

PERSONAL INFORMATION

Full Name:	Kathrin Martina Seibt
Date of Birth:	02.07.1984 (Görlitz, Germany)
Marital Status:	married
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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, 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

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|-------------------|---|
| 07/2021 – present | Career Break for Maternity Leave <ul style="list-style-type: none">contributions to data analyses, project reports, and publications |
| 1/2021 – 06/2021 | potato breeder NORIKA GmbH
<u>Methods</u> <ul style="list-style-type: none">computational work: sequence analyses & quality control, database analysis, optimization & conversion from dBase, bioinformatics workshop |
| 04/2012 – 10/2020 | Technische Universität Dresden , Plant Cell & Molecular Biology (late Prof. Thomas Schmidt/Dr. Tony Heitkam)
<u>Topics</u> <ul style="list-style-type: none">BMBF projects "AVIMA" and "MASEPA" – development of resistance-linked molecular markers for marker-assisted potato breedingtransposable element genomics in Solanaceae & higher plants
<u>Methods</u> <ul style="list-style-type: none">bioinformatics: comparative genomics, sequence analyses, development of analysis workflows in Python, statistical analyses and data visualization in Rmolecular 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

- 2019 MOOC on **open science** by Technische Universität Dresden
 Science 2.0 and open research methods (Moving MOOC)
- since 2013 **Bioinformatics and programming** MOOCs on Coursera platform
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| Improving Deep Neural Networks: Hyperparameter Tuning, Regularization and Optimization | (DeepLearning.AI; 5 weeks) |
| Bioinformatics algorithms [part 1] | (University of California, USA; 14 weeks) |
| Bioinformatics: Introduction and methods | (Peking University, China; 15 weeks) |
| Command line tools for genomic data science | (John Hopkins University, USA; 4 weeks) |
| Computational molecular evolution | (Technical University of Denmark, Denmark; 6 weeks) |
| 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) |
- since 2013 MOOCs on **data analysis und writing** on Coursera platform
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|--|--|
| 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) |
- 2015 – 2017 Graduate Academy courses at Technische Universität Dresden
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| Research data managements | Fundamentals in R |
| Reading strategies and 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
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| 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**
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| 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 RStudio, Sublime, GitHub Endnote, Mendeley Adobe Photoshop, Inkscape

EXPERIMENTAL SKILLS

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

PUBLISHED SOFTWARE

Seibt KM, Schmidt T & Heitkam T (2018) *FlexiDot: Highly customizable, ambiguity-aware dotplots for visual sequence analyses*. **Bioinformatics** 34:3575-3577

GitHub: <https://github.com/molbio-dresden/flexidot>

Mann L, **Seibt** KM, Weber B & Heitkam T (2022) *ECCsplorer: A pipeline to detect extrachromosomal circular DNA (eccDNA) from next-generation sequencing data*. **BMC Bioinformatics** 23:1-15

GitHub: <https://github.com/crimBubble/ECCsplorer>

RESEARCH PUBLICATIONS

Sultana N, Menzel G, **Seibt** KM, Garcia S, Weber B, Serge S & Heitkam T (2022) *Genome-wide analysis of long terminal repeat retrotransposons from the cranberry Vaccinium macrocarpon*. **Journal of Berry Research** 12:165-185

Schmidt N, **Seibt** KM, Weber B, Schwarzacher T, Schmidt T & Heitkam T (2021) *Broken, silent, and in hiding: tamed endogenous pararetroviruses escape elimination from the genome of sugar beet (Beta vulgaris)*. **Annals of Botany** 128:281-299

Reiche B, Kögler A, Morgenstern K, Brückner M, Weber B, Heikam T, **Seibt** KM, Tröber U, Meyer M, Wolf H, Schmidt T & Krabel D (2021): *Application of retrotransposon-based inter-SINE amplified polymorphism (ISAP) markers for the differentiation of common poplar genotypes*. **Canadian Journal of Forest Research** 51:1650-1663

Maiwald S, Weber B, **Seibt** KM, Schmidt T & Heitkam T (2021) *The Cassandra retrotransposon landscape in sugar beet (Beta vulgaris) and related Amaranthaceae: Recombination and re-shuffling lead to a high structural variability*. **Annals of Botany** 127:91-109

