

Marc J. Williams

Computational Oncology, MSKCC
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Current employment

10/2019– **Postdoctoral Research Fellow**, MSKCC, New York.
Present Postdoc with Prof. Sohrab Shah in the department of Computational Oncology at Memorial Sloan Kettering Cancer Center.

Research area: Drug resistance and evolution in ovarian and breast cancers using single-cell multiomics and liquid biopsies.

Supported by a “K99/R00 NCI Pathway to Independence Award for Outstanding Early Stage Postdoctoral Researchers”

Previous employment

10/2018– **Postdoctoral Research Associate**, *Barts Cancer Institute*, London.
10/2019 Postdoc in Prof. Trevor Graham’s lab at Barts Cancer Institute.

Education

02/2019– **Academic Visitor**, *Memorial Sloan Kettering Cancer Center*, NYC.
05/2019 Funded by a CRUK travel award.
10/2014– **PhD**, *University College London*.
10/2018 Computational biology, cancer evolution and genomics.
Supervisors: Prof. Trevor Graham & Prof. Chris Barnes
09/2013– **MRes, Modelling Biological Complexity**, *University College London*, Distinction.
09/2014
09/2008– **MPhys, Physics**, *University of Manchester*, 1st Class.
06/2012

Grants and funding

- o K99/R00 NCI Pathway to Independence Award for Outstanding Early Stage Postdoctoral Researchers (K99CA256508) **Amount:** \$948,618
- o Cancer Research UK postdoctoral travel fellowship to visit Prof. Sohrab Shah’s lab in Memorial Sloan Kettering for 3 months **Amount:** £9320
- o London interdisciplinary doctoral programme (LIDo) summer student research placement grant for summer 2018. Grant to fund a summer student to work on an 8 week project. **Amount:** £2500

Publications

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

Articles and preprints with major contributions

Marc J Williams#, Ignacio Vazquez-Garcia, Grittney Tam, Michelle Wu, Nancy Varice, Eliyahu Havasov, Hongyu Shi, Gryte Satas, Hannah J Lees, Jake Lee, et al. Tracking clonal evolution of drug resistance in ovarian cancer patients by exploiting structural variants in cfDNA. *bioRxiv*, pages 2024–08, 2024.

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*, pages 1–10, 2024.

Tyler Funnell*, Ciara H O’Flanagan*, **Marc J Williams*#**, Andrew McPherson, Steven McKinney, Farhia Kabeer, Hakwoo Lee, Sohrab Salehi, Ignacio Vázquez-García, Hongyu Shi, et al. Single-cell genomic variation induced by mutational processes in cancer. *Nature*, pages 1–10, 2022.

Marc J Williams#, Luiz Zapata, Benjamin Werner, Chris Barnes, Andrea Sottoriva, and Trevor A Graham. Measuring the distribution of fitness effects in somatic evolution by combining clonal dynamics with *dn/ds* ratios. *eLife*, page 661264, 2020.

Marc J Williams, Benjamin Werner, Timon Heide, Christina Curtis, Chris P Barnes, Andrea Sottoriva, and Trevor A Graham. Quantification of subclonal selection in cancer from bulk sequencing data. *Nature Genetics*, page 1, 2018.

Marc J Williams*, Benjamin Werner*, Chris P Barnes, Trevor A Graham, and Andrea Sottoriva. Identification of neutral tumor evolution across cancer types. *Nature Genetics*, 2016.

Other Articles

Adam C Weiner, **Marc J Williams**, Hongyu Shi, Ignacio Vázquez-García, Sohrab Salehi, Nicole Rusk, Samuel Aparicio, Sohrab P Shah, and Andrew McPherson. Inferring replication timing and proliferation dynamics from single-cell DNA sequencing data. *Nature Communications*, 15(1):8512, 2024.

Hongyu Shi, **Marc J Williams**, Gryte Satas, Adam C Weiner, Andrew McPherson, and 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.

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.

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 Abdul-Jabbar, 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.

Ignacio Vázquez-García, Florian Uhritz, Nicholas Ceglia, Jamie LP Lim, Michelle Wu, Neeman Mohibullah, Juliana Niyazov, Arvin Eric B Ruiz, Kevin M Boehm, Viktoria Bojilova, **Marc J Williams** Fong, Christopher J, et al. Ovarian cancer mutational processes drive site-specific immune evasion. *Nature*, pages 1–9, 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*, pages 1–6, 2021.

Emily A Saunderson, Ann-Marie Baker, **Marc J Williams**, Kit Curtius, J Louise Jones, Trevor A Graham, and 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.

Inês Sequeira, Mamunur Rashid, Inês M Tomás, **Marc J Williams**, Trevor A Graham, David J Adams, Alessandra Vigilante, and Fiona M Watt. Genomic landscape and clonal architecture of mouse oral squamous cell carcinomas dictate tumour ecology. *Nature communications*, 11(1):1–13, 2020.

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.

Benjamin Werner, Jack Case, **Marc J Williams**, Ketevan Chkhaidze, Daniel Temko, Javier Fernández-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.

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.

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.

Katevan Chkhaidze, Timon Heide, Benjamin Werner, **Marc J Williams**, Weini Huang, Giulio Caravagna, Trevor A Graham, and 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*, pages gutjnl–2018, 2019.

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*, pages gutjnl–2018, 2018.

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.

Preprints

Andrew McPherson, Ignacio Vázquez-García, Matthew A Myers, Matthew Zatzman, Duaa Al-Rawi, Adam Weiner, Samuel Freeman, Neeman Mohibullah, Gryte Satas, **Marc J Williams**, et al. Ongoing genome doubling promotes evolvability and immune dysregulation in ovarian cancer. *bioRxiv*, pages 2024–07, 2024.

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, and Trevor A Graham. Measuring clonal evolution in cancer with genomics. *Annual Review of Genomics and Human Genetics*, 20, 2019.

Timon Heide, Luis Zapata, **Marc J Williams**, Benjamin Werner, Giulio Caravagna, Chris P Barnes, Trevor A Graham, and Andrea Sottoriva. Reply to 'neutral tumor evolution?'. *Nature genetics*, 50(12):1633, 2018.

Marc J Williams, Benjamin Werner, Chris P Barnes, Trevor A Graham, and Andrea Sottoriva. Reply: Is the evolution of tumors darwinian or non-darwinian? *National Science Review*, 2018.

Marc J Williams, Benjamin Werner, Timon Heide, Chris P Barnes, Trevor A Graham, and Andrea Sottoriva. Reply to 'revisiting signatures of neutral tumor evolution in the light of complexity of cancer genomic data'. *Nature genetics*, page 1, 2018.

Benjamin Werner, **Marc J Williams**, Chris P Barnes, Trevor A Graham, and Andrea Sottoriva. Reply to 'currently available bulk sequencing data do not necessarily support a model of neutral tumor evolution'. *Nature Genetics*, page 1, 2018.

Marc J Williams, Benjamin Werner, Chris P Barnes, Trevor A Graham, and 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, and 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, Plön, Germany, September 2015

Invited seminars

- Somatic Mosaicism Across Human Tissues (SMaHT) Network, December 2024 (Online)
- 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

Workshops

- Quantification and modeling of spatial structures in colorectal cancer, Adelaide, November 2015
- Integrated Mathematical Oncology Workshop, Tampa Florida, November 2014

Peer Review

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