CURRICULUM VITAE

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NAME	Arthur Zwaenepoel
DATE OF BIRTH	20 February 1995
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EDUCATION

2017 - 2022   **PhD candidate in Bioinformatics**
Ghent University, Belgium
VIB/UGent department of plant systems biology
Fellow of the Flanders Fund for Scientific Research (FWO)
Thesis: *Bayesian Statistical Methods in Evolutionary Genomics*
Promotor: Prof. Dr. Yves Van de Peer

2015 - 2017   **Master of science in Bioinformatics (systems biology)**
Ghent University, Belgium
summa cum laude

2013 - 2015   **Honours programme 'Quetelet Colleges'**
Ghent University, Belgium

2012 - 2015   **Bachelor of science in Biochemistry & Biotechnology**
Ghent University, Belgium
summa cum laude

TEACHING

Teaching assistant / co-lecturer for the following courses:

- *Bioinformatics II* (Prof. Yves Van de Peer)
  2018 – 2022, 3 ECTS, MSc Biochemistry & Biotechnology
  I developed and organized practical sessions on statistical phylogenetics for this course.

- *Evolutionary biology* (Prof. Yves Van de Peer)
  2018 – 2022, 3 ECTS, MSc Bioinformatics
  I have taught theory and organized practical sessions on statistical phylogenetics for this course.

- *Philosophical issues in the life sciences* (Prof. Gertrudis Van de Vijver)
  2020 – 2022, 5 ECTS, MA philosophy
  I co-organized this course with professor Van de Vijver, guiding discussions on key texts

in the history and philosophy of biology. I have also lectured on 20th century evolutionary biology and the history of genetics in this course.

MENTORSHIP

Supervisor for Master 1 group projects (MSc Bioinformatics, Ghent University – 9 ECTS)
- In the 2018 – 2019 academic year I supervised a group of four students working on a project related to bioinformatic inference of ancient genome duplications.
- In the 2019 – 2020 academic year I supervised a group of five students working on a phylogenomics project, solving hard phylogenetics problems using advanced statistical tools.

Master thesis students (Msc. Bioinformatics, Ghent University – 30 ECTS):
- Sam Vanmassenhove (2019-2020)
  Thesis: *Variational inference for Bayesian models of gene family evolution*
- Michael Vandevoorde (2020-2021)
  Thesis: *PolyStab: Individual-based modeling to study polypoid establishment from an eco-evo perspective*

SKILLS

Languages: Dutch (native), English (fluent), French (advanced).

Programming languages: Julia (language of choice), Python (proficient), R (good), Perl (rusty), Haskell (learning with great interest). I have hacked new features on existing C++ codebases.

Other relevant skills: Bayesian statistics, probabilistic modeling, probabilistic programming, Bayesian computation (MCMC, SMC, ABC, VI), simulation, statistical phylogenetics, population genetics, comparative genomics, individual-based modeling, evolutionary theory, Bioinformatics (genomics, transcriptomics), high-performance computing, parallel computing, UNIX environments, git version control, LaTeX.

COURSES AND WORKSHOPS

EMBO practical course: Computational Molecular Evolution – 2018, Heraklion (Crete, Greece).

ForBio workshop on polyploid population genetics – 2019, Drøbak (Norway)

OTHER ACADEMIC

Co-organizer of the International Conference on Poyploidy in Ghent, Belgium (2019) (I did the scheduling of the talks, designed the conference programme booklet and various other tasks). With Yves Van de Peer and Polina Novikova.

Co-editor for the book "Methods in Molecular Biology: Polyploidy", with Yves Van de Peer and Zhen Li.

Reviewer. I have reviewed for Molecular Biology & Evolution, PLOS Genetics, Journal of Evolutionary Biology, Communications Biology, Proceedings of the Royal Society B.

Reading groups. I have organized various reading groups at Ghent University on evolutionary biology with a focus on population genetics and classical papers in theoretical evolutionary genetics. I have been involved in reading groups on important authors in the philosophy of biology (focusing in particular on Georges Canguilhem and Robert Rosen).

OTHER INTERESTS

I am highly interested (and fairly well-read) in philosophy, with a particular interest in Kantian epistemology in the philosophy of science, the French historical epistemology tradition, philosophy of biology (in particular the work of Robert Rosen) and the philosophical issues associated with probability and statistics in the sciences (I particularly enjoy the works of Jeffreys, de Finetti, Savage and Jaynes).

