

Dr. Philipp Bayer

Postdoctoral researcher

contact

philippbay@gmail.com
github.com/philippbayer
twitter.com/philippbayer

languages

German: mother tongue
English: fluent
French & Japanese:
advanced

programming

Python + R
Go, Perl, Bash, Java
Ruby on Rails,
JavaScript, HTML
SLURM, PBS Pro

research

Genomics of complex
traits in plants

statistics

Citations: 4,132
h-index: 25
i10-index: 38

education

- 2012–2015 **PhD Applied Bioinformatics** University of Queensland, Brisbane
Working in the Applied Bioinformatics group on the use of genotyping by sequencing to improve the genome assembly of canola.
Thesis submission date: 23rd September 2015. Date of acceptance: 4th May 2016.
- 2010–2012 **Master of IT** Bond University, Gold Coast
Graduated with High Distinction
- 2006–2009 **Bachelor of Science Biology** University of Münster, Germany
Thesis: Analysis of splicing in two populations of marine plants using bioinformatic approaches

employment

- 2021–2023 **DECRA Fellow** UWA, Perth
My first step towards an independent lab with funding for the first PhD-student primarily supervised by me and with \$448,781 in government and \$418,772 UWA funding. 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.
- 2017–2020 **Forrest Fellow** UWA, Perth
Edwards Lab. Continued work on genomics of complex plants with Forrest Foundation support. Supervised three PhD students and four MSc students to completion.
- 2015–2017 **Postdoctoral researcher** UWA, Perth
Edwards Lab. Researched genetics of complex plants with a focus on canola and wheat. Worked closely with industry partners to improve their breeding programs. Preparing, writing, and publishing research. Supervised two interns, Co-supervised four PhD students and one MSc student, system-administrator for the local computational infrastructure and group data manager. Worked extensively on an ARC Industrial Transformation Training Centre application (2018 round).

publications

- Yang, H., Saad, N. S. M., Ibrahim, M. I., **Bayer, P. E.**, Neik, T. X., Severn-Ellis, A. A., Pradhan, A., Tirnaz, S., Edwards, D., Batley, J., “Candidate Rlm6 resistance genes against *Leptosphaeria. maculans* identified through a genome-wide association study in *Brassica juncea* (L.) Czern” *Theoretical and Applied Genetics* (2021) pp. 1–16. Springer Berlin Heidelberg
- Yang, H., **Bayer, P. E.**, Tirnaz, S., Edwards, D., Batley, J., “Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in *Brassica juncea*” *Biology* 10.1 (2021) p. 17. Multidisciplinary Digital Publishing Institute
- Valliyodan, B., Brown, A. V., Wang, J., Patil, G., Liu, Y., Otyama, P. I., Nelson, R. T., Vuong, T., Song, Q., Musket, T. A., “Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing” *Scientific data* 8.1 (2021) pp. 1–9. Nature Publishing Group
- Danilevicz, M. F., Fernandez, C. G. T., Marsh, J. I., **Bayer, P. E.**, Edwards, D., “High-Throughput Genotyping Technologies in Plant Taxonomy”. In: *Molecular Plant Taxonomy*. Humana, New York, NY, 2021, pp. 149–166 Li, P., Su, T., Zhao, X., Wang, W., Zhang, D., Yu, Y., **Bayer, P. E.**, Edwards, D., Yu,

