Art F. Y. Poon

Contents

Education

2000–2005 **PhD**, *University of California, San Diego*, La Jolla, Biology.
Thesis: Evolutionary consequences of the genetic environment on mutations in bacterial viruses (Dr. Lin Chao)

1998–2000 **MSc**, *University of British Columbia*, Vancouver, Zoology.
Thesis: The evolution of the genetic load caused by recurrent mutations in small populations: genetic context and demographic history (Dr. Sarah P. Otto)

1994–1998 **HonBSc**, *University of Toronto*, Toronto, Biology.
Thesis: Estimates of mutational variance in *Drosophila melanogaster* (Dr. David Houle)

Appointments

August 2016– present **Assistant Professor**, *Department of Pathology and Laboratory Medicine*, Western University.
Primary appointment.

June 2017– present **Assistant Professor**, *Department of Microbiology and Immunology*, Western University.
Cross-appointment.

November 2016– present **Assistant Professor**, *Department of Applied Mathematics*, Western University.
Cross-appointment.

March 2012–July 2016 **Assistant Professor (Partner), non-tenure track**, *Department of Medicine*, University of British Columbia.
As an employee of Providence Health Care, I held this honorary unpaid appointment through the Partner Stream mechanism to provide teaching, scholarly and service activities at the university.

October 2015–July 2016 **Senior Research Scientist**, BC Centre for Excellence in HIV/AIDS.

October 2009 – October 2015 **Associate Research Scientist, Bioinformatics**, BC Centre for Excellence in HIV/AIDS.

July 2010 – June 2015 **Adjunct Assistant Professor**, *Faculty of Health Sciences*, Simon Fraser University.

August 2008 – August 2010 **Postdoctoral Fellow**, *Department of Experimental Medicine*, University of British Columbia.
Supervisor: Dr. P. Richard Harrigan.

August 2005 – July 2008 **Postdoctoral Fellow**, *Antiviral Research Center*, University of California, San Diego.
Supervisor: Dr. Simon Frost.

Awards and Recognitions

2013–2018 **CIHR New Investigator Award**, *CIHR Priority Announcement: CHVI Vaccine Discovery and Social Research*, CAD$300,000.
Project title: Applied phylogenetics for HIV prevention.

2012-2020 **Career Investigator Scholar Award**, *Michael Smith Foundation for Health Research, St. Paul's Hospital Foundation, and the Providence Health Care Research Institute*, CAD$ 317,500.
Project title: Phylogenetic surveillance of the HIV epidemic in British Columbia. In 2016, I declined the remainder of this award when I left British Columbia to accept a tenure-track appointment at Western University in Ontario.

2008-2010 **CIHR Fellowship**, *CIHR Fellowships Award in the Area of Biomedical/Clinical HIV/AIDS Research*, CAD$97,500.

1998-2000 **Postgraduate Scholarship Award**, *Natural Sciences and Engineering Research Council of Canada (NSERC)*, CAD$37,000.

Manuscripts in progress

1. Jamie FS Mann, Katja Klein, Joshua Pankrac, PF Mckay, DFL King, CN Wijewardhana, T Biru, DH Canaday, **Mariano Avino**, **Art FY Poon**, Y Gao, C Foster, S Fidler, RJ Shattock, and Eric J Arts. "A heterologous activator vector vaccine (ACT-VEC) induces HIV-1 latency reversal in CD4+ T cells". In: *Science* (Revision after review, in progress).
I assisted Dr. Avino in the analysis of next-generation sequence data from these experiments.

2. Leonid Chindelevich, **Art FY Poon**, and Caroline Colijn. "Network science inspires novel tree shape statistics". In: *Syst Biol* (Revision requested, August 18, 2017).
I developed and provided several of the virus sequence data sets that were analyzed in this collaborative study, and ran the kernel analyses of all data sets.

3. **Art FY Poon**, Emmanuel Ndashimye, **Mariano Avino**, Richard M Gibson, Fred Kyeyune, Immaculate Nankya, Miguel E Quiñones-Mateu, and Eric J Arts. "First-line HIV treatment failures in non-B subtypes and recombinants: a cross-sectional analysis of multiple populations in Uganda". In: *AIDS Res Ther* (Submitted, August 26, 2018).
I performed all analyses of sequence and clinical data, wrote the manuscript and generated all figures.

4. Andrea D Olmstead, Vincent Montoya, Celia K Chui, **Jeffrey B Joy**, Vera Tai, Winnie Dong, **Art F Y Poon**, **Thuy Nguyen**, Chanson J Brumme, Marianne Martinello, Gail V Matthews, P Richard Harrigan, Gregory J Dore, Tanya L Applegate, Jason Grebely, and Anita Y M Howe. "A systematic, deep sequencing-based methodology for the identification of mixed genotype hepatitis C virus infections". In: *Infect Genet Evol* (Submitted, August 15, 2018).
I designed the analytical pipeline used for characterizing the hepatitis C virus genotype composition of 'deep sequencing' data sets for this study.

5. **Mariano Avino**, **Bradley R Jones**, and **Art F Y Poon**. "Tree shape-based approaches for the comparative study of cophylogeny". In: *Syst Biol* (Submitted, August 10, 2018).
The first author is a postdoctoral associate in my lab. I helped Mariano conceive of and design the experiments, and I wrote the first implementation of the simulation code used in this study. I wrote about 50% of the paper and generated roughly half of the figures.

6. **Mariano Avino**, Emmanuel Ndashimye, Daniel J Lizotte, Richard M Gibson, Cissy Kityo, Eva Nabulime, Fred Kyeyune, Immaculate L Nankya, Miguel E Quiñones-Mateu, Eric J Arts, and **Art F Y Poon**. "Any single site counts: resistance-associated low-frequency variants in HIV integrase". In: *In prep.* (2018).

   I assisted Mariano (postdoctoral associate) with next-generation sequence data processing, design of imputation strategies, and the interpretation of support vector machine outputs.

7. **Jasper Ho**, **Garway T Ng**, **Mathias Renaud**, and **Art F Y Poon**. "*sierra-local*: A lightweight standalone application for secure HIV-1 drug resistance prediction". In: *bioRxiv* (2018).

   I conceived of and design the study, wrote the initial XML parser, supervised the three undergraduate students (Ho, Ng and Renaud) who implemented the code, and the introduction section of the manuscript.

8. **John Palmer** and **Art F Y Poon**. "Phylogenetic measures of indel rate variation among the HIV-1 group M subtypes". In: *In prep* (2018).

   I conceived of and designed this study, wrote about half of the Python and R scripts used in the analysis, and supervised John throughout the study as his undergraduate thesis advisor.

9. Stephen Solis-Reyes, **Mariano Avino**, **Art Poon**, and Lila Kari. "An open-source k-mer based machine learning tool for fast and accurate subtyping of HIV-1 genomes". In: *PLOS ONE* (Submitted, July 24, 2018).

   I directed the methods comparison component of this study, developed the simulation experiments, and wrote about 25% of the manuscript.

10. **Abayomi Olabode**, **Mariano Avino**, **Garway Ng**, **Faisal Abu-Sardanah**, **David Dick**, and **Art Poon**. "Evidence for a Recombinant Origin of HIV-1 group M from Genomic Variation". In: *Virus Evol* (Submitted, July 10, 2018).

    I conceived of and designed this study, led the collection of data sets, ran the Bayesian analysis and wrote about one-third of the manuscript. All authors are trainees in my lab.

Publications

80 articles in total (74 original research articles, 4 review articles, 2 commentaries). I am listed as first or senior author in 37 articles (46.2%).

According to Google Scholar, my articles have been cited a total of 3,201 times.

My name and the names of my past and current trainees are underlined and **bold**.

Original Research Articles

1. Ann M Dennis, Erik M Volz, Simon DW Frost, A S Md Mukarram Hossain, **Art FY Poon**, Peter F Reberio, Sten H Vermund, Timothy Sterling, and Marcia L Kalish. "HIV-1 transmission clustering and phylodynamics highlight the important role of young men who have sex with men in middle Tennessee". In: *AIDS Res Hum Retroviruses* (2018).

   I assisted with the clustering analysis and provided scripts for calculating patristic distances and for generating the network diagram.

2. **Bradley R Jones**, Natalie N Kinloch, **J Horacsek**, Philip Mwimanzi, Bemuluyigza Barakib, John Huang, Ronald Truong, Bruce Ganasea, Marianne Harrisa, P Richard Harrigan, R Brad Jones, Mark A Brockman, **Jeffrey B Joy***, **Art F Y Poon***, and Zabrina L Brumme*. "A phylogenetic approach to recover integration dates of latent HIV sequences within-host". In: *Proc Natl Acad Sci USA* (* equal contribution) Published ahead of print, September 5, 2018 (2018).

   I was the primary co-supervisor for the first and third authors (Jones and Horacsek) while they

were undergraduate research assistants in my lab. In this role, I conceived of the methodological approach and directed the development and validation of the phylogenetic method for reconstructing HIV-1 integration dates that was the basis for this study. As co-senior author, I wrote about a quarter of the manuscript. Joshua wrote the initial implementation of the dating method in R, which was subsequently extended and validated by Brad, who was primarily responsible for writing the manuscript. Our article is currently scoring in the top 5% of all research outputs tracked by Altmetric and has been featured by several media outlets, including the Vancouver Sun and the Georgia Straight.

3. Emmanuel Ndashimye, **Mariano Avino**, Fred Kyeyune, Immaculate Nankya, Richard M Gibson, Eva Nabulime, **Art F Y Poon**, Cissy Kityo, Peter Mugyenyi, Miguel E Quiñones-Mateu, and Eric J Arts. "Absence of HIV-1 drug resistance mutations supports the use of dolutegravir in Uganda". In: *AIDS Res Hum Retroviruses* Published ahead of print, `doi/10.1089/AID.2017.0205` (2018).
   I generated two figures and edited the manuscript. Mariano (PDF) was responsible for analyzing the sequence data and reconstructing the phylogeny.

4. **Art FY Poon**, Jessica L Prodger, B Lynch, Jun Lai, S Reynolds, J Kasule, A Capoferri, Susanna L Lamers, C Rodriguez, D Bruno, S Porcella, C Martens, Robert Siliciano, Janet Siliciano, Thomas Quinn, and Andrew D Redd. "Quantitation of the latent HIV-1 reservoir from the sequence diversity in viral outgrowth assays". In: *Retrovirology* 15 (July 2018), p. 47.
   This paper is the first product of my ongoing collaboration with the HIV reservoir research group at Johns Hopkins University. I developed and implemented the Bayesian method for estimating the proportion of infected cells in the latent HIV-1 reservoir from sequence data derived from a limiting dilution assay, performed the analysis of simulated and experimental data, generated all figures and wrote the manuscript.

5. Hiroyuki Gatanaga, Zabrina L Brumme, Emily Adland, Gustavo Reyes-Terán, Santiago Avila-Rios, Carlos R Mejía-Villatoro, Tsunefusa Hayashida, Takayuki Chikata, Giang Van Tran, Kinh Van Nguyen, Rita I Meza, Elsa Y Palou, Humberto Valenzuela-Ponce, Juan M Pascale, Guillermo Porras-Cortés, Marvin Manzanero, Guinevere Q Lee, Jeffrey N Martin, Mary N Carrington, Mina John, Simon Mallal, **Art F Y Poon**, Philip Goulder, Masafumi Takiguchi, Shinichi Oka, and International HIV Adaptation Collaborative. "Potential for immune-driven viral polymorphisms to compromise antiretroviral-based pre-exposure prophylaxis for prevention of HIV-1 infection". In: *AIDS* (June 2017).
   I analyzed HLA and HIV-1 RT sequence databases to produce the data required to generate Figure 3.

