

Curriculum Vitae
Hiroshi Mamitsuka

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Institute for Chemical Research, Kyoto University.
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EDUCATION

Dr.Sc. in Information Sciences (October, 1999), University of Tokyo, Japan.

Dissertation title: Stochastic Knowledge Representations and Machine Learning Strategies for Biological Sequence Analysis.

M.E. in Information Engineering (March, 1991), University of Tokyo, Japan.

Thesis title: A Theoretical Study on STM Images Based on Molecular Orbital Calculation. (in Japanese).

B.S. in Biochemistry and Biophysics (March, 1988), University of Tokyo, Japan.

Thesis title: Analyzing Isoleucine Binding Site of *E.coli* Isoleucyl-tRNA Synthetase using $^1\text{H-NMR}$. (in Japanese).

PROFESSIONAL EXPERIENCE

Apr. 2006–Present: Professor, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan.

Apr. 2005–Present: Professor, Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan.

Apr. 2002–Mar. 2005: Visiting associate professor, Institute for Chemical Research, Kyoto University, Japan.

Apr. 1991–Mar. 2002: Research staff member, NEC Corporation, Japan.

PUBLICATIONS

Refereed Journal/Magazine Papers

- Kayano, M., Takigawa, I., Shiga, M., Tsuda, K. and Mamitsuka, H., Efficiently Finding Genome-wide Three-way Gene Interactions from Transcript- and Genotype-Data. *Bioinformatics*, 25 (21), 2735–2743, 2009.
- Zhu, S., Zeng, J. and Mamitsuka, H., Enhancing MEDLINE Document Clustering by Incorporating MeSH Semantic Similarity. *Bioinformatics*, 25 (15), 1944–1951, 2009.
- Zhu, S., Takigawa, I., Zeng, J. and Mamitsuka, H., Field Independent Probabilistic Model for Clustering Multi-Field Documents. *Information Processing and Management*, 45 (5), 555–570, 2009.
- Wan, R., Kiseleva, L., Harada, H., Mamitsuka, H. and Horton, P., HAMSTER: Visualizing Microarray Experiments as a Set of Minimum Spanning Trees. *Source Code for Biology and Medicine*, 4, 8, 2009.
- Hashimoto, K., Takigawa, I., Shiga, M., Kanehisa, M. and Mamitsuka, H., Mining Significant Tree Patterns in Carbohydrate Sugar Chains. *Bioinformatics*, 24 (16) (*Proceedings of the Seventh European Conference on Computational Biology (ECCB 2008)*, Cagliari, Sardinia-Italy, September, 2008), i167–i173, 2008.
- Hashimoto, K., Aoki-Kinoshita, K. F., Ueda, N., Kanehisa, M. and Mamitsuka, H., A New Efficient Probabilistic Model for Mining Labeled Ordered Trees Applied to Glycobiology. *ACM Transactions on Knowledge Discovery from Data*, 2 (1), Article 6, 2008.
- Takigawa, I. and Mamitsuka, H., Probabilistic Path Ranking Based on Adjacent Pairwise Coexpression for Metabolic Transcripts Analysis. *Bioinformatics*, 24 (2), 250–257, 2008.
- Shiga, M., Takigawa, I. and Mamitsuka, H., Annotating Gene Function by Combining Expression Data with a Modular Gene Network. *Bioinformatics*, 23 (13) (*Proceedings of the Fifteenth International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2007)*, Vienna, Austria, July, 2007), i468–i478, 2007.
- Yoneya, T. and Mamitsuka, H., A Hidden Markov Model-based Approach for Identifying Timing Differences in Gene Expression under Different Experimental Factors. *Bioinformatics*, 23 (7), 842–849, 2007.
- Kadowaki, T., Wheelock, C. E., Adachi, T., Kudo, T., Okamoto, S., Tanaka, N., Tonomura, K., Tsujimoto, G., Mamitsuka, H., Goto, S. and Kanehisa, M., Identification of Endocrine Disruptor Biodegradation by Integration of Structure-activity Relationship with Pathway Analysis. *Environmental Science & Technology*, 41 (23), 7997–8003, 2007.
- Mamitsuka, H., Selecting Features in Microarray Classification Using ROC Curves. *Pattern Recognition*, 39 (12), 2393–2404, 2006.
- Aoki-Kinoshita, K. F., Ueda, N., Mamitsuka, H. and Kanehisa, M., ProfilePSTMM: Capturing Tree-structure Motifs in Carbohydrate Sugar Chains. *Bioinformatics*, 22 (14) (*Proceedings of the Fourteenth International Conference on Intelligent Systems for Molecular Biology (ISMB 2006)*, Fortaleza, Brazil, August, 2006), e25–e34, 2006.
- Zhu, S., Okuno, Y., Tsujimoto, G. and Mamitsuka, H., Application of a New Probabilistic Model for Mining Implicit Associated Cancer Genes from OMIM and Medline. *Cancer Informatics*, 2, 361–371, 2006.
- Zhu, S., Udaka, K., Sidney, J., Sette, A., Aoki-Kinoshita, K. F. and Mamitsuka, H., Improving MHC Binding Peptide Prediction by Incorporating Binding Data of Auxiliary MHC Molecules. *Bioinformatics*, 22 (13), 1648–1655, 2006.

