

# dr. philippbayer

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 and  
wheat

## stats

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

## 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 **Postdoctoral researcher** UWA, Perth  
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.
- 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	<b>Research exchange</b> at Bayer CropScience	Ghent, Belgium
	For 4 weeks, worked on the assembly of the <i>Brassica napus</i> 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.	
2011–Current	<b>Co-founder openSNP.org</b>	Germany/Australia
	A project for costumers 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	<b>GRDC Travel Award</b>	GRDC
	\$4000 travel cost scholarship	
2014	<b>SAFS Travel Award</b>	University of Queensland
	\$2500 travel cost scholarship	
2011–2014	<b>Two postgraduate scholarships</b>	University of Queensland
	For the work on genotyping by sequencing, covers tuition and living costs.	
2012	<b>First place in PLOS/Mendeley Binary Challenge</b>	Won with openSNP.org
	Won first price in a competition aimed towards the advancement of open science	
2009–2011	<b>Master IT</b>	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	<b>Teaching Software Carpentry</b>	Curtin University, Perth
	Introduction to version control	
2017	<b>Teaching Software Carpentry</b>	Research Bazaar, Curtin University, Perth
	Introduction to data manipulation using Python	
2016	<b>Teaching and hosting Data Carpentry</b>	UWA, Perth
	Hosted, planned, and set up the first Data Carpentry workshop at UWA, taught best data management practices	
2016–Current	<b>University teaching</b>	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	<b>Teaching Software Carpentry</b>	Research Bazaar, Murdoch University, Perth
	Taught introduction to Python	
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.	
2013–2014	<b>Teaching Software Carpentry</b>	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	<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	

## public speaking

2017	<b>Presentation</b>	COMBINE event, Perth
	Title: Towards better plant breeding at UWA	
2017	<b>Presentation</b>	Plant And Animal Genome conference, San Diego
	Title: Improving Plant Breeding using KNetMiner	
2016	<b>Presentation</b>	CCDM, Curtin University
	Title: Towards a canola pan-genome: cautionary tales from the assembly bench	
2015	<b>Presentation</b>	Plant And Animal Genome conference, San Diego
	Title: Assessing and validating the amphidiploid genome of <i>Brassica napus</i> using genotyping by sequencing	
2014	<b>Presentation</b>	University of Queensland, GenGen Seminar Series
	Title: Assembling and validating the genome of the <i>Brassica napus</i> using skim-based genotyping by sequencing	
2013	<b>Poster</b>	Plant And Animal Genome conference, San Diego
	Title: Genome Assembly Validation and Trait Association using Skim Based Genotyping by Sequencing in Canola	
2012	<b>Presentation</b>	28th Chaos Communication Congress, Berlin
	Presented the work on openSNP, talked about the future of personal genomics and privacy implications	

## publications

**Bayer, Philipp E**, Bhavna Hurgobin, Agnieszka A Golicz, Chon-Kit Kenneth Chan, Yuxuan Yuan, HueyTyng Lee, Michael Renton, Jinling Meng, Ruiyuan Li, Yan Long, et al. "Assembly and comparison of two closely related *Brassica napus* genomes" *Plant biotechnology journal* (2017)

- Conceived of the study, performed the majority of analysis steps, wrote the publication.

Yuxuan Yuan, **Bayer, Philipp E**, Jacqueline Batley, and David Edwards "Improvements in Genomic Technologies: Application to Crop Genomics" *Trends in Biotechnology* (2017). *Elsevier Current Trends*

- Added several citations, added paragraphs, proof-read and error-corrected.

Juan D Montenegro, Agnieszka A Golicz, **Bayer, Philipp E**, Bhavna Hurgobin, HueyTyng Lee, Chon-Kit Kenneth Chan, Paul Visendi, Kaitao Lai, Jaroslav Doležel, Jacqueline Batley, et al. "The pangenome of hexaploid bread wheat" *The Plant Journal* (2017)

- Streamlined the annotation pipeline.

Parwinder Kaur, **Bayer, Philipp E**, Zbyněk Milec, Jan Vrána, Yuxuan Yuan, Rudi Appels, David Edwards, Jacqueline Batley, Phillip Nichols, William Erskine, et al. "An advanced reference genome of *Trifolium subterraneum* L. reveals genes related to agronomic performance" *Plant biotechnology journal* (2017)

- Created the advanced ordering of assembly, performed new gene prediction, analysed cultivar differences.

Katarzyna Gacek, **Bayer, Philipp E**, Iwona Bartkowiak-Broda, Laurencja Szala, Jan Bocianowski, David Edwards, and Jacqueline Batley "Genome-wide association study of genetic control of seed fatty acid biosynthesis in *Brassica napus*" *Frontiers in Plant Science* 7 (2016). *Frontiers Media SA*

- Ran the genome-wide association study, interpreted results.

