

Thibaut Jombart, PhD

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/// Positions

- **Since October 2014:** Lecturer in Genetic Analysis, Imperial College London, UK
- **April 2014 - September 2014:** Research Fellow, Imperial College London, UK
- **2009 - April 2014:** Post-doctoral Research Associate, Imperial College London, UK

/// Other appointments / awards

- Head of the R Epidemics Consortium (RECON: www.repidemicsconsortium.org)
- WHO consultant – outbreak response
- Member of GOARN advisory panel for analysis tools development
- Co-investigator: NERC grant (NE/P001165/1) “*The evolutionary dynamics of multiazole resistance in pathogenic Aspergillus fungi*” 2016-2019
- HPRU project lead: “*Using genomes sequences to impute the origins of food-borne outbreaks*”
- HPRU project lead: “*Integrating statistical tools for outbreak response into public health systems and training programmes*”

/// Education

- **2005-2008:** PhD, Biostatistics, University Lyon 1 (France). *Multivariate analysis of genetic markers*. Supervisors: Dr A-B Dufour, Pr D Pontier, Pr D Chessel
- **2004-2005:** MRes in Ecology, Evolution, Biometry, University Lyon 1 (France) / University of Montreal (Canada). *Coinertia analysis under spatial constraints*. Supervisors: Pr D Chessel, Pr D Boisclair, Pr P Legendre, Dr D Borcard
- **2003-2004:** MSc in Population Biology & Ecosystems. University of Tours (France)
- **2000-2003:** BSc in Biology, University of Tours (France) / University of Montreal (Canada)

/// Teaching

- Short course on outbreak response (5 days)
- Programming using R. MRes Epidemiology, Imperial College London.
- Genetic Data Analysis using R. One-week summer course with PR Statistics.
- Simulation of an Ebola outbreak response. 1.5 days during short course in Infectious Disease Modelling, Imperial College London.

/// Selected publications

(Total number of publications: 64; Citations: 6,097; H-index: 26)[‡]

- **Jombart T**, Kendall M, Almagro-Garcia J, and Colijn C. (2017) *treespace*: statistical exploration of landscapes of phylogenetic trees. *Molecular Ecology Resources*
- Karkey A*, **Jombart T***, Walker AW, Thompson CN, Torres A, Dongol S, et al (2016) The Ecological Dynamics of Fecal Contamination and *Salmonella Typhi* and *Salmonella Paratyphi A* in Municipal Kathmandu Drinking Water. *PLoS Neglected Tropical Diseases* 10(1): e0004346
- Mita T and **Jombart T** (2015) Patterns and dynamics of genetic diversity in *Plasmodium falciparum*: What past human migrations tell us about malaria. *Parasitology international* 64, 238-243
- WHO Ebola Response Team (2015) West African Ebola Epidemic after One Year — Slowing but Not Yet under Control. *The New England journal of medicine*. 372, 584-587.
- WHO Ebola Response Team (2014) Ebola Virus Disease in West Africa — The First 9 Months of the Epidemic and Forward Projections. *The New England journal of medicine* 371, 1481–1495.
- **Jombart T**, Cori A, Didelot X, Cauchemez S, Fraser C, Ferguson N, (2014). Bayesian reconstruction of disease outbreaks by combining epidemiologic and genomic data. *PLoS Computational Biology* 10(1): e1003457
- Cuy Y* , Yan Y*, Li D*, Li Y*, **Jombart T*** et al. (2013) Historical variations in mutation rate in an epidemic pathogen, *Yersinia pestis*. *PNAS*, 110: 577–582.

/// Conference talks and invited seminars (since 2013)

- Jombart T. RECON: building the next generation of tools for outbreak response using R (plenary talk) 2016. Stockholm, Sweden.
- Jombart T. On the emergence of R as a platform for outbreak response. 2016. User2016! conference, Stanford.
- Jombart T. Disease outbreak reconstruction using R. Invited short course, 2015, Epidemics 5, Florida, USA.
- Jombart T. Towards an open-source, unified platform for disease outbreak analysis. NESCent invited seminar, 2015, Durham (NC), USA.
- Jombart T. outbreaker: disease outbreak reconstruction using genetic data. Invited talk, 2013, Epidemics4, Amsterdam, The Netherlands.
- Jombart T. Towards an open-source, unified platform for disease outbreak analysis. Invited talk, 2013, Symposium: Combining genetic and epidemiological data to unravel infectious disease dynamics, Utrecht, The Netherlands.
- Jombart T. outbreaker: disease outbreak reconstruction using genetic data. Invited talk, 2013, Pre-ESCAIDE workshop on Molecular Outbreak Epidemiology, Stockholm, Sweden.
- Jombart T. outbreaker: disease outbreak reconstruction using genetic data. Invited talk, 2013, RAPID-NGS for Public Health Microbiology, Münster, Germany.

