

Kathrin Martina Seibt

About me

I am a **computational and molecular biologist** with an **interdisciplinary background**. In order to address my research questions and to handle large amounts of data, I trained myself to acquire and apply programming skills in **Python** and **R**. I am passionate about problem solving, programming, and data visualization. Therefore, I am keen to expand my skill set and approach challenging tasks by integrating state-of-the-art technologies.

Work Experience

Career break for Maternity Leave

07/2021 – present

- contributions to data analyses, project reports, and publications

NORIKA GmbH, German potato breeder

01/2021 – 06/2021

- computational work: sequence analyses & quality control, database analysis, optimization & conversion from dBase, bioinformatics workshop

Meth.

Technische Universität Dresden, Germany Plant Cell & Molecular Biology

04/2012 – 10/2020

(late Prof. Dr. Thomas Schmidt/Dr. Tony Heitkam)

- BMBF projects "AVIMA" and "MASEPA" – development of resistance-linked molecular markers for marker-assisted potato breeding
- repetitive element genomics in nightshades & higher plants
- bioinformatics: comparative genomics, sequence analyses, creating analysis workflows in Python, statistical analyses & data visualization in R
- molecular biology: molecular markers, molecular cloning, DNA sequencing

Topics

Methods

NORIKA GmbH, German potato breeder

02/2009 – 03/2012

- BMBF project "RetroKartoffel" – development of molecular markers for potato cultivar differentiation
- molecular biology: plant DNA isolation, molecular markers
- bioinformatics: sequence analyses, establishment of a fingerprint database, genotype clustering

Topic

Methods

Medizinisches Labor Ostsachsen (Internship)

08/2006, 08/2007

- molecular/microbiology: cultivation, routine microbiological and molecular biological diagnostics such as ELISA, PCR, agglutination tests

Meth.

Education

Technische Universität Bergakademie Freiberg, Germany

10/2003 – 10/2008

Diploma Natural Scientist (Diplom-Naturwissenschaftler)
(grade 1.4; specialization biotechnology, environmental microbiology)

- course of studies: Angewandte Naturwissenschaft (applied science)
- diploma thesis at the chair of Environmental Microbiology (grade 1.2): "Cultivation & molecular characterization of sulfate-reducing bacteria [...]"
- molecular biology, microbiology, analytical chemistry, mathematics, physics
- basics of computer science and business administration

General

Topics

Gymnasium 2 Annenschule, Görlitz, Germany

2003

Abitur (grade 1.6; specialization mathematics, biology)



02.07.1984
in Görlitz, Germany



23.08.2021 (son Jakob)



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<https://github.com/KathSe1984>

Programming

Python	■■■■■■■■■
R	■■■■■■■■■
Unix/Bash	■■■■■■■■■
HTML	■■■■■■■■■
SQL	■■■■■■■■■
C++	■■■■■■■■■

Bioinformatics

Genomics	■■■■■■■■■
Sequence Annotation	■■■■■■■■■
Orthologue Search	■■■■■■■■■
Phylogenetics	■■■■■■■■■
Transcriptomics	■■■■■■■■■
Statistics	■■■■■■■■■
Protein Structure Prediction	■■■■■■■■■

Languages

German	■■■■■■■■■
English	■■■■■■■■■
Italian	■■■■■■■□
Spanish	■■■■■■■□

Personality

Extrovert	■■■■■□	Introvert
Rational	■□■■■	Emotional
Analytical	■□■■■	Creative
Organized	■□■■■	Chaotic

Soft Skills

problem solving
critical thinking
growth mindset
willingness to learn
quick grasp
decision-making
reliability
self-management
scheduling
effective communication
team work
open-mindedness
adaptability
intrinsic motivation
dedication

Hobbies



Travelling Pilates Photography



Board Games E-Learning

References

Dr. Tony Heitkam
TU Dresden
Plant Cell & Molecular Biology
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Kathrin Martina Seibt

Detailed Information: <https://github.com/KathSe1984/ProfessionalProfile/>

Professional Development (Selection)

Coursera MOOCs on Bioinformatics and Programming since 2013

- *Improving Deep Neural Networks: Hyperparameter Tuning, Regularization and Optimization* DeepLearning.AI; 5 weeks
- *Bioinformatics algorithms [part 1]* University of California; 14 weeks
- *Bioinformatics: introduction and methods* Peking University; 15 weeks
- *Introduction to interactive programming in Python* Rice University; 8 weeks
- *Principles of computing [part 1 and 2]* Rice University; 10 weeks
- *Learn to program: The fundamentals* University of Toronto; 10 weeks
- *Command line tools for genomic data science* John Hopkins University; 4 weeks
- *Computational molecular evolution* Technical University of Denmark; 6 weeks
- *Data analysis and statistical inference* Duke University; 8 weeks
- *Pattern discovery in data mining* University of Illinois at Urbana-Champaign; 4 weeks

Graduate Academy courses & lectures at **TU Dresden** 2015 – 2017

- *Programming for bioinformatics*
- *Applied bioinformatics*
- *Fundamentals in R*
- *Research data managements*
- *Probability, statistics & programming for computational biology*
- *Introduction to mathematical biology*
- *Reading strategies and techniques*

Good Manufacturing Practice (GMP)

2015, 2018

- *GMP* Technische Universität Dresden; 1 week
- *GMP Statistics* Universität Leipzig; 3 days

Software

- **Seibt** KM, Schmidt T & Heitkam T (2018) **FlexiDot**: Highly customizable, ambiguity-aware dotplots for visual sequence analyses. **Bioinformatics** 34(20):3575-3577; GitHub: <https://github.com/molbio-dresden/flexidot>

Selected Publications

- **Seibt** KM, Schmidt T & Heitkam T (2020) *The conserved 3' Angio-domain defines a superfamily of short interspersed nuclear elements (SINEs) in higher plants.* **Plant Journal** 101(3):681-699
- **Seibt** KM, Wenke T, Muders K, Truberg B & Schmidt T (2016) *Short interspersed nuclear elements (SINEs) are abundant in Solanaceae and have a family-specific impact on gene structure and genome organization.* **Plant Journal** 86(3):268-285
- Wenke T, **Seibt** KM, Döbel T, Muders K & Schmidt T (2015) *Inter-SINE amplified polymorphism (ISAP) for rapid and robust plant genotyping.* In: Batley J (ed) **Methods in Molecular Biology - Plant Genotyping: Methods and Protocols.** Springer, New York, pp 183-192
- **Seibt** KM, Wenke T, Wollrab C, Junghans H, Muders K, Dehmer KJ, Diekmann K & Schmidt T (2012) *Development and application of SINE-based markers for genotyping of potato varieties.* **Theoretical and Applied Genetics** 125(1):185-196

Full publication list: <https://scholar.google.com/citations?user=5tWrgxgAAAAJ>