

Marc J. Williams, PhD

Computational Oncology, MSKCC
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Employment

- Postdoctoral Researcher**, Memorial Sloan Kettering Cancer Center, New York *Oct 2019–Present*
Supervisor: Prof. Sohrab Shah
- Postdoctoral Researcher**, Barts Cancer Institute, London *Mar 2019–Oct 2019*
Supervisor: Prof. Trevor Graham
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Education

- Academic Visitor**, Memorial Sloan Kettering Cancer Center, NYC *Feb 2019–May 2019*
Funded by a CRUK travel award.
- PhD**, University College London *Oct 2014–Feb 2019*
Computational biology, cancer evolution and genomics.
Supervisors: Prof. Trevor Graham & Prof. Chris Barnes
- MRes, Modelling Biological Complexity**, University College London, Distinction *Sep 2013–Sep 2014*
- MPhys, Physics**, University of Manchester, 1st Class *Sep 2008–Jun 2012*
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Awards and honors

- Award for Scientific Excellence** *2024*
Computational Oncology, Memorial Sloan Kettering Cancer Center
- K99/R00 NCI Pathway to Independence Award** (K99CA256508) *2021-2024*
Amount: \$189,669
- Society Scholar Prize** *2023*
The Society of Memorial Sloan Kettering
- Award for Scientific Excellence** *2022*
Computational Oncology, Memorial Sloan Kettering Cancer Center
- Cancer Research UK Travel Fellowship** *2019*
Funded a visit to Prof. Sohrab Shah's lab in Memorial Sloan Kettering for 3 months
Amount: £9,320
- Summer student research placement grant** *2018*
Funds to cover a summer placement for an undergraduate student via the London interdisciplinary doctoral programme (LIDO)
Amount: £2,500

Publications

* denotes co-first author, # denotes co-corresponding.

Articles with Major Contributions

- **Marc J Williams**#, Ignacio Vazquez-Garcia, Grittney Tam, Michelle Wu, Nancy Varice, Eliyahu Havasov, Hongyu Shi, Duaa H Al-Rawi, Gryte Satas, Hannah J Lees *et al.* Tracking clonal evolution during treatment in ovarian cancer using cell-free DNA. **Nature**, 2025.
- **Marc J Williams***, Michael UJ Oliphant*, Vinci Au*, Cathy Liu, Caroline Baril, Ciara O’Flanagan, Daniel Lai, Sean Beatty, Michael Van Vliet, Jacky CH Yiu *et al.* Luminal breast epithelial cells of BRCA1 or BRCA2 mutation carriers and noncarriers harbor common breast cancer copy number alterations. **Nature Genetics**, 2024.
- Tyler Funnell*, Ciara H O’Flanagan*, **Marc J Williams***#, Andrew McPherson, Steven McKinney, Farhia Kabeer, Hakwoo Lee, Sohrab Salehi, Ignacio Vazquez-Garcia, Hongyu Shi *et al.* Single-cell genomic variation induced by mutational processes in cancer. **Nature**, 2022.
- **Marc J Williams**#, Luiz Zapata, Benjamin Werner, Chris Barnes, Andrea Sottoriva Trevor A Graham. Measuring the distribution of fitness effects in somatic evolution by combining clonal dynamics with dN/dS ratios. **eLife**, 2020.
- **Marc J Williams**, Benjamin Werner, Timon Heide, Christina Curtis, Chris P Barnes, Andrea Sottoriva Trevor A Graham. Quantification of subclonal selection in cancer from bulk sequencing data. **Nature Genetics**, 2018.
- **Marc J Williams***, Benjamin Werner*, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Identification of neutral tumor evolution across cancer types. **Nature Genetics**, 2016.

