Áine Niamh O'Toole

Curriculum Vitae

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Profile

My work includes developing bioinformatic software for the genomic epidemiology of infectious disease, particularly RNA viruses. I am a member of the ARTIC Network and a post-doctoral researcher at the University of Edinburgh in the Rambaut Lab. I carried out my PhD at the University of Edinburgh as part of the Wellcome Trust PhD programme 'Hosts, Pathogens and Global Health'. I feel strongly about the importance of genomic and bioinformatic capacity building and have regularly engaged in workshops with the ARTIC Network and the Polio Sequencing Consortium.

Education

2017–2021 **PhD**, *Wellcome Trust PhD Programme in Hosts, Pathogens & Global Health*.
Rambaut Lab, University of Edinburgh
The Genomic Epidemiology of SARS-CoV-2: From outbreak investigation to national and international surveillance efforts

2016–2017 **MSc by Research**, *Wellcome Trust Hosts, Pathogens & Global Health*, University of Edinburgh.
Woolhouse Lab *(Novel bat viruses in Viet Nam found in bat metagenomes)*,
Spence Lab *(Early metabolomic response to malaria in humans)*,
Little Lab *(Life history plasticity in response to dietary restriction)*
Distinction

2014–2016 **MSc by Research**, *Genetics (Molecular Evolution)*, *Analysis of evolutionary rates of primate duplicable and singleton genes*.
McLysaght Lab, Trinity College Dublin

2010–2014 **BA Natural Sciences (Mod Genetics)**, Trinity College Dublin, *Honours project: Identification of causal mutations in patients with hereditary retinal disease using Illumina and Sanger sequencing*.
Farrar Lab, Trinity College Dublin
First class honours

Employment

2021–Present **Post-doctoral researcher**, *Rambaut Lab, ARTIC Network & Polio Sequencing Consortium*, *Work on virus phylogenetics, bioinformatic tools for genomics capacity building for virus outbreak surveillance*.
University of Edinburgh

2021–Present	**Scientific consultant**, *Astra-Zeneca*, *Performed a large-scale analysis of lineage information contained in the spike protein of SARS-CoV-2 and developed a wrapper tool Hedgehog that can be used to assign lineage sets to spike nucleotide sequences.* Contract through the University of Edinburgh
2020	**Research associate**, *COVID-19 Genomics UK Consortium*, *Worked as part of the COG-UK phylogenetics core and developed bioinformatic software tools such as civet and pangolin.* University of Edinburgh
2019	**Lecturing**, *Plant.ID Intensive Phylogenetics Course*, *Developed materials and lectured on a phylogenetics course for PhD students in the Plant.ID network.* University of Oslo, Norway
2019	**Demonstrator**, *Evolutionary Biology Field Course*, *Taught on a field sequencing and bioinformatics workshop.* University of Edinbugh, Urra, Spain
2018	**Demonstrator**, *Developed materials for and taught on a real-time sequencing, bioinformatics and epidemiology workshop.* West African Centre for Cell Biology of Infectious Pathogens, University of Ghana
2016–2021	**Demonstrator & Tutor**, *School of Biological Sciences*, *Teach a variety of coding, genomics and bioinformatics courses which are given to undergraduate and postgraduate students.* Biology Teaching Organisation, University of Edinburgh
2014–2016	**Laboratory demonstrator**, *Undergraduate biology*, *Demonstrated various undergraduate biology courses.* Biology Teaching Centre, Trinity College Dublin
2013	**Research Assistant**, *Carried out RNASeq validation of Autism model rats.* Buxbaum Lab, The Mount Sinai Hospital, New York City, NY

First author publications

2017	**Áine O'Toole**, Lawrence Hurst & Aoife McLysaght. Duplicable genes are faster evolving. Molecular Biology and Evolution. doi: 10.1093/molbev/msx270
2021	**Áine O'Toole**, Verity Hill, et al. Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 using grinch, *Wellcome Open Resources*, doi: 10.21956/wellcomeopenres.18372.r43966
2021	**Áine O'Toole**, Emily Scher, et al. Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. *Virus Evolution*, doi: 10.1093/ve/veab064
2021	**Áine O'Toole**, Oliver Pybus et al. Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences. *bioRxiv*, doi: 10.1101/2021.08.10.455799
2021	**Áine O'Toole**, Verity Hill et al. Genomics-informed outbreak investigations of SARS-CoV-2 using civet. *medRxiv*, doi: 10.1101/2021.12.13.21267267

* Full list of publications at `https://www.researchgate.net/profile/Aine-Otoole`

Analytical skills

Languages Python, bash, HTML, CSS, Javascript (basic), $\mathbb{R}$

Theory Knowledge of evolutionary theory, particular emphasis on molecular evolution. A firm foundation in the fields of genomic epidemiology and virus evolution. Familiar with bioinformatic and phylogenetic methods. Fundamentals of statistical analysis.

