

philippbayer

bioinformatician

contact

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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 *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
- 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

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*, 2014

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*, 2014

Kaitao Lai, Michal 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. 2015

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*, 2013

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*, 2014

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*, 2015

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*, 2015

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*, 2016

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*, 2016

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.

An efficient approach to BAC based assembly of complex genomes

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

Bayer, Philipp E

Genomics of Salinity

(2016) pp. 179–194. *Springer New York*, 2016

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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*, 2016

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, 2016

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. 2017

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, 2016

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, 2016

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). 2017

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). 2017

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, 2017

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). 2017