

Our Aim: Scionics wants to become a leading provider of IT products, consulting, and support to enhance the efficiency of scientific research in the life sciences and other knowledge based industries in Europe and North America.

Scionics Computer Innovation GmbH was founded 1999. Today, Scionics specializes in the organization, analysis, and presentation of research results including the integration of research hardware such as microscopes and image capturing systems. Hereby, Scionics applies the skills of its 25 employees in the following technologies and areas of scientific application:

Programming languages

- Python
- Java
- PERL (for bioinformatics applications & systems integration)
- C/C++ (for extensions & performance enhancement only)

Database development platforms

- MySQL (incl. large scale databases)
- Postgres (incl. large scale databases)
- Oracle
- Sequel 7

Operating systems

- Linux (Debian, Ubuntu, Red Hat)
- Solaris
- Mac OS X
- Windows 2000/XP

Technology integration

- LDAP
- NIS
- Apache
- Tomcat
- Others

Areas of special expertise:

- **Bioinformatics**
 - Protein sequence analysis and functional prediction
 - Comparative genomics
 - esiRNA/siRNA design
 - Bioinformatics tool development

- **Laboratory Information Management**
 - RNAi & chemical screening
 - esiRNAi production data management
 - Laboratory data storage

- **Image & Data Analysis**
 - Screening image browsing & statistical pattern recognition
 - Kinetic analysis with clustering
 - Data-dependent acquisition methods for mass spectrometers

- **Administrative Systems**
 - Personnel & resource scheduling
 - Animal facility data management
 - Work-flow & task management
 - Networked data sharing

Through past projects, we have special expertise in above mentioned areas. At the same time, we possess a broad skill set as well as extensive experience in research environments, which enables us to successfully deal with nearly any challenge that arises in a scientific information technology context.

List of publications since 2000 (in descending chronological order):

Schwudke D, Oegema J, Burton L, Entchev E, Hannich JT, Ejsing CS, Kurzchalia T, Shevchenko A. in **Analytical Chemistry** **78(2)**, 585-95, 2006: *Lipid profiling by multiple precursor and neutral loss scanning driven by the data-dependent acquisition.*

Zayas RM, Hernandez A, Habermann B, Wang Y, Stary JM, Newmark PA. in **PNAS** **102**, 18491-6, 2005: *The planarian Schmidtea mediterranea as a model for epigenetic germ cell specification: analysis of ESTs from the hermaphroditic strain.*

Krauß E, Heninger AK, Kittler R, Lohmann A, Poser I, Wagner J, Franke K, Kozak K, Grabner H, Buchholz F. in **BIOspektrum** **11**, 436-441, 2005: *Eine Genom-weite RNA-Interferenz-Bibliothek für die funktionelle Charakterisierung aller Gene in kultivierten, menschlichen Zellen.*

Proszynski TJ, Klemm RW, Gravert M, Hsu PP, Gloor Y, Wagner J, Kozak K, Grabner H, Walzer K, Bagnat M, Simons K, Walch-Solimena C. in **PNAS** **102(50)**, 17981-6, 2005: *A genome-wide visual screen reveals a role for sphingolipids and ergosterol in cell surface delivery in yeast.*

Itoh T, Erdmann KS, Roux A, Habermann B, Werner H, De Camilli P. in **Dev Cell** **9**, 791-804, 2005: *Dynamain and the actin cytoskeleton cooperatively regulate plasma membrane invagination by BAR and F-BAR proteins.*

Kittler R, Heninger AK, Franke K, Habermann B, Buchholz F. in **Nat Methods** **2**, 779-84, 2005: *Production of endoribonuclease-prepared short interfering RNAs for gene silencing in mammalian cells.*

Ozlu N, Srayko M, Kinoshita K, Habermann B, O'toole ET, Muller-Reichert T, Schmalz N, Desai A, Hyman AA. in **Dev Cell**. **9**, 237-48, 2005: *An Essential Function of the C. elegans Ortholog of TPX2 Is to Localize Activated Aurora A Kinase to Mitotic Spindles.*

Maddox AS, Habermann B, Desai A, Oegema K. in **Development** **132(12)**, 2837-48, 2005: *Distinct roles for two C. elegans anillins in the gonad and early embryo.*

Pelkmans L, Fava E, Grabner H, Hannus M, Habermann B, Krausz E, Zerial M. in **Nature** **436**, 78-86, 2005: *Genome-wide analysis of human kinases in clathrin- and caveolae/raft-mediated endocytosis*

Sebastian Hoepfner, Fedor Severin, Alicia Cabezas, Habermann B, Anja Runge, David Gillooly, Harald Stenmark and Marino Zerial in **Cell** **121**, 437-50, 2005: *Modulation of receptor recycling and degradation by the endosomal kinesin KIF16B*