6. Richard M Gibson, Gabrielle Nickel, Michael Crawford, Fred Kyeyune, Colin Venner, Immaculate Nankya, Eva Nabulime, Emmanuel Ndashimye, **Art FY Poon**, Robert A Salata, Cissy Kityo, Peter Mugyenyi, Miguel E Quiñones-Mateu, and Eric J Arts. "Sensitive detection of HIV-1 resistance to Zidovudine and impact on treatment outcomes in low-to middle-income countries". In: *Infectious diseases of poverty* 6.1 (2017), p. 163.
   I advised the first author on the statistical analyses and edited the manuscript.

7. Alejandro Gonzalez-Serna, Arie C Glas, C J Brumme, **Art F Y Poon**, Adriana Nohpal De La Rosa, Tania Mudrikova, Viviane Dias Lima, Annemarie M J Wensing, and Richard Harrigan. "Genotypic susceptibility score (GSS) and CD4+ T cell recovery in HIV-1 patients with suppressed viral load". In: *J Antimicrob Chemother* 72.2 (Feb. 2017), pp. 496–503.
   I developed the bioinformatic pipeline for computing the genotypic susceptibility scores from the HIV treatment database, which were the primary data source for this study.

8. **Bradley R Jones** and **Art F Y Poon**. "node.dating: dating ancestors in phylogenetic trees in R". In: *Bioinformatics* 33.6 (Mar. 2017), pp. 932–934.
    I was the first author's (Jones) primary co-supervisor for the duration of this project. I concived of the project, designed the model validation experiments, and helped write the manuscript. Brad implemented the method in R and was primarily responsible for writing the manuscript.

9. **Katja Klein, Gabrielle Nickel, Immaculate Nankya, C Kwok, PL Chen, Art FY Poon, M Munjoma, T Chipato, Peter Mugyenyi, Robert A Salata, CS Morrison, and Eric J Arts. "Higher sequence diversity in the vaginal tract than in blood at acute and early HIV-1 infection". In: *PLOS Pathog* 14.1 (2017), e1006754.**
    I assisted with the processing and analysis of the next-generation sequence data. This paper was selected to be the feature article on the front page of the PLOS Pathogens website.

10. **Rosemary M McCloskey** and **Art FY Poon**. "A model-based clustering method to detect infectious disease transmission outbreaks from sequence variation". In: *PLoS Comput Biol* (2017).
    I conceived of the study, proposed the mathematical model, performed all simulation experiments and model validation on simulated and real data, wrote the paper and generated all figures. My graduate student (McCloskey) implemented the model and wrote the computer program.

11. Oliver Ratmann, Emma B Hodcroft, Michael Pickles, Anne Cori, Matthew Hall, Samantha Lycett, Caroline Colijn, Bethany Dearlove, Xavier Didelot, Simon Frost, A S Md Mukarram Hossain, **Jeffrey B Joy**, Michelle Kendall, Denise Kühnert, Gabriel E Leventhal, **Richard Liang**, Giacomo Plazzotta, **Art F Y Poon**, David A Rasmussen, Tanja Stadler, Erik Volz, Caroline Weis, Andrew J Leigh Brown, Christophe Fraser, and PANGEA-HIV Consortium. "Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison". In: *Mol Biol Evol* 34.1 (2017), pp. 185–203.
    I led the team based in Vancouver (comprising myself and my trainees Jeff Joy and Richard Liang) that contributed an analysis of the simulated HIV-1 epidemic data sets in this multi-centre collaboration. There were a total of five teams in this study. The team members are alphabetical order in the list of authors.

12. Brendan Jacka, Tanya Applegate, **Art F Poon**, Jayna Raghwani, P Richard Harrigan, Kora DeBeck, M-J Milloy, Mel Krajden, Andrea Olmstead, **Jeffrey B Joy**, Brandon D L Marshall, Kanna Hayashi, Oliver G Pybus, Viviane Dias Lima, Gkikas Magiorkinis, Julio Montaner, Francois Lamoury, Gregory J Dore, Evan Wood, and Jason Grebely. "Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada". In: *J Hepatol* 64.6 (June 2016), pp. 1247–55.
    I contributed analytical tools for this study.

13. **Jeffrey B Joy, Rosemary M McCloskey, Thuy Nguyen, Richard H Liang, Yury Khudyakov, Andrea Olmstead, Mel Krajden, John W Ward, P Richard Harrigan, Julio S G Montaner, and Art F Y Poon**. "The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study". In: *Lancet Infect Dis* 16.6 (June 2016), pp. 698–702.
    I led this study on reconstructing the epidemic spread of hepatitis C virus in North America. The first four authors were my trainees; Joy was my post-doc who was primarily responsible for the phylogenetic analysis and wrote the majority of the paper. I was responsible for collecting and processing the sequence data, editing the manuscript, and developing the response to reviews. My trainees Jeff, Rosemary, Thuy and Richard help me collect and curate the sequence data. Rosemary wrote a Python script for automating some of the data curation process. This paper was featured in several media outlets, including the Globe and Mail, CBC News, Global News,

and the Toronto Star; and was referenced by the U.S. National Viral Hepatitis Action Plan (2017-2020).

14. **Rosemary M McCloskey**, **Richard H Liang**, and **Art F Y Poon**. "Reconstructing contact network parameters from viral phylogenies". In: *Virus Evol* 2.2 (July 2016), vew029.
This manuscript presented findings from my MSc student's thesis project (McCloskey). Rosemary developed the method and performed all the validation experiments. Richard assisted in the development of simulation code. I conceived of the project, supervised the first author throughout the project, and revised earlier versions of the manuscript.

15. Vincent Montoya, Andrea Olmstead, Patrick Tang, Darrel Cook, Naveed Janjua, Jason Grebely, Brendan Jacka, **Art F Y Poon**, and Mel Krajden. "Deep sequencing increases hepatitis C virus phylogenetic cluster detection compared to Sanger sequencing". In: *Infect Genet Evol* 43 (Sept. 2016), pp. 329–37.
I contributed analytical tools for the study, designed Figure 1, and provided extensive feedback on earlier versions of the manuscript.

16. **Art F Y Poon**. "Impacts and shortcomings of genetic clustering methods for infectious disease outbreaks". In: *Virus Evol* 2.2 (July 2016), vew031.
As the sole author, I conceived of the study, performed all analyses, and wrote the manuscript.

17. **Art F Y Poon**, Réka Gustafson, Patricia Daly, Laura Zerr, S Ellen Demlow, Jason Wong, Conan K Woods, Robert S Hogg, Mel Krajden, David Moore, Perry Kendall, Julio S G Montaner, and P Richard Harrigan. "Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study". In: *Lancet HIV* 3.5 (May 2016), e231–8.
As the lead author of this manuscript, I was responsible for creating the monitoring system that is the focus of the case study, developed all figures and wrote the paper. This was the world's first example of an automated real-time monitoring system on an HIV treatment database, which initiated and supported a public health intervention to significantly reduce the spread of transmitted HIV drug resistance in British Columbia. This paper has been featured by UNAIDS, IEEE Spectrum Magazine, and MD Magazine; and it is scoring in the top 5% of all research outputs scored by Altmetric.

18. C K S Chui, W W Y Dong, **J B Joy**, **A F Y Poon**, W Y Dong, T Mo, C K Woods, C Beatty, H Hew, P R Harrigan, and C J Brumme. "Development and Validation of Two Screening Assays for the Hepatitis C Virus NS3 Q80K Polymorphism Associated with Reduced Response to Combination Treatment Regimens Containing Simeprevir". In: *J Clin Microbiol* 53.9 (Sept. 2015), pp. 2942–50.
I developed the bioinformatic pipeline that was used to analyze the next-generation sequence data in this study.

19. **Aram Karakas**, Zabrina L Brumme, and **Art F Y Poon**. "Global Database-Driven Assessment of HIV-1 Adaptation to the Immune Repertoires of Human Populations". In: *J Virol* 89.20 (Oct. 2015), pp. 10693–5.
This manuscript was the product of Aram's undergraduate directed studies project under my supervision. Aram was responsible for running the data analysis and generating figures. I conceived of the project, designed the bioinformatic scripts used to collect and analyze the data, and wrote the manuscript.

20. Natalie N Kinloch, Daniel R MacMillan, Anh Q Le, Laura A Cotton, David R Bangsberg, Susan Buchbinder, Mary Carrington, Jonathan Fuchs, P Richard Harrigan, Beryl Koblin, Margot Kushel, Martin Markowitz, Kenneth Mayer, M J Milloy, Martin T Schechter, Theresa Wagner, Bruce D Walker, Jonathan M Carlson, **Art F Y Poon**, and Zabrina L Brumme. "Population-Level Immune-Mediated Adaptation in HIV-1 Polymerase during the North American Epidemic". In: *J Virol* 90.3 (Nov. 2015), pp. 1244–58.
I performed the phylogenetic analyses of the modern and historic HIV-1 sequences, and reconstructed the ancestral sequence at the origin of the North American epidemic that was recreated in the lab by mutagenesis for functional characterization. The lead graduate student author received a conference scholarship for the presentation of this study at the Canadian HIV/AIDS Research Conference.

21. François M J Lamoury, Brendan Jacka, Sofia Bartlett, Rowena A Bull, Arthur Wong, Janaki Amin, Janke Schinkel, **Art F Poon**, Gail V Matthews, Jason Grebely, Gregory J Dore, and Tanya L Applegate. "The Influence of Hepatitis C Virus Genetic Region on Phylogenetic Clustering Analysis". In: *PLoS One* 10.7 (2015), e0131437.
I contributed analytical tools for this study.

22. H R Lapointe, W Dong, G Q Lee, D R Bangsberg, J N Martin, A R Mocello, Y Boum, A Karakas, D Kirkby, **A F Y Poon**, P R Harrigan, and C J Brumme. "HIV drug resistance testing by high-multiplex "wide" sequencing on the MiSeq instrument". In: *Antimicrob Agents Chemother* 59.11 (Nov. 2015), pp. 6824–33.
I developed the bioinformatic pipeline that was used to process the next-generation sequence data that was the primary result of the manuscript.

23. Anh Q Le, Jeremy Taylor, Winnie Dong, **Rosemary McCloskey**, Conan Woods, Ryan Danroth, Kanna Hayashi, M-J Milloy, **Art F Y Poon***, and Zabrina L Brumme*. "Differential evolution of a CXCR4-using HIV-1 strain in CCR5wt/wt and CCR5δ32/δ32 hosts revealed by longitudinal deep sequencing and phylogenetic reconstruction". In: *Sci Rep* 5 (Dec. 2015), p. 17607.
Rosemary assisted with the phylogenetic sequence analysis. I performed the phylogenetic analysis of the next-generation sequence data sets that formed the basis of the primary results in this study. As a result, I was co-senior author on this manuscript.

24. **Rosemary M McCloskey**, **Richard H Liang**, **Jeffrey B Joy**, Mel Krajden, Julio S G Montaner, P Richard Harrigan, and **Art F Y Poon**. "Global origin and transmission of hepatitis C virus nonstructural protein 3 Q80K polymorphism". In: *J Infect Dis* 211.8 (Apr. 2015), pp. 1288–95.
Rosemary performed the analysis, generated the figures and was primarily responsible for writing the paper. RIchard and Jeff assisted with data collection and revising the manuscript. Richard customized the Path-O-Gen Java program used for rooting the phylogeny. I conceived of and designed this study, and performed the preliminary data collection and phylogenetic analysis.

25. Andrea D Olmstead, **Jeffrey B Joy**, Vincent Montoya, Iris Luo, **Art F Y Poon**, Brendan Jacka, François Lamoury, Tanya Applegate, Julio Montaner, Yury Khudyakov, Jason Grebely, Darrel Cook, P Richard Harrigan, and Mel Krajden. "A molecular phylogenetics-based approach for identifying recent hepatitis C virus transmission events". In: *Infect Genet Evol* 33 (July 2015), pp. 101–9.
Jeff assisted with the phylogenetic analysis. I contributed analytical tools for the analysis of data in this study, and assisted in the interpretation of analytical results.

