evolution in cancer”, Aug 29, 2016 |
|  | University of British Columbia, Department of Bioinformatics; Celia Siu, M.Sc., Thesis Title “Characterization of the human thyroid epigenome”, Feb 28, 2017 |
|  | University of British Columbia, Department of Bioinformatics; Fong Chun Chan, PhD, Thesis Title “Clinical Implications of inter-tumour, intra-tumour, and tumour microenvironment heterogeneity in B-cell lymphomas”, Mar 10,2017 |
|  | University of British Columbia, Department of Bioinformatics; Seyed Alborz Mazloomian, PhD, Thesis Title “A systems biology study of alternative splicing regulations and functions”, Apr 27, 2017 |

*(i) Consultant (indicate organization and dates)*

*(j) Other service to the community*

|  |  |
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|  | Guest Blogger, BC Cancer Foundation, May – Jun 2012. |

**13. AWARDS AND DISTINCTIONS**

*(a) Awards for Teaching (indicate name of award, awarding organizations, date)*

*(b) Awards for Scholarship (indicate name of award, awarding organizations, date)*

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|  | Lap-Chee Tsui Publication Award from the Canadian Institutes for Health Research Institute of Genetics, In recognition of outstanding published health research carried out by trainees, For the discovery of the mutation in FOXL2 in granulosa cell tumors of the ovary (published in NEJM). $1000 |
|  | Senior Graduate Trainee Award, Michael Smith Foundation For Health Research, Canada, 04/2006-04/2008, $45,000 |
|  | University Graduate Fellowship (declined), University of British Columbia, Effective: 05/2006-05/2009, $48,000 |
|  | ISCB travel award, International Society for Computational Biology, United States, 07/2007-08/2007, Travel fellowship to ISMB 2007 conference, $1,100 |
|  | Postdoctoral Fellowship, Michael Smith Foundation For Health Research, Canada ($120,000 over 3yrs), 10/2008-10/2011 |
|  | ISCB travel award, International Society for Computational Biology, United States,, 07/2009-08/2009, Travel fellowship to ISMB 2009 conference, $1,100 |
|  | Canadian Breast Cancer Foundation Bioinformatics Fellowship. (part of $500,000 over 5yrs to Dr. Sam Aparicio), 2008-2013 |
|  | Research Fellowship, Eli Lilly. ($130,000 over 2yrs), 09/2009-09/2011 |
|  | Career Investigator Award, Michael Smith Foundation for Health Research ($635,000 over 8yrs). 07/2011-06/2019 |
| 1. 1 | Associate, Peter Wall Institute for Advanced Studies, $1000. 09/2012-09/2013 |
| 1. 2 | Terry Fox New Investigator Award, Terry Fox Research Institute ($450,000 over 3 yrs) 10/2012-10/2015 |
|  | Distinguished Achievement Award for Overall Excellence – Early Career. Faculty of Medicine, UBC, 2013 |
|  | Canada Research Chair Tier 2 in Computational Cancer Genomics ($500,000 over 5 years), 04/2013-03/2018 |
|  | Award for Early Career Excellence in Research and Discovery. UBC Department of Pathology and Laboratory Medicine, 05/2015 |
|  | UBC Killam Research Prize. Applied Science, Junior Category 01/2016 |

*(c) Awards for Service (indicate name of award, awarding organizations, date)*

|  |  |
| --- | --- |
| 1. 2 | Student service award. Department of Computer Science, UBC, 2008 |

*(d) Other Awards*

**14. OTHER RELEVANT INFORMATION (Maximum One Page)**

**THE UNIVERSITY OF BRITISH COLUMBIA**

***Publications Record***

**SURNAME**: Shah **FIRST** **NAME**: Sohrab **Initials**:SPS

**MIDDLE NAME(S)**: Prakash **Date**: March 31, 2017

**Authorship Statement**

Underline – trainees under my direct supervision

**1. REFEREED PUBLICATIONS**

*(a) Journals*

MANUSCRIPTS SUBMITTED FOR PUBLICATION

|  |
| --- |
| De Souza CPE, Faharani H, Billings R, Yap D, Shumansky K, Aniba MR, Wan A, Mes-Masson AM, Aparicio S, and **Shah SP**. Engineered in-vitro cell line mixtures and robust evaluation of computation methods for clonal decomposition and longitudinal dynamics in cancer. *Scientific Reports.* Submitted (2017) |

