

Alan O'Callaghan

CURRICULUM VITAE

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Skills

- Programming: R, C++, Ruby, Java, Python.
- Statistics: Bayesian modelling, GLM, survival analysis, high dimensional statistics.
- Computing: Linux/Unix, \LaTeX , git, make, snakemake, unit testing, continuous integration.
- Web: HTML/CSS, JS, PHP, htmlwidgets (R).

Education

Ph.D., Biomedical data science

MRC HUMAN GENETICS UNIT, UNIVERSITY OF EDINBURGH

2018 – 2022

- Statistical methods for, and applied statistical analysis of, single cell RNAseq with complex experimental designs.
- Implementation of scalable Bayesian inference (adaptive Metropolis within Gibbs, divide and conquer MCMC).
- Assisting other students and contributing to research and computing environment in the institute.

M.Sc., Bioinformatics and computational genomics

QUEEN'S UNIVERSITY BELFAST

Distinction
2014 – 2015

- Dissertation: Java-based eye-tracking and image analysis of histopathology whole slide images.
- Lectures: programming, image analysis, statistical learning techniques.
- Programming projects: Implementation of alignment, clustering, linear regression and cross-validation algorithms in R; cell detection, Ki67 quantification and image segmentation in Java.

B.Sc. (honours), biopharmaceutical chemistry

NATIONAL UNIVERSITY OF IRELAND, GALWAY

2.1
2008 – 2013

- Research Project: Structure elucidation and structure-activity relationship of bioactive marine compound.
- Lectures: (bio)chemistry, toxicology, pharmacology, molecular modelling, drug discovery and design.

Experience

Research software engineer

CENTRE FOR GENOMICS AND EXPERIMENTAL MEDICINE, UNIVERSITY OF EDINBURGH

April 2023 – present

- Software development associated with QuPath, an open source digital pathology image analysis tool.
- Implementing and maintaining machine learning pipelines using Deep Java Library.
- Building and packaging native library dependencies for the QuPath project.
- Developing and delivering training materials for QuPath users.
- Facilitate research using QuPath by providing technical support and guidance, and leading research when time permits.
- Developing and maintaining documentation and continuous integration pipelines for associated projects.

Postdoctoral research associate

MRC BIOSTATISTICS UNIT, UNIVERSITY OF CAMBRIDGE

2022 – April 2023

- Computational optimisation of Bayesian models for the identification of eQTLs from RNAseq data.
- Computational analysis of RNAseq data using gene signatures.

Research assistant

UNIVERSITY OF EDINBURGH

April 2021 – September 2021

- Developing a Carpentries course in high-dimensional statistics.
- Certification as a trained Carpentries instructor.
- Acted as teacher and helper in Carpentries courses in high-dimensional statistics, R, python and machine learning.

Bioinformatician

FIOS GENOMICS

October 2015 – August 2018

- Communicating regularly with clients to plan projects and explain results.
- Exploratory and statistical analysis for academics and commercial clients.
- Statistical analysis & visualisations for client publications & commercial research projects.
- Developer, author & maintainer of proprietary R packages.
- Minor system administration tasks.

Software

R packages

Package	Platform	Role	Average monthly downloads
scater	Bioconductor	Maintainer	3549
contrast	CRAN	Maintainer	1235
densvis	Bioconductor	Maintainer	1073
iheatmapr	CRAN	Maintainer	623
bayefdr	CRAN	Maintainer	348
snifter	Bioconductor	Maintainer	102
BASiCStan	Bioconductor	Maintainer	63
heatmaply	CRAN	Contributor	8365
BASiCS	Bioconductor	Contributor	123

StackExchange

StackOverflow reputation: [3,038](#)

CrossValidated reputation: [1,226](#)

Publications

- **O'Callaghan, A.**, Vallejos, C. A., *Scalable Inference of Transcriptional Variability with Basics*. 2025. doi: [10.2139/ssrn.5113761](#). (Visited on 02/06/2025)
- Goldsborough, T., Philps, B., **O'Callaghan, A.**, Inglis, F., Leplat, L., Filby, A., Bilen, H., Bankhead, P., *InstanSeg: An Embedding-Based Instance Segmentation Algorithm Optimized for Accurate, Efficient and Portable Cell Segmentation*. Aug. 2024. doi: [10.48550/arXiv.2408.15954](#). arXiv: [2408.15954 \[cs\]](#). (Visited on 02/06/2025)
- Goldsborough, T., **O'Callaghan, A.**, Inglis, F., Leplat, L., Filby, A., Bilen, H., Bankhead, P., *A Novel Channel Invariant Architecture for the Segmentation of Cells and Nuclei in Multiplexed Images Using InstanSeg*. Sept. 2024. doi: [10.1101/2024.09.04.611150](#). (Visited on 02/06/2025)