- S., Zhang, F., “Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson” *Plant Biotechnology Journal* (2020). John Wiley & Sons, Ltd
- Bayer, P. E.**, Edwards, D., “Machine learning in agriculture: from silos to marketplaces” *Plant Biotechnology Journal* (2020)
- Mercé, C., **Bayer, P. E.**, Tay Fernandez, C., Batley, J., Edwards, D., “Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives” *Agronomy* 10.10 (2020) p. 1484. *Multidisciplinary Digital Publishing Institute*
- Tirnaz, S., **Bayer, P. E.**, Inturrisi, F., Zhang, F., Yang, H., Dolatabadian, A., Neik, T. X., Severn-Ellis, A., Patel, D. A., Ibrahim, M. I., “Resistance gene analogs in the Brassicaceae: Identification, characterization, distribution, and evolution” *Plant Physiology* 184.2 (2020) pp. 909–922. *American Society of Plant Biologists*
- Bayer, P. E.**, Golicz, A. A., Scheben, A., Batley, J., Edwards, D., “Plant pan-genomes are the new reference” *Nat. Plants* 6 (2020) pp. 914–920
- Tirnaz, S., Merce, C., **Bayer, P. E.**, Severn-Ellis, A. A., Edwards, D., Batley, J., “Effect of *Leptosphaeria maculans* infection on promoter DNA methylation of defence genes in *Brassica napus*” *Agronomy* 10.8 (2020) p. 1072. *Multidisciplinary Digital Publishing Institute*
- Inturrisi, F., **Bayer, P. E.**, Yang, H., Tirnaz, S., Edwards, D., Batley, J., “Genome-wide identification and comparative analysis of resistance genes in *Brassica juncea*” *Molecular Breeding* 40.8 (2020) pp. 1–14. *Springer Netherlands*
- Tirnaz, Bayer, Inturrisi, Zhang, Yang, Dolatabadian, Neik, Severn-Ellis, Patel, Ibrahim, et al., “Resistance gene analogs in the Brassicaceae: Identification, characterization, distribution, and evolution” Dolatabadian, A., **Bayer, P. E.**, Tirnaz, S., Hurgobin, B., Edwards, D., Batley, J., “Characterization of disease resistance genes in the *Brassica napus* pangenome reveals significant structural variation” *Plant biotechnology journal* 18.4 (2020) pp. 969–982
- Golicz, A. A., **Bayer, P. E.**, Bhalla, P. L., Batley, J., Edwards, D., “Pangenomics comes of age: From bacteria to plant and animal applications” *Trends in Genetics* 36.2 (2020) pp. 132–145. *Elsevier Current Trends*
- Anderson, R., Fernandez, C. T., Yuan, Y., Golicz, A. A., Edwards, D., **Bayer, P. E.**, “Method for Genome-Wide Association Study: A Soybean Example”. In: *Legume Genomics*. Humana, New York, NY, 2020, pp. 147–158
- Hu, H., Yuan, Y., **Bayer, P. E.**, Fernandez, C. T., Scheben, A., Golicz, A. A., Edwards, D., “Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach”. In: *Legume Genomics*. Humana, New York, NY, 2020, pp. 35–47 Danilevicz, M. F., Fernandez, C. G. T., Marsh, J. I., **Bayer, P. E.**, Edwards, D., “Plant pangenomics: approaches, applications and advancements” *Current Opinion in Plant Biology* 54 (2020) pp. 18–25. *Elsevier Current Trends*
- Zhao, J., **Bayer, P. E.**, Ruperao, P., Saxena, R. K., Khan, A. W., Golicz, A. A., Nguyen, H. T., Batley, J., Edwards, D., Varshney, R. K., “Trait associations in the pangenome of pigeon pea (*Cajanus cajan*)” *Plant Biotechnology Journal* (2020)
- Anderson, R., **Bayer, P. E.**, Edwards, D., “Climate change and the need for agricultural adaptation” *Current Opinion in Plant Biology* (2020). *Elsevier Current Trends*
- Yuan, Y., **Bayer, P. E.**, Anderson, R., Lee, H., Chan, C.-K. K., Zhao, R., Batley, J., Edwards, D., “RefKA: A fast and efficient long-read genome assembly approach for large and complex genomes” *BioRxiv* (2020). *Cold Spring Harbor Laboratory*
- Furaste Danilevicz, M., Danilevicz, M. F., Tay Fernandez, C. G., Marsh, J. I., **Bayer, P. E.**, Edwards, D., “Plant pangenomics: approaches, applications and advancements” (2020)
- Valliyodan, B., Cannon, S. B., **Bayer, P. E.**, Shu, S., Brown, A. V., Ren, L., Jenkins, J., Chung, C. Y.-L.,

