

Rosemary McCloskey

github.com/rmcclosk | rmcclosk.math@gmail.com | 604-219-0157

Objective

To launch a challenging and fulfilling career in software development.

Education

M.Sc. Bioinformatics Candidate CIHR Strategic Training Program in Bioinformatics 90% Average University of British Columbia	Sep. 2015 - present
B.Sc. Mathematics Honours, Computer Science Minor 3.98 GPA Simon Fraser University	Sep. 2009 - June 2014

Skills

Programming languages

- Four years experience using C, Python, and R to develop research software.
- Academic experience with Java for software engineering course project.
- Markup languages: LaTeX, Markdown, HTML+CSS.

Computing environment

- Five years experience in Linux, including bash scripting.
- Familiar with development tools such as gdb, valgrind, Make, autotools.
- Working knowledge of SQL.

Mathematics and statistics

- Strong formal mathematics background including calculus, linear algebra, and discrete mathematics.
- Experience performing statistical tests, fitting models, applying Bayesian inference, and creating informative visualizations of data.

Bioinformatics

- Extensive experience processing genetic data and performing phylogenetic analyses.
- Familiar with open source toolkits such as BioPython and Bioconductor.
- Experience interfacing with public databases such as Genbank and the Cancer Genome Atlas.

Experience

M.Sc. Candidate, Bioinformatics
BC Centre for Excellence in HIV/AIDS

May. 2015 - present

- Masters thesis project under the supervision of Dr. Art Poon (Medicine, University of British Columbia).
- Developed a Bayesian inference method using HIV sequence data to investigate properties of human contact networks.
- Implemented method as open source C software (github.com/rmcclosk/netabc).

Research Assistant
Bioinformatics Training Program, UBC

Sep. 2014 - May 2015

- Two four-month rotations under Dr. Ryan Morin (Molecular Biology and Biochemistry, Simon Fraser University) and Dr. Sara Mostafavi (Statistics and Medical Genetics, University of British Columbia).
- Performed bioinformatic analyses of genetic and epigenetic data pertaining to cancer and Alzheimer's research.
- Developed web interface using *shiny* framework to visualize changes in mutation frequency over time.

Research Assistant
BC Centre for Excellence in HIV/AIDS

May - Dec. 2012
Jan. - Aug. 2014

- Two eight-month co-op research assistantships with Dr. Art Poon (Medicine, University of British Columbia).
- Performed extensive computational experimentation for publication-level bioinformatics research on HIV and hepatitis C phylogenetics.
- Produced two first-author peer-reviewed publications with no formal training in biology or bioinformatics.
- Junior developer on Python/Django software project for tracking bioinformatics pipelines (github.com/cfe-lab/Kive).

Research Assistant
Mathematics Department, Simon Fraser University

May - Aug. 2011

- Four month co-op research term with Drs. Marni Mishna and Cedric Chauve (Mathematics, Simon Fraser University).
- Implemented algorithms in Python for generation and analysis of combinatorial structures.

Awards and Scholarships

Department of Statistics Award for Data Science University of British Columbia	June 2015
Strategic Training Program in Bioinformatics Scholarship Canadian Institutes of Health Research	Sep. 2014 - present
Walter C Koerner Fellowship University of British Columbia	Sep. 2014 - May. 2015
NSERC Canadian Graduate Scholarship - Masters University of British Columbia	Sep. 2014 - Aug. 2015
Academic Scholarship, Basic Sciences Canadian Conference on HIV/AIDS Research	Apr. 2013
New Investigator Award Conference on Retroviruses and Opportunistic Infections	Mar. 2013
Vice-President Research Undergraduate Student Research Award Simon Fraser University	May - Aug. 2012
NSERC Undergraduate Student Research Award Simon Fraser University	May - Aug. 2011
Undergraduate Open Scholarship Simon Fraser University	Sep. 2010 - Dec. 2013
Alumni Scholarship Simon Fraser University	Sep. 2010 - Sep. 2011
Kennith M Strand Entrance Scholarship Simon Fraser University	Sep. 2009 - Apr. 2010

