

MORGAN G. I. LANGILLE, PhD

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EDUCATION

| | | |
|----------------|--|--|
| 2004- 2009 | Ph.D. CIHR/MSFHR Bioinformatics Training Program (Department of Molecular Biology and Biochemistry) | Dr. Fiona Brinkman Simon Fraser University Burnaby, BC, Canada |
| 1999 – 2004 | Bachelor's of Science (Biology) First Division | University of New Brunswick Fredericton, NB, Canada |
| 1999 – 2004 | Bachelor's of Computer Science First Division | University of New Brunswick Fredericton, NB, Canada |

RESEARCH & RELEVANT WORK EXPERIENCE

| | | |
|------------------|--|---|
| 2011- Current | Post-Doctoral Fellow <ul style="list-style-type: none">Metagenomics analysis of the human microbiome -- “Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes”Predicting gene functional counts from metagenomic datasets | Dr. Robert Beiko Dr. Ford Doolittle Dalhousie University, Halifax, NS |
| 2009- 2011 | Post-Doctoral Fellow <ul style="list-style-type: none">Development of new environmental and ecological computational methods for the analysis of metagenomics data (see iSEEM project)Leading the comparative genomic analysis of 8 newly sequenced Archaea halophile species.Created BioTorrents, a new open data sharing service for scientists. | Dr. Jonathan Eisen UC Davis, Davis, Ca |
| 2004- 2009 | Ph.D. Thesis <ul style="list-style-type: none">Developed new computational methods for the identification of genomic islands (large regions of horizontal gene transfer) within bacterial genomes using comparative genomics: http://www.pathogenomics.sfu.ca/islandviewer/Led genome annotation and analysis of an epidemic <i>P. aeruginosa</i> strainSee publications and abstracts for more details | Dr. Fiona Brinkman MBB, SFU Burnaby, BC |
| 06/2008- | Bioinformatics Instructor | B.C. Institute of |

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|---------------------|--|--|
| 08/2008 | <ul style="list-style-type: none"> Taught introductory classes on bioinformatics | Technology Burnaby, BC |
| 06/2007 | Private Consulting <ul style="list-style-type: none"> Computational analysis of metagenomic data obtained from a sand sample | Dr. Robert Naviaux UC San Diego San Diego, CA, USA |
| 06/2007 | Canadian Bioinformatics Workshop <ul style="list-style-type: none"> Instructor for 2 lectures Teaching assistant during entire workshop | UBC Michael Smith Laboratories Vancouver, BC |
| 09/2005- 12/2005 | Bioinformatics Graduate Program Lab Rotation <ul style="list-style-type: none"> Ontology development for flow cytometry data Included use of OWL (Web Ontology Language), XML and XSLT languages | Dr. Ryan Brinkman Terry Fox Laboratory BC Cancer Research Centre (BCCRC) Vancouver, BC |
| 01/2005- 04/2005 | Bioinformatics Graduate Program Lab Rotation <ul style="list-style-type: none"> Deconstruction of data transformations using reusable web services Included development of SOAP (Simple Object Application Protocol) web services | Dr. Mark Wilkinson iCapture St. Paul's Hospital Vancouver, BC |
| 12/2004- 02/2005 | Graduate Course Research Project <ul style="list-style-type: none"> Computational algorithm and tool development for improvement of medical image segmentation Included programming in Matlab and C See publications | Dr. Ghassan Hamarneh SFU Burnaby, BC |
| 2003 & 2004 | Summer Research Student <ul style="list-style-type: none"> Detection of retrotransposition gene duplications in <i>Drosophila melanogaster</i> and their expression profiles See publications | Dr. Denise Clark UNB Fredericton, NB |
| 2002 | Summer Research Student <ul style="list-style-type: none"> Analysis and proposal of an improvement on PSI-BLAST | Dr. Patricia Evans UNB Fredericton, NB |
| 09/2001- 05/2003 | Educational Resident Assistant <ul style="list-style-type: none"> Academic/personal advising Organizing and scheduling of seminars Conflict mediation between residents | Residential Life and Conference Services UNB, Fredericton, NB |