- Chan, T.-F., Daum, C. G., “Construction and comparison of three reference-quality genome assemblies for soybean” *The Plant Journal* 100.5 (2019) pp. 1066–1082
- Kreplak, J., Madoui, M.-A., Cápál, P., Novák, P., Labadie, K., Aubert, G., **Bayer, P. E.**, Gali, K. K., Syme, R. A., Main, D., “A reference genome for pea provides insight into legume genome evolution” *Nature genetics* 51.9 (2019) pp. 1411–1422. *Nature Publishing Group*
- Dolatabadian, A., **Bayer, P. E.**, Tirnaz, S., Hurgobin, B., Edwards, D., Batley, J., “Characterisation of disease resistance genes in the Brassica napus pangenome reveals significant structural variation” *Plant Biotechnology Journal* (Aug. 2019). *Wiley*
- Tahghighi, H., Erskine, W., Bennett, R., **Bayer, P. E.**, Pazos Navarro, M., Kaur, P., “Genetic diversity linked to haplotype variation in the world core collection of *Trifolium subterraneum* for boron toxicity tolerance provides valuable marker s for pasture breeding” *Frontiers in Plant Science* 10 (Aug. 2019) pp. 1–19
- M, M.-D., S, C., G, T., M, D., PE, B., D, E., MN, N., W, E., FJ, L.-R., J, C., JK, H., “Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens *Botrytis cinerea* and *Sclerotinia sclerotiorum* via comparative genomics.” *BMC genomics* (May 2019)
- Kreplak, J., Madoui, M.-A., Cápál, P., Novák, P., Labadie, K., Aubert, G., **Bayer, P. E.**, Gali, K. K., Syme, R. A., Main, D., Klein, A., Bérard, A., Vrbová, I., Fournier, C., d’Agata, L., Belser, C., Berrabah, W., Toegelová, H., Milec, Z., Vrána, J., Lee, H., Kougbeadjo, A., Térézol, M., Huneau, C., Turo, C. J., Mohellibi, N., Neumann, P., Falque, M., Gallardo, K., McGee, R., Tar’an, B., Bendahmane, A., Aury, J.-M., Batley, J., Paslier, M.-C. L., Ellis, N., Warkentin, T. D., Coyne, C. J., Salse, J., Edwards, D., Lichtenzweig, J., Macas, J., Doležel, J., Wincker, P., Burstin, J., “A reference genome for pea provides insight into legume genome evolution” *Nature Genetics* 51.9 (Sept. 2019) pp. 1411–1422. *Springer Science and Business Media LLC*
- Valliyodan, B., Cannon, S. B., **Bayer, P. E.**, Shu, S., Brown, A. V., Ren, L., Jenkins, J., Chung, C. Y.-L., Chan, T.-F., Daum, C. G., Plott, C., Hastie, A., Baruch, K., Barry, K. W., Huang, W., Patil, G., Varshney, R. K., Hu, H., Batley, J., Yuan, Y., Song, Q., Stupar, R. M., Goodstein, D. M., Stacey, G., Lam, H.-M., Jackson, S. A., Schmutz, J., Grimwood, J., Edwards, D., Nguyen, H. T., “Construction and comparison of three reference-quality genome assemblies for soybean” *The Plant Journal* (Aug. 2019). *Wiley*
- Scheben, A., Verpaalen, B., Lawley, C. T., Chan, C.-K. K., **Bayer, P. E.**, Batley, J., Edwards, D., “Crop-SNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat” *The Plant Journal* 98.1 (2019) pp. 142–152. *Wiley Online Library*
- Anderson, R., Edwards, D., Batley, J., **Bayer, P. E.**, “Genome-Wide Association Studies in Plants” *eLS* (2019) pp. 1–7. *Wiley Online Library*
- Mousavi-Derazmahalleh, M., **Bayer, P. E.**, Hane, J. K., Valliyodan, B., Nguyen, H. T., Nelson, M. N., Erskine, W., Varshney, R. K., Papa, R., Edwards, D., “Adapting legume crops to climate change using genomic approaches” *Plant, cell & environment* 42.1 (2019) pp. 6–19
- Taylor, C. M., Kamphuis, L. G., Zhang, W., Garg, G., Berger, J. D., Mousavi-Derazmahalleh, M., **Bayer, P. E.**, Edwards, D., Singh, K. B., Cowling, W. A., “INDEL variation in the regulatory region of the major flowering time gene *LanFTc1* is associated with vernalization response and flowering time in narrow-leaved lupin (*Lupinus angustifolius* L.)” *Plant, cell & environment* 42.1 (2019) pp. 174–187. *Impact Factor: 6.173*
- Melonek, J., Zhou, R., **Bayer, P. E.**, Edwards, D., Stein, N., Small, I., “High intraspecific diversity of Restorer-of-fertility-like genes in barley” *The Plant Journal* 97.2 (2019) pp. 281–295. *Wiley Online Library*
- Bayer, P. E.**, Golicz, A. A., Tirnaz, S., Chan, C.-K. K., Edwards, D., Batley, J., “Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome” *Plant biotechnology journal* 17.4 (2019) pp. 789–800

