

Curriculum Vitae

Name Torgeir Rhodén Hvidsten
Born 1975.08.04 in Oslo, Norway. Married. Two children.
Address *Private:* Vädursgatan 2C, 90752 Umeå, Sweden.
Work: Department of Plant Physiology, Umeå University, 901 87 Umeå, Sweden.
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Positions

2008- Assistant professor, Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, Sweden.
2004-2008 Postdoc/Researcher at the Linnaeus Centre for Bioinformatics, Uppsala University, Sweden.

Education

2000 – 2004 **PhD student**
Phd-thesis: *Predicting function of genes and proteins from sequence, structure and expression data.* Linnaeus Centre for Bioinformatics and Department of Information Technology, Uppsala University, Sweden.
Defense: 2004.09.22 [Opponent: Professor Anna Tramontano]
Supervisor: Professor Jan Komorowski
Research visit (Fall 2001): Protein Structure Prediction Centre (Dr. Krzysztof A. Fidelis), Lawrence Livermore National Lab, USA.
1995 – 2000 **Master of Science student**
Department of Computer and Information Science, Norwegian University of Science and Technology, Norway. Grade: 1.90¹
Master-thesis: *Knowledge Discovery in Gene Expression Databases.* Grade: 1.25¹
1994 – 1995 **Sergeant training, Norwegian military**
1995 (Spring) Instructor at Lista Airport, Norway. Examen Philosophicum², University of Bergen.
1994 (Fall) Sergeant training, Kongsvinger, Norway. Ranked 6th of approx. 200 applicants.
Teaching courses
2010 (Spring) *Post graduate supervision in practice*, Umeå University, 2 weeks.
2008 (Spring) *Teacher Training for University Teachers, Stage 1 and 2*, Uppsala University, 5 weeks.

Supervisor experience

Postdocs

- Jonas Wiklund, 2011.01.01-present.
- Sergiu Netotea, 2010.03.01-present.

PhD students (main supervisor)

- Jenny Önskog, 2008.10.13-present. Parental leave 2008.11.10-2009.10.31 and 2010.11.01-2011.10.31.

PhD students (assistant supervisor)

- Ogonna Obudulu, 2010-present (main supervisor: Gunnar Wingsle).
- Helena Strömbergsson, *Chemogenomics: Models of Protein-Ligand Interaction Space*, 2006-2009 (main supervisor: Gerard Kleywegt).

Master students and others

- 2011**
 - Niklas Mähler, Project employee (2.5 months)
 - David Sundell, Project employee (8 months)
 - François Richard, Visiting project student and project employee (3+2.5 months).
- 2010** – Lisa Kruggel and Kerstin Strömvall. *Clustering and Motif Finding of an Expression Data Set from Aspen Tree (Populus) Leaves*, Student project (4ECTS³).
- 2009** – Ali Shamsi and Tarek Elhasi. *Clustering and motif finding in poplar gene expression data*, Student project (4ECTS).
– Peter Boman and Daniel Decker. *Visualisation of gene coexpression networks*, Student project (7.5 ECTS).
- 2008** – Patrik Björkholm. *Method for recognizing local descriptors of protein structures using Hidden Markov Models*, Master thesis.
– Johan Alexander Källberg Zvrskovec. *Protein structure prediction by search among combinations of reoccurring structural components*, Student project (10 points⁴).
- 2006-2007** – Minyan Hong. *Fold recognition using local descriptors of protein structure and hidden Markov models*, Student project (5 points) and Master thesis.
- 2005** – Min Jia. *Proteochemometrics modeling of carbonic anhydrase-ligand interactions using rule-based and linear methods*, Student project (10 points).
– Marta Luksza. *A System for Predicting Protein Function from Structure*, Master thesis.

¹ <2.0: A, 2.0-2.5: B, etc.

² Compulsory course in philosophy required for all degrees at Norwegian universities.

³ One year of studying full time gives 60 ECTS.

