

Curriculum vitae

Sebastian Kloska (Ph.D) *25.12.1962

Hohenstaufenstr. 58

D-10781 Berlin
Germany
fon: +49-176-24621622
e-mail: sebastian.kloska@snafu.de



In Brief

Ph.D. in Biology with specialization in Molecular Plant Genetics. Head of two Bioinformatics departments in academia and industry. Many Years working experiences in small to medium size groups. Excellent programming skills especially in Unix/Linux environment

- >27 years C/C++
time critical environment, multi-threading, IPC, Qt, ODBC, custom templates, work with Visual Studio on Windows and QtCreator under Linux.
- >17 years Java
Swing, JDBC, DOM Parsing, SAX Parsing, participated in the HSQLDB open source project.
- >18 years Perl
usage of "*strict*" coding, CPAN modules, custom modules in C, DBI, FastCGI, lots of complex regular expression mapping.
- >9 years JavaScript
including Script.aculo.us and Prototypes
- >16 years Database programming
MySQL, PostgreSQL, MSSQL, ADABAS, Sybase
- >6 years PDF and Postscript especially working with the Adobe™ PDF Library.

Father of a son (*26.02.99) and a daughter (*27.02.02)

Positions

Oct.:2006 - NOW

Freelance developer in different fields of information technologies. Most of the time working in small to medium size groups using version control systems like GIT and Subversion to share code and bug tracking systems like Mantis and JIRA. Took part in the transition from classical "waterfall" to Scrum based working methodologies.

*** Currently: Senior C++ Developer at here.com**

Platform Integration of *HEREs* (www.here.com) proprietary geolocation, mapping and geocoding technology for SASMSUNG wearable and mobile devices. Platform independent C++ code had to be integrated into the Tizen OS. High performance, frugal data consumption and robust fail save code were a must in this assignment.

*** JAVA EE Backend development for "strandsandale.de" ~1 year**

Development of web-based product management tools with J2EE technologies. The JAVA Hibernate API has been used to model the components of the product infrastructure (shoe warehouse). JPA queries were used to access the model and JSP code finally delivered the GUI via an Apache Tomcat engine.

*** PHP Based Frontend development for "lineup.shoes" ~1 year**

Implementation of an online auctioning system which enables customers to bid on advertisement space. Classical "LAMP" development with MySQL as a data backend and PHP as the CGI engine.

The PayPal API has been integrated in order to implement payment and refunding of payments. jQuery and other Javascript components were used to allow for dynamic HTML changes and backend updates via AJAX requests.

*** Digital Printing for "SOFHA GmbH" and "Atlantic Zeiser" ~6 years**

Linux based C++ development ranging from hardware interaction, e.g. ink jet heads, to RDBMS binding for print job management.

Dynamic generation of PDF Documents with the Adobe PDF Library based on XML source documents read via DOM and SAX parsing. Time critical multi-threading and IPC programming with shared memory segments, mutexes and semaphores.

Involvement in kernel development (USB stack) and other open source projects like Samba. Development of user interfaces with Qt and JAVA on Windows and Linux using QtCreator and Visual Studio. Binding to an PostgreSQL backend were implemented via ODBC for the C++ code and with JDBC, JPA for JAVA.

Usage of various SQL Dialects, design and management of various RDBM Systems like MySQL, MSSQL, PostgreSQL and Sybase.

Development of a custom package management and build system consisting of a derivative of the Debian package manager and a set of Perl scripts responsible for version management and build script initialization.

July::2001 - Oct::2006

Head of Bioinformatics at the Scienion A.G

Active participant in the founding of the start up company. Main responsibilities were the implementation of a database and analysis system for Expression Profiling as well as the development of a large scale primer design facility. Participated in the development of a JAVA/Tomcat based LIMS system.

Applied Techniques included the parsing and analysis of whole genome data, the automatic detection of large sets of primer sequences and their storage in an RDBMS.

Coding included JAVA for user interfaces, Perl for maintenance tasks and C++ for time critical sections. Beside other RDBMS like Sybase SQL Anywhere we were using the HSQLDB DB-Engine which at the time didn't support the "ON (DELETE|UPDATE) (CASCADE|SET NULL|SET DEFAULT)". Therefore I took an active part in implementing the functionality within Sourceforge.

June::1998 - June::2001

Head of Bioinformatics at the Max-Planck-Institute of Molecular Plant Physiology

Establishment of the newly founded Bioinformatics group within the Department of Prof. Lothar Willmitzer. From scratch development of a Web based Database and Analysis System (Haruspex) for large scale Microarray experiments.

Large parts of the server logic has been written in Perl/CGI, many of the user interface components in JAVA. Time critical parts and database binding were implemented in C++ with DB binding via ODBC.

Development of a new method for Mutual Information calculation on large datasets (mis_calc). This number crunching application is a pure C++ program with pthreads in order to achieve maximal performance on multi-CPU machines. Small frontends were written with the Qt library,

Jan::1998 - May::1998

Post Doctorial Position at the Max Planck Institute for Molecular Genetics Berlin . Working in the Group of Dr. Hans Lehrach on automated systems for complex hybridization.

Short Position in the Lab. Establishing new methods for quantitative PCR.

Jul::1997 - Dec::1997

Free Software engineer at SofHa Inc. in Berlin.

Working as a freelance Z80 assembler programmer. Implementing the ECP-mode in a microcontroller for the SofHa-RIP.

