MICHAEL DAVID NICHOLSON

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EDUCATION

University of Edinburgh　　　　　　　　　　　　　　　　　*Edinburgh, Scotland*
Doctor of Philosophy　　　　　　　　　　　　　　　　　　　*November, 2018*
Thesis title: *Applications of branching processes to cancer evolution and initiation*
Supervisors: Dr Tibor Antal (School of Mathematics), Dr Bartlomiej Waclaw (School of Physics and Astronomy)

University of Edinburgh　　　　　　　　　　　　　　　　　*Edinburgh, Scotland*
Master of Mathematics (First Class Honours)　　　　　　　　　　　*July 2014*

Technical skills: R, Matlab, Mathematica, Python, Latex, Linux systems, Cluster computing, Git

RESEARCH CAREER

Institute of Genetics and Cancer　　　　　　　　　　　　　　*Edinburgh, Scotland*
University of Edinburgh
Cross-Disciplinary Research Fellow　　　　　　　　　　　　*September 2020-present*
Primary collaborators: Professor Martin Taylor, Professor Ian Tomlinson.
Research overview: Independent research fellowship developing quantitative methods to investigate the causes and consequences of mutational processes in cancer evolution.

Data Sciences, Dana-Farber Cancer Institute　　　　　　　　　　*Boston, USA*
Department of Biostatistics, Harvard T.H. Chan School of Public Health, and Department of Stem Cell and Regenerative Biology, Harvard University
Postdoctoral Research Fellow　　　　　　　　　　　　*September 2018-August 2020*
Supervisor: Professor Franziska Michor
Projects included: Pairing mathematical models of copy number alteration acquisition with single cell DNA sequencing from triple negative breast cancers, inference of transmission dynamics from genomic data in the spread of COVID-19.

Image Analysis, Canon Medical Research Europe　　　　　　　　*Edinburgh, Scotland*
Research Intern　　　　　　　　　　　　　　　　　　　*June-August 2017*
Supervisor: Dr Marco Razeto
Statistical methods for improving image registration.

Program for Evolutionary Dynamics, Harvard University　　　　　　*Boston, USA*
Guest Researcher　　　　　　　　　　　　　　　　　　　*April-May 2015*
Supervisors: Dr Tibor Antal, Professor Martin Nowak
Research focused on modelling metastasis in cancer. Funded by a Scottish University Physics Alliance grant.

Modelling and Translational Biology, GlaxoSmithKline　　　　　　*Ware, England*
Research Intern　　　　　　　　　　　　　　　　　*July-September 2014*
Supervisors: Dr Enuo He, Mrs Carole Shardlow
Modelling intracellular dynamics for drug specific targeting.

Department of Statistics, University of Oxford　　　　　　　　　*Oxford, England*
Funded Participant, Summer School in Computational Biology　　　　*July - August 2013*
Supervisors: Professor Yee Whye Teh, Dr Paul Jenkins
Technical report: *Importance sampling algorithms for inference under the coalescent*

PUBLICATIONS

denotes co-first author † denotes co-second author

Michael D. Nicholson, David Cheek, Tibor Antal (2023) *Sequential mutations in exponentially growing populations.* PLOS Computational Biology. `https://doi.org/10.1371/journal.pcbi.1011289`

Craig J. Anderson*, Lana Talmane*, Juliet Luft, **Michael D. Nicholson**, John Connelly, Oriol Pich, Susan Campbell1, Vasavi Sundaram, Frances Connor, Paul A. Ginno, Liver Cancer Evolution Consortium, Núria López-Bigas, Paul Flicek, Colin A. Semple, Duncan T. Odom, Sarah J. Aitken, Martin S. Taylor (2022) *Strand-resolved mutagenicity of DNA damage and repair.* Biorxiv preprint, `https://doi.org/10.1101/2022.06.10.495644`. Submitted for review to Nature after invitation by the journal.