MANUSCRIPTS ACCEPTED FOR PUBLICATION

|  |
| --- |
| McPherson A, Roth A, Ha G, Chauve C, Steif A, De Souza CPE, Eirew P, Bouchard-Cote A, Aparicio S, Sahinalp C, **Shah SP**. ReMixT: Accurate Estimation of Clone Specific Genomic Structure. *Genome Biology.* Accepted |

PUBLISHED REFEREED PUBLICATIONS

|  |  |
| --- | --- |
|  | **Shah SP**, McVicker GP, Mackworth AK, Rogic S, Ouellette BF. GeneComber: combining outputs of gene prediction programs for improved results. *Bioinformatics*. 2003 Jul 1;19(10):1296-7. Contribution: designed, implemented and tested the software; wrote the manuscript. |
|  | **Shah SP**, He DY, Sawkins JN, Druce JC, Quon G, Lett D, Zheng GX, Xu T, Ouellette BF. Pegasys: software for executing and integrating analyses of biological sequences. *BMC Bioinformatics*. 2004 Apr 19;5:40. Contribution: designed, implemented and tested the software; wrote the manuscript. |
|  | Kemmer D, Huang Y, **Shah SP**, Lim J, Brumm J, Yuen MM, Ling J, Xu T, Wasserman WW, Ouellette BF. Ulysses - an application for the projection of molecular interactions across species. *Genome Biol*. 2005 Dec;6(12):R106. Contribution:developed the Atlas data warehouse, enabled this analysis |
|  | **Shah SP**, Huang Y, Xu T, Yuen MM, Ling J, Ouellette BF. Atlas - a data warehouse for integrative bioinformatics. *BMC Bioinformatics*. 2005 Feb 21;6:34. Contribution: designed, implemented and tested the software; wrote the manuscript. |
|  | **Shah SP**, Xuan X, DeLeeuw RJ, Khojasteh M, Lam WL, Ng R, Murphy KP. Integrating copy number polymorphisms into array CGH analysis using a robust HMM. *Bioinformatics.* 2006 Jul 15;22(14):e431-9. Contribution: derived implemented and evaluated the algorithm; wrote the manuscript. |
|  | **Shah SP**, Lam WL, Ng RT, Murphy KP. Modeling recurrent DNA copy number alterations in array CGH data. *Bioinformatics*. 2007 Jul 1;23(13):i450-8. Contribution: derived, implemented and evaluated the algorithm; wrote the manuscript. |
|  | **Shah SP**. Computational methods for identification of recurrent copy number alteration patterns by array CGH. *Cytogenet Genome Res*. 2008;123(1-4):343-51. Contribution: sole author, solicited review article |
|  | Cheung KJ\*, **Shah SP**\*, Steidl C, Johnson N, Relander T, Telenius A, Lai B, Murphy KP, Lam W, Al-Tourah AJ, Connors JM, Ng RT, Gascoyne RD, Horsman DE. Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. *Blood*. 2009 Jan 1;113(1):137-48. doi: 10.1182/blood-2008-02-140616 (\*equal contribution) Contribution: led and performed data analysis |
|  | **Shah SP**, Cheung KJ Jr, Johnson NA, Alain G, Gascoyne RD, Horsman DE, Ng RT, Murphy KP. Model-based clustering of array CGH data. *Bioinformatics*. 2009 Jun 15;25(12):i30-8. doi: 10.1093/bioinformatics/btp205 Contribution: derived, implemented and evaluated the algorithm; wrote the manuscript. |
|  | **Shah SP**, Köbel M, Senz J, Morin RD, Clarke BA, Wiegand KC, Leung G, Zayed A, Mehl E, Kalloger SE, Sun M, Giuliany R, Yorida E, Jones S, Varhol R, Swenerton KD, Miller D, Clement PB, Crane C, Madore J, Provencher D, Leung P, DeFazio A, Khattra J, Turashvili G, Zhao Y, Zeng T, Glover JN, Vanderhyden B, Zhao C, Parkinson CA, Jimenez-Linan M, Bowtell DD, Mes-Masson AM, Brenton JD, Aparicio SA, Boyd N, Hirst M, Gilks CB, Marra M, Huntsman DG. Mutation of FOXL2 in granulosa-cell tumors of the ovary. *N Engl J Med*. 2009 Jun 25;360(26):2719-29.  **This paper was the first clinically useful discovery from next generation sequencing of tumours. It has now been implemented as a diagnostic test in several non-Canadian jurisdictions.** |