- Bayer, P. E.**, Edwards, D., Batley, J., “Bias in resistance gene prediction due to repeat masking” *Nature Plants* 4.10 (2018) p. 762. *Nature Publishing Group*
- Mousavi-Derazmahalleh, M., Nevado, B., **Bayer, P. E.**, Filatov, D. A., Hane, J. K., Edwards, D., Erskine, W., Nelson, M. N., “The western Mediterranean region provided the founder population of domesticated narrow-leafed lupin” *Theoretical and Applied Genetics* 131.12 (2018) pp. 2543–2554. *Springer*
- The International Wheat Genome Sequencing Consortium (IWGSC), “Shifting the limits in wheat research and breeding using a fully annotated reference genome” *Science* 361.6403 (Aug. 2018) eaar7191
- Ramírez-González, R. H., Borrill, P., Lang, D., Harrington, S. A., Brinton, J., Venturini, L., Davey, M., Jacobs, J., Ex, F., Pasha, A., Khedikar, Y., Robinson, S. J., Cory, A. T., Florio, T., Concia, L., Juery, C., Schoonbeek, H., Steuernagel, B., Xiang, D., Ridout, C. J., Chalhoub, B., Mayer, K. F. X., Benhamed, M., Latrasse, D., Bendahmane, A., International Wheat Genome Sequencing Consortium, Wulff, B. B. H., Appels, R., Tiwari, V., Datla, R., Choulet, F., Pozniak, C. J., Provart, N. J., Sharpe, A. G., Paux, E., Spannagl, M., Bräutigam, A., Uauy, C., “The transcriptional landscape of polyploid wheat” *Science* 361.6403 (Aug. 2018) eaar6089
- Lee, H., Golicz, A. A., **Bayer, P. E.**, Severn-Ellis, A. A., Chan, C.-K. K., Batley, J., Kendrick, G. A., Edwards, D., “Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution” *Journal of experimental botany* 69.15 (2018) pp. 3689–3702. *Oxford University Press UK*. Impact factor: 5.830
- Mousavi-Derazmahalleh, M., **Bayer, P. E.**, Nevado, B., Hurgobin, B., Filatov, D., Kilian, A., Kamphuis, L. G., Singh, K. B., Berger, J. D., Hane, J. K., “Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin” *Theoretical and Applied Genetics* 131.4 (2018) pp. 887–901. *Springer*
- Hurgobin, B., Golicz, A. A., **Bayer, P. E.**, Chan, C.-K. K., Tirnaz, S., Dolatabadian, A., Schiessl, S. V., Samans, B., Montenegro, J. D., Parkin, I. A., “Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid *Brassica napus*” *Plant Biotechnology Journal* 16.7 (2018) pp. 1265–1274. Impact Factor: 6.09, JCR Plant Sciences 11/209 (Q1), Altmetric score: 6
- Schneider, M. V., Griffin, P. C., Tyagi, S., Flannery, M., Dayalan, S., Gladman, S., Watson-Haigh, N., **Bayer, P. E.**, Charleston, M., Cooke, I., “Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia” *Briefings in bioinformatics* 20.2 (2017) pp. 384–389. *Oxford University Press*
- Kaur, P., Appels, R., **Bayer, P. E.**, Keeble-Gagnere, G., Wang, J., Hirakawa, H., Shirasawa, K., Vercoe, P., Stefanova, K., Durmic, Z., “Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation” *Frontiers in Plant Science* 8 (2017) p. 1463. *Frontiers Media SA*
- Yuan, Y., **Bayer, P. E.**, Lee, H.-T., Edwards, D., “runBNG: a software package for BioNano genomic analysis on the command line” *Bioinformatics* 33.19 (2017) pp. 3107–3109. *Oxford University Press*. Impact factor: 7.3
- Yuan, Y., **Bayer, P. E.**, Scheben, A., Chan, C.-K. K., Edwards, D., “BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data” *BMC Bioinformatics* 18.1 (2017) p. 323. *BioMed Central*. Impact factor: 2.4
- Bayer, P. E.**, Hurgobin, B., Golicz, A. A., Chan, C.-K. K., Yuan, Y., Lee, H., Renton, M., Meng, J., Li, R., Long, Y., “Assembly and comparison of two closely related *Brassica napus* genomes” *Plant Biotechnology Journal* 15.12 (2017) pp. 1602–1610. Impact Factor: 6.09, JCR Plant Sciences 11/209 (Q1), Altmetric score: 11
- Yuan, Y., **Bayer, P. E.**, Batley, J., Edwards, D., “Improvements in Genomic Technologies: Application to Crop Genomics” *Trends in Biotechnology* 35.6 (2017) pp. 547–558. Impact Factor: 12.06, JCR Biotechnology and Applied Microbiology 3/161 (Q1), Altmetric score: 7

