

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, HTML

research

Genomics of complex
traits in canola, wheat
and legumes

statistics

Citations: 504
h-index: 7
i10-index: 6

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 Honours
- 2006–2009 **Bachelor of Science** Biology University of Münster, Germany
Thesis: Analysis of splicing in two populations of marine plants using bioinformatic approaches

employment

- 2015–Current **Postdoctoral researcher** UWA, Perth
Edwards Lab. Researching genetics of complex plants with a focus on canola and wheat. Working closely with industry partners to improve their breeding programs. Preparing, writing, and publishing research. Currently supervising two interns, co-supervising four PhD students and one MSc student, as well as the local computational infrastructure and data management. Assisting researchers.

publications

- Yuan, Y., **Bayer, P. E.**, Lee, H., Edwards, D., “runBNG: A software package for BioNano genomic analysis on the command line” *Bioinformatics* (2017)
- 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*
- 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* in press, accepted 12. April (2017). 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. 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* in press, accepted 23. March (2017). 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). *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* (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.
- 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–Current **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

- 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 prize 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 honours. Recipient of John Oglethorpe Medal for highest GPA of all IT students graduating that semester

teaching

- 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.
- 2016 **Teaching Software Carpentry** Research Bazaar, Murdoch University, Perth
Taught introduction to Python
- 2016 **Teaching and hosting Software Carpentry** UQ, Brisbane
Hosted, planned, and set up the first Software Carpentry workshop at UQ. Taught introduction to programming.

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| 2014 | Teaching Software Carpentry Taught basic to intermediate Python as well as documentation and assisted at bootcamp in Melbourne. | Melbourne |
| 2013 | Teaching Software Carpentry Assisted Software Carpentry bootcamp in Adelaide | Adelaide |
| 2009–2011 | Tutoring Tutored students in Intro to Programming (Java), Database Management (Oracle/MySQL) and Networks & Applications, held several all-day refresher courses before exams | Bond University |

Presentations

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| 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 <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 | |