Martin A.M. Reijns*, David A. Parry*, Thomas C. Williams*, Ferran Nadeu, Rebecca L. Hindshaw, Diana Rios Szwed, **Michael D. Nicholson**, Paula Carroll, Shelagh Boyle, Romina Royo, Alex Cornish, Hang Xiang, Kate Ridout, The Genomics England Research Consortium, Colorectal Cancer Domain UK 100,000 Genomes Project, Anna Schuh, Konrad Aden, Claire Palles, Elias Campo, Tatjana Stankovic, Martin S. Taylor, Andrew P. Jackson (2022) *Topoisomerase 1 causes mutations in cancer and the germline.* Nature, `https://doi.org/10.1038/s41586-022-04403-y`

Michael D. Nicholson, Lukas Endler, Alexandra Popa, Jakob-Wendelin Genger, Christoph Bock, Franziska Michor, and Andreas Bergthaler (2021) *Response to comment on "Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2".* Science Translational Medicine, `https://doi.org/10.1126/scitranslmed.abj3222`

Rachael R. Kirkbride, Emily Larkin, Mark Tuttle, **Michael D. Nicholson**, Brian G Jiang, Rokas Liubauskas, Jason Matos, Michael Gavin, Diana E Litmanovich (2021) *Quality and diagnostic performance of coronary computed tomography angiogram (CCTA): A comparison between pre-liver and pre-kidney transplant patients.* European Journal of Radiology, `https://doi.org/10.1016/j.ejrad.2021.109886`.

Darlan Conterno Minussi*, **Michael D. Nicholson***, Hanghui Ye*, Alexander Davis, Kaile Wang, Emi Sei1, Haowei Du, Mashiat Rabbani, Cheng Peng, Min Hu, Shanshan Bai, Thomas McDonald, Aislyn Schalck, Anna Casasent, Angelica Barrera, Hui Chen, Bora Lim, Banu Arun, Funda Meric-Bernstam, Franziska Michor, and Nicholas Navin (2021) *Breast tumours maintain a reservoir of subclonal diversity during expansion.* Nature, `https://doi.org/10.1038/s41586-021-03357-x`

Alexandra Popa*, Jakob-Wendelin Genger*, **Michael D. Nicholson**†, Thomas Penz†, Daniela Schmid†, Stephan W. Aberle†, Benedikt Agerer†, Alexander Lercher†, Lukas Endler , Henrique Colaço , Mark Smyth, Michael Schuster , Miguel Grau, Francisco Martinez, Oriol Pich, Wegene Borena, Erich Pawelka, Zsofia Keszei, Martin Senekowitsch, Jan Laine, Judith H. Aberle, Monika Redlberger-Fritz, Mario Karolyi, Alexander Zoufaly, Sabine Maritschnik, Martin Borkovec , Peter Hufnagl, Manfred Nairz, Günter Weiss, Michael T. Wolfinger, Dorothee von Laer, Giulio Superti-Furga, Nuria Lopez-Bigas, Elisabeth Puchhammer-Stöckl, Franz Allerberger, Franziska Michor, Christoph Bock, and Andreas Bergthaler (2020) *Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2.* Science Translational Medicine, `https://doi.org/10.1126/scitranslmed.abe2555`.

Martín Carballo-Pacheco*, **Michael D. Nicholson***, Elin E. Lilja, Rosalind J.Allen, and Bartlomiej Waclaw (2020) *Phenotypic delay in the evolution of bacterial antibiotic resistance: mechanistic models and their implications.* PLOS Computational Biology, 16(5): e1007930. `https://doi.org/10.1371/journal.pcbi.1007930`

Michael D. Nicholson and Tibor Antal (2019) *Competing evolutionary paths in growing populations with applications to multidrug resistance.* PLOS Computational Biology, 15(4): e1006866. `https://doi.org/10.1371/journal.pcbi.1006866`

Michael D. Nicholson and Tibor Antal (2016) *Universal asymptotic clone size distribution for general population growth.* The Bulletin of Mathematical Biology, 78(11), 2243-2276. `https://doi.org/10.1007/s11538-016-0221-x`

FUNDING

Cross-Disciplinary Fellowship from the University of Edinburgh	£200K
EPSRC PhD award	Tuition and stipend for 3.5 years
IMO 5 sponsorship	Flights, accommodation and subsistence
Scottish University Physics Alliance short term visits	£1650
Corporate sponsorship of mathematics society	£1300

PROFESSIONAL SERVICES AND MEMBERSHIP

– Referee for: Bioinformatics, Bulletin of Mathematical Biology, Journal of Statistical Physics, Theory in Biosciences, Journal of Biological Dynamics, Frontiers in Ecology and Evolution.

