

Luiz Max Fagundes de Carvalho

lm.carvalho@ed.ac.uk

*Rambaut Group, Institute of Evolutionary Biology, School of Biological Sciences,
University of Edinburgh, UK.*

Last update: March 2017

Summary

Natural biological processes emit signals, which are often too loud or too low for us to “hear”. My goal as a scientist is to develop and apply statistical and mathematical tools to decode and quantify these biological signals, specially those imprinted in pathogens’ – and their hosts’ – genomes. I hope a better understanding of these entities can contribute to the general theory of Biology and also lead to a progressive reduction of the world’s disease burden.

My interests lie in **quantitative Biology** and **Biostatistics**, ranging from complex networks to spatial analysis to statistical phylogenetics. In recent years my main scientific interest has been to understand the complex interactions between rapidly evolving pathogens, such as RNA viruses, and their hosts. My peer-reviewed papers have been published in indexed international journals, such as *Infection*, *Genetics and Evolution*, *Transactions of the Royal Society of Tropical Medicine and Hygiene* and *BMC Bioinformatics* (*Nature*, *Science* and *Cell* too, but don’t get too excited about those).

I have also attended or had work presented at national and international conferences, such as the Brazilian Congress of Virology (BSV), the Gordon Research Conference on Biology of Host-Parasite Interactions, the World Statistics Congress (ISI), the Joint Statistical Meetings (ASA) and, my favourite, the Brazilian Meeting on Bayesian Statistics (ISBra–EBEB).

As you will notice if you continue reading, I am a big fan of collaboration, interacting with colleagues around Brazil and abroad. My current interests are:

- Phylogeny estimation: MCMC exploration of time-tree space – characterising time-tree space, new transition kernels;
- Coupling mathematical models to coalescent-based population reconstructions;
- Bayesian inference of deterministic models;
- Combining (pooling) probability distributions;

Please feel free to contact me if your interests lie anywhere near these topics.

Linkedin: <http://www.linkedin.com/profile/view?id=171872451>

ResearchGate: https://www.researchgate.net/profile/Luiz_Carvalho11

Lattes CV: <http://lattes.cnpq.br/7282202947621572>

A list of PDFs of my publications can be found at <https://github.com/maxbiostat/papers/tree/master/PAPERS>

