



# Armin Scheben

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## Work experience

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10. 2019 – **Cold Spring Harbor Laboratory**, New York  
Postdoctoral Fellow Computational  
Principal Investigator: Adam Siepel  
Project on integrating omics data from wild relatives of sorghum and maize across phylogenetic scales to understand evolutionary processes and detect functional targets for crop improvement

## Education

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01. 2016 – 09.2019 **University of Western Australia (UWA)**, Perth  
PhD student in Applied Bioinformatics  
Advisor: David Edwards  
Thesis focus on “Harnessing genomic variation for breeding in hexaploid bread wheat and *Brassica napus*”, including work on genome assembly, genomic database development, identifying genome editing targets, and genome-wide association studies

10. 2013 – 09. 2015 **Ludwig Maximilian University (LMU)**, Munich  
M.Sc. Evolution, Ecology & Systematics (EES)  
Thesis on “Neotropical origin, transoceanic dispersal, and cryptic speciation in the pantropical leafy liverwort *Ceratolejeunea*”

10. 2010 – 09. 2013 **Georg-August University**, Goettingen  
B.Sc. Biodiversity & Ecology  
Thesis on “Hybrid speciation in the *Ranunculus auricomus* complex inferred from ITS sequence data and geometric morphometrics”

## Teaching

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07. 2015 – 07.2019 **Lecturer**, School of Biological Sciences, UWA, Perth  
Lectured and tutored for Master’s course in Bioinformatics and Data Analysis for Genomics (40 hours per year); the course teaches *de novo* genome assembly, phylogenetics and differential expression analysis

11. 2013 – 12. 2015 **Research Assistant**, Faculty of Biology, LMU, Munich  
Assisted in Master’s course in Systematics and Bachelor’s courses in flowering plant diversity

## Industry internships

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- 11.2018 – 12.2018                      **BASF**, Innovation Centre, Ghent  
Programmed pipeline for crop RNA-seq analysis using MinION long reads to improve genome annotations
10. 2017 – 11. 2017                      **Bayer CropScience**, Innovation Centre, Ghent  
Developed proprietary Python tool for CRISPR/Cas guide RNA design in target crops

## Computational skills

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**Python** – expert user (developed stand-alone tools and web tools, scripting)  
**Bash** – expert user (scripting for data management and analysis pipelines)  
**snakemake** – expert user (reproducible pipeline development for bioinformatics analyses)  
**R** – intermediate user (scripting and data visualization)  
**mySQL** - intermediate user (developed web database for genetic variants)  
Version control (<https://github.com/ascheben>)  
HPC cluster use (SLURM/PBS job management)

## Bioinformatics skills

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- Comparative genomics                      Carried out genome-wide presence-absence variation analyses in blackleg fungus, with a focus on virulence genes, using pangenomics, RNA-seq, bulked segregants analysis and protein function prediction
- Phylogenetics                                      Inferred maximum likelihood and Bayesian phylogenies based on gene sequences and single nucleotide polymorphisms in bryophytes, kelp, bitou bush and canola, using RAxML, IQ-Tree and MrBayes
- Population genetics                              Identified invasion history of bitou and population structure of kelp using RAD-seq-derived markers and approximate Bayesian computation

## Further skills

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- Languages    German (native)  
English (native; TOEFL iBT: 120/120)
- Team work    Lead Academic Mentor, University Hall College UWA  
Led team of four, organising academic events and providing academic support services from January 2017 to November 2018

## Awards

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- UWA Graduate Research School Publication Prize 2018 (\$250)
- Postgraduate Student Association Travel Award 2018 (\$800)
- Spillman Alumni Prize for most outstanding contribution to college, 2017 and 2018 (\$500)
- People's Choice - [3 Minute Thesis Competition UWA 2016](#) and 2018 (\$1000)
- International Postgraduate Research Scholarship 2016 (PhD and living stipend)
- [EES Young Researcher Prize](#), 2014 and 2015 (€300)

## Conferences

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Plant and Animal Genome XXVII 2019, Talk on “Brassica pangenomes as a novel source of disease resistance” in the Brassica Workshop

Plant and Animal Genome XXVII 2019, Poster presentation on “CropSNPdb: a database of SNP array data for *Brassica* crops and hexaploid bread wheat”

Brassica 2016, Melbourne, Poster presentation on “Evaluating genotyping by sequencing approaches for *Brassica napus* breeding”

## Media

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German radio interview [on crop genome editing](#)

Motherboard article based on interview about [crop genome editing and GMOs](#)

## Selected publications

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**Scheben A.**, Verpaalen B., Lawley CT, Chan KCK., Bayer P, Batley J, & Edwards D. CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. *The Plant Journal* 2019, 98:142-152.

**Scheben A**, Chan KCK, Mansueto L, Mauleon R, Larmande P, Alexandrov N, Wing R, McNally KL, Quesneville H, Edwards D: Progress in single-access information systems for wheat and rice crop improvement. *Briefings in Bioinformatics* 2018, 20:565-571.

**Scheben A**, Wolter F, Batley J, Puchta H, Edwards D: Towards CRISPR/Cas crops - bringing together genomics and genome editing. *New Phytologist* 2017, 216:682-698.

**Scheben A**, Edwards D: Genome editors take on crops. *Science* 2017, 355:1122-1123.

Yuan YX, Bayer PE, **Scheben A**, Chan KCK, Edwards D: BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data. *BMC Bioinformatics* 2017, 18:323.

**Scheben A**, Bechteler J, Lee GE, Pocs T, Schafer-Verwimp A, Heinrichs J: Multiple transoceanic dispersals and geographical structure in the pantropical leafy liverwort *Ceratolejeunea* (Lejeuneaceae, Porellales). *Journal of Biogeography* 2016, 43:1739-1749.

Hodac L, **Scheben A**, Hojsgaard D, Paun O, Hörandl E: ITS Polymorphisms shed light on hybrid evolution in apomictic plants: a case study on the *Ranunculus auricomus* complex. *PLoS One* 2014, 9:e103003.

Complete [list of publications](#) available via Google Scholar.

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