

# STEFAN R. MAETSCHKE

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## EXPERTISE & INTERESTS

Computational biology, Machine learning, Data mining, Software development,  
Nonlinear optimization, Image and Signal processing

## PROJECTS & RESEARCH

- Classification of TDR-signals (Ethernet) using neural networks
- Evaluation of training algorithms for neural networks
- Kinematic and dynamic simulation models of multi-axle robots
- Adaptive torque controller for a Manutec robot using neural networks
- Friction compensation and filter optimization for tooling machines
- Welding spot diagnosis based on spot image and welding parameters
- Sound and vibration based diagnosis of tiles and motors
- Speaker, language and topic identification on audio signals
- Promoter site recognition in prokaryotes using phylogenetic footprinting
- Cleavage site prediction in signal peptides
- Topology and localization prediction of transmembrane proteins
- Binding site and protein function prediction
- Inference of protein protein interaction networks

(Details can be found at: <http://www.quuux.com/stefan/projects.html>)

## SOFTWARE

- Libraries for vector and matrix processing (C/Java)
- Libraries for nonlinear optimization (C/Java)
- Libraries for support vector machines, hidden Markov models and conditional random fields (Java)
- Jacobi: Library for the analysis of nucleotide and peptide sequences (Java)
- CALVIN: General purpose machine learning application (C++/MFC)
- Simultan: Image and signal based quality control system (C++/MFC)
- TSpot: Experimental system for topic spotting on sound (Java)
- TOPS: Workflow based data mining system for text (Swing/Java)
- BioPatML: Description language for patterns in biological sequences (Java/XML)
- Footy: Phylogenetic footprinting software for promoter site recognition (Java)
- TMPLoc: Localization predictor for transmembrane proteins (Java/JSP)
- Diana-B: Genome browser (Swing/Java)
- PRIP: Predictor for protein-RNA interfaces (Python/Java/JSP)
- Ceye: Calendar application for Google Android (Java)
- CRPs: Web application for the assessment of medical students (Python/Django)
- SDA: Framework for the statistical analysis of stroke data (Python/Matplotlib/SQL)
- Mosaic: Visual framework for sequence analysis (Python/Matplotlib/NumPy)
- go2ppi: Predictor for protein-protein interaction networks (Scala/Jung2/BerkelyDB)

## PATENTS

- Determining the orientation of subject data in a two-dimensional data set (#6792139)
- Method and apparatus for signal segmentation (#6771804)
- System and method for evaluating characteristics for suitability in classification (#6484122)
- Analysis of weld image to determine weld quality (#6414261)
- Device designed to compensate for non-linearity of machine shafts (#5804940)
- Defect identification in bodies consisting of brittle material (#20030167845)

## PUBLICATIONS

### 2011

- S. Maetschke, M. Simonsen, J. Davis, M. Ragan  
Gene Ontology-driven inference of protein-protein interactions using inducers.  
Bioinformatics 2012, 28: 69-75

### 2010

- S. Maetschke, K. Kassahn, J. Dunn, S. Han, E. Curley, K. Stacey, M. Ragan  
A visual framework for sequence analysis using n-grams and spectral rearrangement.  
Bioinformatics 2010, 26 (6): 737-744

### 2009

- S. Maetschke, Z. Yuan  
Exploiting structural and topological information to improve prediction of RNA-protein binding sites.  
BMC Bioinformatics 2009, 10:341
- S. Maetschke  
Computational protein localization prediction.  
VDM Verlag, ISBN:3639137418

### 2008

- F. Buske, S. Maetschke and M. Bodén  
Its about time: signal recognition in staged models of protein translocation.  
Pattern Recognition special issue on CMLS-2007  
Pattern Recognition 42, 567-574
- S. Maetschke, M. Towsey and J. Hogan  
BioPatML - Pattern Sharing for the Genomic Sciences.  
Microsoft eScience Workshop  
Dec 7-9, 2008, Indianapolis
- I. Arieshanti, M. Bodén, S. Maetschke and F. Buske  
Detecting Sequence and Structure Homology via an Integrative Kernel: A Case-Study in Recognizing Enzymes  
CIBCB 2009  
2009 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, 46-52.