- Montenegro, J. D., Golicz, A. A., **Bayer, P. E.**, Hurgobin, B., Lee, H., Chan, C.-K. K., Visendi, P., Lai, K., Dolezel, J., Batley, J., Edwards, D., “The pangenome of hexaploid bread wheat” *The Plant Journal* 90.5 (2017) pp. 1007–1013. Best paper award (Plant Journal) 2017 Resource - Bronze, Impact Factor: 5.46, JCR Plant Sciences 13/209 (Q1), Altmetric score: 52
- Kaur, P., **Bayer, P. E.**, Milec, Z., Vrana, J., Yuan, Y., Appels, R., Edwards, D., Batley, J., Nichols, P., Erskine, W., Dolezel, J., “An advanced reference genome of *Trifolium subterraneum* L. reveals genes related to agronomic performance” *Plant Biotechnology Journal* 15.8 (2017) pp. 1034–1046. Wiley Online Library. Impact Factor: 6.09, JCR Plant Sciences 11/209 (Q1), Altmetric score: 15
- Gacek, K., **Bayer, P. E.**, Bartkowiak-Broda, I., Szala, L., Bocianowski, J., Edwards, D., Batley, J., “Genome-wide association study of genetic control of seed fatty acid biosynthesis in *Brassica napus*” *Frontiers in Plant Science* 7 (2017) p. 2062. *Frontiers Media SA*. Impact Factor: 4.49, JCR Plant Sciences 15/209 (Q1)
- Golicz, A. A., **Bayer, P. E.**, Barker, G. C., Edger, P. P., Kim, H., Martinez, P. A., Chan, C. K. K., Severn-Ellis, A., McCombie, W. R., Parkin, I. A. P., Paterson, A. H., Pires, J. C., Sharpe, A. G., Tang, H., Teakle, G. R., Town, C. D., Batley, J., Edwards, D., “The pangenome of an agronomically important crop plant *Brassica oleracea*” *Nature Communications* 7 (2016) p. 13390. *Nature Publishing Group*. Citations: 5, Impact Factor: 11.32, JCR Multidisciplinary Sciences 3/63 (Q1), Altmetric score: 50
- Hane, J. K., Ming, Y., Kamphuis, L. G., Nelson, M. N., Garg, G., Atkins, C. A., **Bayer, P. E.**, Bravo, A., Bringans, S., Cannon, S., Edwards, D., Foley, R., Gao, L.-L., Harrison, M. J., Huang, W., Hurgobin, B., Li, S., Liu, C.-W., McGrath, A., Morahan, G., Murray, J., Weller, J., Jian, J., Singh, K. B., “A comprehensive draft genome sequence for lupin (*Lupinus angustifolius*), an emerging health food: insights into plant-microbe interactions and legume evolution” *Plant Biotechnology Journal* 15.3 (2017) pp. 318–330. Citations: 6, Impact Factor: 6.09, JCR Plant Sciences 11/209 (Q1), Altmetric score: 15
- Barash, M., **Bayer, P. E.**, Daal, A., “Candidate gene scan for Single Nucleotide Polymorphisms involved in the determination of normal variability in human craniofacial morphology” *bioRxiv* (2016) p. 060814. *Cold Spring Harbor Labs Journals*. Altmetric score: 9
- Lee, H., Golicz, A. A., **Bayer, P.**, Jiao, Y., Tang, H., Paterson, A. H., Sablok, G., Krishnaraj, R. R., Chan, C.-K. K., Batley, J., Kendrick, G. A., Larkum, A. W., Ralph, P. J., Edwards, D., “The genome of a southern hemisphere seagrass species *Zostera muelleri*” *Plant Physiology* 172.1 (2016) pp. 272–283. *American Society of Plant Biologists*. Citations; 3, Impact Factor: 6.28, JCR Plant Sciences 8/209 (Q1), Altmetric score: 6
- Bayer, P. E.** “Genomics of Salinity”. In: *Plant Genomics and Climate Change*. Ed. by David Edwards and Jacqueline Batley. Springer New York, 2016, 179–194
- Visendi, P., Berkman, P. J., Hayashi, S., Golicz, A. A., **Bayer, P. E.**, Ruperao, P., Hurgobin, B., Montenegro, J., Chan, C.-K. K., Staňková, H., “An efficient approach to BAC based assembly of complex genomes” *Plant methods* 12.1 (2016) p. 2. *BioMed Central*. Impact Factor: 3.4, JCR Plant Sciences 30/209 (Q1)
- Mason, A. S., Rousseau-Gueutin, M., Morice, J., **Bayer, P. E.**, Besharat, N., Cousin, A., Pradhan, A., Parkin, I. A. P., Chevre, A.-M., Batley, J., Nelson, M. N., “Centromere locations in *Brassica A* and *C* genomes revealed through half-tetrad analysis” *Genetics* 202.2 (2016) pp. 513–523. *Genetics*. Citations: 8, Impact Factor: 4.6, JCR Genetics & Heredity 29/166 (Q1)
- Bayer, P. E.** “Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies”. In: *Plant Bioinformatics: Methods and Protocols*. Ed. by David Edwards. Springer New York, 2016, pp. 285–292
- Bayer, P. E.**, Ruperao, P., Mason, A. S., Stiller, J., Chan, C.-K. K., Hayashi, S., Long, Y., Meng, J., Sutton, T., Visendi, P., “High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in *Cicer arietinum* and *Brassica napus*” *Theoretical and Applied Genetics* 128.6 (2015) pp. 1039–1047. *Springer Berlin Heidelberg*. Citations: 14, Impact Factor: 3.9, JCR Agronomy 5/83 (Q1)

