

GILLIAN REYNOLDS

Cambridge, United Kingdom
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PERSONAL NOTES

Formerly known as Gillian Woolard

SUMMARY

I am highly experienced bioinformatician with expertise in a range of biological problems including phylogenetics, phylogenomics, whole genome and whole-exome-based variant identification and RNA-seq-based differential expression and isoform identification. My work in these areas have necessitated the development of novel algorithms incorporating distributed computing and machine learning approaches, alongside the application of pre-existing tools. More recently my work at Mursla Bio focused on biomarker discovery with NGS data using machine learning and bioNLP strategies. At the Earlham institute I am a Senior Bioinformatician/software developer within the core bioinformatics team where my work focuses on the development of novel algorithms and workflows for pangenomic genome annotation as well as supporting the institutes other research projects.

Outside of biological data analysis I have demonstrated my driven and independent, yet collaborative, nature as a research scientist. During my PhD this involved the development and execution of my individual interdisciplinary PhD program and at Mursla Bio this was through the set up of the bioinformatics analysis and research efforts. At the Earlham institute I work with multiple teams across a number research projects to assist with their bioinformatics and software development needs.

ADVISORY ROLES

AI For Global Goals Machine Learning Advisory Committee Member	2023 - present
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EMPLOYMENT

Senior Bioinformatician/Software developer, Earlham Institute.	2024 - present
Bioinformatics Scientist, Mursla Bio.	2023 - 2023
Bioinformatics Research Associate, Mursla Bio.	2022 - 2023
Graduate Research Assistantship, Montana State University	2018 - 2022
Associate Lecturer in Biology, University of Worcester	2016 - 2018
Independent Study Co-Supervisor, University of Worcester	2016 - 2017
Data Quality Improvement Officer, National Health Service (NHS)	2015 - 2017
Guest Lecturer in Biology, University of Worcester	2014 - 2016
Research Assistant, University of Worcester	2014 - 2015

EDUCATION

OxML Summer School	May 2023 - July 2023
Individual Interdisciplinary PhD: Computer Science and Plant Genetics	August 2019 - December 2022
Co-Supervisors : Dr. Brendan Mumey, Dr. Jennifer Lachowicz The Gianforte School of Computing and The Department of Plant Sciences and Plant Pathology Montana State University, USA	
PhD in Plant Genetics - changed programs	January 2018 - August 2019
Interim Supervisor : Dr. Tracy Dougher August 2018- August 2019 Former Supervisor : Dr. Hikmet Budak January 2018 - August 2018 Department of Plant Sciences and Plant Pathology Montana State University, USA	
MRes Biology: Bioinformatics and Genomics The University of Worcester, UK	September 2015 - August 2018

SKILLS

Biological

As a result of the varied projects of which I have been a part of I have developed a number of skills in computational biology. These include biomarker identification, gene and genome alignments, phylogenetic tree construction, RNA-Seq analysis, exome-seq analysis, GBS data analysis, sequence read mapping, genome assembly, genome annotation, comparative genomics and developing machine learning models for the analysis of short-read sequencing data and biological scientific texts. I also have a sound understanding of a range of biological topics including genomics, genetics and evolutionary biology. I have undertaken a number of self-directed courses in topics including genomic technologies and systems biology.

Computational

I am fluent the python and R coding languages and have extensive experience work on the the linux command line. I am currently working on learning c++. I have extensive experience with working with high performance computers, including AWS and those that use the SLURM workload manager. I am also experienced with working with TensorFlow, Keras and SciKit learn tools for both supervised and unsupervised machine learning tasks including the analysis of short-read sequencing data, image classification, and biological natural language processing (BioNLP) tasks. I also have experience in algorithm design, including semi-supervised algorithm development and implementation which feature CPU parallelization capabilities. I am experienced with github for code storage and version control.

Mathematical and statistical

Throughout my PhD and since graduation I have continued to develop my mathematical and statistical skills through a combination of self-directed learning and formal courses. I have focused much of my efforts in these areas towards applications in machine learning and variant calling.

Teaching and Supervision

I have enjoyed several teaching and undergraduate supervision opportunities at the University of Worcester. In addition, I have also been involved in the development of educational tools in Bioinformatics for both undergraduates and pre-university students. I am passionate about education and also access to education, something I was able to put into practice during my development of free educational materials and as an associate lecturer at Worcester University. At Montana State University I mentored both graduate and undergraduate students on the analysis of large scale RNA-Seq data and hosted a number of seminars and more informal teaching workshops on a range of bioinformatics topics.

Interdisciplinary

As a PhD student who worked across two departments at MSU I have been able to hone my skills in interdisciplinary communication through presentations, seminars, meetings, collaborations and initiating and developing a joint PhD proposal. Since graduating, my interdisciplinary skills have continued to hold me in good stead as the sole bioinformatician in a start up consisting of professionals from a range of backgrounds.

Outreach

I have participated in a number of outreach projects to engage students in STEM with audiences from primary schools, high schools and sixth form colleges.