|  | **Shah SP**, Morin RD, Khattra J, Prentice L, Pugh T, Burleigh A, Delaney A, Gelmon K, Giuliany R, Senz J, Steidl C, Holt RA, Jones S, Sun M, Leung G, Moore R, Severson T, Taylor GA, Teschendorff AE, Tse K, Turashvili G, Varhol R, Warren RL, Watson P, Zhao Y, Caldas C, Huntsman D, Hirst M, Marra MA, Aparicio S. Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*. 2009 Oct 8;461(7265):809-13. Contribution: project lead; developed algorithms, performed data analysis  **This paper reported the world’s first fully sequenced epithelial cancer genome and was the first study to compare the complete set of mutations across temporal samples to measure tumour evolution. The announcement of this work led the Globe and Mail, CBC and CTV news.** |
|  | Morin RD, Johnson NA, Severson TM, Mungall AJ, An J, Goya R, Paul JE, Boyle M, Woolcock BW, Kuchenbauer F, Yap D, Humphries RK, Griffith OL, **Shah S**, Zhu H, Kimbara M, Shashkin P, Charlot JF, Tcherpakov M, Corbett R, Tam A, Varhol R, Smailus D, Moksa M, Zhao Y, Delaney A, Qian H, Birol I, Schein J, Moore R, Holt R, Horsman DE, Connors JM, Jones S, Aparicio S, Hirst M, Gascoyne RD, Marra MA. Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. *Nat Genet*. 2010 Feb;42(2):181-5. |
|  | Steidl C, Lee T, **Shah SP**, Farinha P, Han G, Nayar T, Delaney A, Jones SJ, Iqbal J, Weisenburger DD, Bast MA, Rosenwald A, Muller-Hermelink HK, Rimsza LM, Campo E, Delabie J, Braziel RM, Cook JR, Tubbs RR, Jaffe ES, Lenz G, Connors JM, Staudt LM, Chan WC, Gascoyne RD. Tumor-associated macrophages and survival in classic Hodgkin’s lymphoma. *N Engl J Med*. 2010 Mar 11;362(10):875-85. Contribution: supervised data analysis and bioinformatics component of the study |
|  | 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 Mar 15;26(6):730-6. Contribution: project conception and oversight; wrote the manuscript. |
|  | Steidl C, Telenius A, **Shah SP**, Farinha P, Barclay L, Boyle M, Connors JM, Horsman DE, Gascoyne RD. Genome-wide copy number analysis of Hodgkin Reed-Sternberg cells identifies recurrent imbalances with correlations to treatment outcome. *Blood*. 2010 Jul 22;116(3):418-27. |
|  | Jones SJ, Laskin J, Li YY, Griffith OL, An J, Bilenky M, Butterfield YS, Cezard T, Chuah E, Corbett R, Fejes AP, Griffith M, Yee J, Martin M, Mayo M, Melnyk N, Morin RD, Pugh TJ, Severson T, **Shah SP**, Sutcliffe M, Tam A, Terry J, Thiessen N, Thomson T, Varhol R, Zeng T, Zhao Y, Moore RA, Huntsman DG, Birol I, Hirst M, Holt RA, Marra MA. Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. *Genome Biol*. 2010 August;11(8):R82. |
|  | Cheung KJ, Delaney A, Ben-Neriah S, Schein J, Lee T, **Shah SP**, Cheung D, Johnson NA, Mungall AJ, Telenius A, Lai B, Boyle M, Connors JM, Gascoyne RD, Marra MA, Horsman DE. High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copy-neutral loss of heterozygosity and copy number alterations that target single genes. *Genes, Chromosomes Cancer*. 2010 Aug;49(8):669-81. |
|  | 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. *N Engl J Med*. 2010 Oct 14;363(16):1532-43. |
|  | Cheung KJ, Johnson NA, Affleck JG, Severson T, Steidl C, Ben-Neriah S, Schein J, Morin RD, Moore R, **Shah SP**, Qian H, Paul JE, Telenius A, Relander T, Lam W, Savage K, Connors JM, Brown C, Marra MA, Gascoyne RD, Horsman DE. Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. *Cancer Res*. 2010 Nov 15;70(22):9166-74. |
|  | 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. MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. *Nature* 2011 Mar 17;471(7338):377-81. \*Equal contribution. |
|  | McConechy MK, Anglesio MS, Kalloger SE, Yang W, Senz J, Chow C, Heravi-Moussavi A, Morin GB, Mes-Masson AM; Australian Ovarian Cancer Study Group, Carey MS, McAlpine JN, Kwon JS, Prentice LM, Boyd N, **Shah SP**, Gilks CB, Huntsman DG. Subtype-specific mutation of PPP2R1A in endometrial and ovarian carcinomas. *J Pathol*. 2011 Apr;223(5):567-73. |
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|  | Taghiyar MJ, Rosner J, Grewal D, Grande BM, Aniba R, Grewal J, Boutros PC, Morin RD, Bashashati A, **Shah SP**. Kronos: a workflow assembler for genome analytics and informatics. *Gigascience.* 2017 Jun 26. doi: 10.1093/gigascience/gix042. |
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*(b) Conference Proceedings*