- Mamitsuka, H., Query-Learning-Based Iterative Feature-Subset Selection for Learning from High-Dimensional Data Sets. *Knowledge and Information Systems*, 9 (1), 91–108, 2006.
- Zhu, S., Okuno, Y., Tsujimoto, G. and Mamitsuka, H., A Probabilistic Model for Mining Implicit “Chemical Compound - Gene” Relations from Literature. *Bioinformatics*, 21, Supplement 2 (*Proceedings of the Fourth European Conference on Computational Biology (ECCB/JBI 2005)*, Madrid, Spain, September, 2005), ii245–ii251, 2005.
- Mamitsuka, H., Finding the Biologically Optimal Alignment of Multiple Sequences. *Artificial Intelligence in Medicine*, 35 (1), 9–18, 2005.
- Ueda, N., Aoki-Kinoshita, K. F., Yamaguchi, A., Akutsu, T., Mamitsuka, H., A Probabilistic Model for Mining Labeled Ordered Trees: Capturing Patterns in Carbohydrate Sugar Chains. *IEEE Transactions on Knowledge and Data Engineering*, 17 (8), 1051–1064, 2005.
- Mamitsuka, H., Mining New Protein-Protein Interactions - Using a Hierarchical Latent-variable Model to Determine the Function of a Functionally Unknown Protein. *IEEE Engineering in Medicine and Biology Magazine*, 24 (3), 103–108, 2005.
- Mamitsuka, H., Essential Latent Knowledge for Protein-Protein Interactions: Analysis by an Unsupervised Learning Approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2 (2), 119–130, 2005.
- Mamitsuka, H., Efficient Unsupervised Mining from Noisy Co-occurrence Data. *New Mathematics and Natural Computation*, 1 (1), 173–193, 2005.
- Aoki, K. F., Mamitsuka, H., Akutsu, T. and Kanehisa, M., A Score Matrix to Reveal the Hidden Links in Glycans. *Bioinformatics*, 21 (8), 1457–1463, 2005.
Corresponding author.
- Igarashi, Y., Aoki, K. F., Mamitsuka, H., Kuma, K. and Kanehisa, M., The Evolutionary Repertoires of the Eukaryotic-type ABC Transporters in terms of the Phylogeny of ATP-binding Domains in Eukaryotes and Prokaryotes. *Molecular Biology and Evolution*, 21 (11), 2149–2160, 2004.
- Yamaguchi, A., Aoki, K. F. and Mamitsuka, H., Finding the Maximum Common Subgraph of a Partial k-Tree and a Graph with a Polynomially Bounded Number of Spanning Trees. *Information Processing Letters*, 92 (2), 57–63, 2004.
- Aoki, K. F., Ueda, N., Yamaguchi, A., Kanehisa, M., Akutsu, T. and Mamitsuka, H., Application of a New Probabilistic Model for Recognizing Complex Patterns in Glycans. *Bioinformatics*, 20, Supplement 1 (*Proceedings of the Twelfth International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2004)*, Glasgow, UK, August, 2004), i6–i14, 2004.
- Aoki, K. F., Yamaguchi, A., Ueda, N., Akutsu, T., Mamitsuka, H., Goto, S. and Kanehisa, M., KCaM (KEGG Carbohydrate Matcher): A Software Tool for Analyzing the Structures of Carbohydrate Sugar Chains. *Nucleic Acids Research*, 32, W267–W272, 2004.
- Aoki, K. F., Ueda, N., Yamaguchi, A., Akutsu, T., Kanehisa, M., Mamitsuka, H., Managing and Analyzing Carbohydrate Data. *ACM SIGMOD Record*, 33 (2), 33–38, 2004.
- Mamitsuka, H., Okuno, Y. and Yamaguchi, A., Mining Biologically Active Patterns in Metabolic Pathways using Microarray Expression Profiles. *ACM SIGKDD Explorations*, 5 (2), 113–122, 2003.
- Udaka, K., Mamitsuka, H., Nakaseko, Y. and Abe, N., Empirical Evaluation of a Dynamic Experiment Design Method for Prediction of MHC Class I-Binding Peptides. *Journal of Immunology*, 169 (10), 5744–5753, 2002.