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

- Kögler A, **Seibt** KM, Heitkam T, Morgenstern K, Reiche B, Brückner M, Wolf H, Krabel D & Schmidt T (2020) *Divergence of 3' ends as a driver of short interspersed nuclear element (SINE) evolution in the Salicaceae*. **Plant Journal** 103:443-458
- Diekmann K, **Seibt** KM, Muders K, Wenke T, Junghans H, Schmidt T & Dehmer KJ (2017) *Diversity studies in genetic resources of Solanum spp. (section Petota) by comparative application of ISAP markers*. **Genetic Resources and Crop Evolution** 64:1937-1953
- Tomlekova N, Spasova-Apostolova V, Nacheva E, Stoyanova M, Teneva A, Petrov N, **Seibt** KM & Schmidt T (2017) *Genotyping of Bulgarian potato varieties by SINE-based ISAP markers*. **Comptes Rendus de l'Académie Bulgare des Sciences** 70:63-72
- 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** 86:268-285
- Schwichtenberg K, Wenke T, Zakrzewski F, **Seibt** KM, Minoche A, Dohm JC, Weisshaar B, Himmelbauer H & Schmidt T (2016) *Diversification, evolution and methylation of short interspersed nuclear element families in sugar beet and related Amaranthaceae species*. **Plant Journal** 85:229-244
- Menzel G, Heitkam T, **Seibt** KM, Nouroz F, Müller-Stoermer M, Heslop-Harrison JS & Schmidt T (2014) *The diversification and activity of hAT transposons in Musa genomes*. **Chromosome Research** 22:559-571
- 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** 125:185-196

PUBLICATIONS IN PREPARATION

- Hartig N, **Seibt** KM, Schmidt T & Heitkam T: *How to start a LINE: 5' switching rejuvenates LINE retrotransposons in tobacco and related Nicotiana species*.

BOOK CHAPTERS

- Reiche B, Kögler A, Morgenstern K, Brückner M, Weber B, Heitkam T, **Seibt** KM, Tröber U, Meyer M, Wolf H, Schmidt T, & Krabel D (2020): "Anwendung des SINE-basierten Markersystems ISAP zur Identifizierung von Pappelklonen." Chapter in Thünen Report 76: Forstpflanzenzüchtung für die Praxis, M. Liesebach (ed.), pp 144-154
- 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) Plant Genotyping: Methods and Protocols. Springer Science+Business Media, New York, pp 183-192
- Seifert J, Erler B, **Seibt** K, Rohrbach N, Arnold J, Schlömann M, Kassahun A & Jenk U (2008) *Characterization of the microbial diversity in the abandoned uranium mine Königstein*. In: Merkel B & Hasche-Berger A (ed) Uranium, Mining and Hydrogeology. Springer, Berlin, pp 733-742

GRANTS

- 2018 Conference travel grant by the German Academic Exchange Office (DAAD) for the "*Transposable elements meeting*" in Cold Spring Harbor, USA

CONFERENCE TALKS

- RepeatExplorer Meeting** 2019 (workshop on the RepeatExplorer pipeline for repetitive DNA analyses; České Budějovice, Czech Republic) "*The Angio-SINE superfamily with a conserved 3' domain is widely distributed across the Angiosperms and frequently associated with genes*"
- Biopolis** 2018 (PhD conference; Dresden, Germany) "*The Angio-SINE superfamily with a conserved 3' domain is widely distributed across the Angiosperms*"
- iJaDe** 2016 (conference for German-Japanese cooperation; Dresden, Germany) "*Solanaceae short interspersed nuclear elements and their impact on gene structure and genome organization.*"

CONFERENCE POSTERS (LAST 5 YEARS)

- Maiwald M, Weber B, **Seibt** KM, Schmidt T & Heitkam T (2020) "*The highly recombined landscape of Cassandra retrotransposons in Beta vulgaris*" Biopolis (Dresden, Germany) [presented by first author]
- Seibt** KM, Schmidt T & Heitkam T (2019) "*FlexiDot: Customize your dotplots for visual sequence analyses*" Meeting of the GPZ group Cytogenetics (Dresden, Germany)
- Seibt** KM, Schmidt T & Heitkam T (2019) "*The conserved 3' Angio-domain defines a novel superfamily of short interspersed nuclear elements (SINEs) in higher plants*" Meeting of the GPZ group Cytogenetics (Dresden, Germany)

