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Education

Hokkaido University, Graduate School of Engineering Ph.D. 2004
Thesis: Analysis of Solutions in Underdetermined Source Separation
Supervisor: Mineichi Kudo, Division of System and Information Engineering.
Hokkaido University, Graduate School of Engineering M.Eng. 2001
Hokkaido University, Faculty of Engineering B.Eng. 1999

Work Experience

May 2010 – Aug 2010 **Visiting Researcher**
Bioinformatics Program, Boston University

Apr 2007 – **Assistant Professor**
Graduate School of Pharmaceutical Science, Kyoto University

Aug 2005 – **Assistant Professor**
Institute for Chemical Research, Kyoto University

Apr 2005 – Jul 2005 **Research Associate**
Institute for Chemical Research, Kyoto University
The 21st Century Center of Excellence Program (Ministry of Education, Culture, Science and Technology) “Knowledge Information Infrastructure for Genome Science”

Apr 2004 – Mar 2005 **Postdoctoral Fellow**
Graduate School of Information Science and Technology, Hokkaido University
The 21st Century Center of Excellence Program (Ministry of Education, Culture, Science and Technology) “Meme-Media Technology Approach to the R&D of Next-Generation Information Technologies”

Apr 2003 – Mar 2004 **Research Assistant**
Graduate School of Engineering, Hokkaido University

Apr 2002 – Feb 2003 **Adjunct Instructor**
Faculty of Economics, Sapporo University
Course: “Information Theory & Artificial Intelligence” and “Multivariate Statistical Analysis”

Apr 2002 – Jul 2002 **Teaching Assistant**
Hokkaido University

Sep 2001 – Sep 2001 **Adjunct Instructor**
Otaru University of Commerce
2-Week Course: “Introductory calculus”

Apr 2001 – Jul 2001 **Teaching Assistant**
Hokkaido University

Grants

Apr 2011 – Mar 2014	PI	Grants-in-Aid for Scientific Research #23710233 (Ministry of Education, Culture, Science and Technology)
Apr 2008 – Mar 2011	PI	Grants-in-Aid for Scientific Research #20700134 (Ministry of Education, Culture, Science and Technology)
Oct 2007 – Sep 2010	Co-PI	Bioinformatics Research and Development (BIRD) (Japan Science and Technology Agency)
Apr 2006 – Mar 2008	PI	Grants-in-Aid for Scientific Research #10374597 (Ministry of Education, Culture, Science and Technology)
Apr 2005 – Mar 2006	PI	Startup Research Grant (Kyoto University)

Publications

Journal papers:

- 01) M. Kayano, I. Takigawa, M. Shiga, K. Tsuda, H. Mamitsuka, **ROS-DET: robust detector of switching mechanisms in gene expression**. *Nucleic Acids Research*, **39**(11): e74, 2011.
- 02) I. Takigawa, K. Tsuda, H. Mamitsuka, **Mining significant substructure pairs for interpreting polypharmacology in drug-target network**. *PLoS ONE*, **6**(2): e16999, 2011.
- 03) I. Takigawa, H. Mamitsuka, **Efficiently mining delta-tolerance closed frequent subgraphs**. *Machine Learning*, **82**(2): 95-121, 2011.
- 04) M. Shiga, I. Takigawa, H. Mamitsuka, **A spectral approach to clustering numerical vectors as nodes in network**. *Pattern Recognition*, **44**(2): 236-251, 2011;
- 05) T. Hancock, I. Takigawa and H. Mamitsuka, **Mining metabolic pathways through gene expression**. *Bioinformatics*, **26**(17): 2128-2135, 2010;
- 06) M. Kayano, I. Takigawa, M. Shiga, K. Tsuda, H. Mamitsuka, **On the performance of methods for finding a switching mechanism in gene expression**. *Genome Informatics*, **24**: 69-83, 2010.
(from the 10th Annual International Workshop on Bioinformatics and Systems Biology (IBSB2010), Kyoto, Japan, July 26-28, 2010)
- 07) I. Takigawa, M. Kudo, and A. Nakamura, **Convex sets as prototypes for classifying patterns**. *Engineering Applications of Artificial Intelligence*, **22**(1): 101-108, 2009;
- 08) D. duVerle, I. Takigawa, Y. Ono, H. Sorimachi, H. Mamitsuka, **CaMPDB: a resource for calpain and modulatory proteolysis**. *Genome Informatics*, **22**: 202-214, 2009;
(from the 9th Annual International Workshop on Bioinformatics and Systems Biology (IBSB2009), Boston, USA, July 27-29, 2009)
- 09) M. Kayano, I. Takigawa, M. Shiga, K. Tsuda, H. Mamitsuka, **Efficiently finding genome-wide three-way gene interactions from transcript- and genotype-data**. *Bioinformatics*, **25**(21): 2735-2743, 2009;
- 10) S. Zhu, I. Takigawa, J. Zeng, H. Mamitsuka, **Field independent probabilistic model for clustering multi-field documents**. *Information Processing & Management*, **45**(5): 555-570, 2009;
- 11) K. Hashimoto*, I. Takigawa*, M. Shiga, M. Kanehisa, H. Mamitsuka, **Mining significant tree patterns in carbohydrate sugar chains**. *Bioinformatics*, **24**(16): i167-i173, 2008; (* equally contributed)
(from ECCB'08 European Conference on Computational Biology, Cagliari, Italy, Sep 22-26, 2008)
- 12) I. Takigawa, H. Mamitsuka, **Probabilistic path ranking based on adjacent pairwise coexpression for metabolic transcripts analysis**. *Bioinformatics*, **24**(2): 250-257, 2008;
- 13) M. Shiga, I. Takigawa and H. Mamitsuka, **Annotating gene function by combining expression data with a modular gene network**. *Bioinformatics*, **23**(13): i468-i478, 2007;
(from the 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2007), Vienna, Austria, Jul 21-15, 2007)
- 14) I. Takigawa, M. Kudo, and J. Toyama, **Performance analysis of minimum L1-norm solutions for underdetermined source separation**. *IEEE Transactions on Signal Processing*, **52**(3): 582-591, 2004;
- 15) I. Takigawa, N. Abe, Y. Shidara, and M. Kudo, **The boosted/bagged subclass method**. *International Journal of Computing Anticipatory Systems*, **14**: 311-320, 2004;
(from the 6th International Conference on Computing Anticipatory Systems (CASYS'03), Liege, Belgium, Aug 11-16, 2003)

Conference papers:

- 16) A. Nakamura, T. Saito, I. Takigawa, H. Mamitsuka, M. Kudo, **Algorithms for finding a minimum repetition representation of a string.** *Proceedings of the 17th symposium on String Processing and Information Retrieval (SPIRE2010)*, 185-190, Los Cabos, Mexico, Oct 11-13, 2010.
- 17) M. Kudo, A. Nakamura, I. Takigawa, **Classification by reflective convex hulls.** *Proceedings of the 19th International conference on pattern recognition (ICPR2008)*, WeAT9.3, Tampa, Florida, USA, Dec 8-11, 2008.
- 18) M. Shiga, I. Takigawa, H. Mamitsuka, **A spectral clustering approach to optimally combining numerical vectors with a modular network.** *Proceedings of the Thirteenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2007)*, 647-656, San Jose, CA, USA, Aug 12-15, 2007.
- 19) S. Zhu, I. Takigawa, S. Zhang, and H. Mamitsuka, **Probabilistic model for clustering text documents with multiple fields.** *Lecture Notes in Computer Science*, **4425**: 331-342, 2007; (from the 29th European Conference on Information Retrieval (ECIR 2007), Roma, Italy, Apr 2-5, 2007)
- 20) R. Wan, I. Takigawa, H. Mamitsuka, **Applying Gaussian distribution-dependent criteria to decision trees for high-dimensional microarray data.** *Lecture Notes in Computer Science*, **4316**: 40-49, 2006; (from VLDB Workshop on Data Mining in Bioinformatics, Seoul, Korea, Sep 11, 2006)
- 21) I. Takigawa, M. Kudo, A. Nakamura, **The convex subclass method: combinatorial classifier based on a family of convex sets.** *Lecture Notes in Computer Science*, **3587**: 90-99, 2005; (from the IAPR International Conference on Machine Learning and Data Mining in Pattern Recognition (MLDM 2005), Leipzig, Germany, Jul 9-11, 2005)
- 22) A. Tanaka, I. Takigawa, H. Imai, M. Kudo, M. Miyakoshi, **Projection learning based kernel machine design using series of monotone increasing reproducing kernel hilbert spaces.** *Lecture Notes in Computer Science*, **3213**: 1058-1064, 2004; (from the 8th International Conference on Knowledge-Based Intelligent Information & Engineering Systems (KES2004), Wellington, New Zealand, Sep 20-24, 2004)
- 23) I. Takigawa, M. Kudo, A. Nakamura, J. Toyama, **On the minimum L1-norm signal recovery in underdetermined source separation.** *Lecture Notes in Computer Science*, **3195**: 193-200, 2004; (from the 5th International Conference on Independent Component Analysis and Blind Signal Separation (ICA2004), Granada, Spain, Sep 22-24, 2004)
- 24) I. Takigawa, M. Kudo, J. Toyama and M. Shimbo, **Error analysis of MAP solutions under Laplace prior in underdetermined blind source separation.** *Proceedings of the Second International ICSC Symposium on Advances in Intelligent Data Analysis (AIDA'01)*, paper 1724-169, Bangor, U.K., June 19-22, 2001; (Proceedings CIMA'2001, ISBN 3-906454-26-6)
- 25) I. Takigawa, J. Toyama, M. Shimbo, **A modified LEGION using a spectrogram for speech segregation.** *Proceedings of IEEE International Conference on Systems, Man, and Cybernetics (SMC'99)*, paper I 526-531, Tokyo, Japan, Oct 12-15, 1999; (ISBN 0-7803-5734-5, IEEE Catalog Number 99CH37028C)

Not-peer-reviewed papers:

- 26) I. Takigawa, K. Hashimoto, M. Shiga, M. Kanehisa, H. Mamitsuka, **Mining patterns from glycan structures.** *Proceedings of the International Beilstein Symposium on Glyco-Bioinformatics*, 13-14, 2010. (Invited Talk, Proceedings of the International Beilstein Symposium on Glyco-Bioinformatics (Glyco-Bioinformatics2009), Potsdam, Germany, 4-8 October, 2009.)
- 27) I. Takigawa, M. Kudo, A. Nakamura, **Subclass covering by balls for pattern classification.** *Proceedings of The 2nd International Workshop on Ubiquitous Knowledge Network Environment*, Sapporo, Japan, Mar 16-18, 2005.
- 28) I. Takigawa, N. Abe, Y. Shidara, M. Kudo, **The subclass method using adaptive sampling.** *Proceedings of The 1st International Workshop on Ubiquitous Knowledge Network Environment*, Sapporo, Japan, Nov 25-27, 2003.

Poster presentations:

- 29) I. Takigawa, H. Mamitsuka, **Parametric summarization of frequent subgraphs for characterizing structural features of bioactive compounds.** *The 2010 Annual Conference of the Japanese Society for Bioinformatics (JSBi 2010)*, P109, Fukuoka, Dec 13-15, 2010.
- 30) M. Kayano, I. Takigawa, M. Shiga, K. Tsuda, H. Mamitsuka, **Finding three-way gene interactions from transcript and genotype data.** *The 2010 Annual Conference of the Japanese Society for Bioinformatics (JSBi 2010)*, P69, Fukuoka, Dec 13-15, 2010.