⁴ One year of studying full time gives 40 points. 1 point corresponds to one week of studying full time.

- Anna Hennecke. *Predicting protein function from its 3-dimensional structure - Biological validation of protein function predictions*, Student project (10 points).

Teaching experience

Abbreviations

S/F	Spring/Fall	KBC	Chemical Biological Centre
UPSC	Umeå Plant Science Center	KRS	KBC Research School
UmU	Umeå University	EBC	Evolutionary Biology Centre
LCB	Linnaeus Centre for Bioinformatics	FarmBio	Department of Pharmaceutical Biosciences
UU	Uppsala University	SLU	Swedish University of Agricultural Sciences
IDI	Dep. of Computer and Information Science	IBG	Biology Education Centre
NTNU	Norwegian Univ. of Science and Technology		

Responsible teacher (* developed courses)

- 2011** F **Computational life Science* (15 ECTS), UPSC and KRS, UmU.
2010 F **Next-generation sequencing - techniques and applications* (2 ECTS), KRS, UmU.
 **Computational life Science* (15 ECTS), UPSC and KRS, UmU.
 S **Computer Programming Languages and Algorithms in Bioinformatics* (2 ECTS), KRS, UmU.
2009 F **Computational life Science* (15 ECTS), UPSC and KRS, UmU.
 S **Computer Programming Languages and Algorithms in Bioinformatics* (2 ECTS), KRS, UmU.
2008 F **Discrete Structures for Bioinformatics II* (Level: C⁵, 5 points), LCB, UU.
2007 F **Discrete Structures for Bioinformatics II* (Level: C, 5 points), LCB, UU.
Knowledge-based systems in Bioinformatics (Level: D, 5 points), LCB, UU.
2006 F **Discrete Structures for Bioinformatics II* (Level: C, 5 points), LCB, UU.

Lectures/labs

- 2011** S Lecture (1), *Basic Bioinformatics*, Master program for biotechnology, UmU.
 Lectures (2), *Functional genomics*, UPSC, UmU.
 Lecture (1), *Multivariate Data Analysis with Biological and Medical Applications*, KRS, UmU.
2010 S Lecture (1), *Basic Bioinformatics*, Master program for biotechnology, UmU.
 Lectures (2), *Functional genomics*, UPSC, UmU.
 Lecture (1), *Multivariate Data Analysis with Biological and Medical Applications*, KRS, UmU.
2009 S Lectures (2), *Functional genomics*, UPSC, UmU.
 Lecture (1), *Multivariate Data Analysis with Biological and Medical Applications*, KRS, UmU.
2008 S Lecture, *Boolean reasoning in Bioinformatics* (Level: D), LCB, UU.
 Lectures (3), *Molecular Bioinformatics X3* (Level: C), IBG, UU.
2007 S Lecture, *Boolean reasoning in Bioinformatics* (Level: D), LCB, UU.
 Lectures (3), *Molecular Bioinformatics X3* (Level: C), IBG, UU.
 Lecture (Internet course), *Pharmaceutical bioinformatics* (Level: PhD students), FarmBio, UU.
2006 F Lecture, *Pharmaceutical bioinformatics*, FarmBio (Level: PhD students), UU.
 S Lectures (3), *Molecular Bioinformatics X3* (Level: C), IBG, UU.
 Lecture, *Boolean reasoning in Bioinformatics* (Level: D), LCB, UU.
2005 S Lectures (2) and computer labs, *Boolean reasoning in Bioinformatics* (Level: D), LCB, UU.
2004 F Lecture and computer labs, *Bioinformatics - Models and Algorithms*, EBC, UU.
 S Lecture and computer lab, *Bioinformatics VT04*, SLU.
2003 F Lecture and computer labs, *Bioinformatics - Models and Algorithms*, EBC, UU.
 S Lecture and computer lab, *Bioinformatics VT04*, SLUs.
 Lectures (2) and responsible for computer labs, *A Course on Analysis and Informatics of Microarray Data*, LCB, UU.
 Responsible for computer labs, *Molecular Bioinformatics X3* (Level: C), IBG, UU.
2002 S Teaching Assistant⁶, *Programming Languages*, IDI, NTNU.
2001 S Teaching Assistant, *Logic*, IDI, NTNU.
2000 F Teaching Assistant, *Knowledge Systems (AI)*, IDI, NTNU.
1999 S Student Assistant⁷, *Logic*, IDI, NTNU.
1998 F Student Assistant, *Digital Design and Computers*, IDI, NTNU.
 S Student Assistant, *Control Technique*, Department of Engineering Cybernetics, NTNU.
1997 F Student Assistant, *Mathematics 1*, Department of Mathematical Science, NTNU.