*(c) Other*

**2. NON-REFEREED PUBLICATIONS**

*(a) Journals*

*(b) Conference Proceedings*

*(c) Other*

|  |  |
| --- | --- |
|  | McPherson A, **Shah S**. Gene fusion discovery in paired end RNA-Seq data with application to ovarian cancer. Oral presentation. ISMB 2010 (HiTSeq 2010). Boston, MA; July 11, 2010 |
|  | McPherson A, **Shah S**. Integrated analysis of multiple next generation sequencing datasets with application to gene fusion discovery. Oral presentation. Genome Informatics 2010. Hinxton, UK; Sept 15, 2010 |
|  | McPherson A, **Shah S**. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq. Oral presentation. Third Annual RECOMB Satellite Workshop on Computational Cancer Biology. Vancouver, BC; March 28, 2011 |
|  | Roth A, Crisan A, Aparicio S, **Shah S**. Detecting Somatic Mutations In Tumour/Normal Paired Sample Sequence Data. Third Annual RECOMB Satellite Workshop on Computational Cancer Biology. Vancouver, BC; March 28, 2011 |
|  | Ding J, Roth A, Giuliany R, Aparicio S, **Shah S.** Accurate somatic point mutation prediction using supervised machine learning algorithms. Third Annual RECOMB Satellite Workshop on Computational Cancer Biology. Vancouver, BC; March 28, 2011 |
|  | McPherson A, **Shah S**. Comrad: Detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data.  Oral presentation and poster. ISMB 2011 / HitSeq 2011. Vienna, Austria; July 16, 2011 |
|  | Giuliany R, Roth A, Huntsman D, Aparicio S, **Shah S**. Auditor: exploring RNA-editing in cancer through simultaneous analysis of tumour genome and transcriptome sequencing data. HitSeq 2011. Vienna, Austria; July 16, 2011 |
|  | Roth A, Ding J, Crisan A, Ha G, Giuliany R, Bashashati A, Aparicio S, **Shah S**. JointSNVMix: A Probabilistic Model For Accurate Detection Of Somatic Mutations In Nor- mal/Tumour Paired Sample Sequence Data. HitSeq International Conference. Vienna, Austria; July 16, 2011 |
|  | Giuliany R, Roth A, Huntsman D, Aparicio S, **Shah S**. A survey of RNA-editing in Forme Fruste tumours using a novel statistical method. BC Cancer Agency Annual Cancer Conference. Vancouver, BC; Nov 29-Dec 1, 2012 |
|  | Chan FC, Ben-Neriah S, Lim R, Hu S, Gunawardana J, Telenius A, Ennishi D, Boyle M, Ding J, Rogic S, Johnson N, Morin R, Ha G, Scott DW, Sehn L, Connors JM, Marra M, Gascoyne RD, **Shah S**\*, Steidl C\*. Large-Scale High Resolution Integration of Copy Number and Gene Expression in DLBCL Reveals Focal and Frequent Deletions in Chromatin Modifying Genes with Outcome Correlation. BC Cancer Agency Annual Cancer Conference. Vancouver, BC; Nov 29-Dec 1, 2012 (\* equal contribution) |
|  | Ding J, Bashashati A, Aparicio S, Condon A, **Shah S**. A probabilistic model to simultaneously infer functional mutations and driver genes. BC Cancer Agency Annual Cancer Conference. Vancouver, BC; Nov 29-Dec 1, 2012 |
|  | Lefebvre C, Aparicio S, Huntsman D, Wasserman W, **Shah S**. The Impact of Somatic Insertions and Deletions in Regulatory Elements in Epithelial Cancers. BC Cancer Agency Annual Cancer Conference. Vancouver, BC; Nov 29-Dec 1, 2012 |