26. **Art F Y Poon**. "Phylodynamic Inference with Kernel ABC and Its Application to HIV Epidemiology". In: *Mol Biol Evol* 32.9 (Sept. 2015), pp. 2483–95.

As sole author of this manuscript, I conceived and designed the study, performed all analyses and wrote the paper.

27. **Art F Y Poon**, **Jeffrey B Joy**, Conan K Woods, Susan Shurgold, Guillaume Colley, Chanson J Brumme, Robert S Hogg, Julio S G Montaner, and P Richard Harrigan. "The impact of clinical, demographic and risk factors on rates of HIV transmission: a population-based phylogenetic analysis in British Columbia, Canada". In: *J Infect Dis* 211.6 (Mar. 2015), pp. 926–35.

Jeff contributed analytical tools and helped revise the paper. I performed all analyses in this study and wrote the manuscript. This article remains one of the largest retrospective analyses of genetic clusters in a regional HIV treatment database, and was featured in an editorial commentary.

28. Laura A Cotton, Xiaomei T Kuang, Anh Q Le, Jonathan M Carlson, Benjamin Chan, Denis R Chopera, Chanson J Brumme, Tristan J Markle, Eric Martin, Aniqa Shahid, Gursev Anmole, Philip Mwimanzi, Pauline Nassab, Kali A Penney, Manal A Rahman, M-J Milloy, Martin T Schechter, Martin Markowitz, Mary Carrington, Bruce D Walker, Theresa Wagner, Susan Buchbinder, Jonathan Fuchs, Beryl Koblin, Kenneth H Mayer, P Richard Harrigan, Mark A Brockman, **Art F Y Poon**, and Zabrina L Brumme. "Genotypic and functional impact of HIV-1 adaptation to its host population during the North American epidemic". In: *PLoS Genet* 10.4 (Apr. 2014), e1004295.

I performed the phylogenetic, molecular dating and ancestral sequence reconstruction analyses for this study. This paper was featured by Science Daily.

29. B Jacka, T Applegate, M Krajden, A Olmstead, P R Harrigan, B D L Marshall, K DeBeck, M-J Milloy, F Lamoury, O G Pybus, V D Lima, G Magiorkinis, V Montoya, J Montaner, **J Joy**, C Woods, S Dobrer, G J Dore, **A F Poon**, and J Grebely. "Phylogenetic clustering of hepatitis C virus among people who inject drugs in Vancouver, Canada". In: *Hepatology* 60.5 (Nov. 2014), pp. 1571–1580.

I performed the preliminary data analyses for this study, contributed analytical tools, and advised the lead author on the usage and interpretation of phylogenetic methods. In this year of publication, the journal *Hepatology* received an impact factor of 11.06.

30. David J H F Knapp, Rachel A McGovern, **Art F Y Poon**, Xiaoyin Zhong, Dennison Chan, Luke C Swenson, Winnie Dong, and P Richard Harrigan. ""Deep" sequencing accuracy and reproducibility using Roche/454 technology for inferring co-receptor usage in HIV-1". In: *PLoS One* 9.6 (2014), e99508.

I assisted in the analysis of the next-generation sequence data and helped revise the manuscript in response to reviewers.

31. **Richard H Liang**, Theresa Mo, Winnie Dong, Guinevere Q Lee, Luke C Swenson, **Rosemary M McCloskey**, Conan K Woods, Chanson J Brumme, Cynthia K Y Ho, Janke Schinkel, **Jeffrey B Joy**, P Richard Harrigan, and **Art F Y Poon**. "Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing". In: *Nucleic Acids Res* 42.12 (July 2014), e98.

Richard Liang was a post-doctoral fellow under my supervision. Richard performed the analysis and was primarily responsible for generating figures and writing the manuscript. I conceived of and designed the study, and helped write the manuscript. The current impact factor for this journal is 10.2.

32. **Rosemary M McCloskey**, **Richard H Liang**, P Richard Harrigan, Zabrina L Brumme, and **Art F Y Poon**. "An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data". In: *J Virol* 88.11 (June 2014), pp. 6181–94.
I was the lead author's undergraduate co-op supervisor during this study. Rosemary performed all analyses and primarily wrote the paper. I conceived of and designed the study and instructed Rosemary on HIV evolution, phylogenetics and ancestral reconstruction throughout the study.

33. Brejnev Muhizi Muhire, Michael Golden, Ben Murrell, Pierre Lefeuvre, Jean-Michel Lett, Alistair Gray, **Art Y F Poon**, Nobubelo Kwanele Ngandu, Yves Semegni, Emil Pavlov Tanov, Adérito Luis Monjane, Gordon William Harkins, Arvind Varsani, Dionne Natalie Shepherd, and Darren Patrick Martin. "Evidence of pervasive biologically functional secondary structures within the genomes of eukaryotic single-stranded DNA viruses". In: *J Virol* 88.4 (Feb. 2014), pp. 1972–89.
I contributed a custom HyPhy batch language script for detecting secondary structures from nucleotide coevolution for this study.

34. Chanson J Brumme, Kelly D Huber, Winnie Dong, **Art F Y Poon**, P Richard Harrigan, and Nicolas Sluis-Cremer. "Replication fitness of multiple nonnucleoside reverse transcriptase-resistant HIV-1 variants in the presence of etravirine measured by 454 deep sequencing". In: *J Virol* 87.15 (Aug. 2013), pp. 8805–7.
For this study, I developed population genetic models of viral fitness to measure the selective advantage of mutations associated with drug resistance.

35. David J H F Knapp, Rachel A McGovern, Winnie Dong, **Art F Y Poon**, Luke C Swenson, Xiaoyin Zhong, Conan K Woods, and P Richard Harrigan. "Factors influencing the sensitivity and specificity of conventional sequencing in human immunodeficiency virus type 1 tropism testing". In: *J Clin Microbiol* 51.2 (Feb. 2013), pp. 444–51.
I was responsible for anonymizing the clinical data sets used in this study so that they could be analyzed by the lead author, who had started employment at another institution during the preparation of this manuscript, and wrote the scripts used to generate Figure 4A.

36. Guinevere Q Lee, P Richard Harrigan, Winnie Dong, **Art F Y Poon**, Jayvant Heera, James Demarest, Alex Rinehart, Doug Chapman, Hernan Valdez, and Simon Portsmouth. "Comparison of population and 454 "deep" sequence analysis for HIV type 1 tropism versus the original trofile assay in non-B subtypes". In: *AIDS Res Hum Retroviruses* 29.6 (June 2013), pp. 979–84.
For this study, I customized the pre-processing script for uploading next-generation sequence data sets to a web-server for coreceptor tropism prediction, which facilitated the batch analysis of data under varying parameters.

37. Rachel A McGovern, Jori Symons, **Art F Y Poon**, P Richard Harrigan, Steven F L van Lelyveld, Andy I M Hoepelman, Petra M van Ham, Winnie Dong, Annemarie M J Wensing, and Monique Nijhuis. "Maraviroc treatment in non-R5-HIV-1-infected patients results in the selection of extreme CXCR4-using variants with limited effect on the total viral setpoint". In: *J Antimicrob Chemother* 68.9 (Sept. 2013), pp. 2007–14.
I developed and applied a method for estimating the selective effect of drug pressure on the composition of the virus population for this study.

38. **Art F Y Poon**, Lorne W Walker, **Heather Murray**, **Rosemary M McCloskey**, P Richard Harrigan, and **Richard H Liang**. "Mapping the shapes of phylogenetic trees from human and zoonotic RNA viruses". In: *PLoS One* 8.11 (2013), e78122.
Three of the authors were undergraduates or a postdoc under my primary supervision. As lead author, I conceived of and designed the study, collected about 80% of the data, developed and applied all analytical methods (Lorne Walker wrote a preliminary implementation of the kernel method), and wrote the manuscript. Richard Liang was a post-doc under my supervision and was given senior authorship to recognize his contributions in deriving a mathematical proof of the kernel as being positive semidefinite. Heather and Rosemary assisted in the collection of human virus sequence datasets.

39. Luke C Swenson, Winnie W Y Dong, Theresa Mo, James Demarest, Doug Chapman, Suzanne Ellery, Jayvant Heera, Hernan Valdez, **Art F Y Poon**, and P Richard Harrigan. "Use of cellular HIV DNA to predict virologic response to maraviroc: performance of population-based and deep sequencing". In: *Clin Infect Dis* 56.11 (June 2013), pp. 1659–66.
I assisted in the analysis and interpretation of tropism prediction data and wrote the description of bioinformatic methods.

40. Jeannette L Aldous, Sergei Kosakovsky Pond, **Art Poon**, Sonia Jain, Huifang Qin, James S Kahn, Mari Kitahata, Benigno Rodriguez, Ann M Dennis, Stephen L Boswell, Richard Haubrich, and Davey M Smith. "Characterizing HIV transmission networks across the United States". In: *Clin Infect Dis* 55.8 (Oct. 2012), pp. 1135–43.
I processed the sequence data and assisted in the interpretation of results.

41. A Gonzalez-Serna, R A McGovern, P R Harrigan, F Vidal, **A F Y Poon**, S Ferrando-Martinez, M A Abad, M Genebat, M Leal, and E Ruiz-Mateos. "Correlation of the virological response to short-term maraviroc monotherapy with standard and deep-sequencing-based genotypic tropism prediction methods". In: *Antimicrob Agents Chemother* 56.3 (Mar. 2012), pp. 1202–7.
I assisted in the analysis of the next-generation sequence data.

42. Guinevere Q Lee, Luke C Swenson, **Art F Y Poon**, Jeffrey N Martin, Hiroyu Hatano, Steven G Deeks, and P Richard Harrigan. "Prolonged and substantial discordance in prevalence of raltegravir-resistant HIV-1 in plasma versus PBMC samples revealed by 454 ''deep'' sequencing". In: *PLoS One* 7.9 (2012), e46181.
I analyzed the next-generation sequence data and generated Figure 2.

43. **Art F Y Poon**, Luke C Swenson, Evelien M Bunnik, Diana Edo-Matas, Hanneke Schuitemaker, Angélique B van 't Wout, and P Richard Harrigan. "Reconstructing the dynamics of HIV evolution within hosts from serial deep sequence data". In: *PLoS Comput Biol* 8.11 (2012), e1002753.
I performed all data analyses, created all figures and wrote the paper.

44. Camilla U Rang, Annie Y Peng, **Art F Poon**, and Lin Chao. "Ageing in *Escherichia coli* requires damage by an extrinsic agent". In: *Microbiology* 158.6 (2012), pp. 1553–1559.
I contributed a Bayesian method for fitting the model of bacterial ageing, which I implemented in the program JAGS (Just Another Gibbs Sampler).

45. David J H F Knapp, P Richard Harrigan, **Art F Y Poon**, Zabrina L Brumme, Mark Brockman, and Peter K Cheung. "In vitro selection of clinically relevant bevirimat resistance mutations revealed by "deep" sequencing of serially passaged, quasispecies-containing recombinant HIV-1". In: *J Clin Microbiol* 49.1 (Jan. 2011), pp. 201–8.

I analyzed the next-generation sequence data using a two-locus deterministic model, screened for potential contaminants using BLAST on patient-specific databases and calculated diversity measures.

46. Susanna L Lamers, **Art F Y Poon**, and Michael S McGrath. "HIV-1 *nef* protein structures associated with brain infection and dementia pathogenesis". In: *PLoS One* 6.2 (Feb. 2011), e16659.

I generated a structural model of the HIV-1 Nef protein by combining two crystal structures and performing an energy minimization/folding analysis. This model was used to generate figures 2 and 3 and for all structural analyses (residue distances, free energies) in the paper.

47. **Art F Y Poon**, Jeannette L Aldous, W Christopher Mathews, Mari Kitahata, James S Kahn, Michael S Saag, Benigno Rodríguez, Stephen L Boswell, Simon D W Frost, and Richard H Haubrich. "Transmitted drug resistance in the CFAR network of integrated clinical systems cohort: prevalence and effects on pre-therapy CD4 and viral load". In: *PLoS One* 6.6 (2011), e21189.