⁵ Levels from lowest to highest: A, B, C and D.

⁶ Teaching Assistant: Responsible for lab exercises and lab lectures.

⁷ Student Assistant: Guiding students in the lab and correcting lab reports.

Presentations

- 2011** – A systems biology view to the regulatory genomes of plants, Max Planck Institute of Molecular Plant Physiology, September 13th, Golm-Potsdam, Germany.
- 2010** – The regulatory network of trees: a comparison of traditional bioinformatics approaches and systems biology, Institute of Biotechnology, April 30, Vilnius, Lithuania.
- 2009** – A systems biology approach to model the transcriptional network in trees. Third UPRA Meeting on Plant Integrative Biology, UPRA (European Open Laboratory UPSC and INRA), November 25 – 27, INRA Nancy Research Centre, Champenoux, France.
- A systems biology approach to model the transcriptional and metabolic network in Populus, 3rd Joint meeting Riken, Golm, UPSC, September 16-18, Umeå, Sweden.
- Local descriptors of protein structure: A universal approach to protein structure representation, Stockholm Bioinformatics Centre (SBC), September 10th, Stockholm, Sweden.
- A systems biology approach to model the transcriptional network in trees, Seminar on novel approaches in physical biology and bioinformatics, May 20, Warsaw, Poland.
- 2008** – Predicting gene function from gene expression trends, protein features and cis-regulatory information – A rough set modeling approach, IGK Workshop: Data driven modelling and optimization, December 15-16, 2008, Warsaw, Poland.
- Dissecting regulatory control in Yeast using rule-based learning, Invited talk at the Norwegian University of science and technology, Bioinformatics seminar series, March 6th, Trondheim, Norway.
- 2007** – Towards computational inference of cellular interaction networks, Invited talk at the Umeå Plant Science Centre, December 4th, Umeå, Sweden.
- 2006** – From sequence to structure to function: towards new approaches to protein function prediction, Invited talk at the Biotech Centre of Oslo, June, Oslo, Norway.
- 2004** – Predicting molecular function from local descriptors of protein structure, 5th Swedish Bioinformatics Workshop for PhD students and Postdocs, November 26-27, Lund, Sweden.
- Discovering regulatory binding site modules using rule-based learning, Workshop: Regulatory Sequence Motif Discovery, May 6-7, Uppsala, Sweden.
- 2003** – A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins, European Conference on Computational Biology, September 27-30, Paris, France.
- 2002** – Protein fold prediction using sequence based features from local structures, 3rd Annual Workshop in Bioinformatics for PhD Students and PostDocs, November 22-23, Stockholm, Sweden.
- Studying Bioinformatics, Inauguration Day of The Linnaeus Centre for Bioinformatics, November 6th.
- 2001** – A Method Based on Rough Set Supervised Learning used to Predict the Biological Function of Unknown Genes from DNA Microarray Gene Expression Data, Seminar in Medical Technology, May 10, Trondheim, Norway.
- A framework for learning gene functions from microarray data, NBS Vintermøte 2001 - 37. Norwegian Biochemical Society's Wintermeeting, Beitostølen.
- 2000** – Predicting Gene Function from Gene Expressions and Ontologies, First annual workshop for PhD students and postdocs in Bioinformatics, November 16, Uppsala, Sweden.
- A Methodology for Knowledge Discovery from Gene Expressions, Workshop 3: Knowledge Discovery in Biology, The Fourth European Conference on Principles of Data Mining and Knowledge Discovery (PKDD'2000), September 13, Lyon, France.

