

PERSONAL INFORMATION

Full Name:	Kathrin Martina Seibt
Date of Birth:	02.07.1984 (Görlitz, Germany)
Marital Status:	married
Children:	son born August 2021
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*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, data analyses, 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

- 07/2021 – present **Career Break for Maternity Leave**
- contributions to data analyses, project reports, and publications
 - self-organized road trip through southern Europe (2.5 months)
- 1/2021 – 06/2021 **potato breeder NORIKA GmbH**
- Methods
- data analyses: data extraction, profiling & transformation from dBase database using Python and R, sequence analyses & quality control, providing a bioinformatics workshop
- 04/2012 – 10/2020 **Technische Universität Dresden**, Plant Cell & Molecular Biology (late Prof. Thomas Schmidt/Dr. Tony Heitkam)
- Topics
- BMBF projects "AVIMA" and "MASEPA" – development of resistance-linked molecular markers for marker-assisted potato breeding
 - transposable element genomics in Solanaceae & higher plants
- Methods
- bioinformatics: comparative genomics, sequence analyses, development of analysis workflows in Python, statistical analyses and data visualization in R
 - molecular biology: molecular markers, cloning, DNA sequencing

02/2009 – 03/2012 **potato breeder NORIKA GmbH**

Topics

- BMBF project "RetroKartoffel" – development of a marker system for potato cultivar differentiation

Methods

- molecular biology: plant DNA isolation, molecular markers, molecular cloning
- bioinformatics: sequence analyses, establishment of a fingerprint database, genotype clustering

11/2007 – 10/2008 **Freiberg University of Mining & Technology,**
Diploma thesis Environmental Microbiology (Prof. Michael Schlömann)

Topic

- "Cultivation and molecular characterization of sulfate-reducing bacteria from mining sites" (grade 1,2)

Methods

- molecular/microbiology: cultivation of anaerobic bacteria, characterization of substrate utilization, DNA isolation, molecular cloning, molecular markers, Sanger DNA sequencing

03/2007 – 11/2007 **Freiberg University of Mining & Technology,**
Student project Environmental Microbiology (Prof. Michael Schlömann)

Topic

- "Bacterial diversity of a water sample from the uranium mine Königstein (Germany)"

Methods

- molecular/microbiology: DNA isolation, molecular cloning, molecular markers, Sanger DNA sequencing

08/2006, 08/2007 Medizinisches Labor Ostsachsen, Görlitz
Internship (Medical Laboratory East Saxony; Dr. med. Roger Hillert)

Methods

- molecular biology: routine microbiological and molecular biological diagnostics like ELISA, PCR, agglutination tests
- microbiological routine techniques

EDUCATION

10/2008	Diploma degree Diplom-Naturwissenschaftler (diploma natural scientist, grade 1.4)
10/2003 – 09/2008	Course of studies „ Angewandte Naturwissenschaft “ (applied natural science) at Freiberg University of Mining & Technology (TUBAF; Germany) Specialization: biotechnology, environmental microbiology
2003	Abitur (grade 1.6) at Gymnasium 2 Annenschule, Görlitz (Germany) Specialization: mathematics, biology

FURTHER EDUCATION AND PROFESSIONAL DEVELOPMENT

since 2013 **Bioinformatics and programming** MOOCs on Coursera platform

Introduction to interactive programming in Python	(Rice University, USA; 8 weeks)
Principles of computing [part 1 and 2]	(Rice University, USA; 5 weeks each)
Learn to program: The fundamentals	(University of Toronto, Canada; 10 weeks)
Bioinformatics algorithms [part 1]	(University of California, USA; 14 weeks)
Bioinformatics: Introduction and methods	(Peking University, China; 15 weeks)
Computational molecular evolution	(Technical University of Denmark, Denmark; 6 weeks)
Command line tools for genomic data science	(John Hopkins University, USA; 4 weeks)
Improving Deep Neural Networks: Hyperparameter Tuning, Regularization and Optimization	(DeepLearning.AI; 5 weeks)
PH525.1x: Statistics & R for the Life Sciences	(Harvard & Dana Farber Cancer Institute; via edX platform)

since 2013 MOOCs on **data analysis und writing** on Coursera platform

Data analysis and statistical inference	(Duke University, USA; 8 weeks)
Pattern discovery in data mining	(University of Illinois at Urbana-Champaign, USA; 4 weeks)
Crafting an effective writer: Tools of the trade	(Mt. San Jacinto College, USA; 6 weeks)
Creativity, innovation and change	(Penn State University, USA; 4 weeks)