- Udaka, K., Mamitsuka, H., Nakaseko, Y. and Abe, N., Prediction of MHC Class I Binding Peptides by a Query Learning Algorithm Based on Hidden Markov Models. *Journal of Biological Physics*, 28 (2), 183–194, 2002.
- Mamitsuka, H., Predicting Peptides That Bind to MHC Molecules Using Supervised Learning of Hidden Markov Models. *PROTEINS: Structure, Function, and Genetics*, 33 (4), 460–474, 1998.
- Abe, N. and Mamitsuka, H., Predicting Protein Secondary Structures Using Stochastic Tree Grammars. *Machine Learning*, 29 (2-3), 275–301, 1997.
Both authors contributed equally to this work.
- Mamitsuka, H., A Learning Method of Hidden Markov Models for Sequence Discrimination. *Journal of Computational Biology*, 3 (3), 361–373, 1996.
- Mamitsuka, H., Representing Inter-residue Dependencies in Protein Sequences with Probabilistic Networks. *Computer Applications in the Biosciences (Currently, Bioinformatics)*, 11 (4), 413–422, 1995.
- Mamitsuka, H., and Yamanishi, K., Alpha-Helix Region Prediction with Stochastic-rule Learning. *Computer Applications in the Biosciences (Currently, Bioinformatics)*, 11 (4), 399–411, 1995.

Refereed Conference Papers

- Shiga, M., Takigawa, I. and Mamitsuka, H., 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)*., pp. 647–656, San Jose, CA, USA, August 2007, ACM Press.
- Zhu, S., Takigawa, I., Zhang, S. and Mamitsuka, H., A Probabilistic Model for Clustering Text Documents with Multiple Fields. *Proceedings of the 29th European Conference on Information Retrieval (ECIR 2007) (Lecture Notes in Computer Science, vol. 4425)*, pp. 331–342, Roma, Italy, April 2007, Springer-Verlag.
- Hashimoto, K., Aoki-Kinoshita, K. F., Ueda, N., Kanehisa, M. and Mamitsuka, H., A New Efficient Probabilistic Model for Mining Labeled Ordered Trees. *Proceedings of the Twelfth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2006)*., pp. 177–186, Philadelphia, PA, USA, August 2006, ACM Press.
- Mamitsuka, H. and Okuno, Y., A Hierarchical Mixture of Markov Models for Finding Biologically Active Metabolic Paths using Gene Expression and Protein Classes. *Proceedings of the IEEE Computational Systems Bioinformatics Conference (CSB 2004)*., pp.341–352, Stanford, CA, USA, August 2004, IEEE Computer Society Press.
- Ueda, N., Aoki, K. F. and Mamitsuka, H., A General Probabilistic Framework for Mining Labeled Ordered Trees. *Proceedings of the Fourth SIAM International Conference on Data Mining (SDM 2004)*., pp. 357–368, Orlando, FL, USA, April 2004, SIAM.
- Aoki, K. F., Yamaguchi, A., Okuno, Y., Akutsu, T., Ueda, N., Kanehisa, M. and Mamitsuka, H., Efficient Tree-Matching Methods for Accurate Carbohydrate Database Queries. *Proceedings of the Fourteenth International Conference on Genome Informatics (GIW 2003)*. (*Genome Informatics*, 14), pp. 134–143, Yokohama, Japan, Dec. 2003, Universal Academy Press, Inc.
- Mamitsuka, H., Hierarchical Latent Knowledge Analysis for Co-occurrence Data. *Proceedings of the Twentieth International Conference on Machine Learning (ICML 2003)*., pp. 504–511, Washington DC, USA, Aug. 2003, AAAI Press.
- Mamitsuka, H., Efficient Unsupervised Mining from Noisy Data Sets: Application to Clustering Co-occurrence Data. *Proceedings of the Third SIAM International Conference on Data Mining (SDM 2003)*., pp. 239–243, San Francisco, CA, USA, May 2003, SIAM.

