

Dr. Christian H.C. Spieth



Background

- 1993-2000 Studies of Civil Engineering at the [University of Stuttgart](#), Germany with emphasis on numerical methods.
Thesis: "Zur Simulation von instationären Strömungs-Schalen-Interaktionsproblemen".
Degree: Diplom-Ing.
- 1997 "Construction Management Award 1997".
- 1998 "IPCE Software Design Award 1998".
- 1996-2000 Teaching assistant at the [Institute of Structural Mechanics](#), University of Stuttgart, Germany.
- 2000-2001 Studies of Computer Science at the [University of Oxford](#), UK, with emphasis on Bioinformatics.
Master Thesis: "Analyzing DNA Sequences of Bacteria to Find Promoter Regions".
Degree: MSc. in Computer Science (Bioinformatics)
- Since October 2001 Research assistant at the Department of Computer Architecture of the University of Tuebingen, Germany.

Research Interests

- Gene Regulatory Networks
- Data analysis of Microarrays
- Bioinformatical Databases

Current Projects

- JCell: Inference of regulatory networks from microarray data and simulation of pattern formation in Artificial Life.
- JPrints: Genome Fingerprint analysis of expression data under various environmental conditions.
- Modeling of the CD3/CD28 costimulation of human T-Cells: [Prof. Dr. Brock](#) - Cell Biology, University of Tübingen
- Identifying Gene Expression Modules in Arabidopsis thaliana: [Dr. Dierk Wanke](#), [Prof. Dr. Harter](#) - Plant Physiology, University of Tübingen
- Modeling of the glycolysis pathway of E. coli: [Prof. Dr. Reuss](#) - Biochemical Engineering, University of Stuttgart
- Analysis of *Zea Mays* Time Series Gene Expression Experiments: [Michaela Sauer](#), [Dr. Hochholdinger](#) - ZMBP, General Genetics, University of Tübingen
- Analysis of Pericycle specific Gene Expression in *Zea Mays*: [Diana Dembinsky](#), [Dr. Hochholdinger](#) - ZMBP, General Genetics, University of Tübingen
- Haplotype analysis of SNPs related to Adipocytokines: [Dr. Norbert Stefan](#), [Prof. Dr.med. Häring](#) - Internal Medicine, University Hospital Tübingen
- Genotype-Phenotype association study related to voltage-gated potassium channel Kv1.3: [Otto Tschritter](#), [Prof. Dr.med. Häring](#) - Internal Medicine, University Hospital Tübingen
- BMBF-Project: [NGFN 2](#) (National Genome Research Network): Explorative Project - Inferring Genetic Networks from Gene Expression Data.

Completed Projects

- BMBF-Project: [TuebinGENome](#) (Genome Reserach Network Tuebingen): Functional Genomics of Infectious Disease Susceptibility, Bioinformatic methods for microarray data analysis.
- [xTWIF](#): eXtended TuebinGENome Web InterFace for genome data analysis. Password protected.
- TuebinGENomeDB: TuebinGENome microarray database system based on Oracle Enterprise DB 9x.

Awards

doIT Software Award 2005

3rd prize endowed with 8.000€

[doIT Softwareforschungspreis](#), State of Baden-Württemberg

IPCE Software Design Award 1998

Institute of Information Processing in Civil Engineering, University of Stuttgart

Construction Management Award 1997

[Institute of Construction Management](#), University of Stuttgart

Publications

JCell - a Java based framework for inferring regulatory networks from time series data

C. Spieth, J. Supper, F. Streichert, N. Speer, and A. Zell

Bioinformatics, 22, pp. 2051-2052

[Abstract](#)

Ongoing Coxsackievirus Myocarditis Is Associated with Increased Formation and Activity of Myocardial Immunoproteasomes

G. Szalay, S. Meiners, A. Voigt, J. Lauber, C. Spieth, N. Speer, M. Sauter, U. Kuckelkorn, A. Zell, K., K. Stangl, and R. Kandolf

American Journal of Pathology, 168 (5), pp. 1542-1552

Comparing Mathematical Models on the Problem of Network Inference

C. Spieth, N. Hassis, F. Streichert, J. Supper, N. Speer, K. Beyreuther, and A. Zell

Genetic and Evolutionary Computation Conference (GECCO 2006), Seattle, USA, to be published

nominated for GECCO Best Paper Award 2006

Comparing Evolutionary Algorithms on the Problem of Network Inference

C. Spieth, R. Worzischek, F. Streichert, J. Supper, N. Speer, and A. Zell

Genetic and Evolutionary Computation Conference (GECCO 2006), Seattle, USA, to be published