As the lead author, I performed all analyses – including Bayesian network analyses and detection of transmitted drug resistance – and wrote the paper.

48. Vera Tai, **Art FY Poon**, Ian T Paulsen, and Brian Palenik. "Selection in coastal Synechococcus (Cyanobacteria) populations evaluated from environmental metagenomes". In: *PloS one* 6.9 (2011), e24249.

I developed a Python script for parsing ACE files (at the time, there were no parsing modules available) and for screening the resulting sequences for evidence of diversifying selection.

49. **Wayne Delport, Art F Y Poon, Simon D W Frost, and Sergei L Kosakovsky Pond. "Data-monkey 2010: a suite of phylogenetic analysis tools for evolutionary biology". In: *Bioinformatics* 26.19 (Oct. 2010), pp. 2455–7.**

I developed a machine learning toolkit (stochastic context free grammars and Bayesian graphical models) that was directly incorporated into the HyPhy software C++ source, and represented one of the major advances in this version. This applications note has been cited over 700 times.

50. Weerawat Manosuthi, David M Butler, Josué Pérez-Santiago, **Art FY Poon**, Satish K Pillai, Sanjay R Mehta, Mary E Pacold, Douglas D Richman, Sergei Kosakovsky Pond, and Davey M Smith. "Protease polymorphisms in HIV-1 subtype CRF01_AE represent selection by antiretroviral therapy and host immune pressure". In: *AIDS* 24.3 (Jan. 2010), pp. 411–6.

I performed a Bayesian network analysis of amino acid covariation and helped edit the manuscript.

51. Sergei L Kosakovsky Pond, Konrad Scheffler, Michael B Gravenor, **Art F Y Poon**, and Simon D W Frost. "Evolutionary fingerprinting of genes". In: *Mol Biol Evol* 27.3 (Mar. 2010), pp. 520–36.

I created Supplementary Figure S2, assisted with data collection and edited the manuscript.

52. **Art F Y Poon**, Luke C Swenson, Winnie W Y Dong, Wenjie Deng, Sergei L Kosakovsky Pond, Zabrina L Brumme, James I Mullins, Douglas D Richman, P Richard Harrigan, and Simon D W Frost. "Phylogenetic analysis of population-based and deep sequencing data to identify coevolving sites in the nef gene of HIV-1". In: *Mol Biol Evol* 27.4 (Apr. 2010), pp. 819–32.
This paper was one of the first studies to utilize next-generation sequencing to examine the composition of a virus population within patients. As lead author, I performed all analyses, wrote custom Python scripts to generate figures, and wrote the manuscript.

53. Brad H Davis, **Art F Y Poon**, and Michael C Whitlock. "Compensatory mutations are repeatable and clustered within proteins". In: *Proc Biol Sci* 276.1663 (May 2009), pp. 1823–7.
I performed data collection and processing for this study.

54. Parris S Jordan, **Art Poon**, Joseph Eron, Kathleen Squires, Caroline Ignacio, Douglas D Richman, and Davey M Smith. "A novel codon insert in protease of clade B HIV type 1". In: *AIDS Res Hum Retroviruses* 25.5 (May 2009), pp. 547–50.
I contributed a structural model of HIV-1 protease that was edited to include the amino acid insertion, and generated energy-minimized fold predictions of the resulting structure.

55. Sergei L Kosakovsky Pond, David Posada, Eric Stawiski, Colombe Chappey, **Art F Y Poon**, Gareth Hughes, Esther Fearnhill, Mike B Gravenor, Andrew J Leigh Brown, and Simon D W Frost. "An evolutionary model-based algorithm for accurate phylogenetic breakpoint mapping and subtype prediction in HIV-1". In: *PLoS Comput Biol* 5.11 (Nov. 2009), e1000581.
I assisted with data collection and preliminary analysis.

56. S J Lycett, M J Ward, F I Lewis, **A F Y Poon**, S L Kosakovsky Pond, and A J Leigh Brown. "Detection of mammalian virulence determinants in highly pathogenic avian influenza H5N1 viruses: multivariate analysis of published data". In: *J Virol* 83.19 (Oct. 2009), pp. 9901–10.
For this study, I performed a Bayesian network analysis to detect associations between sequence variation and the type of mammalian host.

57. **Art F Y Poon**, Kimberly C Brouwer, Steffanie A Strathdee, Michelle Firestone-Cruz, Remedios M Lozada, Sergei L Kosakovsky Pond, Douglas D Heckathorn, and Simon D W Frost. "Parsing social network survey data from hidden populations using stochastic context-free grammars". In: *PLoS One* 4.9 (Sept. 2009), e6777.
I performed all analyses and wrote the paper.

58. **Art F Y Poon**, Simon D W Frost, and Sergei L Kosakovsky Pond. "Detecting signatures of selection from DNA sequences using Datamonkey". In: *Methods Mol Biol* 537 (2009), pp. 163–83.
This was an invited and peer-reviewed review paper that provided an overview of the phylogenetic sequence analysis methods on the Datamonkey webserver. As lead author, I wrote about half of the manuscript and coordinated the contributions from the other authors.

59. Edward R Cachay, Simon D W Frost, **Art F Y Poon**, David Looney, Sherry M Rostami, Mary E Pacold, Douglas D Richman, Susan J Little, and Davey M Smith. "Herpes simplex virus type 2 acquisition during recent HIV infection does not influence plasma HIV levels". In: *J Acquir Immune Defic Syndr* 47.5 (Apr. 2008), pp. 592–6.
I contributed some statistical analyses of the experimental data for this study.

60. P Richard Harrigan, Chih-Wei Sheen, Vikram S Gill, Brian Wynhoven, Erin Hudson, Viviane D Lima, Pierre Lecocq, Rosalia Aguirre, **Art F Y Poon**, and Nicolas Sluis-Cremer. "Silent mutations are selected in HIV-1 reverse transcriptase and affect enzymatic efficiency". In: *AIDS* 22.18 (Nov. 2008), pp. 2501–8.
I verified the main finding of the study by carrying out an analysis of bulk sequence mixtures in a similar data set.

61. S L Kosakovsky Pond, **A F Y Poon**, S Zárate, D M Smith, S J Little, S K Pillai, R J Ellis, J K Wong, A J Leigh Brown, D D Richman, and S D W Frost. "Estimating selection pressures on HIV-1 using phylogenetic likelihood models". In: *Stat Med* 27.23 (Oct. 2008), pp. 4779–89.
I contributed about one-eighth of the text in this manuscript, which was an invited review article for a peer-reviewed journal.

62. Sergei L Kosakovsky Pond, **Art F Y Poon**, Andrew J Leigh Brown, and Simon D W Frost. "A maximum likelihood method for detecting directional evolution in protein sequences and its application to influenza A virus". In: *Mol Biol Evol* 25.9 (Sept. 2008), pp. 1809–24.
I collected data sets for model validation and edited the manuscript.

63. **Art F Y Poon**, Fraser I Lewis, Simon D W Frost, and Sergei L Kosakovsky Pond. "Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models". In: *Bioinformatics* 24.17 (Sept. 2008), pp. 1949–50.
As lead author, I developed the method described in this applicatio note and wrote the paper. The web tool it describes has averaged about 2,000 job submissions per year since going online in 2007.

64. Hendrik Streeck, Bin Li, **Art F Y Poon**, Arne Schneidewind, Adrianne D Gladden, Karen A Power, Demetre Daskalakis, Suzane Bazner, Rosario Zuniga, Christian Brander, Eric S Rosenberg, Simon D W Frost, Marcus Altfeld, and Todd M Allen. "Immune-driven recombination and loss of control after HIV superinfection". In: *J Exp Med* 205.8 (Aug. 2008), pp. 1789–96.
I performed the recombination detection analysis of HIV-1 sequences for this study.

65. H Lapp, S Bala, JP Balhoff, A Bouck, N Goto, M Holder, R Holland, A Holloway, T Katayama, PO Lewis, AJ Mackey, BI Osborne, WH Piel, Pond SL Kosakovsky, **AFY Poon**, W Qiu, JE Stajich, A Stoltzfus, T Thierer, and AJ Vilella. "The 2006 NESCent Phyloinformatics Hackathon: A Field Report." In: (2007).
This contribution reported the results from a 'hackathon' that was held at Duke University in 2006, at which I was a workshop participant and developed Python wrappers for the software package *HyPhy*.

66. **Art F Y Poon**, Sergei L Kosakovsky Pond, Phil Bennett, Douglas D Richman, Andrew J Leigh Brown, and Simon D W Frost. "Adaptation to human populations is revealed by within-host polymorphisms in HIV-1 and hepatitis C virus". In: *PLoS Pathog* 3.3 (Mar. 2007), e45.
I performed all analyses, developed and analyzed the mathematical model, generated all figures and wrote the manuscript.

67. **Art F Y Poon**, Sergei L Kosakovsky Pond, Douglas D Richman, and Simon D W Frost. "Mapping protease inhibitor resistance to human immunodeficiency virus type 1 sequence polymorphisms within patients". In: *J Virol* 81.24 (Dec. 2007), pp. 13598–607.
As lead author, I conceived of, designed and performed all analyses and wrote the paper.

68. **Art F Y Poon**, Fraser I Lewis, Sergei L Kosakovsky Pond, and Simon D W Frost. "An evolutionary-network model reveals stratified interactions in the V3 loop of the HIV-1 envelope". In: *PLoS Comput Biol* 3.11 (Nov. 2007), e231.
I conceived of, designed and performed all analyses for this study and wrote the paper.

69. **Art F Y Poon**, Fraser I Lewis, Sergei L Kosakovsky Pond, and Simon D W Frost. "Evolutionary interactions between N-linked glycosylation sites in the HIV-1 envelope". In: *PLoS Comput Biol* 3.1 (Jan. 2007), e11.
For this paper, I implemented a binary covarion model of glycosylation site evolution and ran the Bayesian network analyses on the same data, generated all figures and wrote the manuscript.

70. **Art F Y Poon** and Lin Chao. "Functional origins of fitness effect-sizes of compensatory mutations in the DNA bacteriophage phiX174". In: *Evolution* 60.10 (Oct. 2006), pp. 2032–43.
I designed the study, performed all experiments and wrote the manuscript.

71. **Art Poon and Lin Chao. "The rate of compensatory mutation in the DNA bacteriophage ϕX174". In: *Genetics* 170.3 (July 2005), pp. 989–99.**
I conceived of and designed the study, developed the experimental system, performed all mutagenesis experiments, analyzed the data, and wrote the manuscript. This work has been described as "a revolutionary set of experiments" that were "largely ahead of their time [and] address questions that are only now entering the mainstream" [Curr Opin Struct Biol 26:104].

72. **Art Poon**, Bradley H Davis, and Lin Chao. "The coupon collector and the suppressor mutation: estimating the number of compensatory mutations by maximum likelihood". In: *Genetics* 170.3 (July 2005), pp. 1323–32.
I conceived of and designed the study, collected over half of the data, and wrote the manuscript.

73. **Art Poon** and Lin Chao. "Drift increases the advantage of sex in RNA bacteriophage phi6". In: *Genetics* 166.1 (Jan. 2004), pp. 19–24.
I performed all experiments, analyzed the data and wrote the manuscript.

74. **A Poon** and S P Otto. "Compensating for our load of mutations: freezing the meltdown of small populations". In: *Evolution* 54.5 (Oct. 2000), pp. 1467–79.
I conceived of the study, carried out over half of the theoretical model analyses, generated all figures and wrote the manuscript.

Review Articles

75. Kate Grabowski, Joshua Herbeck, and **Art FY Poon**. "HIV phylogenetics, clusters, and molecular epidemiology". In: *Curr Opin HIV AIDS* 15 (2018), pp. 1–8.
I wrote roughly a third of this invited review as part of the Topical Collection on *The Science of Prevention*.