- Mamitsuka, H., Iteratively Selecting Feature Subsets for Mining from High-Dimensional Databases. *Proceedings of the Sixth European Conference on Principles and Practice of Knowledge Discovery in Databases (PKDD 2002)*. (Lecture Notes in Artificial Intelligence, vol. 2431), pp. 361–372. Helsinki, Finland, Aug. 2002, Springer-Verlag.
- Mamitsuka, H. and Abe, N., Efficient Mining from Large Databases by Query Learning. *Proceedings of the Seventeenth International Conference on Machine Learning (ICML 2000)*., pp. 575–582, Stanford Univ., CA, USA, Jun. 2000, Morgan Kaufman.
- Abe, N. and Mamitsuka, H., Query Learning Strategies Using Boosting and Bagging. *Proceedings of the Fifteenth International Conference on Machine Learning (ICML98)*., pp. 1–9, Madison, WI, USA, Jul. 1998, Morgan Kaufman.
- Nakamura, A., Abe, N., Mamitsuka, H., and Toba, H., Learning Personal Preferences by On-line Prediction Algorithms, *Poster Session Abstracts of the Fifteenth International Joint Conference on Artificial Intelligence (IJCAI97)*., pp. 75, Nagoya, Japan, Aug. 1997.
- Mamitsuka, H., Supervised Learning of Hidden Markov Models for Sequence Discrimination. *Proceedings of the First International Conference on Computational Molecular Biology (RECOMB97)*., pp. 202–208. Santa Fe, NM, USA, Jan. 1997, ACM Press.
- Mamitsuka, H. and Abe, N., Predicting Location and Structure of Beta-Sheet Regions Using Stochastic Tree Grammars. *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology (ISMB94)*., pp. 276–284. Stanford Univ., CA, USA, Aug. 1994, AAAI Press.
- Abe, N and Mamitsuka, H., A New Method for Predicting Protein Secondary Structures Based on Stochastic Tree Grammars, *Proceedings of the 11th International Conference on Machine Learning (ICML94)*., pp. 3–11. Brunswick, NJ, USA, Jul. 1994, Morgan Kaufman.
- Mamitsuka, H and Yamanishi, K., Protein Alpha-Helix Region Prediction based on Stochastic-rule Learning. *Proceedings of the 26th Annual Hawaii International Conference on System Sciences (HICSS26)*., Vol I, pp. 659–668. Maui, HI, USA, Jan. 1993, IEEE Computer Society Press.

Refereed Symposium Papers

- Wan, R, Vo, A. N. and Mamitsuka, H., Efficient Probabilistic Latent Semantic Analysis Through Parallelization. *Proceedings of the Fifth Asian Information Retrieval Symposium (AIRS 2009)*. (Lecture Notes in Computer Science , vol. 5839), pp. 432–443, Sapporo, Japan, Oct. 2009, Springer-Verlag.
- Ching, W-K., Li, L., Chan, Y-M. and Mamitsuka, H., A Study of Network-based Kernel Methods on Protein-Protein Interaction for Protein Functions Prediction. *Proceedings of the Third International Symposium on Optimization and Systems Biology (OSB 2009)*. (Lecture Notes in Operations Research, vol. 11), pp. 25–32, Zhangjiajie, China, Sep. 2009, APORC Press.
- Wan, R., Mamitsuka, H. and Aoki, K. F., Cleaning Microarray Expression Data Using Markov Random Fields based on Profile Similarity. *Proceedings of the Twentieth ACM Symposium on Applied Computing (SAC 2005)*., pp. 206–207, Santa Fe, NM, USA, Mar. 2005, ACM Press.
- Yamaguchi, A. and Mamitsuka, H., Finding the Maximum Common Subgraph of a Partial k-Tree and a Graph with a Polynomially Bounded Number of Spanning Trees. *Proceedings of the Fourteenth International Symposium on Algorithm and Computation (ISAAC 2003)*. (Lecture Notes in Computer Science, vol. 2906), pp. 58–67, Kyoto, Japan, Dec. 2003, Springer-Verlag.
- Mamitsuka, H., Selective Sampling with a Hierarchical Latent Variable Model. *Proceedings of the Fifth International Symposium on Intelligent Data Analysis (IDA 2003)*. (Lecture Notes in Computer Science, vol. 2810), pp. 352–363, Berlin, Germany, Aug. 2003, Springer-Verlag.

Mamitsuka, H., Detecting Experimental Noise in Protein-Protein Interactions with Iterative Sampling and Model-based Clustering. *Proceedings of the Third IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2003)*., pp. 385–392, Bethesda, MD, USA, Mar. 2003, IEEE Computer Society Press.

Mamitsuka, H., Empirical Evaluation of Ensemble Feature Subset Selection Methods for Learning from a High-Dimensional Database in Drug Design. *Proceedings of the Third IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2003)*., pp. 253–257, Bethesda, MD, USA, Mar. 2003, IEEE Computer Society Press.

Refereed Workshop Papers

Hancock, T. and Mamitsuka, H., A Markov Classification Model for Metabolic Pathways. *Proceedings of the Ninth Workshop on Algorithms in Bioinformatics (WABI 2009)*. (*Lecture Notes in Bioinformatics*, vol. 5724), pp. 121–132, Philadelphia, PA, USA, September 2009, Springer.

Hancock, T. and Mamitsuka, H., Active Pathway Identification and Classification with Probabilistic Ensembles. *Proceedings of the Ninth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2009)*. (*Genome Informatics*, 22), pp. 30–40, Boston, USA, Jul. 2009, Imperial College Press.

Li, L., Shiga, M., Ching, W.-K. and Mamitsuka, H., Annotating Gene Functions with Integrative Spectral Clustering on Microarray Expressions and Sequences. *Proceedings of the Ninth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2009)*. (*Genome Informatics*, 22), pp. 95–120, Boston, USA, Jul. 2009, Imperial College Press.