I have a very broad interest in mathematics, and, although not formally trained as a mathematician, I do a lot of self-study in mathematical topics (special interests include probability theory and category theory).

I take great interest in literature (Dutch, English and French), music (classical, Jazz, contemporary, electronic) and play music (guitars, computer music) myself. I enjoy running, cycling and skateboarding.

PUBLICATIONS

1. T. Zhao, **A. Zwaenepoel**, J.-Y. Xue, S.-M. Kao, Z. Li, M. E. Schranz, and Y. Van de Peer, "Whole-genome microsynteny-based phylogeny of angiosperms," *Nature Communications*, vol. 12, no. 1, pp. 1–14, 2020.
2. X. Wang, S. Chen, X. Ma, A. E. Yssel, S. R. Chaluvadi, M. S. Johnson, P. Gangashetty, F. Hamidou, M. D. Sanogo, **A. Zwaenepoel**, *et al.*, "Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (digitaria exilis)," *GigaScience*, vol. 10, no. 3, p. giab013, 2021.
3. **A. Zwaenepoel** and Y. Van de Peer, "Model-based detection of whole-genome duplications in a phylogeny," *Molecular biology and evolution*, vol. 37, no. 9, pp. 2734–2746, 2020.
4. D. Roelofs, **A. Zwaenepoel**, T. Sistermans, J. Nap, A. A. Kampfraath, Y. Van de Peer, J. Ellers, and K. Kraaijeveld, "Multi-faceted analysis provides little evidence for recurrent whole-genome duplications during hexapod evolution," *BMC biology*, vol. 18, pp. 1–13, 2020.
5. J. Zhang, X.-X. Fu, R.-Q. Li, X. Zhao, Y. Liu, M.-H. Li, **A. Zwaenepoel**, H. Ma, B. Goffinet, Y.-L. Guan, *et al.*, "The hornwort genome and early land plant evolution," *Nature plants*, vol. 6, no. 2, pp. 107–118, 2020.

6. **A. Zwaenepoel** and Y. Van de Peer, "Inference of ancient whole-genome duplications and the evolution of gene duplication and loss rates," *Molecular biology and evolution*, vol. 36, no. 7, pp. 1384–1404, 2019.
7. **A. Zwaenepoel** and Y. Van de Peer, "wgd—simple command line tools for the analysis of ancient whole-genome duplications," *Bioinformatics*, vol. 35, no. 12, pp. 2153–2155, 2019.
8. **A. Zwaenepoel**, Z. Li, R. Lohaus, and Y. Van de Peer, "Finding evidence for whole genome duplications: a reappraisal," *Molecular plant*, vol. 12, no. 2, pp. 133–136, 2019.
9. **A. Zwaenepoel**, T. Diels, D. Amar, T. Van Parys, R. Shamir, Y. Van de Peer, and O. Tzfadia, "Morphdb: prioritizing genes for specialized metabolism pathways and gene ontology categories in plants," *Frontiers in plant science*, vol. 9, p. 352, 2018.

PREPRINTS

1. H. Chen, Y. Fang, **A. Zwaenepoel**, S. Huang, Y. Van de Peer, Z. Li "Revisiting Ancient Polyploidy in Leptosporangiate Ferns," *bioRxiv*, 2022.
2. **A. Zwaenepoel**, & Y. Van de Peer. "A two-type branching process model of gene family evolution," *bioRxiv*, 2021.

CONTRIBUTED PRESENTATIONS

1. Probabilistic Modeling in Genomics, Aussois, France, (2020),
   Modeling and Bayesian inference of ancient whole-genome duplications.
2. International Conference on Polyploidy, Ghent, Belgium, (2019),
   Inference of ancient whole-genome duplications and the evolution of gene duplication and loss rates.
3. ALPHY (Alignment & Phylogeny) meeting, Paris, France, (2019),
   Inference of ancient whole-genome duplications using statistical gene tree reconciliation.

INVITED PRESENTATIONS

1. Polyploidy webinar (April 2021) – https://www.barkerlab.net/polyweb,
   Statistical inference of whole-genome duplications in a phylogenetic context using phylogenetic birth-death process models.