## 2007

- S. Maetschke, M. Gallagher, M. Bodén  
A Comparison of Sequence Kernels for Localization Prediction of Transmembrane Proteins. Computational Intelligence and Bioinformatics and Computational Biology (CIBCB). IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, 367-372.
- S. Maetschke, M. Towsey and J. Hogan  
BioPatML - an XML description language for patterns in biological sequences. Technical Report, Department of Software Engineering and Data Communications, QUT.
- J. Hawkins, D. Mahony, S. Maetschke, M. Wakabayashi, R. Teasdale, M. Bodén  
Identifying novel peroxisomal proteins. Proteins: Structure, Function, and Bioinformatics 69(3), 606-616.
- J. Watson, S. Maetschke, J. Wiles  
An introduction to Dsweep, a lightweight tool for distributed parameter sweeps Proceedings of the Seventh International Workshop on Information Processing in Cells and Tissues (IPCAT), Oxford 29-31 August 2007, 400-408.
- B. Grech, S. Maetschke, S. Mathews, P. Timms  
Genome wide analysis of chlamydiae for promoters that phylogenetically footprint. Research in Microbiology, doi: 10.1016/j.resmic.2007.08.005
- S. Maetschke  
Topological models of transmembrane proteins for subcellular localization prediction. PhD thesis, School of Information Technology and Electrical Engineering, 2007.

## 2006

- L. Davis, J. Hawkins, S. Maetschke, M. Bodén  
Comparing SVM Sequence Kernels: A Subcellular Localization Theme. In Proc. 2006 Workshop on Intelligent Systems for Bioinformatics (WISB 2006), Hobart, Australia. CRPIT, 73. Boden, M. and Bailey, T. L., Eds., ACS. 39-47.
- S. Maetschke, M. Bodén, M. Gallagher  
Higher Order HMMs for Localization Prediction of Transmembrane Proteins. In Proc. 2006 Workshop on Intelligent Systems for Bioinformatics (WISB 2006), Hobart, Australia. CRPIT, 73. Boden, M. and Bailey, T. L., Eds., ACS. 49-53.
- S. Maetschke, M. Towsey and J. Hogan  
Bacterial Promoter Modeling and Prediction for E. Coli and B. Subtilis with Beagle. In Proc. 2006 Workshop on Intelligent Systems for Bioinformatics (WISB 2006), Hobart, Australia. CRPIT, 73. Boden, M. and Bailey, T. L., Eds., ACS. 9-13.

## 2005

- S. Maetschke, M. Towsey, M. Bodén  
BLOMAP: An encoding which improves signal peptide cleavage site prediction.  
Third Asia Pacific Bioinformatics Conference, Singapore, 141-150.
- M. Wakabajashi, J. Hawkins, S. Maetschke, M. Bodén  
Exploiting sequence dependencies in the prediction of peroxisomal proteins.  
Intelligent Data Engineering and Automated Learning (IDEAL 2005), Brisbane, 454-461.

## POSTERS

- P. Madhamshettiwar, S. Maetschke, M. Davis, A. Reverter and M. Ragan (2012) Gene regulatory networks in cancer systems biology  
Asia Pacific Bioinformatics Conference (APBC2012), Melbourne, Australia.
- S. Maetschke, M. Gallagher, M. Bodén (2007).  
Localization Prediction of Transmembrane Proteins: A Comparison of Sequence Kernels  
Computational Intelligence and Bioinformatics and Computational Biology (CIBCB), Oahu, Hawaii.
- S. Maetschke, M. Towsey, M. Bodén (2007).  
Topological Models for the Localization Prediction of Transmembrane Proteins.  
Bioinformatics Australia Conference 2007, Brisbane, Australia.
- S. Maetschke, M. Towsey and J. Hogan (2007).  
BioPatML & Diana - A Discription Language and a Browser for Patterns in Biological Sequences.  
Bioinformatics Australia Conference 2007, Brisbane, Australia.
- S. Maetschke, Z. Yuan (2008).  
Exploiting structural and topological information to improve prediction of RNA-protein binding sites.  
IMB ECR Symposium, Brisbane, Australia.