Assignments

- 2011-** – Editorial Board of ISRN Bioinformatics.
- 2010-** – Board of the Computational Life Science Cluster (CLiC), UmU.

Reviews

- Reviewer for journals; *BMC Bioinformatics*, *Bioinformatics*, *FEBS Journal*, *Genomics*, *BMC Structural Biology*, *ISRN Bioinformatics*, *Plant, Cell and Environment*, *Artificial Intelligence in Medicine*, *Transactions on Rough Sets*, *Soft Computing*, *Control & Cybernetics*, *Engineering Applications of Artificial Intelligence*, *Journal of Biomedical Informatics*, *Handbook of Granular Computing*, *IEEE Transactions on NanoBioscience and Fundamenta Informaticae*.
- Reviewer for conferences; *ISMB*, *ECCB*, *Rough Sets*, *Fuzzy Sets*, *Data Mining*, and *Granular Computing*, and *Workshop on State-of-the-Art in Scientific and Parallel Computing*.
- Reviewer for the *Swedish Research Council* (VR), 2010. Postdoc applications.
- Reviewer and grade assigner for several student projects and master theses from NTNU, UU and University of Witwatersrand, Johannesburg, South Africa.
- Member of the grading committee for the licentiate exam of Pär J. Höglund, UU. 2005.05.10.
- Chairman and member of the examining board for the PhD defense of Pär J. Höglund, UU. 2008.11.15.
- Member of the examining board for the PhD defense of Nicolas Joannin, KI. 2010.10.18.

Grants awarded

- 2011 – *Bioinformatics infrastructure for life sciences* (BILS). 2011. 50% funding of a senior researcher (1:e forskningsingenjör). Main applicants: Johan Normark, Torgeir R. Hvidsten, Pär Larsson (FOI), Per Stenberg and Johan Trygg.
– *Kungl. Skogs- och Lantbruksakademien, Stiftelsen Gunnar och Birgitta Nordins fond*, 150 000 SEK.
– *UPSC Berzelii Centre for Forest Biotechnology* for RNA-Seq of transgenic trees (276 750 SEK) and for building a UPSC research for NGS analysis (371 250 SEK, Co-applicant: Nat Street).
- 2010 – *Carl Tryggers Stiftelse för Vetenskaplig Forskning*, 220 000 SEK.
– UPSCs internationalization program: One postdoc fellowship financed by the Kempe Foundations.
- 2009 – *SSF centre for Developmental Biology of Plants* (900k SEK) and the *UPSC Berzelii Centre for Forest Biotechnology* (600k SEK) for next-generations sequencing of RNA and miRNA: A systems biology approach to model regulation of wood development in *Populus*. Co-applicants: 9 group leaders at UPSC.
- 2008 – *Kempe Foundations*, Utveckling av en högdensitets-SNP-array för tall: vägen till genomvid selektion (Genome Wide Selection: GWS). Principle investigator: María Rosario García-Gil. 750k SEK.
- 2008 – Travel grants to Critical Assessment of Techniques for Protein Structure Prediction (CASP 5, 6, 7 and 8). 2002-2008.
- 2003 – Travel grant to European Conference on Computational Biology, September 27-30, Paris, France.
- 2001 – *Norwegian Research Council*, Six month research visit at LLNL (grant 145609/432).

Software tools

- Network visualization tools in PopGenIE. <http://www.popgenie.org/>.
- FragHMMent; a method for residue-residue contact prediction in proteins. <http://fraghmmment.limbo.ifm.liu.se/>.
- The “genomic analysis”-package of the Rosetta system; a rough set-based software system for data mining and knowledge discovery: <http://rosetta.lcb.uu.se/>.
- Some contributions to the LCB Datawarehouse: <https://dw.lcb.uu.se/>.