Kittler R, Putz G, Pelletier L, Poser I, Heninger AK, Drechsel D, Fischer S, Konstantinova I, Habermann B, Grabner H, Yaspo ML, Himmelbauer H, Korn B, Neugebauer K, Pisabarro MT, Buchholz F. in **Nature** **432**, 1036-40, 2004: *An endoribonuclease-prepared siRNA screen in human cells identifies genes essential for cell division*

Dammermann A, Muller-Reichert T, Pelletier L, Habermann B, Desai A, Oegema K. in **Dev Cell** **7**, 815-29, 2004: *Centriole assembly requires both centriolar and pericentriolar material proteins*

Putta S, Smith JJ, Walker JA, Rondet M, Weisrock DW, Monaghan J, Samuels AK, Kump K, King DC, Maness NJ, Habermann B, Tanaka E, Bryant SV, Gardiner DM, Parichy DM, Voss SR. in **BMC Genomics** **5**, 54, 2004: *From biomedicine to natural history research: EST resource for ambystomatid salamander*

Habermann B, Anne-Gaelle Bebin, Stephan Herklotz, Michael Volkmer, Kay Eckelt, Kerstin Pehlke, Hans H Epperlein, Hans K Schackert, Glenis Wiebe and Elly M Tanaka, in **Genome Biology** **5**, **2004**: *An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries*

Liska AJ, Popov AV, Sunyaev S, Couhglin P, Habermann B, Shevchenko A, Bork P, Karsenti E and Shevchenko A, in **Proteomics** **4**, **2707-21**, **2004**: *Homology-based functional proteomics by mass spectrometry: Application to the Xenopus microtubule-associated proteome*

Bernauer S, Croft D, Gardina P, Minch E, de Rinaldis M, Vatcheva I. in **Appl Bioinformatics** **3(1)**, **63-75**, **2004**: *Case study: data management strategies in an integrated pathway tool*

Joosten M, Blazquez-Domingo M, Lindeboom F, Boulme F, Van Hoven-Beijen A, Habermann B, Lowenberg B, Beug H, Mullner EW, Delwel R, Von Lindern M. in **J Biol Chem** **279**, **38169-76**, **2004**: *Putative protooncogene Nm23-M2: translational control by cytokines via phosphoinositide-3-kinase signaling*

Henschel A, Buchholz F, Habermann B. in **Nucleic Acids Res.** **32 (web server issue)**, **W113-20**, **2004**: *DEQOR: a web-based tool for the design and quality control of siRNAs*

Pelletier L, Ozlu N, Hannak E, Cowan C, Habermann B, Ruer M, Muller-Reichert T, Hyman AA. in **Curr Biol.** **14**, **863-73**, **2004**: *The Caenorhabditis elegans centrosomal protein SPD-2 is required for both pericentriolar material recruitment and centriole duplication*

Schwickart M, Havlis J, Habermann B, Bogdanova A, Camasses A, Oelschlaegel T, Shevchenko A, Zachariae W. in **Mol Cell Biol.** **24**, **3562-76**, **2004**: *Swm1/Apc13 is an evolutionarily conserved subunit of the anaphase-promoting complex stabilizing the association of Cdc16 and Cdc27*

Miaczynska M, Christoforidis S, Giner A, Shevchenko A, Uttenweiler-Joseph S, Habermann B, Wilm M, Parton RG, Zerial M. in **Cell** **116**, **445-56**, **2004**: *APPL proteins link Rab5 to nuclear signal transduction via an endosomal compartment*

Habermann B. in **EMBO Rep.** **5**, **250-5**, **2004**: *The BAR-domain family of proteins: a case of bending and binding?*

Habermann B, Oegema J, Sunyaev S, Shevchenko A. in **Mol Cell Proteomics.** **3**, **238-49**, **2004**: *The power and the limitations of cross-species protein identification by mass spectrometry-driven sequence similarity searches*

Peri S, et al. in **Nucleic Acid Research** **32(Database issue)**, **D497-501**, **2004**: *Human protein reference database as a discovery resource for proteomics*

Peri S, et al. in **Genome Research** **13(10)**, **2363-71**, **2003**: *Development of human protein reference database as an initial platform for approaching systems biology in humans*

Spitzenberger F, Pietropaolo S, Verkade P, Habermann B, Lacas-Gervais S, Mziaut H, Pietropaolo M, Solimena M. in **J Biol Chem.** **278(28)**, **26166-73**, **2003**: *Islet cell autoantigen of 69 kDa is an arfaptin-related protein associated with the Golgi complex of insulinoma INS-1 cells*