RESEARCH PUBLICATIONS AND CONFERENCE PRESENTATIONS

Reynolds, G., Mumey, B., Strnadova-Neeley, V. and Lachowiec, J., 2024. Hijacking a rapid and scalable metagenomic method reveals subgenome dynamics and evolution in polyploid plants. *Applications in Plant Sciences*, p.e11581

Upton, R.N., Correr, F.H., Lile, J., **Reynolds, G.L.**, Falaschi, K., Cook, J.P. and Lachowiec, J. Design, execution, and interpretation of plant RNA-seq analyses. *Frontiers in Plant Science*

Figueiras,R., Vagueiro, S., **Reynolds, G.**,Persia,E., Kay, R., Tomás Dias. Targeted capture of hepatocyte-derived extracellular vesicles from plasma and subsequent multi-omic analysis reveals potential diagnostic markers of hepatocellular carcinoma. *ISEV*. 2023

Chroak, G., Correr, F., Lachowiec, J., **Reynolds, G.**, Thum, R. Transcriptional Responses to 2,4-D Herbicide Treatment of a Eurasian (*Myriophyllum Spicatum*) and a Hybrid (*M. Spicatum* × *M. Sibiricum*) Genotype of Watermilfoil that Differ in Their Sensitivity to 2,4-D. *Aquatic Botany*. 2023

Reynolds,G., Strnadova-Neeley,V., Mumey,B., Lachowiec,J.. Hijacking a metagenomic strategy for rapid comparative subgenomics for polyploids and their progenitors. *Botany*. 2022

Reynolds,G., Strnadova-Neeley,V., Mumey,B., Lachowiec,J.. Leveraging a metagenomic strategy to reveal patterns of accessory and subgenomic chromosomal evolution *Plant Genomes Online Conference*. 2022

Reynolds,G., Strnadova-Neeley,V., Mumey,B., Lachowiec,J.. Computational strategies reveal subgenome-specific signatures of polyploid evolution *Barker Lab Polyploidy Webinar*. 2022

Reynolds,G., Strnadova-Neeley,V., Lachowiec,J. MinHash k-mer sketching highlights allopolyploid subgenome sequence differentiation. *ISCB-Africa ASBCB*. 2021

Reynolds,G., Lachowiec,J., Strnadova-Neeley,V. Identifying features for subgenomic sequence identification in a De Bruijn Graph (DBG). *Tech talks at the CRA-WP Grad Cohort Workshop for Women Conference*. 2021

Williams,L., **Reynolds, G.**, Mumey, B. (2019). RNA Transcript Assembly Using Inexact Flows. *In 2019 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE, 2019

Manuweera, B., **Reynolds, G.**, Kahanda, I. (2019). Computational Methods for the *Ab initio* Identification of Novel microRNA in Plants: A Systematic Review. *PeerJ Computer Science* 5:e233 2019.

Pourreza Shahri, Morteza, **Gillian Reynolds**, Mandi Marie Roe, and Indika Kahanda. "PPPred: Classifying Protein-phenotype Co-mentions Extracted from Biomedical Literature." In Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, pp. 414-422. ACM, 2019.

Shahri, Morteza Pourreza, Madhusudan Srinivasan, **Gillian Reynolds**, Diane Bimczok, Indika Kahanda, and Upulee Kanewala."Metamorphic Testing for Quality Assurance of Protein Function Prediction Tools." In 2019 IEEE International Conference On Artificial Intelligence Testing (AITest), pp. 140-148. IEEE, 2019.

Rajasekar, Karthik V., Shuangxi Ji, Rachel J. Coulthard, Jon P. Ride, **Gillian L. Reynolds**, Peter J. Winn, Michael J. Wheeler, Eva I. Hyde, and Lorna J. Smith. "Structure of SPH (self-incompatibility protein homologue) proteins: a widespread family of small, highly stable, secreted proteins." *Biochemical Journal* 476, no. 5 (2019): 809-826.

Wheeler, M., **Woolard, G.** 'Trickle down teaching' informing The Biosciences Curriculum with Bioinformatics. *Beyond Boundaries - University of Worcester Learning & Teaching Conference*. June 2017.

Sherrad, G., **Woolard, G.**, Wheeler, M. Investigating the function of a small secreted protein family in physcomitrella patens. *MOSS 2016 Conference*. 2nd-5th September 2016, University of Leeds, U.K.

TEACHING & UNDERGRADUATE SUPERVISION

Teaching

Guest Lecturer in Cell Biology- *Introduction to bioinformatics*

First year class, The University of Worcester 2020

Co-module Leader in Bioinformatics and Genomics

Final (third) year class, The University of Worcester 2017-2018

Module Leader in Human Genetics

Second year class, The University of Worcester 2017

Guest Lecturer in Genomics and Bionformatics - *Phylogenetics*

Final (third) year class, The University of Worcester 2014-2016

Guest lecturer in Introduction to Biological Chemistry - *Phylogenetics*

First year class, The University of Worcester 2014-2015

PROFESSIONAL MEMBERSHIPS

Royal Society of Biology

International Society for Computational Biology

REFERENCES

Available on request