DuVerle, D., Takigawa, I., Ono, Y., Sorimachi, H. and Mamitsuka, H., CaMPDB: a Resource for Calpain and Modulatory Proteolysis. *Proceedings of the Ninth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2009)*. (*Genome Informatics*, 22), pp. 202–214, Boston, USA, Jul. 2009, Imperial College Press.

Hancock, T. and Mamitsuka, H., Semi-Supervised Graph Partitioning with Decision Trees. *Proceedings of the Eighth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2008)*. (*Genome Informatics*, 20), pp. 102–111, Berlin, Germany, Jun. 2008, Imperial College Press.

Wan, R., Wheelock, Å. and Mamitsuka, H., A Framework for Determining Outlying Microarray Experiments. *Proceedings of the Eighth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2008)*. (*Genome Informatics*, 20), pp. 64–76, Berlin, Germany, Jun. 2008, Imperial College Press.

Yoneya, T. and Mamitsuka, H., PURE: A PubMed Article Recommendation System Based on Content-based Filtering. *Proceedings of the Seventh Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2007)*. (*Genome Informatics*, 18), pp. 267–276, Tokyo, Japan, Jul. 2007, Imperial College Press.

Wan, R., Takigawa, I. and Mamitsuka, H., Applying Gaussian Distribution-dependent Criteria to Decision Trees for High-Dimensional Microarray Data. *Proceedings of 2006 VLDB Workshop on Data Mining in Bioinformatics*. (*Lecture Notes in Bioinformatics*, vol. 4316), pp. 40–49, Seoul, Korea, Sep. 2006, Springer-Verlag.

Yamada, T., Kawashima, S., Mamitsuka, H., Goto, S. and Kanehisa, M., Comprehensive Analysis and Prediction of Synthetic Lethality Using Subcellular Locations. *Proceedings of the Fifth International Workshop on Bioinformatics and Systems Biology*. (*Genome Informatics*, 16 (1)), pp. 150–158, Berlin, Germany, Aug. 2005, Universal Academy Press, Inc.

- Mamitsuka, H., Efficient Mining from Heterogeneous Data Sets for Predicting Protein-Protein Interactions. *Proceedings of the Fourteenth International Workshop on Database and Expert Systems Applications.*, pp. 32–36, Prague, Czech Republic, Sep. 2003, IEEE Computer Society Press.
- Mamitsuka, H. and Abe, N., Prediction of Beta-Sheet Structures Using Stochastic Tree Grammars. *Proceedings of Genome Informatics Workshop V (GIW94)*. (*Genome Informatics*, 5), pp. 19–28. Yokohama, Japan, Dec. 1994, Universal Academy Press, Inc.
- Mamitsuka, H., Representing Inter-residue Dependencies in Protein Sequences with Probabilistic Networks. *Proceedings of Genome Informatics Workshop IV (GIW93)*. (*Genome Informatics*, 4), pp. 46–55. Yokohama, Japan, Dec. 1993, Universal Academy Press, Inc.
- Mamitsuka, H. and Yamanishi, K., Protein Secondary Structure Prediction based on Stochastic-rule Learning. *Proceedings of the Third Annual Workshop on Algorithmic Learning Theory (ALT92)*., pp. 240–251. Tokyo, Japan, Oct. 1992, Ohm-sha. (*Lecture Notes in Artificial Intelligence*, vol. 743, pp. 240–251. Springer-Verlag.)

Books and Conference Proceedings

- Ng, S.-K., Mamitsuka, H. and Wong, L., *Genome Informatics, Vol. 19*, Imperial College Press, 2007, ISBN-10: 1-86094-984-3 (ISBN-13: 978-1-86094-984-3).
- Heinrich, R., Mamitsuka, H., Kanehisa, M., Takagi, T. and Miyano, S., *Genome Informatics, Vol. 16, No.2*, Universal Academy Press, Inc., 2005, ISBN: 4-946443-96-7.
- Mamitsuka, H., Smith, T. F., Holzhütter, H.-G., Kanehisa, M., DeLisi, C., Heinrich, R. and Miyano, S., *Genome Informatics, Vol. 15, No.1*, Universal Academy Press, Inc., 2004, ISBN: 4-946443-88-6.

Book Chapters and Reviews

- Wan, R. and Mamitsuka, H., Discovering Network motifs in Protein Interaction Networks. *Biological Data Mining in Protein Interaction Networks. Chapter 8*, pp. 117–143, Eds. Li, X.-L. and Ng, S.-K., IGI Global, 2009. (ISBN: 978-1-60566-398-2)
- Mamitsuka, H., Informatic Innovations in Glycobiology: Relevance to Drug Discovery. *Drug Discovery Today*, 13 (3/4), 118–123, 2008.
- Cios, K. J., Mamitsuka, H., Nagashima, T. and Tadeusiewicz, R., Computational Intelligence in Solving Bioinformatics Problems. *Artificial Intelligence in Medicine*, 35 (1), 1–8, 2005.
- Mamitsuka, H. and Abe, N., Efficient Data Mining by Active Learning. *Progress in Discovery Science, Lecture Notes in Artificial Intelligence*, vol. 2281, pp. 258–267, Eds. Arikawa, S., Shinohara, A., Springer-Verlag, 2002.
- Abe, N., Yamanishi, K., Nakamura, A., Mamitsuka, H., Takeuchi, J. and Li, H., Distributed and Active Learning. *Foundations of Real World Intelligence, Chapter IV*, pp. 189–250, Eds. Uesaka, Y., Kanerva, P., and Asoh, H., CSLI Publications, 2001.

