Thibaut Jombart, PhD

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/// Positions

- **April 2022 – present:** Software Design and Implementation Lead, Data.Org (80%FTE)
- **September 2021 – present:** consultant in outbreak analytics (WHO, World Bank)
- **September 2018 – present:** Senior Lecturer in Outbreak Analytics, Imperial College London (20% FTE)
- **September 2018 – March 2022:** Associate Professor in Outbreak Analytics, London School of Hygiene and Tropical Medicine (80% 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 / grants

- Principal Investigator: £3M Data.Org grant for Outbreak Analytics Software Development (LSHTM), Nov 2021 – Oct 2024.
- Member of SPI-M UK since March 2020
- Founder, president, treasurer of the R Epidemics Consortium (RECON: www.repidemicsconsortium.org), 2018-2021
- WHO consultant – outbreak response 2017-2021
- Member of GOARN working group for integrated outbreak analytics, 2021
- Co-investigator: MRC grant (MC_PC_19065) "*COVID-19: Understanding the dynamics and drivers of the COVID-19*", 2020-2021
- Core member of the UK Public Health Rapid Support Team, 2018-2020
- Member of GOARN advisory panel for GoData2 development, 2018-2019
- 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*", 2016-2017
- HPRU project lead: "*Integrating statistical tools for outbreak response into public health systems and training programmes*", 2016-2017

/// Outbreak responses

- **March 2020 – September 2021:** COVID-19 response in the UK (member of SPI-M)
- **February 2021 – August 2021:** Lead Data Scientist, WHO COVID-19 analytics team
- **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: Introduction to outbreak analytics using R (5 days), LSHTM
- Programming using R. MRes Epidemiology, Imperial College London
- Reproducible Data Science for Population Genetics. One-week course with PR Statistics
- Simulation of an Ebola oubtreak response. 1.5 days during short course in Infectious Disease Modelling, Imperial College London

/// Selected publications

(Total number of publications: 84; Citations: 12,931; H-index: 41)[‡]

- **Jombart T** (2021) Why development of outbreak analytics tools should be valued, supported, and funded. Lancet ID 21:4, 458-459.
- **Jombart T,** Ghozzi S, Schumacher D, Taylor TJ, Leclerc QJ, Jit M, *et al.* (2021) Real-time monitoring of COVID-19 dynamics using automated trend fitting and anomaly detection. Philos Trans R Soc Lond B Biol Sci. 2021;376: 20200266.
- **Jombart T**, van Zandvoort K, Russell TW et al. Inferring the number of COVID-19 cases from recently reported deaths. *Wellcome Open Res* 2020, 5:78 (https://doi.org/10.12688/wellcomeopenres.15786.1)
- **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).
- 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*

‡ source: web of science, 13-12-2021

- 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

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

- Jombart T. Outbreak analytics: using data science to inform the response to health emergencies. 2021. French Statistical Society plenary. Paris, France.
- Jombart T. The role of WGS in outbreak investigations: a silver bullet against COVID-19? 2021. ICPIC, Geneva, Switzerland.
- Jombart T. When coding matters: reproducibility in outbreak analytics. 2021. OUCRU seminars, Ho Chi Minh City, Vietnam.
- Jombart T. When data integration matters, and why modular platforms are needed. 2021. Outbreak Reconstruction Workshop, London, UK.
- Jombart T. Reproducible data science to inform outbreak response: Report from the North-Kivu Ebola outbreak. 2019. UserR2019, Toulouse, France
- 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, Forida, USA.
- Jombart T. Reconstructing disease outbreaks from pathogen genome sequences: a

/// Workshops (since 2013)

- [organiser] Defining a roadmap for outbreak analytics. Virtual workshop, December 2020
- [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, Bogotà, 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 (Forida), USA, January 2013.
- [organiser] *Hackout*: a hackathon for the analysis of disease outbreaks in R, London, UK, January 2013.

/// Supervision

- Bethany Evans (MPH student, LSHTM, 2021)
- Dr Tim Taylor (Research Fellow, LSHTM, 2020-2021)
- Anne Suffel (MSc student, LSHTM, 2019-2020)
- Emily Meyer (MSc student, LSHTM, 2019-2020)
- Allegra Wilson (MSc student, LSHTM, 2019-2020)
- Srikant Mohan (MSc student, LSHTM, 2019-2020)
- Amy Gimma (Research Assistant, LSHTM, 2019-2020)
- Janetta Skarp (MRes student, ICL, 2018-2019)
- Dr Armish Baidjoe, postdoctoral research associate, ICL, 2017-2018
- Amy Dighe (PhD student – main supervisor, ICL, 2017-2021)
- Dr Martin Hinsch (Research Associate, ICL, 2017)
- Dr Finlay Campbell (MRes student, ICL, 2015-2016; PhD student – main supervisor, ICL, 2016-2018)
- Anil Keshwani (MSc student, ICL, 2017)
- Tim McMackin (MPD student, ICL, 2015-2016)
- Lucy Tran (MSc student, ICL, 2015-2016)
- Camilla Strang (MSc student, ICL, 2015)
- Joel Hellewell (MRes, ICL, 2014-2015)
- Yee Loong Low (MSc student, ICL, 2014)
- Yemisi Khalidson (MPH, ICL, 2014)
- Caitlin Collins (MPH student, ICL 2013; Research Assistant, ICL, 2013 -2014)
- Veronika Valovicova (MSc student, ICL, 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
- *epiflows*: tools for modelling traveller flows
- *epitrix*: a collection of practical tools for epidemiologists
- *geoGraph*: graph algorithms for spatial processes
- *incidence*: computation and visualization of incidence from outbreak data
- *incidence2*: epicurves for the reconverse
- *i2extras*: additional features for *incidence2*
- *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
- *trending*: unified interface for epidemic trend modelling
- *trendeval*: model comparison and selection for *trending*
- *trendbreaker*: trend analysis for epidemic surveillance
- *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)
- Personnal 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
- 25+ years of martial arts practice (Muay Thai, MMA, Yoseikan Budo, Karate, Aikido, Judo)
- Hobbies: extreme metal vocalist, mandolin, cooking, computer security, yoga, meditation, bushcrafting