Publications

Published/Accepted – peer reviewed

- [1] F. P. Camara, A. L. Gomes, Carvalho, L. M., and L. G. Castello, “Dynamic behavior of sylvatic yellow fever in Brazil (1954-2008),” *Rev. Soc. Bras. Med. Trop.*, vol. 44, no. 3, pp. 297–299, 2011.
- [2] Carvalho, L. M. and F. P. Camara, “Epidemiological aspects of acquired immunodeficiency syndrome in older Brazilians: a comparative approach,” *Braz J Infect Dis*, vol. 16, no. 1, pp. 34–37, 2012.
- [3] F. P. Camara, Carvalho, L. M., and A. L. Gomes, “Demographic profile of sylvatic yellow fever in Brazil from 1973 to 2008,” *Trans. R. Soc. Trop. Med. Hyg.*, vol. 107, pp. 324–327, May 2013.
- [4] Carvalho, L. M., L. B. Santos, N. R. Faria, and W. de Castro Silveira, “Phylogeography of foot-and-mouth disease virus serotype O in Ecuador,” *Infect. Genet. Evol.*, vol. 13, pp. 76–88, Jan 2013.
- [5] F. Bielejec, P. Lemey, Carvalho, L. M., G. Baele, A. Rambaut, and M. A. Suchard, “BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios,” *BMC Bioinformatics*, vol. 15, p. 133, 2014.
- [6] D. Mir, H. Romero, Carvalho, L. M., and G. Bello, “Spatiotemporal dynamics of DENV-2 Asian-American genotype lineages in the Americas,” *PLoS ONE*, vol. 9, no. 6, p. e98519, 2014.
- [7] F. C. Coelho and Carvalho, L. M., “Estimating the attack ratio of dengue epidemics under time-varying force of infection using aggregated notification data,” *Scientific reports*, vol. 5, 2015.
- [8] A. Rambaut, T. T. Lam, Carvalho, L. M., and O. G. Pybus, “Exploring the temporal structure of heterochronous sequences using tempest (formerly Path-O-Gen),” *Virus Evolution*, vol. 2, no. 1, p. vew007, 2016.
- [9] A. Rambaut, G. Dudas, Carvalho, L. M., D. J. Park, N. L. Yozwiak, E. C. Holmes, and K. G. Andersen, “Comment on mutation rate and genotype variation of ebola virus from mali case sequences,” *Science*, vol. 353, no. 6300, pp. 658–658, 2016.
- [10] C. Codeço, D. Villela, M. F. Gomes, L. Bastos, O. Cruz, C. Struchiner, Carvalho, L. M., and F. Coelho, “Zika is not a reason for missing the olympic games in rio de janeiro: response to the open letter of dr attaran and colleagues to dr margaret chan, director-general, who, on the zika threat to the olympic and paralympic games,” *Memórias do Instituto Oswaldo Cruz*, vol. 111, no. 6, pp. 414–415, 2016.
- [11] W. E. Diehl, A. E. Lin, N. D. Grubaugh, Carvalho, L. M., K. Kim, P. P. Kyawe, S. M. McCauley, E. Donnard, A. Kucukural, P. McDonel, *et al.*, “Ebola virus glycoprotein with increased infectivity dominated the 2013–2016 epidemic,” *Cell*, vol. 167, no. 4, pp. 1088–1098, 2016.
- [12] F. C. Coelho, B. Durovni, V. Saraceni, C. Lemos, C. T. Codeco, S. Camargo, Carvalho, L. M., L. Bastos, D. Arduini, D. A. Villela, *et al.*, “Higher incidence of zika in adult women than adult men in rio de janeiro suggests a significant contribution of sexual transmission from men to women,” *International Journal of Infectious Diseases*, vol. 51, pp. 128–132, 2016.

- [13] D. A. Villela, L. Bastos, Carvalho, L. M., O. G. Cruz, M. F. Gomes, B. Durovni, M. C. Lemos, V. Saraceni, F. C. Coelho, and C. T. Codeco, “Zika in rio de janeiro: Assessment of basic reproduction number and comparison with dengue outbreaks,” *Epidemiology and Infection*, pp. 1–9, 2017.
- [14] G. Dudas, Carvalho, L. M., T. Bedford, A. J. Tatem, G. Baele, N. Faria, D. Park, J. Ladner, A. Arias, D. Asogun, F. Bielejec, S. Caddy, M. Cotten, J. Dambrozio, S. Dellicour, A. Di Caro, J. Diclaro, S. Duraffour, M. Elmore, L. Fakoli, M. Gilbert, S. M. Gevao, S. Gire, A. Gladden-Young, A. Gnirke, A. Goba, D. Grant, B. Haagmans, J. Hiscox, U. Jah, B. Kargbo, J. Kugelman, D. Liu, J. Lu, C. Malboeuf, S. Mate, D. Matthews, C. Matranga, L. Meredith, J. Qu, J. Quick, S. Pas, M. Phan, G. Poliakakis, C. Reusken, M. Sanchez-Lockhart, S. Schaffner, J. Schieffelin, R. Sealfon, E. Simon-Loriere, S. Smits, K. Stoecker, L. Thorne, E. Alice Tobin, M. Vandi, S. Watson, K. West, S. Whitmer, M. Wiley, S. Winnicki, S. Wohl, R. Wölfel, N. Yozwiak, K. Andersen, S. Blyden, F. Bolay, B. Dahn, M. Carroll, B. Diallo, P. Formenty, C. Fraser, G. Gao, R. Garry, I. Goodfellow, S. Günther, C. Happi, E. Holmes, B. Kargbo, P. Kellam, M. Koopmans, N. Loman, N. Magassouba, D. Naidoo, S. Nichol, T. Nyenswah, G. Palacios, O. Pybus, P. Sabeti, A. Sall, K. Sakoba, U. Ströher, I. Wurie, M. Suchard, P. Lemey, and A. Rambaut, “Virus genomes reveal the factors that spread and sustained the west african ebola epidemic.,” *Nature*, In press.