Other work experience

- 1999 Summer Programming and Software design, Computas, Oslo, Norway.
- 1998 Summer Programming, ABB Kraft, Drammen, Norway.
- 1997 Summer Programming, ABB Kraft, Drammen, Norway.
- 1996 Summer Electromechanical assembling, AS Eltek, Drammen, Norway.

Peer-reviewed research articles

h-index: 10 [Citation statistics from Google scholar. Updated 2011.05.23.]

1. J. Önskog, E. Freyhult, M. Landfors, P. Rydén and **T. R. Hvidsten**. Classification of microarrays; synergistic effects between normalization, gene selection and machine learning. *BMC Bioinformatics* 12: 390, 2011. [*Impact factor* 2010: 3.028, *Citations*: 0]
2. K. Baba*, A. Karlberg*, J. Schmidt, J. Schrader, **T. R. Hvidsten**, L. Bako and R. P. Bhalerao. Activity-dormancy transition in the cambial meristem involves stage specific modulation of auxin response in Hybrid Aspen. *Proceedings of the National Academy of Sciences* 108 (8): 3418-3423, 2011. [*Impact factor* 2010: 9.771, *Citations*: 0]
3. N. Street, S. Jansson and **T. R. Hvidsten**. A systems biology model of the regulatory network in *Populus* leaves reveals interacting regulators and conserved regulation. *BMC Plant Biology* 11: 13, 2011. [*Impact factor* 2010: 4.085, *Citations*: 0]
4. E. Freyhult, M. Landfors, J. Önskog, **T. R. Hvidsten** and P. Rydén. Challenges in microarray class discovery: a comprehensive examination of normalization, gene selection and clustering. *BMC Bioinformatics* 11: 503, 2010. [*Impact factor* 2010: 3.028, *Citations*: 1]
5. V. Srivastava, **T. R. Hvidsten**, P. Ryden, R. Nilsson, E. Freyhult, J. Bygdell, J. Quanstrom, T. Moritz, J. Karlsson, J. Trygg and G. Wingsle. A systems biology approach to study the global responses to oxidative stress in *Populus*. In: *Active Oxygen Involvement in Developmental Processes in Populus*, Doctorial Thesis No. 2009:21, Faculty of Forest Sciences, SLU. (In the process of being submitted to a journal). [*Impact factor*: NA, *Citations*: 0]
6. **T. R. Hvidsten**, A. Lægreid, A. Kryshafovych, G. Andersson, K. Fidelis and J. Komorowski. A comprehensive analysis of the structure-function relationship in proteins based on local structure similarity. *PLoS ONE* 4(7): e6266, 2009. [*Impact factor* 2009: 4.351, *Citations*: 2]
7. P. Björkholm, P. Daniluk, A. Kryshafovych, K. Fidelis, R. Andersson and **T. R. Hvidsten**. Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residue-residue contacts. *Bioinformatics* 25: 1264-1270, 2009. [*Impact factor* 2009: 4.926, *Citations*: 7]
8. **T. R. Hvidsten***, A. Kryshafovych* and K. Fidelis. Local descriptors of protein structure: A systematic analysis of the sequence-structure relationship in proteins using short- and long-range interactions, *Proteins: Structure, Function, and Bioinformatics* 75 (4): 870-884, 2009. [*Impact factor* 2009: 3.085, *Citations*: 8]
9. K. Wabnik, **T. R. Hvidsten**, A. Kedzierska, J. Van Leene, G. De Jaeger, G. T. S. Beemster, J. Komorowski and M. T. R. Kuiper. Gene expression trends and protein features effectively complement each other in gene function prediction, *Bioinformatics* 25 (3):322-330, 2009. [*Impact factor* 2009: 4.926, *Citations*: 4]
10. H. Strömbergsson, P. Daniluk, A. Kryshafovych, K. Fidelis, J. E. S. Wikberg, G. J. Kleywegt and **T. R. Hvidsten**. An Interaction