|  | McPherson A, Ha G, Prentice L, Shumansky K, Le A, McAlpine J , Huntsman D, **Shah S**. Intratumoural Genomic Diversity in High-grade Serous Ovarian Cancer Revealed Through High- throughput Sequencing. BC Cancer Agency Annual Cancer Conference. Vancouver, BC; Nov 29-Dec 1, 2012 |
|  | Chan FC, Ben-Neriah S, Lim R, Hu S, Gunawardana J, Telenius A, Ennishi D, Boyle M, Ding J, Rogic S, Johnson N, Morin R, Ha G, Scott DW, Sehn L, Connors JM, Marra M, Gascoyne RD, **Shah S**\*, Steidl C\*. Large-Scale High Resolution Integration of Copy Number and Gene Expression in DLBCL Reveals Focal and Frequent Deletions in Chromatin Modifying Genes with Outcome Correlation. 2012 American Society of Hematology Annual Meeting. Atlanta GA; Dec 10, 2012 (\* equal contribution) |
|  | Ding J, Bashashati A, Condon A, Aparicio A, **Shah S**. iSeq: a probabilistic model to simultaneously infer functional mutations and driver genes. 11th Asia Pacific Bioinformatics Conference (APBC). Vancouver, BC; Jan 21-23, 2013 |
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|  | Wang Y, Gilks B, Prentice L, Huntsman D, Mes-Masson AM, Mcalpine J, **Shah S**. The genomic landscapes of high-grade serous ovarian cancers: contrasting long term survivors and “platinum-resistant” disease. 10th Biennial Ovarian Cancer Research Symposium.  Seattle, WA; Sep 8-9, 2014 |
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|  | Steif A\*, Eirew P\*, Khattra J\*, Ha G, Yap D, Farahani H, **Shah SP**, Aparicio S. Population dynamics of genomic clones in breast cancer patient xenografts at single cell resolution. Single Cell Genomics Meeting. Stockholm, Sweden; Sept 9-11, 2014  (\* denotes equal contribution) |
|  | Chan FC, Mottok A, Gerrie A, Power M, Savage KJ, Connors JM, Gascoyne RD, **Shah S**, Scott DW, Steidl C. Analysis of Relapse Biopsies in Classical Hodgkin Lymphoma Reveals Correlations with Outcome After Autologous Stem Cell Transplantation. ASH 2014; San Francisco, CA; Dec 5-9, 2014 |
|  | Chan FC, Kridel R, Mottok A, Boyle M, Farinha P, Meissner B, Shumansky K, Aniba R, Scott DW, Sehn LH, Connors JM, Steidl C, Gascoyne RD, Marra M, **Shah S**. Characterization of Genomic Somatic Alterations in Transformed and Treatment Resistant Follicular Lymphoma. TFRI Annual Scientific Meeting. St. Johns, NL; May 7-9, 2015 |
|  | Chan FC, Kridel R, Mottok A, Boyle M, Farinha P, Meissner B, Shumansky K, Aniba R, Scott DW, Sehn LH, Connors JM, Steidl C, Gascoyne RD, Marra M, **Shah S**. Evolutionary Dynamics and Driver Mutations Underlying Transformed and Treatment Resistant Follicular Lymphomas. BCCA Research Day 2015. Vancouver, BC; June 11, 2015 |
|  | Wang YK, Gilks B, Prentice L, Huntsman D, Provencher D, Mes-Masson AM, McAlpine J, **Shah SP**. The genomic landscape of platinum-sensitive and -resistant disease in high-grade serous ovarian cancers. HITSeq2015. Dublin, Ireland; July 10-11th, 2015 |