Education

Oct::1993 - Jan::1997

Ph.D. Student in the group of Axel Brennicke at the IGF Berlin.

Thesis title: "Investigation of the Regulation of nuclear encoded mitochondrial Genes and two novel PR-1 Genes in *Arabidopsis thaliana*".

Beside the classical techniques in molecular genetics I have also written and published my first bioinformatics program written in C. D5scan has been successfully applied to the automated search for Group II Introns.

July::1992 – Sept::1993

Graduate student at the Institute of Genbiological Research (IGF) in Berlin under supervision of Dr. Wolfgang Schuster in the group of Prof. Dr. Axel Brennicke. Title of dissertation: "Characterization of a novel Gene for the Adenine Nucleotide Translocator of *Arabidopsis thaliana*."

Publications

In Paper

1. Daub CO, Steuer R, Selbig J, Kloska S.: **“Estimating mutual information using B-spline functions--an improved similarity measure for analysing gene expression data”**. BMC Bioinformatics. 2004 Aug 31 5 118
2. Colebatch G, Desbrosses G, Ott T, Krusell L, Montanari O, Kloska S, Kopka J, Udvardi MK.: **“Global changes in transcription orchestrate metabolic differentiation during symbiotic nitrogen fixation in *Lotus japonicus*”**. Plant J. 2004 Aug 39(4) 487-512
3. Daub CO, Kloska S, Selbig J.: **“MetaGeneAlyse: analysis of integrated transcriptional and metabolite data”**. Bioinformatics 2003 Nov 22 19(17) 2332-3
4. Stephan Brandt, Sebastian Kloska, Thomas Altmann and Julia Kehr: **“Using array hybridization to monitor gene expression at the single cell level”**. Journal of Experimental Botany Dec. 1 2002 53(379) 2315-2323
5. Colebatch G, Kloska S, Trevaskis B, Freund S, Altmann T, Udvardi MK.: **“Novel aspects of symbiotic nitrogen fixation uncovered by transcript profiling with cDNA arrays”**. Mol Plant Microbe Interact 2002 May 15(5) 411-20
6. Thimm O, Essigmann B, Kloska S, Altmann T, Buckhout TJ.: **“Response of *Arabidopsis* to iron deficiency stress as revealed by microarray analysis”**. Plant Physiol 2001 Nov 127(3) 1030-43
7. Fiehn O, Kloska S, Altmann T.: **“Integrated studies on plant biology using multiparallel techniques”**. Curr Opin Biotechnol 2001 Feb 12(1) 82-6
8. Mozo T, Dewar K, Dunn P, Ecker JR, Fischer S, Kloska S, Lehrach H, Marra M, Martienssen R, Meier-Ewert S, Altmann T.: **“A complete BAC-based physical map of the *Arabidopsis thaliana* genome”**. Nat Genet 1999 Jul 22(3) 271-5
9. Sánchez H, Fester T, Kloska S, Schröder W, Schuster W.: **“Transfer of rps19 to the nucleus involves the gain of an RNP-binding motif which may functionally replace RPS13 in *Arabidopsis* mitochondria”**. EMBO J 1996 May 1 15(9) 2138-49.
10. Knoop V, Kloska S, Brennicke A.: **“On the identification of group II introns in nucleotide sequence data”**. J Mol Biol 1994 Sep 30 242(4) 389-96
11. Schuster W, Kloska S, Brennicke A.: **“An adenine nucleotide translocator gene from *Arabidopsis thaliana*”**. Biochim Biophys Acta 1993 Feb 20 1172(1-2) 205-8

In Books

1. Márquez, A.J. Stougaard, J. Udvardi, M. Parniske, M. Spaink, H. Saalbach, G. Webb, J. Chiurazzi, M. Márquez, A.J.: **“Lotus japonicus expression database”**. *Lotus japonicus Handbook* 149-154 Springer-Verlag GmbH, Heidelberg 2005
2. Michael Udvardi, Thomas Ott, Lene Krusell, Guilhem Desbrosses, Vera Voroshilova, G Colebatch, Maren Wandrey, Ombretta Montanari, Klementina Kakar, Katja Krause, Catrin Günther, Joost van Dongen, Helene Vigeolas, Peter Geigenberger, Ute Kraemer, S. Kloska, J Kopka, Shusei Sato, Yasukazu Nakamura, Satoshi Tabata, Euan K. James, Masayoshi Kawaguchi, Ai Miyamoto, Norio Suganuma, Niels Sandal Jens Stougaard: **“Physiological Responses in Plant-Microbe Interactions Insights into Nodule Physiology and Metabolism from Transcriptomics, Metabolomics, Bioinformatics, and Genetics”**. *Biology of Plant-Microbe Interactions* 5 APS Press 2006

Scientific Projects

1. Martin Steup, Thomas Altmann, Sebastian Kloska, Peter Geigenberger, Gerhard Ritte, Bernd Müller-Röber **Molekulare Physiologie: “Energetik und Regulation primärer pflanzlicher Stoffwechselprozesse”**. Deutsche Forschungsgemeinschaft Sonderforschungsbereich 429, 1999 - 2004
2. Richard Trethewey, Bernd Essigmann, Lothar Willmitzer, Sebastian Kloska, Thomas Altmann, Thomas Linke, Peter-Uwe Zettler, Andre Flöter: **“Entwicklung eines Systems zur Wissensentdeckung in großen biologischen Datenbeständen”**. Universität Potsdam: Informatik 2000