- Aquilina, M., Wu, N. J., Kwan, K., Bušić, F., Dodd, J., Nicolás-Sáenz, L., **O'Callaghan, A.**, Bankhead, P., Dunn, K. E., *GelGenie: An AI-powered Framework for Gel Electrophoresis Image Analysis*. Sept. 2024. doi: [10.1101/2024.09.06.611479](https://doi.org/10.1101/2024.09.06.611479). (Visited on 02/06/2025)
- Kaczmarzyk, J. R., **O'Callaghan, A.**, Inglis, F., Gat, S., Kurc, T., Gupta, R., Bremer, E., Bankhead, P., Saltz, J. H., "Open and Reusable Deep Learning for Pathology with WSInfer and QuPath". In: *npj Precision Oncology* 8.1 (Jan. 2024), p. 9. ISSN: 2397-768X. doi: [10.1038/s41698-024-00499-9](https://doi.org/10.1038/s41698-024-00499-9). (Visited on 02/06/2025)
- **O'Callaghan, A.**, Eling, N., Marioni, J. C., Vallejos, C. A., "BASiCS Workflow: A Step-by-Step Analysis of Expression Variability Using Single Cell RNA Sequencing Data". In: *F1000Research* 11 (Jan. 2022), p. 59. ISSN: 2046-1402. doi: [10.12688/f1000research.74416.1](https://doi.org/10.12688/f1000research.74416.1)
- Harris, B. T., Rajasekaran, V., Blackmur, J. P., **O'Callaghan, A.**, Donnelly, K., Timofeeva, M., Vaughan-Shaw, P. G., Din, F. V. N., Dunlop, M. G., Farrington, S. M., *Transcriptional Dynamics of Colorectal Cancer Risk Associated Variation at 11q23.1 Are Correlated with Tuft Cell Abundance and Marker Expression in Silico*. Preprint. Bioinformatics, Mar. 2022. doi: [10.1101/2022.03.29.485182](https://doi.org/10.1101/2022.03.29.485182)
- Reijns, M. A. M., Thompson, L., Acosta, J. C., Black, H. A., Sanchez-Luque, F. J., Diamond, A., Parry, D. A., Daniels, A., O'Shea, M., Uggenti, C., Sanchez, M. C., **O'Callaghan, A.**, McNab, M. L. L., Adamowicz, M., Friman, E. T., Hurd, T., Jarman, E. J., Chee, F. L. M., Rainger, J. K., Walker, M., Drake, C., Longman, D., Mordstein, C., Warlow, S. J., McKay, S., Slater, L., Ansari, M., Tomlinson, I. P. M., Moore, D., Wilkinson, N., Shepherd, J., Templeton, K., Johannessen, I., Tait-Burkard, C., Haas, J. G., Gilbert, N., Adams, I. R., Jackson, A. P., "A Sensitive and Affordable Multiplex RT-qPCR Assay for SARS-CoV-2 Detection". In: *PLOS Biology* 18.12 (Dec. 2020). Ed. by Bill Sugden, e3001030. ISSN: 1545-7885. doi: [10.1371/journal.pbio.3001030](https://doi.org/10.1371/journal.pbio.3001030)
- Morgan, R., Keen, J., Halligan, D., **O'Callaghan, A.**, Andrew, R., Livingstone, D., Abernethie, A., Maltese, G., Walker, B., Hadoke, P., "Species-Specific Regulation of Angiogenesis by Glucocorticoids Reveals Contrasting Effects on Inflammatory and Angiogenic Pathways". In: *PLOS ONE* 13.2 (Feb. 2018). Ed. by Christina L Addison, e0192746. ISSN: 1932-6203. doi: [10.1371/journal.pone.0192746](https://doi.org/10.1371/journal.pone.0192746)

Teaching

Presenter/helper

CARPENTRIES WORKSHOPS

Online, 2021 – ongoing

- Data carpentries R for social sciences (presenter)
- Python Intro for Libraries (helper)
- Statistics with R (helper)
- Data analysis and visualisation with Python for Genomics (helper)

IGMM statistical seminar series

LECTURES

Online, 2020

- Exploratory data analysis
- Experimental design, hypothesis testing, statistical power

Applied analysis workshop for single cell RNAseq

ONE DAY WORKSHOP

IGMM, 2020

- Exploratory analysis
- Normalisation
- Feature selection
- Differential expression analysis
- Clustering

Teaching materials

AUTHOR/MAINTAINER

2021 – ongoing

- [High dimensional statistics with R](#)
- [Orchestrating single cell analysis, multisample chapter](#)

Conferences and meetings

Images to Knowledge

PRESENTATION

Milan, 2024

QuPath for Python Programmers

European Mathematical Genetics Meeting

PRESENTATION

Cambridge, 2022

Optimising eQTL discovery with BaseQTL using a screening approach

IGMM internal meetings

POSTER

Edinburgh, 2019 – 2020

Scalable Bayesian analysis of single cell RNAseq

Bayesian analysis of multi-donor scRNAseq data (2nd prize)

UoE Centre for Statistics conference

POSTER

Edinburgh, June 2019

Scalable Bayesian analysis of single cell RNAseq

Quantitative Genomics

PRESENTATION

Francis Crick Institute, June 2019

Scalable Bayesian analysis of single cell RNAseq

Genomic Medicine

POSTER

Edinburgh, May 2019

Scalable Bayesian analysis of single cell RNAseq

Edinbr (R user group)

PRESENTATION

Edinburgh, March 2019

Building interactive modules using htmlwidgets

Edinburgh Bioinformatics

PRESENTATION

Edinburgh, November 2018

Interactive data visualisation using R and plotly.

Extracurricular

Society committees

EDINBURGH/GALWAY

Various

- **IGMM Postgraduate Society (Edinburgh):** Organising student events, advocating for improvements in student working conditions and well-being.
- **IGMM social committee (Edinburgh):** Organising social events for students/postdocs/staff. Editor of noteworthy student Christmas movie, 2018.
- **Lotus society (Galway):** Organising yoga classes and events for students/postdocs/staff.

Honors & Awards

- Best savoury food (mattar paneer), IGMM Christmas Party, 2018
- School of Chemistry Medal in Molecular Modelling and Drug Design, NUI Galway, 2011
- Entrance Scholarship, NUI Galway, 2008