Mathieu Fourment

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CURRENT POSITION

Senior Postdoctoral Fellow (Level B)   10/2015 – Present
University of Technology Sydney, Australia.
Computational and statistical methods to investigate genome evolution. Developed a C++ sequential Monte Carlo program for online analysis of bacterial outbreaks.
Principal investigator: Aaron Darling.

PROFESSIONAL EXPERIENCE

Postdoctoral Fellow   05/2013 – 09/2015
The University of Sydney, Australia.
Investigation of viral and bacterial evolution and development of phylogenetic methods.
Principal investigator: Edward Holmes.

Postdoctoral Fellow   04/2011 – 04/2013
Duke-NUS Graduate Medical School Singapore.
Analysis of influenza viruses (human, H5N1, avian influenza) and development of statistical models of evolution. Development of maximum likelihood and genetic algorithm-based methods to date sequences.
Principal investigator: Gavin Smith.

Postdoctoral Fellow   04/2010 – 04/2011
University of California, San Diego, USA.
Investigation of episodic selection using a mixture of Markov processes in the random effects likelihood framework.
Principal investigators: Sergei L. Kosakovsky-Pond and Douglas D. Richman.

Visiting Fellow   01/2008 – 03/2009
Pasteur Institute of Cambodia, Phnom Penh, Cambodia.
Molecular analysis of influenza A viruses and Plasmodium in Cambodia.

Visiting Fellow   02/2005 – 08/2006
Australian National University, Canberra, Australia.
Analysis influenza viruses and development of bioinformatics methods and software.

Visiting Fellow   06/2004 – 08/2004
Australian National University, Canberra, Australia.
Analysis influenza viruses and development of bioinformatics methods and software.

EDUCATION

Doctor of Philosophy in Biological Sciences   2006 – 2010
Macquarie University, Sydney, Australia.
Thesis title: Virus Sequence Analysis and Compilation.
Advisors: Michael R. Gillings and Mark J. Gibbs.

Master by Research in Bioinformatics with Merit   2004
Glasgow University, United Kingdom.

Master degree in Computer Science with Merit   2003
Université Francçis Rabelais, Tours, France.

Bachelor degree in Cellular Biology and Physiology   2002
Université de Nice Sophia-Antipolis, Nice, France.

CONFERENCES Oral presentation. 12th Australian Influenza Symposium. Peter Doherty Institute, Mel-
WORKSHOPS bourne, Australia, 10/2017.

Invited public talk. University of Adelaide, Australia, 11/2016.

Oral presentation. Phylomania - Theoretical Phylogenetics meeting. University of Tas-
mania, Australia, 11/2016.

Invited talk. Centre for Computational Evolution, University of Auckland, New Zealand,
07/2016.

Oral presentation. Sydney Bioinformatics Research Symposium, Australia, 07/2016.

Oral presentation. Annual meeting of the Society of Molecular Biology and Evolution,
Gold Coast, Australia, 07/2016.

11th Australian Influenza Symposium. Deakin University, Geelong, Australia, 10/2015.

10th Australian Influenza Symposium. Peter Doherty Institute, Melbourne, Australia,
11/2014.

Australasian Virology Society annual meeting, Queenstown, New Zealand, 12/2013.

Phylomania - Theoretical Phylogenetics meeting. University of Tasmania, Australia,
11/2013.

9th Australian Influenza Symposium. University of Sydney, Australia, 10/2013.

Centers for Excellence for Influenza Research and Surveillance (CEIRS) Network Annual
Meeting. New York, USA, 07-08/2012.

Mathematical Modelling Workshop: Within and Between-Host Dynamics of Drug-Resistant
Pathogens. Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand, 06/2012.

Next-generation molecular and evolutionary epidemiology of infectious disease: challenges
and opportunities. The Royal Society, Chicheley Hall, United Kingdom, 05/2012.

Next-generation molecular and evolutionary epidemiology of infectious disease. The Royal
Society, London, United Kingdom, 05/2012.

Molecular epidemiology and evolutionary patterns of infectious diseases in South East
Asia, Siem Reap, Cambodia, 2010.

Summer Institute in Statistical Genetics, Seattle, USA, 2009.

Bayesian Phylogeny Workshop, Budapest, Hungary, 2008.

TEACHING   Advanced Bioinformatics workshop for early career researchers: Phylogenetics and genome analysis, 7-11th. Adelaide, Australia, 11/2016.

Bioinformatics workshop organised by the Joint Academic Microbiology Seminars: Introduction to phylogenetics. Sydney, Australia, 03/2016.

SKILLS   **Programming**: Java, C, C++, Perl, Python, Objective-C/Cocoa, R, SSE vectorization, and OpenMP.

Database: MySQL and SQLite.

