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
Go, Perl, Bash, Java
Ruby on Rails,
JavaScript, HTML

research

Genomics of complex
traits in domesticated
plants

statistics

Citations: 1719
h-index: 17
i10-index: 20

edu**cation**

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

emp**loyment**

2018-Current	**Forrest Fellow**	UWA, Perth

Edwards Lab. Continued work on genomics of complex plants with Forrest Foundation support. Supervised one PhD student and two 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).

pub**lications**

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., Cápal, 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., Cápal, 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., Lichtenzveig, 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., "CropSNPdb: 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-leafed 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

2012–Current   **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–Current   **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–Current   **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

2019	**Woodside Early Career Scientist of the Year, finalist**	UWA

Finalist in Premier's Science Awards 2019

2018	**Rising Stars nomination**	UWA

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

2018	**Forrest Research Foundation Non-stipendiary Fellowship**	UWA

Three year fellowship to pursue research at UWA, part of the three inaugural Forrest Fellows

2017	**UWA Research Collaboration Award**	UWA

$28,100 to fund a seagrass microbiome sequencing project

2014	**GRDC Travel Award**	GRDC

Travel cost scholarship

2014	**SAFS Travel Award**	University of Queensland

Travel cost scholarship

2013	**Bayer Grants4Apps**	Bayer HealthCare

Grant to cover openSNP running costs

2011–2014	**Two postgraduate scholarships**	University of Queensland

My PhD was supported by two scholarships from UQ for tuition fees and living costs.

2012	**First place in PLOS/Mendeley Binary Challenge**	Won with openSNP.org

Won first price in a competition aimed towards the advancement of open science

2009-2011	**Master IT**	Bond University

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

teaching

2019	**Introduction to genomics on the command line**	Research Bazaar, Curtin University, Perth

Introduction to the command line, bioinformatics analyses and pipelines, and basic SNP analysis in R

2019	**Introduction to tidyverse and caret in R**	UWA School of Human Sciences, Perth

Introduction to R, tidyverse, ggplot2, caret, and basic statistics in R. Taught over two days.

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

2019	**Eukaryotic pangenomics: where we've been, where we're going**
	Bayliss Seminar Series, Perth

2019	**Assembling complex plant genomes – things I wish someone would have told me earlier**
	AGRF Seminar Series, Perth

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

2018	**The path of least resistance (genes) - mining plant genomes for disease resistance**
	COMBINE/Pawsey bioinformatics symposium

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
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 *Brassica napus* 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 Brassica napus**
	Plant And Animal Genome conference, San Diego
2014	**Assembling and validating the genome of the *Brassica napus* using skim-based genotyping by sequencing**
	University of Queensland, GenGen Seminar Series
2012	**openSNP: Crowdsourcing Genome Wide Association Studies**
	28th Chaos Communication Congress, Berlin