- Model Based on Local Protein Substructures Generalizes to the Entire Structural Enzyme-Ligand Space, *Journal of Chemical Information and Modeling* 48 (11): 2278–2288, 2008. [Impact factor 2008: 3.643, Citations: 11]
11. R. Andersson, C. Bruder, A. Piotrowski, U. Menzel, T. D. de Ståhl, **T. R. Hvidsten**, J. Dumanski, J. Komorowski. A Segmental Maximum A Posteriori Approach to Genome-wide Copy Number Profiling, *Bioinformatics* 24(6): 751-758, 2008. [Impact factor 2008: 4.328, Citations: 17]
 12. C. R. Andersson*, **T. R. Hvidsten***, A. Isaksson, M. G. Gustafsson, J. Komorowski. Revealing cell cycle control by combining model-based detection of periodic expression with cis-regulatory descriptors, *BMC Systems Biology* 1: 45, 2007. [Impact factor 2007: 3.710, Citations: 7]
 13. U. Bergström, J. A. Olsson, **T. R. Hvidsten**, J. Komorowski, I. Brandt. Differential gene expression in the olfactory bulb following exposure to the olfactory toxicant 2,6-dichlorophenyl methylsulphone and its 2,5-dichlorinated isomer in mice, *NeuroToxicology* 28 (6): 1120-1128, 2007. [Impact factor 2007: 3.009, Citations: 0]
 14. B. Wilczyński, **T. R. Hvidsten**, A. Kryshatovych, J. Tiuryn, J. Komorowski, K. Fidelis. Using Local Gene Expression Similarities to Discover Regulatory Binding Site Modules, *BMC Bioinformatics* 7:505, 2006. [Impact factor 2006: 3.617, Citations: 12]
 15. H. Strömbergsson, A. Kryshatovych, P. Prusis, K. Fidelis, J. E. S. Wikberg, J. Komorowski and **T. R. Hvidsten**. Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures, *Proteins: Structure, Function and Bioinformatics* 65: 568-579, 2006. [Impact factor 2006: 3.730, Citations: 16]
 16. **T. R. Hvidsten**, B. Wilczyński, A. Kryshatovych, J. Tiuryn, J. Komorowski and K. Fidelis. Discovering regulatory binding site modules using rule-based learning, *Genome Research* 15: 856-66, 2005. [Impact factor 2005: 10.139, Citations: 36]
 17. J. L. Dennis, **T. R. Hvidsten**, J. Komorowski, E. C. Wit, A. Bell, I. Downie, J. Mooney, C. Verbeke, C. Bellamy, W.N. Keith and K.A. Oien. Markers of Adenocarcinoma Characteristic of the Site of Origin – Development of a Diagnostic Algorithm, *Clinical Cancer Research* 11(10): 3766-72, 2005. [Impact factor 2005: 5.715, Citations: 112]
 18. **T. R. Hvidsten**, A. Lægreid and J. Komorowski. Learning rule-based models of biological process from gene expression time profiles using gene ontology, *Bioinformatics* 19:1116-23, 2003. [Impact factor 2003: 6.701, Citations: 80]
 19. A. Lægreid, **T. R. Hvidsten**, H. Midelfart, J. Komorowski, and A. K. Sandvik. Predicting Gene Ontology Biological Process from Temporal Gene Expression Patterns, *Genome Research* 13(5): 965-979, 2003. [Impact factor 2003: 9.635, Citations: 91]
 20. **T. R. Hvidsten**, A. Kryshatovych, J. Komorowski and K. Fidelis. A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins, ECCB2003, *Bioinformatics* 19 Suppl 2: II81-II91, 2003. [Impact factor 2003: 6.701, Citations: 27]
 21. **T. R. Hvidsten**, J. Komorowski, A. K. Sandvik and A. Lægreid. Predicting Gene Function from Gene Expressions and Ontologies, in *Pacific Symposium on Biocomputing* 6: 299-310, 2001. [Citations: 80]
 22. J. Komorowski, **T. R. Hvidsten**, T.-K. Jenssen, D. Tjeldvoll, E. Hovig, A. K. Sandvik and A. Lægreid. Towards Knowledge Discovery from cDNA Microarray Gene Expression Data, in *Principles of Data Mining and Knowledge Discovery* (PKDD'2000) edited by Djamel A. Zighed, Jan Komorowski and Jan Zytkow, Lecture Notes in Computer Science, 4:470-475, 2000. [Citations: 7]
 23. **T. R. Hvidsten**, M. S. Bjanger, J. Komorowski, M. F. White and B. Guanglai. Fault Diagnosis in Rotating Machinery using Rough Sets and Rosetta, in *European Congress on Intelligent Techniques & Soft Computing* (EUFIT'99), Aachen, September 1999. [Citations: 6]