Development Experience developing bioinformatic software, mainly in Python, and pipelines with Snakemake. Some experience with CI. Automated testing via GitHub actions. Trialling accuracy and speed using simulations (read simulations and reference-based simulations). All work has been open source and can be found on github @aineniamh.

Software Very comfortable managing and using command line tools. Experience analysing Illumina and long-read data, accounting for differences in error profile. Specific experience using a variety of basecalling (e.g. guppy, albacore), demultiplexing (e.g. Porechop, qcat, native-guppy demultiplexing), mapping and assembly tools (e.g. minimap2, miniasm, Canu, wtdgb2, Spades), quality-control tools (e.g. FastQC, MultiQC), alignment tools (e.g. MAFFT, MUSCLE), phylogenetic tree estimation software (e.g. IQTree, BEAST, FastTree, RaXML), metagenomic and taxonomic assignment tools (e.g. Kraken), various alignment tools, BaTS, Poretools, SAMtools

Practical LaTeX, GitHub, Adobe Illustrator, BioPython, ggplot2, Matplotlib

Laboratory experience

- Experience performing Illumina and Nanopore sample and library preparation.
- Experience implementing many standard laboratory protocols, such as DNA and RNA extraction, PCR, running poly-acrylamide and agarose gels.
- Experience loading and running a MinION.

Lecturing Experience

2021 **Edinburgh University**, *HPGH Phylogenetics Lectures*, Analysing SARS-CoV-2 Genomes, Lectures and practical tutorials.

2021 **Trinity College Dublin**, *Junior Sophistor Mathematical Genetics Guest Lecture*, SARS-CoV-2 genomic epidemiology.

2020 **NIH Islamabad, Pakistan**, *Poliovirus reference lab*, 2 weeks of Nanopore sequencing, bioinformatics and phylogenetics, Lectures and practical tutorials.

2020 **NIH Islamabad, Pakistan**, *Poliovirus reference lab*, 2 weeks of Nanopore sequencing, bioinformatics and phylogenetics, Lectures and practical tutorials.

2019-2021 **University of Edinburgh**, *Graduate development programme*, Imposter Syndrome, Lectures.

2019 **Plant-ID Network**, *Bayesian Phylogenetics*, 1 week, Lectures and practical tutorials.

2018 **West African Centre for Cell Biology of Infectious Pathogens, Ghana**, *ARTIC Network*, 1 week on real-time sequencing and analysis for acute viral outbreaks, Lectures and practical tutorials.

Invited Talks

2021-12	**CADDE Meeting**, *Cluster investigation and surveillance with civet*.
2021-11	**Fred Hutch Comp Bio Seminar Series**, *Genomic Epidemiology of SARS-CoV-2: From outbreak investigation to national and international surveillance efforts*.
2021-07	**ARTIC Network and CLIMB Big Data Workshop 2**, *Practical phylogenetics: lineages and variants*.
2021-06	**Microbial (Gen)omics Meeting Sanger Institute**, *Tools for tracking the spread of SARS-CoV-2*.
2021-04	**Edinburgh Disease Transmission Workshop**, *Tracking the spread of SARS-CoV-2 lineages of concern*.
2021-03	**COG-UK Showcase**, *Tracking the international spread of SARS-CoV-2 lineages of concern using grinch*.
2021-03	**BMJ Webinar**, *Tracking the international spread of SARS-CoV-2 lineages of concern*.
2021-02	**Cambridge Pathogen Dynamics Seminar**, *Tracking the international spread of SARS-CoV-2 lineages of concern*.
2021-02	**COG-UK Mutation Tools Seminar**, *Lineage of concern identification and tracking with grinch and polecat*.
2021-01	**CADDE Meeting**, *Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351 501Y-V2*.
2021-01	**ARTIC Network and CLIMB Big Data Workshop**, *Practical phylogenetics: lineages and variants*.
2020-12	**Plenary Lecture, American Society of Microbiology NGS**, *200,001: A Tree-Space Odyssey. Pandemic phylogenetics and reporting in 2020*.
2020-11	**Nanopore Community Meeting**, *SARS-CoV-2 outbreak investigation: from sample to response in a day*.
2020-10	**CZ BioHub**, *Tools for SARS-CoV-2 phylogenetics to inform public health*.
2020-10	**Genetical Society, Trinity College Dublin**, *SARS-CoV-2 molecular epidemiology*.
2020-09	**ESCMID Conference on Coronavirus Disease (ECCVID)**, *Panelist for Phylogenetic analysis and molecular epidemiology of SARS-CoV-2*.
2020-09	**ESCMID Conference on Coronavirus Disease (ECCVID)**, *SARS-CoV-2 diversity, clades and lineages*.
2020	**State Public Health Bioinformatics Network, USA**, *Tools for using genomic epidemiology to inform public health*.
2020	**SARS-CoV-2 Dynamics and Evolution**, *Genetic typing in an emerging pandemic as an epidemiological tool*.
2019	**ARTIC Network AGM, Cambridge**, *ARTIC-Accra: Workshop on real-time sequencing for viral outbreaks, Ghana*.

