

Marc Williams

Computational biologist

MSKCC
1275 York Avenue, New York
USA

+447865399863

✉ marcjwilliams1@gmail.com

📄 <https://marcjwilliams1.github.io>

🐦 [marcjwills_](#)

🌐 [marcjwilliams1](#)

Current employment

- 10/2019– **Postdoctoral Research Fellow**, *MSKCC*, New York.
Present Postdoc with Prof. Sohrab Shah at Memorial Sloan Kettering Cancer Center

Previous employment

- 10/2018– **Postdoctoral Research Associate**, *QMUL*, London.
10/2019 Postdoc with Prof. Trevor Graham at Barts Cancer Institute
10/2017– **Research Assistant**, *QMUL*, London.
10/2018 Employed as research associate with Prof. Trevor Graham at Barts Cancer Institute during final year of PhD

Education

- 02/2019– **Academic Visitor**, *Memorial Sloan Kettering Cancer Center*, NYC.
05/2019 3 Month research placement funded via CRUK postdoctoral travel award in Prof. Sohrab Shah's laboratory
10/2014– **PhD**, *University College London*, London.
10/2018 Title: Methods and practice of detecting selection in human cancers
Supervisors: Prof. Trevor Graham & Dr. Chris Barnes
09/2013– **MRes, Modelling Biological Complexity**, *University College London*, London,
09/2014 Distinction.
Research projects in Computer Vision, Evolutionary Biology, Systems Biology and Evolutionary Cancer Biology
09/2008– **MPhys, Physics**, *University of Manchester*, Manchester, 1st Class.
06/2012 Final year project was developing experimental and computational methods to accurately quantify radioactivity of isotopes used in PET imaging (conducted at the Wolfson Medical Imaging Centre.)

Areas of expertise

- Bioinformatics Analysis of high throughput cancer genomics data including whole genome sequencing, whole exome sequencing and targeted sequencing data.
- Mathematical modelling Mathematical modelling using stochastic processes, differential equations and simulation based methods, particularly with applications to evolutionary systems.

Statistics Regression, survival analysis, hypothesis testing, Markov Chain Monte Carlo methods for Bayesian inference, Approximate Bayesian Computation methods for likelihood free Bayesian inference.

Grants and funding

- Cancer Research UK postdoctoral travel fellowship to visit Prof. Sohrab Shah's lab in Memorial Sloan Kettering for 3 months **Amount:** £9320
- Travel grant to attend *Evolution 2018 conference* from Life Sciences Initiative, QMUL **Amount:** £500
- 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
- Travel grant to attend *European Conference in Mathematical and Theoretical Biology* from University College London. **Amount:** £250
- Travel grant to attend *Integrated Mathematical Oncology Workshop, Tampa Florida* from Moffit Cancer Centre. **Amount:** £1000

Student supervision

- Abdur Sheikh (Undergraduate Student, 2018) *Spatial modelling of colon cancers*
- Callum Gabutt (Masters Student, 2018) *Stem cell dynamics in the colonic epithelium*
- Laura Tomas (Visiting PhD student, 2019) *Clonality of colorectal cancer driver mutations*

Teaching

- 2015-2016 **Tutor**, *Introduction to R Course*, UCL, London.
Taught "Introduction to R" over a semester to first year undergraduate students in biology. Held weekly tutorials with 10-15 students.
- 2014-2016 **Tutor**, *SysMIC*, UCL, London.
Demonstrated on the SysMIC Quantitative Skills for Bioscientists course for bioscience PhD students. Supported students with assignments in R, Matlab and bash.
- 2012-2013 **Classroom assistant**, Technical School, Nova Gorica, Slovenia.
Delivered lessons in English, Mathematics and Physics.

Computing

Programming languages R, Julia, Git and Bash (daily) Mathematica (often) Python, Matlab, C++, Java (occasionally)

Operating systems Windows, macOS, Linux and Linux based high performance clusters, cloud computing infrastructure such as Microsoft Azure and Amazon Web Services

Writing and design L^AT_EX, Markdown, Microsoft Office Suite, Adobe Illustrator

Publications

Articles with Major Contributions

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.

Preprints

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. *BioRxiv*, 2019.

Giulio Caravagna, Timon Heide, **Marc J Williams**, Luis Zapata, Daniel Nichol, Ketevan Chkhaidze, William H Cross, George D Cresswell, Benjamin Werner, Ahmet Acar, et al. Model-based tumor subclonal reconstruction. *bioRxiv*, 2019.

Benjamin Werner, Jack Case, **Marc J Williams**, Kate Chkhaidze, Daniel Temko, Javier Fernandez-Mateos, George D Cresswell, Daniel Nichol, William Cross, Inmaculada Spiteri, et al. Measuring single cell divisions in human cancers from multi-region sequencing data. *BioRxiv*, 2019.

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. *bioRxiv*, 2019.

Other Articles

Daniel Temko, Inge C Van Gool, Emily Rayner, Mark Glaire, Seiko Makino, Matthew Brown, Laura Chegwiddden, 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*, pages gutjnl–2018, 2018.

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.

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.

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

- 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

Seminars

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