Unrefereed Journal Papers

- Zhu, S., Okuno, Y., Tsujimoto, G. and Mamitsuka, H., Predicting Implicit Associated Cancer Genes from OMIM and MEDLINE by a New Probabilistic Model, *BMC Systems Biology* 1(Suppl 1), 16, 2007.
- Mamitsuka, H. and Abe, N., Active Ensemble Learning: Application to Data Mining and Bioinformatics, *Systems and Computers in Japan*, 38 (11), 100–108, 2007.

Unrefereed Conference Proceedings Papers

Wan, R., Ngoc, V. A., and Mamitsuka, H., Passage Retrieval with Vector Space and Query-Level Aspect Models, *The Sixteenth Text REtrieval Conference (TREC 2007) Proceedings* (NIST (National Institute of Standards and Technology) Special Publication: SP 500-274), 37, Washington D.C., USA, 2007.

Wan, R., Takigawa, I., Ngoc, V. A., and Mamitsuka, H., Combining Vector-Space and Word-Based Aspect Models for Passage Retrieval, *The Fifteenth Text REtrieval Conference (TREC 2006) Proceedings* (NIST Special Publication: SP 500-272), 45, Washington D.C., USA, 2006.

Journal Papers in Japanese

Shiga, M., Takigawa, I. and Mamitsuka, H., Clustering Analysis for Combining Multiple Genomic Data, *Seibutsu-butsuri (Biophysics)*, 48 (3), 190–194, 2008. (in Japanese)

Mamitsuka, H. and Abe, N., Active Ensemble Learning – Applications to Data Mining and Bioinformatics – (in Japanese). *IEICE Transactions*, J85-DII (5), 717–724, 2002. (Invited paper).

Book Chapters/Articles in Japanese

Udaka, K. and Mamitsuka, H., Predicting Peptides Binding to Major Histocompatibility Complex Antigens. *Bioinformatics-ga-wakaru.*, pp. 68–71, Ed. Sugawara, H., Yodo-sha, 2003. (in Japanese)

Abe, N. and Mamitsuka, H., Active Learning and Discovery Science. *bit – Special issue on Discovery Science and Data Mining –.*, Chapter 7, pp. 64–72, Eds. Morishita, S. and Miyano, S., Kyoritsu Shuppan, 2000. (in Japanese)

PATENTS

USA, No. 6973446, Mamitsuka, H. and Abe, N.

Japan, P3237606, Mamitsuka, H.

Japan, P3094860, Mamitsuka, H.

Japan, P3012411, Mamitsuka, H.

Japan, P2980037, Mamitsuka, H.

Japan, P2940529, Mamitsuka, H.

Japan, P2870458, Mamitsuka, H., Nakamura, A. and Toba, H.

Japan, P2739825, Mamitsuka, H.

Japan, P2658823, Mamitsuka, H. and Abe, N.

Japan, P2551297, Mamitsuka H. and Yamanishi, K.

PROFESSIONAL ACTIVITIES

Research Visiting

May 2009–Present: Senior Visiting Scholar, Fudan University, China.

May–Jun. 2009: Visiting Professor, Université Louis Pasteur Strasbourg, France.

Mar. 2009, Nov.–Dec. 2007, Mar. 2006: Visiting Scientist, Institute for Infocomm Research (I2R), Agency for Science, Technology and Research (A*STAR), Singapore.

Dec. 2007: Visiting Researcher, School of Computing, National University of Singapore.

Book/Journal/Magazine Editing

Associate Editor, *Knowledge and Information Systems*, Springer. November, 2009–Present.

Associate Editor, *International Journal of Knowledge Discovery and Bioinformatics*, IGI Global. December, 2008–Present.

Member of Editorial Advisory Review Board, *Biological Data Mining in Protein Interaction Networks*, Editors: Xiao-Li Li and See-Kiong Ng, 2008, IGI Global.

Member of Editorial Advisory Board, *The Open Medical Informatics Journal*, Bentham Science Publishers. November, 2007–Present.

Guest Co-editor, *Asia Pacific Biotech News*, Vol. 11, No. 15, Special issue: *Bioinformatics in Japan*, August 15, 2007, Biotech Services PTE. Ltd.