Co-authored Articles

- Andrew McPherson, Ignacio Vazquez-Garcia, Matthew A Myers, Duaa H Al-Rawi, Matthew Zatzman, Adam C Weiner, Samuel Freeman, Neeman Mohibullah, Gryte Satas, **Marc J Williams** *et al.* Ongoing genome doubling shapes evolvability and immunity in ovarian cancer. **Nature**, 2025.
- Adam C Weiner, **Marc J Williams**, Hongyu Shi, Ignacio Vazquez-Garcia, Sohrab Salehi, Nicole Rusk, Samuel Aparicio, Sohrab P Shah Andrew McPherson. Inferring replication timing and proliferation dynamics from single-cell DNA sequencing data. **Nature Communications**, 15(1):8512, 2024.
- Alice Antonello, Riccardo Bergamin, Nicola Calonaci, Jacob Househam, Salvatore Milite, **Marc J Williams**, Fabio Anselmi, Alberto d’Onofrio, Vasavi Sundaram, Alona Sosinsky *et al.* Computational validation of clonal and subclonal copy number alterations from bulk tumor sequencing using CNAqc. **Genome Biology**, 25(1):1–40, 2024.
- Hongyu Shi, **Marc J Williams**, Gryte Satas, Adam C Weiner, Andrew McPherson Sohrab P Shah. Allele-specific transcriptional effects of subclonal copy number alterations enable genotype-phenotype mapping in cancer cells. **Nature Communications**, 15(1):2482, 2024.
- Farhia Kabeer, Hoa Tran, Mirela Andronescu, Gurdeep Singh, Hakwoo Lee, Sohrab Salehi, Beixi Wang, Justina Biele, Jazmine Brimhall, David Gee, ..., **Marc J Williams** *et al.* Single-cell decoding of drug induced transcriptomic reprogramming in triple negative breast cancers. **Genome Biology**, 25(1):191, 2024.
- Sohrab Salehi, Fatemeh Dorri, Kevin Chern, Farhia Kabeer, Nicole Rusk, Tyler Funnell, **Marc J Williams**, Daniel Lai, Mirela Andronescu, Kieran R Campbell *et al.* Cancer phylogenetic tree inference at scale from 1000s of single cell genomes. **Peer Community Journal**, 3, 2023.

