R. Jordan Price

Website: rjprice.bio   **GitHub:** github.com/rj-price

Professional Profile

Highly skilled bioinformatician and molecular biologist with a background in functional genomics across diverse species. Over a decade of molecular biology expertise coupled with 5+ years of hands-on bioinformatics experience. Demonstrated expertise in genomics, comparative analysis, and data-driven research. From sample preparation and sequencing to computational analyses, I bring a comprehensive biological understanding to the implementation of informative genomic data. Adept at leading projects, managing teams, and providing guidance to colleagues. Seeking a full-time bioinformatics position to further apply and expand upon this experience and contribute to innovative research.

Skills

- Proficient using several NGS data pipelines (including WGS, RNA-seq and ChIP-seq)
- Experience utilising long and short read datasets, including quality control
- Comfortable coding in Python, Bash, and R
- Familiar with data visualisation packages (matplotlib, seaborn, ggplot2)
- Proficient working in Linux and Slurm-based HPC environments
- Working knowledge of NextFlow pipeline management, including nf-core and DSL2 features
- Use of version control software (git)
- Familiar with containerisation (Docker, Singularity)

Work Experience

2022 – Present   *Senior Specialist, Cambridge Crop Research, NIAB*

- Utilising whole genome sequencing and variant analysis pipelines, transcriptomics, and CRISPR based deletion and base editing to identify candidate genes responsible for hyper-branching phenotype in the Quorn mycoprotein fungus *Fusarium venenatum*.
- Regularly engaging with project partners, providing summary reports and visualisations of complex data, to ensure that we are meeting project milestones and delivering high-quality results.
- Involvement in several side projects, including the assembly, annotation, and comparative analysis of raspberry cultivars and fungal pathogens.
- Training other lab members in the analysis of RNA-seq datasets and genome assembly methods.

2020 – 2022   *Specialist, Cambridge Crop Research, NIAB*
2019 – 2020   *Specialist, Genetics, Genomics and Breeding, NIAB EMR*

- Used comparative genomics to investigate the evolutionary underpinnings of actinorhizal nitrogen fixing symbiosis, both from the host plant and bacterial symbiont perspectives.
- Carried out sequencing, assembly and annotation of several plant and bacterial genomes.
- Performed comparative analyses across phylogenies to identify orthologs, gene presence/absence, and cis-regulatory elements involved in actinorhizal symbiosis that are now being used to further engineering strategies.

2015 – 2019   *Postdoctoral Research Associate, School of Biosciences, University of Kent*

- Explored the epigenetic and genomic modifications underpinning the pathogenicity of the human fungal pathogen *Candida albicans*.
- Implemented and optimised a novel quantitative ChIP-seq method in *Candida albicans*, performed computational analysis of resulting datasets.
- Created novel deletion strains to explore the genomic modifications underpinning the pathogenicity of a human fungal pathogen and analysed RNA-seq datasets resulting from these strains.

2012 – 2015   *Postdoctoral Research Fellow, Faculty of Medicine, University of Southampton*

- Designed and performed high throughput multiplex TaqMan qPCR assays, Western blot optimisation and analysis, and computational analysis of expression microarray and DNA methylation data to determine the role of BRCA1 and BRCA2 in a variety of cancer and primary human cell lines.

Management Responsibilities

I am currently responsible for management of research project budgets, communication with project partners, and efficient allocation of resources to ensure timely completion of milestones. Throughout my time at NIAB, I have line manged four research technicians and two postdoctoral research associates and have co-supervised three postgraduate students. I also assist with the day-to-day supervision of junior lab members.

Education

2008 – 2012   *PhD in Developmental Biology, University of Portsmouth*
2007 – 2008   *MSc (by research) in Biomedical Science, Lancaster University*
2004 – 2007   *BSc Biochemistry (2:1), Lancaster University*

Selected Publications

- Bates, H. J., Pike, J., **Price, R. J.**, Jenkins, S., Connell, J., Legg, A., Armitage, A., Harrison, R. J. & Clarkson, J. P. Comparative genomics and transcriptomics reveal differences in effector complement and expression between races of *Fusarium oxysporum* f.sp. *lactucae*. Frontiers in Plant Science (2024, accepted).
- **Price, R. J.**, Davik, J., Fernandez, F.F., Bates, H., Lynn, S., Nellist, C., Buti, M., Šurbanovski, N., Harrison, R. & Sargent, D.J. Chromosome-scale genome sequence assemblies of the 'Autumn Bliss' and 'Malling Jewel' cultivars of the highly heterozygous red raspberry (*Rubus idaeus* L.) derived from long-read Oxford Nanopore sequence data. *PLOS ONE* **18**, e0285756 (2023).
- Rizzo, M., Vega-Estevez, S., Soisangwan, N., **Price, R.J.**, Uyl, C., Iracane, E., Shaw, M., Soetaert, J., Selmecki, A. & Buscaino, A. Stress combined with loss of the *Candida albicans* SUMO protease Ulp2 triggers selection of aneuploidy via a two-step process. *PLoS Genet* **18**, e1010576 (2022).
- **Price, R. J.**, Weindling, E., Berman, J. & Buscaino, A. Chromatin Profiling of the Repetitive and Nonrepetitive Genomes of the Human Fungal Pathogen *Candida albicans*. *mBio* **10**, e01376-19 (2019).
- Freire-Benéitez, V., **Price, R. J.**, Tarrant, D., Berman, J. & Buscaino, A. *Candida albicans* repetitive elements display epigenetic diversity and plasticity. *Sci Rep* **6**, 22989 (2016).
- **Price, R. J.**, Lillycrop, K. A. & Burdge, G. C. Folic acid supplementation in vitro induces cell type-specific changes in BRCA1 and BRCA 2 mRNA expression but does not alter DNA methylation of their promoters or DNA repair. *Nutr Res* **35**, 532–544 (2015).