Guest Co-editor, *Artificial Intelligence in Medicine*, Vol. 35, Issues 1-2, Special issue: *Computational Intelligence Techniques in Bioinformatics*, September-October, 2005.

Book/Journal/Magazine Referee

ACM Transactions on Knowledge Discovery from Data (2007), *Acta Biotheoretica* (2001), *Artificial Intelligence in Medicine* (2007), *Bioinformatics* (2004–2009), *BMC Bioinformatics* (2006–2009), *BMC Structural Biology* (2008), *BMC Systems Biology* (2009), *Data and Knowledge Engineering* (2009), *Data Mining and Knowledge Discovery* (2001, 2007), *IEEE Intelligent Systems* (2005), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (2006), *IEEE Transactions on Information Technology in Biomedicine* (2008), *IEEE Transactions on Knowledge and Data Engineering* (2006–2009), *International Journal of Data Mining and Bioinformatics* (2008), *International Journal of Foundation of Computer Science* (2009), *Journal of Bioinformatics and Computational Biology* (2006), *Journal of Biomedical Informatics* (2007), *Journal of Machine Learning Research* (2008), *Molecular Oncology* (2008), *Molecular Pharmaceutics* (2006), *New Generation Computing* (2009), *Nucleic Acids Research* (2004–2005), *OR spectrum* (2006), *Pattern Recognition* (2005), *PLoS Computational Biology* (2008), *PLoS One* (2008), *Theoretical Computer Science* (1997), *Wiley Encyclopedia of Chemical Biology* (2007)

Conference Committee

- Program Committee Co-chair
BIBE (2009), GIW (2005, 2007), IBSB (2004)
- Program Committee Member or Scientific Committee Member
APBC (2008–2010), BIODDD (2002), BIOT (2005–2006), ECCB (2007, 2009), GIW (2003–2009), ISMB (2007–2009)

Grant Referee

Strategic Research Funding, City University of Hong Kong. (Feb. 2008)

Extramural Programme, Biomedical Research Council (BMRC), A*STAR, Singapore. (Sep. 2007)

Professional Societies

- Membership

ACM (Association for Computing Machinery), IEEE (Institute of Electrical and Electronics Engineers), ISCB (International Society for Computational Biology), JSBi (Japanese Society of Bioinformatics)

- Services

1. JSBi

Co-founder (1999), Board Member (Apr. 2005–Mar. 2007), Secretary (Apr. 2007–Mar. 2008)

2. AASBi (Association of Asian Societies for Bioinformatics)

Board Member (Jan. 2007–Present)

AWARDS

Recipient for Certificate of Appreciation, Service Award, IEEE Computer Society, USA, 2009.

RECENT PRESENTATIONS

- Oct. 9, 2009: Seminar, *Humboldt University Berlin*, Germany.
- Oct. 5, 2009: Invited Lecture, *International Beilstein Symposium on Glyco-Bioinformatics*, Potsdam, Germany.
- Sep. 29, 2009: Seminar, *Fudan University*, Shanghai, China.
- Jun. 22 & 24, 2009: Invited Lecture, *TISE Summer School on Statistical Modeling and Machine Learning in Computational Systems Biology*, Tampere, Finland.
- Jun. 6, 2009: Keynote Speech, *IEEE International Conference on Computational Intelligence and Natural Computing (CINC 2009)*, Wuhan University of Science and Technology, Wuhan, China.
- May 28, 2009: Seminar, *The Image Sciences, Computer Sciences and Remote Sensing Laboratory (LSIIT), Université Louis Pasteur Strasbourg*, France.
- May 25, 2009: Seminar, *Faculty of Chemistry, Université Louis Pasteur Strasbourg*, France.
- May 13, 2009: Keynote Speech, *Bioinformatics Workshop*, Fudan University, Shanghai, China.
- Mar. 24, 2009: Seminar, *I2R, A*STAR*, Singapore.
- Jan. 15, 2009: Invited Talk, *Workshop, Bioinformatics on Herbel Medicine*, Toyama, Japan.
- Dec. 21, 2008: Keynote Speech, *IEEE International Symposium on Knowledge Acquisition and Modeling (KAM 2008)*, Huazhong Normal University, Wuhan, China.
- Oct. 22, 2008: Seminar, *Max Planck Institute for Biological Cybernetics*, Tübingen, Germany.
- Oct. 14, 2008: Seminar, *The Graduate University for Advanced Studies (Sokendai)*, Hayama, Japan.
- Jun. 22, 2008: Invited Talk, Workshop on *Relations with Computer Science, Foundations of Computational Mathematics (FoCM'08)*, City University of Hong Kong, China.
- Jun. 19, 2008: Invited Talk, *Research Meeting, The Institute of Electronics, Information and Communication Engineers (IEICE)*, Otaru, Japan.
- Jun. 17, 2008: Seminar, *Nara Institute of Science and Technology*, Nara, Japan
- May 27, 2008: Seminar, *University of Melbourne*, Australia.
- May 27, 2008: Keynote Speech, *Systems Biology Workshop: From Molecules to Life*, Melbourne, Australia.
- Dec. 13, 2007: Seminar, *Helsinki University of Technology*, Finland.
- Dec. 3, 2007: Opening Address, *Eighteenth International Conference on Genome Informatics*, Biopolis, Singapore.
- Dec. 2, 2007: Invited Talk, *AASBi Symposium 2007*, Biopolis, Singapore.
- Nov. 28, 2007: Seminar, *I2R, A*STAR*, Singapore.
- Sep. 20, 2007: Invited Talk, *Symposium on Bioinformatics and Chemical Genomics*, Kyoto, Japan
- Aug. 22, 2007: Keynote Speech, *International Conference on Intelligent Computing (ICIC 2007)*, Academic Exchange Center, Ocean University of China, Qingdao, China.
- Aug. 10, 2007: Seminar, *University of California Berkeley*, USA.