- Luis Zapata, Giulio Caravagna, **Marc J Williams**, Eszter Lakatos, Khalid AbdulJabbar, Benjamin Werner, Diego Chowell, Chela James, Lucie Gourmet, Salvatore Milite *et al.* Immune selection determines tumor antigenicity and influences response to checkpoint inhibitors. **Nature Genetics**, 55(3):451–460, 2023.
- Adam M Passman, Magnus J Haughey, Emanuela Carlotti, **Marc J Williams**, Bianca Cereser, Meng-Lay Lin, Shruthi Devkumar, Jonathan P Gabriel, Enrico Gringeri, Umberto Cillo *et al.* Hepatocytes undergo punctuated expansion dynamics from a periportal stem cell niche in normal human liver. **Journal of Hepatology**, 2023.
- Amir A Jazaeri, Rachel Grisham, Anne Knisely, Stefani Spranger, Dmitriy Zamarin, R Tyler Hillman, Barrett C Lawson, Kathleen H Burns, Sanghoon Lee, Shannon N Westin, **Marc J Williams** *et al.* Transforming ovarian cancer care by targeting minimal residual disease. **Med**, 4(11):755–760, 2023.
- Ignacio Vazquez-Garcia, Florian Uhlig, Nicholas Ceglia, Jamie LP Lim, Michelle Wu, Neeman Mohibullah, Juliana Niyazov, Arvin Eric B Ruiz, Kevin M Boehm, Viktoria Bojilova, Fong, Christopher J, Williams, Marc J *et al.* Ovarian cancer mutational processes drive site-specific immune evasion. **Nature**, 2022.
- Sohrab Salehi, Farhia Kabeer, Nicholas Ceglia, Mirela Andronescu, **Marc J Williams**, Kieran R Campbell, Tehmina Masud, Beixi Wang, Justina Biele, Jazmine Brimhall *et al.* Clonal fitness inferred from time-series modelling of single-cell cancer genomes. **Nature**, 2021.
- Eszter Lakatos, **Marc J Williams**, Ryan O Schenck, William CH Cross, Jacob Househam, Benjamin Werner, Chandler Gatenbee, Mark Robertson-Tessi, Chris P Barnes, Alexander RA Anderson *et al.* Evolutionary dynamics of neoantigens in growing tumours. **Nature Genetics**, 52(10):1057–1066, 2020.
- Giulio Caravagna, Timon Heide, **Marc J Williams**, Luis Zapata, Daniel Nichol, Ketevan Chkhaidze, William Cross, George D Cresswell, Benjamin Werner, Ahmet Acar *et al.* Subclonal reconstruction of tumors by using machine learning and population genetics. **Nature Genetics**, 52(9):898–907, 2020.
- Benjamin Werner, Jack Case, **Marc J Williams**, Ketevan Chkhaidze, Daniel Temko, Javier Fernandez-Mateos, George D Cresswell, Daniel Nichol, William Cross, Inmaculada Spiteri *et al.* Measuring single cell divisions in human tissues from multi-region sequencing data. **Nature communications**, 11(1):1–9, 2020.
- Inês Sequeira, Mamunur Rashid, Inês M Tomá, **Marc J Williams**, Trevor A Graham, David J Adams, Alessandra Vigilante Fiona M Watt. Genomic landscape and clonal architecture of mouse oral squamous cell carcinomas dictate tumour ecology. **Nature communications**, 11(1):1–13, 2020.
- Emily A Saunderson, Ann-Marie Baker, **Marc J Williams**, Kit Curtius, J Louise Jones, Trevor A Graham Gabriella Ficiz. A novel use of random priming-based single-strand library preparation for whole genome sequencing of formalin-fixed paraffin-embedded tissue samples. **NAR genomics and bioinformatics**, 2(1):lqz017, 2020.
- Ketevan Chkhaidze, Timon Heide, Benjamin Werner, **Marc J Williams**, Weini Huang, Giulio Caravagna, Trevor A Graham Andrea Sottoriva. Spatially constrained tumour growth affects the patterns of clonal selection and neutral drift in cancer genomic data. **Plos Computational Biology**, 2019.
- Ann-Marie Baker, Calum Gabbutt, **Marc J Williams**, Biancastella Cereser, Noor Jawad, Manuel Rodriguez-Justo, Marnix Jansen, Chris P Barnes, Benjamin D Simons, Stuart AC McDonald *et al.* Crypt fusion as a homeostatic mechanism in the human colon. **Gut**, 2019.
- Sukaina Rashid, Marta O Freitas, Danilo Cucchi, Gemma Bridge, Zhi Yao, Laura Gay, **Marc J Williams**, Jun Wang, Nirosha Suraweera, Andrew Silver *et al.* MLH1 deficiency leads to deregulated

mitochondrial metabolism. **Cell death & disease**, 10(11):1–11, 2019.

- Daniel Temko, Inge C Van Gool, Emily Rayner, Mark Glaire, Seiko Makino, Matthew Brown, Laura Chegwidan, Claire Palles, Jeroen Depreeuw, Andrew Beggs, Chaido Stathopoulou, John Mason, Ann-Marie Baker, **Marc J Williams** *et al.* Somatic POLE exonuclease domain mutations are early events in sporadic endometrial and colorectal carcinogenesis, determining driver mutational landscape, clonal neoantigen burden and immune response. **The Journal of pathology**, 2018.
- Ann-Marie Baker, William Cross, Kit Curtius, Ibrahim Al Bakir, Chang-Ho Ryan Choi, Hayley Louise Davis, Daniel Temko, Sujata Biswas, Pierre Martinez, **Marc J Williams** *et al.* Evolutionary history of human colitis-associated colorectal cancer. **Gut**, 2018.