Agnieszka A Golicz, **Bayer, Philipp E**, Guy C Barker, Patrick P Edger, HyeRan Kim, Paula A Martinez, Chon Kit Kenneth Chan, Anita Severn-Ellis, W Richard McCombie, Isobel AP Parkin, et al. “The pangenome of an agronomically important crop plant *Brassica oleracea*” *Nature Communications* 7 (2016). *Nature Publishing Group*

- Ran different orders of the *B. oleracea* assembly steps, ran annotation, helped with biological analysis and plotting.

James K Hane, Yao Ming, Lars G Kamphuis, Matthew N Nelson, Gagan Garg, Craig A Atkins, **Bayer, Philipp E**, Armando Bravo, Scott Bringans, Steven Cannon, et al. “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

- Helped with setup of annotation and repeat pipeline.

Mark Barash, **Bayer, Philipp E**, and Angela van Daal “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*

- Ran the entire genome-wide association study, interpreted results.

HueyTyng Lee, Agnieszka A Golicz, **Bayer, Philipp E**, Yuannian Jiao, Haibao Tang, Andrew H Paterson, Gaurav Sablok, Rahul R Krishnaraj, Chon-Kit Kenneth Chan, Jacqueline Batley, et al. “The genome of a southern hemisphere seagrass species (*Zostera muelleri*)” *Plant Physiology* (2016) pp–00868. *American Society of Plant Biologists*

- Supervised part of the analysis, helped with biological interpretation.

**Bayer, Philipp E** “Genomics of Salinity” (2016) pp. 179–194. *Springer New York*

- Collected literature, wrote the review.

Paul Visendi, Paul J Berkman, Satomi Hayashi, Agnieszka A Golicz, **Bayer, Philipp E**, Pradeep Ruperao, Bhavna Hurgobin, Juan Montenegro, Chon-Kit Kenneth Chan, Helena Stařková, et al. “An efficient approach to BAC based assembly of complex genomes” *Plant methods* 12.1 (2016) p. 2. *BioMed Central*

- Helped with streamlining and error removal of the assembly pipeline, helped interpret results, plotting.

Annaliese S Mason, Mathieu Rousseau-Gueutin, Jérôme Morice, **Bayer, Philipp E**, Naghmeh Besharat, Anouska Cousin, Aneeta Pradhan, Isobel AP Parkin, Anne-Marie Chèvre, Jacqueline Batley, et al. “Centromere locations in brassica A and C genomes revealed through half-tetrad analysis” *Genetics* 202.2 (2016) pp. 513–523. *Genetics*

- Analysed different alleles ratios between individuals, wrote analysis script to find outlier regions.

**Bayer, Philipp E** “Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies” *Plant Bioinformatics: Methods and Protocols* (2016) pp. 285–292. *Springer New York*

- Collected literature, wrote the review.

**Bayer, Philipp E**, Pradeep Ruperao, Annaliese S Mason, Jiri Stiller, Chon-Kit Kenneth Chan, Satomi Hayashi, Yan Long, Jinling Meng, Tim Sutton, Paul Visendi, et al. “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*

- Conceived the study, carried out the majority of the research, wrote the majority of software, wrote publication.

Agnieszka A Golicz, **Bayer, Philipp E**, and David Edwards “Skim-based genotyping by sequencing” *Plant Genotyping: Methods and Protocols* (2015) pp. 257–270. Springer New York

- Wrote parts of the review, collected literature.

Kaitao Lai, Michał T Lorenc, Hong Ching Lee, Paul J Berkman, **Bayer, Philipp E**, Paul Visendi, Pradeep Ruperao, Timothy L Fitzgerald, Manuel Zander, Chon-Kit Kenneth Chan, et al. “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

- Helped with analysis and phylogenetic analysis.

Boulos Chalhoub, France Denoeud, Shengyi Liu, Isobel AP Parkin, Haibao Tang, Xiyin Wang, Julien Chiquet, Harry Belcram, Chaobo Tong, Birgit Samans, et al. “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

- Carried out genotyping by sequencing analysis, manually validated contig placement, compiled report of misassemblies.

Annaliese S Mason, Jacqueline Batley, **Bayer, Philipp E**, Alice Hayward, Wallace A Cowling, and Matthew N Nelson “High-resolution molecular karyotyping uncovers pairing between ancestrally related *Brassica* chromosomes” *New Phytologist* 202.3 (2014) pp. 964–974. Wiley Online Library

- Performed the technical analysis and wrote the R-script.

Bastian Greshake, **Bayer, Philipp E**, Helge Rausch, and Julia Reda “OpenSNP—a crowdsourced web resource for personal genomics” *PLoS One* 9.3 (2014) e89204. Public Library of Science

- Built large parts of the website, co-wrote the publication.

Emanuela Dattolo, Jenny Gu, **Bayer, Philipp E**, Silvia Mazzuca, Ilia Anna Serra, Antonia Spadafora, Letizia Bernardo, Lucia Natali, Andrea Cavallini, and Gabriele Procaccini “Acclimation to different depths by the marine angiosperm *Posidonia oceanica*: transcriptomic and proteomic profiles” *Frontiers in plant science* 4 (2013) p. 195. Frontiers

- Ran EST-based differential expression analysis of seagrasses grown in different depths.