Kernel Based Functional Gene Grouping

H. Fröhlich, N. Speer, C. Spieth, and A. Zell

International Joint Conference on Neural Networks (IJCNN 2006), Vancouver, Canada, to be published

A New Variant in the Human Kv1.3 Gene Is Associated With Low Insulin Sensitivity and Impaired Glucose Tolerance

O. Tschritter, F. Machicao, N. Stefan, S. Schäfer, C. Weigert, H. Staiger, C. Spieth, H.-U. Häring, and A. Fritsche

Journal of Clinical Endocrinology & Metabolism, February 2006, 91: 654-658, Endocrine Society

Polymorphisms in the gene encoding adiponectin receptor 1 are associated with insulin resistance and high liver fat

N. Stefan, F. Machicao, H. Staiger, J. Machann, F. Schick, O. Tschritter, C. Spieth, C. Weigert, A. Fritsche, M. Stumvoll and H. U. Häring

Diabetologia, November 2005, 48(11): 2282-2291, Springer-Verlag

Predicting Single Genes Related to Immune-Relevant Processes

C. Spieth, F. Streichert, N. Speer, C. Sinzger, K. Eberhard, and A. Zell

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2005, San Diego, USA

Proceedings, pp. 461-468, IEEE press

Feedback Memetic Algorithms for Modeling Gene Regulatory Networks

C. Spieth, F. Streichert, J. Supper, N. Speer, and A. Zell

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2005, San Diego, USA

Proceedings, pp. 61-67, IEEE press

Functional Distances for Genes Based on GO Feature Maps and their Application to Clustering

N. Speer, H. Fröhlich, C. Spieth, and A. Zell

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2005, San Diego, USA

Proceedings, pp. 142-149, IEEE press

*Reverse Engineering Non-Linear Gene Regulatory Networks Based on the Bacteriophage λ *ci* Circuit*

J. Supper, C. Spieth, and A. Zell

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2005, San Diego, USA

Proceedings, pp. 325-332, IEEE press

Inferring Regulatory Systems with Noisy Pathway Information

C. Spieth, F. Streichert, N. Speer, and A. Zell

German Conference on Bioinformatics (GCB 2005), Hamburg, Germany

LNI, vol. P-71, pp. 193-203, GI

Clustering-based Approach to Identify Solutions for the Inference of Regulatory Networks

C. Spieth, F. Streichert, N. Speer, and A. Zell

IEEE Congress on Evolutionary Computation (CEC 2005), Edinburgh, UK

Proceedings, vol. 1, pp. 660-667, IEEE Press

Spectral Clustering Gene Ontology Terms to Group Genes by Function

N. Speer, C. Spieth, and A. Zell

5th Workshop on Algorithms in Bioinformatics (WABI 2005), Eivissa, Spain

LNBI 3692, pp. 001-012, Springer-Verlag

Identifying Valid Solutions for the Inference of Regulatory Networks

C. Spieth, F. Streichert, N. Speer, and A. Zell

Genetic and Evolutionary Computation Conference (GECCO 2005), Washington DC, USA

Proceedings, pp. 469-471, ACM Press

Biological Cluster Validity Indices Based on the Gene Ontology

N. Speer, C. Spieth, and A. Zell

6th International Symposium on Intelligent Data Analysis (IDA 2005), Madrid, Spain

LNCS 3646, pp. 429-439, Springer-Verlag.

Functional Grouping of Genes Using Spectral Clustering and Gene Ontology

N. Speer, Holger Fröhlich, C. Spieth, and A. Zell

IEEE International Joint Conference on Neural Networks (IJCNN 2005), Montreal, Canada

Proceedings, pp. 298-303, IEEE Press

Multi-Objective Model Optimization for Inferring Gene Regulatory Networks

C. Spieth, F. Streichert, N. Speer, and A. Zell

Conference on Evolutionary Multi-Criterion Optimization (EMO 2005), Guanajuato, Mexico

LNCS 3410, pp. 607-620, 2005, Springer-Verlag

A Memetic Clustering Algorithm for the Functional Partition of Genes Based on the Gene Ontology

N. Speer, C. Spieth, and A. Zell

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2004), San Diego, USA

Proceedings, pp. 252-259, IEEE press

Optimizing Topology and Parameters of Gene Regulatory Network Models from Time-Series Experiments

C. Spieth, F. Streichert, N. Speer, and A. Zell

Genetic and Evolutionary Computation Conference (GECCO 2004), Seattle, USA,

LNCS 3102 (Part I), pp. 461-470, Springer-Verlag

A Memetic Inference Method for Gene Regulatory Networks Based on S-Systems

C. Spieth, F. Streichert, N. Speer, and A. Zell
IEEE Congress on Evolutionary Computation (CEC 2004), Portland, USA
Proceedings, vol. 1, pp. 152-157, IEEE Press

