Connor O. McCoy

1220 East Columbia St. Unit 106
Seattle, Washington 98122

phone: (206) 605-8782
email: connormccoy@gmail.com

Work Experience

Fred Hutchinson Cancer Research Center, Seattle, WA (March 2011 – present)

Systems Analyst/Programmer III

Planned and implemented analyses of high-throughput sequencing data for a variety of projects, from QA and QC of raw sequence data, through exploratory data analysis and development of reproducible bioinformatics pipelines, to statistical analysis and creation of summaries/figures. Projects include:

- Investigating associations between bacterial community diversity and clinical outcomes in 16S rRNA surveys of the human microbiome.
- Detecting and characterizing cases of HIV superinfection in a long-term prospective cohort.
- Assessing clinical samples for low-frequency drug-resistance mutations in HIV polymerase and reverse transcriptase.
- Identifying clusters of somatically-hypermutated, rearranged B-cell receptors from longitudinal samples of HIV-positive individuals.

Contributed to the development and description of new algorithms and tools for analyzing biological data, including:

- A Bayesian method for detecting selection pressures from deep sequencing data.
- An online algorithm for Bayesian phylogenetic inference.
- A variant of k-medoids clustering for discrete mass distributions on a phylogenetic tree.
- A suite of utilities for taxonomic classification and statistical comparison of samples from microbiome studies.
- A generic command-line tool for biological sequence manipulation and format conversion.

Seattle Biomedical Research Institute, Seattle, WA (October 2008 – March 2011)

Bioinformatics Programmer – Supervisor January 2010 – March 2011
Bioinformatics Programmer October 2008 – January 2010

- Led collection, management, and software development for international malaria studies in Tanzania and Mali.
- Planned data collection, developed trial database, and analyzed results of first human malaria challenge trial in Seattle.
- Provided biostatistical support to study investigators.

- Supervised a group of four database assistants.
- Created various tools to integrate, visualize, and analyze clinical data.

Alaska Children's Services, Anchorage, AK (July 2007 - August 2008)

Data Analyst

- Aggregated and analyzed patient outcome data at mental health nonprofit.
- Created automated data cleaning procedures to increase data validity, integrity, and usability.
- Developed web application for scoring behavioral assessments.

Education

- **University of Colorado at Boulder** 2003 – 2007
  B.A., Physics
  Minor: Computer Science

Publications

[1] D.A. Lehman, J. Baeten, C.O. McCoy, et al. FTC/TDF PrEP increases the risk of low-frequency resistance compared to TDF alone. *submitted*, 2014.

[2] D.A. Lehman, D.C. Wamalwa, C.O. McCoy, F.A. Matsen, A. Langat, B.H. Chohan, S. Benki-Nugent, R. Custers-Allen, F.D. Bushman, G.C. John-Stewart, et al. Low-frequency nevirapine resistance at multiple sites may predict treatment failure in infants on nevirapine-based treatment. *JAIDS Journal of Acquired Immune Deficiency Syndromes*, 60(3):225–233, 2012.

[3] M.T. Levine, C.O. McCoy, D. Vermaak, Y.C.G. Lee, M.A. Hiatt, F.A. Matsen, and H.S. Malik. Phylogenomic analysis reveals dynamic evolutionary history of the Drosophila heterochromatin protein 1 (HP1) gene family. *PLoS Genetics*, 8(6):e1002729, 2012.

[4] E.S. Lim, O.I. Fregoso, C.O. McCoy, F.A. Matsen, H.S. Malik, and M. Emerman. The ability of primate lentiviruses to degrade the monocyte restriction factor SAMHD1 preceded the birth of the viral accessory protein Vpx. *Cell Host & Microbe*, 2012.

[5] F.A. Matsen, A. Gallagher, and C.O. McCoy. Minimizing the average distance to a closest leaf in a phylogenetic tree. *Systematic Biology*, in press, 2013.

[6] C.O. McCoy, T. Bedford, V.N. Minin, P. Bradley, H. Robins, and F.A. Matsen. Substitution and site-specific selection driving b cell affinity maturation is consistent across individuals. *submitted; arXiv preprint arXiv:1403.3066*, 2014.

[7] C.O. McCoy, A. Gallagher, N.G. Hoffman, and F.A. Matsen. nestly– a framework for running software with nested parameter choices and aggregating results. *Bioinformatics*, 29(3):387–388, 2013.

[8] C.O. McCoy and F.A. Matsen. Abundance-weighted phylogenetic diversity measures distinguish microbial community states and are robust to sampling depth. *PeerJ*, 1:e157, 9 2013.

[9] K. Ronen, C.O. McCoy, F.A. Matsen, D.F. Boyd, S. Emery, K. Odem-Davis, W. Jaoko, K. Mandaliya, R.S. McClelland, B.A. Richardson, et al. HIV-1 superinfection occurs less frequently than initial infection in a cohort of high-risk Kenyan women. *PLoS pathogens*, 9(8):e1003593, 2013.

[10] S.J. Salipante, D.J. Sengupta, C. Rosenthal, G. Costa, J. Spangler, E.H. Sims, M.A. Jacobs, S.I. Miller, D.R. Hoogestraat, B.T. Cookson, C.O. McCoy, F.A. Matsen, J. Shendure, C.C. Lee, T.T. Harkins, and N.G. Hoffman. Rapid 16S rRNA next-generation sequencing of polymicrobial clinical samples for diagnosis of complex bacterial infections. *PLoS ONE*, 8(5):e65226, 05 2013.

[11] S. Srinivasan, N.G. Hoffman, M.T. Morgan, F.A. Matsen, T.L. Fiedler, R.W. Hall, F.J. Ross, C.O. McCoy, R. Bumgarner, J.M. Marrazzo, et al. Bacterial communities in women with bacterial vaginosis: high resolution phylogenetic analyses reveal relationships of microbiota to clinical criteria. *PLoS ONE*, 7(6):e37818, 2012.