Mathematics: probabilities, bootstrapping, hypothesis testing, optimization, Monte Carlo methods, genetic algorithms

Other: Git, LaTeX, and Unix/Linux operating systems.

SERVICE   Reviewer for *BMC Evolutionary Biology*, *BMC Bioinformatics*, *Bioinformatics*, *PLoS ONE*, *PLoS Computational Biology*, *Virus Evolution*, and *Infection, Genetics and Evolution*.

PUBLICATIONS

28. **Fourment M.**, Claywell B.C., Dinh V., McCoy C., Matsen F.A., Darling A.E. Effective online Bayesian phylogenetics via sequential Monte Carlo with guided proposals. Syst Biol, 2017 In Press (doi: 10.1101/145219)

27. Claywell BC, Dinh V, **Fourment M**, McCoy CO, Matsen FA . A surrogate function for one-dimensional phylogenetic likelihoods. *Mol Biol Evol*, 2017 (doi: 10.1093/molbev/msx253).

26. **Fourment M.**, Darling A.E., Holmes E.C. The Impact of Migratory Flyways on the Spread of Avian Influenza Virus in North America. *BMC Evol Biol*, 2017, 17:118.

25. Duchene S., Holt K.E., Weill F.X., Hello S.L., Hawkey J., Edwards D.J., **Fourment M.**, Holmes E.C. Genome-scale rates of evolutionary change in bacteria. Microbial Genomics, 2016, 2, 11.

24. **Fourment M.** & Holmes E.C. Seqotron: a user-friendly sequence editor for Mac OS X. *BMC Research Notes*, 2016, 9:106.

23. Bos K.I., Herbig A., Sahl J., Waglechner N., **Fourment M.**, Forrest S.A., Klunk J., Schuenemann V.J., Poinar D., Kuch M., Golding G.B., Dutour O., Keim P., Wagner D.M., Holmes E.C., Krause J., Poinar H.N. Eighteenth century Yersinia pestis genomes reveal the long-term persistence of an historical plague focus. *eLife*, 2016, e12994.

22. Sam I.C., Su Y.F., Chan Y.F., Nor'E S.S., Hassan A., Jafar F.L., Joseph U., Halpin R.A., Ghedin E., Hooi P.S., **Fourment M.**, Hassan H., AbuBakar S., Wentworh D.E., and Smith G.J. Evolution of influenza B virus in Kuala Lumpur, Malaysia between 1995 and 2008. *J Virol*, 2015, 89(18):9689-92.

21. **Fourment M.** & Holmes E.C. Avian influenza virus exhibits distinct evolutionary dynamics in wild birds and poultry. *BMC Evol Biol*, 2015, 15:120.

20. Vijaykrishna D., Holmes E.C., Joseph U., **Fourment M.**, Su Y.C.F., Halpin R., Lee R.T.C., Deng Y.M., Gunalan V., Lin X., Stockwell T.B., Fedorova N.B., Zhou B, Spirason N., Kühnert D., Bŏsková V., Stadler T., Costa A.M., Dwyer D.E., Huang Q.S., Jennings L.C., Rawlinson W., Sullivan S.G., Hurt A.C., Maurer-Stroh S., Wentworth D.E., Smith G.J.D., and Barr I. The contrasting phylodynamics of human influenza B viruses. *eLife*, 2015, 4:e05055.

19. **Fourment M.**, Holmes E.C. Novel non-parametric models to estimate evolutionary rates and divergence times from heterochronous sequence data. *BMC Evol Biol.*, 2014, 14:163.

18. Wagner D.M., Klunk J., Harbeck M., Devault A., Waglechner N., Sahl J.W., Enk J., Birdsell D.N., Kuch M., Lumibao C., Poinar D., Pearson T., **Fourment M.**, Golding B., Riehm J.M., Earn D.J., Dewitte S., Rouillard J.M., Grupe G., Wiechmann I., Bliska J.B., Keim P.S., Scholz H.C., Holmes E.C., Poinar H. Yersinia pestis and the Plague of Justinian 541-543 AD: a genomic analysis. *Lancet Infect Dis*, 2014, 14(4):319-26.

17. Bahl J., Krauss S., Kühnert D., **Fourment M.**, Raven G., Pryor P., Niles L.J., Danner A., Walker D., Mendenhall I., Su Y.C., Dugan V.G., Halpin R.A., Stockwell T.B., Webby R.J., Wentworth D.E., Drummond A.J., Smith G.J.D., and Webster R.G. Influenza A Virus Migration and Persistence in North American Wild Birds. *PLoS Pathog*, 2013, 9(8):e1003570.