76. Chanson J Brumme and **Art F Y Poon**. "Promises and pitfalls of Illumina sequencing for HIV resistance genotyping". In: *Virus Res* (Dec. 2016).
I wrote roughly half of this review and perspective article, which was an invited contribution to a peer-reviewed collection of articles on deep sequencing in virology.

77. **Jeffrey B Joy**, **Richard H Liang**, **Rosemary M McCloskey**, **T Nguyen**, and **Art F Y Poon**. "Ancestral Reconstruction". In: *PLoS Comput Biol* 12.7 (July 2016), e1004763.
This manuscript was co-authored by my trainees (two post-docs and two graduate students) and myself. I was responsible for writing about a third of the material and coordinated the contributions from the other authors. This article has been accessed over 7,000 times since publication and is now the template for the topic of ancestral reconstruction on Wikipedia.

78. Sergei L Kosakovsky Pond, Ben Murrell, and **Art F Y Poon**. "Evolution of viral genomes: interplay between selection, recombination, and other forces". In: *Methods Mol Biol* 856 (2012), pp. 239–72.

    I wrote about a third of this phylogenetic methods tutorial article (including the sections on epistasis and identifying selective factors) and wrote the introduction.

    Commentaries

79. **Art FY Poon** and Bethany L Dearlove. "Quantifying the aftermath: recent outbreaks among people who inject drugs and the utility of phylodynamics". In: *J Infect Dis* 217.12 (May 2018), pp. 1854–1857.

    I was invited to contribute this Editorial Commentary on a featured article appearing in the same issue. I invited my colleague Dr. Dearlove to help me compose the article, for which I wrote about one-half of the final content.

80. Joshua T Herbeck, Roxanne P Kerani, and **Art F Y Poon**. "What proportion of HIV-infected foreign-born individuals in the U.S. have been infected after immigrating to the U.S.?" In: *J Acquir Immune Defic Syndr* (2017).

    I contributed one of two core concepts and wrote about 20% of this commentary on a previous publication, which was contributed as a Letter to the Editor. Accepted, November 8, 2017.

Book chapters

1. **Mariano Avino** and **Art F Y Poon**. "Detecting amino acid coevolution in homologous proteins with Bayesian graphical models". In: *Computational Methods in Protein Evolution*. Methods in Molecular Biology 1851 (2018). Ed. by Tobias T Sikosek, p. 444. ISSN: 1064-3745.

2. **Jeffrey B Joy**, **Richard H Liang**, **T Nguyen**, **Rosemary M McCloskey**, and **Art FY Poon**. "Origin and Evolution of Human Immunodeficiency Viruses". In: *Global Virology I-Identifying and Investigating Viral Diseases* (2015), pp. 587–611.

3. ZL Brumme, **AFY Poon**, JM Carlson, and Bruce D Walker. "Identifying HLA-associated polymorphisms in HIV-1". In: *HIV Molecular Immunology* 2011 (2010), pp. 1–14.

4. SL Kosakovsky Pond, **AFY Poon**, and SDW Frost. "Estimating selection pressures on alignments of coding sequences". In: *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing. Cambridge Univ. Press, Cambridge, UK* (2009), pp. 419–490.

Conference publications

1. **J Joy**, **R Liang**, **T Nguyen**, R McCloskey, B Brenner, T Lynch, J Gill, J Buller, Z Brumme, A Burchell, S Rourke, M Loutfy, J Raboud, C Cooper, D Kelly, C Tsoukas, N Machouf, M Klein, A Wong, P Levett, S Hosein, M Wainberg, P Sandstrom, J Montaner, R Hogg, **A Poon**, and PR Harrigan. "Phylodynamic insights into HIV epidemic dynamics within Canada". In: *JOURNAL OF THE INTERNATIONAL AIDS SOCIETY*. Vol. 20. INT AIDS SOCIETY AVENUE DE FRANCE 23, GENEVA, 1202, SWITZERLAND. 2017, pp. 100–101.

2. Paul N Levett, David Alexander, Naveed Gulzar, Prabvir S Grewal, **Art F Y Poon**, Zabrina Brumme, P Richard Harrigan, James I Brooks, Paul A Sandstrom, Stryker Calvez, Stephen E Sanche, and Jamie K Scott. "Analysis of HIV pol diversity in the concentrated HIV epidemic in Saskatchewan". In: *BMC Infectious Diseases* 16.Suppl 2 (2016), p. 315.

3. **Jeffrey B Joy**, Weiyan B Dong, Celia B Chui, Chanson J Brumme, **Art Poon**, Huong Hew, and Richard Harrigan. "Stability and prevalence of the NS3 Q80k polymorphism over time within Hcv genotype 1a infected patients in Canada". In: *Hepatology* 62 (2015), 1102A–1103A.

4. **Jeffrey Joy**, **Richard Liang**, **Rosemary McCloskey**, **Thuy Nguyen**, Chanson Brumme, Guillaume Colley, Robert Hogg, Julio Montaner, P Richard Harrigan, and **Art Poon**. "Phylogenetically estimated HIV diversification rates reveal prevention of HIV-1 by antiretroviral therapy". In: *JOURNAL OF THE INTERNATIONAL AIDS SOCIETY*. Vol. 18. INT AIDS SOCIETY AVENUE DE FRANCE 23, GENEVA, 1202, SWITZERLAND. 2015.

5. Natalie Nicole Kinloch, Daniel R Macmillan, Anh Q Le, Laura A Cotton, Rosemary Mccloskey, David R Bangsberg, Susan Buchbinder, Mary Carrington, Jonathan Fuchs, P Richard Harrigan, Beryl Koblin, Martin Markowitz, Kenneth Mayer, M-J Milloy, Martin T Schechter, Theresa Wagner, Bruce D Walker, Jonathan M Carlson, **Art FY Poon**, and Zabrina L Brumme. "Population-level spread of immune-driven mutations in HIV-1 polymerase during the North American epidemic". In: *JOURNAL OF THE INTERNATIONAL AIDS SOCIETY*. Vol. 18. INT AIDS SOCIETY AVENUE DE FRANCE 23, GENEVA, 1202, SWITZERLAND. 2015.

6. Anh Le, Jeremy Taylor, Winnie Dong, **Rosemary McCloskey**, Conan Woods, Kanna Hayashi, MJ Milloy, P Richard Harrigan, **Art FY Poon**, and Zabrina L Brumme. "Within-host evolution of X4 HIV-1 in a rare transmission pair revealed by phylogenetic reconstruction of deep-sequence data". In: *JOURNAL OF THE INTERNATIONAL AIDS SOCIETY*. Vol. 18. INT AIDS SOCIETY AVENUE DE FRANCE 23, GENEVA, 1202, SWITZERLAND. 2015.

7. Andrea D Olmstead, Vincent Montoya, **Jeffrey B Joy**, **Art F Poon**, Brendan Jacka, Francois Lamoury, Tanya L Applegate, Julio S G Montaner, Yury Khudyakov, Jason Grebely, D Cook, P Richard Harrigan, and Mel Krajden. "PO81: Birth cohort and risk factors in Hepatitis C patients recorded at the Sentinal Units Network in Argentina 2007-2014". In: *15th International Symposium on Viral Hepatitis and Liver Diseases*. Berlin, Germany, 2015.

8. B Jacka, T Applegate, **A Poon**, R Harrigan, GJ Dore, A Olmstead, K DeBeck, M-J Milloy, F Lamoury, C Woods, Z Brumme, S Dobrer, VD Lima, et al. "P762 TEMPORAL CHANGES IN HEPATITIS C VIRUS GENOTYPE 3A DISTRIBUTION AMONG PEOPLE WHO INJECT DRUGS IN VANCOUVER, CANADA". In: *Journal of Hepatology* 60.1 (2014), S324–S325.

9. Brendan Jacka, **Art Poon**, Tanya L Applegate, Mel Krajden, Andrea Olmstead, Richard Harrigan, Brandon D Marshall, Kora Debeck, Mj Milloy, Francois Lamoury, et al. "Hepatitis C virus network dynamics among people who inject drugs in Vancouver, Canada". In: *Hepatology* 60 (2014), 907A–908A.

10. **Jeffrey B Joy**, **Richard H Liang**, Conan K Woods, Susan Shurgold, Guillaume Colley, Chanson J Brumme, Robert S Hogg, Brendan Jacka, Andrea Olmstead, Jason Grebely, Mel Krajden, Julio S G Montaner, P Richard Harrigan, and **Art FY Poon**. "Genetic diversification and population level phylodynamic analysis of the British Columbia Human Immunodeficiency Virus (HIV) and Hepatitis C (HCV) epidemics". In: *23rd Annual Canadian Conference on HIV/AIDS Research*. 2014.

11. Guinevere Q Lee, Christopher Lachowski, Eric Martin, Charlotte Charpentier, Christophe Rodriguez, Benoit Visseaux, Catherine Fagard, Jean-Michel Molin, Christine Katlama, Yazdanand Yazdanpanah, Diane Descamps, **Art F Y Poon**, and P Richard Harrigan. "Comparison of 454 (Roche) versus MiSeq (Illumina) deep sequencing technologies in clinical samples from the (ANRS) 139 TRIO trial". In: *ANTIVIRAL THERAPY*. Vol. 19. INT MEDICAL PRESS LTD 2-4 IDOL LANE, LONDON EC3R 5DD, ENGLAND. 2014, A79–A79.

12. Andrea D Olmstead, Mel Krajden, Vincent Montoya, Jason Grebely, **Art FY Poon**, P Richard Harrigan, and **Jeffrey B Joy**. "Molecular phylogenetics of hepatitis C virus (HCV) as a tool to understand the HCV epidemic in British Columbia (BC), Canada". In: *49th annual meeting of the European Association for the Study of the Liver*. 2014.

13. Andrea Olmstead, Vincent Montoya, **Jeffrey Joy**, Iris Luo, Naveed Z Janjua, **Art Poon**, Brendan Jacka, Francois Lamoury, Tanya L Applegate, Jason Grebely, et al. "Molecular sequencing and phylogenetics as enhanced surveillance tools for monitoring Hepatitis C virus transmission dynamics in British Columbia". In: *Hepatology* 60 (2014), 283A.

14. AR Rutherford, Ali Nadaf, Bojan Ramadanovic, Krisztina Vasarhelyi, Benita Yip, **Art Poon**, **Richard Liang**, Richard Harrigan, Ralf W Wittenberg, and JSG Montaner. "Estimating HIV Incidence: A Mathematical Modelling Approach". In: *Operational Research Applied to Health Services (ORAHS) 2013 Conference Proceedings*. Ed. by T Cayirli, M M Gunal, E D Gunes, and E L Ormeci. 2013.

15. L Cotton, D Chopera, K Penney, J Carlson, E Martin, A Le, T Kuang, B Walker, J Fuchs, S Buchbinder, T Wagner, M John, S Mallal, B Koblin, K Mayer, **A Poon**, M Brockman, and Z Brumme. "Limited evidence for alterations in Gag-mediated HIV replication capacity over the course of the North American epidemic (1979-present)". In: *Retrovirology* 9.2 (2012), P157.

16. Susanna L Lamers, Gary B Fogel, Leanne Huysentruyt, **Art Poon**, and Michael S McGrath. "The HIV nef protein within ARL is genetically and structurally distinct from those in the brain of patients with HAD". In: *Infectious Agents and Cancer*. Vol. 5. S1. Springer. 2010, A77.

Grants

Only grants on which I am Principal Investigator/Applicant, Co-applicant or Co-investigator are listed. These lists omit grants in which I was included as a Collaborator or a Consultant without direct research or salary support.

Active

2018/6 – 2020/5   ★ **Co-Principal Investigator**, *National Institutes of Health (NIH) R21*, Genetics, dynamics and fitness of the HIV-1 latent reservoir, Total funding: $300,200 USD.

