

# Philipp Bayer

DECRA FELLOW

School of Biological Sciences, University of Western Australia

✉ philippbay@gmail.com | 🏠 philipp-bayer.net | 📧 philippbayer | 📺 philippbayer | 🐦 philippbayer

## About me

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I use computers and large data sets to answer biological questions, especially in crops. I use genomics, pangenomics, k-mer/SNP/QTL-association studies, biostatistics, and interpretable machine learning to find new approaches to breed climate change-ready crops.

## Education

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- 2012 to 2016 **PhD**, University of Queensland, Brisbane, Australia  
Pure bioinformatics PhD in the Edwards group. Developed computational pipeline SkimGBS for cheaper genotyping. Worked extensively with industry (Bayer CropScience, later BASF).
- Master of IT**, Bond University, Gold Coast, Australia  
2010 to 2012 Focused on coding and business IT. 5x Top of class, 3x Vice-Chancellor List of Academic Excellence, 1x IT Award Academic Excellence. Graduated with High Distinction. John Oglethorpe Medal for highest GPA of all IT students graduating.
- 2006 to 2009 **Bachelor of Life Sciences**, University of Muenster, Muenster, Germany  
Studied general life sciences with a focus on microbiology. In my final project I worked on EST-based differential gene expression in seagrasses.

## Employment

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- 2021 to 2023 **DECRA Fellow**  
My first step towards an independent lab. I am modeling mechanisms of gene loss and birth in crops to learn where new genes come from, and how to avoid loss of agronomically important genes.
- 2017 to 2020 **Forrest Fellow**  
One of three inaugural Forrest Fellows. Worked on genomics of complex plants with Forrest Foundation support.
- 2015 to 2017 **Postdoctoral researcher**  
Researched genetics of complex plants with a focus on canola and wheat in Edwards lab.

## Current roles

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- 2021 **Member, Scientific Advisory Panel Machine Learning**  
Member of the scientific advisory panel for ongoing machine learning projects supported by the ARDC.
- Hacky Hour Founder**  
2017 Founded a weekly get-together of researchers and staff working with programming and data, doubles as a help-desk for students with programming problems.
- 2013 **Certified Carpentries Instructor**  
Certified Software Carpentry and Data Carpentry instructor
- 2011 **Co-founder openSNP.org**  
Partially wrote and maintain the Ruby on Rails code-base

## Current awards and funding

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- 2020 **Grant: ARC Discovery Early Career Research Award**  
Awarded DECRA for 2021-2023. Total funding: AUD\$ 448,781 and ASUD 418,772 in UWA funding.
- 2020 **Grant: Identifying genetic contributors to canola blackleg resistance in the presence of environmental effects using Machine Learning**  
With Prof. Dave Edwards, Prof. Mohammed Bennamoun, Prof. Farid Boussaid, Prof. Jacqueline Batley. Total funding: AUD\$ 309,524.
- 2020 **Grant: Machine Learning - Project E: Deep Learning for early detection and classification of crop disease and stress**  
With Prof. Mohammed Bennamoun, Prof. Farid Boussaid, Prof. Dave Edwards, Dr. Nic Taylor. Total funding: AUD\$ 344,971.

## Recent presentations

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- 2021 **CCDM/Curtin University** - Machine learning in bioinformatics – where are we and what’s next?
- 2021 **Cinvestav/online** - Machine learning in plant breeding and bioinformatics
- 2021 **UWA DVCR Forrest Fellow series** - Future-ready crops for a changing climate: the role of bioinformatics
- 2021 **Pawsey Supercomputing Centre** - Bioinformatics at scale Q and A
- 2021 **ABACBS online seminars** - Interpretable Machine Learning in Bioinformatics
- 2020 **GRDC Tech Seminars** - Our machine learning technical stack
- 2020 **PAG Conference, San Diego** - Predicting Gene Loss in Plants: Lessons Learned from Laptop-Scale Data
- 2019 **Bayliss Seminar Series** - Eukaryotic pangenomics: where we’ve been, where we’re going
- 2019 **AGRF Seminar Series** - Assembling complex plant genomes – things I wish someone would have told me earlier
- 2019 **PAG Conference, San Diego** - Helping Biologists Make Sense of Plant Variant and Annotation Data

## Relevant publications

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- 8 **Bayer et al.** (2021). Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. *The Plant Genome (TSI)*, NA, NA:1–12.
- 10 **Bayer et al.** (2021). Yield is negatively correlated with nucleotide-binding leucine-rich repeat gene content in soybean. *bioRxiv*, NA, NA:NA.
- 9 **Marsh et al.** (2021). Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003. *bioRxiv*, NA, NA:NA.
- 7 **Valliyodan et al.** (2021). Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. *Scientific data*, 8, 1:1–9.
- 6 **Bayer et al.** (2020). Plant pan-genomes are the new reference. *Nature plants*, 6, 8:914–920.
- 5 **Valliyodan et al.** (2019). Construction and comparison of three reference-quality genome assemblies for soybean. *The Plant Journal*, 100, 5:1066–1082.
- 4 **Appels et al.** (2018). Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361, 6403:NA.
- 3 **Montenegro et al.** (2017). The pangenome of hexaploid bread wheat. *The Plant Journal*, 90, 5:1007–1013.
- 2 **Golicz et al.** (2016). The pangenome of an agronomically important crop plant Brassica oleracea. *Nature Communications*, 7, 1:1–8.
- 1 **Chalhoub et al.** (2014). Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. *science*, 345, 6199:950–953.