[‡] source: web of science, 22-12-2017

- Jombart T. Discriminant Analysis of Principal Components as a tool for pathogen GWAS. Invited talk, 2013, Permafrost workshop, Bormio, Italy.
- Jombart T. Reconstructing disease outbreaks from pathogen genome sequences: a Bayesian approach. Invited talk, 2013, Permafrost workshop, Bormio, Italy.
- Jombart T. Reconstructing disease outbreaks from pathogen genome sequences: a Bayesian approach. Invited talk, 2013, RAPIDD-EPI workshop, Gainesville, Florida, USA.
- Jombart T. Reconstructing disease outbreaks from pathogen genome sequences: a

/// Workshops (since 2013)

- [organiser] *Hackout 3: Statistical Tools for Emergency Outbreak Response*, Berkeley (CA), USA, June 2016.
- Microbial source attribution using genomic data, London, UK, May 2016.
- Permafrost workshop, Bormio, Italy, January 2016.
- [teacher] Genetic data analysis using R, Glasgow, UK, August 2015.
- [teacher] Genetic data analysis using R, Barcelona, Spain, October 2015.
- [co-organiser] Population genetics in R hackathon, Durham (NC), USA, March 2015.
- [organiser] *Hackout 2: Graphical Resources for Infectious Disease Epidemiology in R*, London, UK, February 2015.
- Permafrost workshop, Bormio, Italy, January 2015.
- [teacher] Genetic data analysis using R, Leuven, Belgium, October 2014.
- Permafrost workshop, Bormio, Italy, February 2014.
- [teacher] Pre-ESCAIDE workshop on Molecular Outbreak Epidemiology, Stockholm, Sweden, November 2013.
- [teacher] Genepi workshop, London, UK, April 2013.
- RAPID-NGS for Public Health microbiology workshop, Münster, Germany, March 2013.
- Permafrost workshop, Bormio, Italy, February 2013.
- RAPIDD-EPI workshop, Gainesville (Florida), USA, January 2013.
- [organiser] *Hackout: a hackathon for the analysis of disease outbreaks in R*, London, UK, January 2013.

/// Supervision

- Dr Armish Baidjoe, postdoctoral research associate, Imperial College London, since September 2017.
- Dr Martin Hinsch, postdoctoral research associate, Imperial College London, since March 2017.
- Mr Finlay Campbell, PhD in Infectious Disease Modelling, Imperial College London, since September 2016.
- Mr Anil Keshwani, MSc in Epidemiology, Imperial College London, 2017.
- Mr Tim McMackin, Master in Public Health, Imperial College London, 2015-2016.

- Mr Finlay Campbell, Master in Research, Imperial College London, 2015-2016.
- Ms Lucy Tran, MSc in Epidemiology, Imperial College London, 2015-2016.
- Ms Camilla Strang, MSc in Epidemiology, Imperial College London, 2015.
- Mr Joel Hellewell, Master in Research, Imperial College London, 2014-2015 (starting PhD in September 2015).
- Mr Yee Loong Low, MSc in Epidemiology, Imperial College London, 2014.
- Ms Yemisi Khalidson, Master in Public Health, Imperial College London, 2014.
- Ms Caitlin Collins, Research Assistant, Imperial College London, September 2013 - October 2014.
- Ms Caitlin Collins, Master in Public Health, Imperial College London, 2013.
- Ms Veronika Valovicova, MSc in Epidemiology, Imperial College London, 2013.

/// Reviewing activities

Reviewer for

Acta Oecologica, Annals of Applied Statistics, Bioinformatics, BMC Bioinformatics, Genetic Epidemiology, Journal of Heredity, Landscape Ecology, Marine Biology, Methods in Ecology and Evolution, Molecular Ecology, Molecular Ecology Resources, Molecular Phylogenetics and Evolution, PLoS Computational Biology, PLoS Pathogens, Proceedings of the Royal Society B, Statistical Applications in Genetics and Molecular Biology, Springer, United States - Israel Binational Science Foundation Associate

Editor for

Colombian Journal of Statistics (Special Issue)

/// Software (R packages)

- *adegenet*: multivariate analysis for population genetics
- *adephylo*: exploratory approaches for the phylogenetic comparative method
- *apex*: multi-gene phylogenetic analysis
- *bmmix*: Bayesian multinomial mixture model
- *dibbler*: analysis of foodborne outbreaks
- *earlyR*: early estimation of reproduction number
- *epicontacts*: visualisation and analysis of epidemiological contacts
- *epicontacts.ui*: a web-based graphical user interface for *epicontacts*
- *epitrix*: a collection of practical tools for epidemiologists
- *geoGraph*: graph algorithms for spatial processes
- *incidence*: computation and visualization of incidence from outbreak data
- *incidence.ui*: a web-based graphical user interface for *incidence*
- *outbreaker*: disease outbreak reconstruction using genomic data
- *outbreaker2*: disease outbreak reconstruction by integrating genomic and epidemiological data
- *OutbreakTools*: base package for the handling, visualization and analysis of

outbreak data

- *projections*: projecting future incidence using a Poisson model
- *treespace*: statistical exploration of landscapes of phylogenetic trees
- *vimes*: visualization and monitoring of epidemics