*Contributed equally.

Reviews, book chapters and theses

24. B. Wilczynski and **T. R. Hvidsten**. A computer scientist's guide to the regulatory genome. *Fundamenta Informaticae* 103: 323-332, 2010.
25. J. Fahlén, M. Landfors, E. Freyhult, J. Trygg, **T. R. Hvidsten** and P. Rydén. Bioinformatic strategies for cDNA-microarray data processing. Chapter 6 in *Batch Effects and Noise in Microarray Experiments: Sources and Solutions*, John Wiley & Sons, 2009.
26. **T. R. Hvidsten** and J. Komorowski. Rough sets in bioinformatics, *Transactions on Rough Sets VII* edited by E. Orlowska, J. F. Peters and A. Skowron, Lecture notes in computer science 4400, pp. 225-243, Springer-Verlag Berlin Heidelberg New York, 2007.
27. **T. R. Hvidsten**. A tutorial-based guide to the ROSETTA system: A Rough Set Toolkit for Analysis of Data, 2006.
28. **T. R. Hvidsten**. Predicting function of genes and proteins from sequence, structure and expression data, PhD thesis, Department of Information Technology and Linnaeus Centre for Bioinformatics, Uppsala University, 2004.
29. **T. R. Hvidsten**. Computational gene expression analysis; correlating data and knowledge, *EMBnet.news*, 9(1): 10-12, 2003.
30. **T. R. Hvidsten**, Computational Molecular Biology - an overview, NTNU Computer Science Graduate Student Conference, 2001.
31. J. Komorowski, **T. R. Hvidsten**, T.-K. Jenssen, D. Tjeldvoll, E. Hovig, A. Lægreid and A. K. Sandvik. New knowledge derived from measurement of gene expression with the DNA microarray method, *Tidsskr Nor Lægeforen* 121 (10): 1229-1232, 2001.
32. **T. R. Hvidsten**. Knowledge Discovery in Gene Expression Databases, Master Thesis, Department of Computer and Information science, Norwegian University of Science and Technology, 2000.

Abstracts

33. V. Srivastava, O. Obudulu, J. Bygdell, P. Ryden, R. Nilsson, P. Jonsson, E. Freyhult, J. Quarnström, J. Karlsson, T. Moritz, T. R.