━━━━━ Workshops and Conferences

2019	**Manchester**, *Meeting of the Society of Molecular Biology and Evolution*, Poster Presentation.

2019   **Edinburgh**, *IONBru: Edinburgh MinION User Group Meeting*, Oral Presentation.

2019   **Hinxton**, *Applied Bioinformatics and Public Health Microbiology*.

2019   **Cambridge**, *ARTIC Annual Meeting*, Oral Presentation.

2019   **Edinburgh**, *Bayesian Inference and PyStan for Biologists, Workshop*.

2018   **Yokohama, Japan**, *Meeting of the Society of Molecular Biology and Evolution*, Poster Presentation.

2018   **Hinxton, Cambridge**, *Virus Genomics and Evolution*.

2018   **University of Glasgow**, *Annual meeting of Evolution and Ecology of Infectious Disease*.

2017   **Edinburgh Genomics**, *Linux and Workflows for Biologists Workshop*.

2017   **University of Lisbon**, *Virus Evolution and Molecular Epidemiology Workshop*, Poster Presentation, won best poster.

2017   **Centre for Immunity, Infection and Evolution**, *Annual Retreat*, Presentation.

2017   **University of Edinburgh**, *Edinburgh Infectious Diseases Annual Symposium*.

2017   **Moredun Institute, UofE**, *Metagenomics Workshop*, Workshop.

2017   **University of Glasgow**, *Next-Gen Bioinformatics User Group Meeting*.

2016   **Trinity College Dublin**, *Virtual Institute of Bioinformatics and Evolution in Ireland Conference*, Oral Presentation.

2014   **Edinburgh Genomics**, *Python for Biologists Workshop (Introductory & Advanced)*.

Funding and Awards

2020   **$20,000 Fast Grant Award**, Awarded by Patrick Collison. Fast Grants scheme to support SARS-CoV-2 research.

2019   **Best Poster Presentation Prize**, Institute of Evolutionary Biology Graduate Poster Symposium.

2019   **MBE Graduate Student Paper of the Year 2018, highly commended**, Society of Molecular Biology and Evolution 2019.

2017   **Best Poster Presentation Prize**, Virus Evolution and Molecular Epidemiology Workshop, Lisbon.

2016   **£119,290, Wellcome Trust Award**, four year duration, University of Edinburgh.

2013   **€50,000 (est.), Elected 'Scholar' of Trinity College Dublin**, a five-year scholarship, the benefits of which include tuition fees, evening meal, annual salary, accommodation on Trinity Campus.

2013   **Ronald A. Fisher prize in Genetics**, Trinity College Dublin.

2012   **€1,500, Bill Vincent American–Ireland Scholarship**, American–Ireland Fund. This scholarship sponsored me to travel to the U.S., where a paid position as a research assistant was organized in the Buxbaum Lab in Mount Sinai Hospital, New York.

2011   **First Class Book Prize**, Trinity College Dublin

Public Outreach

- Regularly engage with reporters about COVID-19 lineages and nomenclature, from the Guardian, Wired and the New York Times
- Guest on BBC CWR Radio discussing SARS-CoV-2 epidemiology.
- Stand at the Mid-Lothian Science Festival 2017 'Pathogens in and around you'.
- Volunteer in "Byte-sized Bioinformatics", which is an Edinburgh-based public engagement project that involves using raspberry-pi computers to give bioinformatics workshops in high schools across Scotland.