- Schmidt N, Weber B, **Seibt** KM, Schwarzacher T, Schmidt T & Heitkam T (2019) "*Endogenous pararetroviruses in the genome of sugar beet (Beta vulgaris)*" Meeting of the GPZ group Cytogenetics (Dresden, Germany) [presented by first author]
- Heitkam T, Weber B, **Seibt** KM, Hoffmann J, Badstübner M & Schmidt T (2019) "*Taking the retro-ride: Long terminal repeat retrotransposons carry tandem repeats and disperse them through plant genomes*" Meeting of the GPZ group Cytogenetics (Dresden, Germany) [presented by first author]
- Seibt** KM, Heitkam T & Schmidt T (2019) "*The conserved 3' Angio-domain defines a novel superfamily of SINEs in higher plants*" Crossroads between transposons and gene regulation (London, United Kingdom)
- Seibt** KM, Schmidt T & Heitkam T (2019) "*FlexiDot: Customize your dotplots for visual sequence analyses*" Biopolis (Dresden, Germany)
- Seibt** KM, Heitkam T & Schmidt T (2018) "*The Angio-SINE superfamily with its conserved 3' domain is widely distributed across the Angiosperms*" Transposable elements meeting (Cold Spring Harbor, USA)
- Seibt** KM, Schmidt T & Heitkam T (2018) "*SINEs contribute to gene evolution, regulation and genome rearrangement in Solanaceae plants*" EMBO Workshop plant genome stability and change (IPK Gatersleben, Germany)
- Hübler N, **Seibt** KM, Schmidt T & Heitkam T (2018) "*The impact of allopolyploidization on retrotransposable elements in Nicotiana*", Plant Science Student Conference (IPK Gatersleben, Germany) [presented by first author]
- Seibt** KM, Wenke T, Muders K, Truberg B & Schmidt T (2017) "*SINEs in Solanaceae – gene association and use as molecular markers*" EMBL symposium: The mobile genome: Genetic and physiological impacts of transposable elements (Heidelberg, Germany)
- Weber B, **Seibt** KM, Hoffmann J, Ha HB, Bannack E & Schmidt T, Heitkam T (2017) "*Where it starts and how it ends – the evolution of tandem repeats within LTR retrotransposons*" EMBL symposium: The mobile genome: Genetic and physiological impacts of transposable elements (Heidelberg, Germany) [presented by first author]
- Seibt** KM, Wenke T, Muders K, Truberg B, Heitkam T & Schmidt T (2017) "*SINEs in Solanaceae – chromosomal localization, gene association and utilization as molecular markers*" XIX international botanical congress (Shenzhen, China)
- Seibt** KM, Wenke T, Muders K, Truberg B & Schmidt T (2017) "*SINEs in Solanaceae – genome organization, evolution and application as molecular markers*" Biopolis (Dresden, Germany)
- Seibt** KM, Wenke T, Muders K, Truberg B & Schmidt T (2015) "*Informative retrotransposon-based markers are facilitated by recent amplificational bursts and a dispersed genomic organization*" Plant Science Student Conference (IPB Halle, Germany)

TEACHING

2021	Bioinformatics trainings for TU Dresden and NORIKA lab members: software BioNumerics (genotype database), software Geneious, sequence analysis in general
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, 23.11.2020

My research focused on non-autonomous transposable elements, their genomic impact, evolution, and use as molecular markers for plant breeding.

Potatoes are among the most consumed crops with varieties specifically developed for different purposes and adapted to varying environmental conditions. Accordingly, a clear distinction of potato cultivars is crucial to protect the rights of breeders and customers. In cooperation with the German potato breeder NORIKA GmbH, I have developed a **molecular marker** system to genotype potato cultivars, landraces, and wild species during three projects funded by the German Federal Ministry of Education and Research (BMBF) [1]. The markers are based on insertional polymorphisms of short interspersed nuclear elements (SINEs). For the practical application of the markers by the NORIKA GmbH, I established a fingerprint database. Based on this work, the research group is currently searching for resistance trait-associated markers in potato using my R workflow to identify candidate marker bands for site-specific markers. Such trait-associated markers enable the cost-saving and accelerated breeding of new varieties with desired traits.

To study the genomic basis of our molecular markers, I comparatively analyzed five nightshade genomes using bioinformatics tools and customized Python scripts [2]. **Nightshade SINEs** are enriched in distal, euchromatic chromosome regions, with individual SINE families associated with genes to a varying extent. Thereby, they potentially contribute splice sites, regulatory and coding sequences. Remarkably, 10% of the annotated genes in the five nightshade genomes harbor at least one SINE insertion. The presence of young copies implies a recent SINE amplification in potato, contrasting tomato and pepper. In addition to their mere insertional activity, SINEs can affect the genome through their involvement in sequence rearrangements, evident from tandem-like arrangements and the transduction of flanking sequence regions upon SINE transposition.

Previous studies in plants have indicated a rather narrow phylogenetic distribution of SINE families. In contrast, my computational analysis of a hundred genome assemblies revealed the occurrence of a highly conserved 3' SINE domain in at least 24 SINE families, widespread across the plant kingdom in a patchy manner [3]. This led us to the postulation of the **Angio-SINE superfamily**. Using multiple complementary approaches, I investigated and visualized the modular relationships within this SINE superfamily. When considering all full-length copies, Angio-SINEs are frequently enriched in and nearby genes with a potential impact on the expression or splicing of these genes.

To study repetitive sequences, traditional dotplot visualizations are helpful, but available tools either lacked specific features or their use could not be automated. Due to this, I developed the **cross-platform software FlexiDot**, with novel features like the visualization of sequence annotations to generate highly informative and customizable dotplots [4]. This has been published in the journal *Bioinformatics*. Other **bioinformatics pipelines**, that I designed and implemented during my work, have been applied to other transposable element types and species leading to co-authorships in multiple publications from our research group.

[1] Seibt *et al.* (2012) Theoretical and Applied Genetics

[2] Seibt *et al.* (2016) The Plant Journal

[3] Seibt *et al.* (2020) The Plant Journal

[4] Seibt *et al.* (2018) Bioinformatics