I am a co-PI on this grant along with Dr. Zabrina Brumme and Dr. Mark Brockman of Simon Fraser University (SFU). I will receive about $80,000 USD of the budget through a sub-contract between SFU and Western. The objectives of this grant are to develop a new phylogenetic framework for dating HIV reservoir sequences within a host, and to use this framework to examine the dynamics of the HIV reservoir within individuals on long-term suppressive antiretroviral treatment.

2018/6 – 2023/5   ★ **Principal Applicant**, *NSERC Discovery Grant*, Modeling the evolution of virus genomes, Total funding: $160,000.

The objectives of this application are (1) to develop empirical models of sequence insertions in virus genomes; (2) to develop simulation-based methods for measuring the impact of selection on rates of evolution within overlapping reading frames in viruses; and (3) to develop models of gene birth-death in virus genomes.

2018/4 –
2023/3 ★ **Principal Applicant**, *CIHR Project Grant*, Phylodynamics of HIV within hosts, Total funding: $451,350.

The objectives of this project are to develop and validate new simulation-based methods to fit dynamic models to within-host HIV-1 sequence variation, and to use these methods to elucidate the mechanisms that sustain the latent viral reservoir and to reconstruct the migration of the virus between anatomical and cellular compartments of the host. This application is a resubmission of my Project Grant that received one year of bridge funding.

2018/4 –
2023/3 ★ **Principal Applicant**, *CIHR Project Grant*, Development, evaluation and implementation of genetic clustering methods for the real-time molecular surveillance of HIV outbreaks, Total funding: $401,625.

This research proposal will support the development of a completely new method for genetic clustering in application to HIV molecular epidemiology; to evaluate clustering methods in the context of HIV prevention with computer simulations and the retrospective analysis of population databases; and to support the implementation and evaluation of real-time monitoring systems based on these methods in Uganda and Malaysia.

2018/4 –
2021/3 **Lead investigator (1 of 6)**, *Canadian Statistical Sciences Institute (CANSSI) Collaborative Research Team Project*, Statistical methods for challenging problems in public health microbiology, Total funding: $180,000 (portion received: $30,000).

Principal Applicants: Dr. Leonid Chindelevich and Dr. Alexandre Bouchard-Côté
This team grant combines lead investigators from 5 different universities throughout Canada (Simon Fraser University, Centre Hospitalier Universitaire Sainte-Justine, University of British Columbia, Western University, and Université de Montreal). The aims of this grant are to develop computational methods to call genomic variants of pathogens by fitting evolutionary models; to develop machine learning classifiers to combine multiple inputs to predict drug resistance from whole genome sequencing data; and to detect genotype-phenotype associations in bacteria.

2017/9 –
2019/3 **Co-investigator**, *CIHR Operating Grant: Innovative Biomedical and Clinical HIV/AIDS Research*, Developing the ACT-VEC as an HIV therapeutic vaccine and cure approach, Total funding: $250,000 (portion received: $86,445).

Principal Applicant: Dr. Eric Arts (and 3 others)
The objective of this application is to develop vectors containing near-complete HIV genomes as a heterologous subtype-specific vaccine to induce the reactivation of infected CD4+ T cells from the latent reservoir, as a primary component of an HIV cure strategy. My role will be to design and implement a bioinformatic/phylogenetic algorithm for selecting patient-derived HIV genomes to incorporate into the vaccines.

2014/1 –
2018/12 **Co-investigator**, *CIHR Team Grant: HIV Cure Research*, The Canadian HIV Cure Research Enterprise (CanCURE), Total funding: $8,760,000 (portion received $45,391).

Principal Applicant: Dr. Eric Cohen (and 8 others)
The objective of this grant is to investigate the role of myeloid cells in maintaining the latent HIV reservoir. My role is to provide bioinformatic support for the basic science component led by Drs. Zabrina Brumme and Mark Brockman.

2017/10 –
2018/9 ★ **Principal Investigator**, *CIHR Project Grant: Bridge Funding*, Phylodynamics of HIV within hosts, Total funding: $100,000.

The main objectives of this grant are to develop a new branch of phylodynamics for studying the evolution of HIV within hosts, and to use these methods to test hypotheses on the maintenance of the latent HIV reservoir, and to study the compartmentalization of HIV evolution between the blood and genital tract.

2016/10 – ★ **Principal Investigator**, *Genome Canada/CIHR: Bioinformatics and Computational Biology*,
2019/3 Kamphir: a versatile framework to fit models to tree shapes, Total funding: $205,365.
The objective of this grant is the development and validation of a software module in R for fitting epidemic and diversification models to the shapes of phylogenetic trees, as an innovative means of studying the spread and evolution of viruses.

Completed

2013/6 – **Co-investigator**, *National Institutes of Health (U.S.) R01*, Seek and treat for the optimal
2018/2 prevention of HIV & AIDS in BC, Total funding: $530,331.
The objective of this grant is to support the implementation of strategic 'test and treat' initiatives for HIV prevention in British Columbia. My role was to provide bioinformatic support, including the phylogenetic and geographic analysis of HIV incidence trends based on the population HIV treatment database.

2013/01 – ★ **Co-applicant**, *Genome Canada: Genomics and Personalized Health*, Viral and Human
2017/12 Genetic Predictors of Response to HIV Therapies, Total funding: $4,100,000 (portion received: $69,908).
Project Leaders: Dr. P. Richard Harrigan, Dr. Julio Montaner
The main objectives of this grant was to develop and validate a clinical next-generation sequencing (NGS) pipeline for diagnosing HIV drug resistance; and to build a real-time monitoring system of transmitted HIV drug resistance. My role was to design and implement both the clinical NGS pipeline and the real-time system, and eventually to supervise a team of developers to enhance and maintain these systems as lead developer. Out of three Project Deliverables, I made major contributions to the first, and was entirely responsible for the second.

2012/9 – **Co-investigator**, *National Institutes of Health (U.S.) R01*, Impacts of universal access to
2017/8 HIV/AIDS care among HIV+ injection drug users, Total funding: $2,424,355 (portion received: $98,160).
Principal Investigator: Dr. Evan Wood
This application requested continued funding support for the Vancouver Injection Drug User Study (VIDUS) and ACCESS cohorts in British Columbia, for the further evaluation of increasing access to antiretroviral treatment and harm reduction resources in Vancouver. My role was to provide phylogenetic support for characterizing the effects of these initiatives on transmission rates.

2014/7 – **Co-investigator**, *Bill & Melinda Gates Foundation Grant*, Biostatistical, Computational Biology,
2017/7 and Mathematical Modeling for the Assessment of Immune Correlates of Protection in the HVTN 701 and 702 Efficacy Trials of South Africa, Total funding: $1,051,333 (portion received: $8,000).
Principal Investigator: Dr. Peter B. Gilbert The purpose of this project was to develop, validate and apply phylogenetic methods to characterize the dynamics and adaptation of HIV in individuals who had become infected while participating in the vaccine efficacy trials HVTN 701 and 702. My role was to implement some of the standard phylogenetic methods into a Python module to facilitate batch processing and testing.

2012/10 – **Co-investigator**, *CIHR Operating Grant*, Measuring mitochondrial aging, application to HIV
2015/9 infection and therapy, Total funding: $330,150 (portion received: $0).
Principal Investigator: Dr. Hélène Côté
My role in this project was to assist in the analysis of next-generation sequence data that was collected to discriminate between the *de novo* emergence and clonal expansion of mtDNA variants within patients undergoing antiretroviral treatment.

2011/10 – 2014/9	**Co-investigator**, *CIHR Operating Grant*, HIV adaptation to immune selection pressures: historic trends and future implications, Total funding: $318,132 (portion received: $5,000).

Principal Investigator: Dr. Zabrina Brumme

My role was to perform phylogenetic, molecular clock and ancestral reconstruction analyses on historic and modern HIV sequences.

2011/10 – 2014/9	**Co-investigator**, *CIHR Operating Grant*, Hepatitis C virus transmission dynamics among injection drug users, Total funding: $336,569.

Principal Investigator: Jason Grebely

My role was to provide phylogenetic and genetic analysis software tools and expertise on their usage and interpretation of results in the context of HCV epidemics.

2011/4 – 2014/3	★ **Principal Investigator**, *CIHR Operating Grant*, Reconstructing within-host evolution of HIV-1 from next-generation sequencing data, Total funding: $169,441.

The objective of this grant was to develop phylogenetic methods for the analysis of next-generation sequence data to reconstruct the evolution of HIV within hosts. Specific objectives were to develop methods to estimate the date of HIV infection from sequence variation, and to map the emergence of specific variants associated with pathogenesis to the timeline of infection.

2012/3 – 2013/2	★ **Principal Applicant**, *NIH RO1 Administrative Supplement*, Evaluating the natural history of injection drug use, Total funding: $81,687.

Principal Investigator of parent grant: Dr. Thomas Kerr

The purpose of this supplement was to develop methods to estimate the dates of HIV infection from bulk sequence chromatograms, to develop next-generation sequence (NGS) processing pipelines, and methods to estimate dates of HIV infection from NGS data sets.

Presentations

Only conference presentations in the last five years where I am the lead author and presenter or the senior author are listed below.

Conferences

2018-08-20	**Can we quantify cophylogeny?**, *Joint Congress on Evolutionary Biology*, oral, Montpellier, France.

M Avino and A Poon

2018-07-26	**Every site counts: Detecting low frequency variants in non-subtype B HIV-1 integrase associated with drug resistance in Uganda**, *22nd International AIDS Conference*, poster discussion, Amsterdam, Netherlands.

M Avino, E Ndashimye, D Lizotte, F Kyeyune, I Nankya, R Gibson, E Nabulime, C Kityo, P Mugyenyi, M Quiñones-Mateu, E Arts, A Poon

2018-03-06	**First-line HIV treatment failure in non-B subtypes and recombinants in Uganda**, *25th Conference on Retroviruses and Opportunistic Infections*, poster, Boston, USA.

AFY Poon, E Ndashimye, M Avino, RM Gibson, F Kyeyune, I Nankya, ME Quiñones-Nateu and EJ Arts

2018-03-06	**Phylogenetic and geographic separation in HIV infected people in British Columbia**, *25th Conference on Retroviruses and Opportunistic Infections*, poster, Boston, USA.

DA McVea, RH Liang, JB Joy, PR Harrigan and AFY Poon

2017-05-24	**A model-based genetic clustering method for detecting variation in HIV transmission rates**, *24th International HIV Dynamics & Evolution Meeting*, oral, Sleat, Scotland.

