Mathieu Fourment

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Current position

Postdoctoral Fellow

The University of Sydney, Australia.

Investigation of viral and bacterial evolution and development of phylogenetic methods.

Principal investigator: Edward Holmes.

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.

Professional Experience

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.
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.

Conferences/workshops

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

Phylomania. Theoretical Phylogenetics meeting. University of Tasmania, Australia, November 2013.

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

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

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

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

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

Fellowships/Grants

CoI - Evolutionary consequences of reassortment of influenza A viruses. Academic Research Fund Tier 2, Ministry of Education, Singapore S$691,194. 2012-2015.

CoI - Evolutionary genomics of the 2009 swine-origin H1N1 influenza A pandemic virus. Individual Research Grant, National Medical Research Council, Singapore S$1,140,450. 2011-2014.

CoI - Ecology, evolution and population genetics of influenza A (H5N1) virus. NIAID Centers of Excellence for Influenza Research and Surveillance, NIH, USA US$1,614,805. 2007-2014.

National Science Foundation, Mathematical Biology program: Identifying Selection Pressures on Viral Genomes, University of California, San Diego, 2010-2011.

International Macquarie University Research Scholarship, Australia, 2006-2010.

Service

Reviewer for *BMC Evolutionary Biology*, *BMC Bioinformatics*, *Bioinformatics*, *PLoS One*, *PLoS Computational Biology*, and *Infection, Genetics and Evolution.*

Research

Interests

Viruses, seasonal and H5N1 Influenza, malaria, HIV, SIV, computational methods, phylogenetics, molecular evolution, molecular epidemiology.

Skills

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

Database: MySQL and SQLite.

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

Publications

23. **Fourment M.** & Holmes E.C. Seqotron: a user-friendly sequence editor (*Submitted to Bioinformatics*).

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.

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

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., Bǒsková 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.

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.

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., and Poinar H. Yersinia pestis and the Plague of Justinian 541-543 AD: a genomic analysis. *Lancet Infect Dis*, 2014.

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. Spatial diffusion of avian influenza A virus between North American migratory bird populations maintains genetic diversity and persistence. *PLoS Pathog*, 2013.

16. Shanmuganatham K., Feeroz M.M., Jones-Engel L., Smith G.J.D., **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., and Webster R.G. Antigenic and molecular characterization of avian influenza A(H9N2) viruses, Bangladesh. *Emerg Infect Dis*, 2013.

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.

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.

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.

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.

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.

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.

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.

7. Duval L., Nerrienet E., Rousset D., Sadeuh S., Houze, S., **Fourment M.**, Robert V., and Ariey, F. Chimpanzee malaria parasites exhibit phylogenetic relationships with *Plasmodium ovale* in Africa. *PLoS ONE*, 2009.

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.

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

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

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.

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.

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

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