

Thibaut Jombart, PhD

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/// Positions

- **September 2018 – present:** Associate Professor in Outbreak Analytics, London School of Hygiene and Tropical Medicine (80% FTE), Senior Lecturer, Imperial College London (20% FTE)
- **October 2014 – August 2018:** 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

/// Appointments / awards

- Founder, president, treasurer 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*”

/// Outbreak responses

- **February 2019 – November 2019:** WHO Ebola response (lead data analyst), Beni / Goma, DRC.
- **May 2017:** WHO Ebola Likati response team (data manager), Kinshasa, DRC.
- **2014-2016:** WHO Ebola response team (analysis and sitrep pipeline design), Imperial College London
- **2013:** MERS-CoV analysis team for KSA (modeller), Imperial College London

/// 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.
- Reproducible Data Science for Population Genetics. One-week 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: 71; Citations: 10,244; H-index: 32)[‡]

- **Jombart T**, Jarvis CI, Mesfin S, Tabal N, Mossoko M, Mpia LM, Abedi A, Chene S, Forbin EE, Belizaire MRD, de Radiguès X, Ngombo R, Tutu Y, Finger F, Crowe M, Edmunds WJ, Nsio J, Yam A, Diallo B, Gueye AS, Ahuka-Mundeke S, Yao M, Fall IS (2020) The cost of insecurity: from flare-up to control of a major Ebola virus disease hotspot during the outbreak in the Democratic Republic of the Congo, 2019. *Eurosurveillance* 25(2). <https://doi.org/10.2807/1560-7917.ES.2020.25.2.1900735>
- Polonsky JA, Baidjoe A, Kamvar ZN, Cori A, Durski K, Edmunds JW, Eggo RM, Funk S, Kaiser L, Keating P, le Polain de Waroux O, Marks M, Moraga P, Morgan O, Nouvellet P, Ratnayake R, Roberts CH, Whitworth J & **Jombart T** (2019). Outbreak analytics: a developing data science for informing the response to emerging pathogens *Philosophical Transactions B*
- Cori A, Nouvellet P, Garske T, Bourhy H, Nakouné E & **Jombart T** (2018). A graph-based evidence synthesis approach to detecting outbreak clusters: an application to dog rabies *PLoS Computational Biology*
- Campbell F, Didelot X, FitzJohn R, Ferguson N, Cori A & **Jombart T** (2018). outbreaker2: a modular platform for outbreak reconstruction *BMC Bioinformatics* doi:10.1186/s12859-018-2330-z
- Campbell, F., Strang, C., Ferguson, N., Cori, A. & Jombart, T. (2018). When are pathogen genome sequences informative of transmission events? *PLoS Pathogens*
- 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

[‡] source: web of science, 14-02-2020

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

- Jombart T. Outbreak response analytics: when are pathogen genomes useful? 2018. SMBE satellite meeting Kyoto, Japan.
- Jombart T. Data analytics in early outbreak response: academic exercise or operational tool? 2018. ASTMH New Orleans, USA.
- Jombart T. vimes: an evidence synthesis approach for detecting outbreak clusters. 2018. IDD Cumbria, UK.
- Jombart T. RECON: building the next generation of tools for outbreak response using R. 2017. Epidemics6 Barcelona, Spain.
- Jombart T. RECON: building the next generation of tools for outbreak response using R (invited seminar) 2017. Institut Pasteur Paris, France.
- 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.
- 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] RECON short course: introduction to outbreak analytics using R (with WHO Afro), Cotonou, Bénin, December 2018
- [organiser] RECON hackfest 3: sitreps and case studies (satellite event to ESCAIDE), Malta, November 2018.
- [organiser] 2-days introduction to outbreak response analytics using R (satellite event to ESCAIDE), Malta, November 2018.
- [organiser] 4-days short course on epidemiological case studies and outbreak

- response, Sofia, Bulgaria, October 2018.
- [organiser] 3-days short course on early outbreak assessment, CDC Atlanta, USA, April 2018.
- [organiser] Short course on Epidemic Analysis, Modelling and Response, Bogotá, Colombia, December 2017.
- [organiser] Epidemics 6 workshop on Outbreak Response Analytics, Barcelona, Spain, December 2017.
- [organiser] RECON hackfest 2, London, September 2017.
- [lead teacher] PR Statistics course 'Reproducible Data Science for Population Genetics', UK, October 2017.
- [organiser] RECON hackfest 1, London, March 2017.
- [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

- Ms Amy Gimma, research assistant, London School of Hygiene and Tropical Medicine, 2019-2020.
- Dr Armish Baidjoe, postdoctoral research associate, Imperial College London, since September 2017.
- Ms Amy Dighe, PhD in Infectious Disease Modelling, Imperial College London, since September 2017.
- Dr Martin Hinsch, postdoctoral research associate, Imperial College London, since March 2017.
- Dr 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

/// 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*
- *linelist*: easy cleaning and standardisation of linelist data
- *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
- *reportfactory*: keeping reports tidy using R markdown
- *treespace*: statistical exploration of landscapes of phylogenetic trees
- *vimes*: visualization and monitoring of epidemics

/// Miscellaneous

- UN SSAFE training, Goma, DRC (WHO / UNDSS, 2019)
- Personal field security training in fragile environment (KBS SAFE / SAFE+ training, 2018)
- Personal field security training (Clarity's HEAT training, 2017)
- UN Basic and Advanced Field Security Trainings (certified in 2017)
- Field first aid training (certified in 2016)
- Languages: English (fluent), French (native), notions of Russian
- 20+ years of martial arts practice (Muay Thai, MMA, Yoseikan Budo, Karate, Aikido, Judo)
- Hobbies: music (vocalist for 'The Brood' 2014-2018), computer security, cooking, yoga, meditation