

STEFAN R. MAETSCHKE

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EXPERIENCE

Software development, Machine learning, Bioinformatics, Data mining
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

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)
- Library for the analysis of nucleotide and peptide sequences (Java)
- General purpose machine learning application (C++/MFC)
- Image and signal based quality control system (C++/MFC)
- Experimental system for topic spotting on sound (Java)
- Workflow based data mining system for text (Swing/Java)
- Description language for patterns in biological sequences (Java)
- Phylogenetic footprinting software for promoter site recognition (Java)
- Localization predictor for transmembrane proteins (Java/JSP)
- Genome browser (Swing/Java)

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

- S. Maetschke, M. Towsey, M. Bodén (2005).
BLOMAP: An encoding which improves signal peptide cleavage site prediction.
Third Asia Pacific Bioinformatics Conference, Singapore, 141-150.
- M. Wakabayashi, J. Hawkins, S. Maetschke, M. Bodén (2005).
Exploiting sequence dependencies in the prediction of peroxisomal proteins.
Intelligent Data Engineering and Automated Learning (IDEAL 2005), Brisbane, 454-461.
- L. Davis, J. Hawkins, S. Maetschke, M. Bodén (2006).
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 (2006).
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 (2006).
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.
- S. Maetschke, M. Gallagher, M. Bodén (2007).
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.
- J. Hawkins, D. Mahony, S. Maetschke, M. Wakabayashi, R. Teasdale, M. Bodén (2007).
Identifying novel peroxisomal proteins.
Proteins: Structure, Function, and Bioinformatics, (accepted)
- J. Watson, S. Maetschke, J. Wiles (2007).
Dsweep: A lightweight tool for distributed parameter sweeps.
Seventh International Workshop on Information Processing in Cells and Tissues (IPCAT). (accepted)
- B. Grech, S. Maetschke, S. Mathews, P. Timms (2007).
Genome wide analysis of chlamydiae for promoters that phylogenetically footprint.
Research in Microbiology, (accepted)
- S. Maetschke, M. Towsey and J. Hogan (2007).
BioPatML - an XML-based description language for patterns in biological sequences.
BMC Bioinformatics, (submitted)

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

- 2007 - today 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
- Java, Python, C/C++, Matlab, Perl, Pascal, Lisp, Fortran
- XML, HTML, CSS, JSP, JDBC, SQL
- Eclipse, JBuilder, Visual C++

LANGUAGES

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

REFERENCES

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