- Golicz, A. A., **Bayer, P. E.**, Edwards, D., “Skim-based genotyping by sequencing”. In: *Plant Genotyping: Methods and Protocols*. Ed. by David Edwards. Citations: 6. Springer New York, 2015, pp. 257–270
- Lai, K., Lorenc, M. T., Lee, H. C., Berkman, P. J., **Bayer, P. E.**, Visendi, P., Ruperao, P., Fitzgerald, T. L., Zander, M., Chan, C.-K. K., “Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat” *Plant Biotechnology Journal* 13.1 (2015) pp. 97–104. Citations: 17, Impact Factor: 6.09, JCR Plant Sciences 11/209 (Q1)
- Chalhoub, B., Denoeud, F., Liu, S., Parkin, I. A. P., Tang, H., Wang, X., Chiquet, J., Belcram, H., Tong, C., Samans, B., Correa, M., Da Silva, C., Just, J., Falentin, C., Koh, C. S., Le Clainche, I., Bernard, M., Bento, P., Noel, B., Labadie, K., Alberti, A., Charles, M., Arnaud, D., Guo, H., Daviaud, C., Alamery, S., Jabbari, K., Zhao, M., Edger, P. P., Chelaifa, H., Tack, D., Lassalle, G., Mestiri, I., Schnel, N., Le Paslier, M.-C., Fan, G., Renault, V., **Bayer, P. E.**, Golicz, A. A., Manoli, S., Lee, T.-H., Thi, V. H. D., Chalabi, S., Hu, Q., Fan, C., Tollenaere, R., Lu, Y., Battail, C., Shen, J., Sidebottom, C. H. D., Canaguier, A., Chauveau, A., Berard, A., Deniot, G., Guan, M., Liu, Z., Sun, F., Lim, Y. P., Lyons, E., Town, C. D., Bancroft, I., Meng, J., Ma, J., Pires, J. C., King, G. J., Brunel, D., Delourme, R., Renard, M., Aury, J.-M., Adams, K. L., Batley, J., Snowdon, R. J., Tost, J., Edwards, D., Zhou, Y., Hua, W., Sharpe, A. G., Paterson, A. H., Guan, C., Wincker, P., “Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome” *Science* 345.6199 (2014) pp. 950–953. *American Association for the Advancement of Science*. Citations: 384, Impact Factor: 34.6, JCR Multidisciplinary Sciences 2/62 (Q1), Altmetric score: 175
- Mason, A. S., Batley, J., **Bayer, P. E.**, Hayward, A., Cowling, W. A., Nelson, M. N., “High-resolution molecular karyotyping uncovers pairing between ancestrally related *Brassica* chromosomes” *New Phytologist* 202.3 (2014) pp. 964–974. *Wiley Online Library*. Citations: 16, Impact Factor: 7.21, JCR Plant Sciences 5/209 (Q1)
- Greshake, B., **Bayer, P. E.**, Rausch, H., Reda, J., “OpenSNP—a crowdsourced web resource for personal genomics” *PLoS One* 9.3 (2014) e89204. *Public Library of Science*. Citations: 26, Impact Factor: 3.057, JCR Multidisciplinary Sciences 11/63 (Q1), Altmetric score: 61
- Dattolo, E., Gu, J., **Bayer, P. E.**, Mazzuca, S., Serra, I. A., Spadafora, A., Bernardo, L., Natali, L., Cavallini, A., Procaccini, G., “Acclimation to different depths by the marine angiosperm *Posidonia oceanica*: transcriptomic and proteomic profiles” *Frontiers in Plant Science* 4 (2013) p. 195. *Frontiers*

