

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 <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

High resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in chickpea and canola

Bayer, P. E., P. Ruperao, A. S. Mason, J. Stiller, C.-K. K. Chan, S. Hayashi, Y. Long, J. Meng, T. Sutton, P. Visendi, R. K. Varshney, J. Batley, and D. Edwards

TAG (submitted) (2014). 2014

Improving the assembly of the *Brassica napus* cultivars Darmor and Tapidor using genotyping by sequencing

Bayer, P. E., A. A. Golicz, C.-K. K. Chan, J. Stiller, J. Batley, and D. Edwards

Plant Biotechnol J (in preparation) (2014). 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, Sahana Manoli, Jiri Stiller, Jacqueline Batley, and David Edwards

Plant Biotechnol J (Aug. 2014). 2014

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

Boulos Chalhoub, France Denoeud, Shengyi Liu, Isobel A P. Parkin, Haibao Tang, Xiyin Wang, Julien Chiquet, Harry Belcram, Chaobo Tong, Birgit Samans, Margot Corr  a, Corinne Da Silva, J  r  my Just, Cyril Falentin, Chu Shin Koh, Isabelle Le Clainche, Maria Bernard, Pascal Bento, Benjamin Noel, Karine Labadie, Adriana Alberti,

Mathieu Charles, Dominique Arnaud, Hui Guo, Christian Daviaud, Salman Alamery, Kamel Jabbari, Meixia Zhao, Patrick P. Edger, Houda Chelaifa, David Tack, Gilles Lassalle, Imen Mestiri, Nicolas Schnel, Marie-Christine Le Paslier, Guangyi Fan, Victor Renault, **Bayer, Philipp E.**, and et al.

Science 345.6199 (Aug. 2014) pp. 950–953. 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 Phytol (Jan. 2014). 2014

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

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

Front Plant Sci 4 (2013) p. 195. 2013