Nicholas R. Waters

S nickp60☑ nickp60@gmail.com

Technical Skills

Python, R, Bash
Docker, SGE, Nativescript
tidyverse, pandas
Shiny, ggplot2, matplotlib, Inkscape
git, Rmarkdown/knitr, Jupyter
STAN, caret, scikit-learn

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Objective

As I finish my microbial bioinformatics PhD, I am looking for opportunities requiring expertise in data science, microbial genomics, machine learning, modelling, and open source software development. I am passionate about research reproducibility and developing tools to benefit the global community.

Recent Work Experience

 National University of Ireland, Galway, Galway, Ireland <i>PhD Researcher</i> Conceived and implemented riboSeed, a genome assembly polisher Developed happie to perform pan-mobilome analysis on <i>E. coli</i> genomes Mentored undergraduates throughout their capstone projects, and secured 3 months funding for one student to continue their research Contributed 16S amplicon data analysis, metagenome assembly, Bayesian modelling, and software to various other projects 	June 2016 – Present
 Georgetown University, Washington, D.C. Research Assistant with Dr. Shaun Brinsmade Constructed S. aureus mutant; performed various gene expression assays Implemented an RNA-seq pipeline for expression and clustering analysis Created a locally-hosted Shiny application for accessing lab resources 	Jan. 2015 – May 2016
 Indigo Ag formerly Symbiota LLC, Cambridge, MA Laboratory Technician Preprocessed, analyzed, and visualized for field trials Provided 3 month's data analysis consulting services post-employment 	Aug. 2014 – Dec. 2014
 AstraZeneca R&D Boston, Waltham, MA Bioscience Intern: Infection Used RNA-seq to better understand membrane proteins in Pseudomonas sp. Determined MIC's, growth kinetics, and metabolic requirements for various strains 	May 2014 - Aug. 2014
 Antimicrobial Discovery Center, Northeastern University, Boston, MA Undergrad Lab Assistant with Dr. Kim Lewis Screened toxin/antitoxin E. coli mutants for changes in persister phenotypes Fulfilled occasional electron microscopy requests Characterized metabolic pathways of "uncultured" bacteria 	July 2013 – April 2014

Education

National University of Ireland, Galway, Galway, Ireland	PhD Microbiology, 2016 – Spring 2020 [anticipated]
MIT OpenCourseWare (MOOC)	Introduction to Algorithms; 6.046, 2016
HarvardX (MOOC)	Statistics and R for the Life Sciences PH525.1x, 2015
Northeastern University, Boston, MA	Bachelor of Science in Biology, 2014

Awards

Travel Award, Ryan Institute at NUIG, 2019: awarded funds to travel to Microbiology Society Annual Meeting in Belfast, UK **Anthony P. Moran Prize**, Microbiology Department NUIG, 2018: awarded for best student-driven research paper **Poster Prize**, Environ Conference, 2017: "Best Soil Presentation" **Joint Studentship**, James Hutton Institute and NUIG, 2016: awarded additional project funding

Publications

Authored:

"Easily phylotyping E. coli via the EzClermont web app and command-line tool"; Nicholas Waters, Florence Abram, Fiona Brennan, Ashleigh Holmes, and Leighton Pritchard. bioRxiv 2018 10.1101/317610.

"riboSeed: leveraging prokaryotic genomic architecture to assemble across ribosomal regions"; Nicholas Waters, Florence Abram, Fiona Brennan, Ashleigh Holmes, and Leighton Pritchard. NAR 2018 10.1093/nar/gky212.

"A spectrum of CodY activities drives metabolic reorganization and virulence gene expression in *Staphylococcus Aureus*"; Nicholas Waters, David Samuels, Ranjan Behera, Jonathan Livny, Kyu Rhee, Marat Sadyko and Shaun Brinsmade. **Molecular Microbiology** 2016 10.1111/mmi.13404.

Contributed to:

"The potential for polyphosphate metabolism in Archaea and anaerobic polyphosphate formation in *Methanosarcina mazei*"; Paula and Chin, Schnurer, Muller, Manesiotis, Waters, Macintosh, Quinn, Connolly, Abram, McGrath and O'Flaherty. Scientific Reports 2019 10.1038/s41598-019-53168-4.

"Chordomics: a visualisation tool for linking function to phylogeny in microbiomes"; McDonnell, Waters, Howley, Abram. Bioinformatics 2019 10.1093/bioinformatics/btz711.

"Toward Assessing Farm-Based Anaerobic Digestate Public Health Risks: Comparative Investigation With Slurry, Effect of Pasteurization Treatments, and Use of Miniature Bioreactors as Proxies for Pathogen Spiking Trials"; Nolan, Waters, Brennan, Auer, Fenton, Bolton, O'Flaherty, Abram. Frontiers in Sustainable Food Systems 2018 10.3389/fsufs.2018.00041.

"Thermophilic versus mesophilic dark fermentation in xylose-fed fluidised bed reactors: Biohydrogen production and active microbial community"; Dessi, Porca, Waters, Lakaniemia, Collins, Lens. Int. Journal of Hydrogen Energy 2018 10.1016/j.ijhydene.2018.01.158.

"Bioconda: Sustainable and comprehensive software distribution for the life sciences."; Grüning, Dale, Sjödin, Chapman, Row, Tomkins-Tinch, Valieris, Köster, Perez-Riverol, Khan, Wollmann, Brueffer, **The Bioconda Team**, Urgese, Eggenhofer. **Nature** Methods 2018 10.1038/s41592-018-0046-7. (contributed and maintain 10 recipes, commented on early draft of manuscript)

"Absence of Curli in Soil-Persistent Escherichia coli Is Mediated by a C-di-GMP Signaling Defect and Suggests Evidence of Biofilm-Independent Niche Specialization.": Somorin, Vollmerhausen, Waters, Pritchard, Abram, Brennan, O'Byrne. Frontiers Microbiology 2018 10.3389/fmicb.2018.01340

Open Source

Select GitHub Repos

- plentyofbugs: identify a compatible reference genome for your sequenced isolate
- sraFind: database linking NCBI's SRA, BioProject, BioSample, Assembly, and Nucleotide accessions
- annofilt: filter questionable annotations for before building a pan-genome

WebApps

Organizations

Bioconda: member and contributor

The Carpentries: certified instructor

EzClermont: quickly find the Clermont 2013 phylotype of an *E. coli* assembly cgfind: quickly fetch microbial reference genomes

Leadership

Microbiology Society, National University of Ireland, Galway

President: initiated incoming student mentorship program; managed bi-monthly seminars *Vice President*: organized training event; secured funds for brewing demonstrations 2017-2019 2016-2017