R McCloskey and A Poon

2017-05-24 **Reconstructing within-host HIV dynamics from sequence variation with a simulation-based phylodynamic method**, *24th International HIV Dynamics & Evolution Meeting*, poster, Sleat, Scotland.
BR Jones and AFY Poon

2017-04-08 **HIV genetic clustering for molecular epidemiology: why it doesn't work and how we can fix it**, *26th Annual Canadian Conference on HIV/AIDS Research*, oral, Montréal, Canada.
R McCloskey and A Poon

2017-02-14 **Blind dating: phylogenetic determination of latent HIV sequence ages within host**, *24th Conference on Retroviruses and Opportunistic Infections*, poster, Seattle, WA, USA.
BR Jones, J Horacsek, J Joy, Z Brumme, and A Poon

2017-02-14 **A framework for predicting phylogenetic clusters of HIV at high risk for growth**, *24th Conference on Retroviruses and Opportunistic Infections*, poster, Seattle, WA, USA.
D McVea, R Liang, J Joy, PR Harrigan, and A Poon

2016-05-13 **Next generation sequencing reveals the temporal complexity of mixed hepatitis C infections among people who inject drugs in Vancouver, BC, Canada**, *25th Annual Canadian Conference on HIV/AIDS Research*, oral, Winnipeg, Canada.
JB Joy, W Dong, DR Kirkby, J Grebley, RH Liang, V Tai, A Howe, PR Harrigan, and AF Poon

2016-05-13 **Blind Dating: A Phylogenetic Approach to Dating HIV Reservoir Sequences**, *25th Annual Canadian Conference on HIV/AIDS Research*, poster, Winnipeg, Canada.
BR Jones, J Horacsek, JB Joy, ZL Brumme, and AF Poon

2016-04-25 **Phylogenetic estimation of contact network parameters with kernel ABC**, *23rd International HIV Dynamics & Evolution Meeting*, oral, Woods Hole, Massachusetts, USA.
RM McCloskey and <u>AFY Poon</u>

2015-12-07 **Implementation of a near real-time monitoring system for localized HIV outbreaks in British Columbia, Canada**, *2015 National HIV Prevention Conference*, oral, Atlanta, Georgia.
<u>AFY Poon</u>, CK Woods, S Shurgold, G Colley, RS Hogg, DM Moore, M Krajden, R Gustafson, JSG Montaner, and PR Harrigan

2015-07-21 **Kive: a framework for version control of bioinformatics pipleines and data, and its application to HIV resistance genotyping**, *8th IAS Conference on HIV Pathogenesis, Treatment & Prevention*, poster, Vancouver, Canada.
RH Liang, E Martin, RM McCloskey, D Kirkby, J Nakagawa, J Horacsek, T Nguyen, H Lapointe, CJ Brumme, PR Harrigan, and <u>AFY Poon</u>

2015-07-22 **Near real-time tracking of localized HIV outbreaks using an automated phylogenetic monitoring system: Implementation and translation to public health**, *8th IAS Conference on HIV Pathogenesis, Treatment & Prevention*, oral, Vancouver, Canada.
<u>AFY Poon</u>, CK Woods, S Shurgold, G Colley, RS Hogg, M Krajden, DM Moore, R Gustafson, JSG Montaner, and PR Harrigan

2015-07-21 **A new framework for reconstructing epidemic dynamics from virus sequences: model validation and application to the HIV CRF07-BC epidemic in China**, *8th IAS Conference on HIV Pathogenesis, Treatment & Prevention*, poster, Vancouver, Canada.
AFY Poon

2014-05-08 **A tree shape kernel method to infer epidemiological parameters from RNA virus phylogenies**, *21st International HIV Dynamics & Evolution Meeting*, oral, Tucson, Arizona.
AFY Poon

2014-05-08 **Selection profiles from shotgun sequencing of RNA virus populations by localized phylogenetic analysis**, *21st International HIV Dynamics & Evolution Meeting*, poster, Tucson, Arizona.
Nguyen, T and AFY Poon

2014-05-08 **Global origin and transmissibility of HCV NS3 substitution Q80K that is associated with lower simeprevir susceptibility**, *21st International HIV Dynamics & Evolution Meeting*, poster, Tucson, Arizona.
Liang, R, J Joy, R McCloskey, T Nguyen, M Krajden, J Montaner, PR Harrigan, and AFY Poon

2014-05-08 **HIV diversification rate correlates with evolution and distribution of drug resistance**, *21st International HIV Dynamics & Evolution Meeting*, oral, Tucson, Arizona.
Joy, J, S Shurgold, G Colley, R Hogg, J Montaner, PR Harrigan, and AFY Poon

2014-05-08 **Detection of within-host adaptation by its effect on the pattern of mutations in the phylogeny**, *21st International HIV Dynamics & Evolution Meeting*, oral, Tucson, Arizona.
Liang, R, J Joy, PR Harrigan, and AFY Poon

2014-05-03 **Application of change detection and ancestral state reconstruction to the detection of natural selection**, *23rd Annual Canadian Conference on HIV/AIDS Research*, poster, St. John's, NL.
Liang, R, JB Joy, PR Harrigan, and AFY Poon

2014-05-03 **Genetic diversification and population level phylodynamic analysis of the British Columbia Human Immunodeficiency Virus (HIV) and Hepatitis C (HCV) epidemics**, *23rd Annual Canadian Conference on HIV/AIDS Research*, poster, St. John's, NL.
Joy, JB, RH Liang, CK Woods, S Shurgold, G Colley, CJ Brumme, RS Hogg, B Jacka, A Olmstead, J Grebely, M Krajden, JS Montaner, PR Harrigan, and AF Poon

2014-05-03 **Population-level phylogenetic analyses quantify the impact of clinical, demographic, and risk factors on variations in HIV transmission rates in British Columbia, Canada**, *23rd Annual Canadian Conference on HIV/AIDS Research*, oral, St. John's, NL.
Poon AFY, JB Joy, CK Woods, S Shurgold, G Colley, CJ Brumme, RS Hogg, JSG Montaner, and PR Harrigan

2014-03-05 **Global origin of HCV NS3 substitution Q80K that is associated with lower simeprevir susceptibility (Late Breaker)**, *21st Conference on Retroviruses and Opportunistic Infections*, poster (Late Breaker), Boston, MA.
AF Poon, RH Liang, JB Joy, T Nguyen, RM McCloskey, M Krajden, JSG Montaner, and PR Harrigan

2014-03-06 **Phylodynamic analysis of a regional HIV epidemic**, *21st Conference on Retroviruses and Opportunistic Infections*, poster, Boston, MA.
Joy, JB, R Liang, CK Woods, S Shurgold, G Colley, C Brumme, RS Hogg, JSG Montaner, PR Harrigan, and AFY Poon

2013-04-24 **Large-scale phylogenetic analysis of HIV sequences to reconstruct historical epidemic dynamics and transmitted drug resistance in British Columbia, Canada**, *3rd International HIV Treatment as Prevention Workshop*, oral, Vancouver, BC.
AFY Poon, C Woods, S Shurgold, G Colley, CJ Brumme, and PR Harrigan

2013-04-12 **Impact of experimental conditions on the utility of "primer ID" tagging for next-generation HIV sequencing**, *22nd Annual Canadian Conference on HIV/AIDS Research*, oral, Vancouver, BC.
Liang, RH, PR Harrigan, T Mo, WY Dong, G Lee, L Swenson, R McCloskey, C Woods, C Brumme, and A Poon

2013-04-12 **Reconstructing transmitted HIV genotypes by phylogenetic analysis of serial samples**, *22nd Annual Canadian Conference on HIV/AIDS Research*, oral, Vancouver, BC.
McCloskey, RM, ZL Brumme, PR Harrigan, RH Liang, and <u>AFY Poon</u>.
★ My student (McCloskey) was awarded an Academic Scholarship to attend this meeting on the strength of the submitted abstract.

2013-04-13 **Large-scale phylogenetic analysis of HIV sequences to reconstruct historical epidemic dynamics and transmitted drug resistance in British Columbia, Canada**, *22nd Annual Canadian Conference on HIV/AIDS Research*, poster, Vancouver, BC.
<u>AF Poon</u>, C Woods, CJ Brumme, and PR Harrigan

2013-03-15 **An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data**, *20th Conference on Retroviruses and Opportunistic Infections*, poster, Atlanta, GA.
McCloskey, R, R Liang, PR Harrigan, Z Brumme, and <u>AFY Poon</u>

2013-03-15 **Impact of experimental conditions on the utility of primer ID tagging for next-generation HIV sequencing**, *20th Conference on Retroviruses and Opportunistic Infections*, poster, Atlanta, GA.
Liang, R, T Mo, W Dong, G Lee, L Swenson, R McCloskey, C Woods, C Brumme, PR Harrigan, and <u>AFY Poon</u>

2013-03-15 **Robust phylogenetic method to reconstruct dates of infection in HIV-1 seroconverters from different risk groups**, *20th Conference on Retroviruses and Opportunistic Infections*, poster, Atlanta, GA.
McGovern, RA, Z Brumme, C Johnson, R Hogg, E Wood, T Kerr, M Milloy, PR Harrigan, <u>AFY Poon</u>, and the VANGUARD and VIDUS/ACCESS Cohort Studies

Invited seminars

2018-06-26 **Western North American Region of the International Biometrics Society**, *Invited Speaker, Institute of Mathematical Sciences (IMS) Invited Session*, University of Alberta, Edmonton, Canada.

2018-02-28 **Applied Math Colloquium**, *Invited speaker*, Western University, London, Canada.

2017-11-17 **Biology Seminar Series**, *Invited speaker*, Western University, London, Canada.

2017-02-17 **Mathematical Approaches to Evolutionary Trees and Networks**, *Invited speaker*, Banff International Research Station for Mathematical Innovation and Discovery, Banff, Canada.

2016-11-24 **Workshop on viruses and next-generation sequencing**, *Instructor, keynote speaker*, Research Center for Cellular Dynamics, Autonomous University of the State of Morelos, Cuernevaca, México.

2016-11-02 **Topical Research in Computer Science (TRICS)**, *Seminar speaker*, Western University, London, Canada.

2016-10-13 **Dr. Robert Zhong Seminar in Pathology and Laboratory Medicine**, *Seminar speaker*, Western University, London, Canada.
"Failure to Launch: Challenges in bringing next-generation sequencing to the clinical HIV laboratory."

2016-09-19 **Phylogenetics Community/Expert Consultation Meeting**, *Invited speaker*, HIV Center for Clinical and Behavioural Studies, the Treatment Action Group, and the New York City Department of Health & Mental Hygiene, New York, USA.

2016-03-31 **1st Annual Third Coast Center for AIDS Research Symposium**, *Invited speaker*, Lurie Cancer Center, Chicago, USA.
"Near real-time monitoring of HIV transmission hotspots"

2016-02-02	**Public Health Grand Rounds**, *Invited speaker*, BC Centre for Disease Control, Vancouver, Canada.
	"New bioinformatics technologies for clinical infectious disease laboratories"
2016-01-20	**Alliance Coordinating Office Webinar**, *Invited speaker*, Online, `http://www.icid.com/event/aco-webinar-bioinformatics-phylogenetics-for-hiv-101`.
	"Bioinformatics: Phylogenetics for HIV 101"
2015-11-04	**Forefront Lecture Series**, *Invited speaker*, BC Centre for Excellence in HIV/AIDS, Vancouver, Canada.
	"Near real-time monitoring of HIV transmisson hotspots in BC: Harnessing Big Data for public health"
2015-06-21	**Bioinformatics Bootcamp, 8th International AIDS Society Conference on HIV Pathogenesis, Treatment & Prevention**, *Instructor*, Vancouver Convention Centre, Vancouver, Canada.
	"Datamonkey: rapid detection of positive selection"
2015-07-18	**United Nations 90-90-90 Target Workshop: Lessons from the Field**, *Invited speaker*, Sheraton Wall Centre, Vancouver, Canada.
	"Lessons from implementing a phylogenetic monitoring system of HIV outbreaks in British Columbia, Canada"
2014-11-18	**RGE Murray Seminar Series**, *Guest speaker*, Western University, London, Canada.
	"Development, testing, and implementation of computational and statistical methods for HIV-1 genetic sequence analysis"
2014-09-18	**TasP/PrEP Evidence Summit, International Association of Providers of AIDS Care**, *Invited speaker*, Royal Garden Hotel, London, England.
	"Implementation of a Near Real-time Phylogenetic Monitoring Program for HIV Transmission Outbreaks"
2013-11-25	**NCAIDS/China Centre for Disease Control and Prevention and BC-CfE Treatment as Prevention Education Event**, *Invited speaker*, National Center for AIDS/STD Control and Prevention and China CDC, Beijing, China.
	"Bridging HIV Treatment to Prevention with Applied Phylogenetics"
2013-07-03	**Vancouver Bioinformatics Users Group (VanBUG)**, *Guest speaker*, BC Cancer Research Centre, Vancouver, Canada.
	"Reconstructing the evolution of HIV within a patient"
2013-03-20	**UBC Centre for Blood Research, Summer Seminar Series**, *Invited speaker*, University of British Columbia, Vancouver, Canada.
2013-01-18	**UBC James Hogg Research Centre, Friday Seminar Series**, *Guest speaker*, St. Paul's Hospital, Vancouver, Canada.