Utilizing an Island Model for EA to Preserve Solution Diversity for Inferring Gene Regulatory Networks

C. Spieth, F. Streichert, N. Speer, and A. Zell
IEEE Congress on Evolutionary Computation (CEC 2004), Portland, USA
Proceedings, vol. 1, pp. 146-151, IEEE Press

Comparing Genetic Programming and Evolution Strategies on Inferring Gene Regulatory Networks

F. Streichert, H. Planatscher, C. Spieth, H. Ulmer, and A. Zell
Genetic and Evolutionary Computation Conference (GECCO 2004), Seattle, USA,
LNCS 3102 (Part I), pp. 471-480, Springer-Verlag

How to evolve the Head-Tail Pattern from Reaction-Diffusion Systems

F. Streichert, C. Spieth, H. Ulmer, and A. Zell
NASA/DoD Conference on Evolvable Hardware (EH 2004), Seattle, USA,
Proceedings pp. 261-268, IEEE Press

A Memetic Co-Clustering Algorithm for Gene Expression Profiles and Biological Annotation

N. Speer, C. Spieth, and A. Zell
IEEE Congress on Evolutionary Computation (CEC 2004), Portland, USA
Proceedings, vol. 2, pp. 1631-1638, IEEE Press

Iteratively Inferring Gene Regulatory Networks with Virtual Knockout Experiments

C. Spieth, F. Streichert, N. Speer, and A. Zell
2nd European Workshop on Evolutionary Bioinformatics (evoBIO 2004), Coimbra, Portugal
LNCS 3005, pp. 102-111, Springer-Verlag

Gene Expression patterns of epithelial cells modulated by pathogenicity factors of Yersinia enterocolitica

E. Bohn, S. Müller, J. Lauber, R. Geffers, N. Speer, C. Spieth, J. Krejci, B. Manncke, J. Buer, A. Zell and I.B. Autenrieth
Cellular Microbiology, February 2004, vol. 6, no. 2, pp. 129-141(13), Blackwell Publishing

Differential overexpression of interferon-associated genes during the innate and acute phase of myocardial coxsackievirus B3 infection contributes to chronic myocarditis

G. Szalay, S. Meiners, K. Klingel, J.-J. Schnorr, J. Lauber, C. Spieth, N. Speer, K. Stangl, R. Kandolf
Immunobiol., 2004, vol. 208, pp. 181, Elsevier

Clustering Gene Expression Data with Memetic Algorithms based on Minimum Spanning Trees

N. Speer, Peter Merz, C. Spieth, and A. Zell
IEEE Congress on Evolutionary Computation (CEC 2003), Canberra, Australia,
Proceedings, vol. 3, pp. 1848-1855, IEEE Press

Evolving the Ability of Limited Growth and Self-Repair for Artificial Embryos

F. Streichert, C. Spieth, H. Ulmer, and A. Zell
7th European Conference on Artificial Life (ECAL 03), Dortmund, Germany,
LNAI 2801, pp. 289-298, Springer-Verlag

Presentations

Upregulation of immunoproteasome gene expression during the acute phase of myocardial coxsackievirus B3 infection contributes to chronic myocarditis

G. Szalay, S. Meiners, K. Klingel, S. Stefanovic, C. Spieth, N. Speer, K. Stangl, R. Kandolf
IUIS/ICI/FOCIS Congress, 19. - 23. July 2004, Montreal, USA

Differential overexpression of immunoproteasome subunits during the innate and acute phase of myocardial coxsackievirus B3 infection contributes to chronic myocarditis

G. Szalay, S. Meiners, K. Klingel, Chr. Spieth, N. Speer, K. Stangl, R. Kandolf
Jahrestagung der Gesellschaft für Virologie, 17. - 20. March 2004, Tübingen

Die differentielle Überexpression von Interferon-assoziierten Genen in der frühen und akuten Phase der Enterovirusmyokarditis als Determinante für eine chronische Verlaufsform

G. Szalay, S. Meiners, K. Klingel, J. Lauber, C. Spieth, N. Speer, K. Stangl, R. Kandolf
70. Jahrestagung der Deutschen Gesellschaft für Kardiologie - Herz- und Kreislaufforschung, 17. April 2004, Mannheim

Gene Expression Patterns of Epithelial Cells Modulated by Pathogenicity Factors of Enteric Yersinia