|  | McPherson A, Roth A, McAlpine J, Bouchard-Côté A, **Shah SP**. The Importance of Mutation Loss in Modelling Evolution and Metastasis in Genomically Unstable Cancers. ISMB 2015 HitSeq SIG. Dublin, Ireland; July 10-14, 2015 |
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|  | Steif A\*, Eirew P\*, Khattra J\*, Zahn H\*, Ha G, Yap D, Farahani H, Wan A, Laks E, Hansen CL, **Shah SP,** Aparicio S. High-resolution clonal dynamics in breast cancer xenografts with single cell whole-genome sequencing. Forecasting Evolution. Lisbon, Portugal; July 8-11, 2015 |
|  | Roth A, McPherson A, Bouchard-Cote A, **Shah SP**. Inference of clonal genotypes from single cell sequencing data. Oral presentation. ISMB 2015. Dublin, Ireland; July 11, 2015 |
|  | Zahn H\*, Steif A\*, **Shah S**, Aparicio S, Hansen CL. A microfluidic device for single-cell genome-wide identification of copy number variation. Single Cell Genomics. Utrecht, The Netherlands; Sept 16-18, 2015. \*co-presenting authors |
|  | Roth A, McPherson A, Bouchard-Cote A, **Shah SP**. Inference of clonal genotypes from single cell sequencing data. Cold Spring Harbor Laboratory Meeting: Probabilistic Modeling in Genomics. Cold Spring Harbor, NY; Oct 14-17, 2015 |
|  | Zhang.AW, McPherson.A, Roth.A, Kroeger.DR, Milne.K,Wasserman.WW, McAlpine.JN, Holt.RA, Nelson.BH, **Shah.SP.** Abstract 4136: Properties of the immune microenvironment associated with clonal diversity in high-grade serous ovarian cancer. AACR 107th Annual Meeting 2016; April 16-20, 2016; New Orleans, LA. Apr 16 – 20 2016 |
|  | Smith M, Nielsen C, Chan FC, Roth A, McPherson A, Machev D, **Shah S** Visualization methods for spatial and temporal evolution analysis in cancer, 15th European Conference on Computational Biology, The Hague, Netherlands 3-7 September 2016 |
|  | Wang Y, Bashashati A, Anglesio MS, Cochrane D, Grewal D, Horlings H,  Karnezis A, Mes-Masson AM, Okamoto A, Yanagida S, Yanaihara N, Saito M,  Gilks B, McAlpine J, Aparicio S, Huntsman D,  **Shah S.** Abstract LB-324: Genomic consequences of aberrant DNA repair stratify ovarian cancer histotypes. AACR 107th Annual Meeting 2016; April 16-20, 2016; New Orleans, LA |
|  | Yung CK, Bourque G, Boutros PC, El Emam K, Ferretti V, Knoppers BM, O’Connor B, Ouellette BFF, Sahinalp C, **Shah SP.** Stein LD. Abstract 3605: ICGC in the cloud. AACR 107th Annual Meeting 2016; April 16-20, 2016; New Orleans, LA |
|  | Taghiyar MJ, Rosner J, Grewal G, Grande B, Aniba R, Grewal J, Boutros PC, Morin R, Bashashati A, **Shah SP.** Kronos: a workflow assembler for genome analytics and informatics. BOSC meeting, ISMB conference Jul 8-9, 2016, Orlando, Florida. |
|  | Ennishi D, Bashashati A, Saberi S, Mottok A, Meissner B, Boyle M, Ben-Neriah S, Kridel R, Dominguez-Sola D, Savage K, Sehn L, Connors JM, Morin RD, Marra MA, **Shah SP**, Steidl C, Scott DW, Gascoyne RD. Frequent Genetic Alterations of PI3K-AKT Pathway and Their Clinical Significance in Germinal Center B-Cell-like Diffuse Large B-Cell Lymphoma. American Society of Hematology 568th Annual Meeting & Exposition; Dec 3-6, 2016; San Diego, CA. |