2019 MOOC on **open science** by Technische Universität Dresden

Science 2.0 and open research methods (Moving MOOC)

2015 – 2017 Graduate Academy courses at Technische Universität Dresden

Research data managements	Fundamentals in R
Reading strategies & techniques	
Writing papers and theses in the life and natural sciences	
Time and self-management for doctoral candidates	
Enhance your visibility: Creating and developing your professional profile	

2009 – 2015 **Bioinformatics and biology** lectures at Technische Universität Dresden

Medical microbiology (grade 1.0)	Probability, statistics and programming for computational biology
Clinical genetics (grade 1.3)	
Interaction bacteria plants (grade 1.0)	Introduction to mathematical biology
Applied bioinformatics	Genes and genomes
Programming for bioinformatics	

2015/2018 **Good Manufacturing Practice**

Good Manufacturing Practice (GMP)	(TU Dresden, Germany; 1 week)
GMP Statistics Course	(Universität Leipzig, Germany; 3 days)

BIOINFORMATICS SKILLS

I quickly learn to apply, interpret, and integrate new software into custom pipelines. Here, I am only listing tools I used frequently.

programming languages	Python, R, RMarkdown (advanced) UNIX tools, bash scripting (intermediate) SQL, HTML (basic)
general sequence analysis	Geneious, Staden package, EMBOSS tools, Galaxy platform
alignment and mapping	Muscle, ClustalW, MAFFT, T-Coffee, Bowtie2
clustering	MEGA, SplitsTree (network analysis), CAFE (k-mer based clustering), SiLiX (similarity-based clustering), STRUCTURE (population structure analysis)
sequence search	BLAST, FASTA, nhmmer
NGS data analysis	FastQC, Trimmomatic, TrimGalore!, samtools, bedtools, SeqMonk, edgeR
transposable element annotation	RepeatExplorer, RepeatMasker, LTRharvest, LTR_Finder, SINE-Finder, and others
visualization	MapChart, IGV, FigTree, FlexiDot, ggplot2
others	handling various biological file formats (fastq, bed, gff, sam, vcf,...)

GENERAL COMPUTATIONAL SKILLS

operating systems	Windows, Linux administrator at the TU Dresden lab responsible for setup and maintenance of dual-boot computers
databases	GelComparII (molecular marker fingerprint manager) ARB (16S rDNA sequence database and analysis package) Microsoft SQL Server
general software	Microsoft Office, Endnote, Mendeley RStudio, Sublime, GitHub, Adobe Photoshop, Inkscape

EXPERIMENTAL SKILLS

I am used to designing and optimizing methodologies and I routinely plan, execute, document, and interpret large scale experiments.

molecular biology	DNA isolation, PCR, electrophoresis, molecular cloning, molecular markers (ARDRA, T-RFLP, ISAP, STS), Southern hybridization, Sanger sequencing, preparation of plant chromosome spreads, fluorescent <i>in situ</i> hybridization
other biological techniques	plant <i>in vitro</i> culture, grafting of potato plants, ELISA assay

LANGUAGES

German	native language	
English	fluent	(Unicert III)
Italian	conversational	(Unicert I, Level B1)
Spanish	basic	
Latin	Latinum	(Abitur, grade 1,0)

OTHER SKILLS

drivers license	German class B
GxP (good scientific practice)	basic knowledge

GRANTS

2018	Conference travel grant by the German Academic Exchange Office (DAAD) for the " <i>Transposable elements meeting</i> " in Cold Spring Harbor, USA
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TEACHING

2021	Bioinformatics trainings for TU Dresden and NORIKA lab members: detailed introduction to the softwares BioNumerics (genotype database) and Geneious (sequence analysis) with theoretical background
2017	Supervision of a Bachelor thesis entitled: „ <i>New ISAP markers based on the widespread plant SINE family Au & their evaluation using reference potato genotypes</i> “
2016 – 2020	Teaching during the practical course " <i>DNA sequencing</i> ": Introduction to bioinformatics (theoretical background of BLAST, file formats, Galaxy platform, trimming of NGS data)
2012	Supervision of a school thesis „Besondere Lernleistung“ (9 months) entitled: „ <i>Mobile DNA sequences as markers in crop breeding</i> “
since 2011	Supervision of visiting students (high-school students, university students, guest students from USA)

PERSONAL INTEREST

Travelling, Board Games, Photography, Pilates, E-Learning, listening to Blinkist



Dresden, 03.02.2023