- Dec. 8, 2006: Invited Talk, *International Workshop on Scientific Computing: Models, Algorithm and Applications*, University of Hong Kong, China.
- Nov. 9, 2006: Invited Talk, *Second Taiwan-Japan Bilateral Symposium on Bioinformatics*, National Cheng Kung University, Tainan, Taiwan.
- Nov. 3, 2006: Invited Talk, *Third Japan-Germany Frontiers of Sciences Symposium*, Heidelberg, Germany.
- Sep. 26, 2006: Seminar, *BioFrontier Laboratories, Kyowa Hakko Kogyo Co., Ltd.*, Machida, Japan.
- Aug. 24, 2006: Seminar, *IBM T. J. Watson Research Center*, USA.
- May 25, 2006: Seminar, *The Tokyo Metropolitan Institute of Medical Science (Rinshoken)*, Japan.
- Mar. 28, 2006: Seminar, *Department of Mathematics and Informatics, Faculty of Sciences, Chiba University*, Japan.
- Mar. 23, 2006: Seminar, *School of Computing, National University of Singapore*.
- Mar. 21, 2006: Seminar, *I2R, A*STAR*, Singapore.
- Mar. 14, 2006: Invited Talk, *First Japan-Taiwan Bilateral Symposium on Bioinformatics*, University of Tokyo, Japan.

TEACHING

Visitors Supervisor

Anh Ngoc Vo (Research Fellow, University of Melbourne, Australia), Jun. 2008–Jul. 2008

Nikolaos Angelopoulos (Postdoctoral Fellow, University of Edinburgh, UK), Oct. 2006

Takashi Yoneya (Senior Scientist, Kirin Brewery Co., Ltd., Japan), Oct. 2005–Sep. 2006

Postdocs Supervisor

Hao Canh Nguyen, Apr. 2009–Present

Mitsunori Kayano, Apr. 2008–Present

Yayoi Natsume, Apr. 2008–Present

Timothy Peter Hancock, Jul. 2007–Present

Motoki Shiga (Currently, Assistant Professor, Kyoto University), Apr. 2006–Mar. 2008

Shanfeng Zhu (Currently, Associate Professor, Fudan University, China), May 2004–May 2008

Raymond Wan (Currently, Research Staff Member, Computational Biology Research Center, Japan), Apr. 2004–Mar. 2009

Nicolas Majeux, Apr. 2003–Jan. 2004

Kiyoko Flora Aoki-Kinoshita (Currently, Associate Professor, Soka University, Japan), Apr. 2003–Mar. 2004

PhD Thesis Supervisor

David DuVerle, Advisor, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Apr. 2009–Present

Merja Oja, Thesis opponent, Department of Computer Science and Engineering, Helsinki University of Technology, Finland, Dec. 2007

Limin Li (Currently still student), Internship supervisor, Department of Mathematics, University of Hong Kong, Jun.–Sep. 2007

Jin Chen, Thesis external examiner, School of Computing, National University of Singapore, Jan. 2007

Masters Thesis Supervisor

Yoshifumi Matsushima, Advisor, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Apr. 2007–Mar. 2009.

Yoshiko Satoh, Advisor, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Apr. 2007–Mar. 2009.

Courses Taught

Faculty of Medicine, Niigata University, Japan (2010)

Pathway

Kyoto Sustainability Initiative (KSI), The Integrated Research System for Sustainability Science (IR3S), Japan (2009)

Biological Sequence Alignment

Graduate School of Pharmaceutical Sciences, Kyoto University (2003–2009)

Introduction to Bioinformatics, Advanced Bioinformatics, Lead Discovery, Chemical Skills

Education and Research Organization for Genome Information Science, Japan (2002–2006)

Machine Learning, Machine Learning and Data Mining for Biological Sequence Analysis, Protein and/or RNA Structure Analysis with Statistical Learning, Protein Network Analysis, Sequence Alignment, Sorting, Technical Writing