PUBLICATIONS

1. Jospin G, Sharpton TJ, Wu D, **Langille MGI**, Pollard KS, Eisen JA (2012) “Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource” (In Review).
2. Jiang X*, **Langille MGI***, Neches RY, Elliot M, Levin SA, Eisen JA, Weitz JS, Dushoff J (2012) “Functional biogeography of ocean microbes: dimension reduction of metagenomic data identifies biological patterns across scale” (In Review).
*Co-first authors.
3. Lynch EA, **Langille MGI**, Darling A, Wilbanks EG, Haltiner C, Shao KSY, Starr MO, Teiling C, Harkins TT, Edwards RA, Eisen JA, Facciotti MT (2012) “Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux” (In Review)
4. **Langille MGI**, Laird MR, Hsiao WWL, Chiu TA, Eisen JA, Brinkman FSL (2012) “MicrobeDB: a locally maintainable database of microbial genomic sequences”, *Bioinformatics*, 28(14), 1947–1948.
5. **Langille MGI**, Meehan CJ, Beiko RG (2012) “Human Microbiome: A Genetic Bazaar for Microbes?”, *Current Biology*, 22(1), R20-22.
6. **Langille MGI**, Hsiao WWL, Brinkman FSL (2010) “Detection of genomic islands using bioinformatics approaches”, *Nature Reviews Microbiology*, 8(5), 373-82.
7. **Langille MGI** and Eisen JA (2010) “BioTorrents: A File Sharing Service for scientific data” *PLoS One*, 5(4): e10071.
 - Highlighted in [Nature \(News Briefing\)](#), [Nature Blog](#), [GenomeWeb](#), [Ars Technica](#), and several other online news sites/blogs.
8. Ho Sui SJ, Fedynak A, Hsiao WWL, **Langille MGI**, Brinkman FSL (2009) “The association of virulence factors with genomic islands”, *PLoS One*, 4(12): e8094.
9. **Langille MGI** (2009) “Computational prediction and characterization of genomic islands: insights into bacterial pathogenicity”, Ph.D. dissertation, Simon Fraser University, Burnaby, BC, Canada.
10. **Langille MGI** and Brinkman FSL (2009) “Bioinformatic detection of horizontally transferred DNA in bacterial genomes”, *F1000 Biology Reports*, 1:25.
11. **Langille MGI** and Brinkman FSL (2009) “IslandViewer: an integrated interface for computational identification and visualization of genomic islands”, *Bioinformatics*, 25(5):664-5.
12. Winstanley C, **Langille MGI**, Fothergill JL, Kukavica-Ibrulj I, Paradis-Bleau C, Sanschagrin F, Thomson NR, Winsor GI, Quail MA, Lennard N, Bignell A, Clarke L, Seeger K, Saunders D, Harris D, Parkhill J, Hancock REW, Brinkman FSL, and Levesque RC (2008). “Newly introduced genomic prophage islands are critical

- determinants of *in vivo* competitiveness in the Liverpool Epidemic Strain of *Pseudomonas aeruginosa*", *Genome Research*, 19(1):12-23.
13. **Langille MGI**, Hsiao WWL, Brinkman FSL (2008). "Evaluation of genomic island predictors using a comparative genomics approach", *BMC Bioinformatics*, 9:329
 14. **Langille MGI** and Clark DV (2007). "Parent genes of retrotransposition-generated gene duplicates in *Drosophila melanogaster* have distinct expression profiles", *Genomics*, 90(3):334-43.
 15. Spidlen, J, Gentleman RC, Haaland PD, **Langille MGI**, Meur NL, Ochs MF, Schmitt C, Smith CA, Treister AS, Brinkman RR (2006). "Data standards for flow cytometry", *OMICS*, 10(2):209-14.
 16. Chodorowski A, Mattsson U, **Langille MGI**, Hamarneh G (2005). "Color Lesion Boundary Detection Using Live Wire", *Proceedings of SPIE Medical Imaging: Image Processing*, 5747:1589-96.
 17. Hamarneh G, Yang J, McIntosh C, **Langille MGI** (2005). "3D live-wire-based semi-automatic segmentation of medical images", *Proceedings of SPIE Medical Imaging: Image Processing*, 5747:1597-603.