experience

- 2021–Current **Member, Scientific Advisory Panel Machine Learning** ARDC
Member of the scientific advisory panel for ongoing machine learning projects supported by the ARDC.
- 2012–2018 **Research collaboration with Bayer CropScience, later BASF** Ghent, Belgium
Continued collaboration with Bayer CropScience on their plant breeding projects which includes several week-long visits to Bayer.
- 2011–Current **Co-founder openSNP.org** Germany/Australia
A project for customers of genotyping companies like 23andMe to share their data with scientists around the world, for free. Partially wrote and still maintain the site's Ruby on Rails code-base, interact and manage with the community of 5000 users, administration of the site's servers, and supervision of contributors.
- 2013–Current **Software Carpentry and Data Carpentry instructor** Australia
Certified Software Carpentry and Data Carpentry instructor. Software Carpentry is a Mozilla/Alfred P. Sloan Foundation funded non-profit organization which teaches best programming practices (structured programming, reproducible research, version control etc.) in bootcamps to scientists around the world. Data Carpentry is a sister-organisation that focuses on teaching best data management practices.
- 2018 **Research Bazaar Organising committee** UWA, Perth
ResBaz is a world-wide three-day festival promoting digital literacy. As member of the organising committee I searched for helpers and teachers, drafted the timeplan, designed the web page, raised funding, succeeded in getting government MP to hold keynote
- 2017–Current **Hacky Hour Founder** UWA, Perth
Founded the Hacky Hour at UWA, a weekly get-together of researchers and staff working with programming and data, doubles as a help-desk for students with programming problems.
- 2017–2019 **Mozilla Open Science Leadership mentor** UWA, Perth
Mentoring open source programmers and researchers on how to streamline and grow open source and open science projects under the umbrella of Mozilla.
- 2016–2019 **EMBL-ABR Head of Nodes member, Open Science Special Interest Group member** UWA, Perth
EMBL-ABR is an Australian-wide network supporting the technical needs of life sciences researchers. Members of the group of Head of Nodes meet monthly to discuss the way forward for the organisation. The Open Science Special Interest Group meets bimonthly to discuss how EMBL-ABR can advance open science in Australia.
- 2016–2017 **COMBINE WA Representative** UWA, Perth
COMBINE is the student and early career researcher subcommittee of the Australian Bioinformatics and Computational Biology Society (ABACBS). As the local representative I organise or help organise workshops and regular networking events.

awards & funding

2021–2023	Grant: ARC Discovery Early Career Research Award Awarded DECRA for 2021-2023. Total funding: \$448,781 and \$418,772 in UWA funding.	UWA
2020–2022	Grant: Identifying genetic contributors to canola blackleg resistance in the presence of environmental effects using Machine Learning With Prof. Dave Edwards, Prof. Mohammed Bennamoun, Dr. Farid Boussaid, Prof. Jacqueline Batley. Total funding: \$309,524.	GRDC
2020–2022	Grant: Machine Learning - Project E: Deep Learning for early detection and classification of crop disease and stress With Prof. Mohammed Bennamoun, Dr. Farid Boussaid, Prof. Dave Edwards, Dr. Nic Taylor. Total funding: \$344,971.	GRDC
2019	Woodside Early Career Scientist of the Year, finalist Finalist in Premier's Science Awards 2019	UWA
2018	Rising Stars nomination Two early career researchers per UWA research school were nominated for Rising Stars, a university-wide event where researchers introduce a public audience to their research	UWA
2018	Forrest Research Foundation Non-stipendiary Fellowship Three year fellowship to pursue research at UWA, part of the three inaugural Forrest Fellows	UWA
2017	UWA Research Collaboration Award \$28,100 to fund a seagrass microbiome sequencing project	UWA
2014	GRDC Travel Award Travel cost scholarship	GRDC
2014	SAFS Travel Award Travel cost scholarship	University of Queensland
2013	Bayer Grants4Apps Grant to cover openSNP running costs	Bayer HealthCare
2011–2014	Two postgraduate scholarships My PhD was supported by two scholarships from UQ for tuition fees and living costs.	University of Queensland
2012	First place in PLOS/Mendeley Binary Challenge Won first prize in a competition aimed towards the advancement of open science	Won with openSNP.org
2009-2011	Master IT 5x Top of class, 3x Vice-Chancellor's List for Academic Excellence, 1x IT Award Academic Excellence. Graduated with High Distinction. Recipient of John Oglethorpe Medal for highest GPA of all IT students graduating that semester	Bond University

teaching

2021–Current	University teaching Organised new MSc Bioinformatics with new unit, SCIE5003 (advanced bioinformatics). Developed content of SCIE5003 and SCIE4002, taught into both units.	UWA, Perth
2019	Introduction to genomics on the command line Introduction to the command line, bioinformatics analyses and pipelines, and basic SNP analysis in R	Research Bazaar, Curtin University, Perth
2019	Introduction to tidyverse and caret in R Introduction to R, tidyverse, ggplot2, caret, and basic statistics in R. Taught over two days.	UWA School of Human Sciences, Perth

