

# Dr. Philipp Bayer

Postdoctoral researcher

## contact

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## 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: 951  
h-index: 12  
i10-index: 13

## 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

- 2018–Current **Forrest Fellow** UWA, Perth  
Edwards Lab. Continued work on genomics of complex plants with Forrest Foundation support.
- 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. Currently supervising two interns, co-supervised four PhD students and one MSc student, as well as the local computational infrastructure and data management. Worked extensively on an ARC Industrial Transformation Training Centre application (2018 round).

## publications

- 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
- 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* (2018). Wiley Online Library
- 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-leaved lupin” *Theoretical and Applied Genetics* (2018) pp. 1–12. 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

- 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., Nelson, M. N., "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.): INDEL variation in the regulatory region of *LanFTc1*" *Plant, Cell & Environment* (2018). Impact Factor: 6.173
- Lee, H., Golicz, A. A., **Bayer, P. E.**, Severn-Ellis, A., Kenneth Chan, C.-K., Batley, J., Kendrick, G. A., Edwards, D., "Genomic Comparison of Two Independent Seagrass Lineages Reveals Habitat-driven Convergent Evolution" *Journal of Experimental Botany* (2018). Impact factor: 5.830
- Mousavi-Derazmahalleh, M., **Bayer, P. E.**, Hane, J. K., Babu, V., Nguyen, H. T., Nelson, M. N., Erskine, W., Varshney, R. K., Papa, R., Edwards, D., "Adapting legume crops to climate change using genomic approaches: climate change legumes" *Plant, Cell & Environment* (2018). Impact Factor: 6.173
- 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-leaved 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
- 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 (2016) 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.-I., 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* (2016) p. 868. *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: 4.495, JCR Plant Sciences 15/209 (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** 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

2018	<b>Forrest Research Foundation Non-stipendiary Fellowship</b> Three year fellowship to pursue research at UWA, part of the three inaugural Forrest Fellows	UWA
2017	<b>UWA Research Collaboration Award</b> \$28,100 to fund a seagrass microbiome sequencing project	UWA
2014	<b>GRDC Travel Award</b> Travel cost scholarship	GRDC
2014	<b>SAFS Travel Award</b> Travel cost scholarship	University of Queensland
2013	<b>Bayer Grants4Apps</b> Grant to cover openSNP running costs	Bayer HealthCare
2011–2014	<b>Two postgraduate scholarships</b> My PhD was supported by two scholarships from UQ for tuition fees and living costs.	University of Queensland
2012	<b>First place in PLOS/Mendeley Binary Challenge</b> Won first prize in a competition aimed towards the advancement of open science	Won with openSNP.org
2009-2011	<b>Master IT</b> 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

2018	<b>Teaching R</b> Introduction to genomics analysis in R	Telethon Kids Institute, Perth
2018	<b>Teaching Data Carpentry</b> Introduction to genomics and shell. Part of the planning committee.	Research Bazaar, University of Western Australia, Perth
2017	<b>Teaching Software Carpentry</b> Introduction to data manipulation using Python	Research Bazaar, Curtin University, Perth
2016	<b>Teaching and hosting Data Carpentry</b> Hosted, planned, and set up the first Data Carpentry workshop at UWA, taught best data management practices	UWA, Perth
2016–Current	<b>University teaching</b> 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.	UWA, Perth
2016	<b>Teaching Software Carpentry</b> Taught introduction to Python	Research Bazaar, Murdoch University, Perth

2016	<b>Teaching and hosting Software Carpentry</b>	UQ, Brisbane
	Hosted, planned, and set up the first Software Carpentry workshop at UQ. Taught introduction to programming.	
2014	<b>Teaching Software Carpentry</b>	Melbourne
	Taught basic to intermediate Python as well as documentation and assisted at bootcamp in Melbourne.	
2013	<b>Teaching Software Carpentry</b>	Adelaide
	Assisted Software Carpentry bootcamp in Adelaide	
2009–2011	<b>Tutoring</b>	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

2018	<b>The path of least resistance (genes) - mining plant genomes for disease resistance</b>	
	COMBINE/Pawsey bioinformatics symposium	
2018	<b>Early Career Researcher Panel - What have I learnt at the beginning of my research career?</b>	
	Combined Biological Sciences Meeting 2018	
2018	<b>ScienceCafe - STEM outreach aimed at year 10 students</b>	
	UWA	
2017	<b>The future of wheat research</b>	
	Wheat showcase, UWA	
2017	<b>Skipping the assembly step – what we can learn from looking at sequences directly</b>	
	Pawsey Roadshow, UWA, Perth	
2017	<b>The State of Bioinformatics in High Performance Computing in 2017</b>	
	HPCAC Conference, Perth	
2017	<b>Towards better plant breeding at UWA</b>	
	COMBINE event, Perth	
2017	<b>Improving Plant Breeding using KNetMiner</b>	
	Plant And Animal Genome conference, San Diego	
2016	<b>Towards a canola pan-genome: cautionary tales from the assembly bench</b>	
	CCDM, Curtin University	
2016	<b>Sharing Experience: What Can We Learn from Each Other Developing Plant Informatics Systems</b>	
	Plant And Animal Genome conference, San Diego	
2015	<b>Assessing and validating the amphidiploid genome of <i>Brassica napus</i> using genotyping by sequencing</b>	
	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