16. Shanmuganatham K., Feeroz M.M., Jones-Engel L., Smith G.J., **Fourment M.**, Walker D., McClenaghan L., Alam S.M., Hasan M.K., Seiler P., Franks J., Danner A., Barman S., McKenzie P., Krauss S., Webby R.J., Webster R.G. Antigenic and molecular characterization of avian influenza A(H9N2) viruses, Bangladesh. *Emerg Infect Dis.*, 2013, 19(9).

15. Vijaykrishna D., Deng Y.M., Su Y.C. **Fourment M.**, Iannello P., Arzey G.G, Hansbro P.M., Arzey K.E., Kirkland P.D., Warner S., O'Riley K., Barr I.G. Smith G.J., and Hurt A.C. The recent establishment of North American H10 lineage influenza viruses in Australian wild waterfowl and the evolution of Australian avian influenza viruses. *J Virol.*, 2013, 87(18):10182-9.

14. Westgeest K.B., de Graaf M., **Fourment M.**, Bestebroer T.M., van Beek R., Spronken M.I., de Jong J.C., Rimmelzwaan G.F., Russell C.A., Osterhaus A.D., Smith G.J., Smith D.J., and Fouchier R.A. Genetic Evolution of Neuraminidase of Influenza A (H3N2) Viruses from 1968 to 2009 and its Correspondence to Hemagglutinin. *J Gen Virol.*, 2012.

13. Wertheim J.O., **Fourment M.**, and Kosakovsky Pond S.L. Inconsistencies in estimating the age of HIV-1 subtypes due to heterotachy. *Mol Biol Evol.*, 2012, 29(2):451-6.

12. Kosakovsky Pond S.L., Murrell B., **Fourment M.**, Frost S.D., Delport W., and Scheffler K. A random effects branch-site model for detecting episodic diversifying selection. *Mol Biol Evol.*, 2011, 28(11):3033-43.

11. Duval L., **Fourment M.**, Nerrienet E., Rousset D., Sadeuh Mba S., Goodman S., Andriaholinirina N., Randrianarivelojosia M., Paul R., Robert V., Ayala F., and Ariey F. African apes as reservoirs of *Plasmodium falciparum* and the origin and diversification of the *Laverania* subgenus. *Proc Natl Acad Sci USA*, 2010, 107(23):10561-6.

10. **Fourment M.**, Wood J.T., Gibbs A.J., and Gibbs M.J. Evolutionary dynamics of the N1 neuraminidases of the main lineages of influenza A viruses. *Mol Phylogenet Evol.*, 2010, 56, 526-535.

9. **Fourment M.**, Mardy S., Channa M., and Buchy P. Evidence for persistence of and antiviral resistance and reassortment events in seasonal influenza virus strains circulating in Cambodia. *J Clin Microbiol.*, 2010, 48, 295-7.

8. Buchy P., **Fourment M.**, Mardy S., Sorn S., Holl D. Ly S., Vong, S., Enouf, V., Peiris J.S.M. and van der Werf S. Molecular epidemiology of clade 1 influenza A viruses (H5N1), Southern Indochina Peninsula, 2004-2007. *Emerging Infectious Diseases*, 2009, 15, 1641-1644.

7. Duval L., Nerrienet E., Rousset D., Sadeuh S., Houze S., **Fourment M.**, Robert V., and Ariey, F. Chimpanzee Malaria Parasites Related to *Plasmodium ovale* in Africa. *PLoS ONE*, 2009, 4(5):e5520.

6. **Fourment M.**, Gibbs A.J., and Gibbs M. J. SWeBLAST: A Sliding Window Web based BLAST tool for recombinant analysis. *J Virol Methods*, 2008, 152, 98101.

5. **Fourment M.** and Gibbs M.J. The VirusBanker database uses a Java program to allow flexible searching through Bunyaviridae sequences. *BMC Bioinformatics*, 2008, 9:83.

4. **Fourment M.** and Gillings M.R. A comparison of common programming languages used in bioinformatics. *BMC Bioinformatics*, 2008, 9:82.

3. Zheng L., Wayper P. J., Gibbs A. J., **Fourment M.**, Rodoni B. C., and Gibbs M.J. Accumulating variation at conserved sites in potyvirus genomes is driven by species discovery and affects degenerate primer design. *PLoS ONE*, 2008, 3(2):e1586.

2. Gibbs M.J., Wayper P., **Fourment M.**, Wood J.T., Ohshima, K., Armstrong J.S., and Gibbs A.J. The variable codons of H3 influenza A virus haemagglutinin genes. *Arch Virol.*, 2007, 152(1):11-24.

1. **Fourment M.** and Gibbs M.J. PATRISTIC: a program for calculating patristic distances and graphically comparing the components of genetic change. *BMC Evol Biol*, 2006, 6:1.

Last updated: October 31, 2017