- Hvidsten, J. Trygg and G. Wingsle. A systems biology approach to studying global response to oxidative stress in *Populus*. Metabomeeting 2011, September 25-28, Helsinki, Finland.
34. S. Netotea, F. Richard and **T. R. Hvidsten**. Modeling adaptive changes in *Populus* metabolic and transcriptional networks. 1st Conference on Constraint-based Reconstruction and Analysis (COBRA), June 24-26, 2011, Reykjavik, Iceland.
 35. F. Lysholm, P. Björkholm, **T. R. Hvidsten** and B. Persson. Residue-residue contact prediction through matching of known motifs. Critical Assessment of Techniques for Protein Structure Prediction (CASP9), December 5-9, 2010, Asilomar Conference Center, Pacific Grove, CA, USA.
 36. P. Björkholm, F. Lysholm, A. Kryshafovich, K. Fidelis, and **T. R. Hvidsten**. FragHMMent – Contact prediction using hidden Markov models trained on alignments of local descriptors of protein structure. Critical Assessment of Techniques for Protein Structure Prediction (CASP9), December 5-9, 2010, Asilomar Conference Center, Pacific Grove, CA, USA.
 37. S. Netotea and **T. R. Hvidsten**. Inferring gene regulatory networks to identify conserved regulation between *Arabidopsis* and *Populus*. ECCB, Sep 26 - Sep 29, 2010, Ghent, Belgium.
 38. P. Björkholm, P. Daniluk, A. Kryshafovich, K. Fidelis, R. Andersson and **T. R. Hvidsten**. FragHMMent: Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residue-residue contacts. ISMB and ECCB, June 27-July 2, 2009, Stockholm, Sweden.
 39. B. Dedicova, **T. R. Hvidsten**, O. Nilsson, U. Egertsdotter. Cryopreservation and survival ability of different Elite embryogenic lines of Norway spruce. 1st International Symposium on Cryopreservation in Horticultural Species, April 5-8, 2009, Leuven, Belgium.
 40. N. Street, S. Jansson and **T. R. Hvidsten**. A systems biology approach to model the transcriptional network in trees. UPSC meeting: Future directions in plant research, March 16-18, 2009, Gålsjö bruk, Sweden.
 41. P. Björkholm, P. Daniluk, A. Kryshafovich, K. Fidelis, R. Andersson and **T. R. Hvidsten**. Predicting residue-residue contacts using hidden Markov models trained on local neighborhoods of protein structure. Critical Assessment of Techniques for Protein Structure Prediction (CASP8), December 3-7, 2008, Cagliari, Sardinia, Italy.
 42. J. E. S. Wikberg, M. Eklund, O. Spjuth, H. Strömbergsson, **T. R. Hvidsten** and M. Lapins. Proteochemometrics. 17th European Symposium on QSAR in "omics" and Systems biology, September 21-26, 2008, Uppsala, Sweden.
 43. P. Björkholm og **T. R. Hvidsten**. Method for recognizing local descriptors of protein structure using Hidden Markov Models. 8th Swedish Bioinformatics Workshop for Ph.D. Students and Postdocs, February 28-29th, 2008, Uppsala, Sweden.
 44. H. Strömbergsson, **T. R. Hvidsten**, J. E. S. Wikberg, A. Kryshafovich, P. Daniluk, K. Fidelis and G. J. Kelywegt. Enzyme Wide Modeling of Protein-Ligand Interactions. ISMB/ECCB: 3DSIG: The 3rd Structural Bioinformatics and Computational Biophysics Satellite Meeting, pp. 62, 19-20 July, 2007, Vienna, Austria.
 45. **T. R. Hvidsten**, A. Kryshafovich, P. Daniluk, K. Fidelis and J. Komorowski. Prediction of protein function using local descriptors of protein structure. Critical Assessment of Techniques for Protein Structure Prediction (CASP7), November 26-30, 2006, Asilomar Conference Center, Pacific Grove, CA, USA.
 46. H. Strömbergsson and **T. R. Hvidsten**. Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. Tenth Annual Conference of the Swedish Structural Biology Network, 16-19 June, 2006, Tällberg, Sweden.
 47. **T. R. Hvidsten**, B. Wilczyński, A. Kryshafovich, J. Tiuryn, J. Komorowski and K. Fidelis. Learning regulatory binding site modules from sequence and expression data. Tenth Annual International Conference on Research in Computational Molecular Biology (RECOMB), April 2-5, 2006, Venice, Italy.
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