Dr. Philipp **Bayer**

Postdoctoral researcher

contact

philippbay@gmail.com
github.com/philippbayer
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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 and wheat

statistics

Citations: 492
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
Dave Edwards Lab. Started after submission of thesis while waiting for visa in Germany. Researching the 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. Supervising the local computational infrastructure and data management. Assisting other researchers. Started and continue to run the group's journal club.

publications

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)*. IF: 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*. IF: 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*. IF: 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)*. IF: 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*. IF: 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, IF: 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, IF: 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, IF: 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*. IF: 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, IF: 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, IF: 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, IF: 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, IF: 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, IF: 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, IF: 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

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.

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.

2012–2012 **Research exchange** at Bayer CropScience Ghent, Belgium
For 4 weeks, worked on the assembly of the *Brassica napus* genome. Learned to work in a corporate science environment. Still regularly involved with Bayer CropScience and continue to collaborate with the company on many projects, including several short visits to Bayer when in Europe.

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.

awards

2014 **GRDC Travel Award** — GRDC
Travel cost scholarship

2014 **SAFS Travel Award** — University of Queensland
Travel cost scholarship

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 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.

2013–2014 **Teaching Software Carpentry** — Adelaide/Melbourne
Assisted Software Carpentry bootcamp in Adelaide, taught basic to intermediate Python as well as documentation and assisted at bootcamp in Melbourne.

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

Oral

2017 **Presentation** COMBINE event, Perth
Towards better plant breeding at UWA

2017 **Presentation** Plant And Animal Genome conference, San Diego
Improving Plant Breeding using KNetMiner

2016 **Presentation** CCDM, Curtin University
Towards a canola pan-genome: cautionary tales from the assembly bench

2015 **Presentation** Plant And Animal Genome conference, San Diego
Assessing and validating the amphidiploid genome of *Brassica napus* using genotyping by sequencing

2014 **Presentation** University of Queensland, GenGen Seminar Series
Assembling and validating the genome of the *Brassica napus* using skim-based genotyping by sequencing

2012 **Presentation** 28th Chaos Communication Congress, Berlin
Presented the work on openSNP, talked about the future of personal genomics and privacy implications

Poster

2016 **Poster** Brassica 2016, Melbourne
Comparison of two canola genome assemblies: the challenge of producing a *Brassica* pangenome

2015 **Poster** Plant and Animal Genome conference, San Diego
Assessing and Validating the Amphidiploid Genome of *Brassica napus* using Genotyping by Sequencing

2013 **Poster** Plant And Animal Genome conference, San Diego
Genome Assembly Validation and Trait Association using Skim Based Genotyping by Sequencing in Canola