E. Bohn, S. Müller, J. Lauber, R. Geffers, N. Speer, C. Spieth, J. Krejci, B. Manncke, J. Buer, A. Zell, I. Autenrieth
Functional Genomics of Infectious Diseases and Inflammation, TuebinGENome Symposium, 18. - 20. September 2003, Tübingen

Microfilariae; Microsatellites and Microarrays. Functional Genomics and identification of Microfilaraemia Resistance Loci in a Murine Model of Filariasis

W. Hoffmann, S. Schumacher, A. Schmidt-Oehm, B. Meyer, A. Lengeling, P. Soboslay, S. Hille, N. Speer, C. Spieth, M. Bonin, P. Nürnberg, H. Schulz-Key
Functional Genomics of Infectious Diseases and Inflammation, TuebinGENome Symposium, 18. - 20. September 2003, Tübingen

Differential Overexpression of Interferon-Associated Genes During the Innate and Acute Phase of Myocardial Coxsackie-Virus B Infection Contributes to Chronic Myocarditis

G. Szalay, S. Meiners, K. Klingel, J. Schnorr, J. Lauber, C. Spieth, N. Speer, K. Stangl, R. Kandolf
Functional Genomics of Infectious Diseases and Inflammation, TuebinGENome Symposium, 18. - 20. September 2003, Tübingen

Posters

JCell - Inferring Genetic Networks

C. Spieth, F. Streichert, N. Speer, and A. Zell
FEBS Workshop on Systems Biology, SysBio 2005, Gosau, Austria

JCell - Inferring Genetic Interactions from DNA Microarray Data

C. Spieth, A. Zell
NGFN Symposium, 20. - 21. November 2004, Berlin

Gene Expression of Human Macrophages in Response to Different Microbial Pathogens of Phylogenetically Very Distant Groups

W. Hoffmann, H. Schulz-Key, G. Szalay, A. Kraus, F. Götz, J. Löffler, H. Einsele, N. Speer, C. Spieth, A. Zell, M. Bonin, G. Jahn, C. Sinzger
Functional Genomics of Infectious Diseases and Inflammation, TuebinGENome Symposium, 18. - 20. September 2003, Tübingen

Differential gene expression of epithelial cells upon infection with enteropathogenic Yersinia enterocolitica

S. Müller, E. Bohn, J. Krejci, J. Lauber, Jan Buer, C. Spieth, N. Speer, A. Zell, I. Autenrieth
The Genetic and Molecular Basis of Human Disease, NGFN/DHGP Symposium, 17. - 19. November 2002, Berlin

Misc

"Neues Softwarewerkzeug mit Zukunft",

[GenomXpress](#) - Informationen der deutschen Genomforschung, p. 36, September 2005>

"Preisgekrönt: Neue Software simuliert das Zusammenspiel der Gene",

[BMBF Newsletter Gesundheitsforschung](#), Nr. 21, p. 9

"Simulationssoftware erhellt Lernprozesse",

[Computer Zeitung](#), Nr. 24, p. 9

"Gut geforscht, für gut befunden",

[Stuttgarter Zeitung](#)

"3. Preis beim doIT Software-Award für Bioinformatiker aus Tübingen",
[BioPro](#)

"doIT Software-Award 2005 - Bioinformatik auf den ersten Plätzen",
[BioPro](#)>

"Software Award - Gut geforscht, für gut befunden",
[Stuttgarter Nachrichten](#)

"doIT Software-Forschungstag zeigt Trends in Bioinformatik",
[MFG Stiftung Baden-Württemberg](#)

"doIT Software-Forschungstag zeigt Trends in Bioinformatik",
[VDI Nachrichten](#)

JCell : a Java framework for inferring genetic networks
C. Spieth
Technical Report, Universitätsbibliothek Tübingen,
URN: urn:nbn:de:bsz:21-opus-17001
[URL:http://w210.ub.uni-tuebingen.de/dbt/volltexte/2005/1700/](http://w210.ub.uni-tuebingen.de/dbt/volltexte/2005/1700/)

"Systembiologie - Vom Experiment zur Struktur"
C. Spieth
[BIOspektrum](#) - Special Edition - 10 Years BIOspektrum, 1/2005, pp. 100-102

"Netzwerke unter der Lupe"
C. Spieth, N. Speer, and A. Zell
[GenomXpress](#) - Informationen der deutschen Genomforschung, pp. 4-6, September 2004

Theses

Zur Simulation von instationären Strömungs-Schalen-Interaktionsproblemen
Diplomarbeit
[Institute of Structural Mechanics](#), University of Stuttgart, 2000, Stuttgart

Analyzing DNA Sequences of Bacteria to Find Promoter Regions
Master Thesis
[Oxford University Computing Laboratory](#), Oxford University, 2001, Oxford, UK

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