Publications

- JB Joy, **RM McCloskey**, T Nguyen, RH Liang, Y Khudyakov, A Olmstead, M Krajden, JW Ward, PR Harrigan, JSG Montaner, and AFY Poon. "The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study". In: *The Lancet Infectious Diseases* 16 (2016), pp. 124-129
- RM McCloskey**, RH Liang, JB Joy, M Krajden, JS Montaner, PR Harrigan, and AFY Poon. "Global origin and transmission of hepatitis C virus nonstructural protein 3 Q80K polymorphism". In: *The Journal of Infectious Diseases* 211.8 (2015), pp. 1288-1295
- AQ Le, J Taylor, W Dong, **R McCloskey**, C Woods, R Danroth, K Hayashi, MJ Milloy, AFY Poon, and ZL Brumme. "Differential evolution of a CXCR4-using HIV-1 strain in CCR5wt/wt and CCR5 Δ 32/ Δ 32 hosts revealed by longitudinal deep sequencing and phylogenetic reconstruction". In: *Scientific Reports* 5 (2015), p. 17607
- JB Joy, RH Liang, T Nguyen, **RM McCloskey**, and AFY Poon. "Origin and evolution of human immunodeficiency viruses". In: *Global Virology I-Identifying and Investigating Viral Diseases*. Springer New York, 2015, pp. 587-611

RM McCloskey, RH Liang, PR Harrigan, ZL Brumme, and AFY Poon. “An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data”. In: *Journal of Virology* 88.11 (2014), pp. 6181–6194

RH Liang, T Mo, W Dong, GQ Lee, LC Swenson, **RM McCloskey**, CK Woods, CJ Brumme, CK Ho, J Schinkel, JB Joy, PR Harrigan, and AFY Poon. “Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing.” In: *Nucleic Acids Research* 42.12 (2014), e98

AFY Poon, LW Walker, H Murray, **RM McCloskey**, PR Harrigan, and RH Liang. “Mapping the shapes of phylogenetic trees from human and zoonotic RNA viruses”. In: *PLoS ONE* 8.11 (2013), e78122

JK Mann, H Byakwaga, XT Kuang, AQ Le, CJ Brumme, P Mwimanzi, S Omarjee, E Martin, GQ Lee, B Baraki, R Danroth, **R McCloskey**, C Muzoora, DR Bangsberg, PW Hunt, PJR Goulder, BD Walker, PR Harrigan, JN Martin, T Ndung’u, MA Brockman, and ZL Brumme. “Ability of HIV-1 Nef to downregulate CD4 and HLA class I differs among viral subtypes”. In: *Retrovirology* 10.1 (2013), p. 1

Oral Presentations

RM McCloskey and AFY Poon. “Phylogenetic estimation of contact network parameters with kernel-ABC”. HIV Dynamics and Evolution, Woods Hole (upcoming). 2016

R McCloskey, R Liang, PR Harrigan, Z Brumme, and AFY Poon. “Reconstructing transmitted HIV genotypes by phylogenetic analysis of serial samples”. Canadian Conference on HIV/AIDS Research, Vancouver. 2013

RM McCloskey. “Statistical methods for ancestral reconstruction”. Canadian Undergraduate Mathematics Conference, Montréal. 2013

Poster Presentations

JB Joy, **RM McCloskey**, T Nguyen, RH Liang, Y Khudyakov, A Olmstead, M Krajden, J Ward, PR Harrigan, JSG Montaner, and AFY Poon. “Phylogenetic estimation of the temporal spread of hepatitis C genotype 1a in North America”. International AIDS Society Conference, Vancouver. 2015

AFY Poon, RH Liang, JB Joy, T Nguyen, **RM McCloskey**, M Krajden, JSG Montaner, and PR Harrigan. “Global origin and transmission of HCV NS3 substitution Q80K that is associated with lower Simeprevir susceptibility”. HIV Dynamics and Evolution, Tucson. 2014

RM McCloskey, R Liang, PR Harrigan, Z Brumme, and AFY Poon. “An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data”. Conference on Retroviruses and Opportunistic Infection, Atlanta. 2013