

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)

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

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
(submitted)

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. A. 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

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.
- 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

- 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.

SUPERVISOR

- Assoc. Supervisor: Isye Ariesanti, 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
- 07.08/09 Python crash course, BIOL3014 Advanced Bioinformatics
University of Queensland, Brisbane, Australia
- 24.06.2008 Python introduction,
Institute for Molecular Bioscience, Brisbane, Australia

OTHER ACHIEVEMENTS

- Member of the editorial board of the Online Journal for Bioinformatics
- Finalist Trailblazer 5 innovation competition

EDUCATION

- 2004 - 2007 PhD in Computer Science,
(Dean's commendation for outstanding PhD thesis),
University of Queensland, Brisbane, Australia
- 1986 - 1990 MSc in Computer Science (Diplom in Informatik),
University of applied science (Fachhochschule), Würzburg,
Germany, Bavaria

EMPLOYMENT HISTORY

- 2009 - today 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, Google Android
- Java, Python, Scala, R, C/C++, Matlab, Pascal, Lisp, Perl, Fortran
- XML, HTML, CSS, JSP, JDBC, SQL, L^AT_EX, Django
- Eclipse, JBuilder, 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@imb.uq.edu.au

Assoc. Prof. James Hogan
Queensland University of Technology, Brisbane, Australia
j.hogan@qut.edu.au

Dr. Michael Towsey
Queensland University of Technology, Brisbane, Australia
m.towsey@qut.edu.au