Conference papers

- [15] Carvalho, L.M., L. Santos, P. Pereira, and W. Silveira, “Phylodynamics of foot-and-mouth disease virus: a complex network approach,” in *Proceedings of the 10th Brazilian Conference on Dynamics, Control and Their Applications*, Brazilian Society for Applied and Computational Mathematics, 2011.

Book chapters

- [16] F. Camara and Carvalho, L. M., “Febres Hemorrágicas virais [Viral hemorrhagic fevers],” in *Introdução à Virologia Humana* (N. Santos, M. T. Romanos, and M. D. Wigg, eds.), Rio de Janeiro: Guanabara Koogan, 3rd ed., 2014.
- [17] Carvalho, L. M., “Métodos bayesianos para inferir o padrão de dispersão de agentes patogênicos : filogeografia do vírus da febre aftosa na América do Sul como um caso de estudo [Bayesian methods to infer spread patterns for pathogens: the phylogeography of Foot-and-Mouth Disease virus in South America as a case study],” in *Abordagens Moleculares em Veterinária* (M. V. Cunha and J. Inácio, eds.), Lisbon: Lidel Editora, 1st ed., 2014.
- [18] Carvalho, L. M., C. Struchiner, and L. Bastos, “Bayesian inference of deterministic population growth models,” in *Interdisciplinary Bayesian Statistics* (A. Polpo de Campos, F. Neto, L. Ramos-Rifo, J. Stern, and M. Lauretto, eds.), vol. 118, pp. 217–228, Springer Verlag, 1st ed., 2015.

Work in progress¹

Carvalho, L.M., G. Baele, N. Faria, A. M. Perez, M. Suchard, P. Lemey, and W. C. Silveira, “Spatiotemporal Dynamics of foot-and-mouth disease virus in South America” In preparation.

¹Drafts in final phase of preparation

L. Zimmermann, Carvalho, L.M., L. Vasconcellos, L. Bastos, C. Struchiner, and A. H. Lopes, “Temperature-dependent oviposition and egg eclosion of Chagas disease vector *Rhodnius prolixus*”, In preparation.

Carvalho, L.M., D.A. Vilella, F.C. Coelho, L. Bastos, “On the choice of the weights for the logarithmic pooling of probability distributions”, In preparation.

Carvalho, L.M., G. Baele, M.A. Suchard, A. Rambaut, “An efficient, tunable time-tree transition kernel for Bayesian phylogenetics”, In preparation.

Education

2009–2012	BSc Microbiology and Immunology, Federal University of Rio de Janeiro, Brazil.
2014–	PhD Evolutionary Biology, University of Edinburgh, UK.

Professional Experience

2010–2013	Pan American Health Organization (PAHO) Position: Statistical Assistant Role: Developed and analysed quality control experiments for veterinary diagnostic tests; Research on Foot-and-Mouth Disease virus phylodynamics
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Academic Experience