Habermann B, Dolznig H, Stangl K, Deiner EM, Moriggl R, Beug H, Mullner EW in **Curr Biol.** **12(13)**, **1076-85**, **2002**: *Apoptosis protection by the epo target bcl-x(l) allows factor-independent differentiation of primary erythroblasts*

Kinoshita K, Habermann B, Hyman AA in **Trends Cell Biol.** **12(6)**, 267-73, 2002: *XMAP215: a key component of the dynamic microtubule cytoskeleton*

Hannak E, Oegema K, Kirkham M, Gonczy P, Habermann B, Hyman AA in **J Cell Biol** **157(4)**, 591-602, 2002: *The kinetically dominant assembly pathway for centrosomal asters in Caenorhabditis elegans is gamma-tubulin dependent*

Fedor Severin, Habermann B, Tim Huffaker and Tony Hyman in **J Biol Chem** **153(2)**, 435-443, 2001: *Stu2 promotes mitotic spindle elongation in anaphase*

Gonczy P, et al. in **Nature** **408(6810)**, 331-6, 2000: *Functional genomic analysis of cell division in C. elegans using RNAi of genes on chromosome III*

Mikulits W., Pradet-Balade B., Habermann, B., Beug H., Garcia-Sanz JA., Muellner EW. in **FASEB J.** **14 (11)**, 1641-52, 2000: *Isolation of Translationally controlled mRNA by Differential Screening*

List of References:

Biopolis Consultants

Dresden, Germany

Cenix Biosciences

Dresden, Germany

JadoLabs

Dresden, Germany

Ludwig Institute for Cancer Research, Department of Cellular & Molecular Medicine

La Jolla, Ca, USA

Ludwig Institute for Cancer Research, Laboratory of Chromosome Biology

La Jolla, Ca, USA

Max Planck Institute for Experimental Medicine, Animal Facility

Göttingen, Germany

Max Planck Institute for Infection Biology, Lab Animals Core Facility

Berlin, Germany

Max Planck Institute of Molecular Cell Biology and Genetics, Biomedical Services

Dresden, Germany

Max Planck Institute of Molecular Cell Biology and Genetics, Light Microscopy Facility

Dresden, Germany

Max Planck Institute of Molecular Cell Biology and Genetics, Shevchenko Lab

Dresden, Germany

Max Planck Institute of Molecular Cell Biology and Genetics, Tanaka Lab

Dresden, Germany

Rush University, Department of Biochemistry

Chicago, IL, USA

University of Illinois at Urbana-Champaign, Newmark Lab

Urbana, IL, USA

Example Project 1 – Lipid Profiling Through MS Data-Dependent Acquisition :

Client: Max Planck Institute of Molecular Cell Biology and Genetics, Shevchenko Lab, Dresden, Germany

Time-frame: August 2005 – November 2005

Objective: Development of a data-dependent acquisition (DDA) method to profile lipids, using precursor and neutral loss scan information of quadrupole – time-of-flight mass spectrometers

Description: DDA involves creating and analyzing multidimensional data files produced by different analytical instruments, such as a suite of mass spectrometers (MS). This allows a greater proportion of the rich array of data generated by MS analysis to be utilized for identifying biological compounds – in this case lipids. Three quadrupole MS provided spectral data on the precursor ions and fragment ions at the client's facility. The data was then analyzed by our software using proprietary algorithms that were developed together with the researchers to link the spectral information to individual lipids. During this project phase, very frequent interaction was necessary to sufficiently coordinate the science/IT collaboration. Upon completion of the prototype, a number of tests were conducted. When it became clear that the underlying principles were correct and that already at this point significant time-savings could be achieved in the field of lipid analysis, the product was refined further. Additional functionality was introduced to allow Boolean searches and thus provide the researchers with options to search for specific compounds. In addition, the user interface was simplified to make such analysis available for researchers without training and extensive prior experience in this field.

Outcome: With the created software, MS generated data on lipids can be analyzed within minutes, thus reducing the time requirement for profiling an unknown sample to a few hours instead of several days with traditional methods. A publication covering this project has been recently published and interest of several lipidomics research groups has been voiced. A follow-up project to extend functionality further is planned.

