PERSONAL INFORMATION

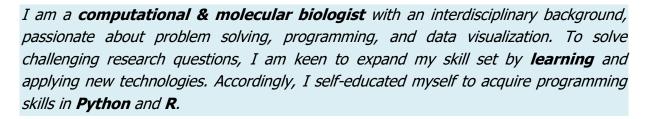|	
Full Name:	Kathrin Martina Seibt
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*I am a **computational & molecular biologist** with an interdisciplinary background, passionate about problem solving, programming, and data visualization. To solve challenging research questions, I am keen to expand my skill set by **learning** and applying new technologies. Accordingly, I self-educated myself to acquire programming skills in **Python** and **R**.*

WORK EXPERIENCE

04/2012 – 10/2020   **Technische Universität Dresden,** Plant Cell & Molecular Biology   (Prof. Thomas Schmidt/Prof. Stefan Wanke)

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 scripting, statistical analyses and data visualization in R, sequence analyses
- 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

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 *in situ* hybridization
other biological techniques	plant *in vitro* culture, grafting of potato plants, ELISA assay

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

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

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

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

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)

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

RESEARCH PUBLICATIONS

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

Maiwald S, Weber B, **Seibt** KM, Schmidt T & Heitkam T (2020) *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** (doi: 10.1093/aob/mcaa176)

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** doi:101111/tpj.14721

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** K & 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

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.), 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.

PUBLICATIONS IN PREPARATION

Hartig N, **Seibt** KM, Schmidt T & Heitkam T: *The impact of allopolyploidization on RTE long interspersed nuclear elements (LINEs) in* Nicotiana.

Schmidt N, Weber B, **Seibt** KM, Schwarzacher T, Schmidt T & Heitkam T: *The genomic organisation and environment of caulimoviruses in* Beta vulgaris *shed a new light on the endopararetrovirus ability to outlast silencing.*

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 recombinated 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)

GRANTS

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

TEACHING

2017	Supervision of a Bachelor thesis entitled: „*New ISAP markers based on the widespread plant SINE family Au and their evaluation using reference potato genotypes* "
since 2016	Teaching during the practical course "*DNA sequencing*": 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: „*Mobile DNA sequences as markers in crop breeding*"
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

REFERENCES

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Prof. Dr. Pat Heslop-Harrison	University of Leicester Department of Genetics Adrian Building University Road Leicester LE1 7RH United Kingdom Phone: +44(0)116 252 5079 E-Mail: phh4@leicester.ac.uk

Dresden, 23.11.2020   *Kathrin Seibt*