BOOK CHAPTERS

1. **Langille MGI**, Zhou F, Fedynak A, Hsiao WWL, Xu Y, and Brinkman FSL. Mobile genetic elements and their prediction, *In* Y. Xu and J.P. Gogarten (eds.), *Computational Methods for Understanding Bacterial and Archaeal Genomes*, Series on Advances in Bioinformatics and Computational Biology, Vol. 7. Imperial College Press, London, 2008.

ABSTRACTS

1. Dhillon BK, Chiu TA, Laird MR, **Langille MGI**, and Brinkman FSL (2012) IslandViewer: an integrated interface for genomic island identification and visualization. Conference of the Canadian Society of Microbiologists, June 20-23, 2012, Vancouver, British Columbia, Canada.
2. **Langille MGI**, Zaneveld JRR, Caporaso JG, Reyes J, Knights D, McDonald D, Knight R, Beiko RG, Huttenhower C (2012) "Inferring microbial community function from taxonomic composition" International Human Microbiome Congress, March 19-21, 2012, Paris, France.
*Received Travel Award from IHMC.
3. Sharpton TJ, Jospin G, **Langille MGI**, Wu D, Eisen JA, Pollard KS (2012) "Quantifying Human Microbiome Functional Variation using Operational Protein Families" International Human Microbiome Congress, March 19-21, 2012, Paris, France.
4. **Langille MGI** and Eisen JA (2010) "Characterizing Protein Families of Unknown

- Function” 18th Annual International Meeting on Microbial Genomics, September 12-16, 2010, Lake Arrowhead, California, USA.
5. **Langille MGI** and Eisen JA (2010) “BioTorrents: a file sharing service for scientific data” 110th General Meeting of the American Society for Microbiology, May 23-27, 2010, San Diego, California, USA.
 6. **Langille MGI** and Eisen JA (2009) “BioTorrents: a file sharing service for scientific data” Biology and Mathematics in the Bay Area Meeting, Nov. 14, 2009, Santa Cruz, California, USA.
 7. Winsor GL, Rossum TV, Fleming LA, Lo R, Yu N, **Langille MGI**, Whiteside MD and Brinkman FSL (2009). “Computational Methods to Aid Comparative Analysis of Microbial Genomes.” Genome Informatics, October 27-30, 2009, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, USA.
 8. **Langille MGI** and Brinkman FSL (2008). "IslandPick and IslandViewer: Tools for the computational identification and visualization of genomic islands." 16th Annual International Meeting on Microbial Genomics, September 14-18, 2008, Lake Arrowhead, California, USA.
 9. **Langille MGI**, Hsiao WWL, and Brinkman FSL (2007). "Automated detection of prokaryotic genomic islands using a comparative genomics approach." 15th Annual International Conference on Intelligent Systems for Molecular Biology, July 21-25, 2007, Vienna, Austria.
 10. Fedynak, A, Ho CK, **Langille MGI**, and Brinkman FSL (2007). “Identification of novel essential genes and pathogen-associated genomic regions”. Canadian Society for Microbiologists Annual General Meeting. June 17-20, 2007, Quebec, Canada.
 11. **Langille MGI**, Hsiao WWL, Fedynak A, Ho CK, and Brinkman FSL (2007). "Development and analysis of data sets of prokaryotic genomic islands." Pacific Symposium on Biocomputing, January 3-7, 2007, Maui, Hawaii, USA.
 12. Hokamp K., Roche FM, **Langille MGI**, Acab M, Fulton DL, Laird M, Li Y, Lo R, Chan SK, Babiuk LA, Hancock REW, and Brinkman FSL (2006). “Bioinformatics Tools for Cross-species Comparisons of Microarray Data.” World Microarray Congress 2006, March 24-25, 2006, Vancouver, B.C., Canada.
 13. **Langille MGI**, Hsiao WWL, Fulton DL, Li Y, Laird M, and Brinkman FSL (2006). “Ortholuge and IslandPath: tools for the genome-wide detection of orthologs and genomic islands.” International Conference on Phylogenomics, March 15-19, 2006. Sainte-Adèle, PQ, Canada.
 14. Hsiao WWL, **Langille MGI**, Fedynak A, Chilana P, and Brinkman FSL (2006). "Genomic island analysis: Improved web-based software and insights into an apparent gene pool associated with genomic islands." ASM Northwest Branch Meeting 2006, March 10-12, 2006, Seattle, Washington, USA.
 15. Hsiao WWL, **Langille MGI**, and Brinkman FSL (2005). “Computational characterization of genomic islands: Insights into a large, novel gene pool.” National