Student/Postdoctoral supervision

Postdoctoral

2017/9 – present	**Abayomi Olabode**, *Postdoctoral associate*, Department of Pathology & Laboratory Medicine, Western University.
	Primary supervisor
2016/10 – present	**Mariano Avino**, *Postdoctoral associate*, Department of Pathology & Laboratory Medicine, Western University.
	Primary supervisor
2013/1 – 2016/1	**Jeffrey B. Joy**, *Postdoctoral fellow*, BC Centre for Excellence in HIV/AIDS.
	Primary supervisor

2011/7 – 2015/8	**Richard H. Liang**, *Postdoctoral fellow*, BC Centre for Excellence in HIV/AIDS. Primary supervisor

Graduate (PhD)

2019/1 – 2023/12	**Everlyn Kamau**, *PhD student (accepted)*, Department of Microbiology & Immunology, Western University. Primary supervisor
2018/8 – 2023/8	**Laura Muñoz Baena**, *PhD student*, Department of Microbiology & Immunology, Western University. Primary supervisor
2016/11 – present	**David Dick**, *PhD student*, Department of Applied Mathematics, Western University. Co-supervisor

Graduate (MSc or MSc-equivalent)

2018/9 – 2020/8	**John Palmer**, *MSc student*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2018/8 – 2020/8	**Connor Chato**, *MSc student*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2016/11 – present	**Erika Chadwick**, *MCISc Pathologists' Assistant Graduate Program*, Department of Pathology & Laboratory Medicine, Western University. Research supervisor
2016/5 – 2016/8	**David McVea**, *Masters of Public Health, research supervisor*, Department of Medicine, University of British Columbia. Research supervisor
2013/9 – 2016/6	**Thuy Nguyen**, *MSc student*, Department of Bioinformatics, University of British Columbia. Primary supervisor
2014/9 – 2016/7	**Rosemary McCloskey**, *MSc student*, Department of Bioinformatics, University of British Columbia. Primary supervisor

Undergraduate

2018/9 – 2019/4	**G. Tammy Ng**, *Undergraduate thesis project, Computational Biochemistry*, Department of Biochemistry, Western University. Primary supervisor
2018/9 – 2019/4	**Lisa-Monique Edward**, *Undergraduate thesis project, Computational Biochemistry*, Department of Biochemistry, Western University. Primary supervisor
2017/10 – 2018/4	**Jasper Ho**, *Scholar's Elective project*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2018/1 – 2018/4	**Yiying (Helen) He**, *Undergraduate research assistant*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor, U Waterloo co-op

2017/9 – 2018/4	**John Palmer**, *Undergraduate thesis project*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2017/9 – 2018/4	**Reid Vender**, *Undergraduate thesis project, Medical Health Informatics*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2017/5 – 2017/8	**Mathias Renaud**, *Waterloo University, Undergraduate Co-op Program*, Western University, Department of Pathology and Laboratory Medicine. Primary supervisor
2017/5 – 2018/4	**Tammy Ng**, *Undergraduate internship*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2016/10 – 2017/4	**Cornelius Nesen**, *Undergraduate thesis project, Medical Health Informatics*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2016/10 – 2017/4	**Enid Chan**, *Undergraduate thesis project, Medical Health Informatics*, Department of Pathology & Laboratory Medicine, Western University. Primary supervisor
2016/1 – 2016/8	**Bradley Jones**, *Undergraduate research co-op*, Faculty of Health Sciences, Simon Fraser University. Primary supervisor
2015/1 – 2015/8	**Joshua Horacsek**, *Undergraduate research co-op*, Faculty of Health Sciences, Simon Fraser University. Primary supervisor

Teaching

Only teaching contributions at Western University are listed.

2018/9 – 2018/12	**Bioinformatics of infectious disease**, *MICB4750F/G*, Department of Microbiology & Immunology, Western University. ○ Development of materials for new course, 2017-12-09 to present (about 40 hours to date). ○ Teaching innovation: developing d3/JavaScript animations as learning tools. ○ Teaching innovation: development and release of online course materials using Jekyll/Markdown framework under a Creative Commons license.
2018/5 – 2018/7	**Bioinformatic data processing with Python**, *PATH9577Q*, Department of Pathology & Laboratory Medicine, Western University. ○ Renewing curriculum based on student evaluations from previous year.
2017/5 – 2017/6	**Bioinformatic data processing with Python**, *PATH9577Q*, Department of Pathology & Laboratory Medicine, Western University. ○ Instructor and coordinator (18 contact hours). ○ Developed materials for new course as Markdown and JavaScript-based online content 2016-09-20 to 2017-06-26 (about 30 hours). ○ Course materials released into public domain at `https://github.com/PoonLab/courses/tree/master/PATH9577Q`.
2017/1 – 2017/3	**Biological and Social Determinants of Infectious Disease**, *MICB3500B*, Department of Microbiology & Immunology, Western University. ○ Guest lectures (2 contact hours)

| 2017/3 – 2017/4 | **Biosystematics and Phylogenetics**, *BIOL4289B*, Department of Biology, Western University. |

○ Guest lectures (2 contact hours)

Academic service

Student committees

| 2018/9 – present | **Dong Kyung Lee**, *Supervisor: Dr. Marc-Andre Lachance*, MSc student, Biology, Western University. |

Advisory committee member.

| 2018/7 – present | **Renee Pang**, *Supervisor: Dr. Michael Rieder*, MSc student, Clinical Investigator Program, Western University. |

Advisory committee member.

| 2017/11 – present | **Daniel Giguere**, *Supervisor: Dr. Greg Gloor*, PhD student, Department of Biochemistry, Western University. |

Advisory committee member.

| 2016 – 2016 | **Tingting (Crystal) Zhao**, *Supervisor: Dr. Alexandre Bouchard-Côté*, PhD student, Department of Statistics, University of British Columbia. |

Comprehensive examination committee member.

| 2012 – 2015 | **Chanson Brumme**, *Supervisor: Dr. Richard Harrigan*, PhD student, Department of Experimental Medicine, University of British Coluimbia. |

Advisory committee member.

| 2013 – 2015 | **Anh Le**, *Supervisor: Dr. Zabrina Brumme*, MSc student, Faculty of Health Sciences, Simon Fraser University. |

Advisory committee member.

| 2011 – 2012 | **Laura Cotton**, *Supervisor: Dr. Zabrina Brumme*, MPH student, Faculty of Health Sciences, Simon Fraser University. |

Advisory committee member.

Internal service

| 2018/7 | **Western Postdoctoral Research Fellowship Program, reviewer**, *Research Development & Services*, Western University. |

| 2018/06/18 | **Chair, Comprehensive Examination Committee (J. Gomes)**, *Department of Pathology*, Western University. |

| 2018/4 – 2019/3 | **Departmental Workload Committee, elected member**, *Department of Pathology & Laboratory Medicine*, Western University. |

| 2018/4 – present | **Collaborative Specialization in Artificial Intelligence, Working Group**, *Vector Institute for Artificial Intelligence, Province of Ontario, and Western University*, (1 hour to date). |

| 2018/3 – 2018/4 | **PaLM Knowledge Creation Task Group**, *Department of Pathology & Laboratory Medicine*, Western University, (3 hours). |

| 2018/2 – 2018/3 | **Awards Committee (Ontario Graduate Scholarships)**, *Department of Pathology & Laboratory Medicine*, Western University, (20 hours). |

| 2018/1 – present | **Bioinformatics Selection Committee**, *Lawson Health Research Institute / Ontario Institute for Cancer Research*, Western University, (3 hours to date). |

| 2017/12 – 2018/1 | **CIHR Internal Review Commitee (Dr. Shuo Li), committee member**, *Lawson Health Research Institute*, Western University, (10 hours). |

2017/10 – 2017/12	**Chair, Workload Committee**, *Department of Pathology & Laboratory Medicine*, Western University, (20 hours).
2017/10 – 2019/9	**Annual Performance Evaluation Committee, elected member**, *Department of Pathology & Laboratory Medicine*, Western University, (10 hours).
2016/12 – 2019/12	**Research Based Graduate Education Committee, elected member**, *Department of Pathology & Laboratory Medicine*, Western University, (20 hours).

External service

2017/12 – 2018/2	**SciNapse - Undergraduate Science Case Competition, judge**, (12 hours).
2017/8 – present	**Editorial Board Member**, *AIDS Research and Therapy*.
2017	**Doctoral Award Committee, member**, *Canadian Institutes for Health Research*.
2016	**Doctoral Award Committee, member**, *Canadian Institutes for Health Research*.
2009/3 – present	**Academic Editor**, *PLOS ONE*.

Peer review - grants

2018/7	**Stichting Joel Lange Institute for Global Health and Development**, *External reviewer*, Amsterdam.
2018/7	**University of Washington/Fred Hutch Center for AIDS Research (CFAR) New Investigator Awards**, *Expert reviewer*, United States.
2018/2 – 2021/1	**CIHR College of Reviewers**, *Member*, Canada.
2018/3	**National Research Foundation, Specialist Committee**, *External reviewer*, South Africa.
2018/1	**NSERC Discovery Grant**, *External reviewer*, Canada.
2017/8	**University of Washington/Fred Hutch Center for AIDS Research (CFAR) New Investigator Awards**, *Expert reviewer*, United States.
2017/3	**Wellcome Trust, Collaborative Award in Science**, *External reviewer*, United Kingdom.
2016/7	**National Institutes of Health**, *Special Emphasis Panel/Scientific Review Group, member*, United States.
2015/3	**Wellcome Trust and Royal Society, Sir Henry Dale Fellowship**, *External reviewer*, United Kingdom.
2014/3	**KU Leuven (University of Leuven) Research Council**, *Expert review*, Belgium.
2012/10	**Netherlands Organization for Scientific Research (NWO)-WOTRO Science for Global Development**, *External reviewer*, Netherlands.
2009/8	**National Science Foundation**, *External reviewer*, United States.
2008/9	**National Science Foundation**, *External reviewer*, United States.

Peer review - conferences

2017/1	**26th Annual Canadian Conference on HIV/AIDS Research**, *Basic Science abstract review team*.
2015/1	**24th Annual Canadian Conference on HIV/AIDS Research**, *Basic Science abstract review team*.

2014/2 – 2014/5	**21st International HIV Dynamics & Evolution Meeting**, *Bioinformatics session co-chair*.
2014/1	**23rd Annual Canadian Conference on HIV/AIDS Research**, *Basic Science abstract review team*.
2013/4	**22nd Annual Canadian Conference on HIV/AIDS Research**, *Basic Sciences: HIV Transmission and Evolution, co-chair*.
2013/1	**22nd Annual Canadian Conference on HIV/AIDS Research**, *Basic Science abstract review team*.

Peer review - articles (2007-present)

My peer review contributions for research journals for the last 3 years are openly tracked at `https://publons.com/author/1494869/art-poon`.

- AIDS Research and Human Retroviruses (3 articles)
- AIDS Research and Therapy (2)
- Annals of Applied Biology
- **Bioinformatics (9 articles)**
- BioSystems
- BMC Bioinformatics
- BMC Evolutionary Biology (2)
- BMC Genomics
- **Clinical Infectious Diseases**
- Emerging Infectious Diseases
- Epidemics
- Evolution (4 articles)
- GENE
- Genome Research
- **Journal of Infectious Diseases (3)**
- Journal of Molecular Biology
- Journal of the International AIDS Society
- Journal of the Royal Society Interface
- Journal of Virology (4 articles)
- **Lancet Infectious Diseases**
- Microbiome
- **Molecular Biology and Evolution (13 articles)**
- Molecular Diagnosis & Therapy
- Philosophical Transactions B
- PLOS Biology (2)
- **PLoS Computational Biology (11 articles)**
- PLOS Genetics (2)
- PLoS ONE (10 articles)
- **PLOS Pathogens (8 articles)**
- Proceedings of the Royal Society, Series B (2)
- Retrovirology (3)
- Sociological Methodology
- Virology
- Virology Journal (2)
- **Virus Evolution (6 articles)**