- 31) L. Takigawa, K. Tsuda, and H. Mamitsuka, **Mining significant substructure-substructure pairs in structural associations.** *The 20th International Conference on Genome Informatics (GIW 2009)*, P107, Yokohama, Dec 14-16, 2009.
- 32) M. Kayano, L. Takigawa, M. Shiga, K. Tsuda, H. Mamitsuka, **Genome-wide three-way gene interactions from transcript and genotype data.** *The 20th International Conference on Genome Informatics (GIW 2009)*, P045, Yokohama, Dec 14-16, 2009.
- 33) D. du Verle, L. Takigawa, Y. Ono, H. Sorimachi, H. Mamitsuka, **CaMPDB: a resource for calpain and modulatory proteolysis.** *The 20th International Conference on Genome Informatics (GIW 2009)*, P114, Yokohama, Dec 14-16, 2009.
- 34) L. Takigawa, K. Hashimoto, M. Shiga, M. Kanehisa, H. Mamitsuka, **Efficiently finding significant substructural patterns conserved in glycans.** *Proceedings of the 2008 annual conference of the Japanese Society for Bioinformatics (JSBi2008)*, P066, Senri-Chuo, Osaka, Dec 15-16, 2008. **(selected as oral talk T05)**
- 35) Y. Matsushima, L. Takigawa, Y. Ono, H. Sorimachi, H. Mamitsuka, **Developing calpain substrate predictor with sequence information.** *The 2008 Annual Conference of Japanese Society for Bioinformatics (JSBi2008)*, P071, Osaka, Dec 15-16, 2008.
- 36) M. Shiga, L. Takigawa, H. Mamitsuka, **A new method for clustering genes by optimally combining expression data with a modular gene network.** *The 2007 Annual Conference of Japanese Society for Bioinformatics (JSBi2007)*, P037, Tokyo, Dec17-19, 2007.
- 37) L. Takigawa, H. Mamitsuka, **Probabilistic ranking for analyzing transcriptional response variations of metabolic gene paths.** *The 17th International Conference on Genome Informatics (GIW2006)*, Yokohama, Dec 18-20, 2006.
- 38) R. Wan, L. Takigawa, H. Mamitsuka, **Applying Gaussian distribution-dependent criteria to decision trees for high-dimensional microarray data.** *The 17th International Conference on Genome Informatics (GIW2006)*, Yokohama, Dec 18-20, 2006.
- 39) S. Zhu, L. Takigawa, S. Zhang, H. Mamitsuka, **Extending multivariate Bernoulli and multinomial models for clustering MEDLINE records.** *The 17th International Conference on Genome Informatics (GIW2006)*, Yokohama, Dec 18-20, 2006.
- 40) M. Shiga, L. Takigawa, H. Mamitsuka, **A gene clustering method using gene expression data and gene networks.** *The 17th International Conference on Genome Informatics (GIW2006)*, Yokohama, Dec 18-20, 2006.
- 41) L. Takigawa, H. Mamitsuka, **Ranking metabolic paths with expression similarities.** *The 16th International Conference on Genome Informatics (GIW2005)*, Yokohama, Dec 19-21, 2005.

Competition:

- 42) R. Wan, V. Ngoc Anh, L. Takigawa, H. Mamitsuka, **Combining vector-space and word-based aspect models for passage retrieval.** *Proceedings of 15th Text Retrieval Conference (TREC 2006)*, Gaithersburg, Maryland, Nov 14-17, 2006.

Talks:

- 43) L. Takigawa, **Ranking metabolic pathways based on transcriptional co-regulation of enzyme-coding genes,** Systems and Integrative Biology Seminar, Boston University, Boston, USA, June 22, 2010. (Host: Dr. Daniel Segré)
- 44) L. Takigawa, **Ranking metabolic pathways based on transcriptional co-regulation of enzyme-coding genes.** Boston College, Boston, USA, June 25, 2010. (Host: Dr. Peter Clote)
- 45) L. Takigawa, **Efficiently finding significant substructural patterns conserved in glycans.** Boston University, Boston, USA, June 23, 2010. (Host: Dr. Charles DeLisi)
- 46) L. Takigawa, **Efficiently finding significant substructural patterns conserved in glycans.** Max Planck Institute for Biological Cybernetics, Tübingen, Germany, Oct 24, 2008. (Host: Dr. Koji Tsuda)