– Co-organiser: Mathematical Biology seminars 2022, University of Edinburgh

– Membership: Society for Mathematical Biology, UK Environmental Mutagen Society

PRESENTATIONS

– *Quantifying the dynamics of transcription coupled repair*
(Invited) Michor lab, Dana-Farber Cancer Institute, July 2023

– *Quantifying the dynamics of transcription coupled repair*
(Invited) Naxerova lab, Massachusetts General Hospital, July 2023

– *Quantifying the dynamics of transcription coupled repair*
(Invited) Somatic Evolution and Tumour Microenvironment Symposium, The Crick, December 2022

– *Characterising the stochastic dynamics of transcription coupled repair via lesion-phasing and mathematical modelling*
(Select meeting) Bertinoro Computational Biology Meeting, September 2022

– *Evolutionary timescales in exponentially growing clonal populations with rare mutations*
(Invited) Conference: "Mathematical Models in Ecology and Evolution", July 2022

– *Mutational bias versus selective advantage in the determination of cancer driving mutations*
(Invited) Chakrabarti lab, NCBS Bangalore (online), May 2022

– *Transient instability in TNBC examined via single cell DNA sequencing and mathematical modelling*
(Invited) Mathematics colloquium at City, University of London, November 2021

– *Transient instability in TNBC examined via single cell DNA sequencing and mathematical modelling*
Cancer Research UK City of London Centre Cancer Evolution Symposium, September 2021

– *TBC. Postponed due to Covid-19 pandemic*
(Invited) Queen Mary University of London complex systems seminar

– *Breast tumours maintain a reservoir of subclonal diversity during expansion*
(Invited) Reiter lab & Naxerova lab joint meeting, Stanford & Harvard, May 2021

- *Power laws in growing populations: 2 seminars*
  (Invited) Nitzan lab & Ovchinnikov lab joint meeting, Harvard, March 2020

- *Competing evolutionary paths in growing populations with applications to multidrug resistance*
  (Invited) Dartmouth applied and computational mathematics seminars, March 2019

- *Competing evolutionary paths in growing populations with applications to multidrug resistance*
  (Invited) Harvard biomathematics initiative, March 2019

- *Competing paths over fitness valleys in growing populations*
  Conference: "Stochastic models of evolving populations: from bacteria to cancer", July 2018

- *Competing paths over fitness valleys in growing populations* (poster)
  Summer School: "Mathematical perspectives in the biology and therapeutics of cancer", July 2018

- *Competing paths over fitness valleys in growing populations*
  Conference: "Modelling Diversity in Cancer and Virus Evolution", May 2018

- *Universal asymptotic clone size distribution for general population growth*
  Spring school: "Probability in mathematics and physics", March 2017

- *Randomly initiated population models*
  Theory Club, School of Physics, Edinburgh, February 2017

- *Universal asymptotic clone size distribution for general population growth*
  Summer school: "Levy processes", August 2016.

- *Universal asymptotic clone size distribution for general population growth*
  Edinburgh physics seminar, May 2016

- *Introduction to regularly varying functions*
  Edinburgh probability working seminar, April 2016

- *Generalised Luria-Delbrück models*
  Program for Evolutionary Dynamics seminar, Harvard, May 2015

TEACHING EXPERIENCE

University of Edinburgh

Topics in mathematical biology (guest lecture)	2022/2023
Introduction to statistics (IGC PhD training)	2021/2022
Fourier analysis and statistics Maths in action: stochastic models in biology (included 1 lecture)	2017/2018
Fourier analysis and statistics Probability Probability with applications Stochastic modelling Applied probability (graduate level)	2016/2017
Introduction to linear algebra Maths in action: computational statistics Mathematics for physics 2	2015/2016
Mathematics for physics 1 Complex analysis (included 1 lecture)	2014/2015

SUPERVISION

University of Edinburgh

Xell Brunet Guasch (PhD Mathematics): secondary supervisor	2022-present
Jo Mattocks (PhD Human Genetics): secondary supervisor	2022-present
Jan Verburg (PhD Human Genetics): secondary supervisor	2022-present

LEADERSHIP EXPERIENCES

University of Edinburgh Mathematics Society   Edinburgh, Scotland
President   2012/2013

References available on request.