Preprints

- William Cross, Maximilian Mossner, Salpie Nowinski, George Cresswell, Abhirup Banerjee, **Marc J Williams**, Laura Gay, Ann-Marie Baker, Christopher Kimberley, Hayley Davis *et al.* Stabilising selection causes grossly altered but stable karyotypes in metastatic colorectal cancer. **bioRxiv**, 2020.

Reviews & Commentaries

- **Marc J Williams**, Andrea Sottoriva Trevor A Graham. Measuring Clonal Evolution in Cancer with Genomics. **Annual Review of Genomics and Human Genetics**, 20, 2019.
- **Marc J Williams**, Benjamin Werner, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Reply: Is the evolution of tumors Darwinian or non-Darwinian?. **National Science Review**, 2018.
- Benjamin Werner, **Marc J Williams**, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Reply to ‘Currently available bulk sequencing data do not necessarily support a model of neutral tumor evolution’. **Nature Genetics**, 2018.
- **Marc J Williams**, Benjamin Werner, Timon Heide, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Reply to ‘Revisiting signatures of neutral tumor evolution in the light of complexity of cancer genomic data’. **Nature Genetics**, 2018.
- Timon Heide, Luis Zapata, **Marc J Williams**, Benjamin Werner, Giulio Caravagna, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Reply to ‘Neutral tumor evolution?’’. **Nature Genetics**, 50(12):1633, 2018.
- **Marc J Williams**, Benjamin Werner, Chris P Barnes, Trevor A Graham Andrea Sottoriva. Reply: Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures.. **Nature Genetics**, 49(9):1289, 2017.
- **Marc J Williams**, Benjamin Werner, Trevor A Graham Andrea Sottoriva. Functional versus non-functional intratumor heterogeneity in cancer. **Molecular & Cellular Oncology**, 3(4):e1162897, 2016.

Talks and Presentations

Conference Talks

- Computational Cancer Biology workshop Bertinoro, September 2024
- Mutations in time and space, Edinburgh, April 2024
- Breakthrough Cancer Annual Summit, Kiawah, November 2023
- Computational Cancer Biology workshop Bertinoro, September 2022
- CRUK City of London Centre Cancer Evolution Symposium, September 2021
- Centers for Excellence in Genomic Science Annual Meeting, September 2021

- Mathematical Models in Ecology and Evolution, Lyon, July 2019 (*Invited*)
- CRUK City of London Centre Symposium February 2019 (*Invited*)
- The Cancer Mosaic, Traits, Strategies and Adaptations, Montpellier, August 2018
- Mathematical perspectives in the biology and therapeutics of cancer, Marseille, July 2018 (*Invited*)
- The International Society for Evolution, Ecology and Cancer, Arizona, November 2017 (*Flash talk*)
- Mathematical Models in Ecology and Evolution, London, July 2017 (*Invited*)
- London Julia Meetup, December 2016 (*Invited*)
- European Conference in Mathematical and Theoretical Biology, Nottingham, July 2016
- Quantitative Genomics, London, June 2016
- European Society of Molecular and Functional Imaging in Radiology, Utrecht, February 2016
- Cancer Evolution Through Space And Time, Plon, Germany, September 2015

Invited Seminars

- Somatic Mosaicism Across Human Tissues (SMaHT) Network, December 2024
- New York Genome Centre, January 2020
- UCL cancer institute, University College London, July 2018
- Genetics Institute, University College London, June 2018
- Department of Genetics and Evolution, University College London, May 2018
- Department of Mathematics, Queen Mary University of London, Complex systems department seminar, March 2018
- Topology and genomics working group, QMUL, London, February 2018
- Barts Cancer Institute, London, April 2017
- Department of Medicine, Sheffield, March 2017

Peer Review

Journals: Nature, Nature Ecology and Evolution, Nature Communications, Annals of Oncology, Giga-Science, PLoS Computational Biology, BMC Evolutionary Biology, Nature Biotechnology