## SUPERVISION

- Supervisor: David Derry, ASPinS Student, 2011
- Assoc. Supervisor: Piyush Madhamshettiwar, PhD Student, 2009-current
- Assoc. Supervisor: Isye Arieshanti, MPhil Student, 2007-2009
- Assoc. Supervisor: Ruth Rule, PhD Student, 1999-2001

## TEACHING

2nd Sem. 08/09	Java: Programming in the Large and Advanced Software Engineering School of Information Technology and Electrical Engineering, Brisbane, Australia
08/09/10	Python introduction, BIOL3014 Advanced Bioinformatics University of Queensland, Brisbane, Australia
08/10/11	Python tutorial for biologists, Institute for Molecular Bioscience, Brisbane, Australia
11	Introduction to Scala language Institute for Molecular Bioscience, Brisbane, Australia

## OTHER ACHIEVEMENTS

- Dean's commendation for outstanding PhD thesis
- Member of the editorial board of the Online Journal for Bioinformatics
- Finalist Trailblazer 5 innovation competition

## EDUCATION

2004 - 2007	PhD in Computer Science, University of Queensland, Brisbane, Australia
1986 - 1990	MSc in Computer Science (Diplom in Informatik), University of applied science (Fachhochschule), Würzburg, Germany, Bavaria

## EMPLOYMENT HISTORY

2010 - today	Research Officer, Institute for Molecular Bioscience, Brisbane, Australia & Research Officer (casual), Faculty of Health Sciences
2009 - 2010	Research Officer, Institute for Molecular Bioscience, Brisbane, Australia & Research Officer (casual), Faculty of Health Sciences Research Officer, Associate Lecturer and Course Coordinator, School of Information Technology and Electrical Engineering, Brisbane, Australia
2008 - 2009	Research Officer, Institute for Molecular Bioscience, Brisbane, Australia & Associate Lecturer and Course Coordinator, School of Information Technology and Electrical Engineering, Brisbane, Australia
2007 - 2008	Research Officer, Institute for Molecular Bioscience, Brisbane, Australia
2004 - 2006	Research Assistant, University of Queensland, Brisbane, Australia

Research Assistant, Queensland University of Technology, Brisbane, Australia  
2001 - 2003 Research & Development, MEDAV GmbH, Uttenreuth, Germany  
1994 - 2001 Research & Development, Siemens AG, Nuernberg, Germany  
1990 - 1994 Research & Development, Siemens AG, Erlangen, Germany

## COMPUTER SKILLS

- Windows, UNIX, Android
- Java, Scala, Python, C/C++, Matlab, R, Pascal, Lisp, Perl, Fortran
- XML, HTML, CSS, JSP, JDBC, SQL,  $\LaTeX$ , Django, BerkelyDB
- Eclipse, IntelliJ, Visual Studio

## LANGUAGES

- English (fluent, CBT 293, Essay 6.0, IELTS 8.5)
- German (native speaker)

## REFERENCES

Dr. Mikael Bodén  
Institute for Molecular Bioscience, Brisbane, Australia  
[m.boden@uq.edu.au](mailto:m.boden@uq.edu.au)

Prof. Mark Ragan  
Institute for Molecular Bioscience, Brisbane, Australia  
[m.ragan@uq.edu.au](mailto:m.ragan@uq.edu.au)

Assoc. Prof. James Hogan  
Queensland University of Technology, Brisbane, Australia  
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