**3. BOOKS**

# *(a) Authored*

*(b) Edited*

|  |  |
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|  | Banerjee, D, **Shah SP** (Editors). Methods in Molecular Biology 973: Array Comparative Genomic Hybridization (Protocols and Applications). 2013. Humana Press |

*(c) Chapters*

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| 1. 1 | Ha G, **Shah S**. Distinguishing somatic and germline copy number events in cancer patient DNA hybridized to whole-genome SNP genotyping arrays. *Methods Mol Biol.* 2013;973:355-72. doi: 10.1007/978-1-62703-281-0\_22. |

**4. PATENTS**

|  |  |
| --- | --- |
|  | **Methods and devices for analyzing particles**  First named inventor: Carl Hansen  Inventors: Hans Zahn, Jens Huft, Marinus Van Loenhout, Kaston Leung, Bill Lin, Anders Klaus, Samuel Aparicio, Sohrab Shah  Application number: PCT/CA2016/0000031  Application Filing Date: February 4, 2016  International Publication Date: August 11, 2016  International Publication Number: WO 2016/123692 A1 |
|  | **Novel biomarkers and targets for ovarian carcinoma - ABANDONED**  First named inventor: David G. Huntsman  Inventors: David G. Huntsman, Marco Marra, Kimberly Wiegand, Martin Hirst, Sohrab Prakash Shah  Application number 13/642337  US Provisional Patent Filed on Apr 22, 2011  Publication Date Aug 01, 2013  US Patent Application 20130197056 |
|  | **Predicting treatment response in cancer patients - ABANDONED**  First named inventor: Andrew Roth  Inventors: Sohrab Shah, Samuel Aparicio, Alexandre Bouchard-Côté, Andrew Roth  Application number 61734456  US Provisional Patent Filed on Dec 07, 2012 |
|  | **Method of Identifying Diffuse large B-cell Lymphoma patients with Poor Outcome - ABANDONED**  First named inventor: Fong Chun Chan  Inventors: Fong Chun Chan, Randy Gascoyne, Sohrab Shah, Christian Steidl  Application number 61734755  US Provisional Patent Filed on Dec 07, 2012 |
|  | **Detection of granulosa-cell tumors - ABANDONED**  First named inventor: David G. Huntsman  Inventors: Marco Marra, Martin Hirst, Ryan D. Morin, Sohrab Prakash Shah, Janine Senz  Application number US 13/123,313  Provisional Patent Filed on Oct 6, 2009  Publication Date Aug 11, 2011  PCT CA2009/001403 |

**5. SPECIAL COPYRIGHTS**

**6. ARTISTIC WORKS, PERFORMANCES, DESIGNS**

**7. OTHER WORKS**

**8. WORK IN PROGRESS (including degree of completion)**

**Collaborations:**

**With Sam Aparicio (BCCA):**

Modeling clonal evolution in xeno-engrafted tumour samples (50% complete)

Single cell genomics to identify somatic genotypes under evolutionary selection (10% complete)

The mutational landscape of triple negative breast cancer (30% complete)

**With David Huntsman (BCCA):**

The mutational landscape of ovarian clear cell carcinomas (50% complete)

**With Alex Cote-Bouchard (UBC Statistics):**

Statistical models for phylogenetic inference of clonal population structures in human cancers (25% complete)

**With Paul Boutros (Ontario Institute for Cancer Research (OICR)):**

A clinical-grade computational platform for cancer genome sequencing analysis (75% complete)

**With Randy Gascoyne (BCCA):**

The evolutionary dynamics of follicular lymphoma and genomic mechanisms for transformation to aggressive DLBCL (75% complete)

**With Christian Steidl (BCCA):**

Integrative analysis of the genomes and transcriptomes of diffuse large B-cell lymphomas (75% complete)

**With Torben Falck-Ortnoft (University of Aarhus, Denmark):**

Evolutionary dynamics of bladder cancer (100% complete)

**With Michael Taylor (OICR):**

Genomic comparisons of primary and metastatic medulloblastomas (100% complete)

**With Lincoln Stein (OICR):**

Analysis of >2500 tumour normal whole genome datasets from the ICGC consortium (25% complete)

**With Karen Gelmon (BCCA):**

Spatial heterogeneity in locally advanced breast cancers (25% complete)

**With Brad Nelson (BCCA)**

How the immune system contends with clonal diversity in high grade serous ovary cancers (25% complete)