Academy of Sciences Sackler Tapestry of Life Colloquium: Lateral Transfers of Heritable Elements, December 12-13, 2005, Irvine, CA, USA.

16. Wang D, **Langille MGI**, Leung S, and Wilkinson M (2005). "Investigation of Data Transformation Frameworks for Enhancing the Interoperability of Bioinformatic Web Services" iCAPTURE Summer Student Research Day, The James Hogg iCAPTURE Centre for Cardiovascular and Pulmonary Research, Department of Pathology and Laboratory Medicine, St. Paul's Hospital / Providence Health Care-University of British Columbia, Vancouver, BC, Canada

INVITED PRESENTATIONS

1. "Leveraging ancestral state reconstruction to infer community function from a single marker gene" iEvoBio, July 11, 2012, Ottawa, ON, Canada.
2. "Computational insights of pathogenic bacteria and the ocean microbiome" University of New Brunswick Biology Seminar Series, Oct. 28, 2011, UNB, Fredericton, NB, Canada.
3. "Predicting function from taxonomy", Microbiome Workshop, June 8th, 2011, Dalhousie University, Halifax, NS, Canada.
4. "BioTorrents: A File Sharing Service For Scientific Data" Open Science Summit, Jul. 30, 2010, Berkeley, California, USA.
5. "BioTorrents: A File Sharing Service For Scientific Data" Bioinformatics Technology Forum, Jun. 1, 2010, UC Davis, Davis, California, USA.
6. "Computational identification of bacterial genomic islands (large regions of horizontal gene transfer)" Bioinformatics Technology Forum, Nov. 17, 2009, UC Davis, Davis, California, USA.
7. "An introduction to systems biology and network visualization" Techniques in Biotechnology, August 11 & 12, 2008, BCIT, Burnaby, BC, Canada
8. "An introduction to bioinformatics, databases, and NCBI" Techniques in Biotechnology, June 9 & 16, 2008, BCIT, Burnaby, BC, Canada
9. "A graduate student's experience in bioinformatics" BiNS - Bioinformatics Night at SFU, Feb. 29, 2008, SFU, Burnaby, BC, Canada
10. "Introduction to Algorithms in Bioinformatics" Canadian Bioinformatics Workshop, June 22, 2007, UBC Michael Smith Laboratories, Vancouver, BC, Canada
11. "Whole Genome Alignments" Canadian Bioinformatics Workshop, June 21, 2007, UBC Michael Smith Laboratories, Vancouver, BC, Canada
12. "Developing an ontology for flow cytometry data" Bioinformatics Graduate Program Colloquium, November 25, 2005, Vancouver, BC, Canada.