2009–2011	Sector of Infectious Diseases Epidemiology (SEDI), Institute of Microbiology, Federal University of Rio de Janeiro Position: Scientific initiation student Advisor: Prof. Dr. Fernando Portela Câmara Role: research on statistical methods in the epidemiology of AIDS, sylvatic yellow fever and dengue
2012–2013	Program for Scientific Computing (PROCC), Oswaldo Cruz Foundation (Fiocruz) Position: Scientific initiation student Advisor: Prof. Dr. Oswaldo Gonçalves Cruz Role: research on spatial partition methods for health areal data
2013–2014	Program for Scientific Computing (PROCC), Oswaldo Cruz Foundation (Fiocruz) Position: Scientific initiation student Advisors: Prof. Dr. Claudio Struchiner and Dr. Leonardo Bastos Role: research on Bayesian inference of deterministic population growth models, multilevel binary regression and opinion pooling
2014–	Institute of Evolutionary Biology (SBS), University of Edinburgh Position: PhD student Advisors: Andrew Rambaut and Darren Obbard Role: research on statistical phylogenetics methods for RNA virus phylodynamics.

Conferences²

Presented work

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|------|---|
| 2009 | Gomes, A.L.B.B; Carvalho, L.M.; Camara, F.P. Dinâmica Espacial da Dengue no Rio de Janeiro: 1986 a 2009 [Spatial dynamics of dengue in Rio de Janeiro: 1986 to 2009], 2009, II International Congress on Geography of Health, Uberlândia -MG, Brazil. |
| 2011 | Vianez Jr., J.L.; Carvalho, L. M.; Bisch, P. Development of a workflow for large-scale epitope prediction: dengue virus as a study of case. In: X Meeting 2011, 2011, Florianópolis-SC, Brazil. X Meeting 2011 Abstract Book, 2011. v. ID 234. |
| 2011 | Carvalho,L.M.; Santos, L.B.; Silveira, W.C. Phylodynamics of Foot-and-Mouth Disease Virus: a Complex Network approach. XXII Meeting of the Brazilian Society of Virology, Águas de Lindóia – SP, Brazil. |
| 2012 | Carvalho, L. M.; Santos, L.B.; Faria, N.R.; Silveira, W.C. Phylogeographic Dynamics of foot-and-mouth disease virus in Ecuador 2002 to 2010 , 2012 In 17th International BioInformatics Workshop on Virus Evolution and Molecular Epidemiology, Belgrade, Serbia. |
| 2012 | Carvalho, L.M.; Faria, N.R.; Silveira, W.C. Phylodynamics of Foot-and-Mouth Disease Virus in South America: a Comprehensive Analysis. XXIII Brazilian Congress of Virology, Foz do Iguaçu – PR, Brazil. |
| 2012 | Vasconcellos, L.R.C.; Dias, F.A.; Soares, J. B. R. C.; Carvalho, L. M.; Oliveira, M. M.; Alves e Silva, T. L.; Gonçalves, I.; Oliveira, M. F.; Lopes, F.G.; Lopes, A. H. C. S. Interaction of the hemipteran <i>Oncopeltus fasciatus</i> with the trypanosomatid <i>Leptomonas wallacei</i>: an insight into parasitism. In: Gordon Research Conference on Biology of Host-Parasite Interactions, 2012, Newport, RI, USA. Annals of the Gordon Research Conference on Biology of Host-Parasite Interactions, 2012. v. 1. p. 1-2. |
| 2013 | Zimmermann, L.T.; Carvalho, L.M.; Vasconcellos, L.R.; Bastos, L.S.; Struchiner, C.J.; Lopes, A.H. Temperature-dependent oviposition and egg eclosion of Chagas disease vector <i>Rhodnius prolixus</i> In XXIX Annual Meeting of the Brazilian Society of Protozoology, 2013, Caxambu-MG, Brazil. Abstract book of the XXIX Annual Meeting of the SBPz, p. 159, ID V004. |
| 2014 | Carvalho, L. M.; Struchiner, C.J.; Bastos, L.S. Bayesian inference of deterministic population growth models In XII Brazilian Meeting on Bayesian Statistics (EBEB), 2014, Atibaia-SP, Brazil. Abstract book of the XII Brazilian Meeting on Bayesian Statistics, p. 63 |
| 2014 | Bastos, L. S.; Carvalho, L. M. Random Effects Binary Model with Misclassified Response In Joint Statistical Meetings, 2014, Boston MS, USA. |

²Main conferences I have attended to or had work presented at. For a complete list please visit my Lattes CV.

