

# Rosemary McCloskey

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## Objective

To use my skills in software development, bioinformatics, and data analysis to launch a challenging and fulfilling career.

## Education

M.Sc. Bioinformatics Candidate CIHR Strategic Training Program in Bioinformatics 90% Average University of British Columbia	Sep. 2014 - Aug. 2016 (expected)
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.
- Contributed to projects in Ruby and Javascript+jQuery.

### Computing environment

- Five years experience in Linux, including bash scripting.
- Familiar with development tools such as gdb, valgrind, Make, autotools, git.
- 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](https://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](https://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 $\Delta$ 32/ $\Delta$ 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 Kraiden, 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 Kraiden, 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