2018	Introduction to modern R	Telethon Kids Institute, Perth
	Introduction to R, tidyverse, ggplot2, and basic statistics approaches in R. Taught over two days.	
2018	Teaching Data Carpentry	Research Bazaar, University of Western Australia, Perth
	Introduction to genomics and shell. Part of the planning committee.	
2017	Teaching Software Carpentry	Research Bazaar, Curtin University, Perth
	Introduction to data manipulation using Python	
2016	Teaching and hosting Data Carpentry	UWA, Perth
	Hosted, planned, and set up the first Data Carpentry workshop at UWA, taught best data management practices	
2016–Current	University teaching	UWA, Perth
	Co-teach and co-supervise SCIE4002, computational analysis for biology and biomedical MSc students. Set up and maintain the computational infrastructure needed for practicals. In 2017, the course has been judged 'consistently excellent' over six semesters based on student evaluations.	
2016	Teaching Software Carpentry	Curtin University, Perth
	Taught introduction to Python	
2016	Teaching Software Carpentry	Research Bazaar, Murdoch University, Perth
	Taught introduction to Python and git	
2016	Teaching and hosting Software Carpentry	University of Queensland, Brisbane
	Hosted, planned, and set up the first Software Carpentry workshop at UQ. Taught introduction to programming.	
2014	Teaching Software Carpentry	Sydney
	Taught basic to intermediate Python.	
2014	Teaching Software Carpentry	PyCon AU/University of Queensland
	Taught basic to intermediate Python.	
2013	Teaching Software Carpentry	Adelaide
	Assisted Software Carpentry bootcamp in Adelaide	
2009–2011	Tutoring	Bond University
	Tutored students in Intro to Programming (Java), Database Management (Oracle/MySQL) and Networks & Applications, held several all-day refresher courses before exams	

presentations

2021	Machine learning in plant breeding and bioinformatics CINVESTAV, online	Invited talk
2021	Future-ready crops for a changing climate: the role of bioinformatics UWA DVCR Forrest Foundation seminar series	Invited talk
2021	Bioinformatics at scale panel Q&A Pawsey Supercomputing Centre	Invited Q&A
2021	Interpretable machine learning in bioinformatics ABACBS online seminar series	Invited talk
2020	Our machine learning technical stack GRDC Tech seminar series	
2020	Predicting Gene Loss in Plants: Lessons Learned from Laptop-Scale Data Plant And Animal Genome conference, San Diego	
2019	Eukaryotic pangenomics: where we've been, where we're going Bayliss Seminar Series, Perth	Invited talk
2019	Assembling complex plant genomes – things I wish someone would have told me earlier AGRF Seminar Series, Perth	Invited talk
2019	Helping Biologists Make Sense of Plant Variant and Annotation Data Plant And Animal Genome conference, San Diego	
2018	Feeding the future world: safe-guarding Australia's food bowl in a changing climate Rising Stars, UWA	

2018	From QTLs to candidate genes, or: There and Back Again Institute of Agriculture Seminar Series, UWA	Invited talk
2018	The path of least resistance (genes) - mining plant genomes for disease resistance COMBINE/Pawsey bioinformatics symposium	Invited talk
2018	Early Career Researcher Panel - What have I learnt at the beginning of my research career? Combined Biological Sciences Meeting 2018	
2018	ScienceCafe - STEM outreach aimed at year 10 students UWA	
2017	The future of wheat research Wheat showcase, UWA	
2017	Skipping the assembly step – what we can learn from looking at sequences directly Pawsey Roadshow, UWA, Perth	
2017	The State of Bioinformatics in High Performance Computing in 2017 HPCAC Conference, Perth	
2017	Towards better plant breeding at UWA COMBINE event, Perth	
2017	Improving Plant Breeding using KNetMiner Plant And Animal Genome conference, San Diego	
2016	Towards a canola pan-genome: cautionary tales from the assembly bench CCDM, Curtin University	Invited talk
2016	Sharing Experience: What Can We Learn from Each Other Developing Plant Informatics Systems Plant And Animal Genome conference, San Diego	
2015	Assessing and validating the amphidiploid genome of <i>Brassica napus</i> using genotyping by sequencing Plant And Animal Genome conference, San Diego	
2015	Using skim-based genotyping by sequencing for trait association and QTL cloning in <i>Brassica napus</i> Plant And Animal Genome conference, San Diego	
2014	Assembling and validating the genome of the <i>Brassica napus</i> using skim-based genotyping by sequencing University of Queensland, GenGen Seminar Series	
2012	openSNP: Crowdsourcing Genome Wide Association Studies 28th Chaos Communication Congress, Berlin	