Participated

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| 2012 | VIII Brazilian Congress of Epidemiology, São Paulo–SP, Brazil. |
| 2013 | 1 st Symposium on Big Data and Public Health, Rio de Janeiro–RJ, Brazil. |

Invited Talks

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| 2011 | <i>Phylodynamics of Foot-and-Mouth Disease Virus: a Complex Network approach.</i> XXII Meeting of the Brazilian Society of Virology |
| 2011 | <i>Playing Dumb: The Misuse of Statistics in Biology.</i> Institute of Microbiology, Federal University of Rio de Janeiro. |
| 2012 | <i>Knowledge Discovery in Databases through Complex Networks: application to phylodynamics.</i> WaFIS 2012 |
| 2014 | <i>Bayesian inference of deterministic population growth models.</i> XII Brazilian Meeting on Bayesian Statistics |
| 2015 | <i>Phylodynamics: how Genetics and Mathematics are changing our understanding of infectious diseases.</i> 30rd Brazilian Mathematics Colloquium |
| 2015 | <i>Choosing the weights for the logarithmic pooling of probability distributions.</i> 60th World Statistics Congress. |
| 2016 | <i>On the choice of the weights for the logarithmic pooling of probability distributions.</i> XIII Brazilian Meeting on Bayesian Statistics. |

Memberships

Brazilian Society for Virology (SBV), Brazilian Statistical Association (ABE), Brazilian Society for the Advancement of Science (SBPC).

Teaching Experience

2007–2011	High School Chemistry and Biology I was a voluntary teacher of whole-year high school courses on organic chemistry, general chemistry and biology.
2010–2013	Basics of Mathematics and Statistics for Microbiology Federal University of Rio de Janeiro Supervisor: Prof. Dr. Fernando Portela Câmara Basics on descriptive statistics, Gaussian distribution and hypothesis testing. Lately, some basic calculus too.
2010	Topics in Human Physiology Federal University of Rio de Janeiro Supervisor: Prof. Dr. Pedro Paulo Elsas By means of seminars and group discussions, we discussed particular aspects of human physiology and stimulate the students to draw general conclusions about the subjacent biological processes going on.
2012	Bioinformatics Federal University of Rio de Janeiro Supervisor: Prof. Andrew Macrae, PhD Basics on Bioinformatics: basic genome annotation, databases, alignment, phylogenetics.

Awards

2010	Honourable Mention - XVI Week of Microbiology and Immunology.
2011	Honourable Mention - XVII Week of Microbiology and Immunology.
2011	Selected for Oral presentation – XXII National Meeting of the Brazilian Society for Virology.
2012	Honourable Mention - XVIII Week of Microbiology and Immunology.
2014	Selected for Oral presentation – XII Brazilian Meeting on Bayesian Statistics.
2014	Principal's Career Development Scholarship, University of Edinburgh.

Languages

Portuguese	Native
English	Fluent (CAE – Grade A)
Spanish	Advanced

References

Reference	What for	email
Prof. Dr. Fernando Portela Câmara	Research and Teaching	<code>portela@micro.ufrj.br</code>
Prof. Ângela Hampshire Lopes, PhD	Research	<code>angela.lopes@micro.ufrj.br</code>
Prof. Andrew Macrae, PhD	Teaching	<code>amacrae@biologia.ufrj.br</code>
Prof. Dr. Pedro Paulo Xavier Elsas	Teaching	<code>pxelsas@micro.ufrj.br</code>
Prof. Claudio Struchiner, PhD	Research	<code>stru@fiocruz.br</code>
Leonardo Bastos, PhD	Research	<code>lsbastos@fiocruz.br</code>
Prof. Philippe Lemey, PhD	Research	<code>philippe.lemey@rega.kuleuven.be</code>