

philippbayer

bioinformatician

contact

philippbay@gmail.com
github.com/philippbayer

languages

German: mother tongue
English: fluent
French & Japanese:
advanced

programming

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

education

- 2012–current **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. Expected to submit in December 2014
- 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

- 2013–Current **Software Carpentry instructor** Australia
Certified Software 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
- 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
- 2011–Now **Co-founder openSNP.org** Germany/Australia
A project for costumers of genotyping companies like 23andMe to share their data with scientists around the world, for free.
Responsibilities:
 - Partially wrote and still maintain the site's Ruby on Rails code-base
 - Interact with the community of 1500 users
 - System administration of the site's server

awards

- 2014 **GRDC Travel Award** GRDC
\$4000 travel cost scholarship
- 2014 **SAFS Travel Award** University of Queensland
\$2500 travel cost scholarship
- 2011–2014 **Two postgraduate scholarships** University of Queensland
For the work on genotyping by sequencing, covers tuition 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

communication skills

2015	Presentation	Plant and animal genome conference, San Diego
	Assessing and validating the amphidiploid genome of <i>Brassica napus</i> using genotyping by sequencing	
2014	Presentation	University of Queensland, GenGen Seminar Series
	Assembling and validating the genome of the <i>Brassica napus</i> using skim-based 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	
2013–2014	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. Currently organizing a bootcamp in Brisbane in July 2014.	
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	

interests

professional: genotyping by sequencing, genome refinement, programming, machine learning, teaching

personal: literature, running, travel

publications

OpenSNP—a crowdsourced web resource for personal genomics

Bastian Greshake, **Bayer, Philipp E**, Helge Rausch, and Julia Reda

PLoS One 9.3 (2014) e89204. *Public Library of Science*, 2014

High-resolution molecular karyotyping uncovers pairing between ancestrally related *Brassica* chromosomes

Annaliese S Mason, Jacqueline Batley, **Bayer, Philipp E**, Alice Hayward, Wallace A Cowling, and Matthew N Nelson

New Phytologist 202.3 (2014) pp. 964–974. *Wiley Online Library*, 2014

Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat

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.

Plant biotechnology journal 13.1 (2015) pp. 97–104. 2015

Acclimation to different depths by the marine angiosperm *Posidonia oceanica*: transcriptomic and proteomic profiles

Emanuela Dattolo, Jenny Gu, **Bayer, Philipp E**, Silvia Mazzuca, Ilia Anna Serra, Antonia Spadafora, Letizia Bernardo, Lucia Natali, Andrea Cavallini, and Gabriele Procaccini

Frontiers in plant science 4 (2013) p. 195. *Frontiers*, 2013

Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome

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

Science 345.6199 (2014) pp. 950–953. *American Association for the Advancement of Science*, 2014

Skim-based genotyping by sequencing

Agnieszka A Golicz, **Bayer, Philipp E**, and David Edwards

Plant Genotyping: Methods and Protocols (2015) pp. 257–270. *Springer New York*, 2015

High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in Cicer arietinum and Brassica napus

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.

Theoretical and Applied Genetics 128.6 (2015) pp. 1039–1047. *Springer Berlin Heidelberg*, 2015

Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies

Bayer, Philipp E

Plant Bioinformatics: Methods and Protocols (2016) pp. 285–292. *Springer New York*, 2016

Centromere locations in brassica A and C genomes revealed through half-tetrad analysis

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.

Genetics 202.2 (2016) pp. 513–523. *Genetics*, 2016

An efficient approach to BAC based assembly of complex genomes

Paul Visendi, Paul J Berkman, Satomi Hayashi, Agnieszka A Golicz, **Bayer, Philipp E**, Pradeep Ruperao, Bhavna Hurgobin, Juan Montenegro, Chon-Kit Kenneth Chan, Helena Staňková, et al.

Plant methods 12.1 (2016) p. 2. *BioMed Central*, 2016

Bayer, Philipp E. “Genomics of Salinity”. In: *Plant Genomics and Climate Change*. Springer New York, 2016, pp. 179–194 The genome of a southern hemisphere seagrass species (*Zostera muelleri*)

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.

Plant Physiology (2016) pp–00868. *American Society of Plant Biologists*, 2016

Candidate gene scan for Single Nucleotide Polymorphisms involved in the determination of normal variability in human craniofacial morphology

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

bioRxiv (2016) p. 060814. *Cold Spring Harbor Labs Journals*, 2016

A comprehensive draft genome sequence for lupin (*Lupinus angustifolius*), an emerging health food: insights into plant–microbe interactions and legume evolution

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.

Plant biotechnology journal 15.3 (2017) pp. 318–330. 2017

The pangenome of an agronomically important crop plant Brassica oleracea

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.

Nature Communications 7 (2016). Nature Publishing Group, 2016

Genome-wide association study of genetic control of seed fatty acid biosynthesis in *Brassica napus*

Katarzyna Gacek, **Bayer, Philipp E**, Iwona Bartkowiak-Broda, Laurencja Szala, Jan Bocianowski, David Edwards, and Jacqueline Batley

Frontiers in Plant Science 7 (2016). Frontiers Media SA, 2016

An advanced reference genome of *Trifolium subterraneum* L. reveals genes related to agronomic performance

Parwinder Kaur, **Bayer, Philipp E**, Zbyněk Milec, Jan Vrána, Yuxuan Yuan, Rudi Appels, David Edwards, Jacqueline Batley, Phillip Nichols, William Erskine, et al.

Plant biotechnology journal (2017). 2017

The pangenome of hexaploid bread wheat

Juan D Montenegro, Agnieszka A Golicz, **Bayer, Philipp E**, Bhavna Hurgobin, HueyTyng Lee, Chon-Kit Kenneth Chan, Paul Visendi, Kaitao Lai, Jaroslav Doležal, Jacqueline Batley, et al.

The Plant Journal (2017). 2017

Improvements in Genomic Technologies: Application to Crop Genomics

Yuxuan Yuan, **Bayer, Philipp E**, Jacqueline Batley, and David Edwards

Trends in Biotechnology (2017). Elsevier Current Trends, 2017

Assembly and comparison of two closely related *Brassica napus* genomes

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.

Plant biotechnology journal (2017). 2017