Technologies applied: Python programming language, wx Python / wx Windows platform independent client interface, Excel and csv reporting

Publication:

Schwudke D, et al. in **Analytical Chemistry 78 (2), 585 -595, 2006: Lipid Profiling by Multiple Precursor and Neutral Loss Scanning Driven by the Data-Dependent Acquisition**

Example Project 2 – MPI-CBG EST Databases :

Client: Max Planck Institute of Molecular Cell Biology and Genetics, Tanaka Lab, Dresden, Germany

Time-frame: August 2002 – January 2003 and ongoing

Objective: Analysis and Management of EST data

Description: Expressed sequence tags (ESTs) are short fragments of transcribed coding and non-coding DNA. Sources of sequenced ESTs have become instrumental in molecular biological work, especially when no sequence information is available for the genome of the model organism. ESTs are generally retrieved by sequencing of cloned cDNAs that have been extracted from different tissues of an organism. The sequence quality of large-scale EST sequencing projects is variable, which makes an *in silico* quality control step mandatory. Their redundant nature furthermore requires an *in silico* step after sequencing that assembles ESTs from identical cDNAs into a single sequence (a so-called Contig). To ease usage of the data, EST sequences also have to be annotated in terms of their sequence homologues in other organisms, identified conserved domains, as well as their putative molecular function, biological process and their localization within a cell. Using standard bioinformatics tools and genomic sequence databases, we have developed a pipeline that performs quality control and assembly of EST sequences, as well as a full, sequence-based annotation of assembled Contigs. Subsequently all the sequences and annotated data were imported into a MySQL database. A web based user interface was designed which can be accessed for internal and external usage (<https://intradb.mpi-cbg.de/axolotl/cgi-bin/login.cgi>). Individual members of the internal user group can add comments for specific sequences of interest, upload expression data from experimental studies, search for sequence similarity by BLAST or retrieve associated information from external databases (NCBI, GO).

Outcome: The software was created as part of a research collaboration with the Tanaka Lab at MPI-CBG, who was working on an in-house EST sequencing project for the Axolotl *Ambystoma mexicanum*, and the Bioinformatics Group of Scionics. A second EST sequence database for *Xenopus laevis* was set up with the same software system in collaboration with the group of Tony Hyman (MPI-CBG). More installations and software extensions are planned as more EST data sets get available. Three publications cover this project.

Technologies applied: Phred, TIGR-Assembler v2, ClustalW, BLAST, RPS-BLAST, Python programming language; MySQL database, server on Linux basis, client systems multi-platform, user authentication via an internal system

Publications:

Habermann B, et al. in **Genome Biology** 5, 2004: *An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries*

Putta S, et al. in **BMC Genomics** 5, 54, 2004: *From biomedicine to natural history research: EST resource for ambystomatid salamander*

Zayas RM, et al. in **PNAS** 102, 18491-6, 2005: *The planarian Schmidtea mediterranea as a model for epigenetic germ cell specification: analysis of ESTs from the hermaphroditic strain.*

Example Project 3 – Management System for Lab Animal Facility :

Client: Max Planck Institute of Molecular Cell Biology and Genetics, Biomedical Services, Dresden, Germany

Time-frame: July 2002 – December 2002 and ongoing

Objective: Proprietary development of a software package to manage a cutting-edge transgenic animal facility and the associated tens of thousands of lab animal data sets

Description: The client manages a rodent lab animal facility with close to 10,000 live mice, keeping a permanent and detailed record for each. Records include a variety of information such as pedigree, genetic strains and mutations, projects, etc. Additionally, information on cages and users (staff and scientists) are also stored in the same system. Prior data management was performed via MS Excel and a Filemaker database, which was unable to provide sufficient functionality.

After a short definition of the functional requirements, in close collaboration with the client, Scionics applied its knowledge from prior large-scale database projects to define the technical basis for this project. Thereby, special attention was paid to intuitive interfaces and high processing speed – in light of the number of data sets within the system. The first model was evaluated by the client and Scionics gave further advice on reporting and administrative functionality for the software, which was highly appreciated by the client and added to the model. During the following programming phase, regular status reports were communicated to the client and small amendments to the specification implemented. The first version of the product was operational at the agreed upon date and used in the daily activities of the facility, saving approximately 1-2 FTE's and enabling extensive services to visiting scientists.

Outcome: The software was created from scratch within a very short time frame (< 6 months). The client is extremely satisfied and continues to very efficiently manage the animal facility and research data with this web-based system. Without active marketing from our side, half a dozen additional institutes have purchased the system because of its user friendliness. Development of additional modules in close collaboration with the clients is ongoing.

Technologies applied: Python programming language, MySQL database, Linux/UNIX server, browser-based client interface, internal user-authentication.

Please feel free to contact us anytime to clarify open points, receive more detail on past projects or talk to one of our references.

Alternatively, visit us at www.scionics.de to get more information and see the state-of-the-art information tools and services that we developed to support the global scientific community.

Scionics Computer Innovation GmbH

Tatzberg 47-51
01307 Dresden
Germany

Telephone: +49 (0) 351 796 53 65

Fax: +49 (0) 351 796 53 64

E-Mail: products@scionics.de

Internet: www.scionics.de

Impressum:

Scionics Computer Innovation GmbH

Trade Register: Amtsgericht Dresden HRB 20337

VAT ID: DE813263791