13. "Identifying Genomic Islands Using Comparative Genomics" Vancouver Bioinformatics Users Group (VanBUG), November 17, 2005, Vancouver, BC, Canada.
14. "Comparative Genomics Approach to Identifying Genomic Islands" Bioinformatics Graduate Program Colloquium, September 12, 2005, Vancouver, BC, Canada.
15. "Deconstruction of data transformations into reusable web services" Bioinformatics Graduate Program Colloquium, March 11, 2005, Vancouver, BC, Canada.

AWARDS AND HONOURS

| | | |
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| 2008 | SFU President's PhD Research Stipend | \$6000 |
| 2008 | MBB Travel Fellowship | \$450 |
| 2006 | MSFHR Junior Graduate Studentship Research award | \$45,000 |
| 2005 | NAS Sackler Colloquium Tapestry of Life Conference Travel Grant | \$350 |
| 2004 | CIHR/MSFHR Strategic Training Program in Bioinformatics Award | \$36,000 |
| 2003 | John J. McCaffrey Scholarship | \$800 |
| 2002 | NSERC - Undergraduate Student Research Award | \$4800 |
| 2001 | Khaki University & YMCA Scholarship | \$700 |
| 2000 | Rolf Riegger Bursary | \$950 |
| 2000 | Purdy MacDonald Scholarship | \$250 |
| 1999 | Martha Fraser McIntosh Scholarship | \$675 |
| 1999 | Brock A. Turner Memorial Scholarship | \$825 |

TEACHING

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|------|---|-------------------------|
| 2011 | SuperNOVA Summer Camp Presenter | Dalhousie University |
| 2008 | BCIT BIOT 5800 Bioinformatics Summer Instructor | Burnaby, BC |
| 2007 | Canadian Bioinformatics Workshop Instructor | Vancouver, BC |
| 2005 | Problem Based Learning Teaching Assistant | Simon Fraser University |
| 2004 | Shad Valley Students Orientation Workshop Teacher | Simon Fraser University |

COMPUTATIONAL SKILLS

Programming Languages

- Extensive use of object oriented programming in Perl.
- Previous use or formal training in Java, C, Matlab, and R.
- Experience with parallel programming on a 50+ computer cluster.

Database and Web Development

- Thorough understanding of relational database design and extensive use of MySQL.
- Comfortable using PHP, JavaScript, HTML, CSS, and XML for web design.

Software

- Operating systems: Windows and Linux/Unix (Suse, Ubuntu)
- Versioning systems: CVS, SVN, and GIT
- Parallel processing and computer cluster usage

- Bioinformatic tools: including but not limited to, Blast, Clustal, Phylip, Cluster, Muscle, Cytoscape, HMMer, and Mauve. Also very familiar with querying public primary and secondary biological databases and the use of genome browsers, structural visualization tools, microarray tools, etc.
- Familiar with common computer science algorithms, such as dynamic programming, hidden Markov models (HMMs), and support vector machines (SVMs).

TRAINING

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|------|---------------------------------------|--------------------------------|
| 2007 | Genome Annotation | Sanger Centre, England |
| 2005 | Ensembl Web/Developer Workshop | UBC Michael Smith Laboratories |
| 2005 | Molecular Biology Techniques Workshop | UBC Michael Smith Laboratories |
| 2004 | ACUC SCUBA Certificate | University of New Brunswick |
| 2001 | Student Orientation | University of New Brunswick |
| 2001 | Conflict Mediation | University of New Brunswick |

COMMITTEES

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| 2007 | SFU MBB Graduate Caucus, Treasurer |
| 2006 | Canadian Society for Systems Biology Steering Committee |
| 2005 | CIHR/MSFHR Training Program in Bioinformatics Student Caucus |
| 2005 | CIHR/MSFHR Training Program in Bioinformatics Steering Committee |

MEMBERSHIPS

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|------|---|
| 2010 | The American Society for Microbiology |
| 2006 | International Society for Computational Biology |

REFERENCES

Available upon request.